Oxidative Stress in Applied Basic Research and Clinical Practice

Stephen M. Roberts James P. Kehrer Lars-Oliver Klotz *Editors* 

# Studies on Experimental Toxicology and Pharmacology

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# **Oxidative Stress in Applied Basic Research and Clinical Practice**

Editor-in-Chief Donald Armstrong

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All books in this series illustrate point-of-care testing and critically evaluate the potential of antioxidant supplementation in various medical disorders associated with oxidative stress. Future volumes will be updated as warranted by emerging new technology, or from studies reporting clinical trials.

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Stephen M. Roberts • James P. Kehrer Lars-Oliver Klotz Editors

# Studies on Experimental Toxicology and Pharmacology

🔆 Humana Press

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# Part I Toxicological Mechanisms and Evaluation of Oxidative Stress

## **Chapter 1 A Historical Perspective on Oxidative Stress and Intracellular Redox Control**

Ethiene Castellucci Estevam, Muhammad Jawad Nasim, Lisa Faulstich, Marina Hakenesch, Torsten Burkholz, and Claus Jacob

#### 1.1 Introduction

Most of us are familiar with the rather curious, popular expression that "History repeats itself". Whilst this may well apply to certain economic cycles and swings in popular political opinion, it seems rather alien to most natural scientists who believe in Science as a unidirectional, ever evolving process. At closer inspection, however, we notice that there are also certain cycles in Science, and research into themes such as Oxidative Stress, intracellular redox processes and related preventive and therapeutic interventions in the form of "antioxidants" form no exception. The history of that particular field of research, which also represents the theme of this book, has witnessed many pioneering studies, leading to the true heydays of research, only to turn into a certain decline to be followed by yet another cycle of rise and fall. Ultimately, the term **Renaissance** not only applies to Italian culture, but also to research, and oxidative stress research even features its very own "Cysteine Chapel" [1, 2].

Indeed, just a couple of months ago, a rather enthusiastic piece has appeared in the journal *Biological Chemistry* entitled "Redox Biology on the rise", apparently ushering in an entirely new era of Redox Biology [3]. Such rather graphic titles do, of course, raise some suspicion. Has Redox Biology only just begun to rise, as one may assume, and if so, where has it been before? What happened to the various previous redox related discoveries in Biology, such as oxidative phosphorylation, the various redox enzymes, free radical oxidative stress theories and glutathione measurements? Or how about everyday products, including the glucose oxidase-based glucose sensor used by diabetics and, on a more trivial note, the antioxidants

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we cherish as part of our daily food? Are these discoveries not "redox" or perhaps not "biology", or just not "on the rise"? Or is the new Redox Biology just old wine in new barrels and the whole matter a cunning PR stunt?

As always, there is no direct answer to such a question, yet a look into the recent history may at least provide some ideas. As part of this chapter, we will therefore take a rather unusual, historical turn and in doing so, direct our attention to the various developments the field of Redox Biology and Biological Redox Chemistry has seen during the last couple of decades. Here, we will find a range of key discoveries which have subsequently led to – or at least influenced – basic concepts in this field which we still value and use today. In order to understand such historic processes fully, we will necessarily have to wear two hats, one of a redox chemist or biologist, and one of a historian of science.

Along the way, we will then dwell on key discoveries, such as the presence of free radicals in the body, or oxidative signaling, we will witness the appearance of new analytical methods, such as techniques for the detection of reactive oxygen species (ROS), and will see the rise, evolution and even demise of certain concepts (Fig. 1.1).

#### **1.2** The Search for the Grandmaster

Our journey will start with a simple yet revealing question often asked by scientists and lawyers alike: "Who invented it?" A more naïve tactic to find a quick answer to this question, unfortunately rather popular those days, may involve the use of one of the many (scientific) search engines to see when "oxidative stress" first appeared on the scene, i.e. in the title of a listed publication.

Here, Web of Science delivers us a very early publication on "oxidative stress" by the Norwegian Svein Ore, published in 1955 in *Acta Chemica Scandinavia*, which unfortunately is on "oxidative stress relaxation of natural rubber vulcanized with di*tertiary*-butyl peroxide" [4]. It is not worth following this lead any further, as comparing this kind of "oxidative stress" with our modern *medical* or *biological* concept of "oxidative stress" would be like comparing apples with horse apples.

Nonetheless, this rather surprising appearance of an homonym provides us with an early warning, namely that certain concepts may be rooted in different disciplines where they may have different meanings altogether, yet could be mutually stimulating once their details are understood correctly.

A more specific, refined search for the first appearance(s) of the expression "oxidative stress" in a biological context then brings us to the 1970s and to a range of publications. Here, we meet groups such as the one of Ernest Beutler (1928–2008), which consider links between glutathione, oxidative stress and wider aspects of metabolism [5]. Yet these studies deal primarily with individual, often rather limited aspects of oxidative stress research, and do not aim at any more general unifying concepts. Ernest Beutler, despite his considerable contribution to haematology and hence also to Redox Biology, is therefore not the one and only 'inventor' either.<sup>1</sup>

<sup>&</sup>lt;sup>1</sup>Curiously, whilst Ernest Beutler never won the Nobel Prize for his groundbreaking work in the field of haematology, his son, Bruce Alan Beutler (*b.* 1957) shared the 2011 Nobel Prize in Physiology or Medicine for "discoveries concerning the activation of innate immunity".





Hence the simple attempt to illuminate the history of oxidative stress research and Redox Biology by using search engines temps us to get lost in the mist of time. Here, another strategy is needed, this time based on contemporary witnesses. Indeed, when posing the question of the founding fathers and mothers of our field of research to more senior colleagues, the latter may contemplate for a moment and then point towards some of the early publications in the field of oxidative stress research they had come across at a time when we were a lot younger and also had a lot more hair, and which were "hot as a two-barrel shotgun", as Bert Vallee tended to put it.

Following this lead, we soon identify such a landmark paper entitled "Free radicals in biological materials". Authored by Barry Commoner and Jonathan Townsend and published in 1957 in *Nature*, this piece describes the widespread presence of (redox active) radical species in organisms [6]. Yet are Commoner and Townsend the founders of oxidative stress research, its true 'inventors'? After all, their work on free radicals predates the concepts of Ernest Beutler by over a decade, although, admittedly, it comes *after* the use of the homonym "oxidative stress" by Svein Ore.

Or should we rather consider Britton Chase and colleagues as inventors, who in 1973 showed that about 2 % of oxygen reduced by mitochondria ends up as superoxide radicals or hydrogen peroxide (and not just water)? Or does this honour, after all, go to Helmut Sies, who in 1985 really coined the expression of "oxidative stress" in the book appropriately entitled "Oxidative Stress"? [7, 8]. At this point "oxidative stress" is no longer just a term with a new, modern meaning, but also a programme, a programme for an entire field of research (see below).

After the rather futile search for a key 'inventor' or 'event' of "oxidative stress" in the laboratory, literature or field, we must admit that the hunt for the one inventor, the grandmaster of our field of research, in the end is an illusion. It is nourished by the common belief that such fields are initiated by one or a few outstanding scientists who subsequently may – or may not – receive the Nobel Prize. As natural scientists, we must therefore depart from yet another of our most cherished ideas. We must face the hard reality that humans do not have a penis bone and that such fields of research do not have just one or a handful of enthusiastic inventors.

We must rather embrace the notion that such concepts have emerged from a range of different strands of investigation, which initially have perhaps been running in parallel in different disciplines for a long time, unaware of each other and with their very own language, terminology and experimental basis. Only much later, such seemingly separate strands of investigation may have come together to develop a common set of ideas and hypotheses which have then slowly crystallized into unified, interdisciplinary theories and perhaps even laid the basis for a true Kuhnian Paradigm (see below).

#### 1.3 The Pre-paradigm Era

As part of our search for the more subtle strands of investigation, which may be seen as the tributaries to the concept of oxidative stress and redox signaling even without mentioning such concepts or terms explicitly, we have to go back further in History, and to take a path which soon parts into several trails winding through different disciplines. These individual trails seem to lead us to several events during the first two-thirds of the twentieth Century. At this time, Redox Biology has not been "on the rise" but has already been "all around us". For researchers investigating redox processes relevant to Biology, such as Otto Warburg, Oscar Loew and Chester Cavallito, the redox theme at the time held considerable promise, yet they were (pre-)occupied with their own research within their own disciplines. In retrospect, we can identify research into what we would nowadays call Redox Biology thriving at that time in various disciplines. This kind of research stretched from the exploration of cellular energy metabolism (e.g. fermentation, oxidative phosphorylation), human host defence (e.g. in form of ROS generating macrophages) and the appearance of free radicals during physical exercise to the presence of glutathione in animal cells, and the rather curious circumstance that the human body contains enzymes able to decompose ROS.

The antioxidant enzyme catalase, for instance, was described rather comprehensively by Oscar Loew (1844–1941) in 1900 and studied extensively afterwards. Considering that this enzyme occurs in the human liver and redox decomposes  $H_2O_2$ , the thought of a particular role of  $H_2O_2$  in human cells would not have been far-fetched, even during these early days of biochemistry. Nonetheless, it still took another couple of decades for researchers to realize that redox events associated with such ROS play an integral and important role in human biochemistry. These decades witnessed the identification of apparently damaging, oxidizing species in the human body (e.g. by Barry Commoner and Jonathan Townsend, 1957), as well as the discovery of additional "antioxidant" enzymes able to remove such reactive species, such as glutathione peroxidase (Gordon C. Mills, 1957) – now known to be a selenoenzyme – and the various metal-containing superoxide dismutases (SOD) by Irwin Fridovich and Joe McCord in 1968 [9–11].

Here it is interesting to highlight the discovery of cytochrome P450 oxidoreductase, originally described by Horecker in 1950 as cytochrome *c* reductase and finally recognized by Martin Klingenberg and David Garfinkel in 1958, later being exhaustively investigated By Jud Coon in the 1960s [12–15]. Many studies concerning P450 oxidoreductase could be cited, but we will highlight the description of the microsomal ethanol-oxidizing system (MEOS) by Lieber and DeCarli in 1968 [16–18].

In 1964 Filippo Rossi and Mario Zatti proposed that a Nicotinamide Adenine Dinucleotide Phosphate (NADPH) oxidase was responsible for the respiratory burst that occurred in activated phagocytes and in 1970 Seymour J. Klebanoff demonstrated that myeloperoxidase (isolated for the first time in the early 1940s by Kjell Agner) contributes to this burst [19–21].

At around the same time, and in an entirely different context, numerous redox active natural products with a pronounced biological activity were identified in and isolated from various plants, including edible ones, and, together with their synthetic analogues, were subsequently studied extensively regarding their biological activity. During this period, we find thriving research programmes into the chemistry and biology of various antioxidant vitamins, chatechins, flavons, anthocyanidins, coumarins, aurones, tannins, resveratrol and related polyphenols, to mention just a few [22]. From the perspective of modern-day Redox Biology, the discovery of numerous biologically active Organic Sulfur Compounds (OSCs) in plants, fungi

and lower organisms is particularly noteworthy, as those compounds – later on – will play a major role as selective, yet also effective redox modulators. Many of these natural substances, such as allicin from garlic, were isolated and characterized in the 1940s and 1950s, i.e. well before their true impact as nutraceuticals became apparent [23]. Indeed, these early studies on redox active natural products have provided the basis – and substances – for emerging new fields of antioxidant and nutritional research, such as the ones dealing with "chemoprevention", "functional foods", "nutraceuticals" and "nutri-epigenetics".

The various discoveries during the first six decades of the twentieth Century have provided a wealth of new insights in the field of redox chemistry and biology, but also new (natural) redox active substances and innovative new analytical methods to follow redox events, which together have paved the way for more comprehensive, systematic concepts.

#### 1.4 The 1980s and the Emergence of More General Concepts

During the 1970s, the individual, mostly independent strands of investigation slowly began to interact and the first holistic concepts entered the scene, heralding a new era of concepts and paradigms.

Our first look to the 1970s will start with the publication by Bernard M. Babior, Ruby S. Kipnes and John T. Curnutte of the paper "The production by leukocytes of superoxide, a potential bactericidal agent", which proposed that superoxide participates in bacterial killing and this could be associated with numerous alternative oxygen dependent mechanisms [24].

During the same decade, nitrogen monoxide (nitric oxide, 'NO) became in evidence although its history de facto began already much earlier, in 1847, with the discovery of nitroglycerine by Ascanio Sobrero and its application for angina treatment by William Murrell in 1876. It was only in 1978, however, that endotheliumderived relaxing factor (EDRF) was described by Robert Furchgott and colleagues, and in 1986 identified as nitrogen monoxide (nitric oxide, 'NO) by Furchgott, Ferid Murad, Louis Ignarro and Salvador Moncada<sup>2</sup> [25, 26]. After this, many other roles of nitric oxide in biological systems were studied, such as its function in activation, recruitment and aggregation of platelets at Joseph Loscalzo's laboratory in 1989 [27–29].

After the discovery of nitric oxide as EDRF, the role of oxidative stress in the pathophysiology of hypertension and atherosclerosis became more evident, although the fact that the relationship between free radicals and hypertension had been suggested already in 1960 by Romanowski, Murray and Huston in a paper entitled "Effects of hydrogen peroxide on normal and hypertensive rats" [30]. In this context, the mode of action of nitroglycerin as an indirect donor of 'NO, was finally understood

<sup>&</sup>lt;sup>2</sup>Furchgott, Murad and Ignarro, but not Moncada, subsequently shared the 1998 Nobel Prize in Physiology or Medicine for this discovery.

[31–33]. Moreover, cytokine-activated macrophages produce high levels of 'NO which leads to the destruction of targeted cells, such as tumor cells and bacteria [34].

At around the same time, in 1978, Dillard and his colleagues published their study on the "Effects of exercise, vitamin E, and ozone on pulmonary function and lipid peroxidation" reaffirming the whole topic of physical stress, redox events, oxidation of biomolecules and subsequent physiological impediments [35]. Interestingly, this and related publications entering the scene during the 1970s possess a new quality: They reflect an emerging holistic approach, which is able to integrate basic (inorganic, radical) chemistry and biomolecule-chemistry with biochemical events and physiological changes. This new approach has many authors, and can also be found in the rather stimulating publication by well-known figures in the field of oxidative stress research, such as Enrique Cadenas, Regina Brigelius, Hermann Esterbauer and Helmut Sies, who in 1983 published together on the "Effects of 4-hydroxynonenal on isolated hepatocytes" [36]. Or we may consider the groundbreaking work of Barry Halliwell and his colleagues on the nature, occurrence and biological impact of various ROS [37]. The 1970s also witnessed the beginning of the studies of Leopold Flohé about the different functions of Glutathione Peroxidase (GPx) [38].

At this point we can see that research began to point to the various physiological roles of oxidative stress and the change in the concept that oxygen, nitrogen and other reactive species were the "bad guys".

At the beginning of the 1980s, the time was therefore ripe for the emergence of new, more general paradigms in oxidative stress and redox signaling research – and the following decade may therefore be seen as the heydays in this field. In 1985, Helmut Sies published his book accurately entitled "Oxidative Stress" and in 1986 the manuscript "Biochemistry of Oxidative Stress" in Angewandte Chemie, pointing out that "This field of research provides new perspectives in biochemical pharmacology, toxicology, radiation biochemistry as well as pathophysiology" [7, 39].

Historically, these publications may well be considered as key events in oxidative stress research. Whilst oxidative stress and Redox Biology research itself were not *invented* at this point, and the authors mentioned above were the proverbial "dwarfs standing on the shoulders of giants", these (and related) publications provided a *common basis for this field across disciplines*. This epistemological difference between inventing or discovering a phenomenon on one side, and inventing a new paradigm on the other, is important. The mid 1980s are the time when this highly interdisciplinary area of research began to consolidate as a separate field, with its own concepts, techniques, experimental methods, mutually accepted tools and, above all, language. As part of this Gestalt Switch, previous discoveries were integrated into the new concepts, revisited or reinterpreted under the new paradigm.<sup>3</sup> It was also the time

<sup>&</sup>lt;sup>3</sup>Unfortunately, the role of language and terminology in science is often belittled, but their power should not be underestimated. The concept of phlogiston was dead once Lavoisier introduced his own language referring to oxidation and entirely removing the "P-word" from his vocabulary and journals, almost like Stalin had the image of Trotzky removed from official photographs. Or as some philosophers would say: "If you have no word for it, it does not exist." While expressions

when researchers from vastly different disciplines, such as Wim Koppenol from inorganic chemistry, and Helmut Sies from biochemistry and physiological chemistry joined forces to provide the expertise for such a highly multidisciplinary adventure.

To supply new tools to this great adventure, Ingold and colleagues in 1985 proposed a quantitative method to measure the total secondary antioxidant content of a biological fluid known as TRAP method and later, in 1993, Guohua Cao and Richard Cutler developed the ORAC method (Oxygen Radical Absorbance Capacity) to assess antioxidant capacities in biological samples *in vitro* [40, 41].

When turning to the 1990s, the paradigms embracing "oxidative stress" and redox signaling in biology were therefore firmly established, analytical methods for the detection and quantification of ROS in biological samples were provided and the role of antioxidants as the "good guys" could be studied. There was also mounting evidence from clinical trials and epidemiological studies pointing towards a specific role of antioxidants in human health, which was subsequently used to discuss apparently healthy foods and opened up the field of nutraceuticals.

#### 1.5 Puzzle Solving

In the words of Thomas Kuhn, the subsequent decades may therefore be characterized as the time when scientists were performing their "puzzle solving activities", i.e. certain post-revolutionary mopping up exercises under the new paradigm(s) of Redox Biology. Here, we find various strands of investigation slowly meandering through their own fields, from bioinorganic and analytical chemistry (e.g. colleagues like Wim Koppenol) all the way to nutrition (e.g. Helmut Sies, Norbert Latruffe), medicine, cosmetics and even to Agriculture (e.g. Alan Slusarenko).

In the field of Redox Biology, we may highlight the rather pivotal research on redox control of the transcription factor NF- $\kappa$ B (by H<sub>2</sub>O<sub>2</sub>) by Patrick Baeuerle and colleagues in the early 1990s [42–44]. These studies were reflected by the work by Toren Finkel and colleagues on the role of H<sub>2</sub>O<sub>2</sub> in (platelet-derived growth factor) signal transduction, published from 1995 onwards [45–47]. Such early discoveries of redox controlled cell signaling events were followed by numerous studies on the redox control of key cellular signaling pathways, for instance by the landmark studies on the redox control of protein tyrosine phosphatases (PTPs) by Sue Goo Rhee and his colleagues [48, 49].

At this point we should mention peroxiredoxins (Prdx, discovered in 1988 by Kanghwa Kim and colleagues from the group of Sue Goo Rhee) and sulfiredoxins (first described by Benoit Biteau, Jean Labarre and Michael B. Toledano in 2003) and their role in signal transduction as well as regulation of post-translational glutathiolation that has been recognized as a means of redox-modulation of enzyme activities [50–54].

such as "oxidative stress" and "free radicals" ultimately ushered in a new era of research, other entities, such as the "caged radical" also appeared on the scene for a while to stimulate research but subsequently escaped from their cages into the mist of time.

#### 1.6 Clouds on the Horizon

Towards the end of the 1990s, the field of oxidative stress research began to move on from ROS and antioxidant research to some of the more hidden redox regulatory events. At this point, the old paradigm defined in 1985, that "oxidative stress" is "a disturbance in the prooxidant/antioxidant balance in favor of the prooxidants, leading to potential damage" [7] was facing its first serious anomalies, clearly demanding a certain refinement.

The traditional view that ROS are entirely 'bad' and damage cells, whilst antioxidants, such as vitamin C or vitamin E are 'good' because they protect cells, came under pressure. First of all, it turned out that antioxidants were not nearly as efficient in preventing or even curing human ailments as early nutritional studies had suggested. In fact, it now seemed that an excessive use of antioxidants such as vitamin E or C may even cause damage (see below). Secondly, there was mounting evidence of widespread cellular redox signaling which involved beneficial, and not just detrimental, oxidative events and pathways. Indeed, it became more and more apparent that a wide range of cellular signaling events rely on the presence of oxidants, such as  $H_2O_2$ , and would not function in their absence. Some beneficial adaptive processes, for instance during physical exercise, even require a build-up of ROS in order to be successful, and fail miserably if antioxidants are used to neutralize such 'good' ROS.

Vincent Bowry, Keith U. Ingold and Roland Stocker (1992), for instance, studied the relationship between ascorbic acid and alpha-tocopherol demonstrating that, depending on some conditions, an antioxidant such as alpha-tocopherol becomes a pro-oxidant [55]. Indeed, in the field of nutrition, Levander and colleagues studying infection and oxidative stress created the term "dietary-induced oxidative stress" in 1995 [56].

At around the same time, Halliwell studied nutrition and oxidative stress searching for optimization strategies of nutritional intake of antioxidants, since the large doses of dietary antioxidants didn't show any preventive or therapeutic effect, and because of this he introduced the "antioxidant paradox" concept [57–59]. Here, the notion of equilibrium is highlighted: "antioxidant defenses act as a balanced and coordinated system and each relies on the action of the others".

This whole conundrum of pro- and antioxidants therefore required an amendment of the previous concepts. At this point, the traditional, crude view of oxidative stress as an entirely damaging event gave way to a more differentiated view on cellular redox signaling. Whilst in 1985, "oxidative stress" was defined by Helmut Sies as "a disturbance in the prooxidant/antioxidant balance in favor of the prooxidants, leading to potential damage"[7], 20 years later, the focus on "damage" had been expanded to a more refined view also paying tribute to "signaling" and "control". "Oxidative stress" was now defined as "an imbalance between oxidants and antioxidants in favor of the oxidants, leading to a disruption of redox signaling and control and/or molecular damage" [60, 61].

Historically speaking, these changes represent an evolution of the original paradigm in response to certain anomalies discovered during the puzzle solving period, rather than a scientific 'revolution' with a change of paradigm. Here, the focus of Redox Biochemistry and Biology has shifted from the damaging effects of free radicals on proteins, membranes and DNA to oxidative modifications involved in cellular signaling. Such oxidative signaling events do not necessarily result in 'negative' actions, such as uncontrolled proliferation or apoptosis, but may also lead to more 'positive' outcomes, such as adaptation, or intrinsic antioxidant responses.

As part of the next two sections, we will therefore briefly consider how such reinterpretations and amendments of the original paradigm(s) have stimulated research into the field of intracellular redox control and also led to a certain renaissance of the antioxidants.

#### **1.7** The Journey to the Cysteine Chapel

The historical developments discussed above may probably be illustrated best when considering the evolution which has taken place during the last 15 years in the field of sulfur-based redox systems and processes. Sulfur-based redox systems have been around for a long time, but research into their darker side only gathered steam during the first decade of the Twenty–first Century. Before then, redox active sulfur was mostly – but not always – considered as a cellular antioxidant in the form of a thiol which could be oxidized to a disulfide. The 1990s were the time, however, when it became obvious that redox active sulfur provides a considerably more diverse and, in any case, extraordinarily facet-rich biological redox chemistry.

Sulfur is a true redox chameleon able to occur in biology in over ten different formal oxidation states ranging from -2 in hydrogen sulfide (H<sub>2</sub>S) to +6 in sulfate (SO<sub>4</sub><sup>2-</sup>), and counting fractional states, such as -1.5 in the disulfide radical anion RSSR<sup>-</sup>. This extraordinary flexibility in oxidation states subsequently translates into numerous different chemical appearances, which range from the better known thiols (RSH) and disulfides (RSSR') to lesser known chemical species, such as thiyl radicals (RS'), sulfenic acids (RSOH), sulfinic acids (RS(O)OH), sulfonic acids (RS(O)<sub>2</sub>OH), thiosulfinates (RS(O)SR'), thiosulfonates (RS(O)<sub>2</sub>SR'), polysulfanes (RSSH and RS<sub>x</sub>H,  $x \ge 3$  and R,  $R' \ne H$ ) and partially reduced per- and hydropolysulfanes (RSSH and RS<sub>x</sub>H,  $x \ge 3$  and  $R \ne H$ , respectively). At the same time, these sulfur species are able to participate in a vast variety of redox processes ranging from one- and two-electron transfer to radical reactions, hydride and oxygen transfer and the omnipresent nucleophilic 'exchange' reactions (e.g. thiol/disulfide exchange).

Not surprisingly, therefore, the last 15 years have witnessed a dramatic increase in the studies addressing the chemistry, biochemistry and biological activity of such Reactive Sulfur Species (RSS). There have also been numerous attempts to use this truly unique 'chemistry' in the fields of medicine, pharmacy and agriculture. Based on extensive prior work on redox active sulfur in biology and medicine, the concept of "Reactive Sulfur Species" (RSS) as a unique class of redox active stressors and regulatory elements emerged in 2001 [62]. This concept represented a further amendment or extension of the original paradigm of oxidative stress and was soon followed by a number of discoveries, which can be divided into three different, mutually not exclusive groups: (a) RSS as oxidative stressors, (b) RSS as a particular group of natural products, similar but not identical to organic sulfur compounds (OSCs), and (c) RSS as posttranslational cysteine modifications found in many proteins and enzymes. The last decade has witnessed considerable progress in all three of these areas.

In the field of oxidative stress research, a number of chemical sulfur species have been identified which are highly reactive and able to cause – sometimes severe – levels of oxidative stress in cells. Such a stress may be useful, for instance in the fight against cancer cells and microbes. Indeed, many rather unusual sulfur compounds found in nature can be described as RSS and are currently under consideration as potential drugs, including thiosulfinates, polysulfanes, 1,2-dithiins, 1,2-dithiole-3-thiones and various isothiocyanates. Such compounds often exhibit considerable cytotoxic activities and have been discussed in the context of chemoprevention, antibacterial activity, antifungal activity, anticancer activity and activity against scleroderma [63–69]. Since many of these agents occur naturally, often even in edible plants (for instance in garlic, onions, mustard, asparagus) or in 'semi-natural' preparations more or less safe for human consumption (e.g. 1,2-dithiole-3-thiones in Haarlem Oil), such RSS feature highly in the arena of nutraceuticals and nutri-epigenetics.

Many of these substances also react fast, efficiently and selectively with cysteine residues in proteins and enzymes and hence exert pronounced, yet well-characterized effects on cells. These 'effects' often include widespread modifications of cysteine residues, a surge in ROS, cell cycle arrest and induction of apoptosis. Whilst the exact chains of events are still not fully understood, it seems that oxidative cysteine modifications play a major role. Here, the hunt for such unusual cysteine modifications is now on, and 'cysteine hunters' such as Kate S. Carroll, Philip Eaton, Jakob R. Winther and Joris Messens have identified quite a number of different RSS in proteins and enzymes during the last 10 years. Such modifications seem to occur in cells during normal cellular metabolism or are induced by internal or external (oxidative) stress. In order to emphasize the importance of such RSS, colleagues like Kate Carroll have even coined a new terminology using expressions such as the "cellular sulfenome" [70, 71]. The latter is referring to the widespread formation of sulfenic acids in proteins and enzymes.

While these investigations have focused primarily on stress situations, other groups, such as the ones of Jenny A. Littlechild, Leslie B. Poole or Michel B. Toledano have begun to search for the presence of unusual sulfur species in catalytic cycles of enzymes, such as the peroxiredoxins (Prdx) [72–74]. The Prdx enzymes catalytically remove  $H_2O_2$  from the cell and also serve as a sensor for oxidative stress. Their normal catalytic cycle involves a thiol, sulfenic acid and disulfide, whilst overoxidation results in the formation of an unusual sulfinic acid, which shuts down the enzyme and opens the 'floodgate' for  $H_2O_2$  to cause damage to the cell and to ultimately lead to apoptosis. The sulfinic acid formed in Prdx may be reduced back to the sulfenic acid (and thiol) in the presence of the redox protein sulfiredoxin (Srx), a process which probably involves the formation of a sulfinic acid phosphoryl ester and a thiolsulfinate as reactive intermediates. As a result, the

catalytic and regulatory cycle of Prdx in concert with Srx includes six different sulfur modifications, of which four (i.e. sulfenic acid, sulfinic acid, sulfinic acid phosphoryl ester, thiosulfinate) clearly represent more unusual forms of RSS.

At the same time, other researchers, such as Pietro Ghezzi and his colleagues, began to shed some light on the events associated with the formation of such post-translational modifications, which obviously do not go unnoticed in the cell. Indeed, many of these oxidative modifications result in a loss of protein function or enzyme inhibition, and hence trigger wider cellular signaling [75, 76].

Indeed, once cell biologists became aware of these developments, the quest for the "cellular redoxome" was truly on [77, 78]. The evaluation of the various chains of oxidative events inside living cells first relied on "intracellular diagnostics" based on a combination of redox sensitive dyes to visualize intracellular redox changes, analytical techniques (such as Western Blots) to monitor oxidative changes to proteins and functional / activity assays to assess oxidatively induced changes in protein function and enzyme activity. These methods were soon joined by sophisticated protein-based 'redox sensors', such as the green fluorescent protein (GFP)-based sensors – "reduction-oxidation-sensitive GFPs" (roGFPs), developed by James Remington and colleagues – or yellow fluorescent protein (YFP)-derived peroxide sensors such as HyPer, developed by Sergey Lukyanov and colleagues [79, 80].

At some stage, the different strands of investigation, which include (a) the effective yet selective modification of cellular thiols by RSS and ROS, (b) the discovery of the resulting, widespread and often reversible cysteine modifications in proteins and enzymes, and (c) the pronounced effects such modifications exert on cellular processes, have merged in the concept of the "cellular thiolstat" first proposed in 2011 [81, 82]. This concept postulates that certain – but not all – intracellular cysteine proteins and enzymes form targets for redox modulation and hence serve as a sophisticated sensing and regulatory network which ultimately controls cell proliferation, differentiation and apoptosis. As redox processes involving cysteine residues are fast, effective and often reversible, the thiolstat enables the cell to respond to internal or external redox changes in an efficient, measured, appropriate and reversible manner.

Epistemologically, the concept of the "cellular thiolstat" represents another important cornerstone of our modern perception of oxidative stress and cellular redox control. Similar to the other concepts sheltered under the general paradigm, it is not an absolute dogma but rather designed to explain certain experimental findings, and to stimulate further research in this field, for instance by providing the necessary problems, leads and directions [83].

#### 1.8 The Rise, Demise and Renaissance of the Antioxidant

A similar development has also taken place in the context of the "antioxidant". As in the field of sulfur biochemistry, changes in the perception of "oxidative stress" in general have resulted in a wealth of knock-on effects, which has also led to a redefinition of the antioxidant concept and a re-evaluation of functional foods. As mentioned before, the 1980s saw the emergence of the traditional concept of "oxidative stress", based on evidence that free radicals cause serious damage to many essential biomolecules and occur in the human body. In parallel, extensive studies on human habits showed that excessive consumption of meat may be damaging to human health whilst the intake of fruits and vegetables, i.e. products rich in antioxidants, may be protective [84]. As such epidemiological studies agreed with their biochemical counterparts supporting the concept of "oxidative stress", the interest in antioxidants and functional foods, culminating in a wave of popular enthusiasm, including the "Five-a-day" movement, should therefore not come as a major surprise.

During the 1990s, however, various reports began to emerge, which found no apparent health benefits associated with antioxidants in isolation, but rather attributed the effects observed previously to a more general healthy lifestyle. At this point, some rather tricky issues emerged, related to the bioavailability of many antioxidants, their relative concentrations in comparison to antioxidants already present in the cell (such as GSH), and the negative impact that some antioxidants (such as vitamins C and E) seem to have on cells, cell signaling and beneficial adaptive processes. Not surprisingly, we have lately witnessed a certain demise of the antioxidant hypothesis, culminating in the removal of the oxygen radical absorbance capacity (ORAC) database from the United States Department of Agriculture (USDA) website in 2012.

Amazingly, however, the ORAC database very lately has been back online again, and so is the concept of the "antioxidant", albeit in a more modern design. Here, the revamped antioxidant hypothesis considers the need for antioxidants in the elderly, an issue related to ageing and demographic changes rampant in many modern societies, and also sees antioxidants as an indicator of "healthy food" (the ORAC value may therefore be more of a quality label for food than a direct health claim). Furthermore, many 'antioxidants' have also turned out to be something else, and are now sailing under the flag of pro-oxidant 'redox modulators' (e.g. allicin), or are considered as epigenetic modulators (e.g. sulforaphane or xanthohumol). Indeed, certain natural and nutritional antioxidants may possess anticancer activities on their own (and unrelated to redox processes), such as carotenoids that facilitate gapjunctional communication, or flavonoids, which modulate Phase I and II xenobiotic detoxification, or vitamin E that inhibits protein kinase C [85–87].

Recently, dietary chemopreventive agents acting via epigenetic mechanisms have received attention. Research on the properties of curcumin, genistein, resveratrol, iso-thiocyanates and xanthohumol have demonstrated the capacity of these substances to modulate DNA methylation, histone modification and miRNA expression [88].

Similar to the notion of "oxidative stress" and the various models describing the role of redox active sulfur in biology, the concept of the "antioxidant" has developed considerably during the last 30 years.

#### 1.9 Conclusions

Our journey through the history of oxidative stress research and Redox Biology is now almost complete. It is extraordinarily difficult to define specific historical epochs in this field, let alone clear beginnings, milestones or inventors. Whilst some events do stand out in our historical review, and may define specific stages of development, they are only lighting rods providing a certain direction.

We have also seen that the field of oxidative stress research has emerged and was shaped during the third quarter of the last century. Redox Biology is therefore not a new invention but can look back on a rather rich history. Importantly, the paradigms which govern this field of research have been established already, and despite the various attempts to revolutionize the field by inventing or re-inventing Redox Biology, the central theories still hold firm and there are no anomalies heralding an entirely new era or area. It is therefore wrong to claim that "Redox Biology is on the rise" at a time when this particular field has already been established firmly across various scientific disciplines for the best of 25 years. It is also not a "doter on the rise" experiencing a certain renaissance, as oxidative stress research and redox regulation have never really seen a serious demise after their first haydays in the 1980s.

We therefore are probably well advised to continue our puzzle solving exercises in the field for a bit longer, for instance by searching for more redox signaling proteins, modifications of cysteine residues and agents able to act as RSS. In doing so, we may well come face to face with certain anomalies, yet those can probably be dealt with by readjusting our existing theories or by inventing some protective auxiliary hypotheses.

Nonetheless, we should always keep an open eye and mind on the possible encounter with the one anomaly which may herald the demise of existing paradigms and the ushering in of new ones. The one of us with her / his eyes most widely open may well catch it and also the Big Prize.

Many names have been cited here and an even greater amount left to be mentioned, not because they are less important, but only for lack of space. And we should, of course, remember that this wonderful journey still continues, although in this paper it ends right here and now.

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# **Chapter 2 An Overview of Free Radicals as Causes and Consequences of Toxicity**

James P. Kehrer, Lars-Oliver Klotz, and Stephen M. Roberts

## 2.1 Introduction

Oxidative stress has been studied extensively for over 40 years as a mechanism of toxicity associated with many drugs, chemicals and environmental agents. Through the numerous studies performed, it has become apparent that changes in the cellular redox state are responsible for some of the adverse effects resulting from exposures to both natural and man-made drugs and chemicals. At the same time, it has also become apparent that the oxidative damage induced by acute exposures may have different mechanisms from the effects resulting from subacute or chronic exposures to low levels of oxidative stress resulting from drugs or toxicants. These latter exposures can involve subtle and not always well-understood changes to proteins/ peptides, DNA, or the cellular gene expression and signaling machinery.

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## 2.2 Radical Chemistry

An atom or molecule that contains one or more unpaired electrons is considered a radical. The absence of such electron pairing makes radicals, in most cases, reactive with other molecules as they seek a lower energy state by either losing or gaining an electron. As a result, radicals have the potential to catalyze various cellular reactions, some of which are beneficial and some of which are detrimental. The former normally occurs in a controlled fashion where the radical is contained within an enzyme or substrate locale. Such radicals are considered "caged". The latter involves radicals that exist without any sort of chemical or biologic control; i.e. "free". This can result in changes that impair cellular functions.

The reactivity of radicals involves the movement of electrons making them integral to redox biochemistry. Oxidation is the removal of one or more electrons from a molecule while reduction involves the addition of one or more electrons. Within a biological system, there is always a balance between oxidation and reduction. Thus, when one substance is oxidized some other must be reduced. Exposure of a biological system to chemicals or stresses can influence redox chemistry in tissues or cells, resulting in compartmentalized changes in the redox status even though overall redox balance is maintained. These localized imbalances can have significant impacts upon cellular functions, depending on the nature and extent of the exposure and the shifts that occur.

Oxygen, which exists as a diradical and thus has the capacity to readily interact with electrons, is a central component of redox biology. Within biological systems, electrons normally flow from food (which provides reducing equivalents) to oxygen, which is ultimately reduced to water. Disrupting this natural redox balance can lead to oxidative stress, a term that was initially defined as "a disturbance in the prooxidant-antioxidant balance in favor of the former" [1]. This definition was later extended to include the concept that oxidative stress leads to potential damage [2]. Other definitions have considered redox balance in terms of a disruption in a biological system's ability to transmit intracellular signals, or to detoxify the reactive species causing the imbalance, or to repair the resultant damage [3]. It is rare that the corollary stress, reductive stress, is considered. However, in the absence of oxygen, reducing equivalents will continue to be generated and will accumulate. This may alter a range of enzymatic and non-enzymatic reactions within a cell, particularly the many redox based reactions, resulting in changes in signal transduction pathways and gene expression, potentially leading to cell damage [4].

Free radicals, particularly oxygen-derived ones known collectively as reactive oxygen species (ROS), are normal products of aerobic cellular metabolism. Thus, biological systems have developed a variety of both enzymatic and non-enzymatic means to minimize the toxicity these reactive products can cause under normal circumstances [5]. Nevertheless, numerous research studies have shown that these antioxidant systems can be inadequate when xenobiotic exposure or disease either impairs their functioning or leads to increased ROS production. In most cases, however, it has proven to be futile to provide protection by enhancing antioxidant

activity in vivo. This may be because in vivo antioxidant systems are naturally optimized or because of complex effects of oxidants on signaling pathways, some of which are beneficial [6].

Exposure to ROS can replicate many of the tissue changes associated with certain xenobiotic toxicities and disease processes [5]. As a result, ROS have been implicated as mechanistic contributors to a wide range of disorders [7]. However, the cause-effect relationship between ROS and different environmental or druginduced diseases and toxicities is difficult to ascertain because most of the experimental endpoints that are measured can be both a cause and a result of toxicity. In addition, some biological changes that are observed may reflect compensatory responses that are not necessarily detrimental to cellular functions. For example, moderate alterations in glutathione levels or the activities of antioxidant enzymes may reflect a tissue's response to oxidative stress but are unlikely to be detrimental to cellular functions.

#### 2.3 Characteristic Oxidative Reactions

Although the toxicity of ROS has been extensively documented, it remains unclear in many systems which of the myriad of changes induced are critical for the observed damage. All cellular molecules are potential targets and thus the ultimate cellular response is the net result of many competing effects, particularly at the mitochondrial level [8]. Macromolecules including DNA, protein and lipids, that make up the bulk of a cell's mass, are the most common targets. But small molecules can also be affected, including signaling molecules, and may be the more critical targets.

## 2.3.1 Proteins and Peptides

Chemically reactive compounds that enter or are formed within cells will commonly bind to cellular proteins. Such binding provides a convenient index of reactivity, but does not always correlate with toxicity. Linking this irreversible binding to specific amino acid residues within proteins that are responsible for toxicity has seen some success in identifying toxic mechanisms [9–11]. However, reversible modifications such as selected thiol oxidations can also cause toxicity [12].

Oxidations of amino acids at non-thiol sites yields the irreversible formation of products such as carbonyls, hydroperoxides and their reduced hydroxy species, or ring cleavage in histidine or tryptophan residues [13]. These amino acid oxidation products, that can be measured as indices of oxidative stress, may cause a myriad of effects to the altered protein including loss (usual) or gain of function, aggregation, enhanced or diminished susceptibility to proteolysis (depends on the extent and duration of oxidation), abnormal cellular uptake (e.g., LDL), changes in gene transcription, and increased immunogenicity [14].

Although oxidation is generally considered a toxic mechanism, there is increasing evidence that an appropriate redox balance or oxidative tonus is critical for cell proliferation and survival [15–17]. This redox hypothesis proposes that the detrimental effects of oxidative stress occur as a consequence of disruption of normal thiol oxidation states thereby altering cell signaling and thus cell functions [18]. The importance of thiol-/cysteine-containing peptides and proteins such as glutathione in regulating cell functions, including redox sensitive signaling cascades involving proteins such as H-Ras and PTP-1B, transcription factors such as Nrf-2 and NF- $\kappa$ B, and enzymes including MAP kinases, PI3 kinase, PTEN [19, 20] provides substantial support for this concept. For example, the binding of glutathione to proteins can protect against the oxidation of critical thiol residues and thereby regulate ion channels, transporters, and enzyme and transcription factor activities. In addition, apoptosis and antioxidant genes are regulated in part by redox balance in the cell [16].

#### 2.3.2 Lipids

Phospholipids are critical structural and functional components of all cell membranes. Because of the susceptibility of polyunsaturated fatty acids to oxidation, phospholipids are important targets for oxidative damage. As the polyunsaturated fatty acids become oxidized, ion channels and membrane proteins may be inactivated, or membrane permeability may be increased as the lipid bilayer is compromised. In addition, some of these lipid oxidation products, that are analogous to prostaglandins or leukotrienes, may have biologic activity and can affect cell signaling [21, 22].

The oxidation of lipids can clearly be a cause of cellular toxicity. However, it is important to remember that membrane lipids become much more susceptible to oxidation as cells die. Thus, when using oxidized lipids as markers of injury, it is essential to determine whether this oxidation is a cause or effect of the observed damage. Such determinations are often difficult but should be based on considerations of the time course of changes, the chemistry of the toxicants, the underlying hypothesis, and the possibility that lipid oxidation is not the proximal cause of injury, but is expanding or modifying the initiating event.

#### 2.3.3 DNA

The mechanisms of free radical-induced DNA damage have been reviewed [23]. The highly reactive hydroxyl radical that can be generated in vivo via Fenton chemistry, appears to be a major mediator of oxidative damage by reacting with DNA bases as well as the sugar moiety. Damage at both sites can lead to errors in DNA replication or transcription and to impaired DNA integrity, e.g. strand breaks. Therefore, similar to proteins, oxidative alterations to DNA can lead to functional changes in gene expression and regulation that are either beneficial or detrimental to cells [24, 25]. In addition, some of the observed changes are adaptive responses [26] that may be beneficial or detrimental, depending on context and duration of the change.

Direct oxidative damage to DNA is usually associated with activation of repair enzymes, such as excision-repair pathways and poly(ADP-ribose) polymerase. However, if the damage reaches a critical threshold, acute toxicity (e.g. cell death) will ensue either through apoptotic or necrotic pathways. Long-term effects of oxidative damage to DNA can include the development of cancer. In addition, ongoing damage to pyridine nucleotides, that are essential for DNA/RNA synthesis as well as being essential cofactors for cellular repair and antioxidant defense systems [27], can result in an increased susceptibility of oxidatively stressed cells to other stresses.

#### 2.3.4 Apoptosis

Extensive oxidant-induced cell damage can cause necrosis, but at lower levels can more subtlety affect numerous intracellular pathways without inducing necrotic cell death. If the effects reach a threshold, the damage cannot be repaired, or the "right" pathways are turned on or off, apoptosis will ensue. This is mediated, in general, by two different mechanisms, known as the intrinsic (mitochondria-mediated) and extrinsic (receptor-mediated) pathways. Numerous publications have suggested that low levels of ROS can either independently induce apoptosis or facilitate apoptosis when death receptor ligands are activated. In both cases, the underlying mechanism appears to be disruption of intracellular redox homeostasis, and irreversible oxidative modifications of lipid, protein, or DNA [28]. In a more general sense, decreases in glutathione levels, often caused by oxidative stress, correlate with apoptosis and seem to have some mechanistic role in this process including activation of Bax, opening the permeability transition pore, and the activation of caspases [29, 30].

## 2.3.5 Role of Metal Ions

Metal ions can be toxic for a number of reasons including their abilities to bind to certain proteins or peptides, and to move electrons resulting in the generation of free radicals. Because of their ability to move electrons, transition metals such as iron and copper, are critical for many enzymatic reactions. When catalyzing such reactions, these transition metals are tightly bound to proteins. However, when in their free (or loosely chelated) states, transition metal ions can be highly toxic by virtue of moving electrons and catalyzing redox reactions in an uncontrolled fashion. For example, oxidative damage to DNA often involves redox-active metal complexes [31] and the toxicity of iron to the gastrointestinal tract is well-known to have a free radical basis.

Metals such as zinc and cadmium exist in only one oxidation state in vivo, thus not directly generating ROS through electron transfer. Nevertheless, the toxicity of these metals involves binding to thiols thereby modulating oxidative reactions. Similarly, other toxic metals, such as lead and mercury, have a high affinity to thiols, thereby altering cellular redox homeostasis. Overall, metal ions often play a key role in the toxicity of oxidants and free radicals.

## 2.4 Summary

Oxidative stress plays an important role in mediating the toxicities resulting from xenobiotic exposures. However, although oxidation resulting from direct reactions or the secondary generation of free radicals has been extensively studied, with few exceptions, the specific oxidations responsible for the toxicities remain largely undefined. Recent studies have yielded an improved understanding of subtle effects at the molecular level and suggest that oxidative processes are more than simply chemical reactions that alter the structure and function of lipids, DNA, and proteins/ peptides. Rather, it is clear that oxidative reactions serve as modulators of normal physiological functions, becoming toxic at high concentrations or when the changes in cellular functions exceed normal parameters in either amplitude or duration. As our understanding of molecular regulation mechanisms improves, the roles that oxidative processes have in adapting, preserving and adversely affecting functions will become more clearly defined. This, in turn, will greatly improve our understanding of toxic mechanisms as well as disease processes associated with exposures to drugs and environmental agents.

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# Chapter 3 Oxidants, Radicals, Free Radicals, and Other Bad Stuff in Mechanisms of Toxicity

**Charles Vincent Smith** 

## 3.1 Free Radicals and Reactivity

In the 1983 movie, *Never Say Never Again*, the threat to human civilization of greatest concern to those selected to protect us from evil was identified thus:

Μ	Too many free radicals. That's your problem.
James Bond	"Free radicals," sir?
Μ	Yes. They're toxins that destroy the body and the brain, caused by eating too much red meat and white bread and too many dry martinis!
James Bond	Then I shall cut out the white bread, sir.
Μ	Oh, you'll do more than THAT, 007. From now on you will suffer a strict regimen of diet and exercise; we shall PURGE those toxins from you!

Yes, readers, the greatest threat to human civilization is from people and institutions who don't understand what they are attempting to manage. Of what am I speaking? Is the primary target of my rapier-like wit the mindless British bureaucrats attempting to manage the clear-thinking spies and killers who are charged with seeking out and eliminating the evil spies and killers hired by the bad guys to do us harm and/or rob us of our precious bodily fluids and other resources? Or am I referencing biomedical investigators who write and talk endlessly about molecular species and mechanisms about which they have ideas that are similarly limited, and often simply incorrect? The domino theory of national defense was simple to explain and easy to understand, but thoroughly misleading many years ago; nevertheless,

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simple explanations persist as foundational elements in present day foreign affairs as well as in mechanistic toxicology. Critical thinking, and the improved understanding that critical thinking produces, are needed in both arenas.

Starting with the idea that assessment and management of anything are not readily possible without the ability to measure the process or effects, we progress to the thought that measurement requires that the process, or products from that process, be defined, and the conditions that form the foundation of the question be described. Note that within this thought framework, 'description' is an essential element, thus challenging the use of 'descriptive' as a dismissive assessment in reviews of proposals and manuscripts. How one proposes to study, much less measure, something any better than one has described that event or process is most puzzling.

Ok, so what is a free radical? Let us start with what is a radical. This is simple. A radical is a molecule with one or more unpaired electrons. Molecular (covalent) bonds are comprised of two electrons with antiparallel spins occupying discrete spatial distributions between two nuclei. Breaking a covalent bond can result in both electrons remaining with one nucleus, the net result being that this nucleus will have an increase in net negative charge, or a decrease in positive charge, with the other molecule or atom exhibiting the reverse. This is heterolytic cleavage, and if the originating molecule was spin-paired (not a radical), the products will not be radicals. In homolytic cleavage, each atom or nucleus parts with one of the electrons of the former covalent bond, hence producing two radicals. Superoxide ( $O_2^{-}$ ) is a radical, a radical anion at that. Hydrogen peroxide ( $H_2O_2$ ) is not a radical. Most of the oxygen ( $O_2$ ) that we breathe is a diradical, meaning that simple (i.e., triplet)  $O_2$  has two unpaired electrons. Egad! Can this be true? Are we in fact surrounded, in fact, perfused, infused, and confused by these toxins [toxicants]? Should M purge all molecular oxygen from James Bond's body?

If being a radical dictates that a molecule is inherently toxic, although seldom stated explicitly, a reasonable interpolation of the thought processes is that the putative mechanisms responsible for those toxicities are due to chemical reactions and molecular alterations of biological molecules, which in turn would be determined by the reactivities of the proposed intermediates. Two major factors limit the toxicities of radicals. One determinant is that, in contrast with the seemingly gratuitous use of the term, not all radicals are free. Although gratuitous attribution of value judgment terms to an entity usually is worthless or misleading, even this generality has exceptions:

Q: Good to see you Mr. Bond, things have been awfully dull around here...Now you're on this, I hope we're going to have some gratuitous sex and violence!

James Bond I certainly hope so too.

As I have said, a radical is an atom or molecule with one or more unpaired electrons. A free radical is a radical that is not compartmentalized, which in a biochemical process might mean that the radical product has escaped or diffused from a site of generation, as from an enzyme. Nonenzymatic chemical reactions also exhibit what amounts to molecular cages, in which homolytic cleavage of a bond formed by two electrons occupying a molecular orbital results in two radicals, each with one unpaired electron. If these species recombine, not necessarily reversing the reaction leading to their generation, but possibly forming a new species, before they diffuse from their site of generation, no free radicals are generated, and therefore the proposed radicals do not have the opportunity to mediate or initiate processes extending beyond their limited scopes. This distinction is most readily understood as interpreting evidence of a toxicity associated with the production of species or transformations that are most reasonably explained as proceeding through the generation of radical species. However, if that radical intermediate is transformed further to a spin-paired product before diffusing from the site of generation, no free radical is produced, much less responsible for any toxicity observed. Correlation is not causation [http://xkcd.com/552/]. This statement should not require explanation, but the reminder does seem to be essential, and with greater frequency than would otherwise not be embarrassing.

Some correlations do link causes with results, and the issues related to distinguishing correlation from causation, particularly insofar as confusion of cause versus result, should be evaluated in light of some very simple principles, the first of which is that causes must precede results. This statement is obvious to the point of being trivial, but is of particular importance in testing hypotheses relating to possible roles of radicals and oxidants in the molecular mechanisms of toxicities, because, in brief, dead meat rots. What this means is that cells and tissues damaged by whatever mechanisms often, even ultimately, lose control of the processes upon which aerobic life depends. In the longer term, much of what we might commonly attribute to 'rotting' may be mediated anaerobically, but in the shorter term, molecules in cells and tissues committed to dying will show oxidative alterations not found commonly in healthy cells and tissues. The non-physiologic oxidations of all sorts of biological molecules that ensue give rise to increases in levels of biomarkers of oxidation, a change that often is interpreted as 'oxidant stress.' Per the above about define and measure, 'oxidant stress' or 'oxidative stress' have been implicated in seemingly countless studies, but with definitions and criteria that are insufficient for the real purpose at hand. The earlier definitions of oxidative stress that generally invoked something along the lines of 'a change in the balance between pro- and anti-oxidant levels to a more pro-oxidant state,' miss the point in several different ways. The first is the assumption that 'a balance' exists in relevant biological systems, and as the noted philosopher and scientist, Benny Hill, has stated, one should not assume [https://www.google.com/?gws\_rd=ssl#q=%22Benny+Hill%22+assum e&safe=active]. The only true chemical equilibrium applicable to biological systems arises from cremation. At equilibrium with our environment, we are more dust, water, and CO<sub>2</sub> than anything else, as our chemical system is surrounded and overwhelmed by our ultimate biological oxidant, O<sub>2</sub>. When considering a human and his/her environment as a chemical system, an essential consideration is that chemical reactions are ones in which neither mass nor charge are created or destroyed. The only real way to increase the content of pro-oxidants is for the person to inhale, thereby increasing his/her content of pro-oxidants (O2). Exhaling decreases prooxidant contents. The other element in the putative oxidation/reduction balance is

comprised of reducing equivalents, which are provided for the most part by food; hence, ingestion of food shifts the oxidation/reduction contents of the chemical system (person) more toward reduction. Ingestion of ethanol, a compound often invoked as a pro-oxidant and free radical generator, imparts a net reductive shift on the chemical system or person. From a chemical perspective, life is a complex set of steady states, something like snow sitting very non-thermodynamically on the tops of mountains, but retarded kinetically from immediate gravitational equilibration (i.e., avalanche, melt, followed by the water running downstream to the ocean). In biology, kinetic concepts are more useful than are principles of thermodynamically determined equilibria. Inasmuch as the bulk of the interest in mechanisms of toxicity has been assembled around the concepts of chemically reactive metabolites and other intermediates, and whether or not a species is reactive is determined kinetically, by the rates at which reactions occur, rather than by the thermodynamic energetics of the reactions involved [1].

Importantly for the present discussion, reactivities are very dependent on context. For example, consider water and hexane. Which is more reactive? Although water would be considered by most biomedical investigators to be chemically inert, and indeed, water does not react appreciably with molecular oxygen, sodium metal would not agree, as water reacts rapidly, indeed violently, with sodium metal. In contrast, sodium metal is not appreciably reactive with hexane. In turn, hexane is stable (reminder: kinetic term) in air, as reactions that mediate the oxidation or burning of hexane in air do not occur rapidly, unless initiated by a source of ignition. Under the right conditions, such as vaporization into a mixture or mist of appropriate hexane/air (oxygen) proportions, a spark for ignition can initiate a reaction that is most robust. If the biological relevance of these examples is not sufficiently evident, please stop writing about mechanisms of cell injury.

#### 3.2 It Is Well-Known That

'It is well known that' N-acetyl-p-benzoquinone imine (NAPQI) is the chemically reactive metabolite of acetaminophen, formed by oxidation of acetaminophen by one or more cytochromes P450. NAPQI reacts preferentially with glutathione (GSH), until GSH is depleted and can no longer scavenge the reactive metabolite, at which point NAPQI reacts with protein thiols, thus binding covalently to proteins. This alkylation of protein thiols compromises cell functions, and with sufficient levels of binding, causes, may cause, or is correlated with cell killing [2–5].

Among other problems with the preceding proclamations, many of the things that are 'well-known' are simply not true. The alert reader should note at this point that I just issued a 'it is well-known that' proclamation stating that such proclamations often are not correct. If you failed to note this problem with my argument until I brought the matter to your attention, please go stand in the corner with the people who were banished for failing to understand the concept of reactivities.

Back to the details of acetaminophen metabolism, binding, and toxicity, synthetic, free, authentic NAPQI reacts with GSH and other thiols to form the respective thioether adduct as well as to be reduced back to acetaminophen, with the latter reaction producing the corresponding disulfides required of the oxidation/reduction reaction. However, as we reported almost 30 years ago, metabolism of acetaminophen in vivo does not increase levels of glutathione disulfide (GSSG), even in animals with markedly compromised GSSG reductase activities [6]. Increases in levels of GSSG in response to the metabolism of acetaminophen have not been reported, and in several studies were not observed. Increases in levels of GSSG in acetaminophen-treated animals have been reported, but these increases have uniformly been observed only after the transformations that irreversibly commit cells and tissue to damage have been initiated. In addition, ascorbate similarly reduces NAPOI back to acetaminophen, and toxic doses of acetaminophen that produce significant covalent binding to protein do not deplete tissue or cell levels of ascorbate [7]. Working the problem backwards, a method that generally is very effective, what might these data suggest? The interpretation that we suggested in 1985 was that NAPQI was not the reactive metabolite of acetaminophen.

Although the thioether products formed in vivo by metabolism of acetaminophen clearly are consistent with thioether products derived from reactions of respective thiols with NAPOI, the absence of evidence of oxidation of biological reductants (GSH, ascorbate) is inconsistent with free NAPQI being the reactive metabolite. Dear reader, if you think I have been beating this poor dead horse pointlessly and beyond the point of diminishing returns, please consider that I thought this horse was dead 30 years ago, so let me keep swinging. To interpret the full body of data available on the topic, we proposed that another species, which we designated as HY in the molecular mechanism scheme presented, formed an intermediate that was not reduced by GSH or ascorbate, but could, through a displacement reaction of the sp<sup>3</sup> species, form the GSH-derived thioether. At that time, Y was used commonly as an abbreviation for glutathione-S-transferases, which is precisely the mechanism we thought would offer the most rational explanation of the data. The scheme proposed implied that GSTs and cytochromes P450 function in assembly line fashion, similar to Lucille Ball's cake packaging enterprise. If this process proceeded smoothly, the NAPQI-HY intermediate would avoid the oxidations of GSH and ascorbate that are characteristic of the chemistry of free NAPQI.

If cellular GSH were depleted, such that the secondary reaction became ratelimiting, the NAPQI-GST adduct might react directly with protein thiols, or NAPQI might be released as a free intermediate that could mediate binding to protein, and possibly thereby lead to toxicity. However, the 'free' NAPQI in such cases should still be reduced by traces of GSH remaining or newly synthesized, or be reduced by ascorbate which does not appear to be affected by acetaminophen in vivo [7]. Much of the discussion above is beyond the hard data in hand, but this analysis is more consistent with the data presently available than are the incredibly simplistic proclamations that continue to be written and spoken on the topic. The objective of our work should be to identify durable concepts and principles upon which useful approaches to significant human health problems can be founded. Efforts to be the first kid on the block to find and report a fragment that proves that the sky is falling are of limited value and more frequently are misleading.

Next, please remember that covalent binding has not been shown or proved to cause cell death. Correlation is not causation. At the same time, I am unaware of any example of acetaminophen-induced cell killing that has been observed in the absence of covalent binding to protein. This is not a statement that extents of injury are correlated linearly with levels of binding. All manner of selectivities and thresholds are to be expected. If alkylation of proteins or other biological molecules can cause or contribute to initiation of cell death, not all sites of binding should be expected to have equal biological consequences. In addition, secondary mechanisms, such as tissue ischemia secondary to cell death-induced swelling, and inflammatory responses to tissue damage, must be considered [8].

A corollary to the last comment is that cell death initiated by processes such as alkylation/covalent binding might well be expanded by process such as inflammatory responses to cell damage. In such cases, the extent of tissue damage might correlate with increases in levels of biomarkers characteristic of oxidative modifications of biological molecules. In this case, one could claim that this secondary wave of cell death was indeed caused by 'oxidative stress' mechanisms. However, those who would claim this as proof that they had indeed identified a piece of the sky that had fallen and hit them on the head are asked to check to see if that piece of the sky does not look suspiciously more like a piece of the roof of the chicken coop in which they live.

Another oddity of acetaminophen binding and toxicity is the 'well-known that' statement that one does not see binding until GSH is depleted substantially. This is simply not true [2-4, 9]. What is true is that binding to protein on the order of 1 nmol/mg protein, which is the level that correlates with substantial hepatic necrosis in vivo, to the best of my knowledge, has not been reported in the absence of substantial depletion of tissue GSH [3]. Nevertheless, measurable binding to protein, on the order of 0.05 nmol/mg protein, is observable at doses well below the threshold for injury in mice and rats. Three different mechanisms can be envisioned to explain this observation. One could be imperfections in Lucy's cake boxing assembly line, meaning that some imperfections might arise in the transfer of the activated species from the CYP active enzyme site to GST, or whatever mechanism or mechanisms limit the oxidative pathways of reactions of the putative initial metabolite. A second possibility is that threshold-level extents of GSH depletion have been achieved, but in very limited subpopulations of cells or subcellular fractions that are not in rapid exchange with other pools of interest. In the case of acetaminophen, the most centrilobular hepatocytes could satisfy such a preferential sequence of depletion, binding, and toxicity, with the extents of depletion and binding being obscured by the relatively unaffected status of cells in the rest of the organ. Alternatively, subcellular fractions, such as a subset of mitochondria or plasma membrane thiols, might account for the effects reported to date, but these potential mechanisms need to be tested more critically [10].

A third possibility is that NAPQI, or its common precursor, is not the only chemically reactive intermediate produced by metabolism of acetaminophen. Synthetic NAPQI does not bind measurably to DNA in vitro, but binding of acetaminophen metabolites to DNA in vivo is observed in mice at doses as low as 10 mg/kg. Although not proved, binding to DNA is best explained as proceeding through the corresponding phenoxyl radical, and this species is not reduced or alkylated preferentially by GSH or GSTs. In fact, alkylation of DNA in vitro by synthetic NAPQI is enhanced quite dramatically by the added presence of proteins, as found in chromatin or intact nuclei, or simply by addition of cysteine, which suggests 1-electron radical addition reactions to DNA, with similar reactions with proteins possibly accounting for the measurable, but low, levels of binding to proteins that are observed with doses of acetaminophen that do not deplete GSH appreciably.

These considerations are noteworthy, not simply as they relate to the academic exercise of elucidating the molecular mechanisms of acetaminophen-induced cell killing, but Perneger et al. [11] reported from an epidemiologic study that the major correlate with end stage renal disease in humans was lifetime ingestion of acetaminophen. Acute hepatic damage caused by doses of acetaminophen that exceed the dose threshold, deplete tissue GSH, and result in marked covalent binding, along the lines of the commonly held tribal wisdom, is a major human health problem. However, the data suggest that this might not be the only problem with acetaminophen, as the epidemiological evidence of cumulative dose exposure association with end stage renal disease places a rather new perspective on the matter, particularly if the mechanisms are driven by cumulative dose effects, rather than by acute dose thresholds. An interesting question that follows would be the relative contributions to this toxicity of binding to protein and DNA. Thus, the sentence used so commonly to introduce discussions of acetaminophen toxicity as 'generally safe in therapeutic doses,' might benefit from a more critical consideration of the differences between absence of evidence (or recognition) and evidence of absence. This point merits added emphasis. The absence of evidence of toxicity associated with use of a pharmacological agent, such as acetaminophen, does not necessarily prove that the agent is safe, just that the drug appears to be safe within the limits of the methods that have been used to test that safety. The trivial nature of this comment is recognized, but I contend that the important principle that is the foundation of the statement is overlooked or neglected in too many instances.

In general, investigation of the possible mechanisms of a toxicity that is observed (and thereby 'described') will be more productive than are efforts to try to find a toxicity that arises from a molecular mechanism that one has envisioned or even observed.

Every reaction has a mechanism, but not every mechanism has a reaction. Richard B. Turner, organic chemistry lectures, Rice University, 1968

However, the need to rely on accumulation of sufficient numbers of human exposures to detect adverse effects, especially in light of the multiple factors that impact possible drug toxicities, is an approach that would allow far too much harm to be incurred before steps to limit that damage were initiated. One approach to limiting harm is to apply what is known about molecular mechanisms, even with the recognition that such actions will not be perfect. For example, let us consider the recent observations of the possible utility of acetaminophen as a means of closing the patent *ductus arteriosis* in infants born prematurely [12]. Even if peroxidase-mediated, low dose and GSH-independent binding to DNA and/or protein of acetaminophen metabolites occurs, as the mechanistic data suggest would happen, that would not necessarily mean that the other options, which range presently from ibuprofen, indomethacin, surgery, or waiting and hoping the duct will close on its own, are preferable. However, appreciation of the fact that acetaminophen metabolites bind covalently to DNA in vivo at therapeutic doses, in fact at doses well below those being studied for duct closure in premature infants, should receive serious consideration, particularly for uses in infants who are early in phases of rapid growth, and cell division and expansion.

As with many research efforts, in our discussion of the studies of the mechanisms by which acetaminophen may or may not cause liver damage, we should continually assess and evaluate the real goals of our efforts. Although lacking many of the molecular details that have been described subsequently and that continue to be guiding objectives in ongoing research, the early studies [2–5] identified a therapeutic approach, namely the administration of N-acetyl-cysteine (NAC), that remains the most effective means for treatment of acetaminophen overdoses. The primary purpose of NAC administration is to support GSH synthesis in temporal windows in which metabolic activation of the parent drug is significant, with far less utility realized by direct reactions of NAC with NAPQI-like intermediates, either by direct alkylation or by reduction [8]. Following that window of therapeutic opportunity, treatments for hepatic damage remain supportive treatment to allow for liver regeneration, or, if the damage is too severe, organ transplantation.

Over the last four decades, quite a number of compounds, elixirs, and mixtures of less well-defined composition have been reported to protect against acetaminophen-induced damage to livers in vivo or in vitro [13]. Quite often, the biological effects associated with such protection are attributed to alterations of signal transduction mechanisms or other elegant molecular interactions, whereas critical examination of relevant mechanisms usually reveals that inhibition of metabolic activation of the parent drug readily accounts for attenuation of injury. The flip side of the benefits of NAC treatment in attenuation of acetaminophen-induced hepatic damage has been that approaches to prevent, treat, or reverse many other examples of tissue damage or other manifestations of toxicity have been attempted that are more along the lines of invocation of magic feather properties than from rational, critical appraisals of molecular mechanisms.

The attempts to use NAC as a universal panacea, something along the lines of a toxicologist's version of WD40 or duct tape, probably have been abetted by the general idea that many toxicities are mediated by oxidative mechanisms, and soaking things in this exogenous reductant can restore a more physiological redox balance. Administration of exogenous NAC can provide benefits, but these benefits are generally mediated by the support of GSH synthesis in situations where the availability of cysteine has become limiting. The oxidant stress balance idea is founded on a conceptual framework that presupposes the existence of a redox balance, and a considerable number of studies have been reported in which assessment and modi-

fication of this 'redox balance' have been central. A simple, critical, test of the applicability of this idea would reveal that, for example, GSH and GSSG are nowhere near in chemical equilibrium with cysteine/cysteine or NADPH/NADP<sup>+</sup>, so that attempts to use any of these or similar chemical redox couples to assess similar ratios in functional molecules in far more complex biological systems would be of questionable relevance.

In a similar effort, a rather large, multi-institutional study was initiated for the stated purpose of identifying 'the' best means of measuring biological oxidant stress status (BOSS) [14–16]. This, as in other efforts, was based upon the presumed existence of something that could be called a singular biological oxidant stress status. A number of different biomarkers of oxidative modifications of biological molecules were measured by investigators who were experienced, and therefore invested, in the measurements of these biomarkers. We had taken previously a rather different approach to the same question and reported data that showed highly divergent responses in specific biomarkers of oxidation among animal models of oxidation [17–19]. These data showed that alignments of biomarkers of oxidation might occur in some examples of toxicity, but the working hypothesis upon which the BOSS studies were founded was not consistent with the data already available. Further, the initial example of 'biological oxidant stress' chosen for the BOSS study was administration of CCl<sub>4</sub>, which we had shown caused rapid and marked elevations in products of lipid (per)oxidation, but did not cause increases in thiol oxidation more characteristic of exposure of biological systems to hydrogen peroxide or other 'reactive oxygen species.'

Consideration of the molecular mechanisms required to produce the specific biomarkers used in the different assay methodologies offered a reasonable explanation as to how these responses could vary so substantially [20]. Many of the biomarkers of oxidative alterations of biological molecules that have been associated with toxic responses are secondary species that represent minor, in many cases very minor, products of the initial oxidations. Ongoing advances in bioanalytical capabilities have placed many of these quantitatively minor products comfortably within the range of measurement by increasing numbers of labs. However, the concept of stoichiometry (how much of the substrate consumed in a process is accounted by the individual product or products measured) is generally overlooked in biological studies of oxidant stress responses [21, 22]. As a consequence, quite large 'foldincreases' can be observed in situations in which the major determinant is less likely to be the initial oxidation than some alteration in the disposition of the products through secondary reactions. For example, increases in the expiration of ethane and pentane by fasted mice given hepatotoxic doses of acetaminophen led some investigators to 'conclude' that acetaminophen-induced hepatic necrosis was mediated by lipid peroxidation [23, 24]. In biological systems, ethane and pentane almost certainly arise from peroxidation of the  $\omega$ -3 and  $\omega$ -6 polyunsaturated fatty acids, but their production also requires that the respective hydroperoxides undergo β-scission, a process that generally requires the availability of redox-active iron chelates, rather than reduction to the corresponding lipid alcohol (or lipid hydroxy acid), which may be reliant largely upon GSH-dependent mechanisms, or other reactions [20]. Even

then, the  $\beta$ -scission reaction does not proceed only to the 1-alkyl radical. Further still, the ethyl and 1-pentyl radicals can react with molecular oxygen, or undergo several other reactions that will preclude formation of ethane or pentane, respectively [25]. In addition, pentane expiration can be affected by CYP-mediated oxidative metabolism of pentane, although this process is less of a factor in ethane expiration. Thus, consideration of the reaction pathways through which ethane and pentane are produced by peroxidation of biological lipids provides a useful example for evaluation of the requirement that one 'assume' a number of untested concepts, principles, and mechanistic relationships for the measurement of any of single product or class of products to be proposed as 'the' measure of lipid peroxidation, much less of 'biological oxidant stress status.'

In our studies, increases in the expiration of ethane and pentane in fasted mice treated with hepatotoxic doses of acetaminophen were dramatic; two or more orders of magnitude, and reproducible. However, these increases were not accompanied by measurable increases in hepatic contents of the hydroperoxide precursors of the hydrocarbons, nor were the contents of other isomeric fatty acid hydroperoxides or their corresponding hydroxy acids increased. The absence of measured increases in lipid hydroperoxides or hydroxy acids in the livers of animals given hepatotoxic doses of acetaminophen is difficult to attribute to limitations of analytical methodologies, as the levels of these species are increased quite rapidly and substantively in mice given comparably hepatotoxic doses of  $CCl_4$  [26, 27].

A basic principle of chemical reactions is that neither mass nor charge are created or destroyed. Stoichiometry (preservation of mass and charge) is an essential feature, but application of this principle is difficult in biological systems in which import, export, and other modes of disposition of peroxidatively modified lipids are investigated. Although limited in biological relevance, model systems in vitro do afford the ability to compare consumption of precursor molecules with measured levels of product molecules. In one such study, specifically the Cu+/ascorbate oxidation of low density lipids in vitro, the lipid hydroxy and hydroperoxy products accounted for up to 70 % of the linoleate and a bit less than 30 % of the arachidonate consumed [21]. In contrast, thiobarbituric acid reactive substances (TBARS), often attributed to malondialdehyde, which is virtually never actually measured, account for at most 2 % of the polyunsaturated fatty acids consumed. Other products, such as 4-hydroxynonenal and the plethora of isoprostanes, formed by peroxidation of fatty acids, account for even smaller fractions of substrate consumption. These specific products may be critical to the biological consequences of lipid peroxidation, but the potential for changes in secondary pathways to effect large changes in levels of these species in absence of changes in overall peroxidation of lipids or in the processes for which the measured biomarkers are intended to be representative must be recognized.

Liver damage caused by acetaminophen overdose persists as a substantial problem in human health. Treatment of acute overdoses with NAC is a reasonably optimized therapy, as such things go. Attempts to diminish intentional and some unintentional overdoses by limiting pack size, although appealing as an idea, do not appear to be exhibiting the beneficial effects that many hoped would be realized. Some progress is being made in decreasing the examples of unintentional overdoses, those incurred in polypharmacy adventures by individuals unaware of the additive effects of acetaminophen in each of the several products being taken. Some of these problems can be aided by greater clarity in contents labeling and education of consumers, possibly including more than a few health care workers. Decreasing the incidence of intentional overdose is more likely to be aided more effectively by investments in mental health care.

## 3.3 Conclusions

A number of factors dictate that fully powered, randomized and double blinded studies of the effects on human health cannot answer all questions of the effects of the potential therapeutic agents needed to improve medical capabilities and environmental substances to which we are exposed presently and will be exposed in the future. Therefore, rational application of our understanding of mechanisms of toxic effects will be essential in setting, revising, and applying limits of exposure, and priorities for more detailed investigation. Certainly, conducting more and better studies will be essential. However, so much of what is known at the present time is not being included in the interpretation of the data presently available. Addressing this disconnect would improve the efficiency of management of awful diseases, such as white bread poisoning.

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# Chapter 4 Lipid Oxidation

#### Norsyahida Mohd Fauzi and Corinne M. Spickett

## Abbreviations

AKR	Aldo-keto reductase
Ch	Cholesterol
CYP450	Cytochrome P450
ECs	Endothelial cells
EGFR	Epidermal growth factor receptor
eNOS	Endothelial nitric oxide synthase
EPA	Eicosapentaenoic acid
5-EpoxyCh	5,6-epoxycholesterol
HETEs	Hydroxyeicosatetraenoic acids
HPETEs	Hydroperoxyeicosatetraenoic acid
4-HNE	4-hydroxynonenal
HO-1	Heme oxygenase-1
HPLC	High performance liquid chromatography
HPODEs	Hydroperoxyoctadecadienoic acid
ICAM1	Intracellular cell adhesion molecule-1
isoLGs	Iso-levuglandins
KEAP1	Kelch-like ECH-associated protein 1
KOdiA-PC	Palmitoyl-2-(5-keto-6-octene-dioyl)-phosphatidylcholine
MAPK	Mitogen activated protein kinase

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MDA	Malondialdehyde
MS	Mass spectrometry
NFκB	Nuclear factor-kappa B
NRF2	Nuclear factor (erythroid-derived 2)-like 2
7α-OHCh	7a-hydroxycholestrol
7α-OOHCh	7a-hydroperoxycholesterol
oxPAPC	Oxidized palmitoyl arachidonoyl phosphatidylcholine
PAF	Platelet activating factor
PC	Phosphatidylcholine
PE	Phosphatidylethanolamine
PECPC	1-palmitoyl-2-cyclopentenone-sn-glycero-3-phosphocholine
$PGG_2$	Prostaglandin G <sub>2</sub>
$PGH_2$	Prostaglandin H <sub>2</sub>
PON-1	Paraoxonase-1
POVPC	1-palmitoyl-2-(5-oxovaleroyl)-sn-glycero-3-phosphocholine
PPAR	Peroxisome proliferator-activated receptor
PS	Phosphatidylserine
PUFAs	Polyunsaturated fatty acids
ROS	Reactive oxygen species
SMase	Sphingomyelinase
TLRs	Toll-like receptors
VCAM-1	Vascular cell adhesion molecule-1
VSMCs	Vascular smooth muscle cells

## 4.1 Introduction

Lipids are fundamental components of cell membranes and also have many important functions in cell signalling. All lipids have hydrophobic elements of high hydrocarbon content, such as fatty acyl chains, which occur in many lipids. Unsaturated fatty acyl chains, especially polyunsaturated chains, are susceptible to attack by a variety of different oxidants, including reactive nitrogen and halogen species, as well as oxygen-based radicals, either through one-electron or twoelectron mechanisms. Even considering only the oxidation of fatty acyl chains by radical attack, a very large number of different products can be formed owing to multiple possible sites of attack and subsequent reaction pathways, while if the products of other oxidants are included, the variety of products increases substantially.

Biological effects of oxidized fatty acids, such as prostaglandins, thromboxanes and leukotrienes have been known for many years [1], but subsequently it was discovered that intact phospholipids had pro-inflammatory effects that were independent of release of the oxidized fatty acid moieties. Much of this research resulted from interest in the role of oxidized low density lipoprotein (LDL) the development of atherosclerosis, and it was discovered that oxidized LDL was cytotoxic to macrophages, endothelial cells and smooth muscle cells, but additionally that it had proinflammatory effects such as inducing monocyte adhesion to endothelial cells [2]. The cytotoxic effects of low molecular weight products of lipid oxidation, such as malondialdehyde (MDA) and 4-hydroxynonenal (4-HNE), have also been recognized for many years [3, 4]. In parallel with work on phospholipid oxidation products, research on cholesterol oxidation products (oxysterols) has also shown these to have important cytotoxic and bioactive effects [5, 6]. It has been known for years that some truncated phospholipids could bind to the receptor for platelet activating factor (PAF) [7], but subsequently several other receptors and sites of interactions have been identified for oxidized lipids, and these have enabled understanding of the wide range of biological activities that they are now known to have [8].

# 4.2 Types of Lipid Oxidation

Lipid oxidation can fundamentally be divided into enzymatic and non-enzymatic processes, with the former generally regarded as essential in physiology to produce signalling molecules that regulate a variety of functions such as immune responses and cardiovascular status. In contrast, until the last 2 decades non-enzymatic modifications were considered as adventitious damage occurring under stress conditions, and hence of limited physiological relevance. It is now recognized that this is an oversimplification, and while lipid oxidation products may indeed be the result of unregulated oxidative attack, nevertheless many have bioactivity and contribute positively to cellular behaviour.

## 4.2.1 Enzymatic Oxidation of Lipids

Several cellular enzymes catalyze lipid oxidation to generate families of physiological signalling compounds such as prostaglandins, thromboxanes, lipoxins and leukotrienes [1]. Lipoxygenases (LOX) catalyze the incorporation of molecular oxygen ( $O_2$ ) at specific sites in the fatty acyl chain (e.g. 5-LOX, 15-LOX) to form hydroperoxides of arachidonic acid [(e.g., hydroperoxyeicosatetraenoic acid (HPETEs)] or linoleic acid [e.g., hydroperoxyoctadecadienoic acid (HPODEs)] [9, 10]; some work only on free fatty acids; while others can oxidize FAs esterified in phosphatidylcholine (PC) or phosphatidylethanolamine (PE) (e.g. 15-LOX). Cyclooxygenases (COX-1/2/3) are prostaglandin endoperoxide synthases, which convert free arachidonic acid initially to prostaglandin G<sub>2</sub> (PGG<sub>2</sub>) by addition of two molecules of O<sub>2</sub> [11, 12]. PGG<sub>2</sub> is then converted enzymatically via prostaglandin H<sub>2</sub> (PGH<sub>2</sub>) to other prostanoids, by a selection of prostaglandin synthases; some of these products are analogous to the isoprostane structures generated by free radical lipid oxidation. They can also peroxidize other C20 fatty acids [e.g., eicosapentaenoic acid (EPA)] to give analogous families of products [13]. Finally, cytochrome P450 enzymes (CYP450) are mono-oxygenase enzymes with hydroxylase or epoxygenase activities [14, 15]. Some CYP450 isoforms generate epoxylated products, which can then be hydrolyzed to di-hydroxylated fatty acids; other CYP450s produces hydroxyeicosatetraenoic acids (HETEs) directly [15]. Arachidonic acid is the main substrate, although other fatty acids are also utilized [16]. A critical feature of the oxidations catalyzed by all these enzymes is that they are stereo- and regio-specific, in contrast to the products of non-enzymatic reactions, which tend to be produced in racemic mixtures.

## 4.2.2 Non-enzymatic Oxidation of Lipids

Non-enzymatic oxidations of lipids can be divided into radical (1-electron) reactions and non-radical (2-electron) reactions. The classical radical attack on polyunsaturated fatty acids (PUFAs) is the process known as lipid peroxidation, whereby the radical abstracts a hydrogen atom (H<sup>•</sup>) from the bis-allylic position between the two double bonds (Fig. 4.1) to form a carbon-centred radical (R<sup>•</sup>), which then reacts readily with molecular oxygen (O<sub>2</sub>, itself a di-radical) to form a peroxyl radical (ROO<sup>•</sup>). As the peroxyl radical still has high reactivity, it is able to abstract a hydrogen atom from another nearby, bis-allylic position, resulting in a chain reaction of damage to unsaturated fatty acids [17, 18]. As fatty acids esterified within phospholipids are densely packed adjacently in bilayers within membranes, a cascade of radical abstractions and oxidations can readily occur, leading to the formation of a



**Fig. 4.1** Schematic diagram showing the chain reaction of lipid peroxidation in a lipid bilayer. (**a**) Process of hydrogen abstraction at a bis-allylic site. (**b**) Addition of oxygen to form lipid peroxyl radical. (**c**) Abstraction of a hydrogen from an adjacent chain by the peroxyl radical, to form a new C-centred radical. (**d**) New C-centred radical reacts with oxygen in essentially the same reaction as b, resulting in a chain reaction. (**e**) The lipid hydroperoxide (or the peroxyl radical) can undergo cleavage reactions to generate breakdown products such as small aldehydes. Note that the lipids are cartoons and the full length of the chains are not shown

large number of hydroperoxides (ROOH) from a single radical attack event. The best radicals for initiating this process are those that are lipophilic and uncharged, and can penetrate into the lipid bilayer. Hydroxyl radical ('OH) is recognized as one of the most reactive species and a good initiator of lipid peroxidation, in contrast to superoxide ( $O_2^-$ ), which is not particularly lipophilic. It is generally thought that lipid peroxidation can be terminated by a lipophilic chain-breaking antioxidant, such as  $\alpha$ -tocopherol, which has relatively high stability and low reactivity in terms of hydrogen abstraction, and can be detoxified by reaction with another  $\alpha$ -tocopheryl radical to form a non-radical species or possibly by synergy with other antioxidant cycles [19]. Ultimately, radical processes can only be terminated by the reaction of two radicals to yield a non-radical compound.

Lipid peroxyl radicals can alternatively undergo rearrangement with attack of the radical on the hydrocarbon chain, and often together with the addition of further oxygen this can result in the cleavage of the hydrocarbon chain, for which several mechanisms have been proposed, including β-scission and Hock rearrangement. β-scission generates a hydrocarbon fragment that is 1 carbon shorter than the chain length to the site of peroxidation, plus a fragment containing the remaining chain terminated in an aldehyde. This leads to formation of small, volatile hydrocarbons such as ethane and pentane [20]. In contrast, Hock rearrangement forms two fragments that both terminate in an aldehyde. Hydroperoxides are not very stable either and if acidified can also undergo degradation. Multiple different products can be formed from these secondary reactions, depending on the nature of the fatty acyl chain and site of radical attack. For example, 4-HNE can be formed by radical attack on  $\omega$ -6 polyunsaturated chains such as linoleic, linolenic, or arachidonic acids, whereas  $\omega$ -3 PUFAs yield the 6 carbon analogue 4-hydroxy-trans-2-hexenal [21, 22]. When these cleavage reactions occur, an aldehyde is also formed on the other section of the hydrocarbon chain; for example, oxidation of linoleic acid (C18:2) can yield 4-HNE and 9-oxo-nonenoic acid [23, 24]. If the oxidized linoleic acid was esterified in a phospholipid, free 4-HNE plus an esterified aldehyde will be generated. Multiple cleavage reactions are also possible and result in the formation of small reactive aldehydes, notably the 3-carbon compounds MDA and acrolein, which are derived from endoperoxides [25, 26]. In this case, several fragmentation products are formed from a single fatty acyl chain. Alternatively, internal rearrangements of the oxidized chain that do not result in cleavage are possible. These products can be either free or phospholipid-esterified, and examples include F<sub>2</sub>-isoprostanes, and a variety of cyclopentane products derived from cross-linking of two carbons within the chain [27, 28]. Subsequent C-C cleavage of cyclopentane endoperoxides gives rise to levuglandins [or isolevuglandins (isoLGs)/ $\gamma$ -ketoaldehydes from non-enzymatic reactions] [27, 29]. Overall, several different oxidized chemical groups can be introduced into the hydrocarbon chain, including epoxides, hydroxides, aldehydes and ketones, and carboxylic acids. The conversion of hydroperoxides to hydroxides can be achieved enzymatically by glutathione peroxidases [30-32], and interconversion of carbonyl, hydroxide and carboxylic acids may be catalyzed by aldose reductases (aldoketo reductases) or dehydrogenases [33-35].

In addition to these partially reduced oxygen species, other radicals can also attack unsaturated lipids. A good example is nitrogen dioxide (NO<sub>2</sub>), but in addition to H abstraction it can also cause other modifications, such as nitration. Other species that result in nitration either directly or indirectly include peroxynitrite (ONOO<sup>-</sup>), NO<sub>2</sub><sup>+</sup> and the nitrosoperoxicarbonate anion (ONOOCO<sub>2</sub><sup>-</sup>) although these are not radicals and the reaction involves a 2-electron mechanism [36]. Similarly, non-radical chlorination reactions can occur in the presence of molecular chlorine (Cl<sub>2</sub>) or oxychloro compounds such as hypochlorous acid (HOCl) or ClO<sub>2</sub> [37]. The reaction of HOCl involves addition across double bonds of unsaturated fatty acids to form chlorohydrins ( $\alpha$ -hydroxy,  $\beta$ -chloro compounds) [38, 39]. In contrast to lipid peroxidation, which is much favoured in PUFAs, chlorohydrin formation occurs readily with mono-unsaturated lipids, and these also yield the most stable products. Highly unsaturated fatty acids can be highly modified by HOCl, but phospholipids containing such modified chains are unstable and tend to degrade to lysolipids [40]. Plasmenyl phospholipids (containing a vinyl ether linkage instead of an ester linkage) are susceptible to attack by HOCl at the vinyl ether, resulting in formation of a lysolipid and  $\alpha$ -chloro fattyaldehyde [41, 42]. These reactions are illustrated in Fig. 4.2. Sphingomyelin is another type of lipid that is susceptible to HOCl attack, and attack of HOCl on this lipid also yields monochlorohydrin and mixed chlorohydrin/chloramide sphingomyelin species [43].

Moreover, it is important to remember that phospholipids have various headgroups, including phosphocholine, phosphoethanolamine, phosphoserine, phosphoinositol and phosphoglycerol. Apart from the fact that this increases the variety of different products, the phosphoethanolamine and phosphoserine headgroups are themselves susceptible to oxidative damage, owing to the presence of a primary amine [44]. For example, in phosphatidylserine (PS), the amine can be oxidatively deaminated to form glycerophosphoacetic acid, as described by Domingues group [45]. Alternatively, the amine in phosphaditidylethanolamine (PE) can be modified by reaction with aldehydes formed during lipid peroxidation, to yield PE-MDA or 15-isoLG-PE, among others [46].

Thus it can be seen that the term lipid oxidation covers several different processes, and results in a multitude of different products, even from a single parent lipid. The structures of the most common non-esterified fragmented products of lipid oxidation are shown in Table 4.1, while some typical esterified and full chain length products are given in Table 4.2. Many of these products have been found to have biological effects ranging from toxicity to bioactivity. These effects will be discussed in the subsequent sections of this chapter.

In addition to phospholipids, cholesterol and cholesterol esters can undergo peroxidation reactions that are essentially analogous to those of phospholipids. With cholesterol esters containing unsaturated chains, such as linoleate, these are oxidized as described above. The cholesterol structure itself can also be oxidized to generate a variety of hydroxyl, keto and epoxy products both on the rings structure and alkyl tail [17]. These compounds are collectively known as oxysterols. Interestingly, some products and stereochemistry are favoured over others: in LDL oxidation it was found that  $7\beta$ -hydroperoxycholesterol ( $7\beta$ -OOHCh) was produced in substantially higher quantities than  $7\alpha$ -hydroperoxycholesterol ( $7\alpha$ -OOHCh) [47], resulting in products such as  $7\beta$ -hydroxy and  $7\beta$  -keto cholesterol being common.



Fig. 4.2 Formation of nitrated and chlorinated lipids by electrophilic attack at unsaturated sites

Chamical Structure (stigle form)	Common nomo	Chain
Chemical Structure (stick form)	Common name	lengui
0	Acrolein	3 carbons
0	Malondialdehyde (MDA)	3 carbons
	Pentane	5 carbons
0 OH	4-Hydroxy-trans-2-hexenal (HHE)	6 carbons
O OH	4-Hydroxy-trans-2-nonenal (HNE)	9 carbons
	4-Oxo-trans-2-nonenal (OHE)	9 carbons
OH OH OH	4-Hydroxy-trans-2-nonenoic acid (HNA)	9 carbons
O OH	4-Hydroxydodecadienal (HDDE)	12 carbons
ОСООН	9,12-dioxo-10-E-dodecenoic acid/9-keto-12-oxo-dodecenoic acid (DODE or KODA)	12 carbons

Table 4.1 Structures of some common aldehyde breakdown products of lipid peroxidation

## 4.3 Reactivity of Lipid Oxidation Products

Many products of lipid peroxidation and oxidation are reactive; only hydroxides and fragmented hydrocarbons are relatively unreactive. By definition, most radicals are unstable and highly reactive: peroxyl and alkoxyl radicals readily abstract hydrogens in intra- and inter-molecular reactions. Hydroperoxides are unstable in the presence of redox metal ions. Epoxides are reactive, and can be hydrolysed to glycols. Many lipid peroxidation products contain carbonyl groups (-C=O), either as aldehydes or ketones, and these react with amines to form Schiff bases [48]. Some products are  $\alpha,\beta$ -unsaturated aldehydes, which makes them highly reactive and electrophilic compounds that can readily form Michael adducts with amines and thiols as well as Schiff bases with amines; of these, the most reactive are the substituted unsaturated aldehydes, such as hydroxyalkenals or ketoalkenals (e.g. 4-HNE or 4-ONE).  $\alpha$ , $\beta$ -Unsaturated aldehydes are bi-reactive, and hence able to cause cross-linking of other molecules, such as proteins and DNA. For example, at physiological pH, MDA occurs predominantly in the enolate form, which is less reactive but still able to modify nucleic acids [49]. The  $\alpha,\beta$ -unsaturated aldehydes and hydroxyalkenals readily form adducts with lysine, histidine and cysteine residues in proteins, a process also referred to as lipoxidation [44, 50]. Some lipid peroxidation products, such as 4-HNE and isoLGs, are so reactive that it is difficult to find them

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Table 4.2 Structures of some common phospholipid-esterified and full c	hain free products of lipid peroxidation	
Chemical structure (stick form)	Common name and abbreviation	Chain length
$H_{3}C \xrightarrow{(CH_2)_{14}} 0$	1-Palmitoyl-2-(5-oxovaleroyl)-sn-3-glycerophosphocholine (POVPC)	5 carbons
$H_{3}C \xrightarrow{(CH_2)_{14}} O \xrightarrow{O} O O O O O O O O O O O O O O O O O O $	1-Palmitoyl-2-glutaroyl-sn-3-glycerophosphocholine (PGPC)	5 carbons
$\overset{H_3C}{\overset{(CH_2)_{14}}{\overset{0}{\overset{0}{\overset{0}{\overset{0}{\overset{0}{\overset{0}{\overset{0}{\overset$	1-Palmitoyl-2-(8-carboxy-5-keto-oct-6-enoyl)-sn-3- glycerophosphocholine (KOdiA-PC)	8 carbons
$H_{3}C (CH_{2})_{14} \int_{0}^{0} O + O + O + O + O + O + O + O + O + O $	1-Palmitoyl-2-(9-oxononanoyl)-sn-3-glycerophosphocholine (PONPC). NOTE: the 9-carbon chain ending in a carboxylic acid is azelaoyl (PAzPC)	9 carbons

Table 4.2 (continued)		
Chemical structure (stick form)	Common name and abbreviation	Chain length
H <sub>3</sub> C <sup>(CH<sub>2</sub>)<sub>14</sub> 0 Me<sub>3</sub>N<sup>(C)</sup> 0 O<sup>-D</sup> 0 O<sup>-D</sup> 0</sup>	1-Palmitoyl-2-(5,6 epoxycyclopentenone)-sn-3- glycerophosphocholine (PECPC)	20 carbons
H <sub>3</sub> C (CH <sub>2</sub> ) <sub>14</sub> 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1-Palmitoyl-2-(5,6 epoxyisoprostane)-sn-3-glycerophosphocholine (PEIPC)	20 carbons
O OH OH	Iso-levuglandin	20 carbons
HOOC	Isofuran	20 carbons

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in free form in biological tissues. Not only small, free aldehydes, but those also esterified in phospholipids can modify proteins. The occurrence of such adducts was first discovered using so-called "natural antibodies" against oxidized PCs, of which the best known is EO6. This is known to recognize 1-palmitoyl-2-(5-oxovaleroyl)-*sn*-glycero-3-phosphocholine (POVPC) adducts on LDL and other lipoproteins, but adducts of other oxidized PCs, such as 1-palmitoyl-2-epoxyisoprostane-sn-glycero-3-phosphocholine (PEIPC), can also be detected. More recently, the occurrence of oxidized PC adducts on apolipoprotein (Apo) B-100 has been confirmed by mass spectrometry, and adducts of POVPC and 1-palmitoyl-2-(9-oxo)nonanoyl-*sn*-glycero-3-phosphocholine (PONPC) on lysine and histidine residues were identified [51].

In many cases, protein adduct formation interferes with the protein's normal function and causes inhibition, thus representing another mechanism of cellular toxicity. However, there is increasing evidence that in a small number of cases, specific adduct formation can increase or alter the activity of a protein without inhibiting it, as will be discussed later.

## 4.4 Types of Biological Effects

The field of phospholipid oxidation has advanced enormously since the days when non-enzymatic oxidation was considered as an interfering artefact, or at best a damaging process with no physiological relevance. As described above, some lipid oxidation products are highly reactive and form covalent adducts with proteins, DNA, carbohydrates, and other lipids. However, it is now well-accepted that many products of phospholipid oxidation affect cellular behaviour by interactions with receptors or signalling proteins that induce specific effects, although it is not always known whether these are covalent or non-covalent interactions. The best established biological effects are summarized in Fig. 4.3. Many of these types of interactions have important effects and have been suggested to have roles in pathology or, more recently, in physiological processes.

#### 4.4.1 Effects on Cell Membranes

Oxidation of membrane phospholipids undoubtedly affects the cell membrane composition and stability. Oxidized phospholipids (oxPLs) are more polar than the parent (unoxidized) lipid and alter the bilayer properties and fluidity. This in itself can affect the activity of membrane proteins, which is often dependent on the lipid present in the annulus [52]. Theoretical modelling and studies in model bilayers have shown that oxPL formation can de-stabilize the membrane and cause loss of membrane asymmetry, but only at relatively high ratios of modified lipids that may not be physiologically relevant [53, 54]. However, the headgroup-modified product



Fig. 4.3 Summary of the major deleterious and beneficial effects of oxidized phospholipids

N-isoLG-PE has been reported to alter membrane curvature, which may be related to ER stress [55]. The elegant lipid whisker model proposes that it is energetically unfavourable for the oxidized, polar chains of membrane phospholipids to remain within the bilayer, and instead they protrude from the membrane into extracellular or cytoplasmic aqueous environment, where they can interact with other molecules, including receptors on other cells, thus initiating some biological effects [56]. In contrast, small oxidized fragmentation products may be lost into the aqueous environment, although it has been suggested that some longer chain non-esterified products may even accumulate in the membrane [57]. Thus while the early concept that oxidative attack on membrane phospholipids led to physical membrane disruption and cell lysis is probably an over-simplification, only relevant at unphysiologically high oxidant treatments, lipid oxidation can lead to more subtle membrane effects that are likely to affect cell behaviour.

## 4.4.2 Toxicity

Many products of lipid oxidation are toxic, although the concentrations required vary considerably between individual species [58]. Lipid hydroperoxides, hydroxy-fatty acids, aldehydes and electrophilic lipids [59] and chlorinated lipids [60–62] have all been found to cause cell death in at least one cell type. The cytotoxicity of small, non-esterified aldehydes such as MDA, acrolein and 4-HNE, which are

reactive  $\alpha,\beta$ -unsaturated aldehydes, has long been known [49, 57, 63]. The basis of their toxicity is thought to be their ability to cause cross-linking of other molecules, such as proteins and DNA. MDA reacts with nucleic acids, giving pyrimido- $[1,2-\alpha]$ purin-10(3H)-one deoxyribose as the major product from DNA [49]. Other aldehydes can also react with nucleic acid bases and yield exocyclic adducts with 5- or 6-membered rings. These products, in particular their ability to cause sequencedependent frameshifts and cross-link DNA strands, are considered to contribute to the genotoxicity of the aldehydes. 4-HNE was found to have selective cytotoxicity versus cancer cell lines and tumoristatic effects, probably reflecting adverse reactions with DNA [26]. The toxicity of the di-aldehyde compounds iso-LGs has long been recognized. For example, free 15-E2-isoLG caused endothelial cell damage and necrosis of brain at concentrations of 100 nM [64]. Iso-LGs have been shown to enhance pro-apoptotic effects following calcium elevation, such as enhancing mitochondrial swelling, inhibiting respiration, and inducing mitochondrial permeability transition. These effects are thought to be caused by covalent modification of cytochrome c, which causes it to be released from mitochondria [65]. Another aldehyde-containing phospholipid, POVPC, as well as its carboxylate-containing analogue 1-palmitoyl-2-glutaroyl-sn-glycero-3-phosphocholine (PGPC), has been found to cause loss of cell viability in vascular cells, such as vascular smooth muscle cells (VSMCs) and macrophages [66]. The ability to cause apoptosis in VSMCs has been linked to activation of acid sphingomyelinase (SMase), involving release of ceramide, mitogen activated protein kinase (MAPK) activation and ultimately signalling via caspase-3 [67, 68]. In contrast, in rat oligodendrocytes, it was found to be the neutral SMase isoform that was responsible for the increase in ceramide and activation of caspases-3 and caspase-8 on treatment with POVPC [69]. Thus it is clear that oxPLs induce cell-specific responses, although they may have detrimental effects in both vascular and brain tissue. Bi-reactive aldehydes may also affect cell viability by proteasomal inhibition, as crosslinking of proteins prevents their degradation by the 20S proteosome, and extensively crosslinked proteins can completely inhibit proteasome function, leading to cell death [70, 71].

There is substantial evidence that several oxysterols show toxicity to a range of different cell types [72], including colonic epithelial cells [73]. Toxicity to vascular cells, including endothelial cells, VSMCs and fibroblasts, has also been observed for several oxysterols such as 7 $\beta$ -hydroperoxycholesterol (7 $\beta$ -OOHCh), 7 $\beta$ - and 7 $\alpha$ -hydroxycholestrol (7 $\beta$  and  $\alpha$ -OHCh), 7-ketocholesterol (7-ketoCh) and cholesterol epoxides, of which the former was reported to be the most toxic [47]. In fibroblasts with lipoprotein-deficient serum supplementation, it was found that the most toxic oxysterol was 7 $\beta$ -OOHCh, closely followed by the 7 $\beta$ -hydroxy form, while 7-ketoCh and 5,6-epoxycholesterol (5-epoxyCh) showed least toxicity [47]. There is evidence that oxysterol treatment of VSMCs results in increased formation of reactive oxygen species (ROS) and release of cytochrome c [74]. In endothelial cells and macrophages, increased intracellular Ca<sup>2+</sup> level is an important signalling event in mediating oxysterol-induced apoptosis [75].

Finally, some specific effects have been observed for oxidized cardiolipin and PS, which are both associated with apoptosis. Cardiolipin is present in the mito-

chondrial membrane, and can be oxidized by cytochrome c during apoptosis, owing to the development of peroxidase activity. The oxidation of cardiolipin contributes to the mitochondrial permeability transition, an important step in apoptosis. PS is also oxidized by the peroxidase form of cytochrome c released from the mitochondria, and this leads to externalization of oxidized PS, in turn signalling to macrophages to phagocytose the apoptotic cell [76].

Thus it can be seen that many products of lipid oxidation cause toxicity to a range of different cell types. Cell death can occur through apoptosis or necrosis; as a generalization, apoptosis tends to be induced at lower concentrations, although the time course of treatment also influences the outcome, and the concentrations required vary considerably between cell types.

## 4.4.3 Pro-inflammatory or Deleterious Effects

Lipid oxidation products have been found at increased levels in a variety of inflammatory diseases, suggesting that they are involved in the pathology, even if it is not clear that they are causative agents. For example, lipid hydroperoxides have been reported in rheumatoid arthritis in human patients [77] and in ischaemic rat inflammatory lung [78]. Many different types of oxidized lipids have been identified in atherosclerosis; including truncated and full length oxidized PCs [79, 80]; aldehyde adducts of HNE and acrolein [63, 81]. There is extensive evidence for the formation of reactive aldehydes and formation of lipoxidation adducts in neurodegenerative diseases such as Alzheimer's and Parkinson's [50, 82]. The highly toxic compounds isoLGs have also been identified in necrotic brain tissue [64, 83]. IsoLG-modified proteins have been detected in glaucoma, an inflammatory eye condition [84]. Although these diseases have different underlying causes, aspects of the inflammatory pathology are often common, such as immune cell activation and production of proinflammatory cytokines, increased expression of adhesion molecules, loss of endothelial function, impaired wound healing and fibrosis.

Much interest in the pro-inflammatory effects of oxidized lipids dates from investigations on the properties of oxidatively-modified LDL and subsequent demonstration that oxidized palmitoyl arachidonoyl phosphatidylcholine (oxPAPC) could mimic the effects of "minimally-modified" oxLDL [85, 86]. It was found that the oxidized PCs POVPC, PGPC and PIEPC were present in atherosclerotic tissue and could induce monocytes to adhere to a HUVEC monolayer, mimicking leukocyte-endothelial adhesion in tissue [87]. Later, it was shown that oxPAPC and POVPC induced adhesion of monocytic U937 cells and human peripheral blood monocytes, but not blood neutrophils, to HUVECs in a static adhesion system [88]. For POVPC, it was found that the adhesion resulted from increased endothelial cell surface expression of fibronectin connecting segment domain, whereas PGPC showed increased expression of E-selectin and vascular cell adhesion molecule-1 (VCAM-1) [89]. OxPAPC was able to induce selective adhesion of monocytes in the air pouch model of inflammation, in contrast to lipopolysaccharide (LPS), which caused adhesion of both neutrophils and monocytes, and depended on cell adhesion molecule expression rather than release of inflammatory cytokines [90]. This study also demonstrated that a variety of different pro-inflammatory proteins were upregulated in this model, including several monocyte chemoattractant proteins (MCPs), Regulated on activation normal T cell expressed and secreted (RANTES), C-X-C motif chemokine (CXCL)-10 and 14, macrophage inflammatory protein 1 (MIP1)- $\alpha$  &  $\beta$ , and growth-related oncogene  $\alpha$ . The increased expression of many pro-inflammatory proteins by oxPLs is not surprising in view of the fact that in endothe-lial cells, treatment with oxPAPC activated more than 1000 genes, many overlapping with those mentioned above [91].

The effects of OxPLs on smooth muscle cell behaviour have been investigated to understand potential roles in atherosclerosis. In two studies POVPC, but not PGPC, was found to mimic minimally modified oxidized LDL and induce VSMC proliferation by a mechanism involving expression and phosphorylation of connexin Cx43 [92, 93]. These different effects could be due to the distinct signalling mechanisms suggested for these oxPLs, specifically that POVPC activates MAP kinases whereas PGPC activates protein kinase C (PKC) [92, 94]. In contrast, a later study reported that both lipids could inhibit proliferation, though POVPC was more potent [66]. In addition to proliferation, the compounds can cause phenotypic switching of VSMCs from the contractile to the proliferative state [95], and, for PGPC, enhanced type VIII collagen expression and migration [96]. These are important processes in the development of atherosclerotic plaques.

Several studies have reported that oxysterols have proinflammatory effects on endothelial cells and macrophages, which appear to overlap considerably with those described above for oxidized PLs. For example, they induce the expression of cytokines and chemoattractants such as MCP1, transforming growth factor- $\beta$ 1 (TGF- $\beta$ 1), MIP-1 $\beta$ , tumor necrosis factor- $\alpha$  (TNF $\alpha$ ), interleukin-1 $\beta$  (IL-1 $\beta$ ), and IL-8, and lead to increased levels of  $\beta$ 1-integrin on the surface of macrophages, which correlates with increase adhesion to endothelial cells [97]. In some cases, effects of specific oxysterols have been identified, such as the ability of 7-KC to polarize M1 and M2 macrophages towards pro-inflammatory, pro-invasive and pro-angiogenic phenotypes [98] or β-hydroxycholesterol to induce expression of adhesion molecules and secretion of IL-1ß by endothelial cells [99]. In endothelial cells, 7-KC and 7-β-OH have been reported to up-regulate the oxidative enzymes COX-2 and endothelial nitric oxide synthase (eNOS) through epidermal growth factor receptor (EGFR) and phosphoinositide 3-kinase/Akt (PI3K/Akt) signaling pathways [100]. These signaling mechanisms show similarity to those reported for oxPLs [101], and depending on the conditions could cause both pro-inflammatory and pro-apoptotic effects.

As mentioned above, the amine headgroup of PE can be attacked by the highly reactive compounds 4-HNE, MDA and isoLGs. The resulting PE-isoLG adducts demonstrate similar proinflammatory effects to those described for simple oxPLs and oxysterols, including increased expression of adhesion molecules intracellular cell adhesion molecule-1 (ICAM1), VCAM1, and E-selectin, and secretion of the pro-inflammatory cytokines, MCP1 and IL-8. The precise effects were found to be dependent on the presence of an N-pyrrole moiety, and involved endoplasmic reticu-

lum (ER) stress [46, 55]. Interestingly, the occurrence of ER stress has also been reported in endothelium following treatment with PEIPC at ~1  $\mu$ M [102], but whereas PEIPC improved the barrier function of endothelium, 15-E2-isoLG worsened it, as did POVPC [64]. Less is known about the cellular effects of PE adducts with 4-HNE and MDA, but the latter is thought to play a role in cataract formation [103].

4-HNE and other  $\alpha$ , $\beta$ -unsaturated aldehydes have also been reported to have effects on cellular processes relevant to endothelial barrier function, acting via activation of several MAPKs [104]. They were able to induce modification of several cytoskeletal proteins, including actin and microtubules, leading to actin aggregation and formation of actin stress fibers. This affects intercellular gap formation and regulates endothelial barrier function in the lung [105].

There are also many reports on effects of oxLDL, but these have not been described as in many cases it is unclear whether oxidation of the lipid or protein is responsible for the effects, and the precise lipids responsible have not always been determined.

## 4.4.4 Cytoprotective Effects

While much of the focus on the biological effects of oxidized lipids has been on their toxic and pro-inflammatory effects, nevertheless it has been known for some years that oxidized lipids can have some beneficial effects. Like many toxic compounds, including free radicals and irradiation, pretreatment with low concentrations or doses can generate resistance. This has been demonstrated in the adrenal medulla neuronal cell line PC12 pretreated with sublethal concentrations of PC hydroperoxides ( $10 \mu M$ ), HODE (50 μM), 7α-OHCh (20 μM), 7β-OHCh (20 μM), 5β,6β-expoxyCh, 4-HNE (15 µM), and 15-deoxy-D12,14-PGJ2 (15d-PGJ2) (7.5 µM) before stressing them with normally lethal concentrations of the known neurotoxin 6-hydroxydopamine, which resulted in increased survival [106]. Such cytoprotective effects appear to depend on the induction of increased antioxidant levels, in particular glutathione, within the cells, effectively by hormesis [107]. Similarly, Moellering et al. [108] reported that oxPAPC can increase glutathione levels in ECs and protect against quinone redox cycling-induced toxicity [108], and 4-HNE has been found to increase expression of  $\gamma$ -glutamyl cysteine ligase, the rate-limiting enzyme in glutathione synthesis [109, 110]. Subsequently, the role of the redox-sensor KEAP-1 and associated transcription factor Nrf2 in this process was identified [111]. Oxidation or adduction of KEAP-1 thiols results in dis-association of Nrf-2 and its translocation to the nucleus, where it can induce expression of genes containing an antioxidantresponse element (ARE), including  $\gamma$ -glutamate cysteine ligase, heme oxygenase-1 (HO-1), and NAD(P)H quinone oxidoreductase-1, all of which have protective effects. This was demonstrated for phospholipids containing an electrophilic epoxyisoprostane ring [112] and oxPLs generated by UV treatment of skin [113], but other electrophilic lipid species capable of reacting with KEAP-1 thiols are expected to have comparable effects. Interestingly, nitrolinoleate was also found to activate Nrf-2 [114]. However, it is also known upregulation of HO-1 can also be achieved through
peroxisome proliferator-activated receptor- $\alpha$  and  $\gamma$  (PPAR $\alpha$  and  $\gamma$ ), although the role of oxPLs in this is less well established [115]. An alternative mechanism for inducing HO-1 expression in response to oxPAPC involves protein kinases A and C, and MAPKs p38 and ERK, leading to phosphorylation of cAMP-responsive element-binding protein (CREB) [115].

Another, now well-established, mechanism by which oxidized lipids can have protective effects is through interference with pathogen-associated molecular pattern (PAMP) receptors, in particular Toll-like receptors (TLRs). These are an essential part of the innate immune system that detect products from micro-organisms or cellular damage, and trigger pro-inflammatory pathways and responses such as leukocyte-endothelial adhesion and chemokine release [116]. Early work showed that various oxPAPC components, such as POVPC [89] and 1-palmitoyl-2-(5-hydroxy-8-oxooct-6-enoyl)-sn-glycero-3-phosphocholine (HOOA-PC) [117] inhibited pro-inflammatory effects of LPS at a cellular level, and the ability of oxPAPC to protect mice against otherwise lethal endotoxic shock following LPS injection was demonstrated [118]. Subsequent research provided further information on the interactions underlying these effects, in particular the competitive interference of oxPLs with LPS binding partners CD14, LPS-binding protein (LBP) and MD-2 [119].

As mentioned briefly in the previous section, various oxPLs including 1-palmitoyl-2-cyclopentenone-*sn*-glycero-3-phosphocholine (PECPC) have been found to improve the barrier function of endothelium in inflammatory conditions of the lung, thus reducing vascular leak. This is beneficial as it decreases the migration of activated leukocytes to the interstitial fluid, and the concomitant oxidative damage. Unmodified phospholipids did not show comparable oxidative effects [120]. Although it might be logical to suppose that in lung injury involving infection, protective effects of oxPAPC might relate to interference with TLRs, most work has been carried out on ventilator-induced injury where other mechanisms appear to be involved. In pulmonary endothelial cells, oxPAPC products induced activation of three small GTPases, Rho, Rac, and Cdc42 [120], and led to formation of VE-cadherin-p120-catenin/ $\beta$ -catenin complexes, which are important in the cyto-skeletal control and maintenance of tight junctions between the cells [121].

## 4.5 Mechanisms of Biological Effects: Interactions with Receptors and Signalling Pathways

Much research has been carried out to elucidate the mechanisms underlying the deleterious and pro-inflammatory effects of oxidized lipids, in particular aimed at identifying cellular receptors with which they interact and components of signalling pathways that are affected. Bearing in mind that many, but not all, oxidized lipids are highly reactive, it can be envisaged that some effects may be achieved through covalent modifications of proteins, while others may involve non-covalent interactions. In many cases, although receptors have been identified, the exact nature of the interactions has not been established.

Nuclear receptors (ligand-activated transcription factors) such as liver X receptors (LXRs) and peroxisome proliferator-activated receptors (PPARs) are well known to respond to non-esterified oxidized lipids [122]. The first endogenous oxidized lipid ligand for PPARy identified was the prostanoid 15d-PGJ2 [123], but oxidized fatty acids, like 9-hydroxyoctadecadienoic acid (9-HODE) and 13-hydroxyoctadecadienoic acid (13-HODE) are found at higher levels in tissue and are thought to be more physiologically relevant agonists [124, 125]. There is now increasing evidence that oxPLs can activate PPARs; for example the O-alkyl truncated lipid 1-palmityl-2-azelaoyl-PC; (PAZ-PAF) can activate PPARy [126], and at low micromolar concentrations, HETE-PE and KETE-PE have also been found to be weak agonists [127]. In contrast, the diacyl-PCs POVPC and PGPC have been found to act on PPAR $\alpha$  [128], and epoxyisoprostane phospholipids have been found to be particularly potent activators, enhancing PPAR $\alpha$  activity 5-15-fold, which represents much stronger effects than the synthetic ligands [117]. Activation of PPARs can lead to pro-inflammatory events like monocyte-endothelial adhesion, but may also result in anti-inflammatory effects via abrogation of NFkB signalling. For example, both beneficial and adverse effects of PPARy activation have been noted in diabetes and cardiovascular diseases [129]. In contrast to oxidized fatty acids, some oxysterols bind directly to LXRs, such as 24-OHCh, 22-OHCh, and 25-epoxyCh [130]. The main effect of LXR activation is regulation of lipid metabolism, for example by upregulating expression of the sterol regulatory element binding protein-1c (SREBP-1c), but it can also induce genes involved in uptake of lipoproteins, such as the LDL receptor (LDLR) [131] and scavenger receptor-B1 (SR-B1) [132]. In addition to acting via PPARs, a G-protein coupled receptor, G2A, has been demonstrated to respond to oxidized free fatty acids (oxFFAs), including 9-HODE and other oxidized FA derivatives of linoleic and arachidonic acids [133]. The downstream effects of G2A activation by oxFFAs include calcium mobilization, inhibition of cAMP formation, and MAPK activation; these effects have been suggested to play a role in oxidative stressinduced pro-inflammatory responses in human skin cells [134].

One of the first receptors considered as a candidate for mediating the effects of oxPLs was the PAF receptor. PAF is a truncated phosphatidylcholine (1-alkyl-2-acetyl-sn-glycero-3-phosphocholine), and therefore has structural similarity to truncated oxidized PCs, some of which can activate the PAF receptor and are known as PAF-like lipids [135]. The most active of these are truncated alkylacyl phospholipids such as butanoyl-PAF, butenoyl-PAF and oxovaleroyl-PAF, as opposed to diacyl-PCs, although POVPC can also bind [136]. In addition to causing aggregation of platelets, PAF-like lipids also cause leukocyte endothelial adhesion. O-alkyl phospholipids induce effects at nanomolar rather than micromolar concentrations, and these effects are more clearly abrogated by PAF receptor antagonists [137, 138].

There is now excellent evidence that A and B class scavenger receptors, notably CD36, scavenger receptor (SRA)-I/II and SR-B1, recognize oxidized phospholipids. The best oxPL ligands for CD36 have been very well characterized in studies by Podrez et al. [139, 140] and the  $IC_{50}$  values determined. It was found that hydroxyalkenal phospholipids, such as 9-keto-10-dodecendioate-PC and 9-keto-12oxo-10-dodecenoate-PC, had the highest binding affinity. As with the PAF receptor, POVPC was found to bind, but with much lower affinity ( $IC_{50}$  approx. 50x higher), while esterified hydroperoxy derivatives of linoleic and arachidonic acids, or oxysterols, showed little activity. Non-esterified oxidized lipids were not good ligands. Although the most active compounds were also more electrophilic, the authors concluded that adduct formation was not involved, based on the fact that oxidized lipids could be transferred between LDL particles [141]. Recognition of oxPC by CD36 has been shown through the use of CD36-/- mice to be important in foam cell formation and atherosclerosis [142]. Although initial work focused largely on PC species, it was also shown that CD36 was instrumental in the recognition of oxPS on apoptotic cells, and contributed to their clearance.

Another category of cell surface receptors that have been investigated in the context of oxPL recognition is TLRs. Evidence that oxPLs could inhibit LPS signalling via TLRs vet also stimulate pro-inflammatory signalling through the same receptors has been accumulating almost in parallel since the end of the last century [89, 117, 118]. The pathways involved are complex and there are some conflicting findings in the literature, which may be explained by the exact oxPLs tested (often but not always oxPAPC was used as a model system) and cell type differences. For example, in some studies induction of IL-8 or adhesion molecule expression appeared to depend on activation of NFkB via the cannonical pathway [143], whereas as other studies found no evidence of NFkB dependence and in cell reporter systems expression of several TLRs was not found to be required for oxPAPC-stimulated IL-8 production [119, 144]. The need for additional soluble binding factors or membrane-associated proteins may also contribute to this discrepancy [143, 145]. Pro-inflammatory pathways involving TLR2-induced phosphorylation and activation of ERK and Jnk [145] or TLR-4 activation of the tyrosine kinase Syk and AP-1 in response to oxysterols [146] have also been reported. However, it is now becoming clear that oxPLs can be considered very much as damage-associated molecular patterns (DAMPs) from free radical damage during inflammation, and that they can be recognized by several TLRs with various effects [147]. The balance of pro-inflammatory versus anti-inflammatory signalling appears to be concentration dependent, with lower concentrations generally required for interference with LPS and higher levels needed to trigger positive effects [8].

Downstream of cell-surface receptors there is considerable cross-talk in the signalling pathways responsible for transducing the biological effects of oxPLs. MAPK pathway components such as ERK and Jnk have already been mentioned above. The mitogen-activated protein kinase phosphatase-1 (MKP-1), which mediates MCP-1 release and monocyte chemotactic activity, was also observed to be rapidly and transiently induced by oxPAPC in human aortic endothelial cells (HAECs) [148]. p38 MAPK activity can be enhanced in HUVECs by treatment of HUVECs with PE adducts with 4-HNE, 5-oxopentanal, or full-chain isoLGs, which also induces endoplasmic reticulum (ER) stress as demonstrated by expression of markers such as CHOP and BiP [55]. OxPAPC has also been found to upregulate the PI3K/Akt pathway in human aortic endothelial cells, leading to a time-dependent activation of eNOS [101].

## 4.6 Metabolism

Pathways for metabolism of oxPLs and their breakdown products are also very important in detoxification and protective responses, and various enzymes are known with specific or non-specific activity against oxidized lipids. The early products of lipid peroxidation, hydroperoxides, can be reduced to less reactive hydroxides by glutathione peroxidases (GPx), of which several isoforms exist [149, 150]. Free fatty acid hydroperoxides can be detoxified by the cellular form, GPx, but esterified lipids are not substrates. In contrast, GPx4, also known as phopholipid hydroperoxide glutathione peroxidase or PHGPx, can catalyze the reduction of phospholipid hydroperoxides, cholesteryl hydroperoxides and cholesteryl ester hydroperoxides [32, 151]. Of these compounds, the former are the best substrates [152]. Thioredoxin reductase (Trx) and selenoprotein P (SeIP) are other selenoen-zymes with lipid hydroperoxidase activity [153–155].

Some of the most damaging and reactive lipid peroxidation products are those containing aldehydes, but these compounds can be detoxified by AKR1 enzymes of the aldo-keto reductase (AKR) superfamily. For example, AKR1A and AKR1B showed POVPC reductase activity (generating hydroxyvaleroyl-PC), while the specific isoforms AKR 1B1 (aldose reductase, AR) and 1B10 were able to detoxify POVPE and free aldehydes containing 7 and 9 carbons [33, 34]. Spite et al also catalogued the activity of AKR1A/B families against a variety of PAPC oxidation products, as well as those of phosphatidylglycerols or phosphatidic acids. The action of AKRs in reduction of phospholipid-esterified and free aldehydes is mostly thought to be protective [34]; for example, increased atherosclerotic lesion size has been found in AKR<sup>-/-</sup>/apoE<sup>-/-</sup> mice maintained on high-fat diet, suggesting that the observed upregulation of this enzyme in atherosclerosis is beneficial. However, reduction of POVPC to the hydroxyvaleroyl form by aldose reductase (AR) appeared to increase production of a panel of pro-inflammatory cytokines (GM-CSF, TNF-α, MCP-1, IL-1β, IL-6, and IL-8) in POVPC-treated THP-1 cells, as it was prevented by the AR inhibitor, tolrestat, or in macrophages from AR-null mice [156]. Non-esterified aldehydes can also be detoxified by conjugation to glutathione by glutathione-S-transferases (GSTs) and subsequent redox metabolism, as reviewed by Alary [157].

In addition to oxidation or reduction, hydrolysis of phospholipid-estified oxidized or truncated fatty acids appears to be important in their turnover and detoxification. The enzyme lipoprotein-associated phospholipase  $A_2$  (Lp-PL  $A_2$ ), previously known as PAF acetyl hydroylase or PAF-AH, is present in high density lipoprotein (HDL) and normally inactivates the PAF but has also been found to catalyse the hydrolysis of modified fatty acids from oxPLs. In some conditions this may facilitate the removal of the resulting products, lysophosphatidylcholine and oxidized free fatty acids, although otherwise they also have proinflammatory actions [158]. Another HDL-associated enzyme with esterase activity is paraoxonase-1 (PON-1), which has been shown to hydrolyse oxidation products of palmitoyl-linoleoyl-PC and PAPC [159]. PON-1 is also thought to have peroxidase activity, and is sometimes described as an antioxidant enzyme; decreased levels have been observed in several diseases and are thought to contribute to decreased ability to metabolize oxPLs [160, 161].

It is important to recognize that many of the oxPLs and fatty acids are more polar than their parent lipids, which makes them more soluble in the aqueous cytosolic compartment and may facilitate their detoxification through interaction with cellular enzymes. Moreover, it has been reported that truncated phospholipids in plasma that are not sequestered within lipoproteins are rapidly cleared by the liver and kidney [162], which may involve uptake into cells via the phospholipid transporter TMEM30a [163].

## 4.7 Effects of Other Lipid Modifications

As mentioned in Sect. 4.2.2, chlorinated (chlorohydrins and chloro-fatty aldehydes) and nitrated (nitro-fatty acids) products of phospholipid modification can also be produced during inflammation, and are known to have biological effects. Early work on chlorinated fatty acids [60, 62] demonstrated toxicity either by necrosis, involving membrane damage or loss of ATP, or apoptosis, as indicated by caspase-3 activation, although these effects occurred at rather high concentrations. Similar effects were observed with phospholipid chlorohydrins [61]. Chlorinated lipids derived from sphingomyelin have been found to activate apoptotic signaling in dopaminergic PC12 neurons by the activation of caspase-3 [43]. Adverse effects on human red blood cells have also been reported, such as membrane deformation and lysis [164, 165]. Overall, chlorinated phospholipid products cause toxicity in several cell types in a concentration- and time-dependent manner. Interestingly, several proinflammatory effects have been reported. Dever et al. [166] reported that 1-stearoyl-2-oleoyl-PC (SOPC) chlorohydrin induced expression of adhesion molecule P-selectin on ECs in atherosclerotic mouse aorta, resulting in an increase in leukocyte adhesion, and increased production of ROS by splenocytes. Fatty acid chlorohydrins have been shown to induce mRNA expression of pro-inflammatory cytokine such as TNF- $\alpha$  and IL-1 $\beta$  [167]. Several inflammatory effects of  $\alpha$ -chloro fatty aldehydes have also been discovered. For example, 2-chlorohexadecanal induces neutrophil chemotaxis [42] and causes damage of myocardiac as shown by release of lactate dehydrogenase (LDH) from isolated perfused heart [168]. Moreover, 2-chlorohexadecanal can form adducts with primary amine-containing molecules such as ethanolamine glycerophospholipids, and results in the disruption of cell membranes [169]. In contrast to lyso-chlorohydrin, it has also been shown to upregulate mRNA and protein expression of COX-2 in ECs [170]. Overall, these actions could contribute to inflammatory responses in diseases where neutrophils and myeloperoxidase are up-regulated.

Comparatively little work has been carried out on nitrated lipids, but there is evidence that they affect cellular actions, such as nitrohydroxyeicosatrienoic acid, which has vasorelaxing effects. Nitrolinoleate has been demonstrated to have beneficial effects, for example by inhibiting thrombin-mediated aggregation of human platelets, calcium mobilization and P-selectin expression [171], suggesting that nitrolinoleate involved in inhibition of both platelet aggregation and adhesion. Subsequently, it was reported that nitrolinoleate reduced production of ROS and degranulation by neutrophils [172]. Thus it can be seen that unlike chlorinated fatty acids, where the emphasis has been on their role in inflammation, nitrated unsaturated lipids may have potent anti-inflammatory and beneficial properties, although as yet the mechanisms involved are not well established.

## 4.8 Analysis of Lipid Oxidation

Much of the research and knowledge described above has depended on the ability to identify products of lipid oxidation and measure their levels. Indeed, understanding of the chemical mechanisms of lipid peroxidation, chlorination and nitration has required the use of sophisticated analytical methods capable of providing structural information. In terms of methods available to determine the occurrence of lipid oxidation, from experiments in vitro to biological and clinical samples, the number is almost as great as the number of different products. The methods vary from simple and economical, which usually involve reaction with a reagent specific for a structural motif (e.g. carbonyls or hydroperoxides), to ones requiring advanced technology such as high performance liquid chromatography (HPLC) interfaced with tandem mass spectrometry (LC-MSMS). It is impossible to give a detailed review of all the methods within this chapter, so a brief overview of the most critical points is given, and the reader is referred to published reviews of the area [17, 18, 173, 174].

The initial products of lipid peroxidation are peroxyl radicals, which can only be detected using electron spin resonance (ESR) following reaction with radical spin traps to stabilize them [175]. Although the sensitivity and resolution of ESR spectrometers has advanced, this is still a method with limited ability to distinguish different lipid peroxyl radicals. Rearrangement of the double bonds following radical attack yield conjugated dienes that can be detected by absorbance at 234 nm, but this is an insensitive method, and only is suitable for hydroperoxide detection from pure lipid samples as many biological compounds absorb at this wavelength [173]. Probably the best colorimetric assay for lipid hydroperoxides is the ferrous oxidation of xylenol (FOX) assay [176], in which Fe<sup>2+</sup> is oxidized to Fe<sup>3+</sup> and forms a complex with xylenol orange at a  $\lambda_{max} \sim 560$  nm, although the sensitivity is variable and depends on which lipid hydroperoxide is present [177]. HPLC with chemiluminescence detection using luminol or isoluminol has the advantage of separating different lipid hydroperoxides, and is a relatively robust method [178, 179].

The best methods for detecting small lipid peroxidation fragmentation products depend on their nature, such at volatility, polarity and reactive chemical groups. Volatile fragments such as ethane and pentane can readily be analysed by gas chromatography (GC) with detection by flame ionization (FID) or MS [180], although the problems of collecting and condensing the samples means there is often large

variability between laboratories [181]. Many of the non-volatile compounds are aldehydes, and these are commonly detected using aldehyde-reactive reagents such as dinitrophenylhydrazine (DNPH), which yields a chromophore of  $\lambda_{max}$  360 nm, and cyclohexanedione (CHD), which forms fluorescent decahydroacridine derivatives with excitation at 380 nm and emission at 445 nm [182]. These reagents are not specific for identification any individual compound, and therefore identification is improved by HPLC separation of the sample components, and use of synthetic standards where possible. Another well known but much criticized assay is the thiobarbituric acid-reactive substances assay (TBARS assay) for MDA, which generates a chromophore/fluorophore with absorbance at 532 nm and emission at 553 nm. Under the conditions most commonly used it actually detects lipid hydroperoxides, which decompose to MDA in the presence of metal ions [183, 184]. As TBA can react with a variety of aldehydes to give similar chromophores, it is essential to separate the products by HPLC, and it is also important to understand that MDA can be derived from exogenous sources and mechanisms other than non-enzymatic lipid peroxidation. However, the TBARS assay has the advantage of being robust and less variable between laboratories [185].

The most informative, although technically challenging, methods use mass spectrometry method coupled either to GC or HPLC; this allows the compound to be identified by its mass-to-charge ratio (m/z) and fragmentation pattern as well as retention time. All mass spectrometric methods have the advantage that they do not require the presence of any functional group or reactivity; so long as the analyte is ionisable, a wide variety of modifications can be monitored. However, in LC-MS, reactivity with a specific probe can be used to improve ionization efficiency or aid identification of reactive aldehydes [186]. Similar approaches can be used to identify the presence of carbonyl-containing adducts of lipid peroxidation products with proteins [187].

GC-MS is most suitable for non-esterified lipid oxidation products, so phospholipids require hydrolysis to release modified fatty acids before derivatization, for example with trimethylsilylating agents, to obtain volatile analytes [18]. For many years, GC coupled to negative ion chemical ionization MS (GC-NICI-MS) was considered the gold standard for analysis of isoprostanes, and there is extensive research on the analysis of F2-isoprostanes (e.g. 8-epi PGF<sub>2α</sub> as markers of lipid peroxidation in disease [188, 189]). GC-MS can also be used for oxidized fatty acids, such HPETEs, HETEs, HPODEs and HODEs, and oxysterols [18, 190–192] and HNE [193]. α-Chlorohexadecanal derived from plasmalogens was detected by GC-MS in material from atherosclerotic vessels [194], and several nitrated fatty acids (e.g. 9/10-NO<sub>2</sub>-oleic acid), as well as other oxidized fatty acids, have been detected in plasma of healthy and disease human subjects using GC-MS/MS, as reviewed by Tsikas et al. [195].

For soft ionization mass spectrometry analysis, electrospray ionization (ESI) has become more popular, as it interfaces easily with HPLC, but matrix assisted laser desorption ionization (MALDI) has also been used. Phospholipids can be observed in either positive or negative ionization, depending on their charge state and counter ions; for example sphingomyelins (SMs), PCs and PEs are readily observed in+ve ion mode, while PSs and PGs are detected best in -ve ion mode, but acetate adducts of PC appear with negative ionization. The ionization modes for different phospholipids have been reviewed and explained by Domingues and Spickett [44, 196]. As MS detects both unmodified and oxidized lipids, with the latter distinguished by differences in m/z, the spectra are often very complex, and hence additional approaches to identifying oxidized species are useful. In the first instance, coupling to reverse phase HPLC separates oxidized lipids from the parent lipid owing to their increased polarity and earlier elution. An additional approach is to use targetted MS methods, where additional information from fragmenting the lipids is used to identify either specific lipid species, or classes. For example, the MS routine neutral loss can be used to find all lipid species that fragment with loss of 34 Da, which is typical of hydroperoxides, or 36 Da/38 Da, which is characteristic of chlorinated lipids [197, 198]. Specific analysis methods for individual lipids, involving multiple reaction monitoring (MRM) for parent ion and daughter ion couples (or transitions), are increasingly being used to identify and quantify oxidized products of a wide range of phospholipid types [199, 200]. These methods have much better sensitivity and selectivity for the analysis of individual oxidized lipids in complex biological samples.

Finally, as mentioned above, many aldehyde products derived from lipid peroxidation react readily with nucleophiles such as amines and thiols to form Schiff's bases or Michael adducts and hence can modify proteins (lipoxidation) [48], and there is increasing interest in detecting these products. Michael adducts, and Schiff base products from dialdehydes, have a free carbonyl group, and can therefore be detected as protein carbonyls by oxyblotting or spectrophotometric analysis with DNPH [201], although it is not possible to distinguish such carbonyls from those formed by oxidative deamination of lysine residues, for example by HOCl. These methods cannot with confidence identify the protein modified or the location of the modification; to do this requires digestion of the sample with proteases followed by sophisticated LC-MSMS techniques to sequence as many peptides as possible [48, 187]. Again, to improve the selectivity, there have been attempts to use targeted MS routines to identify lipoxidation, such as neutral loss of 138 or 156 Da for HNE adducts [202], or precursor scanning for m/z 184 to identify peptides containing PC adducts [51].

## 4.9 Oxidized Lipids and Therapeutics

As discussed above, oxidized lipids can have both deleterious and beneficial effects, depending on the specific compound and situation, so there are two aspects to therapy: protection against lipid oxidation and its products, and oxPLs as therapeutic agents. In terms of protection against lipid oxidation, there have been many studies with antioxidants, some of which appeared to show positive effects, but in clinical trials, clear evidence of a benefit has been scarce. This may be because the levels used were too low to alter the levels of oxidized lipids in the circulation (which often were not measured in the studies), although it appears to be difficult to alter

isoprostane levels in plasma, for example. Alternatively, low levels of certain oxidized lipids may be beneficial, so treatments that alter them could have unforeseen negative effects.

One approach to reducing inflammation involves the use of apolipoprotein (apo) A-I mimetic peptides (e.g. DF-4), which are thought to have anti-inflammatory effects by binding to oxidized lipids; their design is based on the general structure of apoA-1, which is the major apoprotein of HDL [203]. A study in vascular cells indicated that the affinity of mimetic peptides for oxPLs is higher than nonoxidized lipids [204]. A 14-residue peptide similar to DF-4, Oxpholipin 11D, has been shown to be able to bind to several oxidized phospholipids, including PEIPC, POVPC, PGPC, and 1-Palmitoyl-2-(5-keto-6-octene-dioyl)-PC (KOdiA-PC). It has been demonstrated that oxpholipin inhibits monocyte chemotactic factor induced by LDL in HAECs [205].

Another approach that has received considerable interest is the use of selective aldehyde scavengers to prevent the damaging effects of electrophilic lipids covalenting modifying proteins. Scavengers based on carnosine have been known for some years [206], and some synthetic compounds have been reported to have protective effects against HNE in neuronal cultured cells [207]. Another radical scavenging compound, Edaravone, was found to inhibit protein carbonyl formation and protect haemoglobin, but was not selective for lipid derived reactive aldehydes as it could also react with the physiological coenzyme pyridoxal [208]. Salicylamine and pyridoxamine are other aldehyde scavengers that have been used to prevent the formation of isoLG adducts on proteins; salicylamine has been found to improve memory function in a mouse model of Alzheimer's disease [209].

On the other hand, it is important to recognize a number of potentially beneficial and anti-inflammatory effects of certain oxPLs, although as yet there has been little attempt at translation therapeutic work. The interference of several oxidized PCs with PAMP recognition by TLR has been demonstrated in several studies to limit deleterious inflammation during inflammation in animal models [118, 119] improve barrier function and limit excessive inflammation in specific situations. Judicious use of appropriate oxidized PLs could be of benefit in treating sepsis, but requires extensive further investigation [210]. It is also known that the oxPAPC component PEIPC has a protective effect on pulmonary endothelial barrier function [120], which could be important in treating inflammatory lung diseases such acute respiratory distress syndrome (ARDS), but again any translational application of this knowledge appears to be a long way off.

## 4.10 Summary and Perspectives

A broad interpretation of the term "lipid oxidation" includes several types of modifications, such as peroxidation, nitration and chlorination; together, these generate a vast range of different lipid oxidation products, which makes the field extremely complex. Although lipid oxidation has often been regarded as deleterious and linked to a variety of inflammatory diseases, a full understanding of its outcomes requires appreciation of the differing effects of the different oxidation products. Moreover, lipid oxidation products often show concentration-dependent variation in their biological effects; for example, nanomolar to low micromolar levels may be able to induce cell signalling effects, whereas low to mid-micromolar levels tend to have more severe effects such as apoptosis or necrosis. In general, the levels of many individual oxidized lipid species in plasma and tissue are less than 1  $\mu$ M, but the combined effects of such levels are harder to determine, and understanding of the roles of oxidized lipids requires studies both of individual compounds and physiological mixtures of compounds. This is particularly important as some oxidized lipids have opposite effects to others, and interfere with their action.

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## Chapter 5 Protein Oxidation in Toxicology

Sandra Reeg and Tilman Grune

## 5.1 Introduction

Since many toxic xenobiotics (toxins) are able to generate reactive oxygen species (ROS), the toxicity and the pathologic processes of such compounds are likely to be also related to oxidative protein modifications. Physiologically, ROS are generated in low concentrations in the cell. For instance they are a by-product of the mitochondrial electron transport chain (mETC) [1]. However, if ROS generation is increased, for example through toxin exposure, damage of macromolecules and, therefore, proteins occurs. This leads to disturbance of the cellular metabolism. Oxidative protein modifications may impair signal transduction and the function of receptors, enzymes, antibodies and transport proteins. Moreover, secondary damage of other biomolecules can result from protein oxidation, e.g. oxidative damage of DNA repair enzymes may lead to accumulation of DNA damage.

To understand the relation between toxicity of some xenobiotics and protein oxidation, it is important to understand the basic mechanisms and the consequences of protein oxidation. Moreover this chapter shows the different types of oxidative protein modifications, as well as repair and degradation systems which may protect against cell damage. In addition, examples will be shown, demonstrating how protein oxidation and toxicology play together.

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## 5.2 Oxidative Stress and Protein Oxidation

Oxidative protein damage is the result of the reaction of ROS with proteins. The term ROS includes both, radicals and non-radical oxidants (Table 5.1) [2].

A wide range of endogenous systems are known to generate ROS in a highly controlled way. Enzymes, like nitric oxide synthases, NADPH oxidases, ribonucleotide reductase, prostaglandin synthase and lipoxygenases belong to these systems, as well as the mETC, responsible for cellular respiration, and the cytochrome P450 system (CYP 450). Additionally, many exogenous influences are also able to generate ROS, but in contrast, in a random and uncontrolled way. These exogenous sources include UV-radiation, gamma-radiation, metal ions, xenobiotics and drugs (Fig. 5.1).

ROS may interact and generate further reactive species, e.g. the reaction of  $O_2$  with nitric oxide (NO) leads to the formation of peroxynitrite (ONOO) (for review see [3]). In these interactions and decomposition reactions, numerous different reactive oxygen or nitrogen species (RNS) are formed – all of them having different reactivity, half life, diffusion distance, reaction and detoxification pathways. When speaking of ROS and their related species, in the following the generic term reactive species (RS) will be used.

To respond to the oxidant formation and to prevent the cell from extensive oxidative damage, there exists an antioxidative defense system, which scavenges oxidants and converts them into less reactive forms. Antioxidant enzymes, like superoxidedismutase (SOD), catalase and glutathione peroxidase (GPX) as well as glutathione (GSH) and the vitamins C and E are counted to these oxidant-scavenging systems (Fig. 5.1). In case the formation of ROS and their related species outweighs the defense mechanism against them, oxidative stress occurs (Fig. 5.1) and the oxidative damage of macromolecules (nucleic acids, lipids) and especially proteins increases. In this context it is important to mention that oxidants vary in their reactivity. For instance, HO<sup>•</sup> is a highly reactive oxidant, that reacts rapidly with targets after its generation. Oxidants which are less reactive than HO<sup>•</sup> react much slower with their targets and the damage they induce is more specific. However, these RS

Radicals		Non-radical oxidants	
Superoxide	O2	Singlet oxygen	$O_2^1 \Delta g$
Hydroxyl	OH.	Hydrogen peroxide	H <sub>2</sub> O <sub>2</sub>
Hydroperoxyl	HO <sub>2</sub> .	Ozone	O <sub>3</sub>
Peroxyl	RO <sub>2</sub> ·	Hypochlorous acid	HOCl
Alkoxyl	RO•	Hypobromous acid	HOBr
Carbonate	CO3-	Peroxynitrite	ONO0-
Carbon dioxide	CO2-	Peroxynitrous acid	ONOOH
		Nitrosoperoxycarbonate	ONOOCO2-

Table 5.1 Reactive oxygen species [2]



Fig. 5.1 Oxidative stress. The imbalance between ROS generation and oxidant-scavenging via antioxidant defense systems, defined as oxidative stress. ROS are generated by endogenous or exogenous sources. *ROS* reactive oxygen species, *CYP 450* cytochrome P450 system, *SOD* super-oxide dismutase, *GSH* glutathione, *GPX* glutathione peroxidase

can diffuse considerable distances and, therefore, the damage is not as site-specific as damage from highly reactive oxidants.

Proteins are one of the main targets for oxidative modifications. On the one hand because of their abundance in living organisms, on the other hand because of the high rate constants for reactions of radicals with proteins compared with other macromolecules [4]. Oxidative damage of proteins results in a partial unfolding and a loss of function. Since the most oxidative protein modifications are irreversible, there are only a small number of enzymes which are able to repair a few specific modifications. In most cases, the only way to protect against accumulation of damaged proteins is the degradation of oxidized proteins. However, in case of overloading the degradation pathways due to increased RS generation and protein oxidation, oxidized proteins accumulate and tend to aggregate. These protein aggregates can no longer be removed by cellular degradation systems. Moreover, the excessive formation of protein aggregates leads to inhibition of the removal system, what results in further accumulation and aggregation of oxidized proteins. Finally, protein oxidation and aggregation can lead to apoptotic cell death (Fig. 5.2) [6–8].



**Fig. 5.2** Protein oxidation. Formation of ROS and related species leads to damage of macromolecules. Besides lipids and DNA, proteins are major targets for oxidation. To maintain the cellular protein homeostasis, oxidized proteins may either be repaired or degraded. Otherwise they accumulate and form non-degradable protein aggregates. Protein aggregates may inhibit the degradation system. They adversely affect the whole cell and may lead to cell death. *RS* reactive species, *MSR* methionine sulfoxide reductase, *Txr/TxR* thioredoxin/thioredoxin reductase system, *PDI* protein disulfide isomerase (according to Davies [5])

## 5.3 The Chemistry of Protein Oxidation

Radicals and non-radical oxidants are able to react with a wide variety of amino acids, peptides and proteins. These reactions include hydrogen abstraction, electron transfer, addition, fragmentation, dimerization, disproportionation and substitution. Both, the protein backbone and the different amino acid side-chain residues may be damaged by oxidants, the severity of the damage depends on the kind of the oxidant.

## 5.3.1 Backbone Damage

During oxidative stress, the protein backbones are rapidly attacked by radicals, whereas attacks by non-radical oxidants are often slow and without an effect on the protein backbone. First, the reaction with radicals leads to the abstraction of the



**Fig. 5.3** Protein backbone damage. Reactions of radicals with the protein backbone may lead either to protein cross-linkage or to backbone fragmentation (modified from Davies [4])

hydrogen atom from the  $\alpha$ -carbon, resulting in a stabilized carbon-centered radical (Fig. 5.3 (1)). In the absence of O<sub>2</sub>, this radical reacts with another carbon-centered radical, resulting in production of carbon-carbon cross-linked derivates. In contrast, under aerobic conditions, the carbon-centered radical undergoes a fast addition of O<sub>2</sub>, by which a peroxyl radical is formed (Fig. 5.3 (2)) [9]. There are two fates for such a peroxyl radical. On the one hand, the formation of an imine through an elimination reaction, in which HO<sub>2</sub> is released from the peroxyl radical. A following hydrolysis leads to fragmentation of the protein backbone (Fig. 5.3 (3)). On the

other hand, the peroxyl radical can abstract a hydrogen atom from another species, resulting in hydroperoxide formation. The reduction of this hydroperoxide to an alkoxyl-radical, in a further reaction, leads also to protein damage through backbone fragmentation (Fig. 5.3 (4)) [10].

## 5.3.2 Side-Chain Damage

Oxidative damage of amino acid side-chains is a more complex mechanism than the protein backbone damage. There are 20 different amino acid residues. Oxidation of these residues leads to formation of several oxidation products.

#### 5.3.2.1 Aliphatic Amino Acid Residues

Formation of carbon-centered radicals through hydrogen abstraction constitutes the major reaction of radicals with aliphatic residues. Carbon-centered radicals can dimerize with other radicals, but in presence of O<sub>2</sub> and in situations with a low radical flux this reaction is a very rare event. Furthermore the carbon-centered radicals can be repaired by thiols (RSH) under formation of thiyl radicals (RS<sup>•</sup>) [11]. However, the major and most important pathway under aerobic conditions is the reaction with O<sub>2</sub>, which results in the formation of peroxyl radicals [9]. In further radical-radical reactions peroxyl radicals generate either alcohols and carbonyls or alternatively alkoxyl radicals, what again leads to generation of alcohols and carbonyls after hydrogen atom abstraction and fragmentation reactions. These radicalradical reactions constitute a limited process, due to the low radical flux and the high number of other reaction partners for the peroxyl radicals. For example hydrogen atom abstraction from a reaction partner (DNA, lipids, proteins) leads to formation of a hydroperoxide and the generation of a new radical, harboring the possibility of an oxidation chain reaction. In addition, decomposition of these hydroperoxides also results in radical, alcohol and carbonyl compound generation [4].

#### 5.3.2.2 Aromatic Amino Acid Residues

Aromatic amino acid residues are very susceptible to oxidation by several forms of ROS. The major reaction of oxidants with aromatic residues is the addition. However, substitution reactions via a heteroatom substituent (e.g. HOCl) and electron transfer reactions through powerful oxidants are also known.

The reaction of oxidants with tyrosine may lead to tyrosine phenoxyl radical formation. Tyrosine phenoxyl radicals may dimerize under formation of dityrosine. This reaction represents a possibility for intra- and intermolecular cross-linkage in proteins and may lead to protein aggregation. Reaction of tyrosine with RNS may lead to formation of nitrated products (e.g. 3-nitrotyrosine). Chlorinated products



Fig. 5.4 Products of cysteine and methionine oxidation

(e.g. 3-chlorotyrosine) result from reactions of chlorinating species. Further examples for products of tyrosine oxidation are the unstable 3,4-dihydroxypheylalanine (DOPA), 3-bromotyrosine and hydroxyperoxides.

Other amino acids, next to tyrosine, that contain an aromatic ring in their side chain are tryptophan, phenylalanine and histidine. Tryptophan residue oxidation leads to kynurenine, N-formylkynurenine, 5- and 7-hydroxytryptophan formation. Oxidation of phenylalanine gives rise to 2- and 3-hydroxyphenylalanine and tyrosine. A possible product of histidine oxidation is 2-oxohistidine.

#### 5.3.2.3 Sulfur-Containing Amino Acid Residues

Sulfur centers are a sensitive target for oxidation. Therefore, cysteine and methionine residues display the major sites for oxidation in proteins (Fig. 5.4).

A wide range of oxidants may react with cysteine residues. Radicals often lead to the formation of thiyl radicals (RS<sup>•</sup>). These radicals can give rise to disulfides via dimerization (cystine) or peroxyl radicals through reaction with  $O_2$ . The fate of these peroxyl radicals is the formation of oxyacids (RSO<sub>2</sub>H, RSO<sub>3</sub>H), but this chemistry is very complex and not completely understood in proteins. In addition, thiyl radicals may also react with other species, resulting in a wide range of mixed dimers. Reaction with two-electron oxidants in contrast gives rise to adduct species, which are short-lived and undergo fast hydrolysis. This results in formation of oxyacids or, after reaction with other thiol groups, in cystine or mixed disulfide formation.

Methionine residues in proteins are major targets for many oxidants and methionine sulfoxides (MeSOXs) are the main products of these oxidation reactions. Further oxidation of these species leads to the formation of sulfones. However, this reaction takes place only to a limited extent. MeSOXs are generated in two stereoisomers, the S- and R-forms. The ratio of these two stereoisomers varies between different oxidants and different protein structures.

#### 5.3.2.4 Carbonyl Group Formation

Carbonyl groups (aldehydes and ketones) are formed directly via oxidation of proline, arginine, lysine, threonine and other amino acid residues, as well as in oxidative backbone fragmentation. In addition, secondary reactions of cysteine, histidine and lysine residues may also lead to formation of protein carbonyls. These residues may react with bi-functional aldehydes, generated in lipid peroxidation, and carbonyl derivates (ketoamines, ketoaldehydes), resulting from of reactions of reducing sugars (ketoamines, ketoaldehydes) or from glycation and glycoxidation reactions. Thereby the possibility for formation of advanced lipoxidation/glycation endproducts (ALEs/AGEs) exists [12].

Because protein carbonyls are chemically stable, they are an extensively used marker for protein oxidation. The principle of protein carbonyl measurement frequently used is the carbonyl reaction with 2,4-dinitrophenyl hydrazine (DNPH), forming a hydrazone (DNP), which has an absorbance around 360 nm. Often these hydrazones are detected with specific antibodies against DNP, so immunoblot and ELISA display the most widely used techniques.

## 5.4 Consequences of Protein Oxidation

Oxidative damage of proteins results in a loss of function either by unfolding or direct modification of a protein domain which is responsible for their function. In most cases oxidative damage of proteins results in a partial unfolding of proteins. Due to unfolding, hydrophobic amino acids which are normally hidden in the inside of a native protein are moved to the outside and as a result surface hydrophobicity of the oxidative damaged protein is increased [13, 14]. Because of this increased hydrophobicity, in a hydrophilic environment proteins tend to interact with each other, forming hydrophobic bonds. This results in the formation of protein aggregates.

Besides these hydrophobic aggregation reactions, a range of other dimerization and aggregation reactions are known:

- · Interaction of two carbon-centered radicals
- · Disulfide formation after oxidation of cysteine
- Interaction of protein carbonyls with a lysine or an arginine residue forming Schiff's bases

#### 5 Protein Oxidation in Toxicology

- · Reaction of two tyrosine radicals, resulting in dityrosine formation
- · Reaction of aldehydes, resulting from lipid peroxidation, with lysine residues

Protein aggregates are oligomeric complexes of unfolded proteins which normally do not interact with each other. They are insoluble and non-degradable. Additionally, protein aggregates inhibit the proteasome, resulting in further accumulation and aggregation of oxidized proteins [15, 16]. Protein aggregates may be oxidized and modified by secondary reactions. It seems that the aggregates react further with other cellular components, e.g. lipid peroxidation products such as 4-hydroxynonenal (HNE) and malondialdehyde (MDA) leading to the formation of highly cross-linked material, such as lipofuscin [17]. This highly cross-linked material is also non-degradable by the proteasomal system. Finally, protein aggregates can cause a number of cellular reactions, including apoptotic cell death [8] and the occurrence of protein aggregates is associated with a number of diseases and the aging process (for review see [18]).

Next to protein aggregation which often results from side chain damage, fragmentation of proteins displays a further consequence of protein oxidation. Like mentioned above, fragmentation results from oxidative damage of the protein backbone.

Both, oxidative damage of side chains and of the protein backbone may lead to further reactions and the formation of further reactive species in proteins, for example hydroperoxides and peroxides. Consequently, chain reactions can result from protein oxidation (i.e. one initiating event leads to oxidation of multiple sites) [19]. Nevertheless, the chain reaction is not just limited to the protein with the initial oxidation event, it can be transferred to other macromolecules, e.g. DNA or other proteins [20, 21].

## 5.5 Repair and Degradation of Oxidatively Damaged Proteins

To protect the cell from the comprehensive consequences resulting from protein oxidation it is necessary for the cell to remove these oxidative protein modifications by repair or degradation (Fig. 5.2).

## 5.5.1 Repair Systems

A well described class of proteins which is responsible for the refolding of misfolded and damaged proteins is the class of heat shock proteins. With their chaperone function, they can protect the cell either by holding or by refolding their substrate proteins in their native conformation. However, most of the above mentioned protein oxidation products cannot be repaired by cellular repair mechanisms. Thus, these damaged proteins have to be degraded by proteases. Exclusively disulfide bonds and MeSOXs may be repaired by methionine sulfoxide reductases (MSRs), protein disulfide isomerases (PDIs) and the thioredoxin/thioredoxin reductase system.

#### 5.5.1.1 Repair of Disulfides

Thioredoxins (Trx) are able to repair disulfides (S-S bond), by reducing them to thiols (–SH groups). The enzyme Trx has a Cys-Gly-Pro-Cys motif in its active site, the cysteine residues are essential for the reduction. Disulfide reduction of the protein leads to disulfide formation between these cysteine residues. Afterwards the thioredoxin reductase (TrxR) recycles this Trx disulfide using NADPH [22]. A further enzyme class, which is involved in repair of disulfides are the PDIs. PDIs belong to the so-called thioredoxin superfamily. Similar to Trx, PDIs have two cysteine residues in their active centers. For reduction of a disulfide, an intramolecular disulfide is formed which can be reduced by using GSH (reviewed in [23]).

#### 5.5.1.2 Repair of Methionine Sulfoxides

MSRs play a key role in repair of MeSOXs (Fig. 5.5). As mentioned before, there are two stereoisomers of MeSOXs, the S- and the R-stereoisomer. The methionine sulfoxide reductases A (MsrAs) are specific for the S-isomers, the methionine



**Fig. 5.5** Repair of methionine sulfoxides by methionine sulfoxide reductase. Oxidation of the methionine residue leads to formation of methionine sulfoxides. The methionine sulfoxide reductase (MSR) is able to repair this oxidative protein modification being oxidized itself. The thioredoxin/ thioredoxin reductase system may reduce the MSR (modified from Hoshi and Heinemann [24])

sulfoxide reductases B (MsrBs) are specific for the R-isomers. Most of the MSRs have three specific cysteine residues in their active sites. During reduction of MeSOX to methionine, one of the cysteine residues (catalytic cysteine) is oxidized, whereas the other cysteine residues (recycling cysteines) are together with the Txr/TxrR system involved in the re-reduction of the catalytic cysteine [25]. Some animal MsrBs (SelR) have a selenocysteine in their active site, which plays the same role as the catalytic cysteine [26].

## 5.5.2 Degradation Systems

Since oxidative damage of proteins adversely affects the whole cell and can also cause cell death, existence of a fast and effective degradation system is important. The cell is equipped with a variety of proteases, for example calpaines, lysosomale cathepsines, mitochondrial proteases and caspases. Though, the predominant role in the degradation of oxidized proteins takes over the proteasomal system and especially the 20S proteasome [27].

#### 5.5.2.1 The Proteasomal System

The evolutionary high conserved proteasomal system is the most important protein degradation systems in the cytosol. In contrast to other degradation systems, proteasomal removal is a highly regulated process. The 20S proteasome represents the central part of the proteasomal system. It is a 700 kDa, barrel shaped multi-enzymecomplex. The 20S proteasome is referred as "core proteasome", because it is also part of other proteasomal forms. The 20S core is formed of four homologous rings, each of them is composed of seven subunits. The two inner rings, shaped by the  $\beta$ -subunits ( $\beta$ 1- $\beta$ 7), form the catalytic center of the 20S proteasome (Fig. 5.6). Three of these  $\beta$ -subunits show a proteolytic activity.  $\beta$ 1 possesses a peptidylglutamyl-peptide-hydrolyzing activity,  $\beta 2$  a trypsin-like activity and  $\beta 5$  a chymotrypsin-like activity. The two outer rings, consisting of the  $\alpha$ -subunits ( $\alpha 1-\alpha 7$ ), function as a "gate" for the catalytic center of the proteasome [28]. These subunits are also responsible for recognition and access of the substrates. Binding of a damaged and unfolded protein leads to a conformational change of the  $\alpha$ -subunits, the gate-opening and thus to the activation of the 20S proteasome. Consequently, the regulation of substrate entry is the main control mechanism for the activity of the proteasome [29].

Binding of regulators to the  $\alpha$ -subunits of the 20S proteasome, also results in a conformational change of the  $\alpha$ -subunits and a further opening of the "gate", which results in a higher activity of the proteasome and a change in substrate specificity. One of the most important regulators is the 19S regulator, also known as PA700. Binding of the 19S regulator at one or both sites of the 20S proteasome leads to the formation of the 26S proteasome. The 26S proteasome has a molecular mass of



**Fig. 5.6** The proteasomal system in degradation of oxidized proteins. In case of oxidative stress the 26S proteasome is dissociated in the 19S regulators and the 20S core proteasome. Hsp70 proteins keep the 19S regulators in their native conformation until re-association. The 20S proteasome recognizes hydrophobic patches of (partially) unfolded oxidized proteins and degrades them. The resulting amino acids are available for synthesis of new proteins and the maintenance of protein homeostasis. An increased formation of oxidized proteins and an overloaded proteasomal degradation leads to protein aggregation. Protein aggregates may inhibit the proteasomal system, resulting in further aggregation of oxidized proteins

about 2 MDa [30]. In contrast to the 20S proteasome, the 26S proteasomal degradation of proteins is an ATP- and ubiquitin-dependent process. The 19S regulator is composed of 'base' and 'lid' and consists of 17 monomers (Fig. 5.6) [31]. Six of these 17 monomers, the Rpt-subunits, show an ATPase activity by which the gate opening and the unfolding of substrate proteins is enabled. The other monomers are called Rpn-subunits. They are responsible for the recognition of polyubiquitinated proteins and afterwards their deubiquitination.

The products of proteasomal degradation, whether by the 20S or the 26S proteasome, have a length between 2 and 30 amino acids and are available for new protein synthesis and thus regulation of the cellular protein homeostasis [32].

There is increasing evidence that the 20S proteasome takes over the main role in the degradation of oxidized proteins. It was often shown that oxidized proteins are degraded in an ATP- and ubiquitin-independent way [5, 27, 33–35]. Moreover, only the 20S proteasome is able to recognize unfolded proteins. Protein oxidation leads

to a partial unfolding of the proteins by which, under physiological conditions internal, hydrophobic structures come to the surface. The 20S proteasome recognizes these hydrophobic structures of the oxidized proteins (Fig. 5.6) [14, 33]. This leads to the conformational changes of the  $\alpha$ -subunits, the gate opening and therefore to the 'activation' of the 20S proteasome. Due to the high surface hydrophobicity of oxidized proteins no prior ubiquitination and no ATP-dependent protein unfolding of the substrate proteins is necessary.

In addition the 20S proteasome seems to be more resistant towards oxidative stress than the 26S proteasome [36, 37] and there is evidence that the 26S proteasome dissociates to the 20S proteasome and the 19S regulators during oxidative stress. The involvement of Hsp70 in this process was shown. Hsp70 binds 19S and keeps it in its active form until re-association to the 26S proteasome [38]. It is believed that the dissociation should increase the amount of 20S proteasome to improve the degradation of oxidized proteins (Fig. 5.6).

In case of prolonged and/or severe oxidative stress, there is an accumulation of oxidized proteins and aggregation is increased. Protein aggregates are able to inhibit the 20S proteasome, thus the proteasomal degradation of oxidized proteins is slowed down or completely stopped and consequently more protein aggregates are formed (Fig. 5.6) [15–17, 39, 40]. Finally, the balance between oxidative protein damage and removal of oxidized proteins is disturbed.

#### 5.5.2.2 The Lysosomal System

Lysosomes are acidic vesicles (pH 4–5), containing various degrading enzymes, like phosphatases, polysaccharidases, oligosaccharidases lipid-hydrolyzing enzymes and proteases. Thus the lysosomes have an important function in the degradation of macromolecules. The cathepsins, a protease family consisting of 16 members, are responsible for lysosomal protein degradation.

Three mechanism of lysosomal degradation are known, phagocytosis, endocytosis and autophagy. In this chapter, focus should be placed on autophagy. Autophagy is differentiated in macroautophagy, microautophagy and chaperone-mediated autophagy [41]. Macroautophagy is the inclusion of organelles and soluble proteins in a double-membrane vesicle, forming the so called autophagosome [42]. After fusion of the autophagosome and the lysosome, degradation of the content is performed through lysosomal degrading enzymes. Microautophagy describes a process in which cytosolic components are directly taken up into the lysosome. Cytosolic proteins, containing a KFERQpentapeptide as targeting motif, may be degraded via chaperone-mediated autophagy (CMA). The chaperone Hsc70 is able to recognize these proteins via the targeting motif and the co-chaperones CHIP and BAG3 mediate ubiquitination and transport to the lysosomal membrane, where the substrate-chaperoneco-chaperone-complex interacts with the LAMP-2A receptor. With assistance of lysosomal Hsc70 the substrate protein is translocated into the lysosomal lumen where it may be degraded by lysosomal proteases [43, 44].

The degradation of proteins, included into lysosomal organelles, is in contrast to the proteasomal degradation a less selective process. Therefore, the contribution of the lysosomal system in degradation of oxidized proteins is limited and should be considered to be more random. Although CMA has more substrate-specificity than macroautophagy and microautophagy, the role of CMA in selective degradation of oxidized proteins is at the moment only hypothetical.

# 5.6 Reactive Species and Protein Oxidation: Roles in Toxicology

The main reason by which toxins lead to protein oxidation is their ability to generate RS, including ROS and RNS. As a mechanism of toxicity, toxin-induced oxidative stress is implicated in numerous tissues and organs, including liver, kidney, cardio-vascular and nervous systems. There are several mechanisms, leading to generation of RS and protein oxidation due to toxin action (Fig. 5.7) [2].



Fig. 5.7 Toxin actions leading to formation of reactive species. *RS* reactive species, *CYP* 450 Cytochrome P450 system, *GST* Glutathione-S-transferase, *GSH* Glutathione

## 5.6.1 Toxins Might Be Reactive Species

A toxin itself can be a RS, for example the air pollutant nitrogen dioxide (NO<sub>2</sub><sup>•</sup>) (Fig. 5.7 (1)). In large cities the vehicle exhaust emissions are the main source of NO<sub>2</sub><sup>•</sup>, but it is also produced by gas cookers, coal fires, wood burning stoves and cigarette smoking. NO<sub>2</sub><sup>•</sup> can cause lipid peroxidation by hydrogen atom abstraction or addition reactions, thereby carbon-centered radicals are formed. Further reaction with O<sub>2</sub> gives rise to peroxyl radicals [45]. Additionally, protein oxidation as a consequence was also shown. NO<sub>2</sub><sup>•</sup> reacts with cysteine and tyrosine residues, leading to nitrotyrosine formation [46]. NO<sub>2</sub><sup>•</sup> exposure leads to lung damage due to direct injury to cells and due to impairment of the elastase-dependent hydrolysis of lung elastin.

## 5.6.2 Toxins Are Metabolized to Reactive Species

In most cases toxins themselves have no oxidizing ability, but the ability arises in their metabolism. For instance, a toxin such as Carbon tetrachloride (CCl<sub>4</sub>), may be metabolized to a RS after intake (Fig. 5.7 (2)). CCl<sub>4</sub> is used in industry as an organic solvent. Earlier it was also used as a dry-cleaning agent, but because of its hepato-toxicity it was banned in many countries. The main organ which is affected by CCl<sub>4</sub> is the liver, but toxicity in other organs, such as kidney, is also known. CCl<sub>4</sub> is metabolized to trichloromethyl radical (CCl<sub>3</sub>) in the ER by the cytochrom P450 system [47–49]. CCl<sub>3</sub> might directly attack biological molecules. Moreover, reaction of CCl<sub>3</sub> with O<sub>2</sub> leads to formation of the trichloromethyl peroxidation is regarded as the main reason for the CCl<sub>4</sub>-induced liver toxicity [51]. Although protein oxidation is increased after exposure to CCl<sub>4</sub> [52], it is unclear to what extent the oxidative damage of proteins contributes to CCl<sub>4</sub> toxicity.

## 5.6.3 Reactive Species Are Generated in Redox Cycling of Toxins

Some toxins, e.g. paraquat, undergo a redox cycling after intake, in which RS are produced (Fig. 5.7 (3)). The bipyridyl herbicide paraquat is particularly toxic to the lung, because of its accumulation in lung cell types [53]. After intake, paraquat is reduced mainly by microsomal NADPH-cytochrome P450 reductase (CPR), resulting in the formation of a paraquat radical [54–56]. For re-oxidation to paraquat, the radical reacts with O<sub>2</sub>, resulting in O<sub>2</sub><sup>-</sup>release [57, 58]. This O<sub>2</sub><sup>-</sup>formation has a crucial role in paraquat-induced lung toxicity (see Review [59]). O<sub>2</sub><sup>-</sup>gives rise to H<sub>2</sub>O<sub>2</sub> via reaction of superoxide dismutase. In the Fenton reaction and the Haber-Weiss reaction, the highly reactive OH<sup>•</sup> is formed. A broad spectrum of potentially toxic reactions, including oxidative damage of lipids, DNA and proteins may be induced by these RS (Fig. 5.8). In vivo studies have shown that paraquat causes lung


**Fig. 5.8** Paraquat redox cycling and toxicity. NADPH-cytochrome P450 reductase reduces paraquat, leading to paraquat radical formation. Re-oxidation to paraquat gives rise to  $O_2^{-}$ . Superoxide dismutase can detoxify  $O_2^{-}$  by generating  $H_2O_2$ . OH may be produced by Haber-Weiss and Fenton reaction. OH causes oxidation of lipids, DNA and proteins, contributing to the paraquat toxicity. *CPR* NADPH-cytochrome P450 reductase, *SOD* superoxide reductase, *HWR* Haber-Weiss reaction, *FR* Fenton reaction (modified from Bus and Gibson [59])

protein oxidation by carbonyl group formation [60, 61]. However, the toxicity of paraquat is not only caused by generation of RS, but also by NADPH depletion.

#### 5.6.4 Toxins Interfere with the Antioxidant Defense System

The interference between toxins and the antioxidant system can result in increased RS generation and oxidative damage of macromolecules (Fig. 5.7 (4)), e.g. metabolizing of toxins requires a high quantity of GSH and in consequence, not sufficient amounts of GSH are available for oxidant scavenging. Paracetamol (called Acetaminophen in the USA) as an example for this reaction mechanism, in overdoses damages liver and kidney. It is metabolized to the reactive metabolite N-acetyl-p-benzoquinone imine (NABQI) in a CYP 450-dependent process [62]. During detoxification, the NABQI is conjugated with GSH, either spontaneously or catalyzed by Glutathione-S-transferase (GST). Consequently, after a toxic dose, the cellular stock of GSH is depleted [63, 64]. This may lead to oxidative stress, protein oxidation and lipid peroxidation because of a failure in the antioxidative defense system (e.g. glutathion peroxidase). However, it is not known to which extent this process contributes to hepatotoxicity of paracetamol. There are several other paracetamol-mediated mechanisms which may also be an explanation for the toxicity,

e.g. the Kupffer cell activation [65] and the formation of protein adducts after GSH depletion, which results in loss of function of important cellular proteins (e.g. PDI, glutamine synthetase, Ca<sup>2+</sup>-ATPase of the ER, mitochondrial proteins) [64]. For more detailed information on paracetamol hepatotoxicity see review [66].

#### 5.6.5 Toxins Increase the Endogenous RS generation

Some toxins may stimulate endogenous RS generating systems, such as mETC and CYP 450 (Fig. 5.7 (5)). Both, mETC and CYP 450 are very good ROS-producers because they use  $O_2$  either for cellular energy generation (in form of ATP) or for detoxifying of damaging agents. Although, these processes are highly regulated, the normal reaction cycle may be disturbed and  $O_2$ <sup>-</sup> and other RS are formed. These species may be converted into highly reactive radicals, leading to oxidative damage of proteins, lipids and DNA.

#### 5.6.5.1 Mitochondrial Electron Transport Chain

A wide range of mechanisms are known, leading to mETC-mediated increase in ROS generation via toxin action, e.g. the complex I inhibition. Complex I (also called NADH:ubiquinone oxidoreductase) catalyzes the transfer of electrons from NADH to coenzyme Q10, thereby helping to establish the electrochemical potential which is necessary for ATP production. Thus, toxin-mediated slowing down of complex I leads to decreased ATP production and because of the electron storage to increased O<sub>2</sub><sup>•</sup>-generation. The neurotoxin 1-methyl-4-phenyl-1,2,3,6tetrahydropyridine (MPTP) is a precursor of the complex I-inhibitor 1-methyl-4phenylpyridinium (MPP<sup>+</sup>). MPTP is a byproduct produced during synthesis of desmethylprodine, a lipophilic synthetic opioid drug, which can overcome the blood-brain-barrier. The metabolite kills dopamine-producing neurons of the substantia nigra what causes a movement disorder, similar to Parkinson's disease. Thus, it is believed that complex I dysfunction and oxidative damage are also involved in the pathogenesis of Parkinson's disease [67, 68].

The lipid-lowering agent clofibrate has another mechanism to increase the mitochondrial ROS production. Exposure results in decreased mitochondrial membrane potential and induced mitochondrial permeability transition. The contribution of ROS production and oxidative stress to hepatotoxicity of clofibrate has been shown [69].

#### 5.6.5.2 Cytochrom P450 System

The Cytochrome P450 enzymes (CYPs) are important in the detoxification metabolism of xenobiotic agents (phase I metabolism). For oxidation of their target compounds and the cofactor NADPH, they utilize O<sub>2</sub>. ROS are produced via uncoupling of the normal catalytic cycle of CYPs [70, 71]. The CYPs are heme proteins, meaning that they

contain the non-protein component iron bound to a porphyrine. This iron can exist in different oxidation states, either in the ferrous  $(Fe^{2+})$  or in the ferric  $(Fe^{3+})$  state. Before binding of the target substrate, the CYP is in its  $Fe^{3+}$ -state. After binding, a first electron is passed to the iron of CYP ( $Fe^{2+}$ -state) and  $O_2$  binds to the CYP. The electron can move and reduce the oxygen, generating an  $O_2$  bound to the iron of CYP ( $Fe^{3+}$ -state).

$$Fe^{2+} + O_2 \rightarrow Fe^{3+} + O_2^{\bullet}$$

In this step it is possible that the  $O_2^{-i}$  is released from the CYP. Otherwise a second electron is added to the CYP, resulting again in the reduction of heme bound to  $O_2^{-i}$  (Fe<sup>2+</sup> state). Movement of the electron leads to further reduction of  $O_2^{-i}$  generating an iron-bound  $O_2^{-2}$  (Fe<sup>3+</sup> state).

$$\operatorname{Fe}^{2+} + \operatorname{O}_{2}^{\bullet-} \rightarrow \operatorname{Fe}^{3+} + \operatorname{O}_{2}^{2-}$$

Now the CYP can transfer one oxygen atom to the bound substrate, the other oxygen atom becomes  $H_2O$ . After that the metabolized substrate is released from the enzyme.

$$RH + O_2 + 2H^+ + 2e^- \rightarrow ROH + H_2O_2$$

Protons and electrons are supplied by a NADPH-dependent FAD and FMNcontaining reductases, e.g. NADPH-Cytochrome P450 reductase (CPR). However, if the cycle uncouples, the CYP-bound  $O_2^{2-}$  (Fe<sup>3+</sup> state) can also break down and binding of two hydrogen atoms leading to generation of  $H_2O_2$ . (reviewed in [72]).

One special form of the CYPs is the cytochrome P450 2E1 (CYP2E1). Besides the alcohol dehydrogenase, it is involved in alcohol metabolism in the liver (called the microsomal ethanol oxidizing system). CYP2E1 generates ROS more readily than the other 57 different CYPs known in humans. Alcohol consumption will increase the CYP2E1 concentration. For example, it has been shown that the daily intake of 40 g alcohol, after 4 weeks results in a five-fold increase in CYP2E1 levels [73]. Additionally, it was shown that this increased expression of CYP2E1 is correlated with liver injury [74, 75]. Besides ethanol, many other xenobiotics are substrates for CYP2E1. Therefore toxin-induced CYP2E1-mediated ROS production is not only a specific effect of ethanol.

#### 5.6.6 Toxins Provoking the Immune Response

Another reason why toxins lead to ROS generation displays the binding of toxins to biomolecules, creating a new antigen, and thus provoking the immune response. This leads to RS generation (Fig. 5.7 (6)). Macrophages, neutrophils and dendritic cells, members of the unspecific innate immune system, produce NO and ROS during antigen recognition and activation of the immune response.

## 5.7 Conclusion

As mentioned above, there are several toxin actions, which lead to the generation of RS and to oxidative damage of macromolecules including proteins. ROS and their related species may be generated in the metabolism of toxins, e.g. when they are detoxified. Other toxins may stimulate endogenous systems, like the mETC or the CYP 450. CYP450 is an important enzyme system, which is involved in the detoxification metabolism of many xenobiotics. Therefore, and because it utilizes  $O_2$ , it represents a very good ROS producer. A further mechanism of toxin action, which leads to increased RS generation, is the impairment of the antioxidant system. The detoxification of toxins often results in depletion of oxidant-scavenging molecules, such as GSH.

Toxins often act not only via one but via multiple mechanisms. A good example represents cigarette smoke, a complex mixture of toxic agents. It contains free radicals, such as NO<sup>•</sup> and NO<sub>2</sub><sup>•</sup>, the GSH-depleting acrolein, and hydroquinones/quinones, which undergo redox cycling. Cigarette smoke can activate alveolar macrophages to produce  $O_2^{--}$ ,  $H_2O_2$  and NO<sup>•</sup>. A further reason why smoking leads to oxidative stress and protein oxidation is the increased smoking-dependent metal intake. Toxic metals, like cadmium, aluminium, copper, lead, mercury nickel, chromium and zinc are found in tobacco, cigarette papers, filter and the cigarette smoke.

In summary, it is necessary to note that although toxins have the ability to generate RS, the RS must not to be the cause for the toxicity and the injuries which result from the toxin action. Sometimes the toxin-mediated RS generation causes a major damage. Thus, the RS generation may be the major cause for toxicity. However, sometimes the RS generation is only a side-effect which does not cause the leading injury.

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# Chapter 6 Oxidative Stress and DNA Damage Association with Carcinogenesis: A Truth or a Myth?

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# 6.1 Introduction

Living organisms are constantly subjected to oxidative stress and free radicals. The production of a plethora of reactive oxygen and nitrogen species (ROS/RNS) may occur endogenously (intracellularly) or exogenously [1–3]. Exogenous and environmental triggers of oxidation relate to specific exposure of the organism to ionizing radiation (IR), like X-,  $\gamma$ - or cosmic rays and  $\alpha$ -particles from radon decay, oxidizing chemicals and UVA solar light. Endogenous (intracellular) attack corresponds to natural origin such as through cellular signaling and metabolic processes or during inflammation [3–8]. Examples such as hydroxyl radical (°OH), superoxide anion radicals (O<sub>2</sub><sup>--</sup>), hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>), singlet oxygen (<sup>1</sup>O<sub>2</sub>) and peroxynitrite are major toxic forms of oxygen [6, 9]. These forms of oxygen are generated by mono- or divalent reduction of molecular oxygen through normal cellular processes (e.g. respiration) [10–12] and/or produced as metabolic by-products of biochemical pathways (e.g. lipoxygenase pathway) and mitochondrial respiration (e.g. oxidative phosphorylation) [13, 14]. They may also be generated as a result of exposure to

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chemical agents (e.g. tamoxifen derivatives, paraquat) [15, 16]. It is therefore widely accepted that oxygen, even though it is beneficial for the aerobic organisms, can interact with DNA, proteins, lipids and other cellular components, through ROS generation, inducing disruption of normal synthesis and repair of DNA, inhibition/ inactivation of antioxidant key proteins and key enzymes, genomic instability, cellular toxicity and cell death [3]. There is substantial evidence that prolonged exposure of an organism to oxidative stress may be a causative effect of inflammation, imbalance of homeostatic mechanisms and possible tumor formation [3, 17].

In this chapter, we will go through the primary reactions of toxic forms of oxygen and their ability to damage cellular organic compounds such as DNA, proteins and membrane lipids causing in vivo toxicity, the different types of oxidative stressinduced DNA damage, the role of oxidative damage in carcinogenesis and the use of oxidative DNA lesions as possible cancer biomarkers.

# 6.2 Toxic Forms of Oxygen and Primary Reactions

The major intracellular sources of ROS ( $O_2$ ,  $H_2O_2$ , OH) are associated with the stepwise reduction of dioxygen to water during mitochondrial respiration. Specifically,  $H_2O_2$  and  $O_2^{-}$  in combination with redox-active metal ions, contribute to the formation of 'OH in the Haber-Weiss reaction. Hydroxyl radicals may then react with polyunsaturated fatty acids in lipid membranes causing lipid degradation and in vivo toxicity [18, 19] (Fig. 6.1). Many lipid radicals are produced during lipid peroxidation, decompose to the more stable non-radical compounds with aldehyde-, keto-, hydroxyl-, epoxy-, carboxy-, or peroxy- functional groups [20]. The lipid hydroperoxides formed are capable of producing DNA double stand breaks via a mechanism that depends on the presence of transition metals (e.g.  $Fe^{2+}$ ,  $Cu^{2+}$ ,  $Ni^{2+}$ ) in a cell (i.e. Fenton reaction) [21, 22]. Metal ions that are in close proximity to chromatin can catalyse the production of 'OH and induce base damage and interruption of chromosomal replication [23]. Other intracellular processes resulting in the release of ROS include peroxisomal metabolism, the enzymatic synthesis of nitric oxide and the metabolism of phagocytic leukocytes [21]. Moreover, a number of enzymes found in the cells of the mammalian immune system (e.g. myeloperoxidase, NADPH oxidase, nitric oxide synthase, xanthine oxidase, cytochrome P450 reductase) generate toxic forms of oxygen as a part of antimicrobial or antiviral response [19].

A genuine exogenous inducer of oxidative stress and free radicals is ionizing radiation (IR) which has both direct (when directly interacting with DNA) and indirect (when radiation causes production of ROS) effects on DNA [24, 25]. IR generates the 'OH radical through radiolysis, producing more than 100 distinct DNA adducts [19]. Evidence on radiation-induced production of toxic forms of oxygen and oxidative DNA damage arises from studies in several cellular systems. According to Pflaum [26] and Zhang [27], when human keratinocytes (HaCaT cells) and calf thymus DNA are exposed to visible light, oxidative DNA damage occurs [26, 27].

Eqn. 1i	$Fe^{3+} + O_2^{\bullet^-} \rightarrow Fe^{2+} + O_2$
Eqn. 1ii	$Fe^{2+} + H_2O_2 \rightarrow Fe^{3+} + OH- + \bullet OH$
Eqn. 2i	•OH + FA $\rightarrow {}_{FA}R^{\bullet} + H_2O$
Eqn. 2ii	$_{FA}R\bullet + O_2 \rightarrow ROO\bullet$
Eqn. 2iii	$ROO \bullet + \# FA \rightarrow ROOH + \# FAR \bullet$
Eqn. 1i	Oxidised iron (Fe <sup>3+</sup> ) in the presence of superoxide ions ( $O_2^{\bullet^-}$ ) produces molecular oxygen and reduced iron (Fe <sup>2+</sup> )
Eqn. 1ii	$\rm Fe^{2+}$ in the presence of hydrogen peroxide (H_2O_2) produces hydroxyl radical and in so doing oxidizes the iron.
Eqn. 2i	$\scriptstyle \bullet OH$ reacts with a fatty acid (FA) and forms a fatty acid radical ( $_{FA}R \scriptstyle \bullet )$
Eqn. 2ii	In the presence of molecular oxygen the fatty acid radical forms the lipid peroxy radical (ROO•)
Eqn. 2iii	The lipid peroxy radical (ROO•) is able to interact with another fatty acid (# FA) and become a fatty acid hydroperoxide (ROOH) and in doing so gives rise to another lipid peroxy radical (# $_{FA}$ R•). This new lipid peroxy radical may then go through steps 2ii and 2iii again, in a chain reaction.

**Fig. 6.1** Production of hydroxyl radicals via the Haber-Weiss reaction and the subsequent involvement of the hydroxyl radical in lipid peroxidation (Info taken from [18, 19])

Moreover, Wei and his co-workers [28] proposed that  $O_2^-$  involvement also in UV radiation (250 nm) induces base damage (i.e. 8-hydroxy-2'-deoxyguanosine (=8-OH-dG or 8-oxo-dG) formation) in DNA [28]. Furthermore, UV-A irradiation in association with fluoroquinolone antibiotics (Bayer 12–8039 and Y3118) triggers formation of oxidative DNA adducts in cultured liver epithelial cells [29]. Other exogenous sources of ROS that can damage DNA by an iron-dependent radical mechanism are xenobiotic agents (e.g. bleomycin, neocarzinostatin, mitomycin C) [19]. Pesticides like paraquat induce the production of  $O_2^-$  by redox cycling and are highly cytotoxic and mutagenic to epithelial type II cells [19]. Specifically, Tokunaga [30] and his colleagues characterized paraquat-evoked DNA damage and the effect of paraquat on 8-OH-dG formation in rat brain, lung and heart [30]. Furthermore, fumonisin B1 and benzo[a]pyrene are thought as generators of oxidative DNA damage and membrane lipid peroxidation [31].

## 6.3 Types of Oxidative DNA Damage

Toxic oxygen species (ROS and RNS) have sufficient energy to damage cellular organic compounds such as DNA, proteins and membrane lipids, causing in vivo toxicity. Reactions of ROS and RNS with DNA result in strand breaks (single and double strand breaks), small oxidative DNA base lesions (thymine glycol, FaPy lesions, 8-oxo-dG, 8-oxo-dA), abasic sites, crosslinks (DNA-protein, DNA intrastrand, DNA interstrand), exocyclic adducts, intracyclic adducts, alkylated adducts and I-compounds [8, 19, 32-34]. Among these oxidative DNA lesions, oxidative base damage and strand breaks are usually formed by a direct attack of ROS on DNA, while the bulky adducts (exocyclic adducts) probably result from secondary products that arise from reactions with lipids and proteins [20]. A protein oxidation product, 3,4-dihydroxyphenylalanine (DOPA) mediates 8-oxo-dG and 5-OH-dC production and subsequent oxidative DNA damage [35]. According to Sahu [31], fumonisin B1 (FB1) (a contaminant of corn that induces liver cancer formation), causes DNA damage and nuclear membrane lipid peroxidation [31]. One approach to document these alterations has been to treat either cells or DNA with ROS and then analyse the DNA [19] using several methods, such as immunoassays (e.g. ELISA, monoclonal antibodies like N45.1 and PCNA) [36], high performance liquid chromatography (HPLC) [37], gas chromatography – mass spectroscopy [38] and <sup>32</sup>P postlabelling assays [39]. Oxidative attack on the deoxyribose moiety can result in the formation of sugar radicals and release of free DNA bases such as 8-hydroxyguanine, 8-hydroxyadenine, cytosine glycol, 5-hydroxycytosine, 5-hydroxyuracil, 5,6-dihydroxycytosine, 5,6-dihydroxyuracil [19, 22]. Attack of ROS on purines and pyrimidines yields a variety of alterations like intracyclic and exocyclic adducts, hydroxylation, alkylation, crosslinks, strand breaks and production of indigenous adducts (I-compounds) [19-21].

#### 6.3.1 Base Damage

At least 40 different oxidative base modifications are formed when ROS react with DNA [19, 40]. Principally, these are oxidation products of pyrimidines (e.g. thymine glycols, cytosine glycols), purines (e.g. 8-OH-dG, 8-OH-dA) and imidazole ring fragmentation products of purines (e.g. formamidopyrimidines or FAPY) [20].

The 6-hydroxythymine radical intermediate can react with oxygen to yield thymine glycol [21], while 8-OH-dG, resulting from the oxidation of C-8 of guanine, can be specifically generated by the action of methylene blue and UV light (254 nm) under aerobic conditions [21, 28]. 8-OH-dG and FAPY are the major products (>80 %) formed in DNA by 'OH generated by Fenton reaction (or other free radical generating systems like xanthine/xanthine oxidase, tamoxifen derivatives and paraquat), thus providing biomarkers of DNA damage [19, 21, 30, 41]. Another, less frequent lesion is 5-hydroxymethyl-uracil that results from  $\gamma$ -rays or after radiolytic decay of [6-<sup>3</sup>H]thymine in DNA [21, 22]. Thymine glycol and 5-hydroxy-5,6-dihydrothymine lesions were predicted to induce structural distortions of the helix where the base stacking interactions between the lesion and the neighboring A:T base pair are not existing [20]. Some other less frequent lesions are the 5',8-Cyclo-2'-deoxyadenosine and 5',8-cyclo-2'-deoxyguanosine in their 5'*R* and 5'*S* diastereomeric forms. These are considered tandem-type lesions detected among the various DNA modifications and usually identified in mammalian cellular DNA in vivo [42]. It is important to state that these lesions are also detected under hypoxia and at relatively higher levels compared to 8-oxo-dG, therefore opening the possibility for use as markers of tumor-associated hypoxia.

Base damage is detected in DNA in increased amounts after exposure to a variety of agents that produce ROS [19], including IR (254 nm) [21, 28], benzo[a]pyrene [43], as well as nickel(II) [44], chromium (IV) [45] and diesel exhaust particles [46]. Moreover, according to Lodovici [47], the administration of diphenylamine and chlorothalonile (fungicide) induces a dose dependent increase in 8-OH-dG levels in liver DNA in rats [47].

Exposure to osmium tetroxide results in the formation of cytosine glycol and its dehydrated or deaminated derivatives (i.e. 5-OH-dC, 5-OH-dU) [19]. Further studies on the mechanisms of 8-OH-dG formation in vitro by various noxious and carcinogenic agents have been carried out. X-rays [48], cigarette smoke tar, asbestos/ $H_2O_2$  [49], diesel exhaust particles, methylene blue/light and polyphenols are among the oxygen radicals forming agents [19].

#### 6.3.2 Monoalkylated Bases

The most studied medium size alkyl DNA adducts are formed by well known carcinogens such as nitrosourea, nitrosamines, as well as malondialdehyde, ethane and ethylene oxide [20]. Malondialdehyde can be generated by tert-butyl hydroperoxide through lipid peroxidation [50] and may produce  $N_4$ -(3-oxopropenyl)-2'deoxycytosine (in reaction with cytosine) and  $N_6$ -(3-oxopropenyl)-2'deoxyadenosine (in reaction with adenine) [20]. Ethane and ethylene oxide are also formed as products of lipid peroxidation. In vitro treatment of DNA with ethylene oxide yields  $N_7$ -(2-hydroxyethyl)guanine,  $N_1$ -(2-hydroxyethyl)adenine and  $N_3$ -(2hydroxyethyl)adenine [20].

#### 6.3.3 DNA-DNA and DNA-Protein Crosslinks

The nature of DNA-DNA and DNA-protein crosslinks has been investigated through several studies. Malondialdehyde and  $H_2O_2$  (especially when associated with Fe<sup>2+</sup> and Cu<sup>2+</sup>) crosslink DNA and proteins (e.g. in kidney cells of rats) with

nucleotides on the same or the opposite strand. Intrastrand crosslinks have been reported to occur between adjacent adenine-adenine and adenine-guanine nucleotides. DNA-protein crosslinks involve tyrosine and thymine when chromatin is treated with IR, iron or copper ions, xenobiotics (e.g. mitomycin C, cisplatin, paraquat),  $H_2O_2$  and  $O_2^{-1}[20]$ .

## 6.3.4 Intracyclic and Exocyclic Adducts

Lipid peroxidation products (e.g. lipid peroxyl radicals, 4-hydroxynonenal) are the major sources of exocyclic adducts formation with either five- (ethero adducts) or six- (propane adducts) member rings. Among the exocyclic adducts that are mainly induced by lipid peroxidation products are the following:  $1,N^2$ -edG, edA,  $N^2$ , 3-edG, glyoxal-dG, edC, M1dG, AdG, CdG [20]. Exocyclic adducts generated after treatment with halogenated compounds (e.g. vinyl chloride) and malondial-dehyde, were detected by specific monoclonal antibodies in human liver tissues and white blood cells [20].

#### 6.3.5 Abasic Sites and Strand Breaks

ROS can cause the formation of apurinic/apyrimidinic (AP) sites in both prokaryotic and eukaryotic DNA, via oxidation of the sugar moieties [51]. Another interesting aspect of the injurious effects of oxygen radicals is their potential to function as clastogenic factors and chromosomal breakage inducers. Clastogenic activity, either induced by exogenous (e.g. UV irradiation) or endogenous sources of DNA damage, has been detected in plasma, isolated from patients with Bloom's syndrome, Fanconi's anemia, systemic lupus erythematosus, rheumatoid arthritis, chronic active hepatitis and ulcerative colitis. These alterations can result from the loss of a nucleoside moiety, leaving a phosphate group on both the free 5'- and 3'- termini, or from degradation of a sugar residue leaving the altered sugar molecule on the 3'-end of the break and a 5'-phosphate on the other [19].

# 6.3.6 Indigenous Adducts (I-Compounds)

I-compounds produced both by Fenton reaction and lipid peroxidation, have similar migration as intrastrand crosslinks, DNA-protein crosslinks and exocyclic adducts. Randerath examined the prenatal formation of a subclass (type II) of I-compounds in various tissues in neonatal rats exposed to sudden increase in partial oxygen pressure at birth [52, 53].

#### 6.4 Repair Mechanisms of Oxidative DNA Damage

The repair of oxidative DNA damage has been studied extensively both in prokaryotic and mammalian cells, using mutants in the oxidative repair pathways that exhibit enhanced sensitivity to oxidative insult [20, 54, 55]. Specifically, in vitro transcription-coupled repair and viscoelectric DNA repair studies in association with diagnostic techniques (e.g. gas chromatography, mass spectrometry) [56] have shown that oxidative DNA repair processes involve the simultaneous participation of cellular products generated via different biochemical pathways [21].

Technological advancement in cancer cell biology and genetics has enabled us to monitor the detailed DNA repair activities in the tissue microenvironment. In many pathological cases like cancer, we can see a perturbation at the levels of human DNA repair enzymes dealing with oxidative products like OGG1 (oxidized purines), NTH1 (oxidized pyrimidines) and APE1 (abasic sites) (Table 6.1). Understanding of the intracellular activities of DNA repair proteins for oxidative DNA damage could enhance the understanding of the involvement of mitochondria, ROS, DNA damage and repair in cancer transformation [8].

#### 6.5 Oxidative DNA Damage and Diseases

Oxidative DNA damage has been thought to be an important factor in mutagenesis in aerobic organisms and has been postulated to contribute to a wide variety of diseases. It seems to play a key role in hereditary syndromes with a proclivity to malignancy, such as ataxia telangiectasia (Hong, [57]), Bloom's syndrome, Fanconi's anemia, xeroderma pigmentosum and lymphoblastic leukemia [58, 59]. Oxidative DNA damage has been linked with premature ageing and age-related increase in cancer risk [60–63]. Furthermore, it has been considered to be a causative factor in a wide spectrum of other diseases including atherosclerosis, strokes, autoimmune syndromes and neurodegerative diseases like Parkinson's disease, Alzheimer disease and amyotrophic lateral sclerosis [64–66].

#### 6.6 Oxidative DNA Damage and Cancer

Oxidative damage to DNA is a causative factor in human cancer [8] induced by IR [67, 68], UV light [61], transition metals and metal ions [69]. Recent studies have shown the strong correlation between a persistent or chronic oxidative stress and human carcinogenesis. Specifically, oxidative DNA damage, which is attributable to smoking as well as disturbances in DNA repair systems, appears to be closely related to esophageal carcinogenesis [70], colorectal cancer [71], cervical cancer [72], prostate cancer [73, 74], breast cancer [75, 76], lung cancer [77], gastric cancer [123] non-melanoma skin cancer (NMSC) [78] and depression-related cancer [79].

as possible biomarkers	of high oxidative str	ess in the organism			3
Type of cancer	Study model	Biomarkers	Method used	Findings	Reference
Breast cancer	Human mammary tissue: normal, benign hyperplasia (BH), ductal carcinoma in situ (DCIS),	Oxidative stress proteins (APE1/Ref-1, PDI, SOD1, Trx, TrxR), DNA repair proteins (APE1/Ref-1, NM23-H1, MPG), damage markers (8-oxo-G, $\gamma$ H2AX,	Immunohistochemistry	t expression of oxidative stress (SOD1, APE1/Ref-1, Trx, PD1) and repair (APE1/ Ref-1, NM23-H1) Change of cellular localization of APE1/Ref-1, Trx, PDI	[19]
	invasive breast cancer (IBC)	nitrotyrosine)			
Breast cancer	Breast carcinoma patients	Total antioxidant status (TAS), thiobarbituric acid reacting substances (TBARS), total nitrite/nitrate (NOX),	ELISA	1 levels of TBARS, NOx, 8-OHdG 4 levels of TAS, antioxidant enzyme activities	[96]
		nitrotyrosine (NT), 8-OHdG, antioxidant enzyme activities	1	The levels of the above remained the same before and after chemotherapy in cancer patients	
Breast cancer	Breast carcinoma patients	S-oxo-dG	High-performance liquid chromatography (HPLC) electrochemical detection Immunohistochemistry with double-fluorescence labeling and laser-scanning cytometry	1 8-oxo-dG and oxidative stress in breast cancer patients	[79]

Table 6.1 Detection of oxidative DNA damage in several forms of human cancer. The increased levels of DNA lesions like 8-oxodG have often been suggested

[66]					[101]						continued)
J levels of vitamins A, C, E in benign adenoma (AD) and colorectal cancer (CRC) patients	↑ levels of 8-OHdG in both AD and CRC patients	↑ expression of OGG1 and APE1 in both AD and CRC patients	↑ levels of 8-oxoGua in urine of CRC patients with increased	(polymorphism)	Significantly elevated levels	ot att prosprior yrated markers in advanced	carcinoma (compared to normal colon tissue)	Co-localization of all markers in the nuclei of nositive cells	Gradual increase in yH2AX and nChk2 levels during tumor	progression	
High performance liquid chromatography (HPLC)/ electrochemical detection technique, nicking assay,	multitemperature polymerase chain reaction-single-strand	conformation polymorphism method (MSSCP)			Immunohistochemistry, Western	diou ahalysis, 1 uneel assay					
Vitamins A, C, E, 8-OHdG, 8-oxoGua, APE1, OGG1, MTH1, OGG1 polymorphism					pATM, γH2AX, pChk2	(proteins)					
Blood and urine samples from colorectal cancer patients					Resected tissue	samples from colorectal	carcinoma patients				
Colorectal cancer					Colorectal	carcinoma					

Dafaranca	Indialation	[102]	0r		a [103]								[104]					
<b>Findinge</b>	<b>LIIUUIUSS</b>	↑ plasma level of 8-OHdG for adenoma patients (p=0.045)	↑ plasma level of 8-OHdG fc patients with early cancer (p=0.020)	8-OHdG level was not a significant risk factor for advanced cancer	the urine level of of 8-OH-Gua	smoker groups (cancer	patients and healthy smokers compared to non-smokers		48 ovodCua in lauboovta	DNA and a low concentration	of vitamin E in the blood	may predict lung cancer risk	Tumors positive for 8-OHdG	are linked to poor overall	patient survival $(p=0.032)$	Strong relation between	expression of hOGG1 and	detection of 8-OHdG
Mathod wed	INTELLIOU USED	Enzyme-linked immunosorbent assay			HPLC/electrochemical detection technique				HDI C'alactrochamical dataction	technique			Alkaline phosphatase	streptavidin method				
Biomorbare	DIOIIIAIKEIS	8-OHdG			8-OH-Gua				8 ovodGua	0-0700 ut			Levels of 8-OHdG, hOGG1	and p53 in tumor tissues				
Study model	Study Inouer	Colorectal adenoma and cancer patients			Urine samples from: lung cancer	patients	(smokers), healthv smokers	and healthy		natients	patrons		Tumor tissue	from melanoma	patients			
Tune of concer	Type of calicer	Colorectal adenoma and cancer			Lung cancer				I une concer	Lung vanvoi			Melanoma	(cutaneous)				

 Table 6.1 (continued)

[105]	[106]	[109]	(continued)
† levels and co-localized immunoreactivity of 8-NitroG and 8-OHdG in all NPC patients 94.7 % of NPC patients positive for iNOS bacterial, viral or parasitic inflammation in nasopharyngeal tissue may underlie nitrative and oxidative DNA damage	1 of prostate cancer risk for carriers of the XRCC1 Arg399Gln variant allele Protective effect of the hOGG1 Ser 326Cys polymorphism	8-OHdG expression in most lesions. Nitrotyrosine expression was weaker than that of 8-OHdG and there was no association with any studied clinicopathological parameters.	
Double immunofluorescent labeling, Enzyme-linked immunosorbent assay (ELISA)	Genotyping by high-throughput chip-based matrix-assisted laser desorption time-of-flight mass spectrometry	Immunohistochemistry assays Abs: Mouse monoclonal 8-OHdG antibody, rabbit polyclonal nitrotyrosine antibody	
8-NitroG, 8-OHdG and iNOS	hOGGI and XRCC1 single nucleotide polymorphisms (SNPs)	8-OHdG Nitrotyrosine	
Cancer cells of NPC patients	Blood samples from male prostate cancer patients	Invasive epithelial ovarian carcinomas patients	
Nasopharyngeal carcinoma (NPC)	Prostate cancer	Ovarian carcinoma	

Type of cancer	Study model	Biomarkers	Method used	Findings	Reference
Colon tubular adenocarcinoma	Cancerous and normal	Non-DSB oxidatively clustered DNA lesions: oxypurine and	Repair enzymes as damage probes: Hape1, OGG1, NTH1	↑ levels of AP sites in some samples, oxypurine and	[110]
Breast invasive ductal	surrounding tissue from	oxypirimidine clusters, abasic (apurinic/apyrimidinic) sites	( <i>E. coli</i> : Endo III) and constant- field gel electrophoresis	oxypirimidine clusters compared to control	
adenoc-arcinoma	cancer patients				
Ovary				$\uparrow$ of AP sites, oxypurine and	
adenocarcinoma				oxypirimidine clusters	
Hepatoblastoma				compared to control	
Wilms kidney tumor (nenhrohlastoma)					
Bladder cancer	Blood and urine	Long interspersed nuclear	COBRA PCR	1 of LINE-1 methylation	
(BCa)	cells from BCa	element-1 (LINE-1)		levels, even lower in	
	patients	hypomethylation		cancerous tissue	
		Urinary total antioxidant status (TAS)	2,2-diphenyl-1-picryl-hydrozyl (DPPH) reduction assay	↓ of TAS levels	
		Plasma protein carbonyl	2,4-dinitrophenyl hydrazine	↑ of plasma protein	
		content	(DNPH) assay	carbonylation	
Vulvar squamous	Tissue sections	SDHO-8	Immunoperoxidase assay	↑ in 8-OHdG levels	[112]
cell carcinoma	from vulvar		Ab: 1 F7 (specific monoclonal)	as preinvasive lesions	
	cancer patients			progress	

 Table 6.1 (continued)

[113]	[114]	[115]
Patients with low levels of 8-OHdG had significantly longer survival times than those with high levels of 8-OHdG.	↑ of 8-oxo-dG and 8-oxoGua levels in urine samples of cancer patients ↑ of 8-oxo-dG levels in DNA of leukocytes in peripheral blood of cancer patients	↑ in the occurrence of 8-oxo-dG in the lymphocytes and urine of MBL and CLL patients Significant differences in the levels of MDA and GSSG/ GSH ratio ↓ of the antioxidant catalase activity of circulating lymphocytes
Enzyme-linked immunosorbent assay (ELISA)	HPLC/EC technique for determination of 8-oxo-dG, HPLC purification and CG/MS analysis for urine samples	HPLC/electrochemical detection technique
8-OHdG	8-oxo-dG in leukocytes, urrinary 8-oxo-dG and 8-oxoGua	8-oxo-dG, Iipid peroxidation product malondialdehyde (MDA), oxidized/reduced glutathione (GSSG/GSH)
NSCLC patients	Patients with malignant cancer (III and IV degree of clinical stage) and healthy subjects	MBL patients and CLL patients
Non-small-cell lung cancer (NSCLC)	Malignant tumors (head and neck, breast, colon, lung, uterine, ovarian, testicular, prostate and gastrointestinal cancer)	Monoclonal B Lymphocytocis (MBL) and Chronic Lymphocytic Leukaemia (CLL)

Table 6.1 (continued)	(				
Type of cancer	Study model	Biomarkers	Method used	Findings	Reference
Squamous cell carcinoma, small cell lung cancer,	Stage I-IV LC patients and non-cancer	Levels of 8-oxo-dG from whole blood, urinary levels of 8-oxo-dG and 8-oxoGua	HPLC technique for determination of 8-oxo-dG, HPLC purification and CG/MS	↑ urinary 8-oxoGua and 8-oxo-dG levels in stage IV LC patients ( <i>p</i> =0.044)	[116]
adenocarcinoma	controls		analysis for urine samples	↑ urinary 8-oxoGua and 8-oxo-dG levels in stage I-III LC patients ( <i>p</i> =0.034)	1
				↑ of urinary 8-oxo-dG levels during the first week of RT (p<0.001)	I
				fof nuclear 8-oxo-dG levels during RT and 3 months after start of RT	1
				fof nuclear 8-oxo-dG levels between the first two CT cycles $(p=0.043)$	
				↑ of urinary 8-oxo-dG levels during the sixth CT cycle (p=0.009)	1
Cancer related to clinical depression	Patients with clinical	8-OH-dG, in peripheral leukocytes	HPLC/electrochemical detection technique	↑ 8-OH-dG, in cancer patients with depression	[79]
-	depression	\$	٦	↑ 8-OH-dG in female patients	
Oral squamous cell carcinoma (OSCC)	Patients with clinically diagnosed OSCC (n=362) and	Mitochondrial superoxide dismutase 2 (SOD2), Cu/Zn enzyme SOD1 gene polymorphisms. Four single	PCR-restriction fragment length polymorphism, DNA sequencing methods	No significant difference was observed in the rs5746136 SOD2 SNPs between the patients and controls	[121]
	healthy normal individuals (n=358)	nucleotide polymorphisms (SNPs; rs4880, rs5746136, rs1804450 and rs11556620)		CT genotype of SOD2 SNP rs4880 was higher in the patients (smokers and non-smokers) than in normal	1
				subjects	

)varian cancer	Human patients. Tumor and	8-OHdG, human repair protein 0GG1	ELISA Immunohistochemistry	Increased 8-OHdG level and decreased expression of	[34]
	matched tumor-adiacent			hOGG1 in tumor were found in HG-SOC hut not I G-S in	
	normal tissue in			matched normal tissue	
	48 high-grade			adjacent to carcinoma	
	papillary serous				
	carcinomas				
	(HG-SOC), 24				
	low-grade				
	papillary serous				
	carcinomas				
	(LG-SOC)				
Prostate cancer	Male patients	Serum MDA	ELISA	Serum MDA and 8-OH-dG	[122]
	with prostate	(malondialdehyde), 8-OH-dG,		levels were significantly	
	cancer and male	caspase 3		raised $(p < 0.05)$ compared to	
	patients with			benign prostate hyperplasia	
	benign prostate			group $(24.05 \pm 8.06,$	
	hyperplasia			$3.99 \pm 0.54$	
				Serum caspase-3 levels were	
				statistically significantly	
				lowered $(p < 0.05)$	

Indirect effects of oxidative DNA damage on cancer arise from the following evidence: ROS are often postulated to contribute to bacteria-associated tumorigenesis such as gastric cancer in mice induced by *Helicobacter hepaticus* [80] and Helicobacter pylori ([81, 124]. The increased mutagenesis mediated by oxidative DNA damage can also affect RNA replication in certain retroviruses, extending their mutational repertoire [82]. Furthermore, exposure to cigarette smoke is well documented to increase oxidative stress and could account for a higher risk of cervical cancer in smokers, [72] while in the case of hepatitis viruses there is an established connection between chronic infection and induction of oxidative stress [83]. The fact that other conditions in the organism such as replication stress can result in induction of DNA breaks, this creates a 'dangerous' genotoxic cocktail. Experimental findings suggest that, in both precancerous and cancerous lesions, activated oncogenes induce replication stress, stalling and collapse of the DNA replication fork, which in turn leads to formation of complex DNA breaks challenging the repair systems of the cell [84]. This can result in unrepairable DNA damage and consequently genomic instability that characterizes the vast majority of human cancers.

The role of ROS toxicity in spontaneous aneuploidy of cultured cells has also been highlighted [34]. Considering that aneuploidy causes genetic instability, alters the biological properties of cells and has been characterized as one of the most critical causes of carcinogenesis [85–87], the ability of ROS to induce aneuploidy highlights their indirect effect in carcinogenesis.

## 6.7 Biomarkers in Cancer

Research on the role of oxidative DNA damage is well established in experimental carcinogenesis. A large number of human studies on biomarkers of oxidative DNA damage (mostly related to guanine oxidation), have been carried out and the results have shown that the level of oxidative DNA damage and repair activity can be quite different between tumor and normal tissues; case-control studies have shown increased levels of oxidative DNA damage and decreased repair capacity in the cells tested. Similarly, the urinary biomarkers of oxidative DNA damage may be elevated in patients with cancer [88, 89]. Several recent examples on the use of oxidative DNA biomarkers in several forms of human cancer are presented in Table 6.1. In many cases as also reviewed earlier by Kryston et al. [3], human carcinomas induce a state of high oxidative stress in the organism, associated also very often with a high inflammation status. This interplay between inflammation and oxidative stress seems to be a major player in the induction or promotion of carcinogenesis [90].

Notably, Curtis et al. [91] observed that special protein protecting cells from ROS such as Cu/Zn superoxide dismutase (SOD1) [92], superoxide dismutase 1 (SOD1), thioredoxin (Trx) [93], apurinic/apyrimidinic endonuclease 1/redox factor-1 (Ape1/Ref-1) [94] and protein disulfide isomerase (PDI) [95] are overexpressed in human breast cancer tissue, providing cancer cells with protection from oxidative stress and thus interfering with chemotherapy. This effect was amplified

by upregulation of proteins implicated in DNA repair (NM23-H1 and Ape1/Ref-1) [91]. Other examples of oxidative DNA biomarkers in cancer arise from the results of Atukeren et al. [96]. The increased oxidative/nitrosative stress products and particularly 8-OH-dG in breast cancer patients are considered as prognostic risk factors for the magnitude of oxidation in serum [96]. Elevated levels of 8-oxo-dG and oxidative stress have been also reported in breast cancer patients [97].

Additional biomarkers related to oxidative stress metabolism are vitamins A, E and C which are known for their antioxidant action, as they demonstrate a free radical scavenging effect [98]. Recent evidence has shown that a low concentration of these crucial vitamins in plasma could indicate a connection to cancer, since DNA would be prone to considerable damage induced by radicals without the vitamins serving as protective shields. Obtułowicz et al. [99] decided to investigate this concept by measuring the concentrations of these antioxidants in blood plasma of benign adenoma (AD) and colorectal cancer (CRC) patients. Indeed most individuals with AD had lower levels of vitamins A, E and C compared to healthy controls, while in CRC patients the phenomenon was significantly amplified. This finding is consistent with the hypothesis that CRC is a disease which develops with time and its first stage might probably be benign adenoma. Moreover, they observed an increase in 8-oxo-dG in blood and urine samples of both CRC and AD, accompanied by elevated expression levels of repair genes, such as OGG1, APE1 and MTH1. All these indications point to an increase in oxidative stress.

Oka et al. used tissue samples from colorectal carcinoma patients to assess the levels of phosphorylated proteins (pATM,  $\gamma$ H2AX, pChk2) closely associated with DNA damage response (DDR) [100]. Interestingly, the levels of the protein markers were increasingly higher with the progression of cancer, reaching a peak in the case of advanced carcinoma. This finding illustrates the gradual activation of DDR as cancer develops. However, evaluation of apoptosis revealed absence of apoptotic cells, leading to the hypothesis that activation of DDR does not necessarily have apoptotic endpoints unless the damage induced is severe enough, or is dependent on various factors such as impairment of a part of DDR pathway [101].

Furthermore, experiments run by Sato et al. showed association between increased plasma levels of 8-OH-dG and the development of colorectal adenoma and cancer. Enzyme-linked immunosorbent assays revealed significantly increased levels of 8-OH-dG in patients with adenoma and early cancer. In contrast, 8-OH-dG was not detected at high levels in patients with advanced cancer, probably due to the decreased energy intake and nutritional disorders in such patients [102]. In another study, the broad spectrum of oxidative DNA damage biomarker 8-hydroxyguanine (8-OH-Gua) was analyzed in 51 lung cancer patients (all smokers), 26 healthy smokers and 38 healthy non-smokers. The mean level of 8-OH-Gua in the urine of the two smoker groups (cancer patients and healthy smokers) was significantly higher than in non-smokers [103]. Additional experimental work from the same research group, revealed that 8-oxo-dG in leukocyte DNA and a low concentration of vitamin E in the blood may predict lung cancer risk [77]. However, further studies are needed to evaluate whether these phenomena may simply result from disease development [77].

Murtas et al. studied the correlation between expression/levels of 8-OH-dG induced by UV radiation and survival in melanoma patients [104]. The expression of proteins hOGG1 and G6PD, prevalent in repair mechanisms and oxidative damage protection, was also studied in light of overall patient survival. The results show that tumor cells positive for 8-OH-dG are significantly linked to poor overall survival of melanoma patients, which in turn reveals an important weapon for prognosis; primary cutaneous melanoma could be assessed with regard to mortality risk and classified accordingly, thus aiming to treatment optimization and possibly prevention. Moreover, cells positive for 8-OH-dG also demonstrated elevated levels of hOGG1 expression, suggesting that hOGG1 could constitute a damage biomarker as well [104].

Huang et al. have also measured 8-OH-dG in the serum of nasopharyngeal carcinoma (NPC) patients, along with 8-nitroguanine (8-NitroG). 94.7 % of the patients were tested positive for the expression of inducible nitric oxide synthase (iNOS) as well, in contrast with controls. The induction of nitrative and oxidative DNA damage in cells could indicate the potential risk of NPC, through the assessment of 8-OH-dG and 8-NitroG levels and, consequently, their use as predictive biomarkers. In an attempt to link DNA lesions and iNOS expression to inflammation, the researchers studied cases of individuals with chronic nasopharyngitis. The results lacked the intensity observed in NPC patients, however they were still higher than controls, implying a gradual increase in iNOS-induced lesions during the initiation and advancement of carcinogenesis [105].

Zhang and colleagues [106], performed a case-control study of male patients with prostate cancer and investigated the role of single nucleotide polymorphisms on the repair enzymes hOGG1 and XRCC1 resulting in serine to cysteine substitution (Ser326Cys) and arginine to glutamine (Arg399Gln) respectively. Individuals homozygous or heterozygous for hOGG1 variant allele demonstrated a lower risk compared to subjects with wild type allele homozygosity. This finding is consistent with a study by Obtułowicz et al., where the variant allele demonstrated significantly increased 8-oxo-Gua excision capacity in CRC patients [99]. On the contrary, XRCC1 Arg399Gln polymorphism was linked to elevated prostate cancer risk. Apparently, the Arg399Gln polymorphism exhibits a reduced enzymatic activity because the mutation appears in a highly conserved region of the protein. [107, 108]

In another study, Karihtala et al. investigated the role of oxidative stress and major antioxidant enzymes in 68 cases of invasive ovarian carcinomas. The study revealed that 8-OH-dG is a powerful prognostic factor in ovarian carcinoma. 8-OH-dG was prominent in most lesions and this expression was notably higher in tumors of patients whose primary operation was non-optimal, than in those whose optimal operation outcome could not be reached. Nitrotyrosine levels were also evaluated and the results showed that they were lower than those of 8-OH-dG in ovarian carcinomas [109].

Further experimental work from Nowsheen et al. revealed that an increased level of non-DSB clustered DNA lesions might be affiliated with higher oxidative stress in tumor tissues. DNA from colon tubular adenocarcinoma, breast invasive ductual adenocarcinoma, hepatoblastoma, ovary adenocarcinoma, nephroblastoma and normal adjacent tissues was isolated and the levels of non-DSB oxidative clustered DNA lesions were assessed. In most cases, the levels of APE1-clusters in tumors were higher compared to normal tissues, but statistically considerable differences have been tracked only for liver, ovary, kidney and some cases of breast and colon tumors. In addition to that finding, it was revealed that within the same tumor localization, there has been a significant variation in the assessed values [110].

Evidence from a recent study of Patchsung et al. has shown that decreased long interspersed nuclear element-1 (LINE-1) methylation is linked to increased oxidative stress, both in bladder cancer (BCa) patients and healthy groups, implying a dose-response association. Moreover, a positive correlation between methylation of LINE-1 in the blood-derived DNA and urinary total antioxidant status (TAS) was determined in both BCa patients and healthy subjects [111]. A progressive significant increase in the levels of 8-OH-dG was also observed in tissue sections from vulvar cancer patients [112].

In order to evaluate the effects of 8-OH-dG on survival in NSCLC patients, Shen et al. used an enzyme-linked immunosorbent assay (ELISA) to determine the levels of 8-OH-dG in the DNA of 99 lung tumor samples, obtained from patients who had undergone resection for clinical stage I-IV NSCLC. 77 of the 99 lung cancer patients included in the study, passed away during the follow-up. The results demonstrated that subjects who died in the course of the follow-up had notably higher median levels of 8-OH-dG, than those who survived at the end of it. [113].

Evidence from a recent study of Roszkowski [114], which examined samples from 222 cancer patients and 134 healthy volunteers, has shown that 8-oxo-dG (8-oxo-7,8-dihydro-2'-deoxyguanosine) and 8-oxo-Gua (8-oxo-7,8-dihydroguanine) in urinary excretions as well as leukocyte oxidative DNA damage have been characterized as helpful biomarkers in cancer diagnosis [114].

Recent studies on the use of 8-oxo-dG as potential biomarker have shown a significant increase in the occurrence of the mutagenic base 8-oxo-guanine in the lymphocytes and urine of Monoclonal B Lymphocytosis (MBL) and Chronic Lymphocytic Leukaemia (CLL) patients compared with controls. Significant differences were also observed in the levels of the lipid peroxidation product malondialdehyde (MDA) and in the oxidised/reduced glutathione (GSSG/GSH) ratio. Interestingly, the antioxidant catalase activity of circulating lymphocytes decreased in the patient groups. In conclusion, early oxidative stress exists in patients with MBL and CLL, causing damage to DNA and lipid structures [115].

In another study, the increased urinary levels of 8-oxo-guanine (8-oxo-Gua) and levels of 8-oxo-dG from urine and whole blood were determined in 36 non-cancer controls and 65 lung cancer patients before any treatments, indicating an association between those urinary DNA damage biomarker and lung cancer stage [116]. Specifically, stage IV lung cancer patients had statistically significant higher urinary 8-oxo-Gua and 8-oxo-dG levels than patients with stage I-III disease [116].

Furthermore, in an effort to elucidate the potential link between depression and cancer, Irie et al. [79], compared the cancer-related oxidative DNA damage, 8-OH-dG, in peripheral leukocytes between 30 patients with depression and 60 age- and gendermatched healthy controls. The patients showed significantly higher 8-OH-dG levels than the controls. Moreover, a significant positive correlation between 8-OH-dG levels in depressive, particularly female, patients has been shown, suggesting that clinical depression is a risk factor for cancer initiation in view of oxidative DNA damage [79].

Lately, exocyclic DNA adducts are emerging as potential new tools for the study of oxidative stress-related diseases as well as the determination of cancer etiology and cancer risk. It is important to determine whether levels of exocyclic DNA adducts reflect redox stress in vivo and what role these adducts play in human diseases. To answer these important questions, inter-individual differences, tissue distribution, background levels, and repair have to be assessed [117].

# 6.8 Lipid Peroxidation Biomarkers in Carcinogenesis

In recent years, the interest in the use of oxidative DNA damage as biomarkers of carcinogenesis is focused towards lipid peroxidation (LPO) products. It is well known that oxidative stress enhances lipid peroxidation, and that both are implicated in the promotion and progression stages of carcinogenesis, particularly under conditions of chronic inflammation and infections [118]. LPO products are characterized by hydrocarbon chains of different lengths, reactive aldehyde groups and double bonds, which makes these molecules reactive to nucleic acids, proteins and cellular thiols [119]. It has been reported that LPO-derived adducts to DNA bases form etheno-type and propano-type exocyclic rings, have profound mutagenic potential, are executed by several repair systems and have been shown to be elevated in several cancer-prone diseases [119]. Specifically, exocyclic etheno-DNA adducts, which are formed by LPO-products such as 4-hydroxy-2-nonenal, are strongly promutagenic DNA lesions. The development of ultra-sensitive detection methods for etheno-adducts in human tissues (white blood cells, urine) has provided evidence that these adducts are elevated in affected organs of cancer-prone patients, probably acting as a driving force to malignancy [118]. The results have shown that biomonitoring of etheno-DNA adducts in humans are promising tools for understanding better disease aetiopathogenesis, monitoring disease progression and verification of the efficacy of chemopreventive and therapeutic interventions [118].

A striking remark is that a severe oxidative stress manifested as a high level of guanine oxidation in cellular DNA and in urine of cancer patients is a consequence of development of many types of cancer. Although at present it is impossible to directly answer the question concerning involvement of oxidative DNA damage in cancer etiology it is likely that oxidative DNA base modifications may serve as a source of mutations that initiate carcinogenesis [88, 103].

Cohort studies are required to provide evidence that a high level of oxidative DNA damage implies a high risk of cancer. However, this represents a real challenge considering the large number of subjects and the long follow up time required, along with likely spurious oxidation of DNA during collection, assay and/or storage of samples [89]. Future studies, in association with multidisciplinary technological approaches will help in discovery of new biomarkers. Aiming to connect free radical

chemical reactivity with biological processes, Chatgilialoglu et al. [120], developed a chemical biology approach to provide information on the mechanistic pathways and products. The core of this approach was the design of biomimetic models to study biomolecule behavior, including lipids, nucleic acids and proteins, in aqueous systems especially under conditions of physiological oxidative stress mimicking the in vivo situation. By this way we can obtain insights of the reaction pathways as well as building up molecular libraries of the free radical reaction products [120].

#### 6.9 Conclusion

The exploitation of new "cancer biomarkers" in the future will not only contribute significantly in early prognosis but also in the structural design of new and more efficient therapeutic regimes especially in oxidative stress-related malignancies [3]. In addition, the detection of systemic or non-targeted effects in the organism is considered critical. In many cases these phenomena can be triggered by a local type of stress i.e. radiation damage or tumor growth and propagate in the body via activation of innate immune response and inflammatory or oxidative mechanisms [3]. At the same time will shed light on the possible mechanisms leading to sustainable oxidant status often coupled with inflammation. The possible use of anti-oxidant or anti-inflammatory therapies may prove useful towards the mitigation of any type of genotoxic stress and chromosomal instability due to the accumulation of DNA damage.

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# Chapter 7 Glutathione and Thiols

Lou Ann S. Brown and Dean P. Jones

# Abbreviations

Cys	Cysteine
CySS	Cystine
GCL	γ-Glutamylcysteine Ligase
GGT	γ-Glutamyl transferase
GSH	Glutathione (reduced)
GSSG	Glutathione (oxidized)
Gpx	Glutathione Peroxidase
GR	Glutathione Reductase
GS	Glutathione Synthase
Grx	Glutaredoxin
GST	Glutathione S-transferase
$H_2O_2$	Hydrogen Peroxide
Prdx	Peroxiredoxin
ROS	Reactive oxygen species
Trx	Thioredoxin
TrxR	Thioredoxin Reductase
VOC	Volatile Organic Compounds

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## 7.1 Introduction

Reactive oxygen species (**ROS**), oxidative stress, and the availability of antioxidants play key roles in health and pathologies including inflammation [1], aging [2], cardiovascular disease [3], diabetes [4], and other pathologies [5, 6]. ROS can oxidize macromolecules including proteins, DNA, or lipids resulting in altered macromolecule function that ultimately compromises cellular function and contributes to pathogenic processes. ROS have also been linked to essential biological processes that involve redox-sensitive cell signaling pathways where changes in the oxidation state of a molecule, usually a cysteine (**Cys**), initiate signaling events [7–9].

#### 7.2 Thiols and Cellular Defenses

The two main families of relevant oxidants in biology are ROS and reactive nitrogen species (**RNS**). ROS include primarily free radicals or molecular fragments with one or more unpaired electrons that are stabilized by removal of electrons from neighboring molecules. Non-radical species, like hydrogen peroxide ( $H_2O_2$ ) or peroxynitrite, also act as strong electron acceptors due to their highly positive redox potential [10]. Unless the biological molecule has a transition metal center, ROS like  $H_2O_2$  or superoxide do not react directly.

The transition metal sulfur is large, polarizable, and electron rich making it very reactive and able to adopt multiple oxidation states. Sulfur is found in multiple biological compounds and participates in a complicated network of sulfur-based reactions due to its distinct functional groups: thiols, disulfides, polysulfides, sulfenic, sulfinic and sulfonic acids, etc. (Fig. 7.1) [11–14]. The reactivity of the many different sulfur-containing amino acids is dependent upon their accessibility, local pK, and dissociation state. Thiol (X-SH) amino acids can form symmetrical disulfides (XS – SX), asymmetrical thiol-thiol disulfide compounds (XS – SR), or proteinthiol mixed disulfides (XS – SP). Protein-Cys moieties can also react with neighboring thiol groups to form a disulfide bridge within or between proteins (protein-S – S-protein). Within proteins, 10–20 % of the Cys residues interact with ROS under biological conditions and the activities of many enzymes, structural proteins, and protein nuclear factors, are subsequently altered by such posttranslational modifications [7, 15].

Cys plays a key role in the metabolic pathways of other thiols including methionine, taurine, and glutathione (**GSH**). Through the thiol/disulfide couples glutathione (GSH/GSSG), cysteine (Cys/CySS), and thioredoxin ((Trx-(SH)/Trx-SS)), electrons are transferred between molecules depending on the balance between reduced/ oxidized forms of electrons donors and acceptors; this is termed redox balance [16]. Through these redox-sensing thiols, different biologic systems are integrated into a context-dependent and coordinated redox circuit and, in participation with antioxidant enzymes plus other antioxidants like vitamins E and C, redox homeostasis is maintained [17–20].


**Fig. 7.1 Summary of the major oxidative modifications affecting protein cysteine residues.** The Cys moieties in proteins can react with ROS like  $H_2O_2$  to yield a sulfenic acid (protein-SOH), an unstable derivative. The sulfenic acids can form intra- or inter-disulfides which can then be reduced to the thiol form by GSH or Trx. The sulfenic acids can also be glutathionylated through the addition of GSH. In the continued presence of  $H_2O_2$ , sulfenic acid can be oxidized to sulfinic acid (Protein-SO<sub>2</sub>H) and then further oxidized to sulfonic acid (Protein-SO<sub>3</sub>H). Thiol over-oxidation to sulfinic or sulfonic acids generates irreversible modifications

### 7.3 Glutathione/Glutathione Disulfide (GSH/GSSG) System

In cells, GSH ( $\gamma$ -glutamyl-cysteinyl-glycine) is primarily in the biologically active reduced thiol form (SH) and is present at 2–10 mM making it the most abundant cellular thiol [16]. The capacity varies, but every organ synthesizes GSH *de novo* through the rate limiting enzyme  $\gamma$ -glutamylcysteine ligase (GCL, also called  $\gamma$ glutamyl-cysteine synthetase, or GCS) (Fig. 7.2). GCL is a heterodimeric protein composed of catalytic (GCLC) and a modulatory (GCLM) subunits that combine glutamate and cysteine to form a  $\gamma$  carboxyl group [21]. Glutathione synthase (GS) catalyzes the final step by adding glycine to the dipeptide to form GSH. GCL activity, Cys availability, and GSH feedback inhibition are the main factors regulating GSH synthesis. GSH oxidation to GSSG is associated with oxidative stress and the GSH/GSSG ratio is a useful indicator of cellular oxidative stress.

The regeneration of GSH from GSSG is catalyzed by NADPH-dependent GSH reductase (**GR**). GSH uptake from extracellular pools is dependent on GSH metabolism by  $\gamma$ -glutamyl transferase (**GGT**). The released amino acids, particularly Cys, then serve as essential substrates for the synthesis of GSH or proteins [22]. GSH is also consumed during detoxification reactions by GSH-dependent enzymes such as



Fig. 7.2 GSH synthesis, oxidation, and recycling. *Cys* cysteine, *CysGly* cysteinylglycine, *Glu* glutamate, *Gly* glycine, *DP* dipeptidase, *GCL*  $\gamma$ -glutamylcysteine ligase,  $\gamma GT \gamma$ -glutamyl transpeptidase,  $\gamma GluCys \gamma$ -glutamylcysteine, *Gpx* glutathione peroxidase, *GR* glutathione reductase, *GS* glutathione synthetase, *GSH* glutathione, *GSSG* glutathione disulfide, *GST* glutathione-S-transferase,  $H_2O_2$  hydrogen peroxide, *LOOH* lipid peroxide, *NADPH* nicotinamide adenine dinucleotide phosphate; *Pr-SH* protein thiol, *Pr-S-SG* glutathionylated protein

GR, glutaredoxin (**Grx**), GSH peroxidases (**GPxs**), and GSH-S-transferases (**GSTs**). During these detoxification reactions, GSH is critical for the redox modulation of enzyme function making GSH availability an important regulatory mechanism for the removal of ROS, RNS, carcinogens, drugs, and xenobiotics. When comparing monozygotic to dizygotic twins, the concentrations of GSH, GSSG, redox state, and the total GSH pool (GSH plus GSSG) within red blood cells behaved as if the major portion of the phenotype for GSH homeostasis is genetically controlled [23]. In other words, the genetic sequences inherited will determine the specific activities of the enzymes involved in GSH homeostasis and control the GSH and GSSG concentrations present in each cell.

A fast reaction of GSH with  $H_2O_2$  or lipid hydroperoxides requires the dissociated thiolate (– S–) form making the electron transfer, and is strongly dependent on the pH within the microdomain [24]. For GSH, the pKa is ~9.0 so that ~1 % of the GSH pool will be deprotonated in the cytosol (pH of 7.2). However, that percentage changes with physiologically relevant changes in the pH, particularly within organelles. GSH can form glutathione-thiyl radicals (GS(•)) that can combine with other molecules to produce additional radicals [25]. The GS(•) can be converted to GSSG or transferred to a protein forming a mixed disulfide (protein-SSG) [26]. GSH can also react with xenobiotic radicals to form glutathionyl radicals [27]. A glutathionyl radical can react with GSH to form GSSG•–that then reacts with molecular oxygen to produce superoxide anions and GSSG. Proteins can undergo protein S-glutathionylation, the reversible binding of GSH to protein thiols (PSH) which is involved in protein redox regulation. Protein S-glutathionyls serve as a GSH storage pool, and protect protein thiols from irreversible oxidation [28–31]. Once GSH/GSSG is restored, S-glutathionylation can be reversed through an enzyme-dependent or -independent manner. S-glutathionylation has a pivotal role in monocyte/macrophage function [32], ion channel activity [33–35], protein folding in the endoplasmic reticulum [36–38], mitochondrial function, oxidative phosphorylation, mitochondrial permeability transition (MPT), apoptosis, mitochondrial fission and fusion [39–41], and proteasomal protein degradation [31].

The capacity of GSH to accept or donate electrons is determined by its redox potential (E<sub>h</sub>) through the Nernst equation:  $E_h = E_0 + (RT/nF) \ln([GSSG]/[GSH]^2)$ , where R is the gas constant, T is the absolute temperature, F is Faraday's constant, and n is the number of electrons transferred.  $E_0$  is the standard potential for the redox couple and is calculated at equilibrium conditions relative to a standard hydrogen electrode. Assuming factors remain constant, the effective GSH/GSSG redox state is principally modulated by the GSH and GSSG concentrations according to the relationship [GSH]<sup>2</sup>/[GSSG] [42]. Within the cytosol, GSH is highly reduced with a GSH/GSSG redox potential of approximately -260 mV [43, 44]. Cytosolic GSH participates in cytosolic redox signaling and serves as the reservoir for other intracellular compartments. Regulated by transmembranal transport, succinct GSH redox states are maintained in the highly reduced mitochondrial (-300 mV) and the highly oxidized endoplasmic reticular (ER; -170 to -185 mV) environments. For the nucleus, the redox state is uncertain because the GSH concentration is difficult to assess, but is expected to be higher than the cytosol suggesting that the nucleus is more reduced [45]. Furthermore, GSH is sequestered in the nucleus during cell proliferation suggesting that common redox mechanisms exist for DNA regulation in G1 and mitosis in all eukaryotes [46, 47].

Organ GSH pools are dependent on plasma GSH and GSSG concentrations that vary with gender, age, ethnicity, co-morbidities, and diets [48, 49]. There is a diurnal variation with a nadir in GSH concentrations and oxidation of the GSH/GSSG redox potential occurring in the midafternoon [50]. After 45 years of age, the plasma GSH/GSSG redox state becomes progressively more oxidized due to increased GSSG and a decreased ability for *de novo* GSH biosynthesis. This results in an increasing oxidation of the redox potential at a linear rate of 0.7 mV per year [42, 51–54]. The K(m) of glutamate-cysteine ligase (GCL) significantly increases with aging, which adversely affects the ability for rapid GSH biosynthesis during stress [55, 56]. However, Cys metabolism can adapt to meet increased requirements for GSH. For example, critically ill patients receiving enteral or parenteral nutrition enriched with glycine, exhibit decreased Cys catabolism, improved GSH synthesis, and increased plasma GSH [57]. These factors contributing to the plasma GSH concentration and redox state have the potential to subsequently alter the threshold for ROS- or chemically-induced toxicity [58–60]. Given that GSH is the most

abundant cellular thiol antioxidant and controls multiple cellular processes, it is not surprising that perturbations in its homeostasis are associated with multiple pathologies involving drugs, gender, alcohol, diet, and environmental pollutants [61].

Variances in extracellular GSH concentrations can be very important in protection against chemically-induced injury, the supply of GSH or its precursors to the underlying cells, and protection against oxidative damage to underlying cells [61]. In plasma, the GSH concentration (~3  $\mu$ M) is much greater than GSSG (~0.15  $\mu$ M) and the redox potential is ~ -150 mV, which is considerably more oxidized than tissues or cultured cells (-185 to -258 mV) [62]. In contrast, the GSH concentration in the fluid lining the alveolar space is considerably higher at ~500  $\mu$ M [63–65]. The GSSG concentration in the alveolar fluid is ~20  $\mu$ M and the redox potential is ~ -200 mV which is significantly more reduced than plasma and approaches the redox state of cells [65]. This is not unexpected because the alveolar lining fluid serves as a barrier against inhaled agents and detoxifies potentially damaging reactive species that are abundant in the atmosphere.

Chronic pulmonary oxidative stress, as assessed by GSH depletion and oxidation of the alveolar lining fluid, is linked to multiple lung pathologies [66–69]. With exposures to cigarette smoke, wood smoke, or other environmental agents, GSH in the alveolar lining fluid increases suggesting mobilization to the air-lung interface and protective adaptation [70–72]. However, GSH in the alveolar lining fluid decreases with chronic exposures to volatile organic compounds (VOCs), even at low dose exposures [73, 74]. With aging, alveolar lining fluid GSH can decrease by as much as 50 % and the ability to mobilize GSH in response to cigarette smoke is decreased [75]. Aging and smoking are also linked to chronic obstructive pulmonary disease (COPD) and decreased GSH in the alveolar lining fluid suggests that disruption of GSH adaptive responses may contribute to the pathophysiology of COPD [76]. In subjects with an alcohol use disorder, a group also associated with an increased risk of infection and lung injury [77], GSH in the alveolar lining fluid is decreased by 80 % and the GSH/GSSG redox state is oxidized by ~50 mV [65, 78].

The GSH/GSSG redox state in the alveolar lining fluid modulates bacterial killing by alveolar macrophages and the risk of pneumonia or tuberculosis [79, 80]. Strategies to restore extracellular GSH can improve the immune functions of alveolar macrophages. For example, GSH is decreased in the alveolar lining fluid of HIV positive subjects, a population at risk for respiratory infections [81]. However, adding to the GSH pool in vitro decreased the growth of *M. tuberculosis* in alveolar macrophages from HIV positive subjects [82]. Likewise, GSH or GSH precursors in the diet decreased experimentally-induced pneumonia and acute lung injury in control and ethanol-fed mice [83, 84]. In a model of fetal alcohol exposure, experimentally-induced pneumonia was decreased by intranasal GSH [85]. Therefore, the GSH status in these extracellular pools is an important determinant of resilience. Similarly, decreases in the alveolar lining fluid GSH increases the risk of injury from environmental exposures, and the impaired immune functions in the alveolar macrophages related to the decrease in GSH increases the risk of respiratory infections. Correspondingly, strategies like oral thiols may be needed to meet organ needs for GSH, particularly those populations with decreased GSH in these extracellular pools.

#### 7.4 Glutathione-Dependent Enzymes

*Peroxidases* Peroxidases use GSH in a broad range of redox reactions, often with isoforms specific to an organelle. For the seven isoforms of GSH peroxidase (**Gpx**), the selenocysteine at the active site reacts rapidly with peroxides and transfers reducing equivalents from GSH to  $H_2O_2$  to produce GSSG and water [86–88] (Fig. 7.2). The phospholipid hydroperoxide GPx isoform has some unusual structural and catalytic properties enabling it to reduce the lipid hydroperoxides formed in membranes. This prevents the initiation and propagation of lipid peroxidation [88].

Peroxiredoxins A family of thiol-specific peroxidases called peroxiredoxins (Prxs) catalyzes the reduction of  $H_2O_2$  and organic hydroperoxides. The peroxidatic Cys is oxidized to sulfenic acid (Cys-SOH) which then forms a disulfide bond with a C-terminal Cys residue (Fig. 7.1). The regeneration to an active Cys is then catalyzed by thioredoxin (**Trx**) and thioredoxin reductase (**TrxR**) (Fig. 7.3). The Prx isoforms (Prx 1 to 6) are further divided into typical 2-Cys Prxs, atypical 2-Cys Prxs, and 1-Cys Prx [89-92]. The 2-Cys Prxs require no cofactors and are further divided into typical and atypical Prxs. For typical 2-Cys Prxs (Prx1-Prx4), dimers are formed when a peroxidatic Cys of one Prx subunit reacts with a hydroperoxide to form a sulfenic acid. This sulfenic acid subsequently forms a disulfide linkage with the Cys residue in the carboxyl terminus of another Prx subunit. The Prx-S-S-Prx disulfide linkage is then reduced by NADPH through coupling with Trx and TrxR. However, the sulfenic acid form can also be inactivated when a second hydroperoxide molecule reacts to form sulfinic acid [93]. This sulfinic acid can then condense with another Cys on an adjacent Prx to form a disulfide. In the presence of high  $H_2O_2$  concentrations or chronic oxidative stress like alcohol abuse, the sulfinic acid reacts with another  $H_2O_2$  to become hyper-oxidized to sulfonic acid [94, 95]. The typical 2-Cys Prx isoforms have distinct roles based on their organelle distribution: Prx 1 and 2 in the cytosol; Prx 4 in the extracellular space and endoplasmic reticulum; and Prx 3 in the mitochondria. Prx 5 is the only atypical 2-Cys Prx that forms an intramolecular disfulide linkage when it reduces H<sub>2</sub>O<sub>2</sub>. Prx 5 isoforms are widely distributed in mitochondria, cytosol, nucleus, and peroxisomes. Prx 6, found only in the cytosol, involves only one Cys and is reduced by GSH through GSH S-transferases [96, 97]. Because both the Gpxs and Prxs depend on NADPH to maintain their catalytic activity, NADPH regeneration is pivotal for maintaining effective antioxidant defenses and redox sensitive signaling for these thiols.

*GSH S-Transferases* Biological electrophilic intermediates can form covalent adducts with protein-Cys or react with glutathione-S-transferases (**GSTs**), a family of homo- or heterodimer enzymes [98]. GSTs are grouped into seven distinct classes that are either cytosolic or present in mitochondrial and microsomal membranes. GSTs react with a broad range of potentially toxic compounds to form GSSG or a less toxic GSH S-conjugate compound [99]. The GSH-conjugates are generally then transported to vacuoles for GSH recycling, or exported from the cell [100–106]. The primary polymorphisms, GST-M1 and GST-T1, involve complete gene deletion. The loss of these enzymes predisposes to oxidative stress and downstream tissue injury, particularly in subjects with both genes absent [107, 108]. For GST-Pi,



Fig. 7.3 GSH (a) and Thioredoxin (b) Redox Signaling Circuits. (a) GSH Redox Signaling Circuit. Prdx-(SH), Peroxiredoxin – reduced form; Prdx-SOH peroxiredoxin sulfenic acid,  $Grx(SH)_2$  glutaredoxin – reduced form, Grx(S-S) glutaredoxin – disulfide form, GSH glutathione, GSSG oxidized glutathione,  $GR(SH)_2$  glutathione reductase – reduced form, GR(S-S) glutathione reductase – disulfide form. (b) Thioredoxin Redox Signaling Circuit.  $H_2O_2$  hydrogen peroxide, Prdx-(SH) peroxiredoxin – reduced form, Trx-(SH)<sub>2</sub> thioredoxin – reduced form, Trx (S-S) thioredoxin – disulfide form, Prdx-SO<sub>2</sub>H peroxiredoxin – sulfinic acid, Prdx-SO<sub>3</sub>H peroxiredoxin – sulfonic acid, TrxR-(SH)<sub>2</sub>, thioredoxin – sulfinic acid, TrxR (S-S) thioredoxin reductase – disulfide form

the major polymorphism is a substitution of adenine to guanine at codon 103. This nucleotide change leads to the substitution of Ile by Val and subsequent decreases in substrate affinity and enzymatic activity. GST-Pi exists predominantly in a monomeric form that blocks different signaling cascades by binding to components like JNK-1 $\alpha$ 2 and the TNF receptor associated factor (TRAF) [109–111]. As oxidative stress increases, the Cys residues located in the GST-Pi active site dimerize which attenuates enzymatic activity and its capacity to block ROS-dependent signaling [112–114]. Polymorphisms in GST-T1, GST-M1, and GST-Pi have been implicated as risk factors for multiple pathologies including cancers [115–117], glaucoma [118], hypertension [119], and airway diseases [120, 121].

### 7.5 Thioredoxin (Trx) and Trx-Dependent Redox System

The thioredoxin (**Trx**) system is composed of NADPH, thioredoxin reductase (**TrxR**), and Trx which maintain redox homeostasis through its disulfide reductase activity, thereby regulating the protein dithiol/disulfide balance [7, 122-124]

(Fig. 7.3). Trx are small ubiquitous proteins that catalyze the reversible reduction of disulfide bonds (Cys-XX-Cys) formed at the active site Cys in thiol-dependent proteins like Prxs, ribonucleotide reductase, and methionine sulfoxide reductases. For Trx1, the cytosolic isoform is maintained at a redox potential of -280 mV and the nuclear isoform at -300 mV. In mitochondria, the distinct Trx2 isoform maintains a redox potential of -330 mV. Trx1 and Trx2 are regulated independently within their subcellular compartments and are differentially sensitive to various stimuli. The oxidized Cys-XX-Cys protein motifs are reduced by the NADPH-dependent Trx reductase (TrxR) [122]. Like their corresponding Trx isoforms, TrxR1 and TrxR2 are cytosolic and mitochondrial enzymes, respectively, with a C-terminal selenium-Cys residue that is essential for catalytic activity [125–127]. The Trx and GSH systems are independent, but serve each other as a backup system when the other system is compromised [122, 128].

### 7.6 Cysteine/Cystine (Cys/CySS) Redox System

The other thiol pair abundant in biological systems is Cys and its oxidized form cystine (CySS). In plasma, Cys and CySS concentrations are 40 and 8–10  $\mu$ M, respectively. This pair is not in equilibrium with GSH/GSSG or Trx-SH/Trx-SS concentrations, or the overall redox state [62, 124, 128, 129]. The plasma Cys/CySS redox state undergoes diurnal variation [50]. With an insufficient intake of sulfur amino acids, the Cys concentration decreases and the Cys/CySS redox potential becomes more oxidized [130]. The Cys/CySS ratio also varies with age but its oxidation pattern is distinct from that of GSH/GSSG [129] and is relevant to DNA repair, cell proliferation, apoptosis, endoplasmic reticulum stress, and inflammatory responses [131]. Oxidation of plasma Cys/CySS may be a link to sensitivity to environmental influences, smoking, obesity, alcohol abuse, diabetes, cardiovascular disease, and atherosclerosis [20, 129, 132].

### 7.7 Redox Signaling

The redox states for these different thiol pairs are not in equilibrium and are governed by their subcellular localization, the reactivity of their sulfhydryl groups, the ROS species and concentrations, and the duration of exposure [90]. Each thiol/ disulfide pair functions as a localized redox circuit that initiates intracellular signaling cascades through  $H_2O_2$ -mediated reversible oxidation at key Cys sites [15, 133]. The post-translational oxidative modifications of these protein thiols are central to biological events because they control the activity of target proteins [124, 128]. The cascade of signaling events also involves cross-talk between redox couples within and between subcellular compartments [39, 134, 135]. However, disruption of redox homeostasis through an imbalance between reductants and oxidants results in disruption of normal cellular redox signaling events, molecular damage, and disruption of enzymes with redox sensitive sites [44, 136]. It is the duration and reversibility of protein oxidations that determine if the organelle or the cell can maintain healthy redox signaling [10]. Therefore, the redox poise of these critical thiols has a central role in the tolerance and adaptability to environmental challenges or biological insults.

### 7.8 Concluding Remarks

Through subcellular compartmentalization, the thiol pairs GSH/GSSG, Trx-SH/ Trx-SS and Cys/CySS function as unique, independent redox control nodes that integrate different biologic systems in a coordinated manner. Therefore, thiol homeostasis determines the redox milieu and, ultimately, the scavenging of free radicals by thiols like GSH. There is tissue resilience when redox homeostasis is rapidly reestablished after oxidative stress and the redox active thiol switches are reset to their control positions. However, an inability to restore redox homeostasis results in disrupted signaling within the organelles and redox-mediated dysregulation of protein function through oxidation of catalytic sites with redox active Cys sites. Sustained aberrant redox signaling and protein dysfunction produces irreversible alterations in cellular functions. Understanding the dynamic interactions between the different redox circuits, and their dysregulation, should provide a mechanistic understanding of cellular resilience in response to environmental or pharmacological stresses.

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### Chapter 8 Reactive Oxygen Species as Initiators and Mediators of Cellular Signaling Processes

Lars-Oliver Klotz

### 8.1 Introduction

From studies in bacteria, it has been known for decades that oxygen and reactive oxygen species (ROS) affect cellular adaptation mechanisms through modulation of gene expression. For example, the E. coli transcription factors OxyR and SoxR act as sensors of changes in cellular concentrations of hydrogen peroxide and superoxide, respectively, controlling the expression of genes encoding antioxidant proteins [1, 2]. Nevertheless, it was considered unlikely by many that these principles might also apply to more complex mammalian cells; how should something as unspecific as these intracellular "ROS fireworks" stimulate relatively specific signaling cascades in systems as complicated as mammalian cells? Yet some transcription factors were soon identified to be sensitive to an exposure of cells to ROS, including activator protein (AP)-1 and nuclear factor (NF)- $\kappa$ B [3, 4].

It is now widely accepted that ROS affect a multitude of cellular signaling processes, ultimately modulating gene expression and the cellular response to various stimuli. ROS may act both as first and as second messengers; exposure of cells to ROS or to physical stimuli or xenobiotics that cause the generation of ROS may trigger numerous signaling events, with ROS as the actual initiating species. On the other hand, cells generate ROS in a controlled fashion in order to use them as mediator molecules in cellular signaling cascades. Here, both of these aspects of ROS signaling will be briefly dealt with, followed by a discussion of the mode of action of ROS. Finally, some examples of known redox-sensitive signaling cascades will be provided.

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### 8.2 Endogenously Generated ROS as Mediators of Signaling Processes

Major cellular sources of ROS include the mitochondrial respiratory chain, with superoxide generated as a by-product of mitochondrial electron transport from metabolic reducing equivalents to oxygen. Similar processes occur near other electron transport chains, such as those related to xenobiotic metabolism in the endoplasmic reticulum. Moreover, NADPH oxidase complexes are major sources of ROS. These complexes were originally identified as membrane-bound flavoenzymes responsible for the generation of superoxide and  $H_2O_2$  in phagocytes upon stimulation (the "respiratory burst", [5]). NADPH oxidase complexes (with five different isoforms of the catalytic subunit, NOX 1 through 5, identified) are now known to be present in many non-phagocytes and to be activated by numerous stimuli including proinflammatory factors [6–8]. There are several other metabolic sources of ROS, and ROS generating enzymes in mammalian cells include amine oxidases, aldehyde oxidases, or oxidases involved in peroxisomal beta-oxidation of fatty acids.

With mitochondria (see Sect. 8.2.1) and NADPH oxidase (see Sect. 8.2.2), one obvious issue is that of ROS release into the cytoplasm. While reactive radicals such as the hydroxyl radical are unlikely to react anywhere but at their site of formation, the more stable ROS such as hydrogen peroxide and peroxynitrite (likely in its uncharged peroxynitrous acid form) [9, 10] are believed to permeate membranes such as the mitochondrial or plasma membranes. However, it is clear now for  $H_2O_2$  that its permeation of the plasma membrane is "limited" (see [11] for review) and becomes significant and rapid only if facilitated by aquaporins such as AQP3 [12, 13] and AQP8 [13, 14].

ROS derived from mitochondria and from NADPH oxidase activation are linked to endogenous regulatory circuits. This notion of ROS acting as signaling molecules and as parts of signaling cascades has one more important implication: the degree of stimulation of a signaling cascade may be linked to the extent of ROS production – and of oxidative damage.

### 8.2.1 Mitochondrial ROS as Signals for Adaptation

Impairment of mitochondrial electron transport along the respiratory chain may enhance electron leakage and ROS production [15], followed by oxidative damage (e.g. to mitochondrial DNA), and trigger a vicious cycle of elevated ROS formation/ damage accumulation, because mitochondrial DNA integrity is a requirement for the complete biosynthesis of respiratory chain complexes [16]. Although the enhanced formation of ROS in mitochondria with an impaired respiratory chain is well accepted, it should be noted that the vicious cycle theory has been challenged recently [17].

ROS, in addition to other potential mediators released from mitochondria such as calcium ions, NAD(H) or acetyl-CoA, are one possible "retrograde" signal which, upon release from mitochondria into the cytoplasm, may trigger events causing a

nuclear transcriptional response [18, 19]. For example, ROS derived from the mitochondrial respiratory chain (but not changes in AMP/ATP) are responsible for AMPK activation in cells under hypoxia [20], eliciting AMPK-dependent signaling, e.g. to stimulate transcription factors known to be modulated by phosphorylation through AMPK, such as FoxOs and Nrf2 (for review, see [21]). In addition, these and other AMPK-regulated transcription factors are triggered by ROS directly; FoxOs and Nrf2 will be described in further detail below (Sect. 8.5.1).

Mitochondrial ROS release, as a retrograde signal, is linked to the initiation of a cellular stress response and stress resistance. Hence, interference with ROS formation, release, or elimination (e.g. by antioxidants) may also interfere with the adaptation process normally elicited by mitochondrial ROS. Adaptive processes initiated by mitochondrial ROS are responsible for protective and life-prolonging effects of low doses of certain xenobiotics (e.g., arsenite [22]) in model organisms such as *C. elegans*. This phenomenon of cellular processes leading to adaptation to subcytotoxic doses of xenobiotics is termed mitohormesis, owing to the prominent role of mitochondria in that hormetic effect [23, 24].

Interestingly, the link between mitochondrial ROS and AMPK appears to exist in both directions, as recently shown for diabetic kidneys [25]; a lowered superoxide production was detected in kidneys of diabetic relative to control mice, coinciding with lower AMPK activity. Activation of AMPK using aminoimidazole carboxamide ribonucleotide (AICAR), an AMP analog, stimulated mitochondrial superoxide production. The authors hypothesize that this may be due to an AMPK-dependent induction of the transcriptional regulator, PGC-1 $\alpha$  (peroxisome proliferator-activated receptor  $\gamma$  coactivator-1 $\alpha$ ), a known stimulator of mitochondrial biogenesis [26].

### 8.2.2 NADPH Oxidases in Cellular Signaling and Toxicity

Stimulation of receptor tyrosine kinases (RTK) by their natural ligands - stimulation of the insulin receptor with insulin (see below), the epidermal growth factor (EGF) receptor with EGF [27, 28] or the platelet-derived growth factor (PDGF) receptor with PDGF [29] - all come with a transient increase in NADPH oxidasederived ROS and an ROS-mediated modulation of downstream signaling. These signaling events occur through transient oxidative inhibition of protein tyrosine phosphatases (PTP) associated with the respective RTK, which appears to be required for a significant ligand-induced increase in RTK phosphorylation and therefore a significant intracellular signal to be initiated. For example, NOX4 generates H<sub>2</sub>O<sub>2</sub>, attenuating dephosphorylation of EGFR [30]. Similarly, insulin signaling is under redox control by NOX-derived ROS. Not only is H<sub>2</sub>O<sub>2</sub> generated in cells upon stimulation with insulin, but this is essential to insulin signaling in that it oxidatively and transiently inhibits a PTP controlling insulin receptor tyrosine phosphorylation, PTP1B [31-33]. A major H<sub>2</sub>O<sub>2</sub> source in insulin-exposed adipocytes was then identified as NOX4, whose protein levels/activity control PTP1B activity and insulin receptor-dependent signaling [34].

The exact mode of coupling the insulin receptor to NOX4 for an acute increase in ROS generation is unclear at present, particularly considering the current view of NOX4 (in contrast to NOX1 or 2) as largely constitutively active and regulated mainly at the level of expression [35]. However, a link between insulin exposure and a prolonged increase in ROS generation due to NOX4 was established in 3T3-L1 fibroblasts [36]; insulin-induced signaling results in an enhanced expression of NOX4. Interestingly, insulin-induced NOX4 expression entailed an enhanced expression of MAPK-phosphatase-1 (MKP1) in that study, a dual-specificity phosphatase regulating MAPK phosphorylation known as an immediate-early gene expressed under stress [37].

In addition to RTK signaling, the stimulation of G protein-coupled receptors (GPCR) by their natural ligands is linked to NOX activation. For example, angiotensin II stimulation of its receptor in smooth muscle cells causes two waves of ROS generation (seconds versus minutes); one mediated by G-protein-dependent activation of protein kinase C (resulting in phosphorylation of the NADPH oxidase complex subunit, p47phox, and its translocation to the membrane), the other requiring transactivation of the EGF receptor following angiotensin II stimulation and the GTP-binding protein Rac [38].

Enhanced NOX-dependent ROS production in response to stimulation of hormone receptors, including GPCR, nuclear/steroid receptors and other receptor families, by their cognate ligands not only mediates signaling processes, but may also cause damage. For example, oxidative DNA damage was detected in several types of cells following stimulation with adrenalin, angiotensin II or androsterone, only to name a few (for reviews, see [39, 40]).

Similar to the role of mitochondria and mitochondrial ROS in mitohormesis, a role for NOX in ischemic preconditioning (i.e. an adaptation of cells/tissues following a brief ischemic stress, rendering them more resistant to a later ischemic insult [41] (for review, see [8])), a hormesis-like phenomenon, was suggested [42].

# 8.3 Xenobiotic-Induced Signaling: ROS as Initiators of Signaling Elicited by Exogenous Stimuli

With mitochondrial respiratory chain and NADPH oxidases as endogenous sources of ROS, any exogenous stimulus that affects either or both of these will result in an altered generation of ROS. In line with this notion, the list of NOX-activating stresses is extensive and includes physical stimuli (such as ionizing and non-ionizing radiation, or changes in pH and osmolarity) as well as xenobiotics such as heavy metal ions, components of cigarette smoke and others (for a review and recent list, see [8]). However, many xenobiotics and exogenous stimuli result in elevated steady-state levels of ROS, sometimes in a confined cellular environment, such as the cell membrane. This occurs in a NOX-independent fashion, and these xenobiotic-derived ROS will result in cellular stress signaling either in a direct manner or indirectly by generating cellular oxidation products that, in turn, stimulate signaling.

Numerous xenobiotics are capable of stimulating cellular ROS generation in such a manner. It is more difficult, however, to prove the involvement of ROS in xenobiotic-induced signaling. For example, exposure of mammalian cells to redox-active metal ions such as copper ions indeed stimulates cellular ROS formation [43], possibly due to redox cycling processes that have Cu(II) reduced intracellularly to Cu(I), which may reduce physically dissolved oxygen to form superoxide, regenerating Cu(II). In parallel, exposure to Cu(II) strongly stimulates phosphoinositide 3'-kinase (PI3K)-dependent activation of the Ser/Thr kinase Akt, resulting in phosphorylation of FoxO transcription factors [43, 44]. Apparently, one is independent of the other. For example, time courses of ROS formation and Akt stimulation do not match (for review, see [45]).

### 8.3.1 How to Prove the Involvement of ROS in Xenobiotic-Induced Signaling ("Triple-I-Approach")

In order to demonstrate a role for specific ROS in a signaling effect elicited by a xenobiotic, the effect needs to be inhibitable using a specific antioxidant (*interception*); the effect needs to be mimicable using a different source of the suspected ROS (*imitation*); and the presence or formation of the suspected ROS needs to be shown (*identification*). This "triple-I"-approach was employed to demonstrate that  $H_2O_2$  mediates the stimulation of EGF receptor tyrosine phosphorylation following ultraviolet radiation [46]: (i) catalase blocked stimulation of EGFR, (ii) bolus  $H_2O_2$  administration had the same effect as ultraviolet radiation, and (iii)  $H_2O_2$  formation was identified following radiation, using a specific (enzyme-based) assay. The same approach was used to demonstrate that the green tea flavonoid, epigallocatechin gallate (EGCG), may stimulate Akt-dependent signaling via the generation of  $H_2O_2$  [47].

# 8.3.2 1,4-Naphthoquinones: Xenobiotics That Stimulate RTK Signaling

Following their uptake, certain xenobiotics are metabolized to intermediates that may undergo redox cycling, i.e. they may be reduced enzymatically at the expense of cellular reducing equivalents such as NADH or NADPH. In the presence of molecular oxygen, which is found physically dissolved and at high micromolar concentrations in most cells, these intermediates are then reoxidized to the respective starting point, with molecular oxygen in turn reduced to superoxide. This reduction/reoxidation cycle of xenobiotics, generating superoxide from oxygen, may occur repeatedly, provided the supply of reducing equivalents lasts. Quinones are a group of compounds that frequently undergo redox cycling in mammalian cells, with formation of a semiquinone by reduction, followed by reoxidation (and concomitant superoxide



**Fig. 8.1 Redox cycling.** Superoxide and other ROS may be generated by the cyclic reduction/ oxidation of quinones, which may be reduced intracellularly to their corresponding semiquinone, e.g. by microsomal reductases. Semiquinones can be further reduced to the respective hydroquinone. Alternatively, molecular oxygen may reoxidize a semiquinone, regenerating the quinone and producing superoxide (Figure taken from Klotz, 2014 [119], with kind permission from Springer Science +Business Media)

production) to the quinone (Fig. 8.1). A second reduction step from semiquinones to hydroquinones may occur, and similarly result in the formation of superoxide upon reoxidation (Fig. 8.1). The 1,4-naphthoquinone derivatives plumbagin and juglone are found in plants such as leadwort (*plumbago sp.*) and black walnut (*juglans nigra*), respectively, and are typical examples of potent redox cyclers that are capable of generating superoxide in mammalian cells. Figure 8.2 lists some natural and synthetic naphthoquinone derivatives that stimulate the generation of ROS (and induce signaling processes that are referred to below) [48]. Other xenobiotics may be metabolized to form quinoid compounds and redox cyclers. For example, the anti-malarial 8-aminoquinoline primaquine or certain pyrimidine glycosides found in fava beans, such as con-/vicine, are metabolized to form products capable of generating ROS through redox cycling, such as ortho-/para-quinones or quinone-imines [49–51].

Several naphthoquinones are strong stimulators of RTK signaling, eliciting tyrosine phosphorylation of the ErbB-family RTKs, the EGF receptor (EGFR) and ErbB2 [48, 52, 53], or platelet-derived growth factor receptor (PDGFR) [54]. Stimulation of superoxide formation was demonstrated for 1,4-naphthoquinone, menadione (2-methyl-1,4-naphthoquinone), juglone and plumbagin in exposed cells, and all strongly stimulated EGFR and ErbB2 activation and downstream signaling (see Fig. 8.2). No activation of these receptors was detected in cells exposed to lawsone or lapachol [48]. Interestingly, EGFR activation by menadione, juglone or plumbagin was diminished by about 20 % in cells pretreated with a superoxide



**Fig. 8.2** 1,4-Naphthoquinones and activation of epidermal growth factor receptor (EGFR) and its relative ErbB2. Structures of 1,4-naphthoquinone and 1,4-naphthoquinone derivatives. Some naphthoquinones are from natural sources, such as plumbagin (an ingredient of leadwort, plumbago sp.), juglone (from various types of walnut, juglans sp.), lawsone (found in colorants made from henna, i.e. lawsonia sp.) and lapachol (found in lapacho tea). The structure of NSC95397 (2,3-bis-[2-hydroxyethylsulfanyl]-1,4-naphthoquinone), an inhibitor of several protein tyrosine phosphatases that causes strong stimulation of EGFR/ErbB2 signaling, is shown (Figure taken from Klotz, 2014 [119], with kind permission from Springer Science+Business Media)

dismutase and catalase-mimetic manganese-containing porphyrin (MnTBAP). This indicates that ROS formation may be involved in the activation of the RTK, but a larger portion of the activation is due to other factors. In line with this notion, no attenuation of EGFR activation by 1,4-naphthoquinone was achieved using MnTBAP, implying that, while significant ROS production occurs in cells exposed to this quinone, stimulation of EGFR signaling is elicited independently of ROS formation. In fact, all of the actively signaling quinones exhibit alkylating activity, which appears to be a major contributor to naphthoquinone signaling (see also Sect. 8.4.2) [48].

### 8.4 ROS and Signaling: Modes of Action

An important feature of ROS-induced signaling processes is that the initial molecular ROS targets (i.e. ROS sensors) are modified covalently by this interaction – with the exception of heme moieties required for the action of nitrogen monoxide (NO). In essence, therefore, signaling by ROS may be elicited by oxidative damage of biomolecules. One might ask in how far such oxidative damage is capable of conferring specificity to a signaling cascade relying on the

aforementioned "ROS fireworks". The answer lies in three aspects: (i) in ROS signaling, these fireworks are usually confined to certain areas, (ii) the fireworks are tightly controlled by cellular antioxidant extinguishing mechanisms (see Chap. 21 on antioxidants), and (iii) some molecular structures are more susceptible to oxidative modification than others. For instance, several ROS signaling mechanisms are based on the simple fact that thiolates are usually more susceptible to oxidation than their corresponding thiols. This means that the local aminoacyl residue environment in an enzyme can determine the pKa of a cysteine and hence its susceptibility to oxidation. For example, in experiments exposing isolated protein tyrosine phosphatase-1B (PTP1B) to a singlet oxygen source, of all cysteines covered by the sequencing approach, only the active site cysteine (known to be present in its thiolate form) was oxidized [55]. In addition to cysteine oxidation, methionine sulfoxide formation was also hypothesized as a suitable reversible switch in signaling proteins because enzymes (the methionine sulfoxide reductases (MSR)) exist to efficiently reduce methionine sulfoxide back to methionine. One could envisage that control of signaling based on methionine oxidation is achieved through regulation of methionine accessibility both to oxidants and to MSR. For a discussion of how, and in how far, methionine oxidation and its enzymatic reversion may be crucial to signaling events (e.g. in calcium signaling) the reader is referred to a recent review article [56].

The oxidation of biomolecules, even if minor (i.e. not yet noticeably interfering with the cellular well-being), may trigger cellular processes directly (see Sect. 8.4.1) or indirectly (Sect. 8.4.2); oxidative modification of signaling enzymes may cause loss or gain of activity and shift in signaling equilibria. Yet oxidative stress may also act indirectly by eliciting the generation of bioactive oxidation products that, in turn, will affect signaling enzymes, inhibiting them and/or affecting their degradation.

In terms of ROS sensor moieties in proteins, sulfur – as cysteines, iron/sulfur clusters and methionines – is the prominent feature of many molecular structures targeted by ROS already at low steady-state concentrations, and cysteine (thiol)-based mechanisms will be briefly discussed here.

### 8.4.1 Consequences of Signaling Protein Oxidation by ROS

It was previously mentioned that RTK stimulation by their ligands comes with the generation of ROS. Several of these RTK are also stimulated upon exposure of cells to oxidants rather than the RTK ligands; the epidermal growth factor receptor (EGFR), its relative, ErbB2, or platelet-derived growth factor receptors (PDGFR) are among them and were demonstrated to be activated in cells exposed to stimuli such as  $H_2O_2$  [57], peroxynitrite [58, 59], or redox-cycling agents [53, 60]. Knebel et al. [61] demonstrated that inactivation of a protein tyrosine phosphatase (PTP) mediates this stress-induced RTK stimulation. Ligand/RTK interaction causes activation of the receptor's intrinsic tyrosine kinase activity, catalyzing the

phosphorylation of tyrosyl residues, both of other RTK molecules (enhancing their activity) and of non-RTK substrates. The resulting phosphotyrosine moieties are crucial for downstream signaling as they serve as docking sites for signaling proteins. Hence, reversal of tyrosine phosphorylation will shut down this signaling cascade, thereby controlling the activity of RTK. PTPs catalyze the dephosphorylation of activated/phosphorylated RTK, facilitating the hydrolysis of phosphotyrosine moieties by nucleophilic attack of their active site cysteine thiolate at the phosphotyrosine phosphorous. This results in release of a tyrosyl residue and an intermediate phosphocysteine residue at the PTP's active site, which is further hydrolyzed to release phosphate and the original enzyme [62].

Owing to their active site cysteine being present in its deprotonated (thiolate) form, PTPs are exquisitely sensitive to oxidants and alkylating agents [63]. Accordingly, PTP inactivation occurs in cells or isolated PTP exposed to oxidants including  $H_2O_2$  [61, 64, 65], peroxynitrite [66], and singlet oxygen [55], or alkylating agents that rapidly interact with thiolates [52, 53, 67]. At least three active site oxidation products were identified for different PTPs exposed to ROS: (i) sulfenic acid [68, 69], (ii) an intramolecular disulfide, provided a second cysteine is close to the active site thiolate, as is the case in cdc25 phosphatase [70] or PTEN [71], and (iii) a sulfenamide, as in PTP1B exposed to  $H_2O_2$  [64, 65]. All of these are reversible by reducing agents such as GSH. Exposure of cells to oxidants will therefore result in (reversible) oxidative inactivation of PTPs, shifting tyrosine phosphorylation/dephosphorylation equilibria of proteins controlled by the respective PTP (such as RTK) to the phosphorylation side and resulting in a net accumulation of phosphotyrosine moieties.

The signaling mechanism described above is based entirely on oxidative inactivation of a protein (see Fig. 8.3a) – a negative regulator of a signaling cascade. Likewise, some negative regulators of transcription factors are inactivated by oxidative stress in that their function of keeping a transcriptional regulator in check is abrogated through oxidation (Fig. 8.3b; for example, Keap-1 as a negative regulator of the transcriptional activator, Nrf-2; see Sect. 8.5.1). Similar to MSR reactivating methionines, oxidized cysteines may be reduced back to the thiol form by a 12 kDa protein, thioredoxin (Trx), that is present in multiple cellular compartments [72]. Trx, by means of thiol/disulfide exchange, reactivates oxidized proteins, including signaling molecules such as redox factor-1 (Ref-1), which reduces transcriptional regulators, e.g. of the Jun/Fos families, that were inactivated by cysteine oxidation (for review, see [73]). Trx itself needs recycling which is accomplished through thioredoxin reductases, selenoproteins that require NADPH to reduce oxidized Trx [72].

Mechanisms other than oxidative inactivation of a signaling protein contribute to ROS signaling, including the activation of kinases by ROS. For example, this can occur through unfolding and providing access to a hitherto covered active site (Fig. 8.3c), or through generation of an active site by intermolecular disulfide formation (Fig. 8.3d). Such mechanisms were identified for several kinases, including the tyrosine kinase c-Src, isoforms of the serine/threonine kinase Akt, or apoptosis-signal-regulated kinase-1 (ASK-1) (for review, see [74]).



Fig. 8.3 Regulation of protein activity by interaction of ROS with cysteines. See text for further details

# 8.4.2 Indirect ROS Signaling: Oxidation Products as Mediators of ROS Action

The oxidation of several biomolecules will yield reactive products that may further react with proteins or other crucial molecules and thereby initiate signaling processes.

**Lipid Peroxidation Products** Lipid peroxidation, as initiated by exposure of polyunsaturated fatty acids in membranes to ROS, is accompanied by oxidative breakdown of lipids (and the loss of membrane integrity in affected areas), and comes with the generation of products that may interact with secondary targets not initially affected by ROS. Prominent examples of such lipid peroxidation products are



**Fig. 8.4** Lipid peroxidation products and covalent modification of proteins. Lipid peroxidation results in the formation of reactive aldehydes, e.g. (a) acrolein, (b) malondialdehyde or (c) 4-hydroxy-alkenals, that may interact with protein amino acid residues and undergo Michael addition, Schiff base formation and other nucleophilic substitutions to form covalent adducts and cross-links (Figure taken from Klotz, 2014 [119], with kind permission from Springer Science+Business Media)

reactive aldehydes, such as acrolein, malondialdehyde (MDA) and 4-hydroxynonenal (HNE). These aldehydes may form adducts with proteins by interacting with amino acid side chains that are prone to Michael addition or Schiff base formation, such as cysteine, lysine, and histidine, and may include amino acyl residues that were not originally targeted by the primary oxidant (Fig. 8.4), thereby increasing the range of amino acid residues affected by ROS. Such modifications will conceivably impair functionality of affected proteins. Therefore, it has been proposed that adduct formation contributes to the pathogenesis of several phenomena, including atherosclerosis and cardiovascular disease [75].

Similar to the aforementioned net activation of a signaling cascade following inhibition of a signaling protein, the inhibition and alkylation of the lipid and protein dual phosphatase PTEN (phosphatase and tensin homolog) was demonstrated to coincide with, and postulated to mediate, stimulation of PI3K/Akt signaling by exposure of cells to HNE [76]. Further examples of such alkylations by lipid peroxidation products inducing pathophysiologically relevant signaling processes include the stimulated expression of the proinflammatory protein cyclooxygenase-2 (COX-2) via stress-responsive kinase p38<sup>MAPK</sup> upon exposure to HNE [77], or the stimulation of collagen expression (a crucial step in the pathogenesis of fibrosis) in fibroblasts [78] or hepatic stellate cells [79] following exposure to MDA.

Lipid peroxidation products will also contribute to the formation of so-called advanced glycation endproducts (AGE). These are a group of protein modifications derived, in the original sense of the term, from non-enzymatic interactions (e.g., Schiff base formation) between amino groups and reactive sugars (hence glycation), followed by rearrangements that render the formation irreversible (hence "end"-product). AGEs (i.e. proteins harboring such modifications) are recognized by a plasma membrane-bound receptor, RAGE, whose activation by interaction with AGEs may trigger ROS formation by stimulating NADPH oxidase and by stimulating proinflammatory signaling in general. This leads to the upregulation of enzymes such as inducible NO synthase, which may entail enhanced formation of reactive nitrogen species such as peroxynitrite. For a recent comprehensive review on AGE formation and signaling, see [80].

**Glutathione** Owing to its high intracellular concentrations, glutathione (GSH) is a frequent target of various oxidants. GSH oxidation products are capable of glutathiolating proteins by interacting with cysteine thiols/thiolates; these products include glutathione sulfenic acid (GSOH), glutathione disulfide (GSSG), GSSG S-oxide or S-nitroso- (GSNO) and S-nitroglutathione (GSNO<sub>2</sub>). Vice versa, GSH may attack protein cysteine oxidation products (sulfenic acid, cystine, S-oxide, S-nitroso) to form glutathione/protein mixed disulfides (Fig. 8.5) [81–83].

### 8.5 Examples

ROS-induced modulation of gene expression occurs at various levels, including transcriptional, epigenetic and posttranscriptional control of gene expression.

### 8.5.1 Redox-Sensitive Transcription Factors and Upstream Pathways

Redox cycling of quinones (as depicted in Fig. 8.1) is attenuated in vivo by NAD(P) H:quinone oxidoreductase-1 (NQO1, DT diaphorase), an enzyme catalyzing the two-electron reduction of quinones to the corresponding hydroquinones at the expense of NADH or NADPH (indicated in the Figure by "2 [H]"). NQO1 thereby avoids the semiquinone stage and redox cycling because the hydroquinone may



**Fig. 8.5** Mechanisms of glutathiolation of proteins. Glutathiolation of proteins occurs by nucleophilic attack of a thiol(ate) at an oxidation product of another thiol (resulting from its interaction with a reactive oxygen or nitrogen species), such as (from *top* to *bottom*) a sulfenic acid, nitrosothiol, disulfide, or disulfide-S-oxide. Depending on which reaction partner is present in the oxidized form, R may be glutathione or a protein cysteine, attacking an oxidized protein cysteine or glutathione moiety R', respectively (Figure taken from Klotz, 2014 [119], with kind permission from Springer Science+Business Media)

undergo phase II xenobiotic metabolism, i.e. can be coupled to water-soluble molecules such as sulfate or glucuronic acid, and excreted [84, 85]. Expression of NQO1 is regulated at the transcriptional level by "antioxidant response elements" (ARE) in the gene's promoter region [86], which are recognized by the transcription factor Nrf2 [87], a basic leucine zipper (bZIP) family transcription factor stimulated by alkylating agents/electrophiles and ROS. The expression of numerous other proteins considered protective and important for stress response and xenobiotic metabolism is regulated by Nrf2, including phase II enzymes, heme oxygenase or enzymes involved in glutathione biosynthesis, as well as antioxidant enzymes [88].

Another family of transcription factors known to be redox-regulated and to control the expression of antioxidant enzymes are the forkhead box, class O (FoxO) transcription factors. These factors regulate expression of proapoptotic genes, genes involved in fuel metabolism, and antioxidants such as catalase, MnSOD [89], selenoprotein P [90, 91] and ceruloplasmin [92], to name a few. Nrf2 and FoxOs, and the mode of redox regulation in these cases, will be discussed briefly.

**Redox Regulation of Nrf2 Signaling [88]** Most of the synthesized Nrf2 is kept in check in the cytoplasm by Keap-1, a cysteine-rich protein mediating proteasomal degradation of Nrf2 by forming a complex consisting of 2 Keap-1 molecules, Nrf2 and the Cul3 component of a ubiquitin ligase. Similar to the schematic in Fig. 8.3b, Keap1 may be oxidized by ROS (forming disulfides) and alkylated by various

electrophiles, leading to a release of Nrf2 which will then translocate into the nucleus to form heterodimers with another bZIP family protein, such as a Maf transcription factor, to stimulate ARE-dependent transcription.

**FoxO Transcription Factors in Redox Signaling [93, 94]** Four FoxO transcription factor isoforms are found in humans, FoxO1a, FoxO3a, FoxO4 and FoxO6, which are ubiquitously expressed. FoxOs are regulated by posttranslational modification, e.g. phosphorylation, ubiquitination and acetylation. Several stress-regulated kinases phosphorylate FoxOs, with different outcomes with respect to DNA binding and transactivation activity, and subcellular localization. In short, there is both activation of FoxOs by oxidative stress (e.g., via c Jun-N-terminal kinase-dependent phosphorylation) and inactivation. A prominent FoxO regulator is Akt, that not only mediates the effects of insulin but also of stressful stimuli [95, 96]. Phosphorylation of FoxOs by Akt results in their inactivation and nuclear exclusion.

As FoxOs are regulated by signaling cascades emanating from RTKs, they are also affected by ROS that modulate RTK-dependent signals. Redox regulation of FoxO activity occurs at several levels (Fig. 8.6), such as redox control of PTPs regulating RTKs (insulin receptor in Fig. 8.6) or of PTEN, redox control of Akt and redox-regulated interaction of FoxOs with coregulators like p300/CBP acetyl transferase [97]. Fine-tuning of FoxO activity, and of the patterns of genes regulated by FoxOs, is accomplished by interaction with transcriptional coregulators [98]. In addition to ROS, several xenobiotics modulate FoxO activity indirectly through xenosensor coregulators such as constitutive androstane receptor (CAR) and pregnane X-receptor (PXR), allowing for an indirect modulation of FoxOs by CAR/PXR-specific xenobiotics, such as phenobarbital [99]. Moreover, an interaction between the FoxO and aryl hydrocarbon receptor transcriptional regulator systems has been hypothesized [100].

### 8.5.2 Epigenetic Factors

Epigenetic control of accessibility of the genome to transcription factors is modulated by redox processes. Methylation of DNA (as catalyzed by DNA-methyl transferases, DNMT), as well as posttranslational modification of histones to affect DNA/ histone interactions, are affected by various mechanisms, including ROS-induced modulation of expression of DNMT and histone deacetylases [101], or attenuation of their activity by lipid oxidation products (for review, see [102]). Furthermore, redox control of interactions between transcription factors and histone modifying enzymes was reported. For example, the transcription factor FoxO4 forms a disulfide with p300/CBP acetyl transferase upon exposure of cells to hydrogen peroxide, resulting in changes of FoxO4 acetylation, which is known to modulate its activity [97]. In parallel, this implies that a transcription factor, and the enzyme providing it access to DNA through histone acetylation, are covalently linked.



**Fig. 8.6 Insulin signaling to Akt and FoxO via phosphoinositide** 3'-kinase (**PI3K**). Stimulation of the insulin receptor (InsR) or the related insulin-like growth factor-1 receptor (IGF1-R) causes activation of the lipid kinase, phosphoinositide 3'-kinase (PI3K), which, by generating phosphatidylinositol (3',4',5')-trisphosphate (PIP3), triggers phosphorylation and activation of the serine/ threonine kinase Akt. Akt may migrate into the nucleus and phosphorylate FoxO transcription factors. Following phosphorylation by Akt, FoxOs are inactivated. The lipid phosphatase PTEN dephosphorylates PIP3, thereby attenuating Akt activation. The cascade is regulated by cysteine oxidation state at the levels indicated by a yellow circle: protein tyrosine phosphatases (PTP) controlling insulin receptor tyrosine phosphorylation and PTEN are inactivated by oxidation, resulting in stimulation of Akt. Akt activity may be altered by cysteine oxidation, and FoxO transcription factors were demonstrated to interact with coregulators via reversible disulfide formation. See text for further details (Modified from Klotz, 2014 [119], with kind permission from Springer Science+Business Media)

### 8.5.3 Redox Regulation of Posttranscriptional Control of Gene Expression

Posttranscriptional control of gene expression may occur through modulation of mRNA stability – be it through RNA binding proteins (RBP) that recognize specific sequence elements, such as in the 3'-untranslated regions (UTR) of the respective transcripts, or be it through microRNA (miRNA)-mediated degradation.

**Example 1: HuR** Many RBP are controlled by stress-responsive kinases, such as p38<sup>MAPK</sup>. These kinases phosphorylate RBP and thereby affect their capability of binding to, and (de-)stabilizing specific transcripts. For example, stressful stimuli

cause cytosolic accumulation of the RBP HuR. These stimuli include exposure to ROS, such as hydrogen peroxide [103, 104], or those that generate ROS such as UV radiation [103, 105], arsenite exposure [106], 2-acetylaminofluorene, *tert-butylhydroquinone*, sulindac [107] and others. All these stimuli activate p38<sup>MAPK</sup>. HuR is both a direct and indirect (e.g., via MAPK-activated kinase-2, MK2) sub-strate of p38<sup>MAPK</sup>, which mediates stress-induced cytoplasmic accumulation of HuR and enhances its mRNA stabilizing activity [108–110].

Interestingly, in addition to oxidative stress, HuR activity is stimulated as part of a hypoxic response in mammalian cells. HuR not only stabilizes various hypoxia-inducible mRNAs but also enhances translation of hypoxia-inducible factor (HIF)  $1\alpha$  mRNA, which then leads to an enhanced expression of hypoxia-inducible genes (see [111] for review).

In addition to phosphorylation of HuR, there are a few other mechanisms that control HuR localization and activity in response to oxidative stress. ROS-induced cysteine oxidation, disulfide formation and structural alteration of the tat-interacting protein 30 (TIP30), a tumor suppressor protein regulating nuclear import [112], interfere with the nuclear protein import machinery resulting in higher cytoplasmic levels of HuR and in HuR-dependent mRNA stabilization [113]. Similarly, it was proposed recently that HuR itself can act as a redox sensor. HuR forms homodimers, and homodimerization appears to be required for HuR action. A cysteine residue in the first of the three RNA recognition motifs (RRM) (i.e. RNA binding domains) of HuR was identified as crucial for homodimerization [114]. The authors of the study suggest that this cysteine may mediate alteration of homodimerization and of HuR binding affinity in response to oxidative stress. For example, homodimerization of an isolated RRM1 occurred only under non-reducing conditions in vitro.

Example 2: The Role of miRNAs in Regulating Redox Signaling Regulation of gene expression by micro-RNAs (miRNAs - ca. 22 nucleotide RNAs synthesized by transcription and transcript processing [115]) occurs through miRNA binding to target mRNAs, followed by induced mRNA degradation or preventing translation. miRNA-dependent control of gene expression is affected by oxidative stress at multiple levels; (a) At the level of miRNA expression: Several miRNAs are upregulated in cells exposed to oxidative and similar stress, including miR-200 family miRNAs in vascular smooth muscle and endothelial cells [116]; (b) At the level of miRNA precursor processing: 3T3-derived pre-adipocytes were exposed to various stresses, including H<sub>2</sub>O<sub>2</sub>, paraquat and UV, followed by analysis of expression of Dicer, the enzyme required for processing cytoplasmic pre-miRNAs to mature miRNAs. The authors found that Dicer expression was downregulated by these stimuli. Depletion of Dicer resulted in downregulation of several miRNAs, followed by senescencelike changes in gene expression [117]; (c) At the level of miRNA action: HuR, whose activity is affected by ROS (see above), may relieve miRNA-induced repression of target mRNAs through binding to the same mRNAs and interfering with the miRNA-mRNA interaction [118], thus establishing an indirect regulation of miRNA activity by oxidative stress.

### 8.6 Summary

Cellular signaling processes are triggered by ROS generated endogenously as part of regular ligand/receptor interactions or as by-products of normal fuel metabolism. Similar effects are elicited by exposure of cells to xenobiotics, in part due to ROS generating processes like redox cycling.

While signal transduction pathways stimulated by ROS may be protective in that they elicit an adaptive response, some others may also contribute to damage, as discussed in the case of hormone-induced NOX activation. It will be a major task of future research to devise approaches to distinguish and to control these two sides of ROS signaling in order to exploit only the beneficial effects of ROS signals.

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# **Chapter 9 Role of Oxidative Stress in the Process of Carcinogenesis**

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# 9.1 Introduction: Oxidative Stress

Oxidative stress contributes to the pathogenesis of a wide variety of human diseases, such as inflammatory diseases, neurodegenerative diseases, cardiovascular diseases, diabetes and also cancer. Tumor formation (carcinogenesis) is a multistep process involving initiation, promotion and progression, ultimately leading to a clonal expansion of mutated cells. Diverse chemical and physical agents are able to modulate this complex process resulting in a clinical tumor starting from a single cell. Several molecular mechanisms are discussed to explain the formation of tumors, but the generation of oxidative stress in the cell is believed to be a very central mechanism involved in the process of carcinogenesis: an imbalance between reactive oxygen species (ROS) and the antioxidative capacity of a cell may lead to oxidative damage of cellular macromolecules (DNA, proteins, lipids) which can result in (i) the formation of mutagenic DNA lesions and (ii) the modulation of intracellular signaling pathways affecting central parameters of the cell e.g. the redox-status, apoptosis, DNA repair mechanisms and cellular proliferation. DNA bases can be oxidized by ROS which may result in incorrect base pairing leading to mutations. 8-hydroxy-2'-deoxyguanosine (8-OH-dG) is a pivotal oxidative DNA damage in mammalian cells. A further contribution of ROS to the process of carcinogenesis may be mediated by a stimulation of signal transduction pathways e.g. activation of growth factor-related signaling. Both mechanisms, the genotoxic action of ROS (formation of mutagenic DNA lesions  $\rightarrow$  initiation step of carcinogenesis) as well as the non-genotoxic action of ROS (stimulation of cell growth/inhibition of

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apoptosis  $\rightarrow$  promotion step of carcinogenesis) are important parameters to understand the role of ROS in the process of tumor formation (reviewed by [1, 2]).

The generation of ROS is a physiological process due to the oxidative metabolism of the cell. Therefore cells are continuously exposed to these reactive compounds. The term "ROS" summarizes a large variety of pro-oxidative compounds [3], e.g. the superoxide anion radical  $(O_2^{-})$ , hydrogen peroxide  $(H_2O_2)$ , the hydroxyl radical ('OH), hydroperoxides (ROOH), peroxyl radicals (ROO'), singlet oxygen (<sup>1</sup>O<sub>2</sub>) and ozone  $(O_3)$ . The reactivity of the compounds differs dramatically: half-lives range from nanoseconds (e.g. hydroxyl radical) to hours (e.g. hydrogen peroxide in vitro), depending on the stability as well as enzymatic decomposition of the molecule in the physiological cellular compartment. Usually ROS are inactivated by (i) enzymatic mechanisms e.g. antioxidative enzymes like superoxide dismutases (SOD), glutathione peroxidases (GPx) and catalase (CAT), or (ii) by low molecular non-enzymatic radical scavengers like vitamin E or glutathione. Under physiological conditions, a balance between cellular ROS production and elimination by cellular defense mechanisms is maintained (cellular homeostasis). If the generation of ROS exceeds the antioxidative capacity, these reactive molecules accumulate in the cell. This imbalance of prooxidative molecules and antioxidant capacity of a cell is called "oxidative stress" [4, 5]. An excess of these highly reactive substances can cause severe damage to cellular biomolecules like DNA, lipids and proteins with a potential impact on the cell and the whole organism. On the cellular level, oxidative stress may cause the inhibition or induction of apoptotic cell death [6] or a disturbance of intracellular signal transduction pathways [7], depending on the degree of the "imbalance" of ROS. In non-transformed cells, low-level concentrations of ROS are required for signal transduction, while high concentrations may cause toxic effects. In contrast, cancer cells need relatively high concentrations of ROS to proliferate.

#### 9.1.1 Endogenous Formation of ROS

Examples for endogenous sources of ROS-formation include e.g. the process of oxidative phosphorylation, cytochrome P450-mediated metabolism, activity of different oxidases, peroxisomal processes, and activation of inflammatory cells. Superoxide anion radicals ( $O_2^{-}$ ) are the simplest form of ROS that are formed by addition of one electron to molecular oxygen. These radicals are primarily produced in mitochondria (incomplete reduction of  $O_2$  in the mitochondrial electron transport chain). Ubiquinol:cytochrome c oxidoreductase (complex III) and NADH:ubiquinone oxidoreductase (complex I) account for the majority of superoxide production [8]. Mitochondria produce approximately 2–3 nmol of superoxide/min/mg protein [9, 10]. Defective autophagy of old mitochondria can also be a source of ROS. ROS can be produced enzymatically by cellular oxidases and oxygenases, e.g. NADPH oxidases, xanthine oxidase, lipoxygenases and cyclooxgenases [11]. Xanthine oxidase (XO) is a highly versatile enzyme which catalyzes the reaction of hypoxanthine to xanthine and further on to uric acid, forming  $O_2^{-}$  in a first step and H<sub>2</sub>O<sub>2</sub> in the

second step [12]. Neutrophils, eosinophils, and macrophages utilize oxidases, especially NADPH oxidases, to produce ROS in order to defeat bacteria [13]. If these cells are activated, they elicit a rapid but transient increase in ROS ("respiratory burst"). Chronic infection and inflammation have become well recognized as risk factors for a variety of human cancers. Peroxisomal oxidases, including acyl-CoA oxidase involved in peroxisomal  $\beta$ -oxidation and xanthine oxidase, are responsible for the formation of ROS in peroxisomes. Under physiological conditions, peroxisomes produce mainly H<sub>2</sub>O<sub>2</sub>. In the rat liver, peroxisomes produce approximately 35 % of all H<sub>2</sub>O<sub>2</sub> from normal oxygen consumption [14].

ROS are also endogenously produced during cellular metabolism: the production of reactive oxygen species by cytochrome P450 has been reported by Parke [15]. Furthermore, the cyclooxygenase, a rate-limiting enzyme in the metabolism of arachidonic acid, induces the formation of ROS.

## 9.1.2 Exogenous Stimuli Inducing the Formation of ROS

Oxidative stress also can be induced by exogenous sources: radiation (both ionizing and UV/Vis), metal ions, or various xenobiotics (such as barbiturates, phorbol esters, some peroxisome proliferation stimulating compounds, to name a few) have been shown to induce oxidative stress in different model systems [16].

Ionizing radiation (e.g. X-/gamma-/cosmic rays or alpha-particles from radon decay) is a well-established human carcinogen. It can function at all stages of carcinogenesis. Biological consequences of ionizing radiation include DNA damage leading to mutations and cancer [17], but most of the effects of ionizing radiation are mediated by ROS, which are generated rapidly through radiolysis of water molecules and also by secondary reactions, which can persist and diffuse within cells participating in delayed effects [17, 18].

The potential of metals to generate ROS or to alter the cellular redox-status is a crucial mechanism involved in metal-induced carcinogenicity [19, 20]. Many carcinogenic metals, e.g. Cr(III), Co(II) and Ni(II) have been shown to cause the formation of superoxide anion radicals and hydroxyl radicals, for example via the so-called Fenton reaction [20]. Here, a transition metal ion (in its reduced form) reduces endogenous  $H_2O_2$  to generate the highly unstable and reactive hydroxyl radical.

A variety of different metal ions – e.g. Fe(II), Cu(I), Cr(III, V, IV), Co(II), Ni(II), and V(IV) – is able to enter this Fenton reaction to different extents [21, 22]. Another way to explain the generation of ROS by redox-active metal ions is through the Haber-Weiss-reaction, which is catalyzed by metal ions (reduced form) that convert  $H_2O_2$  to form hydroxyl radicals (Fenton reaction) and (in their resulting oxidized form) oxidize superoxide to molecular oxygen. As a sum of both reactions,  $O_2^{-}$ reduces  $H_2O_2$  to form oxygen, OH<sup>-</sup> and a hydroxyl radical, and the respective metal ion catalyzes this reaction. Redox-inactive metal ions, e.g. Cd(II) are not able to generate free radicals directly under physiological conditions. However, indirect production of ROS has been reported, e.g. in cadmium-exposed cells [23, 24].

The generation of oxidative stress is also a postulated mode of action for different rodent hepatic carcinogens: ethanol, TCDD, lindane or dieldrin [25]. The mechanisms discussed as underlying the formation of ROS include the induction of cytochrome P450 enzymes (e.g. phenobarbital, hexachloride and benzene 1.1-bis(*p-chlorophenyl*)-2,2,2-trichloroethane) activation of or peroxisome proliferator-activated receptors (PPARs). For example, 2-butoxyethanol, a chemical that induces the formation of hemangiosarcomas in the liver of male mice, increases the level of 8-hydroxydeoxyguanosine in mouse liver [26].

Chronic viral infections are a generally underestimated source of free radical generation: a variety of viruses has been associated with a decrease in antioxidant enzymes as well as high levels of hydroxyl radicals and DNA damage leading to an enhanced mutagenic rate [27]. However, compared to endogenously induced DNA lesions, DNA lesions induced by environmental factors often reach a lower level [28].

# 9.1.3 Role of Antioxidants

Antioxidants are a cellular defense mechanism against ROS [29], and include both enzymatic and non-enzymatic antioxidants. The most prominent antioxidant proteins are superoxide dismutases, glutathione peroxidase and catalase. Superoxide dismutases (SOD) catalyze the disproportionation of superoxide anions to hydrogen peroxide and oxygen. Three isoforms of SOD exist: copper/zinc SOD (Cu/Zn-SOD), a homodimer of 32 kDa, localized in the cytosol or mitochondrial inter-membrane space; manganese SOD (Mn-SOD), a homotetramer of 88 kDa, localized in the mitochondrial matrix, and an extracellular Cu/Zn SOD form (EC-SOD), a tetrameric glycoprotein of 135 kDa. Overexpression of SOD2 was found to suppress the malignant phenotype of human melanoma cells [30]. However, the antioxidative enzyme SOD can, if conditions allow, also cause a pro-oxidant effect since the product of its reaction is  $H_2O_2$ , which is more toxic to the cells (especially when converted to the hydroxyl radical via transition metal catalysis). It is therefore essential that  $H_2O_2$ production is balanced by the  $H_2O_2$ -reducing enzymes CAT and GPx (Fig. 9.1).

Catalase which is mainly found in the peroxisomes of mammalian cells, is a tetrameric enzyme consisting of four identical subunits of 60 kDa that catalyzes the conversion of  $H_2O_2$  into  $H_2O$  and  $O_2$ .

The glutathione peroxidases (GPx) are a family of selenium-dependent enzymes with several isoenzymes identified in the mammalian genome (GPx1, 2, 3, 4 and 6). GPx1 was the first identified and is the most abundant selenoprotein in mammals [31]. This enzyme is ubiquitously expressed in humans, protecting cells against oxidative damage by reducing  $H_2O_2$  and a wide range of organic peroxides [32]. Glutathione peroxidases which are localized in the cytosol and mitochondria remove the majority of cytosolic  $H_2O_2$ .

Antioxidative enzymes with an "indirect" effect are e.g.  $\gamma$ -glutamylcysteine synthetase, glutathione reductase or thioredoxin reductases. Nonenzymatic antioxidants such as vitamin E, vitamin C,  $\beta$ -carotene, alpha-lipoic acid, glutathione, and



**Fig. 9.1** Schematic illustration of the role of antioxidative enzymes. *SOD* superoxide dismutase, *GPx* glutathione peroxidase, *CAT* catalase

coenzyme Q may directly scavenge ROS in the cell and are thereby oxidized themselves. Apart from their protective role as preventive agents against cancer development, there is evidence that antioxidant supplementation during chemotherapy has the potential to reduce dose-limiting toxicities of chemotherapeutic drugs in patients with cancer [33].

# 9.2 Role of Oxidative Stress in Cancer

In the last two decades, a growing number of reports investigating associations between oxidative stress and carcinogenesis have been published. One common feature associated with cancer cells is an increased ROS generation compared to normal cells due to a higher metabolic rate [34]. The redox balance of tumor cells differs from that in normal cells, resulting in proliferation of the cells as well as resistance to exogenous ROS. It is reported that ROS levels are raised in a wide variety of cancers, e.g. breast cancer [35], lung cancer [36] and brain tumors [37], cervical cancer [38] and gastric cancer [39]. As a result of increased ROS levels, an increase in the amount of oxidized DNA bases was demonstrated in various human cancers [40, 41]. The phenomenon of increased ROS levels in cancer cells leads to the question if ROS may not only be a consequence of the process of carcinogenesis, but also a causal point in the formation of a cancer cell. Diverse chemical and physical agents can modulate the redox state of the cell, resulting in excessive ROS formation, which may lead to a clinical tumor starting from a single cell. Both, genotoxic actions of ROS (formation of mutagenic DNA lesions  $\rightarrow$  initiation) as well as

non-genotoxic actions of ROS (stimulation of cell growth, inhibition of apoptosis...  $\rightarrow$  promotion) are important parameters to understand the role of ROS in the process of tumor formation.

# 9.2.1 Direct Action of ROS: Oxidative DNA Lesions

Initiated cells are generated when normal cells sustain DNA lesions in distinct genes as a result of a genotoxic offence which are fixed by DNA replication. An increased formation of ROS is associated with the formation of apurinic/apyrimidinic (abasic) DNA sites, oxidized purines and pyrimidines, single strand (SSB) and double strand (DSB) DNA breaks. Diverse ROS are able to oxidize DNA, but the highly reactive hydroxyl radical is the predominant radical that targets DNA [42]. Oxidation of the guanine moiety in DNA at the C8 position results in the formation of 8-hydroxydeoxyguanine or 8-hydroxydeoxyguanosine (8-OH-dG) nucleosides. 8-OH-dG is the most abundant mutagenic adduct caused by ROS: it has been shown to cause mutations, predominantly G to T transversions [43] and therefore is strongly implicated in the process of cancer formation. This oxidative DNA lesion has been reported to be increased 8- to 17-fold in breast primary tumors compared with nonmalignant breast tissue [44, 45]. It has further been demonstrated that 8-OH-dG levels are higher in DNA from tumor tissue compared to non-malignant adjacent tissue e.g. in cervical cancer [46], hepatocellular carcinoma [47] and colorectal cancer [48]. Generation of 8-OH-dG in rat hepatic DNA has been demonstrated after single i.p. administration of genotoxic carcinogens including N-nitrosodiethylamine [49]. Induction of 8-OH-dG was also reported in vivo after application of phenobarbital, ethyl tertiary-butyl ether, dimethylarsinic acid (DMA(V)) and 2-amino-3.8-dimethylimidazo[4,5-f]quinoxaline (MeIOx) (reviewed by [50]).

Based on this evidence, 8-OH-dG is used as a biomarker of oxidative DNA damage, and measurement of 8-OH-dG levels is often applied to evaluate the load of oxidative stress [1, 51, 52]. Other examples of ROS-mediated DNA lesions are 8-oxo-adenine, 5-hydroxy-deoxycytidine and thymine glycol [53]. Altogether, more than 100 oxidized DNA adducts have been identified [54]. It has to be concluded that the induction of oxidative DNA lesions, at least for 8-OH-dG, is potentially mutagenic and therefore of high importance in the process of carcinogenesis.

If the oxidative DNA lesion is not repaired prior to DNA replication, mutations may be formed, leading to replication errors and genomic instability. On the other hand, persistent DNA damage may result in the activation of signal transduction pathways which either arrest or induce transcription (Fig. 9.2). It is estimated that  $10^4-10^5$  oxidative lesions are formed per day in each cell due to endogenous ROS formation [55, 56]. Therefore, the importance of highly efficient DNA repair systems is evident.

Compared with the nuclear genome, the mitochondrial genome is more susceptible to oxidative DNA base damage due to a decreased activity of DNA repair



Fig. 9.2 Schematic illustration of the role of oxidative DNA damage in carcinogenesis. *BER* base excision repair, *NER* nucleotide excision repair, *SSB* single strand break, *AP* apurinic/apyrimidinic site

enzymes and lack of protective histone proteins. Mitochondrial DNA mutations have been identified in a number of cancers [57, 58]. Mutations in genes encoding oxidative phosphorylation can affect cellular ATP production and lead to an imbalance of the energy status of the cell. This is supported by the finding that in tumor cells the rate of glycolysis is much higher compared to non-transformed cells.

Aside from a direct oxidation of nucleic acids, ROS may also indirectly lead to the formation of DNA adducts which may be important in the process of chemical carcinogenesis. A plasma membrane rich in polyunsaturated lipids is highly susceptible towards oxidation by reactive species. ROS-mediated peroxidation of these unsaturated cellular lipid membranes is a process that generates a variety of reactive products, e.g. reactive aldehydes including malondialdehyde (MDA) and 4-hydroxy-2-nonenal (4-HNE). Reactive intermediates are generated during the lipid peroxidation process, react with DNA and give rise to exocyclic etheno- and propane-adducts [59], e.g. 1,*N*6-ethenodeoxyguanosine and 3,*N*4-ethenodeoxycytidine. MDA and 4-HNE, the terminal products of lipid peroxidation, possess a high reactivity towards DNA and proteins [60–63]. MDA was shown to have a mutagenic potential in bacterial assays as well as in the mouse lymphoma assay. Furthermore, this compound induces thyroid tumors in chronically treated rats [64].

# 9.2.2 Indirect Action of ROS: Stimulation of Cell Growth

Next to the genotoxicity of reactive oxygen species which may cause initiation of carcinogenesis, there are non-genotoxic actions of ROS contributing to carcinogenesis. Examples for these non-genotoxic effects of ROS which are important in the process of tumor promotion are (i) stimulation of cellular proliferation (e.g. via activation of the extracellular-regulated kinases 1/2 (ERK1/2)), (ii) evasion of apoptosis or anoikis (e.g. via PI3K/Akt activation), (iii) stimulation of invasion and metastasis (e.g. via stimulation of metalloproteinase (MMP) secretion into extracellular matrix), and iv) increased angiogenesis (e.g. via VEGF-release).

#### 9.2.2.1 Activation of Signaling by ROS

While a permanent high concentration of ROS may lead to the induction of apoptotic or necrotic cell death, low or transient levels of ROS can increase cellular proliferation or survival signaling pathways by activation of transcription factors such as AP-1 [65, 66], NF-κB [67], hypoxia-inducible transcription factor 1α (HIF-1 $\alpha$ ) [68] and/or nuclear factor erythroid 2-related factor 2 (Nrf2) [69]. Activation of these transcription factors can lead to the expression of different genes, including those for growth factors, inflammatory cytokines, chemokines, cell cycle regulatory molecules, and anti-inflammatory molecules [70]. Further signaling proteins and cascades affected by ROS include EGF [71], VEGF [72], JAK-STAT cascades [73], cyclin D1 [74], ras, mitogen-activated protein (MAP) kinases or the PI3K/Akt pathway. Oxidative stress can cause a release of Ca<sup>2+</sup> from intracellular stores. This increase in the intracellular Ca2+ concentration can result in an activation of different kinases, e.g. protein kinase C (PKC), which regulates a variety of cell functions including proliferation, cell cycle, differentiation, cytoskeletal organization, cell migration, and apoptosis [75]. H<sub>2</sub>O<sub>2</sub> is able to modulate distinct protein kinases/phosphatases such as extracellular signal-regulated kinase (ERK)1/2, phosphoinositide 3'-kinase (PI3K) and Akt [76] as well as protein tyrosine phosphatases [75]. Epidermal growth factor receptor can be activated by ROS, resulting in an activation of MAP kinases, which regulate diverse cellular processes including proliferation, differentiation, and apoptosis. The mitogenic mechanism of several nongenotoxic carcinogenic compounds is explained by an increase in intracellular ROS levels which activates distinct signaling pathways that modulate the network of gene expression and stimulate proliferation.

**Nrf2** The Nrf2/ARE signaling pathway (NF-E2-related factor-2/Antioxidant response element) is activated by ROS. This pathway is considered to be the master regulator of the cellular response towards prooxidative stimuli. Nrf2 is a member of the "cap'n collar" family of transcription factors that possess a highly conserved basic leucine zipper structure.

The mechanisms for activation of Nrf2 have been intensively investigated (reviewed by [77]). Under physiological conditions, Nrf2 is bound to its cytosolic

inhibitor Keap1. This inhibitor protein contains reactive cysteine residues that form protein-protein crosslinks through intermolecular disulfide bonds upon exposure to electrophiles or oxidant stress. The resulting conformational change leads to the disruption of the Keap1-Nrf2 complex and liberation of Nrf2 from its inhibitor [78]. Furthermore, activation of Nrf2 can be mediated by different protein kinases [79, 80]: PKC phosphorylates Nrf2, thereby enhancing the stability and/or the release of Nrf2 from Keap1 [81].

After disruption of the Nrf2-Keap1 complex, Nrf2 translocates into the nucleus, heterodimerizes with small Maf proteins and induces the expression of distinct phase II- and cytoprotective enzymes like  $\gamma$ -glutamylcysteine-synthetase (GCS), NADPH-quinone-oxidoreductase1 (NQO1), glutathione-S-transferases (GST) and heme oxygenase1 (HO-1) [77].

Because of the important role of Nrf2 in the antioxidative defence of the cell, this transcription factor is discussed to be classified as a protooncogene [82]: A loss of Nrf2 activity will result in an increase of oxidative stress and therefore predisposes cells to tumorigenesis. During oxidative stress conditions, mice lacking Nrf2 develop more severe intestinal inflammation. The Nrf2-deficient mice showed increased numbers of aberrant crypts, suggesting a function for Nrf2 in the prevention of inflammation and carcinogenesis [83]. Somatic mutations in Nrf2 were identified in cancer patients [84]. However, elevated activity of Nrf2 may also be associated with the process of cancer formation [85].

**AP-1** AP-1 is a collection of dimeric bZip proteins that belong to the Jun (c-Jun, JunB, JunD), Fos (FosB, Fra-1, Fra-2), Maf/ATF subfamily, all of which can bind TPA or cAMP response elements [86]. This transcription factor can be activated by  $H_2O_2$  or cytokines. The activation of AP-1 is mediated mainly by JNK and p38 MAP kinase cascades. AP-1 regulates several genes which are important for cell proliferation, e.g. it up regulates cyclin D1 [87]. Thereby, this transcription factor promotes cyclin-dependent kinase activation, which promotes entry into the cell division cycle. Furthermore, AP-1 suppresses expression of p21<sup>waf</sup>, a protein that inhibits cell cycle progression [88].

**NF-\kappaB** NF- $\kappa$ B is an inducible and ubiquitously expressed transcription factor for genes involved in cell survival, differentiation, inflammation, and growth. Activation of this dimeric transcription factor occurs in response to various stimuli, e.g. TNF $\alpha$  and LPS. During the activation process, I $\kappa$ B kinases are activated, resulting in a dissociation of an inhibitory protein thereby unmasking the nuclear localization sequence of NF- $\kappa$ B. The dimeric transcription factor translocates into the nucleus where it binds to specific  $\kappa$ B-sites in the promoter regions of different genes [89]. NF- $\kappa$ B is a direct target for oxidation, which can affect its ability to bind to DNA [67]. Its activation can be blocked by antioxidants, including L-cysteine, NAC and vitamin E.

The expression of various genes, e.g. *bcl-2*, *bcl-xL*, *traf1* and *sod*, is regulated by this transcription factor. NF- $\kappa$ B activation has been linked to carcinogenesis through inhibition of apoptosis as well as promotion of angiogenesis and metastasis [90]. Tumor cells from blood neoplasms, and colon, breast, pancreas, and squamous cell carcinoma cell lines have all been reported to constitutively express activated NF- $\kappa$ B [91].

**Ras** The Ras pathway is another central signaling pathway which is related to oxidative stress and cancer [92]. The Ras family of small GTPases (Ha-, Na, Ki-ras) has emerged as a central node in the coordination of cell proliferation. Approximately 30 % of human tumors contain activating mutations in the Ras family of protooncogenes, rendering the protein constitutively active [93]. Several studies have demonstrated that mutant Ras leads to an increase in ROS levels, which causes DNA damage and contributes to transformation [94, 95]. Mutant RasVal12 positively regulates the NADPH oxidase system Nox4-p22phox, resulting in an increased formation of ROS in the cell.

**PPAR** Peroxisome proliferator-activated receptors (PPARs) play essential roles in the regulation of differentiation, development and metabolism. There are three isoforms, PPAR-alpha, PPAR-beta/delta and PPAR-gamma. The activation of these PPARs has been linked with the process of carcinogenesis in the liver. Several mechanisms are discussed, e.g. enhanced cell replication, promotion of preneoplastic lesions, and inhibition of apoptosis [96]. Furthermore, the activation of PPAR $\alpha$ by peroxisome proliferators in rats and mice was reported to produce oxidative stress, due to the induction of distinct cytochrome P450 enzymes (CYP4A1) and oxidases (fatty acyl coenzyme A oxidase) [97]. Examples for the different compounds that act as PPAR $\alpha$  agonists are hypolipidemic drugs (fibrates), phthalate esters (DEHP), and halogenated solvents. These compounds increase the number as well as the size of the peroxisomes leading to a tumor induction in the liver [98, 99]. The formation of cancer by toxic PPAR-inducing agents shows a mechanistic link between peroxisome proliferation–induced ROS and liver tumorigenesis [100].

**HIF** ROS generated at complex III of the mitochondrial respiratory chain may directly regulate a family of transcription factors, the hypoxia-inducible factors (HIFs) [101]. HIF-1 is a heterodimeric transcription factor and a basic-helix-loop-helix (bHLH) protein of the PAS family. The concentration of this factor is tightly controlled by the intracellular oxygen concentration: several enzymes are involved in the induction of the HIF-1 subunit by activating the PI3K/Akt/p706K and the MEK/ERK pathways [102, 103]. HIF-1 $\alpha$  modulates a broad range of cellular functions including cell proliferation and angiogenesis, processes that are important in tumor development and progression [68, 104]. The involvement of this transcription factor has been implicated in ROS-induced carcinogenesis in a variety of human tumors, including bladder, breast, colon, glial, hepatocellular, ovarian, pancreatic, prostate, and renal tumors [105].

# 9.2.3 Epithelial-Mesenchymal Transition (EMT)

Epithelial-mesenchymal transition is a cellular mechanism that leads to metastasis: epithelial cells transform to a mesenchymal phenotype [106], accompanied by an increase in ECM proteins. This improves migration of the cell leading to a more aggressive form of the tumor. Various ROS-activated signaling pathways are, at least in part, implicated in this cellular process, e.g. E-cadherin, NF- $\kappa$ B signaling,

HIF-1 or integrin-mediated MAPK signaling, transforming growth factor-activated kinase 1 (TAK1), AP-1 and Smad [107–109]. ROS also regulate p21-activated kinase 1 (PAK-1), which is involved in Rac-associated cytoskeleton remodeling, which is directly linked to metastasis and angiogenesis [110].

#### 9.2.4 Neoangiogenesis

Angiogenesis is the physiological process of new blood vessel formation from preexisting vessels. It is an important process in normal growth/development as well as wound healing, but it is also a fundamental step for tumor growth as well as metastasis [111]. In tumor cells, the synthesis of the vascular endothelial growth factor (VEGF) is greatly enhanced to initiate this process. The process of angiogenesis is very complex, other substances which are involved are matrix metalloproteases (MMPs), angiopoietin-1, fibroblast growth factor, interleukin-8, platelet-derived growth factor and TGF- $\beta$ . During angiogenesis, VEGF levels are increased by ROS [112]. Due to the pro-oxidative state of most tumors, VEGF is reported to be highly upregulated in most human cancers. The NADPH oxidase Nox1 which is overexpressed in colon and prostate cancers induces the production of H<sub>2</sub>O<sub>2</sub>, which augments VEGF, VEGFR and MMP levels [113]. ROS derived from these oxidases result in VEGFR2 autophosphorylation, thereby promoting the induction of transcription factors and genes involved in angiogenesis.

#### 9.2.5 Inflammation

Inflammation is part of the biological response of tissues to harmful stimuli, e.g. pathogenic bacteria. In contrast to acute inflammation, different types of cells are present at the site of inflammation in chronic inflammation: neutrophils, eosinophils, and macrophages. These cells, including phagocytes, undergo a "respiratory burst" leading to transient increases in oxygen uptake and generation of ROS through NADPH oxidase [114]. Due to the prolonged activation of NADPH oxidase, these cells contribute significantly to ROS levels and therefore the destructive processes in inflammatory tissue. This prolonged or chronic inflammation is known as a risk factor for a variety of human cancers.

# 9.2.6 Apoptosis

Apoptosis is the process of programmed cell death leading to characteristic morphological changes of the cell, e.g. cell shrinkage, membrane blebbing, chromatin condensation and nuclear fragmentation [115]. Apoptosis is an

active process that is initiated at the molecular level via activation of "death receptors", e.g. Fas/CD95 and TNFR1 or via a mitochondrial pathway. The formation of the mitochondrial permeability transition pore, initiating the apoptotic cascade by release of cytochrome c into the cytosol, is modulated by pro- or antiapoptotic proteins of the Bcl-family. Apoptosis and the genes that control it have a profound effect on the malignant phenotype: loss of apoptosis can impact tumor initiation, progression and metastasis. The antiapoptotic proteins Bcl-2 or Bcl- $x_L$  promote cell survival by blocking programmed cell death. Overexpression of Bcl-2 promotes proliferation of lymphoma cells. In addition to Bcl-2, Bcl- $x_L$  is a potent death suppressor that is upregulated in some tumor types. The regulation of apoptotic gene expression by oxidants is a promising therapeutic approach.

However, the role of oxidative stress in apoptosis is ambivalent: on the one hand it is known that ROS, e.g.  $H_2O_2$  at low doses, induce apoptosis (reviewed by [116]). A variety of pro-apoptotic substances, e.g. redox cycling compounds like the cytostatic drug doxorubicin induce apoptosis via the generation of ROS. Consequently, antioxidants such as *N*-acetyl cysteine, glutathione, and dithiothreitol inhibit the apoptotic process, supporting the link between ROS formation and apoptosis. On the other hand, low doses of  $H_2O_2$  are able to stimulate proliferation via activation of proliferation-sensitive pathways. Several cytostatic drugs have been shown to inhibit ROS production and oxidative DNA damage, thereby inhibiting tumor promotion [116].

# 9.2.7 ROS-Regulated MicroRNAs

MicroRNAs are small (21–24 nucleotides), non-coding, evolutionarily conserved RNA molecules that regulate gene expression by base pairing with the 3'-untranslated region (UTR) of target mRNAs, causing translational repression or mRNA cleavage [117]. MicroRNA (miRNA) expression is associated with cellular proliferation, death, and development. Moreover, miRNAs actively participate in different pathologies, including cancer. Ionizing radiation, etoposide, and  $H_2O_2$  can induce alterations in global miRNA expression patterns [118]. Several ROS-related miRNAs have been described [119]. miR-210, which is overexpressed in breast and hepatocellular carcinomas (HCC), is associated with invasion and poor clinical outcome [120]. miR-141 and miR-200a target the protein kinase p38, which is one of the main sensors of oxidative stress [121]. p38 inactivation is associated with ROS accumulation and the subsequent stimulation of antioxidant defenses. Pre-treatment with the free radical scavenger NAC prevented radiation-induced alterations in miRNA expression, suggesting that miRNAs actively respond to oxidative stress [122]. Primary high-grade human ovarian carcinomas overexpress the miRNA miR-200a. Concomitant miR-200a overexpression and p38-downregulation sensitizes ovarian cancer cells to chemotherapeutic ROS inducers.

# 9.3 Oxidative Stress and Cancer: Clinical Correlations

Several chemical compounds induce the formation of ROS in the cell and also lead to the formation of tumors. Several modes of action by which ROS may influence the multistep process of tumor formation – initiation, promotion and progression – were discussed above. In this section, correlations of polymorphisms in oxidative-stress-related genes and cancer formation will be reviewed, as well as the outcome of antioxidants used in human intervention studies on oxidative parameters.

#### 9.3.1 Polymorphisms of Oxidative-Stress-Related Genes

Single nucleotide polymorphisms (SNPs) constitute the majority of genetic variation observed in the human population and are defined as a variation in a single nucleotide pair occurring at a population frequency of at least 1 %. Recent evidence demonstrates an association between a number of SNPs in antioxidant genes and oxidative DNA repair genes and human cancer susceptibility.

**Superoxide Dismutases (SOD)** The Japan Collaborative Cohort (JACC) Study group [123] analyzed serum SOD activity among the subjects within a large-scale cohort study in Japan: significantly low SOD activity was evident in male heavy smokers. In the JACC Study (914 cancer deaths and 2,739 matched controls) a slightly positive association between serum SOD activities and the risk of all cancermortality was observed [124].

The Breast and Prostate Cancer Cohort Consortium [125] analyzed nine cohorts including over 10,726 post-menopausal breast and 7,532 prostate cancer cases with matched controls. The consortium did not observe a significant association of breast and prostate cancer risks and survival with variants of the manganese superoxide dismutase (MnSOD) gene (rs4880 Val16Ala) and that of glutathione peroxidase (GPx-1; rs1050450 Pro198Leu). However, a weak inverse association between prostate cancer risk and GPx-1 Pro198Leu carriers was observed [125].

In a hospital-based case–control study conducted by the National Cancer Institute, Rajaraman et al. [126] evaluated risk of glioma (n=362), meningioma (n=134), and acoustic neuroma (n=69) compared to non-cancer controls (n=494) with respect to nine single nucleotide polymorphisms in the CAT, GPx1, NOS3, PON1, SOD1, SOD2, and SOD3 genes. Their results suggest that common variants in the SOD2, SOD3, and CAT genes may influence brain tumor risk: an increased risk of glioma and meningioma was observed with the SOD3 variant rs699473. There was also indication of increased acoustic neuroma risk with the SOD2 rs4880 Ala variant and decreased acoustic neuroma risk with the CAT rs1001179 T allele variant.

Gadjeva et al. [127] analyzed 21 patients with melanoma for MDA concentrations as well as SOD and CAT activity compared to healthy volunteers. Plasma levels of MDA and the enzyme activity of CAT were significantly higher in patients with melanoma, and erythrocyte SOD activity was significantly lower. Manju et al. [128] investigated the extent of oxidative stress, the levels of SOD, catalase and ceruloplasmin together with the tumor markers aspartate transaminase (AST), alanine transaminase (ALT), alkaline phosphatase (ALP) and total sialic acid (TSA) levels in the circulation of women with cervical carcinoma. Low levels of SOD and CAT observed in the circulation of cervical cancer patients may be due to their increased utilization to scavenge lipid peroxides as well as sequestration by tumor cells.

Elango et al. [129] analyzed blood samples collected from stage III oral cancer patients before initiating radiotherapy. The concentrations of selenium, all non-enzymatic antioxidants and the activities of enzymatic antioxidants were found to be lowered in oral cancer patients, compared to a control group.

Choi et al. [130] evaluated associations between the gene variants MnSOD Ala16Val, CAT-262 C>T, and GPx1 Pro200Leu and prostate cancer risk among 724 men with incident prostate cancer who participated in the Carotene and Retinol Efficacy Trial (CARET) cohort. However, there were no associations between genotypes of MnSOD, CAT, and GPx1 and prostate cancer risk. Only among men diagnosed before age 65, CAT TT genotype was associated with an increased risk of prostate cancer (OR 2.0).

The authors conclude that variants in MnSOD, CAT, or GPx1 do not seem to have an influence on prostate cancer risk in this cohort of men who were smokers or exposed to asbestos, although it is possible that cumulative defects in protection from oxidative stress may result in increased risk of the disease.

**Catalase (CAT)** A common catalase-262 C/T polymorphism has been identified in the promoter region of human CAT, and the variant of this gene affects transcriptional activity and catalase levels in red blood cells [131]. Several epidemiologic studies have investigated the relationship between SNPs of this gene and human cancer risks; however, also for CAT, results remain inconclusive. Polymorphisms of CAT were not associated with lung cancer risk in a Chinese population [132], non-Hodgkin's lymphoma in the United Kingdom [133], or prostate cancer in the United States [130].

**Glutathione Peroxidases (GPx)** More than 30 SNPs have been identified in the GPx1-gene. A SNP resulting in a proline-to-leucine substitution at codon 198 of human GPx1 has been associated with an increased risk of breast [134], prostate [135], lung [136], and bladder cancer [137] but is not consistent in all populations [138, 139]. A second polymorphism involves a variable number of "GCG" trinucleotide repeats in the first exon of the human GPx1-gene that results in five, six, or seven alanines near the N-terminus. The number of repeats is associated with cancers of several types, but there is no evident pattern for the allele influencing the risk [140]. The role of gastrointestinal glutathione peroxidase (GPx2) in tumor formation is not clear: GPx2 is increased in human colorectal adenomas, in Barrett's esophagus, and in lung adenocarcinomas from smokers (reviewed by [140]), but GPx2 knockout mice have increased susceptibility to develop UV radiation–induced skin cancer [141]. The GPx3 promoter was shown to be hypermethylated in primary prostate cancer samples and distinct human prostate cancer cell lines [142]. Yu et al. [143] reported that an inactivation of the GPx3 gene correlated with a poor clinical outcome.

#### 9.3.2 Intervention Therapies with Antioxidants

In several epidemiological studies, a high intake of fruit and vegetables has been associated with a lower incidence of distinct forms of cancer. Usually, antioxidative effects are discussed as a mechanistic cause – at least in part – for these observations. According to the underlying theory, intake of antioxidants by consumption of fruit/vegetables or food supplements should protect against reactive oxygen species and decrease the formation of oxidative DNA damage. However, the data from literature differ.

Protective effects of polyphenols were reported by various groups. Wilms et al. [144] performed a human intervention study (168 healthy volunteers, 4 weeks) to assess antioxidative and possible anti-genotoxic properties of a blueberry/apple drink (97 mg of the antioxidative flavonoid quercetin and 16 mg ascorbic acid/day). They demonstrated a protective effect against H<sub>2</sub>O<sub>2</sub>-induced DNA damage in lymphocytes (comet assay). It was hypothesized that individuals bearing genetic polymorphisms for genes related to the metabolism of the micronutrient quercetin, oxidative stress and DNA repair differ in their response to DNA protective effects of increased antioxidant intake. Lymphocytes from individuals bearing variant genotype for Cyp1B1\*5 (amino acid change of SNP: V432L) seemed to benefit more than wild-types from DNA damage-protecting effects upon intervention. Variants for COMT tended to benefit less or even experienced detrimental effects from intervention [144].

A further intervention study (18 healthy probands, 7 weeks) showed protective effects of a mixed berry juice [145]. During intervention phase, a decrease of oxidative DNA damage and an increase of reduced glutathione and of glutathione status were observed compared to a polyphenol-depleted juice. Similar results were obtained with uptake of green tea: Hakim et al. [146] demonstrated in a randomized controlled study (133 heavy smokers, 4 months) a decrease in urinary 8-OH-dG after consumption of polyphenol-rich decaffeinated green tea, but not in the control group (black tea group with low content of polyphenols). Luo et al. [147] showed in an intervention study (124 individuals with high risk of liver cancer) that green tea polyphenols (500/1,000 mg/day, 3 months) decreased the level of urinary 8-OH-dG compared to placebo.

On the other hand, diverse studies investigating the effect of fruit and vegetables showed no correlation between dietary intake of antioxidative compounds and oxidative damage. Moller et al. [148] performed a randomized, placebo-controlled intervention study (43 individuals, 24 days) to investigate the effect of fruit and vegetables (600 g/day) on the amount of oxidative DNA damage: consumption of fruit and vegetables had no effect (i) on oxidative DNA damage (detected in urine or in mononuclear cells) and (ii) on the sensitivity against  $H_2O_2$  (comet assay) compared to placebo. Briviba et al. [149] reported that in a randomized controlled trial with 64 healthy individuals (8 weeks) receiving different amounts of fruit and vegetables per day, no differences in the levels of endogenous DNA strand breaks, oxidative DNA damage and plasma markers for lipid peroxidation were detected: although consumption of 8 servings versus 2 servings/day (4 weeks) significantly increased the carotenoid level in plasma, no significant differences in DNA damage, lipid peroxidation, and antioxidant capacity markers among healthy subjects were detected. Kristal et al. [150] examined nutritional risk factors for prostate cancer among 9.559 participants in the Prostate Cancer Prevention Trial. Nutrient intake was assessed using a food frequency questionnaire and a structured supplement use questionnaire; presence or absence of cancer was determined by prostate biopsy. Neither dietary nor supplemental intakes of nutrients, including lycopene, longchain  $\omega$ -3 fatty acids, vitamin D, vitamin E, and selenium were significantly associated with cancer risk. Huang et al. [151] demonstrated that supplementation of diet with vitamin C (500 mg/day) and vitamin E (400 IU d-alpha-tocopheryl acetate/ day) had no significant effect on oxidative DNA damage as measured by urinary 8-OH-dG in 184 nonsmoking adults (2 months). However, fruit and vegetable intake and serum ascorbic acid were found to be inversely associated with urinary 8-OHdG levels. In another trial, vitamin C was demonstrated to reduce oxidative stress among subjects with atrophic gastritis [152]: the adjusted difference in the changes of total ROS between baseline and after 5-year supplementation was statistically significant between the intervention groups.

Regarding a supplementation with lycopene, van Breemen et al. [153] reported no significant changes in the DNA oxidation product 8-oxo-deoxyguanosine and the lipid peroxidation product malondialdehyde in prostate tissue and plasma, respectively, as a result of lycopene (30 mg/day, 3 weeks) administration. Riso et al. [154] reported a decrease in TNF-alpha production (26 participants, 26 days) after consumption of a tomato-based drink (*Lyc-o-Mato*; 5.7 mg lycopene, 1 mg B-carotene, 1.8 mg tocopherol), whereas the other parameters of oxidative stress were not modified by the treatment. Schaumberg et al. [155] demonstrated that  $\beta$ -carotene supplementation had no effect on the risk of non-melanoma skin cancer. Preliminary data of a study by Signori et al. [156] showed that an administration of omega-3 fatty acids (4 g/day, 1 year) in postmenopausal women at increased risk for breast cancer decreased serum triglycerides and increased HDL cholesterol, but did not alter biomarkers of IGF-1-signaling, inflammation or oxidative stress. Harms-Ringdahl et al. [157] showed that tomato juice (150 ml/day=15 mg lycopene/day) has an antioxidant effect (15 participants, 5 weeks).

A reduction of oxidative parameters by dietary supplementation with selenium was shown in oral cancer patients: Elango et al. [129] investigated whether selenium supplementation (400  $\mu$ g/day, 6 months) of radiation treated oral cancer patients improves the status of GSH, vitamin E, vitamin C, vitamin A, SOD, CAT, GPx and GR. The selenium group showed marked increase in the concentrations of antioxidants compared to controls. Hopkins et al. [158] reported that an antioxidant micronutrient cocktail (e.g. 800 mg dl-alpha-tocopherol acetate, 24 mg β-carotene, 1 g ascorbic acid, 200  $\mu$ g L-selenomethionine) modulates biomarkers of oxidative stress and inflammation in humans (decrease in plasma TNF-alpha and oxidized cystein). The role of selenium in the process of carcinogenesis is further reviewed by Davis et al. [140], Hatfield et al. [159] and Nicastro and Dunn [160].

In addition to the nutritional intervention, pharmacological reduction of the cancer risk was also analysed: epidemiologic studies have suggested that long-term

use of the xanthine oxidase inhibitor allopurinol in gout patients is associated with a lower risk of colorectal cancer [161] and an increased survival of patients with advanced colorectal cancer. It was suggested that inhibition of xanthine oxidase may reduce ROS levels and consequently ROS-mediated proliferative pathways. However, in a randomized, double-blind, placebo-controlled preoperative trial in subjects with colorectal adenomatous polyps, it was demonstrated that the level of the proliferation marker Ki-67 (primary endpoint) was not decreased by allopurinol (100, 300 mg/day, 4 weeks). Only a decrease in  $\beta$ -catenin expression levels (a secondary endpoint) was detectable in adenomatous tissue compared to normal adjacent tissue [162]. Oltipraz (125 mg/day, 8 weeks), a potent inducer of phase II detoxification enzymes, caused no major effect on oxidative DNA damage [163] in a double-blind, randomized, placebo-controlled trial (233 healthy individuals at high risk of exposure to aflatoxin).

In addition to the investigation of the effects on "basal" biomarkers of oxidative stress, it may be useful to investigate modulating effects of antioxidative compounds on ROS-mediated signaling pathways in cancer tissue. Magbanua et al. [164] examined the effects of lycopene and fish oil on prostate gene expression in a doubleblind placebo-controlled randomized clinical trial (48 participants, 3-months intervention with lycopene, fish oil supplementation or placebo) via cDNA microarray analysis. The differential gene expression patterns and pathway analyses showed no significant individual gene that was associated with high intake of fish or tomato. Magbanua et al. [164] revealed a modulation of androgen and estrogen metabolism in men who routinely consumed more fish and tomato compared to men who ate less. In addition, modulation of arachidonic acid metabolism was observed after 3 months of fish oil supplementation compared with the placebo group; and modulation of Nrf2-mediated oxidative stress response for either supplement versus placebo.

In summary, data from clinical trials using dietary supplementation with antioxidants are inconsistent with respect to effects on various individual markers of oxidative stress.

#### 9.4 Conclusion

If DNA bases are modified by attack of ROS, and this damage is not corrected by DNA repair enzymes, this may result in the formation of mutations. Although the role of oxidative DNA damage in neoplasia has been established, signal transduction pathways also contribute to the process of carcinogenesis. The role of reactive oxygen species in cell growth regulation is complex, being cell specific and dependent upon the form of the oxidant as well as the concentration of the particular reactive oxygen species. Although plausible, evidence from human studies for a reduction of oxidative DNA damage by antioxidant vitamins has been sparse and inconsistent.

This incoherence may be due to differences in the basal antioxidant defense capacity in different study designs, which may be sufficient to protect tissues from ROS without antioxidant supplementation.

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# Part II Agents That Produce Toxicity: Mechanisms and Therapeutic Interventions

# Chapter 10 Isolation of Murine Adult Bone Marrow and Fetal Liver Cells for Mechanistic Assessment of Hematotoxicity Caused by Organic Solvents

Nicola A. Philbrook and Louise M. Winn

## **10.1 Introduction**

Due to their chemical properties, organic solvents are often used in industrial settings to dissolve water insoluble materials. These properties include being lipophilic, volatile, lacking charge and having a small molecular weight [1]. While organic solvents are used extensively, it is well-known that environmental and occupational exposure to organic solvents is linked to several toxicities including cancer, neurotoxicity, and reproductive effects. These exposures can also cause hematotoxicity in both adults and the developing fetus, which may ultimately lead to leukemias. Leukemias are defined by the uncontrolled proliferation of hematopoietic cells that have lost the ability to differentiate into normal mature blood cells responsible for oxygen transport, host defense and repair, and maintaining hemostasis [2]. Although the cause of most leukemias remains unknown, certain factors have been implicated and include: heredity, radiation, viral infection, treatment with chemotherapeutic agents, and environmental chemical exposures [3, 4]. In addition to leukemia, hematotoxicity also includes anemias, methemoglobinemia, immunosuppression and infection [5].

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While the mechanisms by which organic compounds cause toxicity are not fully understood, many of these compounds can be bioactivated to generate reactive intermediates and/or reactive oxygen species (ROS). These species can act both as signaling molecules, which affect the regulation of gene expression, cell growth, and cell death, and they can also directly damage DNA, protein and lipids. Given that the process of hematopoiesis is tightly controlled and involves a high degree of cell proliferation and differentiation, blood-forming organs are particularly sensitive to toxicities caused by environmental exposures.

Understanding the mechanisms by which organic compounds initiate this toxicity is crucial to setting safe workplace and industrial emissions guidelines. In adult humans and most laboratory animals, hematopoiesis occurs in the bone marrow. In the developing fetus, the site of hematopoiesis begins in the yolk sac and progresses to the aorta-gonad mesonephros region, the placenta, the fetal liver, spleen and finally the bone marrow where it remains throughout life [6, 7]. This chapter describes the procedure for extracting bone marrow from adult mice and other blood forming tissues from developing mouse fetuses. Additionally, this chapter summarizes techniques that can be employed to understand the hematotoxicity initiated by various organic compounds.

### 10.2 Materials

#### **10.2.1** Adult Mice for Bone Marrow Extraction

- 1. CD-1 mice, male or female
- 2. 26-gauge needle
- 3. Mazola® corn oil
- 4. organic solvent of interest
- 5. surgical scissors and rat tooth forceps
- 6. 70 % ethanol
- 7. 1.5 ml Eppendorf tube
- 8. petri dish
- 9. phosphate buffered saline (PBS; pH 7.4)
- 10. microcentrifuge

#### **10.2.2** Breeding Mice and Dissecting Fetal Tissues

- 1. CD-1 mice, male and female (Note 1)
- 2. gross anatomy probe
- 3. forceps and surgical scissors
- 4. 70 % ethanol
- 5. 15 ml conical tube with lid

# 10.2.3 Fetal Liver Cell Culture

- 1. 23-gauge needle
- 2. Iscove's Modified Dulbecco's Media (IMDM)
- 3. 100 % fetal bovine serum (FBS)
- 4. mouse stem cell factor (MSCF)
- 5. interleukin-3 (IL-3)
- 6. interleukin-6 (IL-6)
- 7. β-mercaptoethanol
- 8. sterile reverse osmosis double distilled water
- 9. sterile phosphate buffer saline (PBS; pH7.4)
- 10. 100 mm polystyrene cell culture plates
- 11. 70 % ethanol
- 12. organic solvent of interest

# 10.3 Methods

# 10.3.1 Treatment of Animals and Isolation of Bone Marrow

- 1. To prepare the solution of the organic solvent of interest for intraperitoneal (i.p.) injection, first dilute it with corn oil to the desired concentration. Inject each mouse i.p. using a  $25^{5/8}$ -gauge needle and a dosing volume of 10 µl per gram of mouse body weight.
- 2. To isolate bone marrow (Figs. 10.1 and 10.2), euthanize the treated mouse by cervical dislocation (Note 2) at the desired time-point after exposure to the organic solvent, and spray the hind limbs with 70 % ethanol.
- 3. Using forceps, extend one of the hind legs of the mouse by grasping the foot, and then begin to cut away skin and muscle above the knee with surgical scissors, snipping proximally towards the hip (Fig. 10.1).
- 4. Run the scissors as far up towards the hip joint as possible, and then cut transversely through the femur. Now that the hind limb is detached, remove as much muscle from the bone as possible. Exposed bone should look red from the bone marrow on the interior (Fig. 10.1).
- 5. Once tissue has been cleared, cut the femur directly above the knee and place in a petri dish. Using a 1 ml syringe and 26-gauge needle, aspirate the bone marrow by forcing PBS through the femur by inserting the needle through the hollow portion of the bone at one end. Red-pigmented bone marrow should extrude from the bone, leaving a white bone behind. Pipet the bone marrow to break up clumps (Fig. 10.2).
- 6. Centrifuge at  $900 \times g$  for 3 min to collect a cell pellet of bone marrow cells (Fig. 10.2). Aspirate off PBS and flash freeze in liquid nitrogen. Store at -80 °C until further use.
- 7. Repeat all steps with the other hind limb of the mouse.



**Fig. 10.1** Extraction of bone marrow. A. The hind legs are sprayed with 70 % ethanol and removed using surgical scissors and forceps. Tissue and muscle are removed to expose bone, and the femur is removed from the distal portion of the leg using surgical scissors



**Fig. 10.2** The marrow is expelled from the bone using PBS and a 26-gauge needle. Bone marrow cells are suspended in PBS, centrifuged ( $900 \times g$ ), and collected for later use



**Fig. 10.3** Extraction of fetal-placental units. CD-1 mouse dam is sprayed with ethanol, and the uterus is exposed. The uterus is removed from the dam, and fetal-placental units are gently removed from each uterine horn. Please note that this litter is not representative of the average number of pups found in a CD-1 mouse litter

# 10.3.2 Breeding of Mice for Fetal Liver Extraction

- 1. Female CD-1 mice are housed with male CD-1 mice at a 2:1 ratio from 1700 h until 0900 h. At 0900 h, the presence of vaginal plugs is checked using a gross anatomy probe. The time of pregnancy is denoted as GD 1 if a plug is observed and pregnant females are separated from the colony.
- 2. To isolate the fetal liver (Note 3), euthanize pregnant dams by cervical dislocation and spray the abdomen with 70 % ethanol. Using forceps, tent skin in the lower abdomen and cut up along the mid-sagittal plane to expose internal organs (Fig. 10.3).
- 3. Identify ovaries on either side of the uterine horn, and remove the uteri, including the ovaries, by cutting above the oviducts and across the cervix. Place the uteri on a clean piece of bench paper, and beginning with the left uterine horn, remove the ovary with surgical scissors, creating an opening at the end of the uterine horn. Apply pressure on the proximal side of the most distal fetal-placental unit with gloved fingertips, and gently slide one fetal-placental unit out of the uterus. Try not to burst the amniotic sac in this process (Note 4). Continue this procedure for consecutive fetal-placental units and the right uterine horn (Fig. 10.3).
- 4. Once the fetal-placental units are removed from the uteri, detach the placenta from the rest of the conceptus using surgical scissors, burst the amniotic sac, and expose the fetus (Fig. 10.4).



Fig. 10.4 Exposing the fetus. The placenta is removed using surgical scissors, and the fetus is gently removed from its yolk sac



Fig. 10.5 Removal of the fetal liver: The fetus is decapitated, hind legs are removed, and the fetal liver is gently extracted from the body cavity

5. Decapitate the fetus, and cut the fetal abdomen transversely just above the lower limbs. Using forceps, apply pressure to the body just above the dark red liver, which will cause it to extrude from the open abdomen. Remove the liver by gently pulling it away from surrounding tissue using a pair of curved forceps (Fig. 10.5). Be sure to dissect away any intestinal tissue that may be intertwined

with liver tissue at this point (white/translucent tissue). Finally, place the fetal liver in a 15 ml conical containing culture media (see below).

6. Collect all fetal livers from one dam in the same 15 ml conical and continue to methods for primary cell culture.

## 10.3.3 Primary Cell Culture of GD14 Fetal Liver Cells

- 1. To prepare the pre-stimulation mix (media) add 42.5 ml IMDM, 7.5 ml 100 % FBS, 50  $\mu$ l IL-3 and IL-6 (both made up to 1  $\mu$ g/100  $\mu$ l stock), 250  $\mu$ l MSCF (made up to a 1  $\mu$ g/100  $\mu$ l stock), 500  $\mu$ l antibiotic/antimycotic (1×), 500  $\mu$ l L-glutamine (1×), and 500  $\mu$ l of a 0.1 % stock of  $\beta$ -mercaptoethanol to a sterile glass bottle. Warm media to 37 °C prior to use (Note 5).
- 2. Once fetal livers are isolated, pool together 5–7 fetal livers in 2 to 3 ml of fresh pre-stimulation mix in a 15 ml conical with a lid. Spray outside of the conical with 70 % ethanol, and transfer the tube into a sterile cell culture hood.
- 3. Using sterile technique, create a single cell suspension of fetal liver cells by passing the livers through a 23-gauge needle several times until no clumps are visible.
- 4. Centrifuge cells at  $900 \times g$  for 3 min to pellet cells, wash with 5 ml PBS, and then re-suspend cells in 2–3 ml of fresh pre-stimulation mix.
- 5. Divide cells between 3 or 4 cell culture plates (100 mm), adding more prestimulation mix to bring the final volume to 10 ml per plate. Gently agitate the plate to evenly distribute the cells around the plate. Hematopoietic cells will remain in suspension.
- 6. Cells should be allowed to acclimatize for 24–48 h at 37 °C in a humidified atmosphere of 5 %  $CO_2$  prior to incubation with desired organic solvent.
- 7. Following desired time period of incubation, collect cells and assess for desired molecular markers of toxicity.

# 10.3.4 Molecular Techniques Used to Quantify Toxicity Caused by Exposure to Organic Solvents: Focus on Oxidative Stress

 ROS detection. While there are a number of methods to detect the presence of ROS in cells, the method that our laboratory is most familiar with is detection using the fluorescent dye 2',7'- dichlorodihydrofluorescin diacetate (DCFDA). DCFDA is a non-fluorescent, membrane permeable precursor to the membrane impermeable H<sub>2</sub>DCF, that is produced by intracellular esterases. H<sub>2</sub>DCF is oxidized intracellularly to produce the fluorescent product, carboxydichlorofluorescein (DCF) [8]. The increase in fluorescence emitted by DCF in cells excited at 505 nm can be measured at 535 nm using a fluorescent microscope [9], a spectrophotometer [10], or flow cytometry [8, 11]. Because it is inexpensive
and easy to use, DCFDA is a popular tool used to detect presence of intracellular ROS in a variety of circumstances.

- 2. qRT-PCR. Quantifying mRNA transcript levels of genes that may affected by the presence of oxidative stress in the cell is a technique that can be employed to assess the effect of exposure to an organic solvent. Primers can be synthesized or purchased commercially to detect differences in mRNA transcript levels between exposed and unexposed cells or tissue. RNA extraction can be performed using a variety of commercial RNA extraction kits (i.e.: RNeasy Extraction Kit, Qiagen). RNA can be converted to cDNA, that is subsequently used in qRT-PCR reactions. qRT-PCR is a sensitive technique used to detect alterations in gene expression. However, due to this sensitivity, impurities in cDNA and other types of contamination can significantly affect results.
- 3. Western Blotting and Immunohistochemistry. For western blotting, cells or tissues can be homogenized in a lysis buffer, such as RIPA buffer (50 mM Tris-HCl, pH 7.4, 150 mM NaCl, 0.2 % (w/v) NP-40 and 1 mM EDTA) containing protease and phosphatase inhibitors. For immunohistochemical analysis, cells or tissues are typically fixed and tissue is paraffin embedded. Cells or tissues are affixed to microscope slides and incubated with appropriate dilutions of antibodies. Antibodies for both purposes can be purchased commercially for numerous proteins and enzymes that would indicate changes in redox state, and can be used easily for both cells and tissues. When examining the presence of ROS following exposure to an organic solvent, the levels of numerous proteins and the activities of many enzymes could be modified, including enzymes equipped to deal directly with an influx of ROS, such as catalase or the superoxide dismutases. Additionally, oxidation of certain proteins can be examined using antibodies, measuring a direct change in proteins caused by interaction with ROS. Immunohistochemistry provides the added advantage of being able to visualize the location of probed proteins in the cell, and could, for example, provide information about the nuclear translocation of redox sensitive transcription factors, such as NFkB or Nrf2, indicative of activation by ROS.
- 4. Enzyme activity assays and ELISAs. Measuring the activities of enzymes upregulated by oxidative stress provides an indirect measurement of ROS present in the cell. This could include enzymes that directly detoxify ROS, for example catalase activity, or it could include the activity of numerous enzymes that are upregulated following activation by a redox sensitive transcription factor. One highly studied redox sensitive transcription factor is nuclear factor (erythroid-derived 2)-like 2 (Nrf2). In the nucleus, activated Nrf2 associates with the antioxidant response element on DNA. This results in increased transcription and activity of numerous downstream effectors of Nrf2, many of which are involved in the detoxification of chemicals. For example, Nrf2 activation leads to the increased transcription and activity of the enzyme NADPH quinone oxidore-ductase 1 (NQO1), which is responsible for two-electron reduction of quinones, such as benzoquinone, a metabolite of benzene. This reduction converts these highly reactive quinone molecules into less reactive compounds that allows for

further conjugation with molecules such as glutathione, ultimately producing a stable, water-soluble conjugate that can be easily excreted by the body [12]. NQO1 activity can be measured using a straightforward assay that involves homogenization of cells or tissues in buffer (25 mM Tris HCl, pH 7.4; 250 mM sucrose, 5  $\mu$ M flavin adenine dinucleotide), followed by centrifugation, and collection of the supernatant. NQO1 reduces 2,6-dichlorophenol-indophenol, which is inhibited by the presence of dicumarol. Calculating the rate of color change (purple to clear) in the presence or absence of the inhibitor allows one to calculate the NQO1 activity in a given sample. An increase in activity of enzymes such as NQO1 can indicate an increased presence of ROS and/or an organic solvent in the cell. In addition to a variety of protocols to determine the activities of redox sensitive enzymes, numerous commercially available ELISA kits are available to measure a variety of enzymes that are known to be upregulated by the presence of ROS.

# 10.3.5 The Use of Protective Agents to Ameliorate the Negative Effects Associated with Organic Solvent Exposure

There are a number of protective agents that could be used in an attempt to ameliorate any negative effects caused by organic solvent exposure in an animal model. Our laboratory has successfully utilized polyethylene glycol-conjugated catalase at a dose of 25 kU/kg prior to IP injection with 200 mg/kg benzene in vivo or 400 U/ ml in vitro to reduce the oxidative stress associated with benzene or benzene metabolite exposure [11, 13]. Catalase is conjugated with polyethylene glycol to facilitate cellular uptake and extend the half life of the enzyme [14]. Pretreatment with other antioxidant enzymes, such as Cu/Zn superoxide dismutase, could be employed in the same manner.

Additionally, a number of phytochemicals have been used in recent years to prevent carcinogenesis caused by a wide variety of chemicals. These include sulforaphane, extracted from cruciferous vegetables, and curcumin, extracted from turmeric. Although these compounds are varied in structure, they share some common mechanisms that make them useful in preventing carcinogenesis. These general mechanisms include antioxidant properties, such as inhibition of redox sensitive transcription factors, including NF $\kappa$ B [15, 16]. Inhibition of NF $\kappa$ B not only counterbalances the effects of oxidative stress, but also plays a role in increasing cell death pathways in carcinogenic cells as well as inhibiting angiogenesis necessary for tumor survival [17, 18]. While there is ample evidence supporting a role for these compounds in preventing carcinogenesis in animal models, few studies have been performed to examine their utility in preventing toxicity associated with organic solvent exposure. However, due to some of their mechanisms of action, it is possible that pretreatment with one of these compounds could be advantageous prior to exposure to organic solvents.

# 10.4 Notes

- 1. While most of our studies use CD-1 mice because they are typically larger in size and easier to breed than other strains, we have also used C57Bl/6 in these procedures. Furthermore, we are confident these techniques can be applied to other strains. For example, it may be extremely valuable to utilize genetically engineered mouse strains with altered bioactivating capabilities to address specific mechanisms of toxicity. Similarly, it may be necessary to use other strains based on known differences in susceptibility to different xenobiotics.
- 2. We use cervical dislocation in our laboratory to avoid any potential confounding effects of chemical euthanasia on altering enzyme activities involved in drug metabolism. For example, it is known that carbon dioxide can affect the activities of certain enzymes (i.e. heme oxygenases), and little (if anything) is known regarding the effects of chemical euthanasia on embryonic enzyme activities.
- 3. The fetal liver is of interest because, during gestational days 12 and 14.5 in the mouse, it is a primary site of hematopoiesis. The liver of a mouse is difficult to extract prior to GD13, and so if studies using earlier gestational days are desired, other hematopoietic structures may be used, such as the placenta or yolk sac.
- 4. While not necessary, the advantage of keeping the amniotic sac intact is for ease of fetal-placental unit extraction from the uterus.
- 5. Pre-stimulation mix can also be used to culture bone marrow cells of adults or early postnatal mice. Bone marrow is extracted in the same way as above, but is placed in pre-stimulation mix instead of PBS.

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# Chapter 11 Oxidative Stress and Ethanol Toxicity

Juliane I. Beier and Gavin E. Arteel

## **11.1 Ethanol Consumption and Its Impact**

### 11.1.1 The Ubiquity of Alcohol Consumption

It is assumed that initial discovery of fermented beverages was accidental and was derived from improper storage of foods. With the development of agrarian cultures, the intentional cultivation of crops for alcoholic beverage production occurred simultaneously in several areas of the world. In addition to being a 'social lubricant,' alcoholic beverages were valued in ancient cultures for several reasons [92]. First, it was a relatively safe source of hydration, in a time when potable water was difficult to attain. Second, it had at least moderate nutritive value and supplemented malnourishment. Third, distilled spirits (alcohol is derived from the Arabic term 'al kohl,' which refers to the distillation process), had significant medicinal value as an antiseptic. It is therefore not surprising that alcohol consumption is almost completely ubiquitous in human societies. Even in cultures in which alcohol consumption is considered taboo, the development of social mores against its use speaks to the fact the cultures (at least historically) were exposed to alcohol consumption.

The above potential benefits of alcohol to cultures are clearly obvious. Indeed, in the absence of potable water, one could argue that alcohol was a necessity, especially in urban environments. However, the detriments of alcohol consumption were likely observed simultaneously with its benefits. Almost every culture speaks for a need for moderation in alcohol consumption and frowns upon public drunkenness and alcohol-dependence. For example, Aristotle strongly propounds temperance in his work, "The Nicomachean Ethics." In the modern time, the impact of inappropriate

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alcohol consumption has an even more significant societal impact. For example, there is on average more than one alcohol-related driving fatality every hour in the US [75]. It suffices to say that alcohol has always been a double-edged sword with both benefits and detriments to societies.

#### 11.1.2 Ethanol and Toxicity

In addition to the societal impact, alcohol has significant health impact. Ethanol is arguably not a very potent toxin and requires relatively high concentrations to achieve most of its toxic effects in biological systems. However, this lack of potency is offset by the sheer volume of alcohol consumed by humans. The annual per capita consumption in US adults is ~91 of pure ethanol [63] and is even higher in other countries. Furthermore, alcohol is required to be consumed in relatively high doses to exert any discernable inebriating effect; the legal driving BAC in most US States (0.08 % w/v) translates to ~20 mM ethanol. Indeed, one could argue that alcohol is the most common poison voluntarily consumed at toxic doses by the human population. Chronic alcohol consumption/abuse is thought to directly damage several organs, including liver [10], skeletal muscle and heart [1], the brain [20], and the pancreas [81]. Alcohol consumption increases the risk of developing several cancers and is considered a group 1 carcinogen for cancers of the GI tract, liver, breast and pancreas by the International Agency for Research on Cancer [45]. In toto, alcohol consumption is responsible for ~6 % of all disability-adjusted life years (DALY) lost in the United States [91], most of which are attributable to alcoholinduced toxicity.

# 11.2 The Coevolution of Oxidative Stress and Alcohol Toxicity Research

Although excessive alcohol consumption was associated with organ toxicity by ancient cultures, the first suggestion that alcohol consumption may directly cause organ damage is credited to Thomas Addison [2], when he proposed a direct link between alcohol consumption and liver disease. However, based on the work of Best et al. [12], it was assumed that alcohol-induced liver damage was caused by altered nutrition. This hypothesis held until the 1960s, in which it became increasingly clear that alcohol causes direct hepatotoxicity independent of nutritional status [67]. It was in this time-frame that Di Luzio and colleagues [51] proposed that antioxidants could protect against its pathology. Although our initial understanding on the role of oxidative stress in alcohol-induced organ damage focused on liver, many of the mechanisms and concepts have been validated in other target organs of alcohol toxicity.

#### 11 Ethanol and Oxidative Stress

It is interesting to take these developments into context with that of the oxidative stress field. Gerschman et al. [35] first proposed that radiation-induced cell killing is mediated by oxygen free radicals. The long-standing "free radical theory of aging" by Harman [40] was proposed in the same year. Although these ideas implicated free radicals in vivo, it was generally thought that free radical formation in the cell was limited to either external stimuli or random events. It was not until over a decade later, when McCord and Fridovich [71] described the function of SOD as a catalytic reducer of  $O_2$  to  $H_2O_2$ , that the concept that oxidants are produced by the cell under normal conditions gained hold. Discoveries of other antioxidant enzyme systems (e.g., peroxidases and catalases) and prooxidant enzymes (e.g., NOX enzymes, NOS isoforms, and myeloperoxidases; see Fig. 11.1) illustrated that prooxidants are often intentionally produced by the cell. It became clear that balance between prooxidants and antioxidants is critical for survival and functioning of aerobic organisms. It is an imbalance favoring prooxidants and/or disfavoring antioxidants that is defined as oxidative stress [89].

It is notable that the proposal that oxidative stress contributes to alcohol-induced liver disease [51] preceded the work of McCord and Fridovich [71]. Therefore, the concept that oxidative stress contributes to alcohol-induced organ toxicity coevolved with our understanding of oxidative stress. Although significant advances have been made in the understanding of the role of oxidants in alcohol-induced injury, this work has yet to translate into an accepted antioxidant therapy for humans. With a



**Fig. 11.1 Endogenous sources of prooxidants**. Prooxidants can be produced from electron leakage from endogenous enzymes, such as those involved in microsomal oxidation and electron transport. There also exist several enzymes that directly produce parent ROS (e.g., NADPH oxidases, xanthine oxidase) or RNS (e.g., NOS isoforms). Furthermore, there are several enzymes that react with parent oxidants to produce more potent oxidizing species (e.g., lipoxygenases and myeloperoxidase). Lastly, transition metals (e.g., Fe and Cu) are kept in tight check to prevent Fenton-type reactions; their release can increase potent prooxidant formation

better understanding of the mechanisms by which oxidative stress leads to damage during alcohol exposure, more targeted therapies may be applied in the clinic with potentially better success. This chapter will cover the potential mechanisms by which alcohol causes oxidative stress, putative types of prooxidants produced in response to alcohol, and potential mechanisms by which oxidative stress contributes to organ toxicity. As mentioned above, the understanding of the role of oxidative stress in organ pathology is derived predominantly from experiments in alcohol-induced liver injury, but the principles are applicable to most types of organ damage caused by alcohol [78, 53].

# 11.3 Potential Mechanisms by Which Alcohol Causes Oxidative Stress

As discussed above, any changes in the cell that favor prooxidant formation or disfavor antioxidant defenses can cause oxidative stress. Potential mechanisms by which ethanol increases prooxidant production are via electron leakage from normal biologic processes and increased activity of prooxidant enzymes. Ethanol also causes biochemical changes that favor generation and propagation of potent prooxidant species. Lastly, ethanol consumption can directly or indirectly impair defenses against prooxidants. The potential alterations caused by ethanol are summarized schematically in Fig. 11.2.

## 11.3.1 Electron Leakage

Enzyme-catalyzed transport of electrons from one biologic molecule to another is critical for normal cellular function. Although these are usually tightly coupled reactions, electrons can leak from these reactions to other electron acceptors, such as oxygen (see Fig. 11.1). Furthermore, alcohol can increase the likelihood of uncoupling of these reactions. For example, the reduction of O<sub>2</sub> to H<sub>2</sub>O by the mitochondria is not complete and 1-2 % of O<sub>2</sub> consumption by mitochondria leads to the formation of  $O_2^{-}$  under basal conditions [13]. To put this in context, an 80-kg human would produce 215–430 mmol  $O_2^{-}$  a day from this source alone [17]. Alcohol exposure increases the yield of  $O_2$  from this cellular component in the liver [e.g., [6]] and in other organs [61]. Elevated prooxidant production by mitochondria not only increases the net yield of prooxidants in the cell, but can also directly damage mitochondrial proteins and DNA, which can exacerbate mitochondrial aging and stimulate mitochondrial-mediated apoptotic pathways [see [21] for review]. Moreover, alcohol depletes mitochondrial GSH levels, which increases the response of hepatocytes to apoptotic stimuli [30]. Therefore, it is likely that prooxidant production from this cellular compartment is key for the development of oxidative stress caused by alcohol.



Fig. 11.2 Potential mechanisms of oxidative stress caused by ethanol. Ethanol can cause oxidative stress via a myriad of mechanisms. Ethanol enhances electron leakage from biochemical processes by uncoupling the reactions (e.g., MEOS and mitochondria); some of these processes (e.g., MEOS) are also induced by ethanol consumption. Ethanol increases the production of ROS/ RNS from prooxidant enzymes (e.g., NADPH oxidases and NOS isoforms) both in inflammatory cells and in non-inflammatory cells. Oxidative (e.g., acetaldehyde) and non-oxidative (e.g., FAEE) metabolites of ethanol can directly cause oxidative damage to biomolecules. Ethanol metabolism exerts significant biochemical stress on the cell, which can indirectly increase prooxidant production and/or impair antioxidant defenses. Alcohol consumption also directly impairs antioxidant defenses via nutritional deficiencies, and via impairing mechanisms of repair and restoration (e.g., proteosomal and autophagic responses). Lastly, alcohol consumption mobilizes transition metals, which increases the likelihood of formation of potent prooxidant species. These responses often work in tandem and via 'feed-forward' mechanisms, leading to a vicious cycle of oxidative stress and tissue damage

The major route of metabolism is the oxidation of ethanol to acetaldehyde. Whereas the dominant enzyme system involved in this process is alcohol dehydrogenases (ADH), the cytochrome P450 systems, also called microsomal ethanol oxidizing system or 'MEOS' (mostly CYP2E1) also plays a critical role. Molecular oxygen (O<sub>2</sub>) is the recipient of the electrons from ethanol via the MEOS system, and hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) is reduced to water by catalase. Whereas the relative contribution of the MEOS system to total alcohol metabolism is low *a priori*, CYP2E1 is robustly induced by alcohol and can contribute to a far greater amount of total alcohol metabolism in alcohol-dependent individuals [65]. CYP2E1 is also relatively loosely coupled with cytochrome reductase; it can therefore leak electrons to oxygen to form  $O_2^{+}$ , or catalyze lipid peroxidation [27], a process which increases with CYP2E1 induction by alcohol. It is therefore proposed that this enzyme may contribute to oxidative stress caused by alcohol. This iso-zyme has also been shown to be induced in macrophages; macrophages overexpressing CYP2E1 have a more robust response to stimulation in culture [18], which may contribute to the 'priming' effect of alcohol on these cells (see Sect. 11.3.2).

# 11.3.2 Increased Activity of Prooxidant Enzymes from Inflammatory Cells

In contrast to electron leakage from uncoupled metabolic processes, prooxidant enzymes intentionally produce prooxidant species. Many of these enzymes are found in inflammatory cells and play key roles in mediating the inflammatory/ immune response (see Fig. 11.1). In contrast to non-inflammatory cells, where reactive oxygen species (ROS) production is predominantly caused by electron leakage from biochemical processes, inflammatory cells are 'professional' producers of ROS and reactive nitrogen species (RNS), capable of generating high concentrations of both types of species into their surrounding environment. Indeed genetic deficiencies in these prooxidant enzymes cause severe immunosuppression in humans [e.g., [43]]. A frequent component in the progression of alcohol-induced tissue damage is low-grade inflammation, involving both resident (e.g., Kupffer cells in liver) and recruited (e.g., neutrophils and lymphocytes) inflammatory cells. Whereas the production of these species is critical for host defense, if inappropriately stimulated, they can also cause damage to normal tissue. It is now generally accepted that inappropriate activation of inflammatory cells plays a key role in the initiation of alcoholic liver injury [see [11] for review], and similar effects are hypothesized to be involved in alcohol-induced damage to other organs.

Two major sources of prooxidants in these cells include NAD(P)H oxidase (NOX2) and the inducible form of nitric oxide synthase (NOS2). In experimental alcoholic liver disease, genetic ablation almost completely protected the organ against damage caused by ethanol [60, 72]. Other studies have implicated one or both of these enzymes in alcohol-induced organ damage in other tissues, including brain [93, 86] and lung [98]. Interestingly, whereas RNS production from NOS2 may be damaging in alcohol-induced organ injury, the activity of endothelial NOS (NOS3) is often protective; the different isoforms of NOS may therefore serve different functions in the disease state, as has been suggested to be the case in alcoholic liver disease [96]. Other sources of ROS in include lipoxygenases, and myeloper-oxidases (Fig. 11.1), both of which may contribute to oxidative stress caused by alcohol administration by propagating more potent reactive species (see Sect. 11.3.5 below).

Priming is a key concept that has been established in alcoholic liver injury, and may well play a role in alcohol-induced damage to other organs [69]. As mentioned above, the natural history of alcohol-induced organ damage is often characterized by chronic low-grade inflammation. Inflammatory cells appear to be primed to activation by alcohol administration. For example, peripheral blood monocytes obtained from patients with alcoholic hepatitis spontaneously produce proinflammatory mediators (e.g., TNF $\alpha$ ), and they produce more of these mediators in response to LPS [70]. In addition to cytokine/chemokine production, there are a host of other mediators of inflammation that are increased by alcohol administration, such as adhesion molecule expression, and cytokine receptors (e.g. TNFR1). Not only is oxidative stress likely involved in the mechanism of priming proinflammatory cells, but the stimulation of the inflammatory response recruits prooxidantproducing inflammatory cells to the site of organ damage, thereby likely contributing to a vicious cycle of oxidative stress, inflammation and normal tissue damage.

# 11.3.3 Increased Activity of Prooxidant Enzymes from Noninflammatory Cells

Although electron leakage from normal enzymatic processes is arguably the dominant source of parent ROS in non-inflammatory cells (see Sect. 11.3.1), these cells also possess prooxidant-producing enzymes, which may contribute to organ damage caused by alcohol. For example, oxidative stress plays a role in the transformation of hepatic stellate cells into myofibroblasts, the critical matrix depositioning cell in the fibrotic liver [85]. The contribution of oxidative stress to stellate cells transformation is not solely in response to extrinsic ROS, but also from intracellular prooxidant enzymes. More specifically, non-phagocytic NOX production may also be involved in the transformation of stellate cells [80]. Another example is xanthine dehydrogenase, which is proteolytically cleaved to the  $O_2$  -producing xanthine oxidase in response to hypoxia and other stimuli (Fig. 11.1). Indeed, the xanthine oxidase inhibitor, allopurinol, confers protection against alcohol-induced oxidative stress in hepatic and in extrahepatic tissues [78, 58].

### 11.3.4 Alcohol Metabolism as a Source of Oxidative Stress

The rapid removal of ethanol by the liver is clearly a protective mechanism at the organismal level by preventing CNS depression. However, in addition to inducing CYP2E1 (see Sect. 11.3.1), there are potentially toxic metabolic and biochemical processes of ethanol metabolism that may contribute to alcohol-induced oxidative stress, including production of toxic metabolites, and alteration of biochemical processes.

#### 11.3.4.1 Prooxidant Metabolites of Ethanol

The major route of alcohol metabolism is oxidation to acetaldehyde. Although, acetaldehyde is subsequently oxidized to acetate by aldehyde dehydrogenases (ALDH), the kinetics of this reaction are sufficiently slow to allow for acetaldehyde to accumulate in humans consuming alcohol. Acetaldehyde is toxic, and a number of the systemic toxic effects of ethanol abuse (e.g., flushing, headaches, and nausea) are mediated, at least in part, by direct or indirect effects of elevated acetaldehyde levels. Acetaldehyde is highly electrophilic and can form adducts with reactive

residues on proteins or small molecules (e.g., cysteines). Furthermore, acetaldehyde promotes enhanced glutathione (GSH) utilization and turnover, and depletes the reduced pool of GSH [65], which is critical to maintain catalytic antioxidant defenses. These chemical modifications can also alter and/or interfere with normal biologic processes and be directly toxic to the cell [53]. Modified biologic molecules may also stimulate the host immune response and cause an autoimmune-like disease. Antibodies against acetaldehyde-modified proteins have been reported in both humans and animal models of alcohol exposure [76]. For example, a hybrid adduct of malondialdehyde and acetaldehyde (MAA) unique to alcohol exposure has been shown to induce an immune response both in human alcoholics and in animal models of alcohol exposure [97].

Other products of alcohol metabolism may also induce oxidative stress in organs. In addition to oxidative metabolism, ethanol can also undergo metabolism via a non-oxidative pathway, in which the endproducts are fatty acid ethyl esters [FAEE [62]]. These molecules are thought to accumulate in the mitochondria of cells and to potentially uncouple oxidative phosphorylation and thereby increase ROS production; they are suspected to contribute to tissue damage, especially in organs that effectively lack oxidative metabolism of ethanol [8].

#### 11.3.4.2 Alteration of Biochemical Processes

As mentioned in Sect. 11.1.2, biologically-relevant concentrations of ethanol in the body are quite high (mM). Furthermore, owing to the first-pass effect of the liver on ethanol, hepatic concentrations of ethanol are much higher than systemic concentrations. These high alcohol concentrations, coupled with the impressive rate of metabolism, causes a great deal of biochemical stress to cells. Indeed, whereas acetate from ethanol oxidation can enter the citric acid cycle after conversion to acetyl-CoA, the various metabolic and biochemical alterations caused by ethanol exposure results in a negative energy balance [65]. It is hypothesized that some of these biochemical changes caused by alcohol metabolism may mediate (or at least exacerbate) oxidative stress caused by alcohol.

The oxidation of ethanol to acetaldehyde by ADH and subsequent oxidation to acetate by ALDH utilizes NAD<sup>+</sup> as an electron acceptor, causing a pronounced shift in the NADH:NAD<sup>+</sup> (and by extension, the NADPH:NADP<sup>+</sup>) ratio to a more reduced state. This increase in the reduced state of pyridine nucleotides increases the rate of fatty acid synthesis and esterification, while simultaneously decreasing mitochondrial  $\beta$ -oxidation of free fatty acids. As lipid peroxidation is a key mechanism of free radical propagation, increases in this pool can increase oxidative stress, even in the absence of a true increase in parent ROS formation. This change in the redox state can also impair normal carbohydrate metabolism, which has multiple effects, including decreasing the supply of ATP to the cell [66]. Since the catalytic defense against oxidative stress requires energy to reduce antioxidants, the depletion of ATP pools by alcohol metabolism is likely to affect overall antioxidant defense of the cell.

As mentioned in Sect. 11.3.1, the oxidation of alcohol by the MEOS consumes oxygen. Furthermore, alcohol causes an acute hypermetabolic state, in which the oxygen consumption rate by mitochondria is doubled in liver [101]. This increase in the oxygen extraction rate may increase the arterial to venous oxygen gradient within the tissue [48], and can cause hypoxia [5, 4]. Although this phenomenon has been mostly studied in the liver [14], the metabolic changes caused by alcohol that lead to an increase in oxygen extraction by the cell may be generally applicable to most cells in the body [64]. Alcohol-induced hypoxia will exacerbate the already impaired mitochondria electron flow caused by alcohol by decreasing the delivery of  $O_2$  to the mitochondria, thereby increasing the likelihood of electron leakage. Furthermore, the subsequent reoxygenation after alcohol levels decrease could increase prooxidant production via hypoxia/reoxygenation. This effect coupled with the impairment of free radical defenses caused by hypoxia can contribute to the observed oxidative stress in tissues after alcohol exposure [49].

# 11.3.5 Changes Caused by Alcohol that Favor the Production of Potent Prooxidants

The oxidant that is formed initially (i.e., parent oxidant) is often not highly reactive, per se. For example, although  $O_2^{-}$  is probably the most common parent ROS formed in vivo (see Sect. 11.4.1, below), it has a relatively weak redox potential and a slow reactions rate-constant with most biologic molecules. For example, the  $\alpha$ -hydroxyethyl radical is known to be formed during alcohol intoxication in vivo and to be dependent on  $O_2^{-}$  production [56]; however,  $O_2^{-}$  does not have the redox potential to directly attack ethanol to form this radical. Instead, O<sub>2</sub><sup>-</sup> is further reduced through catalytic pathways in the cell to form more potent oxidants (Fig. 11.3). For example, the reduction of  $O_2$  by SOD forms  $H_2O_2$ ;  $H_2O_2$  and transition metals can lead to formation of 'OH [the Fenton reaction [32]]. Alternatively,  $H_2O_2$  can react with Cl<sup>-</sup> via myeloperoxidase in neutrophils to make HOCl<sup>-</sup> [55]. An additional pathway of  $O_2$  -dependent oxidative stress involves the enzyme independent reaction of O2<sup>-</sup> with NO<sup>•</sup> to form ONOO<sup>-</sup>, a strong oxidizing and nitrating species [9]. All of these oxidant species have been proposed to be involved in liver disease in general and in alcoholic liver injury in particular. For example, ethanol intoxication increases iron mobilization in the cell [19], which makes more free iron available for the Fenton reaction (Figs. 11.1 and 11.3). Alcohol-induced inflammation (see Sect. 11.3.2) increases the concentration of myeloperoxidase in tissues and enhances the formation of HOCI-. Lastly, alcohol increases the production of nitric oxide (NO<sup>•</sup>) in many tissues (see Sect. 11.4.2, below), which likely increases the yield of ONOO<sup>-</sup> within the cell. Importantly, such changes will favor oxidative stress and tissue damage, even under cases in which the production of the parent oxidant  $(O_2^{\bullet})$  is not increased, per se.



Fig. 11.3 Potential pathways of formation of potent oxidants from superoxide. Superoxide  $(O_2^{-})$  can react through catalytic pathways in the cell to form more potent oxidants. For example, the reduction of  $O_2^{-}$  by SOD forms  $H_2O_2$ ;  $H_2O_2$  and transition metals can lead to formation of OH (the Fenton reaction). Alternatively,  $H_2O_2$  can react with Cl<sup>-</sup> via myeloperoxidase in neutrophils to make HOCl<sup>-</sup>. An additional pathway of  $O_2^{-}$ -dependent oxidative stress involves the enzyme independent reaction of  $O_2^{-}$  with NO to form ONOO<sup>-</sup>, a strong oxidizing and nitrating species

# 11.3.6 Changes Caused by Alcohol that Disfavor Antioxidant Defenses

It should be emphasized that any changes in the cell favor prooxidant formation or *disfavor* antioxidant defenses can lead to oxidative stress. In this context, alcohol can cause modifications to the cell that lead to shift in this delicate balance by decreasing antioxidant defenses, even in the absence of increased prooxidant production. The depletion by ethanol of both cytosolic and mitochondrial energy supplies (see Sect. 11.3.4.2) can indirectly impair cellular antioxidant defenses. There exists a host of proteins and systems involved in the "antioxidant network." This family does not directly intercept prooxidants, but serve instead as ancillary reductants and maintain the catalytic activity of antioxidant proteins or small molecules. These reactions of course require cellular energy to maintain these systems. Alcohol consumption also causes nutritional deficiencies that can impair antioxidant defenses. Alcoholics replace up to 50 % of their total daily calories with ethanol (Patek Jr. [82]), which decreases the supply of dietary antioxidants. Furthermore, alcohol consumption often causes malabsorption [16], which further exacerbates the deficiency of dietary antioxidants. These factors combined impair overall antioxidant defenses in those consuming alcohol.

Even under optimal conditions, ROS/RNS will damage biomolecules, which often impairs their normal function. Indeed, secondary and tertiary structure of proteins that make unique amino acid residues critical for electron transfer (e.g., cysteines) and/or signal transduction (e.g., tyrosines), also makes them sensitive to ROS/RNS attack. Alcohol often impairs the systems in place to repair and/or recycle these damaged proteins. For example, alcohol consumption inhibits the 26S proteasome [7], which is a critical system for degrading oxidatively-modified proteins.

Another process that is impaired by alcohol consumption is autophagy [25], which is also important for the clearance of cellular components that are damaged by ROS/ RNS [24]. Impairment of these degradation processes can lead to the accumulation of damaged proteins within the cell, which can subsequently can exacerbate other stresses [e.g., ER stress [23, 68]].

# 11.4 Putative Types of Prooxidants Produced in Response to Alcohol

The term 'ROS/RNS' covers a broad range of diverse chemicals and compounds that induce oxidative stress. The vagueness of the term is due, in part, to the nature of ROS/RNS research. Specifically, due to their inherent reactivity, parent ROS/ RNS generally cannot be measured directly, especially in living systems. One is therefore often left with measuring products of the reaction of these molecules with either other endogenous molecules (e.g., lipid peroxides), or exogenous molecules (e.g., spin traps utilized in ESR spectroscopy). This indirect detection of 'footprints' of ROS/RNS often makes it difficult to conclusively identify the nature of the original prooxidant. However, there are some ROS/RNS for which there are relatively clear data supporting their involvement in alcohol-induced organ damage.

#### 11.4.1 Reactive Oxygen Species: A Role for Superoxide

Of the  $O_2$ -derived prooxidants that can be formed in vivo,  $O_2^{-1}$  is generally accepted to play a central role in alcohol-induced organ injury. The reasons for this fact are two-fold: first, ground state oxygen is relatively abundant within the cell; second,  $O_2^{-1}$  is readily produced by numerous processes in vivo. Ground-state oxygen has two unpaired electrons; this spin restriction means that the most common mechanisms of oxygen reduction in biochemical reactions are those involving transfer of only a single electron (monovalent reduction) to form  $O_2^{-1}$ . As mentioned above (see Sect. 11.3.5),  $O_2^{-1}$  is not a very potent oxidant, but it readily forms more reactive prooxidants via reactions with other biomolecules.

Evidence supporting a role for  $O_2^-$  in alcohol-induced organ injury has been shown predominantly by indirect methods, such correlating damage with endogenous SOD activity, or by administering exogenous SOD in model systems. For example, SOD levels correlated inversely with pathological changes in the experimental alcohol-induced liver [84]. Further support for the role of  $O_2^-$  in alcoholinduced oxidant production has been also shown with exogenous SOD in in situ experiments with cultured cells, or isolated organelles (e.g., mitochondria). In vivo data supporting a role for  $O_2^-$  in damage was lacking for several years until the technical limitations of delivering SOD were overcome with gene delivery approaches. Specifically, delivery of either cytosolic Cu/Zn-SOD or mitochondrial Mn-SOD via adenoviral (Ad) gene delivery prevented alcohol-induced liver injury in rats fed enteral alcohol [94, 95]. These data gave definitive support to the hypothesis that  $O_2^-$  is involved in alcoholic liver injury. Furthermore, the finding that both Cu/Zn-SOD and Mn-SOD were protective suggested that there may be at least 2 distinct pools of  $O_2^-$  production that are involved in alcoholic liver injury.

#### 11.4.2 Reactive Nitrogen Species: A Role for Nitric Oxide

Like O<sub>2</sub><sup>-</sup> for ROS, it is likely that NO<sup>•</sup> serves as the 'parent' molecule for other RNS in vivo. Unlike  $O_2^{-}$ , NO has pleiotropic effects that obfuscate whether it predominantly plays a protective or damaging role in tissue damage caused by alcohol [44]. For example, in liver, it is well known that alcohol-induced dysregulation of vascular tone is mediated, in part, by decreased NO<sup>•</sup> production [79, 96]. It has also been shown that NO' is antiapoptotic in cells [54]. Other potential protective effects of NO<sup>•</sup> include its function of NO<sup>•</sup> as a chain-breaking antioxidant by reaction with lipid peroxyl radicals [87], which blunts propagation of lipid radicals. On the other hand, high levels of NO' can also play a potentially damaging role in alcoholinduced tissue damage by production of RNS, such as ONOO<sup>-</sup> (see Sect. 11.3.5). RNS derived from NO<sup>•</sup> can cause nitration reactions (e.g., 3-nitrotyrosine formation) and nitrosation reactions (e.g., nitrosothiol formation), as well as oxidation reactions during alcohol exposure. Importantly, reactive intermediates formed during ONOOdegradation can also cause one-electron oxidation reactions with ethanol, leading to the formation hydroxyethyl radicals [34], which is a 'fingerprint' of alcohol-induced oxidative stress. Thus, NO' may play a dual role in alcohol-induced organ damage, mediating both protective effects and tissue damage by overproduction of RNS; which of these events predominates in vivo may depend on the cell type, NOS isoform, and stage of disease studied.

# 11.5 Potential Mechanisms by Which Oxidative Stress Contributes to Alcohol-Induced Organ Toxicity

It is not surprising that early foci on oxidative stress-induced damage centered on direct damage to biomolecules (see Sect. 11.2). These chemical modifications can alter and/or interfere with normal biologic processes and be directly toxic to the cell (see Sect. 11.3.6), or may also stimulate the host immune response and cause an autoimmune-like disease, as discussed in Sect. 11.3.2. However, it is now understood that prooxidants can also confer highly specific changes in a cell at concentrations well below observable chemical damage. For example, the amount of oxidants

produced during ischemia/reperfusion are too low to cause significant direct chemical changes [47], although prooxidants clearly play a role in mediating tissue damage under these conditions. It is now clear that prooxidants can mediate and/or amplify their signal by modifying signaling cascades within the cell.

# 11.5.1 Altered Intracellular Signaling Caused by Oxidative Stress

Many reviews have focused on the role of signaling cascades in damage due to oxidative stress [52, 3, 31, 26]; general results of this research will not be reviewed in detail here, but some key areas in context of alcohol-induced tissue damage will be listed. Oxidant sensitive signaling cascades include small molecules [e.g., intracellular Ca<sup>2+</sup> [28]], stress-activated protein kinases [SAPK; e.g., JNK, ERK 1/2, and p38 [90]], transcription factors [e.g., AP-1, HIF-1 and NFkB [22]], and modulators of apoptosis signaling [e.g., caspases, Bad, and Bcl-2 [42]]. Further, the hypothesis that redox modification of thiols is an important post-translational modification within the cell is receiving wider acceptance [88, 31].

Ethanol has been shown to modulate the signal of many of these cascades. For example, the activation of the transcription factor, NF $\kappa$ B, has been clearly linked to oxidant production in response to alcohol. However, the effect of NF $\kappa$ B activation has different biologic effects in different cell types, making its role unclear. Specifically, NF $\kappa$ B is a key mediator in the inflammatory response in Kupffer cells by upregulating proinflammatory genes (e.g., TNF $\alpha$ ). On the other hand, NF $\kappa$ B inhibition mediates cellular apoptosis [15, 41].

Another mechanism of oxidative stress-induced damage is via to the oxidation of thiol disulfide pairs such as cysteine and cystine (Cys/CySS), glutathione and glutathione disulfide (GSH/GSSG), and thioredoxin, which results in alterations in their redox potential, hereafter termed 'Eh' [37]. The Cys/CySS thiol disulfide redox couple is the predominant low molecular weight thiol disulfide pool found in plasma, and it controls intracellular levels of glutathione [36]. Alcohol abuse causes the oxidation of the Eh Cys/CySS, and it has been proposed that these changes in the redox potential of extracellular thiol pairs can serve as independent transducer of oxidant stress [50]. The novelty of this signaling mechanism is that it can trigger intracellular redox signaling by oxidation of membranebound proteins, and this oxidation can trigger the down-stream generation of reactive oxygen species. Altering these thiol redox circuits dramatically impacts several intracellular events [37]. Furthermore, oxidation of the Eh Cys/CySS increases proinflammatory cytokine production [46], activates SAPK dependent pathways [77]. Thus, oxidation of the redox potential of distinct thiol disulfide couples is likely to represent yet another pathway by which alcohol could exert its detrimental effects.

# 11.5.2 Altered Intercellular Signaling Caused by Oxidative Stress

In addition to activating/modulating intracellular signaling, it is now clear that oxidants also modify intercellular signaling through activation/modulation of cytokine expression [38]. The critical importance of TNF $\alpha$  production was demonstrated most clearly in mice deficient in TNFR1 receptors [100]. Interestingly, knocking out TNFR1 had no protective effect on  $\alpha$ -hydroxyethyl radical formation [99]. This observation lends strong support to the hypothesis that prooxidants from inflammatory cells do not directly damage hepatocytes during alcohol-induced liver injury, but instead enhance the production of signaling cascades/molecule which then mediate their effects. It has also been shown that downstream from the binding of TNF $\alpha$  to its receptor is the stimulus of mitochondrial oxidant production mediated at least in part by trafficking of the ganglioside GD3 to mitochondria [33]. TNF $\alpha$ thus appears to be a critical link between prooxidant production in inflammatory cells and hepatocytes.

Another interesting observation during work with antioxidants in experimental alcohol-induced liver injury is that many of these conditions blunt the increase in fatty liver. For example, antioxidant treatments such as ebselen [57], adenoviral overexpression of SODs [94, 95], polyphenolic extracts [73], DPI [59], and allopurinol [58], all prevented the accumulation of lipid droplets in the hepatocytes caused by ethanol. Furthermore, mice deficient in prooxidant-producing enzymes (e.g., NADPH oxidase and iNOS) all had decreased levels of steatosis after ethanol exposure [60, 72]. Hepatic steatosis due to alcohol is historically considered the result of NADH redox inhibition of mitochondrial  $\beta$ -oxidation caused by alcohol metabolism (see Sect. 11.3.4.2). The data obtained from antioxidants and knockouts bring into question whether this redox shift is sufficient in and of itself. Specifically, none of the conditions mentioned above had any apparent effect on alcohol metabolism.

One effect that these conditions do have in common is that the increase in cytokine (e.g., TNF $\alpha$ ) production caused by alcohol was blunted in the antioxidant/ knockout group relative to their controls/wild-types given alcohol. Further support for the role of cytokines in alcohol-induced steatosis is derived from the observation that knocking out TNFR1 almost completely blocks alcohol-induced fatty liver [100]. There are data suggesting that TNF $\alpha$  (and other cytokines) can indeed influence lipid metabolism both in liver and periphery (Fig. 11.4 [83] for review). For example, TNF $\alpha$  increases free fatty acid release from adipocytes in the periphery [39], increases lipogenesis in hepatocytes [29], and inhibits  $\beta$ -oxidation of fatty acids [74]. Moreover, prooxidant production stimulated by TNF $\alpha$  in hepatocytes could impair mitochondrial electron flow and cause lipid peroxidation, processes that could also slow the metabolism of fat by mitochondria. The net consequence during alcohol exposure is that cytokines increase the supply of fatty acids to liver while simultaneously impairing the ability of the hepatocytes to metabolize and secrete them.



**Fig. 11.4** Possible mechanisms by which TNFα and other cytokines contribute to lipid accumulation and oxidative stress. Direct effects of TNFα include increased free fatty acid (FFA) release from adipocytes in the periphery, increased lipogenesis in hepatocytes, and inhibition of β-oxidation of fatty acids. Taken together, the net amount of FFA is increased. Further, TNFα can directly increase ROS formation by impairing mitochondrial electron flow, leading formation of  $O_2^-$ . Indirectly, the oxidation of lipids by ROS/RNS can further impair β-oxidation of fatty acids, and further damage to mitochondria. Other cytokines induced by alcohol (e.g., IL-1 and IL-6), may impair transport and secretion of triglycerides (TG). The net result during alcohol exposure is that cytokines increase the supply of fatty acids, while simultaneously impairing the ability of the cell to metabolize and secrete them

### **11.6 Summary and Conclusions**

As summarized in this chapter, there are multiple proposed mechanisms by which alcohol causes oxidative stress in tissue. These proposed mechanisms are of course not mutually exclusive and likely work in tandem to cause initiation and progression of damage (see Fig. 11.2). Whereas there is no universally accepted therapy available to treat alcohol-induced tissue damage, or halt its progression, there are many potential therapies being tested that target at least one of these potential mechanisms. Likewise, owing to the multiple mechanisms by which alcohol may damage organs, it is unlikely that one therapy will be sufficient to treat or prevent disease. Rather, an effective therapy may be a mix of lifestyle modification, dietary care, and pharmacologic intervention. Antioxidant therapies may be an effective part of such a mix in the future.

Another avenue in which improvements need to be made is in modeling the disease. Specifically, most research to date focuses on early stages of ALD and often involve concomitant administration of the potential therapy with ethanol, or in the case of transgenic/knockout mice, using strains in which the expression of the protein of interest is a life-long event. Such research has given us quite useful information and is the foundation on which we now stand. However, the relevance of this research to the clinical situation in which alcoholics are seeking therapy to reverse existing injury is unclear. Although there are many studies that currently focus on this concern, more work along these lines should be performed.

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# Chapter 12 Pharmaceutical Agents

Abdullah Al Maruf and Peter J. O'Brien

### 12.1 Background

Oxidative stress has been proposed as one of the main and common mechanisms of pharmaceutical agents-induced hepatotoxicity, cardiovascular toxicity, nephrotoxicity, retinopathy, neurotoxicity, ototoxicity, and reproductive toxicity (reviewed in [1, 2]). Oxidative stress was also found to be associated with the pathogenesis of different diseases e.g., cancer, Parkinson's, Huntington's, Alzheimer's, prions, Down's syndrome, ataxia, multiple sclerosis, Creutzfeldt-Jacob disease, amyotrophic lateral sclerosis, schizophrenia, tardive dyskinesia, asthma, chronic obstructive pulmonary disease, cataracts, cardiovascular diseases, etc. (reviewed in [3, 4]).

Oxidative stress is defined as an increased generation of reactive oxygen species (ROS) and reactive nitrogen species (RNS) that exceeds cellular adaptive and repair capacities which causes damage to biomolecules such as nucleic acids, proteins, and membrane phospholipids and may lead to cell death [5]. Thiol/disulfide couples such as glutathione (GSH/GSSG), cysteine (Cys/CySS) and thioredoxin ((Trx-(SH)2/Trx-SS)) are functionally organized in redox circuits controlled by glutathione pools, thioredoxins and other control nodes that vary little among healthy individuals. They are maintained in disequilibrium relative to each other and have significantly altered the concept of oxidative stress. Under this new concept of "Redox Hypothesis", oxidative stress is defined as the disruption of those redox circuits [2, 6, 7]. The deleterious effects of ROS and NOS on cellular targets have been described in other chapters.

Drug-induced toxicity in numerous tissues and organ systems, especially in the liver, is of major concern in clinical studies, as well as in the post-marketing

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surveillance of drugs [8]. Understanding the mechanisms of toxicity and developing therapeutic interventions to combat such toxicities are important for the pharmaceutical industry so as to decrease post-market withdrawals, decrease drug development costs and increase patient safety and well-being.

# 12.2 Mechanisms of Drug-Induced Oxidative Stress and Therapeutic Interventions

Drugs from several classes of pharmaceutical agents were reported to have adverse effects related to oxidative stress, e.g., anticancer drugs, antibiotics, antiretroviral drugs, anti-tubercular drugs, analgesics including non-steroidal anti-inflammatory drugs (NSAID), and antipsychotics as illustrated in Table 12.1. Some drugs are involved in multi-tissue and multi-organ toxicity. Possible mechanisms of oxidative stress-mediated injury are illustrated in Fig. 12.1 for cisplatin (an anti-cancer drug), zidovudin (AZT; an anti-retroviral drug) and doxorubicin (Dox; an anthracycline antineoplastic agent).

Antioxidants, being exogenous or endogenous, are chemical agents that donate an electron to free radical molecules which converts them to a harmless configuration that decreases damaging radical chain reactions [4]. Many natural and synthetic compounds are currently being used as antioxidants with numerous different claims that are prescribed by physicians or sold over the counter. However, not all compounds with antioxidant activities have clinical effectiveness (reviewed in [8]).

Mitochondria are thought to be a major target and source of ROS. Damage in the electron transport chain (ETC) or in the inner mitochondrial membrane may increase superoxide production [2, 9]. The exogenous administration of hydrogen peroxide ( $H_2O_2$ ) induced non-apoptotic neuronal cell death in a c-Jun N-terminal kinase- and poly(ADP-ribosyl) polymerase-dependent manner [9]. Additionally,  $H_2O_2$  treatment induced transient hyperpolarization of the mitochondrial membrane potential and a subsequent delayed ROS production. The inhibition of mitochondrial hyperpolarization with agents, such as diphenylene iodonium or rotenone may protect neuronal cells from oxidative stress-induced necrotic cell death [9]).

### 12.2.1 Endothelial Dysfunction

Endothelium is a single layer of smooth muscle tissue that lines the heart, blood vessels, lymphatic vessels, and serous cavities. The endothelium controls vasodilation, inhibits inflammation, thrombosis, and vascular smooth muscle cell

		Examples and mechanisms	
Pharmacological class	Example drug	of toxicity	References
Antineoplastic	Doxorubicin	Endothelial dysfunction	[11, 12,
		(ROS formation in	20–26]
		endothelial cells may	
		adversely affect the	
		bioavailability of nitric	
		oxide, endothelium-	
		dependent vasodilatation,	
		cell permeability, endothelial	
		cell growth and survival);	
		Cardiotoxicity (increased ROS	
		formation either by reduction	
		to semiquinone free radicals	
		or by forming iron (II)-Dox	
		radical which reacts with	
		molecular oxygen that leads to	
		increased lipid peroxidation,	
		mitochondrial dysfunction,	
		and apoptosis)	
	Cisplatin	Nephrotoxicity (inhibition of	[65–67,
		protein synthesis,	86-88, 98,
		mitochondrial injury, DNA	<b>99</b> ]
		damage, and apoptosis);	
		Neurotoxicity (genotoxicity	
		and neurotoxicity through	
		modulating NF-kappaB	
		pathway);	
		Ototoxicity (increased NOX	
		isoform formation)	
Analgesic/antipyretic	Acetaminophen	Hepatotoxicity (formation of	[2, 45–50,
	-	reactive metabolites,	65, 69]
		depletion of glutathione,	
		activation of proapoptotic	
		proteins, and mitochondrial	
		dysfunction)	
		Nephrotoxicity (increased	
		ROS, MDA and nitric oxide	
		production and depletion of	
		-	

 Table 12.1
 Examples of drugs associated with oxidative stress-mediated toxicity involving single or multiple organs or tissues (Adapted from Deavall et al. 2012) [1]

(continued)

		Examples and mechanisms	
Pharmacological class	Example drug	of toxicity	References
Anti-inflammatory	Nimesulide	Hepatotoxicity (redox imbalance, calcium dependent mitochondrial permeability transition leading to dysfunction, and reactive metabolite formation)	[52–59]
Antibiotic	Gentamicin	<i>Nephrotoxicity</i> (H <sub>2</sub> O <sub>2</sub> production in renal cortical mitochondria)	[72, 73]
Antimicrobial	Mequindox	<i>Reproductive damage</i> (increased superoxide dismutase, reduced glutathione and 8-hydroxydeoxyguananosine levels)	[96]
Antitubercular	Isoniazid	Hepatotoxicity (increased ROS generation along with alteration in levels of enzymatic antioxidants such as SOD, catalase, and glucose-6-phosphate dehydrogenase, altered Bcl-2/Bax content, cytochrome-c translocation, caspase activation, and DNA fragmentation)	[101]
Antiretroviral	Zidovudin	<i>Cardiotoxicity</i> (oxidative damage to cardiac mitochondrial DNA, increased mitochondrial lipid peroxidation and GSH oxidation)	[18]
Antipsychotic	Chlorpromazine	<i>Retinopathy</i> (oxidized to reactive quinones with subsequent adduction to an ocular/retinal macromolecule or ocular glutathione leading to oxidative stress);	[89, 92, 102]
		Dermal toxicity (generation of singlet oxygen and superoxide in response to UVA/B irradiation leading to phototoxicity)	

#### Table 12.1 (continued)



**Fig. 12.1** Doxorubicin (Dox), zidovudin (AZT) and cisplatin-mediated oxidative stress leading to adverse drug reactions. Dox may accumulate in mitochondria of cardiac cells by associating with cardiolipin that causes increased ROS formation either by reduction to semiquinone free radicals or by forming iron (II)-Dox radicals leading to cardiotoxicity. Cisplatin may be transported into renal tubular cells via OCT transporters and increases ROS formation by induction of NOXs. Mitochondrial dysfunction and associated redox imbalance results in apoptic signaling cascades that may lead to a proapoptotic response. These common mechanisms may be responsible for Doxinduced cardiotoxicity, AZT-induced skeletal myopathy, or cisplatin-induced nephrotoxicity and ototoxicity (Adapted from Deavall DG, Martin EA, Horner JM, Roberts R (2012) Drug-induced oxidative stress and toxicity. Journal of Toxicology. 2012: 645460 [1]. Copyright © 2012 Damian G. Deavall et al. Creative Commons Attribution License)

proliferation and maintains the homeostatic balance of vessels and associated organs [10]. Chemotherapeutic agents, immunosuppressive drugs, anti-retroviral drugs, aldosterone and aldosterone antagonists, diethyldithiocarbamate, and nanoparticle drugs have been shown to cause endothelial dysfunction via oxidative stress (reviewed in [11]). ROS formation in endothelial cells may adversely affect the bioavailability of nitric oxide, endothelium-dependent vasodilatation, cell permeability, endothelial cell growth and survival [11]).

Several agents have been reported that have protective effects against oxidative stress-mediated endothelial dysfunction. Gamma-glutamylcysteine ethyl ester (an antioxidant) [12, 13] or N-acetylcysteine (a GSH precursor) was able to abate Dox-induced endothelial dysfunction in rats [14]. Thioredoxin was reported to have a ROS scavenging effect on endothelial cell dysfunction [15]. Probucol was found to attenuate oxidative stress in isoproterenol-induced endothelial injury in rats [16].

Antioxidants were found to be effective in in vitro and animal studies; however, the role of anti-oxidant therapy in patients in attenuating endothelial dysfunction caused by drugs remains unclear [11].

### 12.2.2 Cardiovascular Injury

Oxidative stress-mediated cardiotoxicity has been associated with several drugs and may be caused by energetic imbalance, perturbations in mitochondrial function, activation of stress-related signaling pathways (such as p38 and JNK), p53 accumulation, and, ultimately, cardiac cell death [1].

Cisplatin is an antineoplastic agent used for several types of cancer. Its use has been limited due to the occurrence of several adverse effects including cardiotoxicity, ototoxicity, peripheral neuropathy, and nephrotoxicity. Oxidative stress and apoptosis have been proposed to contribute to cisplatin-induced cardiotoxicity. Increased malondialdehyde (MDA) formation and decreased reduced glutathione (GSH) levels and superoxide dismutase (SOD) activity were reported in cisplatin-treated rats [17]. Zidovudine (AZT) is major antiretroviral drug used for HIV treatment whose use has been limited because of severe side effects, in particular cardiotoxicity in chronic therapy. AZT treatment of mice caused an increase in oxidative damage to cardiac mitochondrial DNA. It also increased mitochondrial lipid peroxidation and GSH oxidation in cardiomycytes that were prevented by dietary supplementation with vitamins C and E in mice [18]. Another antineoplastic agent, 5-fluorouracil (5-FU) induced cardiac cell damage through the triggering of apoptosis due to increased intracellular ROS production that was prevented by N-acetylcysteine [19].

One of the most effective anthracycline antineoplastic drugs, doxorubicin (Dox), has limited clinical use due to cumulative, dose-related, and progressive myocardial damage that potentially can lead to congestive heart failure [20]. Dox produces large amounts of ROS in cancer cells and uncontrolled ROS production in other tissues resulting in oxidative stress-mediated toxicity [21, 22]. Several mechanisms of Dox-mediated ROS production have been reported (Fig. 12.1). Dox is readily reduced by one electron to generate anthracycline semiquinone free radicals catalyzed by reductases in mitochondria. Under aerobic conditions, Dox readily converts molecular oxygen to superoxide anions and H<sub>2</sub>O<sub>2</sub>. Redox reactions subsequently cause an interaction of Dox with iron (III) which generates an iron II-Dox free radical that is capable of reducing molecular oxygen ultimately leading to increased ROS production [1, 21–24]. Redox cycling of Dox in mitochondrial complex I results in mitochondrial damage and disruption of mitochondrial and cellular calcium homeostasis which has also been reported as a possible mechanism of Doxinduced cardiotoxicity [25, 26]. Protection against Dox-induced toxicity has been achieved by using diverse molecules in different model systems, both in vitro and in vivo. Plant extracts, vitamin C and E, L-cartinitine, gamma-glutamycysteine ethyl ester, N-acetylcysteine, coenzyme Q10, dexrazoxane, and carvedilol have

been all reported to attenuate oxidative stress generated by Dox [3, 27–30]. A recent study has demonstrated that propofol attenuated both oxidative stress and cellular apoptosis in Dox-treated cultured rat neonatal cardiomyocytes [31].

#### 12.2.3 Hepatotoxicity

Drug-induced liver injury (DILI) is a major concern in clinical practice [8]. Thirty to fifty percent of acute liver failures and 15 % of liver transplantations are related to chemical-induced hepatotoxicity [32, 33]. DILIs are often idiosyncratic, occurring on a background of transient liver injuries in less than 1 in 10,000 patients [34]. There is also a growing body of evidence suggesting that idiosyncratic drug-induced hepatotoxicity may be mediated, at least in part, by oxidative stress. The proposed pathophysiological mechanisms of most drug-induced hepatoxicities are: inhibition of mitochondrial function, disruption of intracellular calcium homeostasis, activation of apoptosis and oxidative stress, inhibition of specific enzymes or transporters, and formation of reactive metabolites that cause direct toxicity or immunogenic response, potentially leading to idiosyncratic effects [35-38]. Drug-induced mitochondrial dysfunction has been proposed as a key mechanism of DILI. Druginduced mitochondrial dysfunction can be due to the drug itself and/or to reactive metabolites generated through metabolism by cytochrome P450-mediated or other enzyme systems [39–42]. Possible mechanisms of toxicity include inhibiting mitochondrial respiratory complexes of the electron chain; inhibition or uncoupling of oxidative phosphorylation; inducing mitochondrial oxidative stress; or inhibiting DNA replication, transcription or translation. Different mechanisms by which drugs can cause mitochondrial dysfunction are illustrated in Fig. 12.2. Detailed mechanisms have been reviewed in [43, 44].

Acetaminophen is one of the most commonly used analgesics and causes a potentially fatal, hepatic centrilobular necrosis by forming a reactive metabolite N-acetyl-p-benzoquinone imine (NAPQI) that depletes GSH followed by protein binding, especially in mitochondria when taken in overdose. This results in mitochondrial oxidative stress and peroxynitrite formation, in part through c-Jun-Nterminal kinase activation, leading to mitochondrial DNA damage and opening of the mitochondrial transition pore, which subsequently leads to hepatocyte cell death [2, 45, 46]. Cytochromes 2E1, 1A2, 3A4, and 2A6 also oxidize acetaminophen to the reactive metabolites leading to oxidative stress [47–49]. Several agents have been proposed to attenuate acetaminophen-induced hepatotoxicity. However, N-acetylcysteine is the only clinically used antidote which is most effective when administered very early, when it prevents protein binding of NAPQI [50]. Nimesulide is a unique molecule of the sulphonanilides class of non-steroidal anti-inflammatory drugs (NSAIDs) having analgesic, anti-pyretic, potent anti-inflammatory activities and very good gastro-intestinal tolerability [51]. The hepatotoxicity caused by nimesulide is rare, relatively insensitive to accumulated dose, and specific to a patient and is thus considered to be an idiosyncratic toxicity Involvement of ROS



**Fig. 12.2** Proposed mechanisms of drug-induced mitochondrial toxicity. (1) Inhibition of complexes I and III can result in the generation of ROS due to auto-oxidation of reduced complexes. (2a) Uncoupling of mitochondrial oxidative phosphorylation that occurs when protonophoric drugs mediate the transport of protons through the mitochondrial inner membrane causing the membrane potential to dissipate, thus disconnecting the electron transport chain from ATP formation. (2b) Mitochondrial oxidative phosphorylation inhibition occurs when drugs bind to ATP synthase. (3) Mitochondrial oxidative stress is caused by auto-oxidation of Dox semiquinone radicals formed by complex I or by inhibition of complex I. (4) Antiviral drugs impair mitochondria by targeting mitochondrial DNA polymerases, inhibiting mitochondrial DNA replication and protein synthesis. *Cyt c* Cytochrome c, *Mt* Mitochondria (Chan K, Truong D, Shangari N, O'Brien PJ (2005) Drug-induced mitochondrial toxicity. Expert Opin Drug Metab Toxicol 1(4):655–669. Copyright©2005, Informa Healthcare. Reproduced with permission from Informa Healthcare) [44])

formation and mitochondria-mediated pathways in nimesulide-induced apoptotic cell death and resultant hepatotoxicity have also been reported [52, 53].

Nimesulide aggravated redox imbalance and calcium dependent mitochondrial permeability transition leading to dysfunction in vitro [54]. A known nimesulide metabolite (4-hydroxy-nimesulide) can be bioactivated by myeloperoxidase (MPO) through a pathway distinct from human liver microsome-mediated pathways. The generation of reactive species by the MPO-mediated bioactivation pathway at the site of inflammation may contribute to the toxicity associated with nimesulide [55, 56]. The decrease in the viability of hepatocytes exposed to nimesulide was prevented by fructose and, to a larger extent, by fructose plus oligomycin, and was also stimulated by proadifen, a cytochrome P450 inhibitor [57]. Hepatic and pulmonary adverse effects induced by nilutamide, a nonsteroidal antiandrogen, have been associated with oxidative stress. The initial one-electron reduction of the nitro group forms a reactive nitro anion free radical. According to the oxygen tension, the nitro

anion undergoes two main reactions. (1) Under anaerobic conditions, a further oneelectron reduction (probably mediated by disproportionation of the nitro anion radical to form a highly reactive nitroso derivative. The nitroso can be further reduced by two electrons to the hydroxylamine, and, again by two electrons, to a relatively inactive amine. The nitroso and the hydroxylamine are reactive species that can covalently bind to GSH and cellular macromolecules. (2) Under aerobic conditions, molecular oxygen oxidizes the nitro anion free radical, resulting in a redox cycle that regenerates the nitro compound and produces superoxide anions, whose dismutation by SOD yields  $H_2O_2$ . Thus, the reduction of some nitroaromatic compounds e.g., nilutamide, flutamide, nitrofurantoin, nimesulide etc. can lead to the formation of alkylating intermediates and/or potentially toxic oxygen metabolites leading to ROS formation [58, 59]. Nilutamide-induced hepatotoxicity was prevented by GSH precursors, thiol reductants and/or antioxidants, such as L-cystine, L-cysteine, N-acetylcysteine, dithiothreitol, N,N'-diphenyl-p-phenylene-diamine and alphatocopherol [60].

Three thiopurine drugs commonly used in the last 40 years include 6-mercaptopurine (6-MP), 6-thioguanine (6-TG) and azathioprine (AZP) [61]. Hepatotoxicity is an unpredictable side effect of these drugs, whose pathogenic mechanism remains unknown. Previous studies performed with rat hepatocyte primary cultures showed that AZP metabolism leads to intracellular GSH depletion, mitochondrial injury, metabolic activity reduction, decreased ATP levels, and cell death [61–63]. Cyclosporin A and glycine protected against azathioprine hepatotoxicity whereas Trolox (a water-soluble analog of vitamin E) and high-dose allopurinol (a xanthine oxidase inhibitor) attenuated cell injury [63] supporting an oxidative stress mediated hepatic injury mechanism.

### 12.2.4 Nephrotoxicity

Around 20 % of community- and hospital-acquired episodes of acute renal failure are caused by pharmaceutical agents. The incidence of drug-induced nephrotoxicity may be as high as 66 % among older adults [64]. Several drug classes such as anticancer drugs, antibiotics, NSAIDs and immunosuppressants can elicit kidney injury, and oxidative stress has been proposed as a key contributor to cytotoxicity [2].

Several antineoplastic agents e.g., cisplatin, carboplatin, methotrexate, and doxorubicin are nephrotoxic (reviewed in [65]). Nephrotoxicity of cisplatin involves inhibition of protein synthesis, mitochondrial injury and DNA damage. Hydroxyl radicals are responsible for cisplatin-induced apoptosis whereas hydroxyl radical scavengers inhibited cytochrome c release and caspase activation [2, 65–67] (Fig. 12.1). Moreover, cisplatin caused oxidative damage to mitochondrial lipids, oxidation of mitochondrial proteins and decreased aconitase activity in vivo [66]. Methotrexate increased lipid peroxidation in rat kidney and decreased SOD, catalase and GSH peroxidase activities in renal tissue, resulting in a decrease in the antioxidant capacity leading to oxidative stress [68]. Several analgesics e.g., acetaminophen, diclofenac and other nonsteroidal antiinflammatory drugs (NSAIDs) were reported to be associated with oxidative stress mediated nephrotoxicity in vitro and in vivo [65]. Acetaminophen increased ROS, MDA and nitric oxide production whereas GSH was depleted in rat kidney. Rehin, a Chinese herb, attenuated acetaminophen-induced nephrotoxicity [69]. Diclofenac increased MDA levels and DNA fragmentation in rat kidney leading to apoptotic kidney cell death in vivo [70]. Diclofenac-induced nephrotoxicity is caused in part by an intracellular increase in ROS which may be prevented by the antioxidant, N-acetylcysteine [71].

Commonly used aminoglycoside antibiotics including gentamicin can also cause renal toxicity. This toxicity is mainly caused by an induction of oxidative stress in kidney. Gentamicin was reported to form  $H_2O_2$  in renal cortical mitochondria. Radical scavengers and iron chelators provided protection against renal failure in gentamicin-treated rats [72, 73].

#### 12.2.5 Neurotoxicity

Several pharmaceutical agents including antineoplastic drugs, neurogenic drugs and related compounds can induce serious CNS adverse effects resulting from oxidative stress (reviewed in [2, 3]). Relatively high rates of oxygen consumption, abundant supply of transition metals, high content of unsaturated lipids and relatively lower regenerative capacity can make the brain very vulnerable to oxidative stress-mediated toxicity [74].

High-dose administration of amphetamine-like compounds was associated with acute behavioral toxicity as well as long-lasting damage to dopaminergic neurons (reviewed in [75]). Proposed mechanisms included ROS formation, and dopamine quinone formation leading to redox cycling and apoptosis. Dopamine quinones generated in the brain from amphetamine-like compounds can covalently modify and inactivate tyrosine hydroxylase and the dopamine transporter, subsequently inhibiting both dopamine synthesis and uptake leading to toxicity [76–79]. Dopamine quinone formation was prevented by administration of SOD, GSH, some thiol reagents, and also some dopamine agonists through their quinone-quenching activities in vitro and in vivo [77–82].

Antineoplastic drugs including taxol, methotrexate and cisplatin were reported to cause significant clinical neurotoxicities. Taxol, an effective anti-cancer drug that is widely used in breast cancer, causes oxidative stress leading to neuronal cell death in mouse cortical cultures [83]. Apocynin (a potent NADPH oxidase inhibitor) and Trolox inhibit taxol-induced neurotoxicity [83]. Another effective anticancer drug, methotrexate, a folic acid antagonist, has been associated with neurotoxic adverse effects. Methotrexate significantly increased lipid peroxidation and decreased antioxidant enzymes in rat cerebellum. These effects were prevented by administering caffeic acid phenethyl ester [84] and chlorogenic acid [85]. The usage of platinum-based anticancer drugs such as cisplatin has been limited due to the onset

of peripheral nervous system dysfunction, which can be severe and persistent over a long period of time. Dorsal root ganglia oxidative stress has been proposed to be an important cytotoxic mechanism and, possibly, a therapeutic target to limit the severity of platinum-induced peripheral neurotoxicity while preserving the anticancer effectiveness [86]. Schisandrin B (an antioxidant lignin) attenuated cisplatininduced oxidative stress genotoxicity and neurotoxicity through modulating the NF-kappaB pathway in mice [87]. Alpha-tocopherol was also found to protect mice from severe neurologic damage without interfering with the antitumor efficacy of cisplatin [88].

#### 12.2.6 Retinopathy

Drug-induced retinopathy is an infrequent but serious complication associated with diverse classes of pharmaceutical agents including indomethacin, tamoxifen, thioridazine, and chloroquine (reviewed in [89]). Although the etiology of drug-induced retinopathy is largely unknown, preclinical and clinical data indicated that ocular oxidative stress might contribute substantially to retinopathy. Cytochrome P450, monoamine oxidase, xanthine oxidase, and myeloperoxidase present in the eye may activate drugs into oxidants leading to oxidative stress-mediated retinopathy. These activated agents may directly form retinal adducts or may diminish ocular GSH concentrations (reviewed in [89]). Indomethacin, tamoxifan and chlorpromazine could be oxidized to reactive quinones with subsequent adduction to an ocular/retinal macromolecule or ocular GSH leading to oxidative stress. Several animal models indicated that the co-administration of pro-oxidants exacerbated retinal injuries, whereas antioxidants e.g., GSH or N-acetylcysteine afforded some protection against injury [89–92].

#### 12.2.7 Reproductive Toxicity

Several pharmaceutical agents e.g., multivitamin-hematinics complex (used with chloramphenicol) [93], cisplatin [94], tetracycline [95], and mequindox [96] were reported to have reproductive toxicity and oxidative stress has been proposed as one of the key cytotoxic mechanisms. Teratogens cause embryonic oxidative stress leading to severe embryonic damage [97]. Tetracycline, a broad-spectrum antibiotic employed clinically in the treatment of bacterial infections, caused testicular damage in rats which was attenuated by administering ascorbic acid and N-acetylcysteine [95] providing evidence of the involvement of ROS. Mequindox, an antimicrobial agent, increased SOD, GSH and 8-hydroxydeoxyguananosine levels in vivo, whereas the malondialdehyde levels were slightly increased providing evidence of mequindox-induced free radical formation that may be a factor in reproductive toxicity [96].

# 12.2.8 Ototoxicity

Cisplatin is an anti-neoplastic agent that damages the inner ear through ROS and DNA adducts formation. ROS formation was proposed to result from up regulation of nicotinamide adenine dinucleotide phosphate oxidases (NOX-1 and NOX-4) [98, 99] (Fig. 12.1). Cisplatin increased NOX isoform formation and cytotoxicity in HEI-OC1 auditory hair cell lines whereas in mice, it increased expression of NOX in the cochlea. Inhibition of NOX using siRNA was associated with decreased ROS production and caspase-3 activation in HEI-OC1 cells [99]. Several antioxidant agents including N-acetylcysteine, vitamin E, allopurinol and andamifostine were found to protect cisplatin-induced ototoxicity in non-clinical studies (reviewed [100]).

## 12.3 Concluding Remarks

The examples presented above clearly show the involvement of oxidative stress in clinically relevant drug-induced adverse effects. However, the exact mechanisms of ROS generation and how they cause specific adverse effects are not well-established. Insight into one or more of the possible mechanisms by which drugs produce ROS may facilitate the development of future pharmaceuticals with reduced potential for precipitating injury and thus saving time and money in the drug development process. Several antioxidant and related agents are protective against these drug-induced adverse effects in in vitro and non-clinical studies. However, translating protective effects from experimental systems to human may be difficult and will require more focused studies to understand the mechanisms of toxicity.

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# Chapter 13 Insecticides and Herbicides

Georgia K. Hinkley and Stephen M. Roberts

# 13.1 Introduction

## 13.1.1 Historical Overview

Pest control technology is not a novel industry by any means, but one that has evolved over centuries. Dating back to the ancient Greeks and Romans, second century BC, sulfur fumigation was used to control caterpillars in trees and fruit vines, and in 300 AD, ants were imported to control other pests in citrus orchards [1, 2]. In the 1600s, pesticide use took a modern turn when humans began using arsenic compounds mixed with honey to control ant populations, and by the late 1800s more complex arsenical compounds were also being used, including copper acetoarsenite and calcium arsenate [3]. Over the next several decades, a variety of pesticides would become available, with World War II opening a door to more widespread pesticide usage. Due to public pressure and knowledge about pesticide exposure and risk, many industries have moved toward an integrated pesticide management approach [3]. This involves a cooperative application of biological control, similar to the early use of ants to combat other pests in citrus orchards, in combination with chemical pesticides. While this movement in developed countries may allow a decrease in pesticide use, the agricultural industry and common households remain dependent on pesticides. Developing countries are also heavily dependent on pesticides for disease control and food production and often use fewer occupational exposure precautions.

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## 13.1.2 Benefits of Use

The use of pesticides has been at the center of controversy for several decades, with many groups believing the risks of using pesticides far outweigh any benefits. With the publication of *Silent Spring* in the early 1960s, the world became increasingly aware of the broad range of potential risks of pesticide use and public criticism became an ongoing issue. With the vocal concerns surrounding pesticide risks, it is easy to forget the benefits of pesticide use and how hard our lives would be without them. Consider one example of the impact of pesticide use in agriculture: a study done in 1989 estimated that by eliminating the use of fungicides only, food prices would increase 13 % at the consumer level and there would be a loss of 235,000 jobs [4]. This is just a glimpse of how agriculture as we know it would react to life without pesticides.

Putting aside the benefit of sustainable agriculture, pesticide use beneficially impacts our lives on a daily basis in several ways, ranging from global health issues to household luxuries. It is important to consider the global impact that pesticides have in, for example, disease transmission. The United States Environmental Protection Agency recognizes the importance of using pesticides to control things such as vector-borne diseases, and even includes exceptions to pesticide use law for controlling outbreaks of biological agents — anthrax for example. In addition to preventing global disasters, pesticides also prevent our homes from being taken over by noxious and damaging insects like termites and fleas. While there is little doubt that severe risks can associated with high doses of pesticide products, it is always important to consider things in terms of a risk-benefit analysis and not lose sight of the big picture.

## **13.2** Types of Pesticides

It is well known that pesticide exposure leads to the production of reactive oxygen species (ROS) and indicators of oxidative stress are frequently used in a clinical setting to determine the extent of accidental human exposures. Cases of pesticide poisoning often find changes in the levels of enzymes such as glutathione reductase (GR), glutathione peroxidase (GPx), glutathione S-transferase (GST), catalase (CAT) and superoxide dismutase (SOD) [5]. Increases in these enzymes may indicate a compensatory response due to an increase in the presence of ROS, while decreases may indicate that a system has been overwhelmed by ROS production. In addition to enzymes, increases in the products of lipid peroxidation (e.g., malondialdehyde, or MDA) and decreases in antioxidants such as glutathione (GSH) are also used as indicators of pesticide exposure.

There are a large variety of insecticides and herbicides that act through two main mechanisms to induce the production of ROS *in vivo*. Many pesticides will directly generate free radicals and ROS during metabolism, leading to oxidative DNA, lipid

and protein damage [6]. In addition to direct damage, pesticide exposure can influence oxidative damage through the depletion of antioxidants (e.g., GSH) and through the inhibition of enzymes responsible for the production and regulation of antioxidants [7,8]. Many pesticides, as produced, do not cause oxidative damage, instead requiring transformation to their reactive metabolites. In addition, many pesticides are capable of inducing the P450 enzymes that are responsible for their toxification, leading to further production of reactive metabolites [5].

More than 100 human diseases, including Parkinson's disease and various cancers, have been associated with pesticide exposure. Pesticides have also been used to induce animal models for Parkinson's disease, and epidemiological data significantly associates pesticide exposure and farming with the development of Parkinson's-related diseases [9, 10]. The central nervous system (CNS), the target organ in Parkinson's, is particularly susceptible to oxidative damage for several reasons; for example, the large surface area of axonal cell membranes [9]. Pesticideinduced lipid peroxidation could have a devastating effect within the CNS, possibly explaining the association between pesticide exposure and Parkinson's disease. Non-Hodgkin's lymphoma and other cancers have also been associated with pesticide exposure [11, 12]. The carcinogenic mechanisms of pesticides vary based on chemical form and are not fully understood for many pesticides. It is conceivable that pesticide exposure may play an important role in DNA damage and protein dysregulation through adduct formation and oxidative damage.

## 13.3 Insecticides

#### 13.3.1 Organophosphates

Since the discontinuation of organochlorine pesticides, organophosphates have become the most widely used insecticides, with more than 40 forms being marketed and used currently [13]. This family of pesticides has a relatively short environmental half-life due to their UV sensitivity, making their use appealing compared to more persistent alternatives. Organophosphates execute their insecticidal properties through the inhibition of acetylcholinesterase (AChE) by phosphorylation, leading to over stimulation of the nervous system due to excessive acetylcholine (ACh) that cannot be broken down [13].

In humans, organophosphate poisoning at high doses leads to depressed motor function, ultimately leading to fatal respiratory depression [13]. While the production and impact of ROS at high doses of organophosphate exposure is not usually a primary concern compared to nervous system toxicity, it can have important effects at sub-lethal doses. Low-level exposures (1–10 nM) can result in DNA damage and chromosomal aberrations, as well as changes in mitochondrial trans-membrane potential, leading to cell death [14]. Sub-lethal exposure to paraoxon (Fig. 13.1A) has been shown to cause caspase-3 mitochondria-mediated cell death *in vitro* to murine EL4 T cells, while having no effect on AChE activity. In addition, it has

been suggested that there is little correlation between organ damage and AChE inhibition following pesticide exposure, suggesting that redox disruption is more important for non-ACh related toxicities [6]. ROS production measured by chemiluminescence has been observed following oral exposure in rats to chlorpyrifos (Fig. 13.1B) and fenthion (Fig. 13.1C), showing higher levels in liver and brain compared to controls [15]. Chlorpyrifos and fenthion also caused an increase in DNA damage (single-strand breaks or SSBs) in liver and brain nuclei in treated versus control rats [15]. In addition to genetic and general ROS detection, lipid peroxidation and enzymatic disruption have been studied extensively.

Several groups have presented evidence for lipid peroxidation, measured by thiobarbituric acid reactive substances (TBARS) or MDA, following exposure to various organophosphate pesticides. Chlorpyrifos-ethyl has been shown to cause dose-dependent lipid peroxidation, indicated by increased MDA, in primary human erythrocytes *ex vivo*, the effects of which are attenuated by co-incubation with antioxidants [16]. Lipid peroxidation and increased MDA have also been observed in cases of human malathion (Fig. 13.1D) poisoning. Figure 13.2 shows how exposure



Fig. 13.1 The chemical structures of the organophosphate pesticides discussed are shown here



**Fig. 13.2** Malathion exposure can result in the production of super oxide, hydrogen peroxide and hydroxyl radicals as indicated with *red asterisks*. GSH and SOD are also consumed in the process leading to possible depletion of these crucial antioxidants

to malathion can lead to the production of superoxide, hydrogen peroxide and hydroxyl radicals [5]. Lipid peroxidation was also observed in rats following oral exposure to chlorpyrifos and fenthion, with substantially elevated TBARS in liver and brain compared to controls [15]. Lipid peroxidation has also been induced by phosalone (Fig. 13.1E) incubation with primary erythrocytes, even at concentrations as low as 0.27 nM [17]. Chlorfenvinphos (Fig. 13.1F) exposure in rats has been shown to cause lipid peroxidation in serum and liver [6]. Intravenous administration of fenthion in mice has shown an increase in MDA in red blood cells (RBCs), liver, brain, lung, pancreas, intestine and heart 24 h after exposure [6].

As shown in Fig. 13.2, consumption of GSH is common for both detoxification of pesticides and reactive metabolites, as well as the conversion of ROS to water [18, 19]. In addition to glutathione, several enzymes including SOD, have been shown to be affected by pesticide exposure. Incubation of primary erythrocytes with phosalone for 3 h leads to a decrease in SOD, GPx and CAT. This short exposure period does not allow for a compensatory reaction to be observed and may not explain the full *in vivo* response to a similar exposure [17]. Rats orally exposed to chlorfenvinphos and quinalphos (Fig. 13.1G) show changes in SOD, CAT and GPx, in liver, and dermal exposure to a combination of metamidophos (Fig. 13.1H) and acephat (Fig. 13.1I) leads to SOD and CAT changes in RBCs [6]. Another group dosed rats with dimethoate (Fig. 13.1J) subchronically at 1/50th the LD<sub>50</sub> and investigated oxidative stress; no traditional forms of pesticide-related toxicity were observed, such as changes in gait, behavior or body weight [9]. In addition to observing oxidative stress indicators of lipid peroxidation in the brain, kidney and plasma, there was also a significant decrease in SOD and GR in the liver [9].

Most studies investigating pesticide-induced oxidative stress have been performed in mammals; however, several studies have also shown that fish are susceptible to ROS production. Carp (*C. carpio*), catfish (*Ictalurus*) and eels (*A. anguilla*) have shown redox disruption after dichlorvos (Fig. 13.1K) exposure, Characid fish matrinxa (*Brycon cephalus*) after methyl parathion (Fig. 13.1L) exposure, Nile tilapia after trichlorfon (Fig. 13.1M) exposure, *Oreochromis niloticus* after fenthion exposure, and gilthead seabream after malathion exposure [8]. Fish have also shown redox disruption in SOD and CAT following exposure to organophosphates (dichlorvos) in a dose-dependent manner in liver and brain tissues [6].

Many groups have studied the influence of co-exposure with antioxidants as a way to further investigate the importance of oxidative stress following organphosphate (OP) exposure. An in vitro study done with chlorpyrifos and diazinon (Fig. 13.1N) in primary murine cerebellar granular neurons (CGNs) has been very helpful in exploring the role of oxidative stress [20]. Dose-dependent cytotoxicity was observed for both chlorpyrifos and diazinon. In an attempt to elucidate the mechanism of toxicity, CGNs were co-exposed to the OPs and antioxidants (phenyl-N-tert butylnitrone and CAT) or to the OPs and muscarinic/nicotinic receptor antagonists. Co-exposure to antioxidants was able to prevent cytotoxicity caused by both compounds, while the use of muscarinic/nicotinic receptor antagonists did not alleviate any cytotoxicity [20]. This study demonstrates that the cytotoxicity observed was caused by oxidative stress-dependent mechanisms and was independent of AChE inhibition. Another observation supporting the role of oxidative-stress in OP toxicity is the fact that fish survival has been shown to increase with administration of N-acetylcysteine (NAC) following lethal exposures to dichlorvos and that survival rates were correlated with GSH levels [6]. However, a study investigating the antioxidant effects of tocopherol and NAC following diazinon administration in rats shows that the antioxidant protective mechanism is at least partially due to the reversal of AChE inhibition [6]. The influence of pre-dosing mice with vitamins C and E was assessed for chlorpyrifos exposure, showing an attenuation of DNA damage, MDA production and changes in SOD, CAT and GPx in retinal tissue [21]. This study aimed to determine if antioxidants could prevent chlorpyrifos-induced retinal damage, and while they reported that oxidative stress was reduced, there was no mention of restoration of histological changes observed in the retina. Similarly, Attia et al. [22] investigated testicular toxicity in rats after chlorpyrifos administration and the influence of propolis ethanol extract (PPE) on preventing this toxicity. While they report that all of the changes in oxidative enzymes and endpoints (TBARS, GSH, SOD, CAT, GPx, GST) in testicular tissues were restored to near control values, there is no mention of the restoration of sperm counts or reproductive potential [22]. While it is clear that antioxidants are capable of relieving oxidative stress following OP exposure, there is conflicting evidence as to whether the production of ROS is responsible for the ultimate toxicity observed in all cases.

## 13.3.2 N-Methyl Carbamates

Exposure to N-methyl carbamates causes similar symptoms to OP exposure due to the insecticidal mode of action being AChE inhibition. However, in comparison to OP inhibition, carbamylation is a more reversible leading to a shortened half-life of

toxicity and symptoms [13]. In addition to a shorter half-life of toxicity, the reversible inhibition of AChE leads to a larger ratio of lethal to Lowest Observable Adverse Effect Level (LOAEL) doses, making the use of carbamates much safer than OPs.

Similar to organophosphate exposure, studies using carbamates have found evidence of GSH depletion, disruption of antioxidant enzymes and lipid peroxidation. Incubation of aldicarb (Fig. 13.3A) and propoxur (Fig. 13.3B) with CHO-K1 cells showed a decreased ratio of GSH/GSSG compared to controls, along with increases in GR, GPx and GST, showing a compensatory response to exposure [23]. Similarly, oral exposure in rats to propoxur resulted in dose-dependent increases in SOD, GR, GPx and GST as well as a decrease in GSH/GSSG [24]. In contrast, aldicarb incubation in a human hepatoma cell line showed no changes in GSH/GSSG, GR or GST [25]. An *in vivo* exposure to aldicarb showed increases in SOD but had no effect on GPx [26]. In cases of human propoxur poisoning, increased serum MDA and lipid peroxidation have been recorded [5]. In addition to mammalian exposures, evidence for ROS production in fish has also been investigated following carbamate exposure. Diethyldithiocarbamate (Fig. 13.3C) causes oxidative stress in carp and goldfish tissues by the extraction of active copper motifs in oxidative enzymes (e.g. SOD), thiocarbamate (Fig. 13.3D) has been revealed to induce oxidative stress in eels A. Anguilla, and aminotriazole (Fig. 13.3E) has been shown to inhibit catalase in rainbow trout O. mykiss by binding active iron [8]. There is sufficient evidence to assume that carbamate exposure causes disruption in the redox system of cells, mammals and fish; however, the overall health implications of these exposures is not entirely clear and we cannot draw conclusions about the role that ROS production plays in carbamate toxicity.

Fig. 13.3 The chemical structures of the carbamate pesticides discussed are shown here



D. Thiocarbamate

B. Propoxur

ĊН.

E. Amintriazole

C. Diethyldithiocarbamate

#### 13.3.3 Organochlorine Insecticides

The use of some organochlorines (e.g. dichlorodiphenyldichloroethane-DDT, aldrin, dieldrin, heptachlor, mirex, chlordecone and chlordane—Fig. 13.4A–G) has declined in recent years; however, others are still included in many agricultural and home-use insecticides. Lindane (Fig. 13.4H), for example, is the active ingredient in Kwell®, a shampoo used to treat lice and scabies in humans and has been associated with neurological effects, likely due to a high dermal absorption potential [13]. Organochlorine exposure leads to over-excitation of the nervous system through binding to sodium channels and preventing inactivation of neurons [27]. Organochlorine poisoning leads to changes in sensory perception, coordination and speech and can also cause convulsions.

Similar to other pesticides, the metabolism and detoxification pathways for organochlorines often lead to the use and depletion of GSH [18]. In turn, the reactive oxygen species produced both endogenously and by the reactive metabolites of the pesticide have the potential to lead to uncontrolled oxidative damage. Glutathione



Fig. 13.4 The chemical structures of the organochlorine pesticides discussed are shown here

depletion has been shown for exposure to DDT and dieldrin, causing mitochondrialmediated apoptosis [28]. Lindane detoxification also leads to GSH depletion (Fig. 13.5) with time-dependent decreases in liver and RBCs [5].

Organochlorine exposure has also been shown to cause ROS production, lipid peroxidation and DNA damage. For examples, lindane metabolism (Fig. 13.5) results in the production of superoxide and hydroxyl radicals, suspected of being responsible for increases in serum MDA following lindane poisoning in humans [5]. Alachlor (Fig. 13.4I) exposure in rats has been shown to cause ROS production in liver and brain, 2.9-fold and-3.2 fold higher than controls, respectively [15]. This study also demonstrated alachlor-induced lipid peroxidation with an increase in TBARS in liver and brain tissue. Increased urinary excretion of MDA, formaldehyde and acetone also indicated lipid peroxidation caused by alachlor [15]. Single-strand breaks were also investigated by Bagchi et al. to measure oxidative DNA damage; they reported a 1.6-fold and 2.2-fold increase in strand breaks in liver and brain, respectively, following alachlor exposure in rats. Oxidative stress has also been shown in carp C. carpio in liver and brain tissue after exposure to hexachlorobenzene (HCB) (Fig. 13.4J) [8]. HCB can result in oxidative damage through the production of a reactive metabolite, tetrachlorobenzoquinone or TCBQ, capable of direct binding to protein thiols, GSH depletion and hydroxyl radical formation (Fig. 13.6) [29, 30].



Fig. 13.5 Lindane metabolism can lead to GSH depletion and the production of free radical metabolites, super oxide, hydrogen peroxide and hydroxyl radicals, indicated by *red asterisks* 



Fig. 13.6 Hexachlorobenzene metabolism leading to GSH depletion, hydroxyl radical formation and protein adduct formation, indicated with *red asterisks* 

## 13.4 Herbicides

## 13.4.1 Paraquat

Paraquat has been used commercially as a broad, non-selective herbicide since the mid 1960s and has been associated with human poisoning since the year of its release. There were more than 232 deaths associated with paraquat exposure between 1964 and 1973 alone [31]. Unlike the pesticides discussed above, the mode of herbicidal action for paraquat involves uncoupling of photosystem I and the generation of superoxide and hydrogen peroxide [32]. Babbs et al. [33] were also able to show experimentally that high levels of hydroxyl radical were formed during an in vivo paraquat exposure to duckweed Lemma minor and perennial ryegrass Lolium perennel. Considering this, it is easy to consider how ROS production may play a key role in the mechanism of mammalian toxicity for paraquat. The source of oxidative stress following PQ exposure is likely related to its ability to enter into redox cycling (Fig. 13.7), leading to a potentially constant production of superoxide. Paraquat can be reduced by NADPH-cytochrome c reductase, NADPHcytochrome P450 reductase or NADH:ubiquinone oxidoreductase (mitochondrial complex I) and then oxidized back to its original form by oxygen, producing superoxide [34].

While ingestion is the most common route of paraquat exposure, the target organ following an acute, high-level exposure is often the lung, likely due to the requirement of oxygen for redox cycling. [13]. At lower, non-pneumotoxic levels of chronic exposure, paraquat leads to cerebral damage and neuronal death [34]. Despite its charged chemistry, paraquat is able to cross the blood-brain barrier via uptake through amino acid transporters, leading to preferential damage to dopaminergic neurons in the substania nigra [34, 35]. Dose and time-dependent cytotoxicity and



**Fig. 13.7** Paraquat is capable of redox cycling leading to the production of super oxide, hydrogen peroxide and hydroxyl radicals. NADPH-cytochrome *c* reductase, NADPH-cytochrome P450 reductase and NADH: ubiquinone oxidoreductase are all capable of reducing Paraquat. *Red asterisks* indicate potential reactive metabolites



**Fig. 13.8** Shows the structures of MPTP, metabolite MPP+ and Paraquat. MPTP is an accepted animal model for Parkinson's disease and the structures of Paraqat and MPTP metabolite MPP+ are very similar

neuronal lipid peroxidation have been shown *in vivo* in mice, in *ex vivo* rat brain slices, *ex vivo* mouse cerebral cortex nerve terminals and in cultured cerebellar granule cells [34, 36, 37].

Due to the cell-specific effects observed with paraquat exposure, it is unsurprising that paraquat has been investigated as an animal model for Parkinson's disease [35]. Paraquat is also very structurally similar to the active metabolite (MPP+) of 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine or MPTP (Fig. 13.8), a widely used and accepted animal model for Parkinson's disease [38]. The MPTP model for Parkinson's disease leads to apoptosis through cytochrome C release and caspase-3 activation; paraquat exposure has been shown to mimic this apoptotic pathway in cerebellar granule cells [37]. In addition, paraquat exposure has been epidemiologically linked to Parkinson's disease in several agricultural committees, showing a stronger association with longer exposure duration (several to 20+ years) [34, 39]. Due to both the acute toxicity and Parkinson's disease link to paraquat exposure, the use is currently very restricted in the United States.

## 13.4.2 Arsenicals

The use of arsenical herbicides has been largely discontinued in the United States but is still being used from old supplies on some farms and in many other countries. In addition to herbicides, arsenic is found endogenously and is present in several chemical forms [40]. Arsenites (Fig. 13.9A) are trivalent inorganic forms that are lipophilic and can be dermally absorbed. Arsenates (Fig. 13.9D) are pentavalent inorganic forms that are water soluble with higher oral bioavailability [13]. Following exposure, both trivalent and pentavalent inorganic forms are methylated (Fig. 13.9B, C, E, F) allowing renal excretion [13]. Methylation of inorganic arsenic has previously been considered a detoxification reaction; however more recently, methylated arsenic forms have been found to act as tumor initiators and cocarcinogens [40, 41]. Dimethylarsine gas (Fig. 13.10) can also be produced and is by far the most toxic form of arsenic. Inorganic arsenic exposure leads to damage in the nervous system, kidney, liver and blood vessels through oxidative phosphorylation and thiol binding. Acute exposure causes GI disruption, dizziness, muscle weakness and convulsions, while chronic exposure leads to neurological and dermal issues, as well as carcinogenicity [13].

Cancers of the skin, bladder, liver and lung are epidemiologically linked to arsenic exposure [42]. Increased urinary output of 8-OH guanine has been demonstrated following arsenic exposure, indicating oxidative DNA damage [41, 42]. This group



C. Dimethylarsinous Acid or DMA (III)

F. Dimethylarsinic Acid or DMA (V)

Fig. 13.9 Shows the chemical structures for the six most common forms of arsenic. (a) and (d) are the inorganic forms while (b), (c), (e) and (f) are the methylated forms



D. Arsenate (V)



E. Monomethylarsinic Acid or MMA (V)



Fig. 13.10 Shows the pathways for reduction and methylation of arsenic, resulting in the production of reactive oxygen species and GSH depletion. *Red asterisks* indicate sources of oxidative stress

also reported that *in vitro* incubation with arsenicals leads to chromosomal aberrations and sister chromatid exchange in leukocytes, lymphocytes, human fibroblasts and hamster embryo cells. Human exposures at a glass plant in India showed five times more DNA damage to leukocytes in blood samples compared to baseline, and a Taiwanese skin-cancer cohort exhibited increases in p53 mutations due to arsenic contaminated drinking water [42]. Further evidence that the observed DNA damage is due to oxidative stress comes from a trial in West Bengal, an area with high arsenic drinking water levels; people taking antioxidants (curcumin and turmeric) for 3 months showed a decrease in DNA damage, ROS generation and lipid peroxidation compared to their pre-trial levels [42]. Antioxidant vitamin E has also shown a protective effect against micronucleus formation in rats dosed with arsenite [42].

While the cellular source/location of oxidative stress production resulting from arsenic exposure is debated, several groups have demonstrated ROS production (e.g., superoxide,  $H_2O_2$ , nitric oxide, hydroxyl radical), DNA damage and lipid peroxidation as well as changes in antioxidants (GSH) and enzymes (e.g., SOD, CAT, GPx) following exposure [40–43]. The reduction and methylation pathways for arsenic are shown in Fig. 13.10 along with the metabolic sources of oxidative stress. In addition to metabolic ROS generation, some studies have demonstrated that trivalent forms of arsenic are able to increase the availability of free iron from ferritin storage, leading to increased production of hydroxyl radicals [43].

## 13.5 Conclusions

Many herbicides and insecticides have been demonstrated to produce oxidative stress. For some agents such as paraquat, oxidative stress is the principal mechanism of toxicity. For other agents, oxidative stress may be secondary to more critical mechanisms underlying acute toxicity (e.g., acetylcholinesterase inhibition or ion channel dysregulation), but is nevertheless important in adverse outcomes from chronic low-dose exposures. Additional research exploring oxidative stress produced by herbicides and insecticides at environmentally relevant exposures, and the health consequences associated with those effects, will be essential to gaining a full understanding of the potential risks associated with the use of specific herbicide and insecticide compounds.

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# **Chapter 14 Health Effects of Indoor Air Pollution Due to Cooking with Biomass Fuel**

**Dona Sinha and Manas Ranjan Ray** 

## 14.1 Introduction

Air pollution is generally perceived as an urban problem associated with motor vehicles and industries. But the rural people of the developing nations of Asia, sub-Saharan Africa and Latin America face another and more severe form of air pollution. It is the indoor air pollution (IAP) due to the use of traditional, unprocessed biomass fuel such as wood, animal dung and agricultural wastes for daily household cooking and room heating [1, 2-5, 6]. Use of biomass as an energy source can be traced to the prehistoric times when humans first moved to temperate climates approximately 200,000 years ago. Cold climate necessitated the construction of shelters and the use of fire indoors for cooking, warmth and light. Ironically, fire, which allowed man to enjoy the benefits of living indoors, resulted in exposure to high levels of pollution as documented by the soot found in prehistoric caves [7]. Wood was the first fuel that man used and exposure to wood smoke is as old as humanity itself.

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## 14.1.1 Use of Biomass as Domestic Energy Source

An estimated 2.8 billion people around the world, i.e., more than 40 % of the world's population, are still dependent on biomass fuels as the primary source of domestic energy [8–10]. Although the proportion of households relying mainly on biomass for cooking has decreased from 62 % to 41 % between 1980 and 2010, the actual number of exposed persons has remained stable at around 2.8 billion during the past three decades because of the population growth [11]. Use of biomass as household fuel is most prevalent in Africa and Southeast Asia where more than 60 % of households cook with biomass. In other regions, biomass fuel use ranges from 46 % in the Western Pacific to 35 % in the Eastern Mediterranean and less than 20 % in the Americas and Europe [11]. Latin America is responsible for 12 % of the global consumption of biomass, and 27 million people in Mexico use wood as an energy source [12]. Biomass use is especially high in the Indian subcontinent (Fig. 14.1). It provides 75 % of the India's rural energy needs [13–15]. In Pakistan, about 90 % of rural and 22 % of urban households use biomass fuels [16]. Similarly, biomass caters the energy need of 88 % households of Bangladesh, 80 % of Nepal, and over 78 % of Sri Lanka [17].

#### 14.1.2 IAP from Biomass Fuel Use

Biomass has poor combustion efficiency compared with gaseous fuels [18]. Because of this, biomass emits considerable smoke that causes very high level of IAP [19]. Traditional ovens and poor kitchen ventilation aggravate the situation. In a typical biomass-using Indian kitchen, the concentration of PM<sub>10</sub> (particulate matter with an aerodynamic diameter of less than 10 micron) varies between 500 and 2000  $\mu$ g/m<sup>3</sup> [20], or even more (up to 5,000  $\mu$ g/m<sup>3</sup>; [21], which is several times higher than the WHO guideline [22], or the prevailing level of outdoor air pollution in highly polluted Indian cities. The indoor PM25 in biomass-using households varies from 330 to 1930  $\mu$ g/m<sup>3</sup> [23], while the black carbon concentrations vary from 50 to 1000  $\mu$ g/ m<sup>3</sup> [24]. A mean PM<sub>10</sub> level of 300  $\mu$ g/m<sup>3</sup> has been found in indoor air of biomassusing households in Bangladesh [25], and the indoor/outdoor ratio of  $PM_{10}$  and PM<sub>2.5</sub> (particulate matter with an aerodynamic diameter of less than 2.5 micron) were 3.80 and 4.36 respectively in biomass-using households of Pakistan [26]. In China,  $PM_{10}$  levels in biomass-using rural households during cooking time were three-times higher than that of urban households that used cleaner fuel [27]. Thus, IAP appears to be a greater menace than outdoor (ambient) air pollution in these countries, and tens of millions of people in the developing world routinely encounter IAP levels similar to the infamous London killer fog of 1952. Even the households that use clean fuel also face high level of  $PM_{2.5}$  (>1000 µg/m<sup>3</sup>) when the neighbors cook with biomass in densely populated areas [28].

During combustion, biomass fuels release smoke in the environment that contains a wide range of potentially health-damaging pollutants. They include respirable PM of different sizes ( $PM_{10}$ ,  $PM_{2.5}$  and ultrafine particles [UFP] with a diameter of less than 0.1 µm). Approximately 5–20 % of biomass smoke particulate mass



**Fig. 14.1** Photographs showing Indian women collecting firewood (**a**) pine leaves (**b**), dried mango leaves (**c**), dried paddy straw (**d**), preparing cake from raw cow dung with her bare hands (**e**), sundried cow dung cakes (**f**) and cooking with biomass (firewood) in traditional mud ovens (**g**). Children often accompany their mothers in the kitchen (**h**) and get highly exposed to smoke in the process

consists of elemental carbon, the rest is trace elements and organic compounds. The composition of the organic fraction varies dramatically with fuel type and the combustion conditions. Wood smoke consists of two-thirds of sub-micron sized particles and one-third of larger aggregates of fine particles [22, 29]. Biomass smoke is considered even more harmful than diesel, because it contains 10 times more mass concentration of PM having diameter of 0.5–0.8 µm in PM<sub>2.5</sub> range [30]. Biomass smoke also contains carbon monoxide (CO), oxides of nitrogen and sulphur, hydrocarbons, oxygenated organics, transitional metals, free radicals and chlorinated organics [31, 32]. The mean 24-h concentration of nitrogen dioxide (NO<sub>2</sub>) in biomass-using homes of Ethiopia was 97 microg/m<sup>3</sup>, which was more than double the annual mean of WHO air quality guideline [33]. The International Agency for Research on Cancer (IARC) has recognized at least five chemical groups in biomass smoke as established or potential human carcinogens [34]. They include polycyclic aromatic compounds such as benzo(a) pyrene and 1,3-butadiene, and volatile organic compounds like benzene [35]. Other toxic compounds are formaldehyde and cilia-toxic respiratory irritants phenols, cresols and acrolein [1, 36–38].

#### 14.1.2.1 Health Impact of IAP Due to Biomass Fuel Use

Epidemiological studies have shown that chronic biomass smoke exposure increases the risk of a range of common and serious diseases of both children and adults [3]. IAP is the 8th most important contributor to the burden of disease, and responsible for 2.7 % of the global burden of disease. In India it ranks 3rd in contributing to the national burden of disease, just below malnutrition and lack of safe sanitation and drinking water [39].

#### 14.1.3 Excess Mortality

High levels of PM and other pollutants present in biomass smoke can lead to excess mortality, because for every 20  $\mu$ g/m<sup>3</sup> increase in PM<sub>10</sub> the overall mortality increases by 1 % [40]. In conformity with this, 1.6 million deaths per year throughout the world (2.9 % of all deaths), mostly from pneumonia, chronic respiratory disease and lung cancer, have been attributed to breathing IAP from biomass burning. A recent study has put the annual death toll from biomass fuel use to four million [21]. For comparison, mortality due to outdoor air pollution is 0.2–0.57 million per year representing 0.4–1.1 % of total annual deaths [39]. Since women and children are subject to the maximum exposure, adverse health impact of IAP is greatest among them [26]. For example, 410,000–570,000 premature deaths per year that have been attributed to biomass fuel use in India occurred mostly among women, and children below the age of 5 years [31]. IAP accounts for 28,000 deaths and 40 million cases of acute respiratory illness a year in Pakistan [26]. Even in the small island country of Sri Lanka, 4300 annual deaths have been attributed to IAP from household cooking with biomass [41]. In China, use of biomass and coal as fuels for cooking and heating was responsible for approximately 420,000 premature deaths per annum, which is more than the approximately 300,000 annual deaths attributed to outdoor air pollution in the country [42].

## 14.1.4 Increased Morbidity

There is now evidence linking an increased risk of respiratory tract infections, exacerbation of inflammatory lung conditions, cardiac events, stroke, eye disease, tuberculosis (TB), cancer and hospital admissions with air pollution levels [18, 43–45].

#### 14.1.4.1 Effects of IAP from Biomass Burning on Respiratory Health

Greater Prevalence of Respiratory Symptoms

Of all the pollutants present in biomass smoke, PM is considered most damaging to the respiratory system. Particles more than 10  $\mu$ m in diameter are usually removed at the upper airways, but PM<sub>10</sub> may penetrate beyond the trachea and large bronchi and PM<sub>2.5</sub> may be deposited in the smaller airways and alveoli [46]. As a result, the risk of respiratory diseases increases.

Children of biomass fuel-using households suffer more from respiratory symptoms like nasal discharge, cough, shortness of breath, chest tightness, wheezing, or whistling than children from cleaner fuel-using households in Bangladesh [47] and India [48, 49]. Similarly, higher prevalence of respiratory symptoms has been recorded in women who cooked with biomass than those using cleaner fuel in Africa [50], India [43, 51], Bangladesh, Nepal and Turkey [52]. Respiratory symptoms, in general, reflect underlying diseases in the lung. Inhalation of biomass smoke may produce respiratory diseases in a number of ways. Airway lining cells have cilia at the outer surface that beat constantly upward in order to dispose of inhaled pollutants through phlegm (sputum). Cumulative smoke exposures damage these lining cells and impair the clearing mechanism of the respiratory tract. This allows inhaled bacteria and viruses to gain entry into the lower airways [53].  $PM_{10}$  and  $PM_{2.5}$  in breathing air elicit respiratory symptoms in biomass-using women. Gaseous pollutants present in biomass smoke such as NO<sub>2</sub> and formaldehyde are pulmonary irritants and can also induce respiratory symptoms [4].

#### 14.1.5 Pulmonary and Systemic Inflammation

Long-term exposure to biomass smoke evokes pulmonary as well as systemic inflammation. After inhalation, the biomass smoke constituents are deposited on the bronchi and the alveoli. The first cells that encounter the inhaled pollutants

are the alveolar macrophages (AM). The number of AM in sputum is considered a reflection of the adverse lung reaction to air pollution, and the AM count has been used as a biomarker of pollution exposure and effect [54, 55]. Laboratory animals exposed to wood smoke exhibited an increase in the number of AM and inflammatory cells in brocho-alveolar lavage fluid [56]. Microscopic evidence of pulmonary inflammation among biomass using women has been demonstrated by Dutta and her co-workers [57]. Taking sputum samples as a surrogate of airway cells, they showed accumulation of inflammatory cells such as neutrophils, eosinophils, lymphocytes and AM in the airways of women who cooked with biomass fuels [57].

Pulmonary inflammation can lead to systemic inflammatory response [58], associated with increased levels of pro-inflammatory cytokines in the bloodstream [32] as well as increased production, release and activation of neutrophils and monocytes from the bone marrow [59]. AMs phagocytose (engulf) the inhaled particles. Upon processing, they release cytokines like tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) that induces generation of chemokines like the neutrophil chemoattractant interleukin-8 (IL-8) to signal other immune cells to come in to the site of inflammation. In human studies, cumulative exposures to biomass smoke was associated with elevated circulating levels of pro-inflammatory mediators TNF- $\alpha$ , IL-8 [57, 60, 61], interleukin-6 (IL-6), interleukin-12 (IL-12) and C-reactive protein (CRP), elevated myeloperoxidase (MPO) with high inducible nitric oxide synthase (iNOS) expression and two-times more nitric oxide (NO) in serum, but reduced concentration of the anti-inflammatory cytokine interleukin-10 (IL-10) [57, 61]. CRP and IL-6 are markers of systemic inflammation [62, 63]. CRP is produced by the liver and secreted into the blood stream within a few hours of the onset of an inflammatory response [62]. Low socioeconomic status, common among the biomass users, is a risk factor for elevated CRP. IL-10 represses the expression of pro-inflammatory TNF- $\alpha$ , IL-6 and IL-1. In contrast, IL-8 is one of the most potent activators and chemoattractants for neutrophils, and it contributes to neutrophilic inflammation leading to obstructive lung disease as in chronic bronchitis and emphysema [64]. NO, a gaseous free radical, participates in wide range of biological functions including host defence and homeostasis. NO derived in the airways has a double role: either it protects against, or it contributes to, hypoxia/re-oxygenation lung injury [65]. Excess production of NO and subsequent oxidative stress are critically involved in the pathophysiology of pulmonary sepsis [66]. Conversely, suppression of NO generation via down-regulation of iNOS by selective iNOS inhibitors protects from lung injury [65, 67].

Biomass smoke inhalation also raises the circulating cortisol level [68]. It can be linked with elevated IL-6, because IL-6 stimulates cortisol secretion from the adrenal [69].

# 14.1.6 Migration of Inflammatory Cells from Blood to the Tissues

Leukocyte extravasation, i.e., the movement of leukocytes out of the circulatory system towards the site of infection or injury is the initial step of inflammation. This process occurs in an orderly manner in some phases like chemoattraction, rolling adhesion, tight adhesion and endothelial transmigration. Leukocyte marginalization and adhesion to the endothelial cells of the blood vessels are receptor-mediated. Inflammatory mediators promote the immediate expression of P-selectin on endothelial cell surfaces. This receptor binds to carbohydrate ligands on leukocyte surfaces and causes them to roll along the endothelial surface as bonds are made and broken. Carbohydrate ligands on the circulating leukocytes enable them to reach the site of inflammation through a gradient of chemokine concentration. Inhalation of airborne pollutants facilitates trafficking of inflammatory cells from pulmonary capillaries to the airway spaces by increasing alveolo-capillary permeability [70]. Biomass-using women displayed upregulation of CD11b/CD18 expression on leukocytes [61, 71], elevated P-selectin expression on circulating platelets [71, 72] and their blood contained elevated levels of IL-8 and TNF- $\alpha$  [61]. Collectively, these findings suggest that inhalation of biomass smoke for long periods may cause leukocyte and platelet activation that can facilitate migration of leukocytes from blood to the tissues, initiating inflammation [61]. Smoke inhalation not only facilitates traffic of inflammatory cells but also passage of fluid from pulmonary capillaries to the airway spaces by increasing alveolo-capillary permeability causing pulmonary edema [70]. These changes predispose the lower respiratory tract to bacterial infection by interfering with mucociliary clearance and by reducing bacterial killing by the AM [73]. Indeed, chronic exposures to smoke have been linked to pulmonary edema [74], respiratory infections and COPD [3, 4, 31].

Among different types of biomass fuels, smoke emitted from dried cow dung cake elicited the greatest inflammatory response in mice [21]. In humans, even short-term exposure to wood smoke evoked both pulmonary and systemic inflammation [75]. But the mechanism of the inflammatory response to biomass smoke is incompletely understood. Organic as well as inorganic components of the PM, especially the transitional metals, stimulate epithelial cells to produce IL-8 [76]. Incidentally, indoor-generated particulates are more bioactive on AM than is outdoor particulate matter. PM can also generate hydroxyl radicals in aqueous solution by an iron-dependent process [77] that lowers antioxidant enzymes level and generates oxidative stress [78]. Wood smoke generates oxidative stress via overproduction of free radicals through the reaction of iron with  $H_2O_2$ .  $H_2O_2$ , may produce genetic and cellular damage, nuclear factor kappa-B (NF- $\kappa$ B) activation and TNF- $\alpha$  release. Sub-chronic exposure to PM collected from households burning biomass

fuel elicited a persistent pulmonary inflammation largely through activation of tolllike receptor and interleukin-1 receptor pathways, which could increase the risk for chronic respiratory diseases [21]. Organs other than the lung can also generate inflammatory mediators, because lung inflammation was found to be mediated by production of TNF- $\alpha$  in the liver [79].

Oxidative stress also increases the permeability of epithelial cells, which would further facilitate the transfer of particles into the interstitium. The proximity of the interstitial inflammatory cells to the endothelium and the blood spaces facilitates sending signals (cytokines) into the blood causing more systemic changes. Moreover, free radicals could also play a role in the development of pulmonary fibrosis and inflammation from cooking smoke exposure, and may lead to greater susceptibility to allergy and infection with elevated titers of immunoglobulin-E [80].

## 14.1.7 Altered Airway Cytology

Airway epithelial cells that act as a barrier to inhaled pollutants are an important target for the toxic and inflammogenic effects of the PM. Continued biomass smoke exposure can inflict injury and subsequent sloughing off of airway cells. Exposure to wood smoke in mice resulted in alteration of lung histology, airway inflammation [81], and altered epithelial morphology. Figure 14.2 depicts pulmonary inflammation and injury to the airway epithelium of pre-menopausal rural women of eastern India who cooked exclusively with wood, dung cake and crop residues. Similarly, dung smoke caused severe histopathological changes in rabbit lung [82]. As in laboratory animals, biomass smoke exposure was associated with histopathological changes in the lungs of children [83] and non-smoking women [84]. In addition to inflammation, the sputa of biomass users displayed cytological changes like ciliocytophthoria which indicates respiratory viral infections; aggregates of ciliated and non-ciliated columnar epithelial cells (injury to the airway lining cells); goblet cell hyperplasia and Curschmann's spiral (mucus overproduction), Charcot-Leyden crystals (airway eosinophilia), and keratinization of the basal and parabasal cells, implying change in cellular differentiation [57].

## 14.1.8 Decrement in Lung Function

Pulmonary inflammation may lead to tissue damage and impairment of lung function. Several investigators have reported reduction in lung function in women who cooked with biomass fuel [43, 85–88]. Children living in homes that used biomass fuel also had reduced forced vital capacity (FVC) and forced expiratory volume in one second (FEV<sub>1</sub>) [9, 49]. Nepalese youth (16–25 years) from biomass-using households suffer more from airflow obstruction than those from cleaner fuel- using families [89].



Fig. 14.2 Photomicrographs of sputum samples showing massive accumulation of neutrophils ( $\mathbf{a}$ ,  $\mathbf{b}$ ) and eosinophils ( $\mathbf{c}$ ) along with particle-laden macrophages ( $\mathbf{d}$ ,  $\mathbf{e}$ ) embedded in thick mucus ( $\mathbf{f}$ ), aggregates of ciliated columnar epithelial cells ( $\mathbf{g}$ ) and goblet cells ( $\mathbf{h}$ ) in pre-menopausal rural women of eastern India who cooked exclusively with wood, dung cake and crop residues. The pictures indicate pulmonary inflammation and injury to the airway epithelium following chronic inhalation of smoke due to household cooking with biomass fuels. Pap-stained; original magnification  $100 \times (a),400 \times (b)$  and  $1,000 \times (c-h)$ 

The predominant type of lung function impairment in biomass users in India was a restrictive type of ventilatory defect characterized by FVC less than 80 % of the predicted values [85];, whereas obstructive lung disease is more prevalent among biomass users in Mexico [90]. Compared with wood and crop residues, animal dung smoke causes greater reduction of lung function, especially the FEV<sub>1</sub> and FEV<sub>1</sub>/ FVC ratio [88].

Although the lung dysfunction among biomass users has been attributed largely to particulate pollution, the underlying mechanism is still unknown. High resolution computed tomography of the thorax in Turkish women who used biomass as cooking fuel has demonstrated a variety of structural changes including thickening of interlobular septa [52]. Inflammation and consequent generation of oxidative stress in biomass-using mothers and their children [91] can inflict injury to the lung cells impairing its function. During inflammation, the airway neutrophils release several tissue-degrading enzymes like collagenase, elastase, and neutral protease, along with various oxidants which markedly derange the alveolar structure, which may ultimately lead to fibrosis and lung function reduction [92]. The combined occurrences of bronchial anthracostenosis, a disease entity consisting of bronchial destruction, deformity and stenosis, and mediastinal fibrosis have been reported in association with biomass smoke exposure [93].

## 14.1.9 Impairment of Lung Defense

The respiratory system is particularly vulnerable to inhaled pollutants because of its enormous surface area. In view of this, the system is equipped with local, specific, unspecific, cellular and humoral immunological defense mechanisms. They include bronchial and adeno-lymphatic tissue that produces secretory immuno-globulins, the ciliary and the mucus cells, lysozyme, interferon, lactoferrin, and the complement system. Moreover, alveolar macrophages, surfactant, neuropeptides, and inflammatory processes constitute other components of the lung defense system [94].

Biomass smoke exposures have been associated with compromised pulmonary immunity both in animals [95, 96] and humans [57]. Inhalation of biomass smoke causes particle overload of the AM [97, 98], that adversely affects phagocytosis as well as intracellular killing of Gram-negative bacteria by the AM [95, 99]. In fact, biomass smoke impairs the anti-microbial efficacy of both AM and bone marrow-derived macrophages [99]. Interactions of AM with inhaled UFPs lead to impairment of phagocytic activity of the former, particularly after infection that induces an increased production IFN- $\gamma$ . Reduction in pulmonary host defense mediated by the AM increases vulnerability to lower respiratory tract infection in children [100]. PM in inhaled air also generates oxidative stress [77] which increases the permeability of epithelial cells and consequent opportunistic infections.

## 14.1.10 Lung Diseases

Use of biomass as household cooking fuel increases the risk of respiratory diseases [101]. It doubles the risk of pneumonia and is responsible for 900,000 deaths annually [102]. In Mexico, wood smoke-associated lung disease includes obstructive lung disease, chronic bronchitis, emphysema and pulmonary hypertension comparable to smokers [90].

#### 14.1.10.1 ALRI

Biomass fuel use has been associated with increased incidence of acute respiratory infection in children aged  $\leq 5$  years in Pakistan [103]. Exposure to indoor biomass smoke PM<sub>2.5</sub> has been consistently associated with an increased risk of acute lower respiratory infection (ALRI) in young children of Bangladesh [104] and Nepal [105]. In addition, cumulative biomass smoke exposure induces bronchial anthraco-fibrosis [106]. The intimate association between biomass smoke and ALRI became evident from the report showing substantial improvement of the condition following reduction of indoor PM<sub>2.5</sub> through intervention measures [104].

#### 14.1.10.2 COPD

Chronic obstructive pulmonary disease (COPD) includes emphysema and chronic bronchitis (CB). It is a progressive inflammatory airway disease and a leading cause of worldwide morbidity and mortality. Tobacco smoking is an established and major risk factor for COPD, but an estimated 25-45 % of patients with COPD have never smoked [107–112]. The proportion of non-smoking-related COPD in all COPD cases ranged from 17.0 % in Venezuela, 23.1 % in Turkey to 68.6 % in India [111]. Thus, the burden of non-smoking COPD is much higher than previously believed [111, 113]. Globally, exposure to biomass smoke, especially the PM<sub>2.5</sub> fraction [114], is the biggest risk factor for COPD among nonsmokers [111]. In India, COPD prevalence was higher in biomass fuel users than the clean fuel users especially in women who cooked with biomass for more than two hours a day [115]. About 23 % of COPD in rural women of Turkey [116] was due to exposure to biomass smoke, after adjusting for possible confounding factors. Review of the published data supporting an association between biomass smoke exposure and COPD in adult women is fairly robust [117].

The prevalence of CB in communities exposed to indoor biomass smoke has been reported to be high [51, 86, 114, 118, 119–122]. Biomass using women with COPD had more lung fibrosis and thicker pulmonary artery intimae than those with COPD due to tobacco smoking [90]. Pulmonary hypertension (PH), a common and well established complication of COPD associated with decreased survival, was more frequent in women with COPD due to biomass smoke exposure than in male COPD cases due to tobacco smoke [123]. However, Ramírez-Venegas et al. [120] reported that Mexican women who had biomass smoke-associated COPD had similar clinical characteristics, quality of life and mortality compared to those with COPD due to tobacco smoking.

The precise mechanism of COPD pathogenesis among biomass users is still elusive. Smoke inhalation may facilitate migration of inflammatory cells and fluid from blood to the airway spaces by increasing alveolo-capillary permeability [70] leading to pulmonary edema [74], respiratory infections, and COPD; [3, 4, 31]. An imbalance in oxidant-antioxidant status has been proposed for the pathogenesis of COPD by some authors [124]. Serum level of malonyldialdehyde, a marker of oxidant-antioxidant imbalance, was high in Turkish women who used biomass as cooking fuel [125]. Injury and disintegration of the alveolar wall by excess secretion of proteases such as neutrophil elastase is another mechanism proposed for the development of emphysema [126].

#### 14.1.10.3 Tuberculosis

Analysis of data from 200,000 Indian adults as part of the Indian National Family Health Survey (1992–93) revealed that persons living in biomass-using households had more instances of tuberculosis than persons living in households that used cleaner fuels with an adjusted odds ratio of 2.58 (95 % CI: 1.98–3.37) [80]. Biomass smoke exposure can account for up to 59 % of rural and 23 % of urban cases of tuberculosis in India [80]. In addition to smoky rooms, low socio-economic status and poor kitchen ventilation perhaps contribute to tuberculosis [127]. Increased risk of tuberculosis among biomass users may result from reduced pulmonary defense [95, 128], and impaired function of the mucociliary escalator that reduces disposal of deposited pollutants [128].

#### 14.1.10.4 Asthma

Asthma is a chronic respiratory disease characterized by sudden attacks of labored breathing, chest tightness, and coughing. It is a multi-factorial disease having strong genetic predisposition. Analysis of 99,574 women and 56,742 men aged between 20 and 49 in India during 2005–2006 has shown that women living in households using biomass have a significantly higher risk of asthma than those living in households using cleaner fuels (OR: 1.26; 95 %CI: 1.06–1.49), even after controlling for the effects of a number of potentially confounding factors [129]. Even children [49] living in biomass-using households had a higher prevalence of asthma than those living in households using cleaner fuels. However, no such association was found in Nigerian children [130]. Biomass smoke exposure, on the other hand, can increase the frequency and severity of attacks in asthmatic people [131].

Systemic Changes Associated with Biomass Smoke Exposure

The ultrafine particles (UFPs, diameter  $<0.1 \mu$ m) and gaseous pollutants present in biomass smoke can cross the alveolar-capillary barrier and enter into the blood stream and circulate throughout the body. As a consequence, all the important functions of the body can be deranged.

#### 14.1.11 Effects on the Hemato-Immune System

#### 14.1.11.1 Anemia and Elevated Leukocyte Count

Chronic inhalation of biomass smoke lowers the hemoglobin and red blood cell values, but raises the white blood cell, neutrophil, and eosinophil counts in Indian women [72] and children [132]. Toxic granulation in neutrophils and an excess of band cells, regarded as indications of bacterial infection, were more frequent in biomass users [72]. An immediate decrease of neutrophils but increase in lymphocytes and monocytes has been observed in males with chronic pulmonary diseases in response to UFPs and gaseous pollutants [133].

#### 14.1.11.2 Platelet Hyperactivity

Cooking with biomass was associated with a significant increase in the number of circulating platelets, rise in platelet volume, and up-regulation of P-selectin (CD62P) expression on the platelet surface of rural housewives in India [71, 134]. Moreover, biomass-using women showed greater aggregation of platelets to agonists, and increased number of platelet-leukocyte aggregates in circulation when compared with age-and gender-matched controls who cooked with cleaner fuel liquid petroleum gas (LPG; [71]). Collectively, these findings suggest platelet hyperactivity and increased risk of cardiovascular diseases (CVD) among biomass users [134].

The underlying mechanism (s) of platelet and leukocyte activation among biomass users is not clear. UFPs may contribute to platelet hyperactivity and plateletleukocyte aggregate formation, because UFPs alter expression of adhesion molecules on leukocytes [135]. Biomass PM-associated bioaerosols such as bacteria [136], endotoxin [137], respiratory viruses and their products [138], fungal spores and pollen, which remain adsorbed on the surface of PM can directly activate platelets. During these conditions, platelet P-selectin expression and platelet aggregation to soluble agonists are upregulated, enhancing the risk of atherosclerosis and thrombotic vascular occlusions [136, 139]. The importance of bacterial infection in platelet activation has been displayed in an animal study that showed a rise in platelet number, P-selectin expression, and agonist-induced platelet aggregation following bacterial lipopolysaccharide (endotoxin) injection [139].

#### 14.1.11.3 Neutrophil Activation and Platelet-Leukocyte Aggregates

Neutrophils, the most abundant leukocytes, are the major inflammatory cells that form the first line of defense against infection and cell injury [140]. Neutrophils are terminally differentiated cells with a very short lifespan (7–20 h) in circulation and in tissue (1–4 days). Neutrophils respond to infection and tissue injury by recognizing and binding with immunoglobulin G (IgG) molecules and complement proteins that coat the surface of the invading agent. This recognition-binding process is mediated by neutrophil surface receptors, including the complement 1 receptor (CD35), complement 3 receptor (CD11b), and the low-affinity IgG receptor (CD16). The engagement of these surface receptors initiates a cascade of intracellular events leading to the release of enzymes following degranulation and generation of reactive oxygen species (ROS) via respiratory burst activity by neutrophils [141]. Women who cooked with biomass had higher blood levels of nitric oxide (NO) [61]. NO, a gaseous free radical, participates in wide range of biological functions including host defence and homeostasis. NO derived in the airways has a double role: either it protects against, or it contributes to, hypoxia/re-oxygenation lung injury [65].

Activated neutrophils express higher levels of CD11b/CD18 on their surface for transmigration. CD11b is both a complement receptor (CR3) and a cell adhesion molecule present on the surface of leukocytes. Up-regulation of  $\beta_2$  Mac-1 integrin (CD11b/CD18) has been demonstrated in peripheral blood neutrophils, monocytes and lymphocytes of women who cooked with biomass [134]. The integrin molecules trigger chemotaxis and shape change [142]. High levels of endotoxin that are usually present in indoor air of biomass-using households [143] can mediate up-regulation of CD11b on neutrophils. Viruses like influenza-A can also enhance CD11b/CD18 expression on neutrophils and monocytes [144]. Biomass smoke mediated activation of the platelets and the leukocytes increases the number of circulating leukocyte-platelet aggregates [71, 134], which increase the risk of CVD [145].

#### 14.1.11.4 Alteration in Monocyte and Lymphocyte Subtypes

Circulating monocytes and lymphocytes are heterogeneous cells with different subtypes expressing characteristic surface molecules. Biomass smoke exposure alters the relative distribution of these subtypes. In monocytes, it depletes the number of classical monocytes (CD16-CD64+), but increases the fractions with both dendritic cell and monocytic functions (CD16+CD64+), with high antigen-presenting capacity (CD16+CD64-) and the plasmacytoid monocytes (CD16-CD64-) [146]. On the other hand, biomass smoke exposures reduce the number of CD4+ T-helper and CD19+ B cells, but increases the number of CD8+ T-cytotoxic, CD16+CD56+natural killer (NK), memory T and CD4+CD25+regulatory T (Treg) cells in peripheral blood [146]. Increase in NK cells and decline in CD4+ T-helper cells among biomass users may imply tissue damage and inflammation [147]. The increase in Treg cells suggests suppression of immune activation status [148] while increase in memory T-cells indicates underlying pulmonary and systemic inflammation [149].

## 14.1.12 Cardiovascular Risk

#### 14.1.12.1 Hypertension, Atherosclerosis

Biomass smoke exposure can alter the blood pressure and the heart rate, two indicators of cardiovascular health [150]. Cooking with biomass was associated with hypertension in relatively young women in India [71] and Guatemala [151]. Elevated blood pressure correlated with high  $PM_{10}$  and  $PM_{2.5}$  levels in indoor air, platelet hyperactivity, and increased circulating levels oxidized low density lipoprotein [71]. Even short-term increase in  $PM_{2.5}$  increased arterial blood pressure by rapidly triggering autonomic nervous system imbalance [152]. Chronic  $PM_{2.5}$  exposure augments pro-vasoconstrictive pathways, blunting vasodilator capacity [152].

Circulating leukocyte-platelet aggregates, found in excess among biomass users [71, 134], represent a prothrombotic condition [153] and a risk for thrombosis [154–156]. The aggregates produce pro-coagulant, oxidative and mitogenic substances, and can cause microembolism in capillaries as well as acute arterial thrombosis.

#### 14.1.12.2 Arterial Stiffness and Heart Rate Variability

Household wood smoke exposures affect ventricular repolarization [157]. It increases central arterial stiffness with simultaneous reduction of heart rate variability [158]. Besides, biomass smoke inhalation increases the risk of atherosclerosis manifested by increased carotid intima-media thickness, greater prevalence of atherosclerotic plaques and higher blood pressure [159].

#### 14.1.12.3 Biomass Smoke, Inflammation and CVD

Hypertension, common among biomass users, is a known risk factor for cardiovascular disease (CVD; [160]). Systemic inflammation (elevated levels of TNF- $\alpha$ , IL-8, CRP and IL-6 along with reduced IL-10) and oxidative stress (excess generation of ROS and/or depleted antioxidant level) could be the mechanistic link between chronic exposure to biomass smoke and an excess risk of CVD [71, 161]. The pro-inflammatory potential of PM depends largely on the organic fraction of the PM [162]. Rise in CRP has been implicated in the pathogenesis of CVD [163]. CRP is an independent cardiovascular risk marker; its level is directly related to the severity of hypertension [164] and pathogenesis of coronary artery disease [165]. CRP promotes atherogenesis [166, 167] via endothelial dysfunction [165], mediates tissue factor expression in monocytes and induces adhesion molecule and chemokine expression in human endothelial cells [167]. Collectively, CRP could promote inflammation and endothelial dysfunction and participate in the development of CVD [165]. CRP level of greater than 3.0 mg/l is recognized is a predictor of cardiovascular risk [168].
Persistently elevated IL-6 levels seen among biomass users, on the other hand, has been linked with left ventricular diastolic dysfunction in humans [169]. Upregulation of CD11b expression on leukocytes, another finding in biomass users, is positively associated with plasma markers of coagulation activation and endothelial perturbation [170]. Likewise, MPO is a critical mediator in coronary atherosclerosis [171].

#### 14.1.12.4 Biomass Smoke, Oxidative Stress and CVD

The relation between biomass smoke-induced oxidative stress and hypertension has been the subject of investigation of some studies [172]. Oxidative stress is recognized both as a cause and consequence of hypertension [173]. Chronic inflammation generates ROS [135, 174] which is a risk for CVD [168, 175-177]. Increase in ROS generation and decrease in antioxidant enzyme superoxide dismutase (SOD) have been demonstrated in biomass-using women in India in their child-bearing age [71, 161]. Likewise, wood smoke particles elicited oxidative stress in Nepalese women [178], and reduced the antioxidant defense in women and children in Nigeria [91]. In animal studies also, wood smoke exposure led to reduced lung antioxidant enzyme activities and oxidative stress [179, 180], similar to that caused by cigarette smoke [181]. Transitional metals like iron and copper, which are abundant in biomass smoke, can catalyze the formation of ROS via 'Fenton and Haber-Weiss' reactions [182]. But the contribution of redoxactive metals in biomass smoke-induced oxidative stress has been reported negligible [178]. PM<sub>2.5</sub> significantly depletes SOD, catalase and glutathione peroxidase activities and increases lipid in laboratory animals [183]. A study in human subjects also revealed an inverse relationship between SOD activity and  $PM_{2.5}$  levels in breathing air [184].

#### 14.1.12.5 Stress and CVD

In addition to smoke exposure, biomass-using women suffer from psycho-social and physical stress because of their low socio-economic status, strenuous physical work for collection of crop wastes from the field, wood from the jungles, making of cow dung cake and in many cases participation in agricultural work. Physical or psychological stress can increase leukocyte count, raise pro-inflammatory mediator levels [185], trigger changes in lymphocyte subpopulations and CD11b expression on neutrophils, and increase platelet-leukocyte aggregate formation [145]. The changes, possibly mediated by catecholamines via beta 2-adreno receptors of lymphocytes [186], can raise the cortisol level and increase the risk of endothelial dysfunction [160, 187–190], hypertension [191] and early atherosclerosis [189].

### 14.1.13 Endocrine Toxicity and Adverse Pregnancy Outcomes

#### 14.1.13.1 Low Birth Weight

Biomass smoke contains many endocrine disruptors such as polycyclic aromatic hydrocarbons and their derivatives, substituted phenolic compounds, aromatic carbonyl compounds and higher molecular weight alcohol and ketones [192]. Inhaled CO emitted from burning biomass combines with hemoglobin to form carboxyhemoglobin (COHb), a much more stable compound that does not readily give up oxygen to peripheral tissues and organs, including the fetus. Exposure to biomass smoke is associated with COHb levels of 2.5-13 % against a critical level of 2.5 % according to WHO guidelines [193]. Continued exposures to endocrine disrupters and high COHb interfere with transplacental delivery of nutrients and oxygen leading to intra-uterine growth retardation and consequent adverse pregnancy outcomes such as preterm births, low birth weight (LBW; birth weight less than 2,500 g) and post-neonatal infant mortality. LBW and stillbirth are common among biomass-using women [194, 195]. Analysis of 3559 childbirths in Zimbabwe showed an average of 175 g lower body weight of the babies born to mothers who cooked with wood, dung, or straw compared with babies born to mothers using LPG, natural gas, or electricity [196]. Similarly, a study among 11,728 live-born infants in rural India showed an adjusted 49 % increased risk of LBW, 34 % increased incidence of respiratory illness, 21 % increased risk of infant mortality (death within 6 months), and 45 % and 30 % increased risks of underweight and stunting at 6 months, respectively, due to household cooking with biomass [197]. Children born in Indian households that used biomass were 73 g [198] to 78 g lighter [199] than those born in households that used cleaner fuels.

#### 14.1.13.2 Still Birth and Infant Mortality

Biomass fuel use has been linked with infant mortality (death within 28 days of birth) in Ecuador [9], and 11 % excess stillbirths in India [200]. Mother's education also plays an important role in this regard, since biomass use was associated with increased risk of neonatal death among infants born to Indian women with no more than primary education (OR 7.56; 95 % CI: 2.40–23.80) [199].

### 14.1.14 Cataract, Middle Ear Infection

Eye irritation from biomass smoke exposure is widely reported [201]. Long-term cooking with biomass fuel can even lead to cataract [87, 202, 203] and blindness in women [204]. In addition, biomass smoke exposure increases the risk of middle ear infection (otitis media) in children [205], a condition that causes a considerable amount of morbidity.

### 14.1.15 Depression and Neurodegenerative Disease

Significantly higher prevalence of depression with altered platelet serotonin has been reported among pre-menopausal women in rural India who cooked regularly with biomass, compared with control women who cooked with LPG [68]. A considerable comorbidity exists between depression and CVD. But the associated vulnerability is not unidirectional, as the presence of CVD can also influence mood [206].

Studies have demonstrated that the brain can be a target of air pollution, especially the UFPs. UFPs can penetrate through the different tissue compartments of the lungs and eventually reach the capillaries and circulating cells such as the erythrocytes. These particles are then transported to other organs including the liver, the spleen, the kidneys, the heart and the brain, where they are deposited [207]. The UFPs can translocate to the central nervous system (CNS) via the olfactory mucosa and the olfactory nerve [208]. After reaching the CNS, the UFPs can evoke neuroinflammation, oxidative stress, tissue injury and neurodegeneration [207], increasing the risk of Alzheimer's and Parkinson's diseases [209]. In addition, chronic biomass smoke exposure in early life affects the children's neurodevelopmental and behavioral performance [210].

# 14.1.16 Genotoxic Effects

#### 14.1.16.1 MN Formation

Household cooking with biomass is a major contributor to mutagens in the indoor environment [211, 212] with increased risk of cancer [211]. Inhalation of biomass smoke increases the frequency of micronucleus (MN) formation, a biomarker of chromosomal breakage [213, 214]. In addition, biomass smoke exposures mediate chromosomal aberrations [215]. For various biomass fuels, the relative MN frequency decreased in the order: cow dung>wood>kerosene>LPG [213].

#### 14.1.16.2 DNA Damage

Alkaline comet assay demonstrated extensive DNA damage in peripheral blood lymphocytes [214, 216, 217] and buccal epithelial cells [218] of women who cooked with biomass [214, 216, 217]. Airway cells of biomass users displayed increased expression of gamma-H2X that suggests that the damage occurred in both strands of the DNA [214]. The DNA-damaging efficacy of biomass smoke particles was much more than the traffic-generated PM per unit mass, possibly due to the high level of polycyclic aromatic hydrocarbons in the former [219]. The genotoxicity of biomass smoke was thought to be mediated by generation of oxidative stress PM

[214, 217, 218]. The direct involvement of biomass smoke in DNA and chromosomal damage becomes apparent from the report that improved kitchen ventilation and reduction of smoke was associated with decrement in the frequency and intensity of DNA damage [12].

#### 14.1.16.3 Impaired DNA Repair

Biomass smoke has been found to interfere with the non-homologous end joining type of DNA double strand break repair [214] and DNA mismatch repair pathways [220]. As a result, a substantial part of the damaged DNA remained unrepaired that may lead to cellular changes including mutagenesis and carcinogenesis along with upregulation of ribosome biogenesis [221].

### 14.1.17 Altered Cell Signaling

#### 14.1.17.1 ERK, p38 and JNK

Studies in laboratory animals have shown that biomass smoke evokes inflammation by modulating the cell signaling pathways [222]. Smoke exposure activates ERK, p38 and JNK signaling pathways. As a result, the expressions of pro-inflammatory IL-8 and matrix metalloproteinase (MMP) -1,-9, and -12 genes are upregulated [222]. In contrast, the expression of tissue inhibitor of MMPs (TIMP-1) was found to be inhibited following biomass smoke exposure [222].

#### 14.1.17.2 PI3K/Akt

Biomass smoke also activates the phosphatidylinositol 3-kinase/protein kinase B (PI3K/Akt) signaling pathway that controls key cellular processes such as glucose metabolism, cell cycle progression, apoptosis and inflammation. Cooking with biomass fuel upregulated the expression of active (phosphorylated) p-Akt<sup>ser473</sup> and p-Akt<sup>thr308</sup> in bronchial epithelial cells, especially in metaplastic and dysplastic cells, alveolar macrophages, airway neutrophils and peripheral blood lymphocytes of rural women in India in their child-bearing age [223, 224].

Akt activation seems to be involved in the mechanism of inflammation among biomass users, because the PI3K/Akt pathway plays a crucial role in the expression and activation of inflammatory mediators, inflammatory cell recruitment, immune cell function, airway remodeling, and corticosteroid insensitivity in chronic inflammatory respiratory disease [225]. In conformity with this, selective PI3K inhibitors reduce inflammation in experimental animal models [225]. Therefore, PI3K/Akt may prove to be useful in creating novel therapies in the treatment of asthma and chronic obstructive pulmonary disease [225]. On the other hand, Akt activation can

be a consequence of inflammation, as TNF- $\alpha$  stimulates the phosphorylation of Akt, its translocation, and the formation of Akt/p65/p300 complex [226]. In addition to inflammation, airway cell Akt activation contributes to epithelial dysplasia (Fig. 14.3; [227]), lung cancer development [228, 229] and metastasis [227].

Akt activation among biomass users can be attributed in part to respiratory virus infections. Rhinovirus (RV) is responsible for the majority of common colds and it triggers exacerbations of asthma and COPD. RV activates Akt minutes after infection [230]. RV exposure in mice was followed by phosphorylation of Akt in the lung and neutrophilic and lymphocytic airway inflammation [231] along with increased expression of IL-8 [230]. Respiratory viral infections may play a crucial role in lung injury as they target the epithelial cells of the lung producing desquamation, microvascular dilation, edema and an inflammatory cell infiltrate [73]. These changes predispose the lower respiratory tract to bacterial infection by interfering with mucociliary clearance and reducing bacterial killing by alveolar macrophages [73].

# 14.1.18 Metaplasia, Dysplasia and Lung Cancer

Chronic air pollution exposures increase the risk of lung cancer, the leading cause of cancer death and the third most common form of malignancy affecting 1.30 million people worldwide in 2004 [232, 233]. The incidence of lung cancer is showing a general upward trend especially in the developing countries like China and India [234].

Biomass smoke exposures increases the risk of multinucleation, metaplasia and dysplasia of bronchial epithelial cells in women (Fig. 14.3; [57, 223, 224]). Metaplasia and dysplasia of airway cells are the initial morphological changes in the journey towards neoplasia [235]. Consistent with this, IARC has identified IAP from coal usage as a known (class 1) human carcinogen, while that from biomass as a probable (class 2A) human carcinogen [236]. Studies from India [237] and Mexico [238] have shown that household cooking with biomass increases the risk of adenocarcinoma of the lung in non-smoking women. Similarly, modest increase in the risk of lung cancer was shown associated with cooking, but not space heating, with biomass fuel [239], and the risk was greater in females [10]. Overall, the association between biomass use and lung cancer is inconsistent, however [10]. In addition to lung cancer, biomass smoke increases the risk of cancer in the upper aero-digestive tract [240], hypopharynx [236], nasopharynx [241]. Moreover, it increases the risk of uterine cervix cancer via activation of human papilloma virus [242]. Airway PI3K pathway activation is an early and reversible event in lung cancer development [229]. Figure 14.3 depicts genotoxicity, activation of Akt signaling and increased cancer risk among biomass users.



**Fig. 14.3** Photomicrographs showing intense comet formation in lymphocyte (**a**), micronucleus formation in parabasal cell (**b**), multicucleated epithelial cells (**c**, **d**), metaplasia (**e**) and dysplasia (**g**) of epithelial cells exfoliated in spontaneously expectorated sputum of biomass-using Indian women in their child-bearing age. Strong phosphorylated Akt protein expression was observed in the nuclei of metaplasic (**f**) as well as dysplastic cells (**h**). The observations imply genotoxicity, activation of Akt signaling and increased cancer risk among biomass users. Alkaline, single cell gel electrophoresis (**a**); Pap-stained (**b**–**e**, **g**) and immunocytochemistry with hematoxylin staining for nuclei (**f**, **h**); original magnification  $400 \times (a)$ ,  $1,000 \times (b-h)$ 

#### 14.1.18.1 Biomass Smoke, Chronic Inflammation and Lung Cancer

As early as in 1863, Virchow first proposed that tumorigenesis may be induced by chronic inflammation [243]. Now it is well recognized that chronic inflammation, common among biomass users, is a risk factor for many human cancers including cancer of the lung. According to induction hypothesis theory, chronic inflammation may lead to excessive cell proliferation and cell activation, thereby causing induction of irreversible DNA damage. Generation of superoxide and other reactive oxygen and nitrogen species by macrophages and neutrophils that infiltrate the sites of inflammation may cause damage to biological molecules including DNA, which can drive the cells towards carcinogenesis [244]. Consequently, persistent irritation, inflammation, and immunosuppression promote tumor growth in these initiated cells, leading to the development of invasive cancer [245]. It has been suggested that the pro-inflammatory cytokines released through inflammatory response promote tumor growth, while tumor growth further stimulates the inflammatory response [246]. Inflammation can initiate and promote carcinogenesis in multiple steps like genomic instability, epigenetic modifications, localized immunosuppression, and angiogenesis [247]. Activation of the pro-growth PI3K-Akt signaling pathway could be a significant factor in this regard, since Akt activation contributes to epithelial dysplasia [227], lung cancer [228, 229] and metastasis [227]. Considering these, it has been suggested that p-Akt [223] and pro-inflammatory cytokines [248] could be used as potential biomarkers of IAP-associated lung cancer among nonsmokers.

#### 14.1.18.2 Summary and Concluding Remarks

Household cooking with unprocessed biomass, a common practice among poor, rural people of the developing nations, is a significant cause of mortality and morbidity. It enhances the prevalence of lung diseases including COPD, causes immune suppression, platelet hyperactivity, pulmonary and systemic inflammation, hypertension and CVD. In addition, cumulative exposure to biomass smoke inflicts chromosomal and DNA damage, impairs the DNA damage repair process, and increases the risk of carcinogenesis in the lungs. Women who cook with biomass suffer more from depression, and they often give birth to a pre-term underweight baby. In terms of mortality, it kills an estimated four million people each year globally. Black carbon and methane released during biomass combustion are also the primary anthropogenic contributors to global warming from the populations of Southeast Asia, sub-Saharan Africa, and India.

Although biomass fuels are cheaper, IAP from household use of biomass fuels incurs high health costs. In India alone, it amounts to 885–4,250 billion rupees per year. Importantly, the annual health cost per household due to burning of dungbriquette is 61.3 % higher than that of biogas [249]. Since biomass remains the main source of household energy for millions of people throughout the globe, the magnitude of the problem of health impairments among biomass users seems enormous and it warrants immediate attention of all concerned. As an immediate measure, introduction of user-friendly smokeless ovens and better kitchen ventilation may be undertaken on a priority basis. Improved cook stoves (IC) provides significant climate and health benefits [250, 251]. IC can reduce indoor cooking-time black carbon concentrations remarkably [24]. Pronounced improvements in respiratory health-related quality of life and significant reductions of household CO levels have been observed after installation of ventilated cook stoves in Bolivia [252]. Exploitation of alternative energy sources, including solar power and/or supply of cleaner fuels such as LPG to the rural people at an affordable price, could be the long-term solution to the problem. Research priorities should include development of simple but sensitive biomarkers that would be helpful for regular health monitoring for initiating medical intervention at the early stage of the disease.

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# Chapter 15 Outdoor Air Pollutants

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# 15.1 When Did the Air Pollution Start?

Although it is a common idea that "air pollution" started in our planet concomitant with the Industrial Revolution, there are documents showing that pollution started well before the eighteenth century. A recent study by Sapart et al. [1] from the Utrecht University in the Netherlands, shows that methane emissions, a gas implicated in climate changes, increased significantly already more than 2000 years ago, during the Roman Empire. The increase was not correlated to increased warming but with human activities. It should be mentioned that metallurgy and large-scale agriculture started around 100 B.C. During the Roman Empire, the population kept domesticated livestock – cows, sheep and goats – which excrete methane gas, a byproduct of digestion. At the same time, in Asia, the Han dynasty expanded its rice fields, which harbor methane-producing bacteria. Also, blacksmiths in both empires produced methane and  $CO_2$  gas when they burned wood to fashion metal weapons.

In the third Century B.C., Theophrastus (a student of Aristotle) wrote "smell of burning coal was disagreeable and troublesome" and later the Roman philosopher Seneca, in 61 A.D., defined the air in Rome as heavy, a sign of air pollution.

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Furthermore, it was during this period that Romans started the use of beach houses as a way to escape from the city pollution.

In the Middle Ages, the use of coal in cities such as London was beginning to increase. In the latter part of the thirteenth century, in an effort to reduce air pollution, England's King Edward I threatened Londoners with harsh penalties if they did not stop burning sea-coal. However, the king's regulations–and those of subsequent leaders–had little effect. In the United Kingdom, the Industrial Revolution in the eighteenth century was based on the use of coal that dramatically increased urban air pollution. In this period, the word smog was coined, as in foggy condition, and pollution levels escalated when urban smog (smoke and fog) was formed. Reports of hazardous effects induced by smog reach as far back as the thirteenth century when, during the reign of Richard III (1377–1399), the first reports of human diseases were attributed to severe air pollution. The 1875 Public Health Act in England contained a smoke abatement section in an attempt to reduce smoke pollution in urban areas.

Starting from the eighteenth century, increased smog and soot levels had serious health impacts on the residents of growing urban centers. For example, in 1952, pollutants from factories and home fireplaces mixed with air condensation killed at least 4,000 people in London over a few days. A few years earlier, in 1948, severe industrial air pollution created a deadly smog that asphyxiated 20 people in Donora, Pennsylvania, and made 7,000 sick. Acid rain, first discovered in the 1850s, was another problem resulting from coal-powered plants. The release of human-produced sulfur and nitrogen compounds into the atmosphere negatively impacted plants, fish, soil, forests and some building materials.

Today, the leading cause of air pollution is motor vehicles, (which were first mass-produced in the U.S. by Henry Ford, in the early twentieth century); auto emissions also increase the amount of greenhouse gases in the atmosphere, which in turn contribute to global warming.

# 15.2 Air Pollution in Life

A good quality of life for humans and other living organisms is assured by low concentrations of air pollutants that must not exceed threshold limits, established by empirical and/or experimental methods. Atmospheric air is a mixture of nitrogen, oxygen, noble gases (such as Ar, Ne, He,), and carbon-dioxide. In addition, atmospheric air is a gas-mixture where solid and liquid particulates are present and thus could be considered as an aero-disperse system. The ideal composition of pure air can not be defined because, in nature, air is always polluted by various components (gases, solid particles and aerosols) that change the base composition of the atmosphere. Pollutants can be harmful to human health, living organisms, soil, water and other elements of the environment.

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More than 3,000 substances that are not part of the base atmospheric composition can be considered air pollutants [2]. Some substances that are normally present in the atmosphere at nominal non-toxic concentrations can be considered pollutants if their concentration reaches much higher than usual levels. Also, some substances that are normally present in certain layers of the atmosphere (e.g. ozone in the stratosphere), when present in the troposphere, are considered pollutants. There is no an ideal method for defining a standard air quality index. In fact, in each country, or even within a country in different cities, the air quality index is determined following different methods and even simple air quality indices need skills in mathematical statistics [3]. Although there is not any unique and comprehensive classification of pollutants, generally they can be classified in several ways according to their origin (natural or anthropogenic, chemical or biological), phase (solid, liquid, gaseous), formation mechanism (primary and secondary), and their effect on human health (toxic, allergic or carcinogenic) (Fig. 15.1). Modern industrial and technical progress has resulted in a significant increase of the concentration of pollutants in the atmosphere and, consequentially, an ever-increasing frequency of allergic illnesses [4].

Pollutants may originate from natural or anthropogenic sources. Biogenic or natural sources include windborne dust, sea spray, wild fires, and volcanic eruptions. Hence, H<sub>2</sub>S, SO<sub>2</sub>, HCl, NO, NO<sub>2</sub>, NO<sub>3</sub>, CO, CO<sub>2</sub>, CH<sub>4</sub>, NH<sub>3</sub>, dust, pollen, fungus spore, bacteria are natural pollutants [5]. Anthropogenic sources are mainly related to human activities, in particular combustion of fuels, both as industrial process or nonindustrial fugitive fonts such as exhaust gas of transportation vehicles [6]. Combustion engines produce nitrogen oxides, volatile organic chemicals



Fig. 15.1 Health effects of air pollutants

(VOCs), carbon monoxide, carbon dioxide, sulfur dioxide and particulates. Cars gas, stoves, incinerators, and farming activities produce carbon monoxide and dioxide, as well as particulates. Other human-made sources include aerosol sprays and solvent spills or leaks.

These anthropogenic pollutants are basically the same as natural pollutants except maybe the biological pollutants and some specific synthetic organic compounds (chlorofluorocarbon (CFC), dioxin and benzene derivatives), soot and ash [4]. According their physical state, air pollutants are classified into **gas forms** (such as oxidized and reduced forms of carbon (CO<sub>2</sub>, CO, CH<sub>4</sub>), of sulphur (SO<sub>2</sub>), of nitrogen (NO<sub>2</sub>, NO, N<sub>2</sub>O<sub>4</sub>, NH<sub>3</sub>), O<sub>3</sub>, halogens, benzene vapors, Hg, VOCs, **particles in suspension** (including heavy metals with toxic effect (Pb, Ni, Cd, As), polycyclic aromatic hydrocarbons (PAHs), PM<sub>10</sub> and PM<sub>2.5</sub> particulate matter and different ionizing radiation.

Because it is not possible to discuss all the air pollutants in this chapter, the main air pollutants to which terrestrial life are exposed based on the EPA classification and for which EPA has set National Ambient Air Quality Standard, will be considered. These pollutants are found throughout the USA and are defined as "most common" or "criteria pollutants". They are (1) particulate pollution or particulate matter, (2) carbon monoxide, (3) sulfur oxides, (4) nitrogen oxides, (5) lead and (6) trophospheric ozone. Particulate matter and ground-level ozone are the most widespread health threats.

# 15.2.1 Particulate Matter

Particulate matter (PM) is defined as any substance (except pure water) that exists as a liquid or solid in the atmosphere under normal conditions and is microscopic or submicroscopic in size, but larger than molecular dimensions [7]. PM have both biogenic and anthropogenic origins. Biogenic or natural sources include windborne dust, sea spray, wild fires, and volcanic eruptions, while anthropogenic sources include combustion of fuels, industrial processes and transportation sources [6]. Particulate matter is generally classified as  $PM_{10}$  and  $PM_{2.5}$ ; particles with aerodynamic diameters lower than 10 and 2.5 µm, respectively, that can induce morbidity and mortality [8–12]. It is further possible to discriminate particles as coarse particles, with diameters >2.5 µm, and fine particles with diameters <2.5 µm. The size of atmospheric particles plays an important role in their chemical and physical properties as well as their climatic and health effects, based on the number of particles, surface area, and volume distribution [13].

The concentrations of PM changes in urban sites as the result chemical and physical processes, vertical and/or horizontal transport, condensation, photochemical reactions [14].

Coarse particles typically originate from primary sources such as dust and traffic, while fine particles arise from secondary sources such as the reaction of gases in the atmosphere [15].

Four main source types for PM<sub>10</sub> and PM<sub>2.5</sub> were identified in a recent study [16]:

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- a vehicular source (traced by carbon/Fe/Ba/Zn/Cu);
- a crustal source (Al/Si/Ca/Fe);
- a sea salt source (Na/Cl/Mg);
- a mixed industrial/fuel oil combustion source (V/Ni/SO<sub>4</sub><sup>2-</sup> and a secondary aerosol (SO<sub>4</sub><sup>2-</sup>/NO<sub>3</sub><sup>-</sup>/NH<sub>4</sub><sup>+</sup>).

Biomass combustion or shipping emissions were also identified, although their contribution to PM levels is less relevant.

The health risks related to inhaled airborne particles depends on both the penetration and deposition of particles in the various regions of the respiratory tract. The larger particles that are inhaled are usually removed in the extrathoracic region, while the smaller particles can easily reach and deposit in the alveolar region where gas exchange occurs. As this region is not coated with a protective mucus layer that is rapidly moved and eliminated, the residence time for the particles deposited in the alveolar region is more significant than in the extrathoracic region [15].

Epidemiologic studies have shown a direct correlation between increased mortality and levels of airborne particles, especially for  $PM_{2.5}$  [17].

Of note is a recent work that assessed the association between long-term exposure to ambient air pollution and lung cancer incidence in European populations using seven cohort studies based in nine European countries. The study showed a statistically significant association between risk for lung cancer and PM exposure. Interestingly, an increase in road traffic of 4,000 vehicle-km per day within 100 m of a residence was associated with an increased risk for lung cancer. These data showed, for the first time, that particulate matter air pollution contributes to lung cancer incidence in Europe [18].

### 15.2.2 Carbon-Monoxide (CO)

Carbon-monoxide (CO) consists of one carbon atom and one oxygen atom, connected by a triple bond which consists of two covalent bonds as well as one dative covalent bond. It is the simplest ox-carbon and it is produced during incomplete combustion of organic matter due to insufficient oxygen supply to enable complete oxidation to carbon dioxide (CO<sub>2</sub>). Worldwide, the largest source of carbon monoxide is natural in origin; due to photochemical reactions in the troposphere which generate about  $5 \times 10^{12}$  kg per year, other natural sources of CO include volcanoes, forest fires, and other forms of combustion [19].

Carbon monoxide is a colorless, odorless, tasteless, and initially non-irritating gas, and thus it is very difficult for people to detected [20]. In biology, carbon monoxide is naturally produced by the action of heme oxygenase 1 and 2 on the heme from hemoglobin breakdown [21]. Although it is produced in low quantities by animal metabolism and is involved in some normal biological functions, in higher quantities it is toxic to humans and animals. The affinity between hemoglobin and CO is approximately 230-fold higher than the affinity with oxygen so hemoglobin

binds preferentially to CO. This results in a proteic complex and squeezes out oxygen. Hemoglobin becomes carbon-monoxide hemoglobin, preventing blood oxygen transport through the body. This results in oxygen depletion of the heart, brains and blood vessels, eventually causing death if the exposure is severe or extended for long time [4]. CO also binds to the hemeprotein myoglobin, with a 60-fold higher affinity than oxygen, reducing its functionality [22]. This causes reduced cardiac output and hypotension, which may result in brain ischemia [23].

Acute CO poisoning brings on headache, heavy breathing, heart problems, in serious cases unconsciousness and even breath paralysis. Chronic symptoms are headache, dizziness, insomnia, heart ache, nervous system symptoms and increase of heart attack frequency.

### 15.2.3 Sulphur Dioxide (SO<sub>2</sub>)

Sulphur dioxide (SO<sub>2</sub>) is the most abundant among the highly reactive gasses known as "oxides of sulfur" (SO<sub>x</sub>). SO<sub>2</sub> is a colorless gas with a pungent odor and dissolves readily in water. SO<sub>2</sub> in the air results primarily from activities associated with the combustion of coal and other fuels in industrial and domestic use. Minor sources of SO<sub>2</sub> include industrial processes such as extracting or smelting metal from ore. Once released into the environment, SO<sub>2</sub> can be converted to sulfuric acid, sulfur trioxide, and sulfates. Once dissolved in water, SO<sub>2</sub> can form sulfurous acid. Soil can absorb SO<sub>2</sub>, but it is not known if or how it moves in soil. Humid weather promotes the transformation of the oxide into sulphuric acid causing acid rains and winter smog [4]. However, SO<sub>2</sub> concentrations in air have been decreasing over the past two decades due to the use of alternative energetic sources [24].

 $SO_2$  is responsible for several adverse effects on the respiratory system. Shortterm exposures to  $SO_2$ , ranging from 5 min to 24 h, are associated to bronchoconstriction and increased asthma symptoms especially during exercise or other hyper-ventilated conditions. Children, elderly people and asthmatics are more sensitive to the actions of  $SO_2$ . Furthermore, SOx can react with other compounds in the atmosphere generating small particles that reach deep sensitive parts of the lungs and can cause or worsen respiratory disease, such as emphysema and bronchitis, and can intensify existing heart disease, and induce premature death.

### 15.2.4 Nitrogen Oxides (NOx)

Nitrogen dioxide  $(NO_2)$  is one component of the complex mixture of different highly reactive gasses known as "oxides of nitrogen," or "nitrogen oxides  $(NO_x)$ ." Other nitrogen oxides include nitrous acid and nitric acid. The Environmental Protection Agency (EPA) established  $NO_2$  as the indicator for the larger group of nitrogen oxides. Nitrogen oxides are produced naturally (by bacterial and volcanic action and lightning) but emissions from cars, trucks and buses, power plants, and off-road equipment represent the major sources of NO<sub>2</sub> [25].

NO<sub>2</sub>, reacting with ammonia in the presence of moisture, is a precursor for a number of harmful secondary air pollutants, and other compounds to form small particles, that increase the formation of ground-level ozone. Fine particle pollution thus is responsible for severe effects on the respiratory system such as emphysema and bronchitis, and can aggravate existing heart disease [26].

Nitrogen-oxides irritate the mucous membrane, cause coughing, nausea, headache, and dizziness. These symptoms usually disappear in a few hours although with acute poisoning, after a few hours, pneumonia and pulmonary edema can emerge [27]. When NO<sub>2</sub> reaches the mucous membrane it forms nitrous or nitric acid, and induces local tissue damage. If it gets into the bloodstream, haemoglobin is converted to methehemoglobin, becoming unable to carry oxygen to the organs. Longer exposures reduce the resistance to infections, aggravate asthmatic diseases, causes frequent respiratory illnesses, and, later on, decreased lung-functions may occur [4]. Recent data from a 73,000 cohort study showed that NO<sub>2</sub> is associated with lung cancer and ischemic heart disease mortality confirming the theory that pollution exposure causes premature mortality [28].

# 15.2.5 Heavy Metals (Lead)

Some elements naturally present in the earth's crust, with metallic properties and an atomic number higher than 20, such as lead, mercury, cadmium, silver, nickel, vanadium, chromium and manganese, are considered heavy metals [29]. Combustion, waste water discharges and manufacturing facilities represent sources of such metals. As metals are not biodegradable (although organic forms can result from metabolism) they can enter into the food chain.

Some metals, such as zinc and iron, are indispensable as essential elements at very low concentrations. However, others, and all at higher doses and after prolonged exposure tend to bio-accumulate in the human body causing severe toxic effects disrupting the functions of vital organs such as brain, kidneys and liver [30]. The toxic effects of heavy metals are due to their ability to substitute or interfere with the actions of diverse polyvalent cations (calcium, zinc, and magnesium) that function as charge carriers, co-factors in catalyzed reactions, or as structural elements of protein.

Lead is one of the most toxic heavy metals and can cause serious adverse effects on different body tissues and organs. In particular, prolonged exposure to Pb even at low levels damage the nervous system. The toxic effects of Pb are mainly due to its capability to substitute for calcium in the body, altering its accumulation, transport, and thus all its physiological functions. Detrimental effects associated to lead exposure are directly related to a persons age. In particular, exposure to high lead levels during pregnancy is directly related to spontaneous abortion, low birth weight and impaired neurodevelopment together with impairment of childhood cognitive functions [31–33]. Several studies also confirmed the carcinogenic properties of lead [31].

# 15.2.6 Ozone (O<sub>3</sub>)

Ozone (O<sub>3</sub>) or trioxygen, is a triatomic molecule consisting of three oxygen atoms. The word ozone derives from the Greek  $\delta\zeta\epsilon\nu$ , which means "to give off a smell". It is an unstable gas of a soft sky-blue color, with a pungent, acrid smell already perceptible at a concentration of 0.01 ppb. The molecule has a molecular weight of 48 KD. Ozone does not have a stable structure but exists in several mesomeric states in dynamic equilibrium.



Ozone is naturally present in the atmosphere surrounding the earth. In the upper part of the atmosphere, the stratosphere, circa 20–30 Km from the earth<sup>2</sup> surface, the ozone layer can reach the concentration of 10 ppm. The ozone occurring in the stratosphere, where the majority of atmospheric ozone is found, forms a "filtering layer" that acts as a barrier to the dangerous radiation from the sun.

$$O_2 \xrightarrow{\langle 242 \text{ nm}} O + O$$
  

$$O + O_2 \xrightarrow{} O_3$$
  

$$O_3 \xrightarrow{} O_2 + O$$

In contrast,  $O_3$  present within the lower troposphere (10 miles from the ground level) is very noxious to the terrestrial health. It is a ubiquitous pollutant of the urban environment but it is not emitted directly by any man-made source in significant quantities. Ozone arises from chemical reactions in the atmosphere through the action of sunlight on oxygen molecules. Among the most common molecules that lead to  $O_3$  formation at the ground level are nitric oxides ( $NO_x$ ).  $NO_2$  can be photolyzed by solar ultraviolet radiation (UV) resulting in NO and the atomic oxygen that can react with molecular oxygen leading the formation of  $O_3$ . Ozone can also be destroyed by nitric oxide; NO can react with  $O_3$  to form  $NO_2$  and  $O_2$ . Under these

steady-state conditions, the concentration of  $O_3$  cannot increase until most of NO has been converted to NO<sub>2</sub> by additional reactions occurring within the complex. This accumulation occurs as the rate of NO<sub>2</sub> photolysis is much faster than that of  $O_3$ .

Other species in photochemical smog also undergo photodecomposition to yield free radicals that may participate either directly or indirectly in the conversion of NO to  $NO_2$ . Hydroxyl and hydroperoxyl radicals are an example of compounds that can react with nitrogen radicals with the destruction of  $O_3$  by NO.

$$\begin{array}{ccc} \text{NO}_2 & \xrightarrow{<310 \text{ nm}} & \text{NO} + \text{O} \\ \text{O} + \text{O}_2 & \xrightarrow{} & \text{O}_3 \\ \text{O}_3 + \text{NO} & \xrightarrow{} & \text{NO}_2 + \text{O}_2 \end{array}$$

In large metropolises like Mexico City, but also European cities such as Rome, Milan and Paris,  $O_3$  can reach toxic concentrations (0.8 ppm) especially during the summer. Anthropogenic emissions, mainly of NOx but also methane (CH<sub>4</sub>), carbon monoxide (CO) and sulphuric compounds, have caused a progressive increase of ozone concentration over 1 ppm [34]. It has been estimate that the level of tropospheric  $O_3$  will increase 5-fold at the end of this century because the increase of cars and industrial fumes, leading to dangerous consequences to terrestrial life [35].

Ozone is strongly toxic to human health especially the respiratory tract.  $O_3$  reacts with the respiratory tract lining fluid (RTLF) components and may never directly reach the underlying respiratory tract epithelial cells, at least in areas where they are covered by RTLFs [36]. Therefore, the toxic effects of  $O_3$  on the underlying epithelial cells may be mediated by products of its reaction with RTLF constituents. These products would include lipid hydroperoxides, cholesterol ozonization products, ozonides, aldehydes, and oxidation products proteins or even antioxidants themselves (e.g., thyol and thyol-derived radicals).

As O<sub>3</sub> is relatively insoluble in water, interactions of O<sub>3</sub> with RTLFs are primarily governed by reactive absorption (i.e., the more oxidizable substrate that is present in RTLFs, the more O<sub>3</sub> will be absorbed by the RTLFs). Therefore, inhaled O<sub>3</sub> may be effectively removed by antioxidants present in the more abundant, proximal RTLFs, thus delivering less inhaled O<sub>3</sub> to more distal and susceptible gas-exchanging regions of the lung [37]. This results in activation of cell defense systems or initiation of inflammatory-immune processes. Several researchers have shown that O<sub>3</sub> reacts readily with water-soluble antioxidants leading to a depletion of this defense at respiratory tract levels [37]. O<sub>3</sub> in sufficient amounts activates regulators of the expression of mediators of airway inflammation such as cytokines, chemokines, and adhesion genes [37]. Critical in this regard are investigations of the effects of  $O_3$  in so called susceptible populations already known to have inflammatory airway diseases (e.g., subjects with asthma and cigarette smokers). Many of these subjects may actually have augmented RTLF antioxidant levels due to increased glandular secretions and plasma leakages and cellular adaptations to the oxidant stress provided by their chronic inflammatory states.

In addition, a the recent work by Jerrett et al. [38] has been shown for the first time that exposure to ozone increases the risk of death from ischemic heart disease, which accounts for more than 7 million deaths worldwide each year. These findings underline how not only the directly exposed organs are affected by air pollutants but once in contact with the toxicants there is a noxious systemic effect on our bodies [38]. Recently, the toxic effects of O<sub>3</sub> exposure have been shown also in other "target" organs, such as skin and eyes. One of the first studies on the effect of  $O_3$  on skin, Thiele et al. demonstrated that  $O_3$  induced significant antioxidants skin depletion and a clear increase in lipid peroxidation [39]. In vivo exposure to ozone depletes vitamins C and E and induces lipid peroxidation in epidermal layers of murine skin [40]. In addition to increased levels of oxidative stress markers, such as lipid peroxidation, aldehydes, and protein carbonyl, and decreased antioxidant levels, such as GSH and vitamins C and E, an induction of proinflammatory markers, such as cyclooxygenase-2 (COX-2), along with increased levels of heat shock proteins (HSP-32, -70, and -27) and activation of NF- $\kappa$ B, were observed in skin of hairless mice exposed to 0.8 ppm of O<sub>3</sub> [41]. The study by Valacchi et at. [41] was the first to show that O<sub>3</sub> exposure induces an active cellular response in the skin, and that  $O_3$  can therefore alter skin physiology. Recently, Xu et al. have confirmed the cutaneous toxic effect of  $O_3$  in humans [42], showing a clear correlation between ozone levels and skin conditions such as urticaria, eczema, contact dermatitis, rash/ other nonspecific eruption, and infectious skin disease. Other pollutants such as particulates, SO<sub>2</sub>, and NO<sub>2</sub>, did not show an association with skin conditions. Furthermore, it has been proposed that the effects of  $O_3$  on skin are mediated by the activation of the aryl receptor (AhR) and by the induction of the cytochrome P450 isoform CYP1, an enzyme in a detoxifying pathway usually activated in the cell by xenobiotics and carcinogens, suggesting that toxicological consequences follow the exposure of cutaneous tissues to  $O_3$  [43].

Finally, although few reports have focused on the effect of ozone on eyes, there is a very early work that demonstrated that ozone exposure was able to affect tear protein stability thereby making the eye more susceptible to damage [44]. More recently, the work by Lee et al. [45] has elegantly shown the toxic effect of  $O_3$  on ocular tissue using both *in vivo* and in *in vitro* models. This is the first report showing that ozone induced the breakdown of corneal epithelial integrity, decreased the number of mucin-secreting cells, and induced the production of inflammatory cytokines. This effect was mediated by the activation of NF- $\kappa$ B as also reported for lung and skin tissues [41].

# 15.2.7 Criteria Pollutants

Besides the "criteria pollutants" as classified by EPA, it is worth mentioning the socalled halogens and halogenated hydrocarbons, pollutants. They include: – Fluorine ( $F_2$ ). Fluoride is present in air pollutant mixtures both as a gas (HF, SiF<sub>6</sub>, CF<sub>4</sub> and F<sub>2</sub>) and particulate ( $F_3$ AlF<sub>6</sub> (cryolite), CaF<sub>2</sub>, NH<sub>3</sub>F, AlF<sub>6</sub>, CaSiF, NaF and Na<sub>2</sub>SiF<sub>6</sub>). Aluminum factories, glassworks, steelworks, ceramic factories, phosphate fertilizer plants, uranium smelters and combustion of coal are the major sources of fluorine pollutants [46]. Fluoride air pollution can adversely affect human health and more than 90 % of fluoride ingested with food or water accumulates in the bodies through incorporation into the crystal structure of bone and tooth. Most of the fluorine that is not deposited in the bones, teeth, and other calcified tissues, is excreted in the urine within hours of ingestion.

**Chlorine** ( $Cl_2$ ) Although chlorine concentrations change rapidly in the atmosphere due to atmospheric chemistry and light, rain can remove all the chlorine from the air in a very short time. The impact of chlorine pollution increases in bright sunlight and decreases in drought and low temperature.

**Hydrogen chloride (HCl)** This gas is released in large quantities through combustion of polyvinylchloride and other chlorinated hydrocarbon materials, and by incinerators. HCl gas is very hygroscopic and quickly reacts with atmospheric moisture and forms aerosol droplets.

**Bromine** ( $Br_2$ ) and Iodine ( $I_2$ ) At high temperatures, organo-bromine compounds are easily converted to free bromine atoms, a process which acts to terminate free radical chemical chain reactions. This makes such compounds useful fire retardants. Well-drilling fluids, as an intermediate in manufacture of organic chemicals, and in film photography represent the most important sources of such a gas. Volatile organic-bromine compounds, under the action of sunlight, form free bromine atoms in the atmosphere which are highly effective in ozone depletion.

In nature, iodine is a relatively rare element and its compounds are primarily used in nutrition, the production of acetic acid and polymers. Iodine's relatively high atomic number, low toxicity, and ease of attachment to organic compounds have made it a part of many X-ray contrast materials in modern medicine.

**Halogenated Hydrocarbons** Halogenated hydrocarbons are produced by reacting fluorine, chlorine, bromine, or iodine with a hydrocarbon molecule and are toxic for human health. They affect the stratospheric ozone layer tending to degrade into their component elements, which include halogen radicals having great affinity towards ozone. CFCl<sub>3</sub> and hydrochlorofluorocarbons HCFCs have been widely used as refrigerants, propellants and solvents, contributing to ozone depletion [47].

**Polycyclic Aromatic Hydrocarbons (PAHs)** More than 60 hydrocarbons and almost 20 aldehydes and ketones are emitted by incomplete combustion of solid fuel (i.e. wood, charcoal, peat, coal) as a complex mixture of particulate and gaseous species (benzene, formaldehyde, 1,3–butadiene, and styrene) that are known to be carcinogenic. The higher molecular weight polycyclic aromatic hydrocarbons (PAHs), PAH derivatives, methylated and alkylated PAHs, and nitrogen-containing heterocyclic aromatic compounds are emitted in the form of particles from the combustion of bituminous smoky coal that contains organic and inorganic materials including intrinsic concentrations of sulfur, arsenic, silica, fluorine, lead, nickel, chromium, and mercury. On combustion, these elements are released as such or in

the form of their oxides causing smog, soot, acid rains, and toxic air emissions. Microfibrous quartz can also be found in some smoky coals and the resulting coal smoke [48].

**Volatile Organic Compounds (VOC)** VOC are a complex mixture of many different contaminants such as carbohydrates, organic compounds and solvents, mainly derived from industrial processes and fuel combustion, paint and cleanser use, or agricultural activities. Depending of the nature of any components, VOC can cause different health problems, offensive odors, reduction of lung capacity and cancer. VOC also play an important role in raising ozone levels in the lower atmospheric layer, the main cause of smog.

# 15.3 The Singular Case Cigarette Smoke

Cigarette smoke is now considered part of the air pollutants. There are reports showing how cigarette smoke produces 10 times more particulates than diesel car exhaust [49]. Tobacco smoke is a complex aerosol, composed of several thousand chemical substances distributed between the gas and the particulate phases. Therefore, cigarette smoke can be classified as both a gaseous and particulate pollutant. The smoke emitted from a lit cigarette is a dense aerosol where microscopic droplets (particulate phase) are distributed in a vapor of air and other gases derived by burning tobacco. There are circa  $10^{10}$  particles per cubic centimeter in fresh mainstream smoke (the combination of inhaled and exhaled smoke after taking a puff on a lit cigarette) and the particle sizes can reach 1 µm in diameter. Smoke particles can be collected using a filter paper (Cambridge filter pad) and are defined as total particulate matter (TPM) or tar. A small portion of the overall components of cigarette smoke are distributed between the gas and the particulate phases and are called "semivolatile components". The gas phase of cigarette smoke includes O<sub>2</sub>, N, NO, CO<sub>2</sub>, CO, etc.) and volatile compounds.

It has been calculated that mainstream cigarette smoke contains circa 5,000 chemicals suspended in the gaseous phase [50]. The presence of high levels of prooxidants, such as free radicals, in smoke is well-documented, and it is estimated that gas-phase smoke contains more than  $10^{14}$  low-molecular-weight carbon- and oxygen- centered radicals per puff [51, 52]. In addition, as mentioned, the gas phase of smoke contains up to 500 ppm nitric oxide (NO), which slowly undergoes oxidation to nitrogen dioxide (NO<sub>2</sub>) [53]; both these gases are radicals.

Radicals in gas-phase smoke have a very short life spam. The small organic radicals in gas-phase smoke are not produced in the flame: flame radicals are too shortlived to pass through the cigarette [52-54]. In addition, the radicals in tar phase are relatively stable and can reduce O<sub>2</sub> to generate superoxide, hydrogen peroxide and other ROS [52, 54, 55]. Although, cigarette smoke contains thousands of toxic chemicals including many carcinogens, a wealth of evidence supports the notion that a major part of the toxicity associated with cigarette smoking is related to oxidative stress, caused by reactive oxidants and radical species in tobacco smoke itself, or by secondary oxidative events such as lipid peroxidation activated by smoke exposure [56, 57].

Both smokers and nonsmokers can incur adverse health effects from the smoke of burning cigarettes. Smokers inhale mostly mainstream smoke, which is drawn through the burning tobacco column and filter tip and exits through the mouthpiece of the cigarette. Nonsmokers inhale mostly sidestream (SS) smoke, which is emitted into the surrounding air between puffs from the end of the smoldering cigarette. Sidestream smoke is the major source of environmental tobacco smoke (ETS).

Numerous epidemiological studies covering the experience of millions of men and women over many years show that smokers' increased risks of developing cancer, cardiovascular diseases and COPD is related to the number of cigarettes smoked daily, the lifetime duration of smoking, and early age of starting smoking. Based on United States statistics, the lifetime risk that an individual (men and women combined) will develop lung cancer is 6.9 %, or 1 in 13 people. Clearly, this number would be higher for people who smoke and much lower for people who have never smoked.

In a 2006 European study, the risk of developing lung cancer was: 0.2 % for men who never smoked (0.4 % for women); 5.5 % for male former smokers (2.6 % in women); 15.9 % for current male smokers (9.5 % for women); 24.4 % for male "heavy smokers" defined as smoking more than 50 cigarettes per day (18.5 % for women). An earlier Canadian study quoted the lifetime risk for male smokers at 17.2 % (11.6 % in women) versus only 1.3 % in male non-smokers (1.4 % in female non-smokers).

From these statistical data it is easy to understand that, although CS is one of the main risk factors for lung cancer, only a percentage of smokers develop the disease, suggesting that, beside the different habits and the kind and number of cigarettes smoked, there is also a possible genetic predisposition. It should also be mentioned that about one nonsmoker dies from secondhand smoke exposure for every eight smokers who die from smoking, even though secondhand smoke doses (in terms of total mass inhaled) are substantially lower. Recent work by Schick and Glantz [58] showed that freshly generated sidestream CS is 3–4 times more toxic to laboratory animals than mainstream smoke (the smoke that the smoker inhales). In addition, the same group has very recently demonstrated that aged SS smoke is even more toxic than the fresh SS smoke. These are important data because in typical indoor spaces secondhand smoke lingers for 1.5–2.0 hours going through chemical transformations that make the smoke even more toxic for humans [59, 60].

# 15.4 Exposure and Toxicity of Air Pollutants

Airborne pollution can fall to the ground in precipitation, in dust, or simply due to gravity. These phenomena are defined "atmospheric deposition". Once deposited from the air, pollution can enter our bodies via direct deposition in water or indirect

deposition in land. Therefore, humans enter in contact with air pollutants not only via inhalation but also by ingestion and dermal contact. Once in our system, the pollutants can affect several organs, not only the one directly exposed to the toxicants. This explains the toxic effects that air pollutants can have at systemic levels. In addition to the respiratory tract system, chronic exposure to pollutants like CO can indirectly reduce the speed reflexes and induce dizziness and fatigue. Lung inflammation due to ozone or particulate matter exposure can affect blood coagulation [61] and even induce myocardial infraction. It is well-known that exposure to high levels of nitrogen oxides [62, 63] sulphur dioxide [64] and heavy metals promote an initial irritation of the first airways and, in particular in asthmatic individuals, a successive bronchoconstriction and dyspnea. Particulate matter and ozone can easily reach the alveolar epithelium [65] inducing lung irritation and inflammation [66] Analogous effects can be observed with long-term exposures to lower pollutant concentrations, while it is known that chronic exposure to ozone and heavy metals lead to a reduced functionality of lungs, including asthma, emphysema, and even lung cancer [67-70].

As mentioned before, pollutants are able to also reach organs that are not directly exposed to the pollutants. For example, the nervous system is mainly affected by heavy metals and several papers have shown symptoms like memory and sleep disorders, tremors, and blurred vision after lead exposure [71]. In particular, lead exposure causes the alteration of the dopamine system, glutamate system, and N-methyl-d-Aspartate (NMDA) receptor complex [72, 73]. Of note are also the effects of metals on the cardiovascular system; in fact mercury, nickel and arsenic can alter the blood pressure and inhibit hematopoiesis anemia [74]. Heavy metals can also affect the urinary system by damaging kidney tubular excretion and decreasing the glomerular filtration rate. Finally, maternal exposure to lead increases the risks of abortion and pre-term delivery, congenital malformations [75] and impairment in the nervous system development [76].

# 15.5 Pollution and Oxidative Stress

Most air pollutants act directly as prooxidants of lipids and proteins or as free radical generators. This common cellular mechanism promotes oxidative stress and induction of inflammatory responses [77, 78]. On the other hand, it is now confirmed that air pollutants play an important role in the initiation, promotion and progression of cancer.

Reactive oxygen and nitrogen species are very injurious inhibiting the normal functions of mitochondrial and nuclear DNA, cellular lipids, and proteins, in addition to their involvement in many signaling pathways [79]. During normal metabolism and in response to exogenous environmental exposures such as cigarette smoke, metals, ozone and free radicals are constantly produced leading to an "oxidative-stress" status. This oxidative state induces a wide variety of adverse effects in many organs and tissues, that easily can led to central nervous system

disorders such as Parkinson's, and Alzheimer's disease, atherosclerosis, or heart attacks, stroke, and even chronic inflammatory diseases such as rheumatoid arthritis. Heavy metals can also induce oxidative stress, but the negative effects are due generally due to their abilities to substitute calcium, magnesium and zinc cations in the maintenance of cellular functions and protein conformation. Heavy metals can also accumulate in cellular organelles leading to dysfunction. Lead, the most dangerous of the heavy metals, can accumulate in mitochondria causing a significant reduction of transmembrane potential [80]. Nickel enters the nucleus, silences the expression of genes such as tumor suppressor genes, interacting with chromatin and inducing carcinogenesis [81]. In conclusion, some metals interfere with various voltage-and ligand-gated ionic channels and cause neurotoxic diseases [82, 83].

### 15.6 Conclusion

Humans are exposed to not only one pollutant, but to several toxicants simultaneously and often this induces an additive if not a synergistic effect. For instance, in the work by Goldberg [84], the effect of exposure to three pollutants such as  $NO_2$ ,  $O_3$  and PM were analyzed. The exposure to fine particulate matter,  $O_3$ , and  $NO_2$  was positively associated with ischemic heart disease mortality.  $NO_2$  (a marker for traffic pollution) and fine particulate matter were also associated with mortality from all causes combined while only  $NO_2$  had significant positive association with lung cancer mortality.

Not everybody that is exposed to toxicants develop diseases or the same diseases. This is a consequence not only of a genetic predisposition but also of the age, nutritional status and time of exposure. All these variables make the understanding of pollution effect in human health very difficult. Thus, the results of animal experiments are often difficult to be extrapolated for the benefit of humans.

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# Chapter 16 Oxidative Stress and the Inorganic Carcinogens

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# 16.1 Introduction

Oxidative stress can be viewed as a state where a toxicological or pathological increase in the formation of reactive oxygen species (ROS) occurs and overwhelms the natural antioxidant capacities of a cell or of the body [1, 2]. Excess ROS and resultant oxidative stress can also occur when the toxicants, like metals, depress or otherwise deplete the normal antioxidant systems inhibiting a cells ability to deal with ambient ROS [1, 2]. These excess or unscavenged ROS subsequently damage critical biomolecules like DNA, proteins, and lipids, and it is this damage that eventually leads to disease [1-3]. Oxidative stress is associated with a number of human diseases including cancer, diabetes, neurological disorders, cardiovascular disease, atherosclerosis, and chronic inflammation [1, 2]. Inorganic toxicants, potentially through the generation of oxidative stress, are associated with all these aforementioned diseases [1, 2]. It is clear that occupational or environmental exposure to several different metals is associated with an elevated risk of cancer in humans or rodents, and oxidative stress may be an important mechanism in this effect [1-3]. In this chapter, we focus on metal-induced ROS and their relation to cancer development. Inorganic carcinogens of concern were selected based on the criteria of the International Agency for Research on Cancer (IARC), a unit of the World Health Organization that, in part, evaluates agents for human carcinogenic potential.

Based on IARC evaluations, several toxic metals or metalloids are considered human carcinogens [4]. These include arsenic, beryllium, cadmium, and nickel, and their related compounds, as well as chromium(VI) compounds [4]. Additional toxic metals considered probable human carcinogens include inorganic lead compounds

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[5] and indium phosphide [6]. Vanadium pentoxide is also possibly carcinogenic to humans [6]. The carcinogenic behavior of cobalt metal depends on the presence of tungsten carbide (with tungsten carbide it is considered a probable human carcinogen, without it cobalt is only a possible carcinogen; [6]), while cobalt sulfate and other soluble divalent cobalt salts are possible human carcinogens [6]. Over-exposure to iron is emerging as a potential carcinogenic threat [7, 8]. All these metallic agents can be linked to oxidative stress [1–3].

In living cells, there is always some endogenously generated ROS including superoxide and hydroxyl radicals, produced by mitochondrial respiration, P450 metabolism, inflammation, etc. [2]. Cells have endogenous defensive mechanisms ranging from simple molecules like glutathione, to complex enzymes like catalase, superoxide dismutase, and glutathione peroxidase [2]. These systems are adaptive and can be induced, to some extent, to deal with exposures that cause oxidative stress.

There are two general mechanisms by which metals, as ions, can generate excessive ROS and thereby oxidative stress [1–3]. These are the direct chemical generation of ROS and indirect generation by displacing an endogenous metal ion capable of direct generation of ROS [1–3]. An additional indirect mechanism could be depletion of antioxidant systems, which could come into play with chronic exposures to metals. For instance, with direct generation in what is known as the Fenton reaction, hydrogen peroxide is reduced while a transition metal is oxidized producing the hydroxyl radical [1, 2]. The ability to participate in such reactions depends on the metal's redox potential. Carcinogenic metals like chromium(VI) are known to produce ROS in this manner while cadmium(II), which is not redox active in biological systems, likely produces ROS in an indirect fashion by displacing other metals [1–3]. The individual sections of this chapter will cover potential mechanisms for ROS generation for the known, probable, and potential human carcinogenic metals compounds.

Assuming oxidative stress has occurred with a carcinogenic metal, the potential outcome relevant to cancer would be ROS attacking DNA. Oxidative DNA damage (ODD) could result and may lead to modifications of DNA bases and resultant mutations or genomic instability. ODD has been directly related to the eventual malignant transformation of target cells with some inorganic carcinogens like arsenic and cadmium [9, 10].

#### 16.2 Known Human Carcinogens

### 16.2.1 Arsenic and Arsenic Compounds

Arsenic is a ubiquitous toxic and carcinogenic metalloid. Inorganic arsenic compounds are human carcinogens in the lung, skin, and bladder, and are suspected kidney, liver, and prostate carcinogens [4]. Human environmental inorganic arsenic exposure occurs mainly from arsenic-contaminated drinking water, which generally comes from natural sources [4]. Occupational exposure to arsenicals occurs in the manufacturing of various agricultural products, such as pesticides and herbicides, from fumes and dusts that occur in smelting industries, and during wood preservation [4]. The common oxidation states of arsenic are +5 and +3, and arsenic can form both inorganic and organic compounds in the environment and in the human body.

Inorganic arsenic is enzymatically methylated to form mono- or di-methylated trivalent and pentavalent forms using *S*-adenosylmethionine as the methyl donor [11]. The methylation of arsenic was originally believed to be a detoxification mechanism. However, recent experimental work has shown that methylated metabolites are more potent toxicants than the non-methylated forms [12]. In fact, it is now thought that the trivalent methylated metabolites are the most reactive oxidants [1, 11], possibly due to their greater ability to release iron from the iron storage protein ferritin [13], which can then catalyze the reduction of hydrogen peroxide to form DNA-damaging hydroxyl radicals. Methylation of arsenic can vary depending on factors such as age, gender, pregnancy, genetic polymorphisms in methylation-associated enzymes, and/ or variability in the activities of different reductants [11, 14, 15]. These factors can play key roles in susceptibility to arsenic-induced diseases.

Arsenic metabolism can lead to the generation of ROS that can have indirect or direct effects on the genotoxicity of arsenic [1, 16]. Although their formation is not fully defined, the major arsenic-induced ROS include superoxide anions, hydrogen peroxide, singlet oxygen, peroxyl radicals, and hydroxyl radicals via the Fenton reaction. These ROS alter cellular redox status by depleting thiols such as glutathione and by modulating thioredoxin reductase. These changes alter signal transduction pathways that regulate gene expression [1, 4, 16]. Arsenic-induced oxidative stress has been linked with the development of various diseases including hepatic and renal disorders, cardiovascular disorders, atherosclerosis, and cancers.

Exposure to arsenic and arsenic compounds induces cancers in animals and malignant transformation in cells [4, 17]. Arsenic-induced ROS mediate oxidative damage to lipids, proteins, and perhaps most importantly to DNA during carcinogenesis and mutagenesis [1, 16]. Arsenic can also interfere with DNA repair mechanisms and induce proteins involved in oxidative stress [16]. ODD has been observed in cells, animals, and humans exposed to arsenic [4, 9, 15, 18]. Although not all cells methylate inorganic arsenic [9, 15], methylation appears necessary for the formation of ODD but is not necessary for malignant transformation of a given target cell [9, 15]. This indicates that inorganic arsenic has both genotoxic and non-genotoxic (i.e. epigenetic) mechanisms.

## 16.2.2 Beryllium and Beryllium Compounds

Beryllium is an alkaline earth metal that is widely used, mostly as an alloy, in the aerospace, automotive, biomedical, defense, energy, and electrical industries because of its unique qualities [4]. Beryllium and beryllium compounds are classified as known human carcinogens [4]. Occupational exposure to beryllium and

beryllium compounds is associated with human lung cancer, and various routes of exposure to the metal or its compounds cause lung and bone tumors in several animal species [3, 4]. Human exposure can also occur via ingestion of contaminated drinking water and food, or inhalation of ambient air or cigarette smoke [4]. Similar to some other metals (e.g. cadmium), beryllium is not redox active under physiological conditions.

The carcinogenic mechanism of beryllium is not yet clear although multiple mechanisms have been proposed [3, 4]. Evidence of direct mutagenic effects of beryllium is inconclusive, with studies being negative or weakly positive [4]. Direct genotoxic effects include chromosomal aberrations, gene mutations, and sister chromatid exchange, and appear to depend on the compound, dose, and experimental conditions [3, 4]. Evidence for epigenetic effects include the hypermethylation of the p16 tumor suppressor and estrogen receptor-alpha, which leads to the inactivation of both genes in lung tumors in rats [3, 4].

The induction of ROS and oxidative stress by beryllium exposure is a possible carcinogenic mechanism. Beryllium-induced ROS and/or oxidative stress is associated with the activation of mitogen protein kinases (e.g. MEK1, ERK1, p38, MAPK and JNK), increased levels of growth factors (e.g. EGF, VEGF) and abnormalities in the functioning of their receptors, the induced expression and/or mutation of oncogenes (e.g. H-Ras, K-Ras), and down-regulation of DNA repair genes [3, 4, 19, 20]. Together, these alterations could contribute to tumorigenesis through indirect genotoxicity and/or unregulated and error-prone cell turnover.

### 16.2.3 Cadmium and Cadmium Compounds

Cadmium is a highly toxic transition metal [4]. Cadmium toxicity is partly due to its strong capacity to replace essential elements, like zinc, in critical sites of biomolecules, such as enzymes [3, 21]. In fact, cadmium often mimics zinc but in a nonfunctional manner [3, 21]. Occupational exposure to cadmium and cadmium compounds mainly occurs via inhalation while exposure in the general population is from a mixture of ingestion and inhalation [4]. Cadmium and cadmium compounds are classified as known human carcinogens [4]. Strong evidence links occupational cadmium exposure to human lung cancer [4, 21] and there are suspected associations between cadmium and renal and prostate cancers [4]. Inhalation of cadmium compounds is associated with lung cancers in rodents [4, 21].

Cadmium and cadmium compounds can be genotoxic [3, 4]. Cadmium is not a redox active metal but none-the-less produces oxidative stress at mechanistically relevant levels [3, 4]. Thus, cadmium likely produces ROS and oxidative stress in an indirect manner [3, 4] by depletion of glutathione resulting in overwhelming a cell's antioxidant capacity [4]. It also appears that cadmium inhibits critical antioxidant enzymes such as catalase, superoxide dismutase, and glutathione reductase leading

to oxidative stress [3, 4]. Alternatively, cadmium could displace Fenton capable metals, like copper or iron, from cellular binding sites and thus allow those metals to cause oxidative stress [2]. It is clear that cadmium can indirectly cause ODD in vitro and this damage can be mitigated by the presence of the metal binding protein metallothionein (MT; [22]).

# 16.2.4 Chromium(VI) Compounds

Chromium is a transition element that is used in metallurgy, and dye and pigment production [4]. There are indications that chromium may be an essential nutrient and it is found in dietary supplements. Trivalent(III) and hexavalent(VI) chromium ions are the two most stable and biologically relevant forms, although the hexavalent form is not naturally occurring and stems from industrial processes [23]. Chromium(VI) compounds are human lung carcinogens [4]. The epidemiological data primarily come from occupational settings where inhalation was the primary route of exposure. There are also studies associating exposure to chromium(VI) compounds with cancer of the nose and nasal sinuses in humans [4]. Various chromium(VI) compounds can be carcinogenic in rodent lung (by intratracheal instillations, implantation in cholesterol filled wire baskets, etc.), but there are no positive carcinogenic inhalation studies with chromium(VI) compounds [4]. In a bioassay run by the National Toxicology Program, sodium dichromate dehydrate, a hexavalent chromium compound, in the drinking water, induced adenocarcinoma of the small intestine of mice, and squamous cell carcinoma of the oral mucosa and tongue in rats [23]. Given the rarity of these tumors and the potential for oral exposure from the environment, these data should stimulate additional epidemiological investigation.

Chromium(VI) ions, with appropriate cellular reduction, are clearly genotoxic [4]. As chromium(VI) is reduced to chromium(III) by cellular reductants, various toxic intermediates, including radicals of chromium, oxygen, and sulfur, are likely generated and can react with key biomolecules relevant to carcinogenesis [4], such as DNA. It is likely that some chromium(VI) reductants undergo Fenton-type reactions to produce hydroxyl radicals, and subsequently attack DNA [1–3]. Chromium(VI) can stimulate the formation of superoxide and deplete glutathione [1, 2]. However, oxidative stress, although clearly an important aspect of the mechanisms of carcinogenesis of chromium(VI) metabolites (e.g. chromium(III)) can be directly genotoxic [1]. Chromium(VI) compounds also cause inflammation and stimulate tumor growth pathways in cell culture systems [4]. With chromium(VI) compounds it is probable that multiple, interactive, mechanisms including ODD and direct attack by chromium(VI) reductants are operative during acquisition of a cancer phenotype.

#### 16.2.5 Nickel and Nickel Compounds

Nickel is a transition metal primarily used in metal alloys and plating [4]. Nickel compounds are considered known human carcinogens [4]. Occupational exposure to nickel compounds is associated with cancers of the lung, nasal cavity and paranasal sinuses [4].

Multiple mechanisms have been proposed for nickel carcinogenesis although it is thought that the ultimate carcinogenic species of the various nickel compounds is the nickel ion (Ni(II)), and that the divalent ion is the driving force in whatever carcinogenic mechanism is involved [4]. Direct interactions of nickel compounds with DNA are likely of minor importance for induction of a carcinogenic response [4]. However, there is evidence of nickel genotoxicity, although the exact mechanism is debatable [3, 4, 24]. Potential carcinogenic mechanisms involving genotoxicity include inhibition of DNA repair at various key points, oxidative stress, and several epigenetic events [3, 4, 24]. It is clear that oxidant stress is linked to treatment with soluble or insoluble nickel compounds in many different cell types [3, 4]. Nickel ions can chemically catalyze the production of hydroxyl radicals from hydrogen peroxide in a Fenton-style reaction [3]. These radicals, in turn, could attack important biomolecules such as DNA. Nickel ions can produce ODD damage in the presence of hydrogen peroxide [3], confirming this catalytic capacity. The source of nickel ions (soluble or insoluble compounds) appears to make little difference in its capacity to produce hydroxyl radicals once the nickel ion has gained access to the cell [2]. Disruption of iron homeostasis could also add to the impact of nickel-induced oxidative stress [2]. The ability of nickel ions to produce oxidative stress via redox activity appears to be dependent on the cell in question and potential ligands involved (histones, etc.) [3]. Overall, it would appear oxidative stress is likely a contributing factor in some cases of nickel carcinogenesis.

#### 16.3 Probable or Possible Human Carcinogens

#### 16.3.1 Cobalt Compounds

Cobalt metal with tungsten carbide is considered a probable human carcinogen, while cobalt metal without tungsten carbide, and soluble cobalt(II) salts, are considered possible human carcinogens [6, 25]. Occupational exposure to hard metal dust containing cobalt and tungsten carbide is associated with an increased risk for lung cancer and lung cancer mortality, with a greater risk associated with an increased duration of exposure. Effects of exposure to cobalt in the absence of tungsten carbide are less clear, but there is evidence to suggest an increased risk of lung cancer in humans because soluble and particulate inorganic cobalt compounds cause lung tumors in animals [6, 25].

Potential carcinogenic mechanisms of cobalt include the release of cobalt ions, increased production of ROS followed by oxidative stress, inhibition of DNA repair, altering critical cell functions by replacing other metals, genotoxicity, inflammation, and effects on apoptosis [3, 6, 25]. There is convincing evidence that both cobalt ions and cobalt metal particles can produce mutagenic effects. Cobalt ions are capable of performing redox reactions in biological systems and can induce the formation of ROS in vivo and in vitro by catalyzing the generation of DNAdamaging hydroxyl radicals from hydrogen peroxide in a Fenton-style reaction. Similarly, cobalt metal can reduce oxygen in ROS independently of the Fenton reaction, a process that can produce soluble cobalt ions which may then take part in a Fenton reaction in the presence of hydrogen peroxide [6]. Thus, both metallic cobalt and ionic cobalt can have genotoxic effects involving ROS and oxidative stress, although the former does this via a much more complex process that may, in turn, involve the latter. Both metallic and ionic cobalt can also indirectly augment DNA damage through the inhibition of DNA repair [3, 6, 25]. Furthermore, cobalt metal can be mixed with metallic carbide particles (e.g. tungsten carbide) to produce higher ROS levels than cobalt alone. This chemical mixture can be mutagenic in vitro and in vivo [6].

Given that metallic cobalt forms particles that can be inhaled, when assessing its ROS production and possible resultant genotoxic effects, consideration should be given to the possible increased ROS production by inflammatory cells, to specific surface properties including size and shape, uptake of the metallic particles, and the presence of transition metals [6].

### 16.3.2 Inorganic Lead Compounds

Lead is a post transition metal that is considered highly toxic. If ingested, it can cause central nervous system damage and renal toxicity [5]. Lead poisoning has been documented in early civilizations such as ancient Greece. The evidence for the carcinogenicity of inorganic lead compounds is considered clear in rodents but limited in humans, leading to a classification of probably carcinogenic to humans [5, 39]. Lead exposure causes renal tumors in mice and rats treated as adults, generally on a background of chronic nephropathy [5]. It appears that early life lead exposure of rodents increases their sensitivity to lead carcinogenesis because renal tumors and hyperplasia occur after perinatal lead exposure with no signs of chronic nephropathy [27].

Inorganic lead compounds show evidence of genotoxicity by indirect mechanisms in vitro [5]. For example, lead inhibits closing of UV-induced DNA strand breaks and enhances UV-induced mutation and sister chromatid exchanges, suggesting lead inhibits DNA repair and acts synergistically with other mutagens [5]. Other proposed mechanisms for lead carcinogenesis are through the indirect generation of free radicals by depletion of cellular antioxidants, or by the direct production of ROS [5]. Lead stimulates lipid peroxidation in vivo which may then deplete cellular antioxidants like glutathione [5]. The loss of the ability to protect against ROS generated by other substances would increase free radical levels and cause oxidative damage to DNA. In addition, low expression of MT, a metal-binding protein, sensitizes mice to lead carcinogenicity [28]. MT is also known to sequester radicals produced by various other metals and oxidants, thereby indirectly reducing metal toxicity [22, 29].

A remarkable characteristic of lead poisoning is the formation of inclusion bodies (IBs), a protein-lead complex protein, in renal cells of poisoned humans or animals [30, 31]. These IBs contain MT and may mitigate lead toxicity [31]. Taken together, a plausible mechanism of lead carcinogenicity could be the generation of ROS and resultant ODD, although precise mechanisms remain to be more fully defined.

# 16.3.3 Indium Phosphide

Indium phosphide (IP) is used in the microelectronics industry as a semiconductor [6]. Indium is considered a post-transition metal occupying a place in the periodic table between transition metals and metalloids. It is produced mainly from residuals of zinc ores [6]. Indium appears to have no biological function. Some epidemiology studies looking at cancer end-points have been conducted on workers in the semiconductor industry, but these are generally negative and considered uninformative for specific compounds such as IP because the exposures in such industries are complex and mixed with other potential carcinogens [6]. In animals, IP was carcinogenic in a single robust study in rats and mice, producing lung tumors by inhalation [32]. The lung cancer response after IP inhalation was dose-dependent in both males and females [32]. This one study was considered to provide sufficient evidence to classify IP as a carcinogen in experimental animals [6].

With regard to genotoxicity, indium was negative in bacterial reverse mutation and chromosomal aberration tests in cultured mammalian cells [33]. However, in concert with the study showing the carcinogenic potential of IP, evidence of oxidative stress was provided in IP-induced lung neoplastic lesions [32]. This included increased expression of glutathione S-transferase and evidence of ODD in IP-induced lung carcinoma, consistent with the pulmonary inflammation associated with oxidative stress driven progression from hyperplasia to neoplasia [32]. Thus, IP appears to act as a lung carcinogen through a mechanism that involves oxidative stress.

### 16.3.4 Iron

Iron is a transition metal that is an essential element and widely used for numerous applications. The carcinogenic potential of iron in humans is complex, and appears to depend on the exposure method and form of the metal. Occupational exposures

during iron and steel founding are known to be carcinogenic, causing lung cancer in humans. However, these exposures are complex and include other known carcinogenic agents along with the iron [34]. Injection of iron-dextran complex is considered a possible human carcinogen based on sufficient carcinogenic evidence in animals [34]. Hematite and ferric oxide are not classifiable as to their carcinogenic-ity to humans [34], but underground hematite mining with exposure to radon is considered carcinogenic to humans [34]. Recent evidence suggests an association between dietary and supplemental iron and colorectal cancer in humans [7]. Recent rodent work indicates excess dietary iron causes colonic inflammation and promotes colon tumor development in mice [35]. Various examples of in vitro genotoxic potential can be cited including the fact that iron-fatty acid complexes induce mutagenesis in lung cells in vitro [36]. Clearly, further consideration should be given to assessing iron as a human carcinogen.

Iron is relatively nontoxic because, as an essential element, there are numerous elastic and safe biologic transport and storage mechanisms. Nevertheless, an excess of the metal can have serious health consequences [8, 37]. Iron excess amplifies oxidative stress by catalyzing Fenton and Haber-Weiss reactions that convert relatively less reactive oxidative molecules (e.g. superoxide, hydrogen peroxide) into the highly reactive hydroxyl radical. These hydroxyl radicals then cause damage to membranes and important biomolecules, including proteins and DNA. Iron overload disorders can be hereditary, acquired, or iatrogenic. Individuals with these disorders may be more susceptible to iron-associated oxidative stress/damage and the resultant health consequences (i.e. cancer formation). For example, hereditary hemochromatosis is a condition in humans in which a genetic deficit causes hepatic iron overload and predisposes the individual to the development of hepatocellular carcinoma, usually, but not always, on a background of non-alcoholic cirrhosis [8]. Whatever the mechanism of iron carcinogenesis, it is likely that oxidative stress is involved.

# 16.3.5 Vanadium Pentoxide

Vanadium pentoxide (VP) is the major commercial form of vanadium [6], a transition metal. VP's major uses are in production of alloys with aluminum and as an oxidation catalyst in industrial applications [6]. Vanadium is an essential metal in animals, although its exact physiological function is unclear. There are no data on the carcinogenic potential of vanadium compounds in humans [6], and vanadium complexes have actually been proposed as cancer chemotherapeutics [38], a dichotomy not uncommon with inorganic carcinogens (i.e. arsenicals). VP was tested for carcinogenicity by inhalation in a single study in rats and mice and found to be active in the lung [6, 40]. Specifically, VP increased alveolar/bronchiolar neoplasms in male and female mice, and male rats [6, 40]. Thus, VP is considered possibly carcinogenic to humans [6]. In humans, inhalation exposure to VP causes an acute respiratory irritation, known as "boilermakers bronchitis", which is reversible. Pentavalent vanadium compounds are genotoxic and can induce micronuclei, chromosomal aberrations, and aneuploidy [3]. Various studies show VP can stimulate DNA damage via generation of ROS [2, 6]. It is thought that the pentavalent vanadium ions may be reduced to vanadium(IV) which can react with cellular oxygen or hydrogen peroxide to form the corresponding oxygen or hydroxyl radicals [2]. The production of the hydroxyl radicals by vanadium(IV) is via a Fenton-type reaction [2]. Cell-free systems show that the genotoxicity of vanadium can largely be attributed to oxidative stress mechanisms [2, 3].

# 16.4 Summary

Many metallic elements are considered to be clearly carcinogenic in humans (arsenic, beryllium, cadmium, chromium (VI), nickel). Although there is clear evidence for the carcinogenicity of other metals in rodents, the evidence in humans is limited or inadequate. Most metallic elements that are linked to cancer also have a capacity to induce oxidative stress relevant to carcinogenic mechanisms [1–3]. Induction of oxidative stress by metals can be direct (e.g. Fenton-like chemistry) or indirect (e.g. glutathione consumption). Oxidative stress may not be the only, or even the primary, mechanism of metal carcinogenesis for every metal and it needs to be investigated on a metal-by-metal basis. Metal-induced oxidative stress may also be associated with a variety of other disease states that are not discussed here.

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# Chapter 17 UV-induced Signaling: Role of Reactive Oxygen Species

Lars-Oliver Klotz

### 17.1 Introduction

Exposure to ultraviolet radiation (UV) is both essential and potentially hazardous to humans. On one hand, it is required for endogenous vitamin D biosynthesis from 7-dehydrocholesterol, on the other hand, extensive exposure to UV is known to cause eye and skin irritations, ranging from inflammatory reactions, such as the classical sunburn, to carcinogenesis. Of the three common UV bands in the 200–400 nm region – UVC (200–280 nm), UVB (280–320 nm) and UVA (320–400 nm)<sup>1</sup> – UVB and UVA are considered of biological significance, as wavelengths above ca. 290 nm pass the stratospheric ozone layer to reach the surface of the earth.

Absorption of UV is key to its phototoxic action. Whereas major chromophores absorbing UVB include DNA and protein, as well as protein degradation products such as urocanic acid, UVA is absorbed by several biomolecules of low molecular mass, such as porphyrins, flavins and certain quinones. Due to these different chromophores, skin transmittance in the UV regions significantly differs: with nucleic acids absorbing in the 260 nm region and proteins in the 280 nm region (and keratin being a prominent absorber in skin), UVC hardly penetrates beyond the upper epidermal layers, whereas transmittance of the epidermis in the UVB and UVA regions is in the 0.2-2% and 2-20% range, respectively [1, 2]. Both UVB and UVA would thus reach dermal (i.e., subepidermal) layers (Fig. 17.1).

<sup>&</sup>lt;sup>1</sup>The division between the UVC/UVB and UVB/UVA regions varies with the literature source chosen and may also be set at 290 nm (rather than 280 nm) and 315 nm (rather than 320 nm), respectively.

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Absorption of UV by these chromophores will result in photochemical reactions that lead to intra- and intermolecular rearrangements and cross-links, in generation of reactive oxygen species (ROS) and in photooxidative processes. As a result, UV damages biomolecules in at least two different ways, i.e. by direct photochemical damage to the absorbing biological chromophores, and indirectly through formation of ROS following absorption of UV by photosensitizers. These processes contribute to the fact that both UVA and UVB are now regarded as complete carcinogenesis, such as initiation, promotion and metastasis.

# 17.2 From Photooxidation to Signaling

Both UVA and UVB cause DNA damage. Exposure of cells to UV radiation results in base rearrangements, e.g. the formation of cyclobutane thymine dimers, and oxidative DNA damage, such as the formation of oxidized guanine nucleosides (8-oxo deoxyguanosine, 8-OH-dG) via the generation of ROS. Whilst oxidative damage is induced indirectly through UV-induced generation of ROS, and cyclobutane pyrimidine dimer (CPD) formation by UVB is through direct absorption of UVB photons, the mechanism of CPD formation by UVA is still being debated and is not clear yet (for recent reviews on UV-induced DNA damage, see [3]).

Whereas the link between DNA damage and mutations (i.e. the initiation stage in the process of carcinogenesis) is easy to draw, the connection between UVA/UVB and the other stages in carcinogenesis is indirect. For example, UV stimulates signaling processes that are known to support proliferation or proinflammatory processes (promotion stage) as well as regulate the expression of metalloproteases – i.e. proteins degrading the extracellular matrix (and thus contributors to the metastasis stage) [4, 5].

# 17.2.1 Photooxidation

Molecular oxygen is a diradical, with two unpaired electrons in its outermost molecular orbitals. These electrons are in a triplet state in ground-state molecular oxygen, i.e. they have parallel spins. Oxygen may be activated and transformed into ROS in one of two ways, i.e. by electron transfer – yielding reduction products of oxygen, such as superoxide  $(O_2^{\bullet})$  – or by energy transfer, which may result in the formation of "singlet" oxygen ( $^1O_2$ ), an electronically excited form of molecular oxygen. In  $^1O_2$ , the outermost electrons have antiparallel spins (either paired, occupying the same molecular orbital, or unpaired – for the biochemistry of  $^1O_2$ , see [6–8]). Electron and energy transfer reactions occur in the presence of photosensitizers, i.e. molecules that facilitate these processes upon absorption of light of appropriate wavelength. Following irradiation, photosensitizers transition into an excited state, from where further reactions with suitable reaction partners (including solvent molecules, biological molecules or oxygen) occur, i.e. energy transfer to molecular oxygen or an initiation of electron transfer/hydrogen abstraction.

These photosensitized electron transfer (coming with the generation of radicals, such as  $O_2^{-}$ ) and energy transfer reactions (with nonradicalic intermediates such as  ${}^{1}O_2$ ) are referred to as type I and type II photosensitized reactions, respectively [3]. A slightly different definition was provided by Foote [9], who distinguished these reactions not with respect to radicalic/nonradicalic intermediates (which, he states, may not be easy to establish experimentally) but with respect to the dependence of the reaction on – or independence of – oxygen. Here, type I reactions would be such reactions where excited photosensitizer reacts with anything but oxygen (such as with solvent), whereas in type II reactions excited photosensitizer would react with oxygen – irrespective of whether superoxide or singlet oxygen is generated. Figure 17.2 summarizes basics on type I and II reactions. Photosensitizers in skin include porphyrins, flavins and others (for a comprehensive list, see [10]), and their presence contributes to the formation of ROS in tissues upon exposure to UVB or UVA.

# 17.2.2 Signaling Pathways Stimulated by UV: Stress Response, Proliferation and Inflammation

Several physiological effects of UV radiation are mediated by ROS – for example, singlet oxygen contributes to UVA cytotoxicity [11]. In addition, UV radiation – also at subtoxic levels – elicits numerous cellular signaling responses. The signaling pathways activated include the usual suspects, i.e. stress signaling pathways as well as such cascades that are known to be stimulated by ROS. For example, singlet oxygen mediates the stimulation of p38 and c-Jun N-terminal kinase (JNK) mitogenactivated protein kinases (MAPK) by UVA [12, 13], hydrogen peroxide – under certain circumstances – mediates epidermal growth factor receptor (EGFR)



**Fig. 17.2** Type I and type II photooxidation reactions. *Boxes*: definition used in this chapter; *dashed lines (bottom)* indicate an alternate definition (see text for further details). Photosens, PS – photosensitizer. Type I reaction: excited PS (in a triplet state) reacts with (triplet, i.e. ground state) molecular oxygen or a non-oxygen reaction partner (R-H). Reduction of oxygen or oxidation of RH generate superoxide or a PS anion radical, respectively. The latter may further react to reduce oxygen to superoxide (not shown). Additionally, hydrogen abstraction is shown. Type II reaction: excited PS reacts with oxygen to transfer energy rather than electrons and generates singlet oxygen and PS

stimulation and EGFR-dependent signaling by UVA [14, 15] and JNK<sup>MAPK</sup> stimulation by UVB [16] is similarly elicited by ROS generated upon exposure of cells to UV radiation.

**Proliferation** Demonstrated for the first time using UVC radiation in a laboratory setting [17], receptor tyrosine kinases (RTK) have now clearly been shown to be stimulated in mammalian cells also by UVB and UVA. EGFR activation triggers several signaling cascades, culminating in stimulation of members of the MAPK family [18, 19] as well as phosphoinositide 3'-kinase (PI3K)-dependent signaling [20]. Both these cascades are involved in UV-dependent stimulation of proliferation. ERK<sup>MAPK</sup> (i.e. MAPK of the ERK – extracellular signal-regulated kinase – subfamily) activate various transcription factors [21], including Elk-1 and Sap-1, thus regulating the expression of genes involved in the regulation of cellular proliferation, such as cyclin D1 or an inhibitor of cyclin-dependent kinases, p27kip1. Further, ERK<sup>MAPK</sup> support general protein biosynthesis/translation [22] as well as nucleotide synthesis – for example, at the level of pyrimidine biosynthesis [23] – as a preparatory step for DNA biosynthesis. Both protein synthesis and DNA replication are prerequisites for cell growth. In parallel, PI3K-dependent signaling via the antiapoptotic serine/threonine kinase Akt will attenuate cell death and support proliferation [24].

**Inflammation** Cyclooxygenases (COX, with two isoforms, COX-1 and -2) catalyze the rate-limiting step in the biosynthesis of important eicosanoid inflammatory mediators, i.e. the conversion of arachidonic acid to prostaglandin H2, which is further converted by various synthases to thromboxane A2 or different prostaglandins. Both UVB [25] and UVA [26] were demonstrated to enhance the expression of the inducible COX variant, COX-2, in human keratinocytes. As a consequence, production and levels of prostaglandin E2 (PGE2) were elevated in skin. UVB appears to be a much stronger inducer of COX-2 expression than UVA, as shown in cultured cells [27] as well as in artificial human epidermis exposed to simulated solar light [28]. Elevated levels of COX-2 and of PGE2 were linked to the development of UV-induced skin cancer (for review, see [29]).

MAPK and PI3K appear to be crucial for UV-induced stimulation of COX-2 expression. At the transcriptional level, stimulation of cAMP response element (CRE) binding protein (CREB)-dependent expression of the gene coding for COX-2 is regulated by p38<sup>MAPK</sup> (directly phosphorylating and activating CREB) and PI3K (in essence, inhibiting an inhibitory phosphorylation of CREB) pathways (for review, see [29]). Moreover, p38<sup>MAPK</sup> further stimulates COX-2 expression by inducing phosphorylation of histone H3, which was suggested by the authors of the study to support recruitment of RNA polymerase II to the *cox-2* promoter [30].

In addition to transcriptional processes, UVB affects RNA stability and posttranscriptional regulation of gene expression [31, 32]. This finding also applies for COX-2 mRNA, which was shown to be stabilized in HaCaT keratinocytes exposed to UVB [33]. The mRNA stabilizing protein, HuR – a protein known to be modulated by stressful stimuli, including UV [34, 35] – was then demonstrated to mediate UVB-induced stabilization of COX-2 mRNA in HaCaT cells in combination with p38<sup>MAPK</sup> [27]. Depletion of HuR attenuated the UVB effect and blocked UVB-induced COX-2 induction and PGE2 accumulation [27]. As HuR is phosphorylated by p38<sup>MAPK</sup>, followed by its cytoplasmic accumulation [36], the authors hypothesize a direct link from UVB via p38<sup>MAPK</sup> to HuR and the stabilization of COX-2 mRNA [27].

### 17.3 Signaling Triggered by UV – Two More Mechanisms

As UV-induced signaling is mediated in large parts by ROS, it is obvious that the same mechanisms apply that were outlined in the earlier chapter on "Reactive oxygen species as initiators and mediators of cellular signaling processes". For example, the stimulation of EGFR signaling by UV was demonstrated to be mediated by oxidative inhibition of a regulatory protein tyrosine phosphatase [37]. Therefore, these mechanisms will not be reiterated here. Rather, two relatively recent examples will be outlined, focusing in the first part on a somewhat indirect mode of stimulating transcription factor activity in response to UVA, and describing the role of a ubiquitous amino acid in UV signaling in the second.

# 17.3.1 Signaling by Oxidative "Clogging"

Recently, the oxidation of proteins as well as the degradation of oxidized proteins were linked to enhanced signaling. Oxidized proteins are frequent substrates to, and therefore degraded by, the proteasome [38]. This does not appear to require ubiquitination of the target proteins, implying that the 20S proteasome is crucial to degradation of oxidized proteins (rather than the 26S proteasome) [39]. However, extensive oxidation, resulting in cross-linking and aggregation of oxidized proteins, may cause the inhibition of the proteasomal system (by "clogging" the proteasomal active site) [40]. The inhibition of the proteasome by overoxidized proteins has consequences for the turnover of other cellular proteins, including proteins involved in the regulation of gene expression. For example, exposure of skin fibroblasts to UVA caused proteasomal inhibition and a subsequent accumulation of c-Jun and phosphorylated c-Jun. These effects appear to be mediated by singlet oxygen and result in an activation of activator protein-1, i.e. transcription factors known to respond to stressful stimuli [41].

# 17.3.2 Tryptophan and Signaling: Regulation of Transcription Factor Activity by Photoproducts

Tryptophan, more specifically its indole moiety, absorbs in the UVB region. Irradiation of tryptophan solutions, and of cells and tissue containing Trp, results in the formation of Trp photoproducts, including products with biological activity, such as 6-formylindolo[2,3-*b*]carbazole (FICZ), which was shown to be present in humans [42] and to potently stimulate aryl hydrocarbon receptor (AhR)-dependent signaling [43]. AhR and FICZ mediate UVB-induced stimulation of expression of genes coding for the production of enzymes such as the phase I xenobiotic metabolism enzyme cytochrome P450 1A1 (CYP1A1) [44]. They were then demonstrated to also stimulate melanogenesis by upregulating tyrosinase expression and to mediate UVB-induced skin tanning [45, 46] – implying that the photoproduct FICZ might have protective functions (Fig. 17.3). Furthermore, UVB, via FICZ and AhR, stimulates EGFR-dependent COX-2 expression, resulting in another mechanism of transcriptional control for UVB-induced COX-2 production [47].

In addition to serving as a precursor of bioactive UVB-photoproducts, Trp also mediates signaling effects in the UVA region. It does so by serving as a reaction partner to a physiological chromophore absorbing in the UVA region, riboflavin (vitamin B2). Upon absorption of UVA, riboflavin will interact with Trp to generate hydrogen peroxide – presumably via dismutation of superoxide, which would make this a type I reaction according to both of the aforementioned definitions (Fig. 17.2) [15, 48, 49]. A similar reaction was found to occur in cell culture systems employing the buffering compound HEPES [N-(2-hydroxyethylpiperazine)-N'-2-ethanesulfonic acid] (Fig. 17.4) [15]. ROS gener-



**Fig. 17.3** Generation of a bioactive photoproduct from tryptophan. Exposure of tryptophan to UVB results in formation of 6-formylindolo[2,3-b]carbazole (FICZ), which is an activator of aryl-hydrocarbon receptor (AhR), a transcription factor that regulates the expression of genes involved in xenobiotic metabolism (such as the gene coding for CYP1A1), melanogenesis (such as the tyrosinase gene) and other biological processes



**Fig. 17.4** Schematic representation of a type I photoreaction for the riboflavin (RF)-dependent generation of hydrogen peroxide in the presence of tryptophan or HEPES. See text for details



Fig. 17.5 Roles of tryptophan in UV-induced signaling. See text for details

ated under these conditions (UVA+riboflavin/Trp or UVA+riboflavin/HEPES) were demonstrated to stimulate cellular signaling [15].

Trp is both a direct and indirect UV target. It may generate a photoproduct (upon exposure to UVB) that stimulates AhR-dependent transcriptional processes, and it may interact with excited riboflavin (resulting from UVA irradiation) to undergo type I photooxidation, generating ROS, which will then elicit signaling (Fig. 17.5).

In summary, ultraviolet radiation, via formation of ROS as well as through the formation of photoproducts, stimulates the expression of genes by stimulating signaling pathways that control transcriptional and posttranscriptional regulatory processes.

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# Chapter 18 Oxidative Stress and Nanomaterial-Cellular Interactions

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Nanotechnology promises to power new innovations across many sectors of society, including medicine, energy technologies, and industrial manufacturing. Engineered nanomaterials (ENMs), formally defined as manmade materials with length scales of less than 100 nm in at least one dimension, have found their way into many everyday consumer products such as sunscreen lotions and cosmetics, textiles, and candy [1–5]. The ability to precisely control the size, shape and aspect ratio of materials, such as silicon nanowires, provides exciting new opportunities for production of high-performance batteries, electronics and solar cells [6, 7]. Indeed, more than 1,300 commercial products enabled by nanotechnology are currently on the market, and as of May 2011, over 6,930 patents classified as nanotechnology-related inventions were issued [8, 9]. It is estimated that by 2014 nanotechnology-enabled products will reach a global market potential of \$2.6 trillion and create 10 million jobs [10].

Widespread acceptance and full realization of the benefits of nanotechnology ultimately depends upon achieving consumer confidence in the safety of these materials. With the dramatic rise in ENM production, there is also increased concern for unintended human exposures, particularly under occupational settings. Emerging evidence that respirable sized nanoparticles can be released in occupational settings during processes such as synthesis, grinding, cutting, or workplace cleaning, contribute to these concerns [11–16]. Direct evidence of human toxicity due to environmental ENM exposure is limited, although reports of serious adverse effects of occupational exposures have been published [17–19]. Most notably, one case report described a worker who died from respiratory distress syndrome following acute inhalation of an estimated gram of nickel nanoparticles [19]. Toxicities

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associated with occupational exposure to nanoparticles in factories in China and India have been also reported [17, 18]. However, due to a myriad of confounding co-exposures to solvents, cigarette smoke, and other agents in these settings, causal relationships between the toxicities observed in humans and internal exposure to ENM remain unclear. Nonetheless, lessons learned from decades of research on environmental particulates suggest caution toward understanding the potential hazards of emerging classes of engineered materials is warranted. In particular, numerous epidemiological studies support causal relationships between human exposure to ultrafine ambient particulates and increased morbidity and mortality due to cardiovascular disease, lung infections and lung cancer associated with ultrafine air pollution, particularly in the elderly [20–24]. Similarly, welders exposed to fumes rich in ultrafine metal oxides have increased susceptibility to lung infections [25–27].

The same properties that make ENM attractive for commercial and biomedical applications are also a source of uncertainty over their biological reactivity. This uncertainty is driven by notions that unusual or unique mechanisms of toxicity may arise from intrinsic physico-chemical properties that occur exclusively at the nanoscale. For instance, many metal oxides exhibit critical sizes for which new material properties emerge when compared to bulk scale materials, including changes in lattice structure and crystallinity, optical and electronic band gap properties, phase transformations, photocatalytic activity, adsorptive capacity, and redox activity [28]. In most cases, these transitions occur at length scales below 20 nm. For example, the photocatalytic activity of TiO<sub>2</sub>, which is thought to drive production of reactive oxygen species (ROS) in biological systems, increases significantly with transitions from rutile to anatase phases, which is optimum at size ranges below 25 nm. Unusual oxidative catalytic properties of gold nanoparticles have been associated with electronic structures that occur below 2 nm, whereas larger particles do not display these catalytic activities [29]. Thus, from a material properties viewpoint, the conventional size threshold definition used to classify and define nanomaterials (≤100 nm) is more of practical convenience than of mechanistic importance. In fact, it has been argued that there is no evidence of "nano-specific" toxicity, where particles below 100 nm diameter display a threshold-like change in their intrinsic potential to cause hazard [30]. On the other hand, particle size is undoubtedly an intrinsic physical property that directly influences the toxic potential of a material in multiple ways. The size of the particle dictates the density of surface molecules available for reactivity in biological systems, influences the receptor and non-receptor mediated pathways utilized for cell uptake, and modifies the biodistribution of ENMs in vivo. In the following sections, we provide an overview of intrinsic and extrinsic properties of ENMs that have been linked to their hazard potential, with particular attention to oxidative stress as a hypothesized mechanism of action that underlies the toxicity of many ENMs.

*Size and Surface-Volume Relationships* One of the most direct impacts that primary particle size plays in determining the potential toxicity of a material is in modulating the effective biological dose. Several metrics can be used to describe cell dose for ENMs, including particle mass, particle number, and surface area. The appropriateness of these metrics for characterizing the relative potencies of particles has been a subject of debate [31]. For a spherical particle of 100 nm diameter, less than  $\sim 2\%$  of the molecules are displayed on the particle surface, whereas this fraction increases to  $\sim 20$  % and 50 % for 10 nm and 3 nm particles, respectively [32]. Thus, if biological effects such as oxidative stress and inflammation are initiated by surface reactive molecules, nanoscale particles will invariably elicit significantly greater responses than the same mass dose of larger particles. This fundamental relationship holds true regardless of whether or not a particle acquires new molecular properties at the nanoscale. Unfortunately, this mass dose relationship is often misinterpreted to imply that small particles are inherently more biologically reactive than larger particles of the same bulk chemistry [33]. This concept was effectively demonstrated by Oberdorster and coworkers [27, 31], who compared the relative potency by which 20 nm and 250 nm diameter TiO<sub>2</sub> particles caused acute lung inflammation in rats. As expected, exposure to small TiO<sub>2</sub> particles caused greater lung neutrophil influx and interstitial inflammation than did an equal mass dose of larger particles. However, when particle surface area was used as the comparative dose metric, the dose-response profiles for small and large particles directly overlapped, indicating equivalent potencies on a surface area dose basis. Similar correlations have been observed between rat lung tumor incidence and total surface area dose for a variety of ultrafine (<0.1  $\mu$ m) and fine (<2.5  $\mu$ m) particles [27]. Proportional relationships between particle surface area dose and pulmonary inflammation have also been observed with polystyrene nanoparticles [34] and other material types [35, 36]. Waters et al. [37] extended these analyses at the cellular level and demonstrated that the genome-wide transcriptional response of macrophages treated with either 10 nm or 500 nm silica nanoparticles was statistically identical when compared at equivalent particle surface area exposure levels. Among over 1,000 biological processes identified in this study using gene enrichment analysis, no processes were statistically enriched in a size-dependent manner when compared at equivalent particle surface area dose metrics. It is not clear that surface area is universally the most appropriate measure of biologically effective dose for all nanomaterials. However, the alignment of a broad array of biological responses across particles which vary in size by 50-fold provides strong support for the appropriateness of surface area as a comparative dose metric.

Particle size is an intrinsic material property that plays a critical role in determining the mode of cellular uptake and biodistribution of ENMs. Cellular uptake of quantum dots, silica, liposomes, gold and polymeric nanoparticles have all been reported to be size-dependent [38–42]. Although no firm predictive rules governing cell uptake of particles have been established, passive uptake mechanisms are generally utilized by very small particles whereas active transport occurs across a range of particle sizes via multiple types of endocytic pathways. Using a panel of gold particles with finely controlled diameters, Van Lein et al. [43] demonstrated that passive penetration of the plasma membrane of cells occurred only for particles below a critical size limit of 3.4 nm. Lu et al. [44] quantified the uptake of a series of well dispersed mesoporous silica nanoparticles ranging from 30 to 280 nm diameter and found maximum cell uptake occurred for ~50 nm particles. Similar findings with gold and polystyrene nanoparticles [45–47] suggest that, in non-phagocytic cells, nanoparticle uptake through classical receptor-mediated endocytic pathways is optimum for particle diameters of ~40–50 nm, and is limited to diameters less than the physical diameter of clathrin-coated pits (<200 nm). These experimental estimates fit well with theoretical models of viral particle uptake which suggest that the mechanics of membrane wrapping around a spherical particle determines the optimum size limits for particle uptake by cells [48]. As discussed further in subsequent sections, the physical limits by which phagocytic cells can internalize and remove ENMs have important implications for the mechanism of toxicity for carbon nanotubes and other ENMs with high aspect ratios.

Surface Chemistry and Charge Relationships The surface charge of ENMs also has large ramifications on the mechanisms of particle uptake, biodistribution and bioreactivity. Because surface charge is a direct function of the material surface chemistry, ligand density, and the neighboring molecules within a specific biological environment, it is difficult to predict the role that charge alone plays on the biological reactivity of ENMs. Nonetheless, some generalities regarding relative differences between cationic and anionic materials have emerged. For instance, positively charged particles are internalized in cells at faster rates than neutral or anionic particles, likely due to the more favorable electrostatic interactions between the particle's cationic surface and the slightly negatively charged cell membrane [49–52]. Studies using functionalized gold particles demonstrated that anionic particles have lower affinity for cell membrane than cationic particles, and that the process of particle adsorption to the cell membrane is a rate-limiting step for overall uptake [52]. The enhanced adsorption of cationic particles to cell membranes can alter cell membrane fluidity and cause local membrane depolarization. This can lead to cytotoxicity through creation of membrane 'holes' and loss of cellular ion homeostasis [53-56]. Following adsorption to the cell surface, the surface charge of particles also determines its interactions with specific endocytic receptors that govern intracellular fate and trafficking [57–61]. For example, whereas anionic amorphous silica nanoparticles are internalized into endolysomal pathways via scavenger receptor binding and clathrin-dependent trafficking, amine-modified silica particles are recruited into cells via interactions with negatively charged proteoglycans via a macropinocytotic route [61–63].

When considering the impact of surface charge in the biocompatibility of ENMs from a general structure-activity perspective, it is critical to note that the surface electrostatic potential of a particle is inextricably linked to several physical factors that are often difficult to control or not easily characterized in biological systems, such as agglomeration state and protein adsorption. Indeed, ENMs bearing cationic surface modification (e.g. primary amines) often agglomerate in aqueous biological systems to a greater extent than the same materials bearing anionic modifications. This agglomeration can have large influences on the rate of ENM delivery and uptake in cells [33, 51, 64]. Unfortunately, the impact of agglomeration status on cell dose rate is often not appropriately controlled for in cellular studies. Furthermore,

the effective surface charge of an ENM is rapidly altered by a corona of adsorbed proteins in all biological systems [65, 66].

The composition of the protein corona is directly dependent on the net surface charge as well as the size/surface curvature of the particle, and can be a major determinant of mechanisms of uptake and toxicity potential of ENMs [59, 67–70]. For instance, the adsorption of serum proteins, which on average are slightly negatively charged, enhances the binding of cationic nanoparticle to cells and inhibits the binding of anionic particles [59]. While such observations seem in conflict with the general view that the anionic charge of the cell membrane limits interactions with negatively charged particles, they are in agreement with the concept that adsorbed proteins may target ENMs to specific cell surface receptors. Proteomic analyses, that show the corona 'footprint' of an ENM can comprise hundreds of protein or lipoprotein species, illustrate the complexity of this problem [69, 71]. The biological role of the protein corona remains one of the least understood factors underlying the biodistribution and toxicity potential of ENMs. A more complete discussion of this important area can be obtained in recent reports [65, 72–74].

Oxidative Stress Mechanisms in ENM-Mediated Cellular Damage Although our understanding of the physicochemical properties of ENMs that cause adverse biological effects is woefully incomplete, the ability of ENMs to stimulate cellular oxidative stress has emerged as a leading predictive hypothesis in nanotoxicology [75, 76]. This hypothesis proposes that the toxicity of ENMs can be predicted from hierarchical analyses of their ability to generate oxidative stress in cells, proceeding from induction of antioxidant response genes, to induction of proinflammatory pathways, ultimately leading to cell death [77]. Indeed, the induction of ROS in target cells is commonly observed for many particles that cause pathology in vivo, particularly at high treatment concentrations. However, the underlying mechanisms of ENM-induced oxidative stress are not well understood and vary dramatically depending on the ENM chemistry. Furthermore, some materials such as singlewalled carbon nanotubes (SWCNT) cause substantial toxicity in the absence of measureable oxidative stress or proinflammatory cytokine induction in cells [78, 79]. Thus, the concept that oxidative stress is a key initial event broadly involved in initiating toxicity by ENMs has been questioned [80-82].

As discussed in subsequent sections, cellular ROS can be generated by both direct and indirect means following ENM treatment (Fig. 18.1), and the loss of redox control is a common phenomena in virtually all processes that lead to cell death. Although oxidative stress remains an important biological endpoint for screening strategies in nanotoxicology, caution should be applied in extending this concept to implicate underlying causal mechanisms.

*Direct Mechanisms of ROS Induction by ENMs* The direct generation of ROS has been demonstrated for a variety of ENMs, most notably metals and metal oxides (Table 18.1). Transition metals such as iron, cobalt, copper, and manganese have the capacity to generate ROS through Haber-Weiss and Fenton reactions, resulting in highly reactive superoxide and hydroxyl radicals [51, 83, 84]. Spin-trapping electron paramagnetic resonance analyses show that for superparamagnetic iron oxide





Oxidative stress mechanism	Examples	References
Radical generation on surface defects (grinding, etching)	Quartz silica Fumed amorphous silicas MWCNT	[85, 86, 89, 127]
Photoactivation	TiO <sub>2</sub>	[90]
Catalytic redox cycling	Transition metals, Metal oxides (Fe, Cu, Cr, V, Co)	[51, 77, 83, 84]
Protein thiol binding	Nanosilver, Nanogold	[115, 116]
Particle dissolution	Nanosilver, ZnO, CuO, Quantum dots	[108–113]
Mitochondrial depolarization	Cationic nanospheres, Nanosilver, Nanocopper, ZnO	[55, 76, 115, 119]
Phagocyte activation (NADPH oxidase, Nitric oxide synthase)	SWCNT, MWCNT, Graphene, Cerium nanorods	[79, 82, 123–125, 136]
Catalytic surface contaminants	MWCNT, SWCNT (Fe, Ni)	[94–97]
Biologically active contaminants	Endotoxin	[132]

Table 18.1 Direct and indirect mechanisms of ROS induction by engineered nanomaterials

(SPIO) nanoparticles, hydroxyl radical production via Fenton chemistry is more efficiently catalyzed at the particle surface as compared to dissolved metal ions, and is not significantly impacted by protein adsorption to the nanoparticle surface [83]. This observation is consistent with results from cellular studies demonstrating that the cytotoxic effects of carboxylated SPIO nanoparticles, when delivered to lung cells as controlled agglomerates, correlates directly with the total surface area of agglomerates delivered to the cell surface, and are less directly related to the total iron buried within the agglomerate core [51]. Co-treatment with the antioxidant N-acetylcysteine efficiently rescues cells from SPIO cytotoxicity [51], indicating ROS generation is a key factor in the toxicity of these materials.

Surface defects in freshly ground crystalline silica particles form silanol-derived radical centers, and in aqueous (acellular) environments these centers can catalyze hydrogen peroxide formation [85]. Differences in surface radical generation across aged and fresh silica samples may explain the variability in the pathology caused by various environmental sources of silica dusts. Furthermore, wide variability in the cytotoxic potential of colloidal and fumed forms of amorphous nanosilica may be due to radical formation associated with straining of siloxane bonds (Si-O-Si) on the particle surface caused by different methods of particle synthesis and processing [86]. Because of interest in the use of nanosilica as a drug carrier, the hemolytic potential of various forms of silica particles has been widely investigated, and generally found to correlate with surface area of the particles [87–89]. The hemolytic activity of silica ENPs depends on the distribution of siloxane and free silanol (Si-OH) groups on the particle surface that interact with specific epitopes on erythrocyte membranes [89], which can also vary with the increased curvature of very small particles.

Titanium dioxide (TiO<sub>2</sub>) nanoparticles, like amorphous forms of SiO<sub>2</sub>, provide another example of a material whose potential for direct ROS induction depends on

the crystalline state of the material, which is also a size-dependent property. The phototoxicity of  $TiO_2$  is reported to be influenced by particle size [90]. Both anatase and rutile forms of TiO<sub>2</sub> can be excited by UV light to produce electron hole pairs, and in acellular systems can catalyze production of hydrogen peroxide. Most nanoscale TiO<sub>2</sub> preparations are composed of a mixture of anatase and rutile, although the anatase phase is generally the more photoactive phase. Although a wealth of studies have demonstrated TiO<sub>2</sub> induces oxidative stress in biological systems (for review, see [91]), a direct contributing role of photoactivation in the generation of cellular ROS is less certain. Rather, studies have reported rutile TiO<sub>2</sub>-induced hydrogen peroxide production and oxidative DNA damage in human bronchial cells in the complete absence of light, whereas other researchers found TiO<sub>2</sub> nanoparticles did not induce oxidative stress in macrophages, despite being photocatalytically active in acellular systems [76, 92]. Still, others have reported TiO<sub>2</sub> nanoparticles cause DNA damage in lung cells independent of evidence for ROS generation [93]. Such reports suggest that the amount of ROS directly generated by TiO<sub>2</sub> through photocatalytic mechanisms is likely to be very low, raising questions over the general importance of direct ROS production in mediating biological effects of this material.

Beyond their use as nanoparticles in semiconductor applications, over 20 metals have been used as catalysts for carbon nanotubes, most frequently including Fe, Ni, Y, Co and Mo [94], and hence are ubiquitous contaminants of these materials. Commercial vendor purification processes are generally not adequate to efficiently remove metals, and significant mobilization of free nickel and iron from commercial sources of 'purified' nanotubes can occur under acidic conditions typical of lysosomal environments [94]. While it is expected that these metals would be capable of stimulating ROS production, equivocal findings concerning the bioactivity of these contaminating metals and their contributing role in redox reactions in biological systems have been reported. Contaminating iron in SWCNT samples catalyzes radical production in cell free systems, and significantly enhances oxidative stress and the cytotoxic effects of SWCNT in some cell types [95, 96]. Contaminating nickel is also associated with inflammasome activation by multi-walled carbon nanotubes (MWCNT) in isolated macrophages [97]. In contrast, recent studies reported that removal of metal contaminants by acid washing had limited or no impact on the pro-inflammatory effects of MWCNT in vivo [98, 99]. It is important to note that acid purification may introduce new surface defects in nanotubes, and generally enhances their aqueous dispersion, which can significantly alter dosimetry in experimental systems. However, as cell uptake of carbon nanotubes is often not measured and is generally difficult to quantify, interpretation of comparative studies of SWCNT or MWCNT toxicity can be challenging.

While many metal oxide ENMs are remarkably stable in aqueous and cellular environments, nanoparticles that are prone to dissolution often recapitulate the pattern of redox toxicity of the soluble constituent metal ions. For instance, the important contributions of ion dissolution in the biological effects of nanosilver are widely recognized [100–104]. Nanoscale silver particles, of growing interest for their bacteriocidal properties, display greater hemotoxicity than their micron sized

counterparts [105, 106]. The enhanced hemolytic activity of nanosilver is mediated not only by increased particle surface area available for direct interactions and redox modification of membrane components, but also through increased dissolution and release of silver ions, that have strong avidity for protein thiol groups [105, 106]. Dissolution of silver ions is initiated at points of particle surface defects. Thus, the rate of ion release is dependent on both surface area and curvature of the particle and the crystal structure. However, the rate of silver particle dissolution can vary by over four orders of magnitude depending on surface modifications, oxidation states, and the local environment [107].

Other materials, including ZnO, CuO and Cd/Se quantum dots, are now well-recognized to produce oxidative stress and toxicity through dissolution-dependent mechanisms [77, 108–112]. The dissolution of CuO and ZnO nanoparticles is facilitated at lysosomal pH (4–5) and occurs over rapid time scales typically used in cell culture studies [108, 110], which makes it challenging to disentangle the relative contributions of nanoparticles and dissolved ionic species in toxicity studies.

Mihai et al. [108] used quantitative microscopy techniques to elucidate the dynamics of focal ZnO dissolution in cultured lung cells in situ, and demonstrated that low but critical levels of  $Zn^{2+}$  formed within endo-lysosomal compartments were necessary for toxicity to occur. Studies using X-ray scanning fluorescence microscopy in macrophages have revealed similar findings, demonstrating that with toxic concentrations of ZnO nanoparticles, intracellular zinc ion levels are elevated by over 400 %, or up to 13-fold greater than an equitoxic concentration of ZnCl<sub>2</sub> [113]. Like nanosilver, dissolution rates of ZnO nanoparticles can be relatively low at neutral pH in the absence of organic material (e.g., protein), emphasizing that intracellular fate and environment of nanoparticles have dramatic influences on particle stability and potential for releasing redox-active metal ions.

Indirect Mechanisms of Cellular ROS Production Although not all ENMs have electronic or surface chemistry properties that directly facilitate spontaneous ROS generation, many materials nonetheless indirectly generate oxidative stress by altering cell metabolism and gene regulation. The most common mechanisms for indirect generation of oxidative stress by ENMs include the disruption of normal control of mitochondrial respiration and activation of inducible nitric oxide and NADPHdependent enzyme pathways in phagocytic cells.

Mitochondria play a critical role in control of redox homeostasis, in part by maintaining a strong net negative potential between the inner and outer mitochondrial membranes. In healthy cells the concentration of superoxide radicals is also strictly compartmentalized in the mitochondrial matrix at levels ~5–10 fold higher than in the cytosol [114]. Cationic polystyrene nanospheres and ultrafine ambient particles can disrupt normal mitochondrial membrane potential and integrity, resulting in cellular ROS production, glutathione depletion and cytotoxicity [76].

Mitochondrial oxidative phosphorylation, which supplies more than 95 % of total cellular energy requirements, is disrupted by nanosilver [115], potentially through perturbation of mitochondrial membrane permeability by interactions
between silver ions and thiol groups of inner mitochondrial membrane proteins [116]. Dissolved metal cations such as Cu<sup>2+</sup> can pass through mitochondrial proton or cationic pumps, causing osmotic swelling and proton loss [117]. Beyond the loss of redox and energy homeostasis, disruption of mitochondrial membrane integrity by ENMs also disrupts intracellular calcium gradients and promotes release of cytochrome c. These effects are ultimately responsible for triggering cell death modalities ranging from apoptosis to necrosis [118].

Given that many of the ENMs reported to disrupt mitochondrial permeability are relatively large in size, an unanswered question is how (or whether) these ENMs are targeted to mitochondria in the first place? Studies using well defined gold nanoparticles suggest that there is a strict permeability size limit (<6 nm) by which nanoparticles can pass though ion channels of the outer mitochondrial membrane [119]. These observations raise the question of whether the disruption of mitochondrial permeability by ENMs is primarily mediated by dissolved metal ions that are small enough to transit across mitochondrial pores.

Phagocytes, (e.g., resident macrophages), are among the first cells to encounter ENMs. Due to their scavenging function, macrophages may harbor high intracellular particle doses following exposure to ENMs. Several reports have shown that the same scavenger receptor-mediated pathways macrophages use to respond to bacterial pathogens also recognize many ENMs [61, 120, 121]. Active phagocytic internalization of ENMs can result in robust oxidative and nitrative stress through stimulation of NADPH oxidase and nitric oxide synthase pathways associated with the phagocytic burst. This indirect mechanism of ROS production may be particularly prevalent for nanotubes and other materials with long aspect ratios that exceed the dimensions for efficient receptor-mediated uptake, resulting in 'frustrated phagocytosis' [79, 122–125].

While metal impurities can contribute to intrinsic ROS generation by nanotubes, there is also evidence that purified carbon nanotubes display antioxidant properties and can directly quench free radicals [126, 127]. However, studies in mice lacking functional NADPH oxidase demonstrated that ROS generated through the phagocytic burst are critical in determining the pulmonary response to SWCNT, contributing to both acute phases of inflammation and later anti-inflammatory and fibrotic responses [122]. Dietary manipulation of levels of the antioxidant vitamin E can modulate nanotube toxicity [128, 129], supporting the concept that cell-mediated ROS production and lipid peroxidation events play important roles in the pathogenic effects of these materials.

A direct link exists between ROS-mediated NADPH oxidase activity following phagocytosis of ENMs and activation of the NALP3 inflammasome, a molecular complex whose activation triggers inflammation via secretion of interleukin-1 $\beta$  [130]. A variety of ENMs stimulate inflammasome activity, including TiO<sub>2</sub>, crystal-line silica, asbestos fibers, and carbon nanotubes [131–134]. Long carbon nanotube fibers and asbestos activate the inflammasome by similar mechanisms that are dependent on phagocytosis and ROS production [134]. It was recently proposed that the generation of ROS is the crucial element by which multiple signals converge on inflammasome activation [135]. However, inflammasome activation is often not

observed in phagocytes treated with highly purified MWCNT in vitro, and some reports indicate ROS generation is not a requirement for activation [132, 133]. Inflammasome activation by nano-TiO<sub>2</sub> may also occur independent of cytoskeletal-dependent phagocytosis [131]. The inflammasome-activating properties of carbon nanotubes may be overestimated in the literature due to the presence of immunologically-active contaminants such as endotoxin commonly found in commercial nanotube preparations [132]. Thus, the physicochemical properties of ENMs that govern activation of the inflammasome have yet to be clearly defined.

The phagocytic uptake of ENMs can cause strong immunomodulatory effects independent of stimulating classical pro-inflammatory pathways. In some experimental models, macrophage uptake of ENMs results in immune suppression and enhanced susceptibility to infection by bacterial pathogens [136–139]. For example, uptake of iron oxide nanoparticles through scavenger receptor-dependent mechanisms dramatically alters macrophage gene regulation in response to Toll 4 receptor activation and downregulates the phagocytic activity of macrophages toward Streptococcus pneumoniae, the leading cause of community-acquired pneumonia [137]. Similarly, exposure to SWCNT was associated with diminished nitric oxide production in macrophages and enhanced susceptibility to lung infection by Lysteria monocyotegenes [136]. Macrophages exposed to SWCNT also exhibit a decreased ability to engulf apoptotic cells [140]. It is important to note that these immunomodulatory effects can occur at cellular ENM levels that are far below those required to cause macrophage overload ( $\sim 6$ % of total macrophage volume [141]), and in the absence of any direct cytotoxic or proinflammatory effects of the ENM alone [137]. Furthermore, these 'indirect effects' may only be manifested during co-exposure scenarios, or when the cells are challenged with additional stressors such as bacteria. Consequently, biological endpoints commonly used in nanotoxicology screening strategies that are heavily focused on cytotoxicity and pro-inflammatory endpoints alone may fail to identify these potential adverse effects.

To date, the immunosuppressive effects of ENMs have received limited research attention. Nonetheless, these recent findings are consistent with numerous epidemiological studies that have linked exposure to ultrafine ambient particulates with increased risk of pneumonia and other lung infections [142–144]. It is intriguing to speculate that such subtle changes in innate immune susceptibility may be particularly relevant to chronic low level or accidental exposures that would be typical of human occupational scenarios.

Improved Mechanistic Markers of Oxidative Stress Are Needed The extent to which ROS production, through either direct or indirect mechanisms, is responsible for the immunomodulatory effects of ENMs is not clear. Although oxidative stress remains an important principle in nanotoxicology, uncertainties in the sources and mechanistic roles of ROS in mediating adverse effects of ENMs means care must be taken in how this principle is used in toxicity screening. Many current nanotoxicology strategies for assessing the ROS production potential if ENMs rely on fluorescent reporter dyes, such as dichorofluorescein (DCFH) derivatives, as generic ROS indicators. Unfortunately, these methods have limited dynamic range, sensitivity and specificity, and are prone to interference by nanomaterials [145]. Broad-based measures of oxidative stress such as assays for cellular glutathione status also provide limited insight into specific biological pathways that are affected by ENM-mediated ROS. While such generic measures of ROS are rapid to employ, their mechanistic and predictive value is questionable.

Key future goals for nanotoxicology are to determine whether (and how) the chemical nature and molecular targets of oxidative modifications within the cell are dependent on the physicochemical attributes of the ENM [81], and whether this site-specific information will be more predictive of specific biological pathways affected by different ENMs. For instance, reversible and site-specific redox modifications of protein cysteines, such as S-nitrosylation and S-glutathionylation, play important roles as regulatory switches for control of specific inflammatory signaling and innate immunity pathways in response to oxidative stressors [146–150]. Despite the development of new methods and tools for measuring these 'pathway-specific' redox modifications at a proteome-wide scale [151, 152], their potential roles in mediating cellular effects of ENMs have yet to be investigated. Ultimately, these more targeted approaches are needed in order to understand whether ROS-mediated signaling events are non-stochastic processes that can result in very different cellular and in vivo outcomes for different types of ENMs.

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### Chapter 19 Chemical Warfare Agents

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### **19.1 Introduction**

Chemical warfare agents have been used since the beginning of the twentieth century, and unfortunately are being a serious threat to army as well as civilian populations. Of these devastating compounds, the mostly commonly used chemical weapon was the blistering agent mustard gas (sulfur mustard, 2,2'-dichlorodiethyl sulfide; SM).

This chemical is a potent vesicating chemical warfare agent, which was first used in World War I [1–4] in 1917 by Germany against French troops near Ypres, Belgium. This early use earned the gas two nicknames: Yperite, and Yellow Cross (due to the special sign on mustard gas-containing shells) [3]. Since then, there has been evidence or allegations of SM use in 11 conflicts, including use by Italy against Ethiopia in 1936, by Japan against China in 1937, by Poland against Germany in 1939, by Egypt against Yemen from 1963 to 1967, and by Iraq against Iran in the 1980s [5]. Accidental exposures have also occurred. Following World War II, large stockpiles of chemical weapons including mustard gas were dumped in the Baltic Sea. Corrosion of the containers led to the liberation of shells which were accidently brought on board by fishing trawlers, resulting in exposure of fishermen to the

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© Springer International Publishing Switzerland 2015 S.M. Roberts et al. (eds.), *Studies on Experimental Toxicology and Pharmacology*, Oxidative Stress in Applied Basic Research and Clinical Practice, DOI 10.1007/978-3-319-19096-9\_19 vesicant [2, 5-7]. In the recent 15 years several cases of accidental exposure to SM have been reported [8-10].

The second type of chemical weapons are the organophosphorous (OP) nerve agents that include sarin, soman, tabun, VX and VR as well as various insecticides, such as parathion, malathion and chlopyriphos. Sarin was used in the terrorist attacks in Matsumoto City and Tokyo subways in 1994 and 1995, respectively [11–19]. In the latter mass exposure more than 3,500 persons were injured while relatively low rate of mortality of 11 victims was documented [11], likely due to the low grade of purity (about 30 %) of the nerve agent. More recently in August 2013, 1,500 civilians including 400 children were killed by a nerve agent, probably sarin, in the civil war in Syria [20–22].

Apart from the steps that should take place for prevention of both synthesis and use of chemical warfare agents, the responsibility of science is to develop physical, chemical and pharmacological countermeasures to reduce as much as possible the toxic effects of these devastating agents. The availability of gas mask and protecting clothing is limited particularly in undeveloped countries. Nevertheless, both nerve agents and mustard gas will penetrate the skin; hence, even a civilian population equipped with gas masks may be affected via dermal exposure. Thus, the pharmacological protection against chemical warfare is of great importance and should be of the highest priority in policy decisions.

The currently available pharmacological antidotes against both mustard gas and nerve agents are of limited therapeutic value. Due to the highly toxic activities of chemical warfare agents and short and long term adverse effects that do not respond to the current treatments, there is a great need for improved antidotes. In particular, new insights and novel pharmacological approaches should be developed to cope with mass exposure to these devastating agents.

The strategy of drug development requires understanding of the cellular, molecular, and physiological actions in the affected organs. The greater the understanding of the mechanism of action of a toxic agent, the better the chance of developing potent antidotes. The present review will be focused on the pathological processes and cellular and molecular events occurring upon exposure to the chemical warfare agent mustard gas, with special emphasis on the inflammation and oxidative stress in the affected organs.

### **19.2 Sulfur Mustard**

SM is a powerful alkylating agent that primarily attacks the main sites of exposure namely, skin, ocular and respiratory tissues [23]. Nevertheless, due to its oily nature and low water solubility [3] it rapidly penetrates the skin and may affect internal organs, such as bone marrow and the nervous system [24]. Because of its volatility, SM affects the respiratory tract and easily reaches the circulation and adversely affects internal target organs [3].

### Structural formula of SM



### 19.2.1 SM-Induced Pathologies

Mass exposure to SM was documented in several conflicts [3–5]. A detailed pathology and evolution of skin and other lesions in SM-exposed Iranian soldiers was documented by Willems [24], Momeni [25], Kehe [26] and their colleagues [25]. Similar properties of SM-induced skin lesions were reported by Sinclair [27–29] in a controlled mass exposure of volunteers protected with a gas mask.

Unlike heat burns, the typical characteristics of SM-induced skin burns are its delayed effects. These start to appear several hours after poisoning. Exposure of humans to SM vapor resulted in erythema, itching and burning sensation, which developed after 8-24 h in the majority of subjects [28]. However, onset of symptoms 20 min to 4 h after exposure has also been reported [24]. In mild cases it was delayed for 3-4 days, and in severely affected persons it appeared within 4 h. In most cases the erythema gave place gradually to the pigmentation characteristic of SM burns. Subcutaneous edema was detected 3-9 days after exposure depending on the region of the body. Vesication of the skin occurred later, appearing as numerous blisters about the size of a pin's head or smaller, and sometimes developing into large blisters [28]. In most cases, the mean time for first onset of vesication in the various regions of the body was 7.2 days; blisters involved superficial layers, which healed in a few days. By contrast, in severe cases (11 % of the exposed individuals) deep vesicles appeared during the first four days. Deep vesication or desquamation produced breaches in the epithelium surface leading to painful raw surfaces, which were the main portals of infection. The mean time for the first appearance of raw surfaces was 8.8 days, while maximal severity of the lesions was observed after a mean of 10.9 days. The average time for healing was 19 days, while in severe cases it could lengthen to months, particularly on the penis. Mustard gas vapor differentially affected various regions of the body. The most severely injured organs were the wet and warm areas, i.e. scrotum, axillae, penis and buttocks. The trunk, dorsum of hands (palms and soles were rarely affected) and forearms were also frequently injured to different degrees of severity [27-29].

#### Typical lesions of guinea pig skin exposed to neat SM (1 µl)



Additional delayed symptoms, such as epigastric distress and vomiting, appearing hours after exposure were observed in soldiers attacked by mustard gas during World War I [30]. Iranian patients suffered from eye irritation 3–4 h after exposure to mustard gas in the Iran-Iraq conflict [25]. The ocular damage progressed to conjunctivitis, lacrimation, photophobia and eyelid edema which occurred in most of the affected individuals, while in severe cases corneal involvement, iritis and chemosis also appeared [30]. The respiratory system was also highly vulnerable to mustard gas vapor. Laryngitis and bronchitis were primarily irritating and in severe cases were complicated, 3–4 days after exposure, by bronchopneumonia or pulmonary edema. The fatal cases (2–5 % of exposed individuals) following attack by SM were largely due to respiratory complications [31, 32] Bone-marrow toxicity was recorded in the most severely affected soldiers [31], as well as in accidental exposure [33].

The main long-term effect of mustard gas is its tumorigenic activity. The mutagenic and carcinogenic potential of the vesicant was proven by *in vitro* and *in vivo* experiments, as well as by epidemiological studies [34]. A 40-year follow-up of workers in British mustard gas manufacture during World War II has shown that the death rate from respiratory tract malignancies was higher (up to 5.5 times) than that of the unexposed population [35]. An even higher incidence of lung cancer (up to 35-fold) was observed in employees in Japanese and German mustard gas factories [34]. Duration of employment significantly affected risk for certain cancers [35]. A recent longitudinal epidemiological study showed that SM decreased the age at which people were at risk of developing lung cancer [36]. A case of cutaneous squamous cell carcinoma was reported long after dermal exposure to SM [37]. High mortality from chronic non-malignant respiratory diseases was also observed [35]. Long-term keratopathy, including deposition of hyaline, calcium and crystals, was also detected 35–50 years after exposure to mustard gas during World War I [38].

### 19.2.2 SM-Induced Inflammation

In an aqueous environment, the key reaction of mustard gas is the intramolecular cyclization to form the electrophilic ethylene episulfonium intermediate [4]. This intermediate alkylates nucleophilic residues of macromolecules, such as N-7 and N-3 of the guanine and adenine residues [39–43], respectively, and cysteine residue in proteins and peptides. Thus, chromatid aberrations occur [44], synthesis of DNA, RNA and proteins is inhibited and cell cycle is blocked [44, 45].

Concomitant to these molecular events, inflammation is present as an early sign of toxicity in the exposed tissues. Exposure of haired guinea pig skin to SM resulted in recruitment of inflammatory cells, microvesicle formation, ulceration and necrosis [46, 47]. Similar processes were observed in heat burns and in other types of chemical burns (hydrofluoric acid), but with faster kinetics [48]. Infiltration of CD4+ and CD8+ T cells was observed in SM-exposed skin of euthymic hairless guinea pigs [49]. Activated neutrophils and macrophages recruited in the affected area produce and secrete a variety of inflammatory factors such as cytokines, prostaglandins and proteinases. Involvement of TNF $\alpha$  was reported in SM-exposed guinea pig skin [50], while in the hairless SKH-1 mice mRNA transcripts of IL-1 $\beta$ ,

IL-6, CXCL2, CCR1 and TNF $\alpha$  were upregulated in skin exposed to the vesicant [51, 52]. The inflammatory response is not limited to the immune cells present at the site of exposure; keratinocytes take active part in the process of inflammation. For instance, human HaCaT keratinocytes generate hydrogen peroxide in response to lysophosphatidic acid [53]. Several reports on the effect of SM on keratinocytes demonstrated upregulation of various proinflammatory cytokines and chemokines. Exposure of HaCaT keratinocytes to the vesicant caused elevation of TNF $\alpha$ , IL-6 and IL-8 [50, 54, 55]. Similar profile was observed in normal human epidermal keratinocytes [56]. Increased levels of PGE2 upon vesicant exposure were found in the hairless guinea pig [57] and mouse ear swelling test [58] models. Additional inflammatory components like matrix metalloproteinases were shown to be induced by SM. Metalloproteinase-2 and 9 activities were elevated during the wound development in the hairless guinea pig skin following SM exposure [57]. Induction of MMPs was also observed in haired guinea pig skin exposed to nitrogen mustard [59] and hairless SKH-1 mice topically applied with SM [51].

### 19.2.3 Oxidative Stress Induced by SM and Its Analogs

It is well accepted that inflammation is associated with oxidative stress. This link was evidenced in a variety of biological and toxicological systems including chemical irritation. SM and its alkylating derivatives cause the production of reactive oxygen species (ROS) which play a central role in skin pathologies [60] and vesicant injuries. The review by Laskin and coworkers [61] describes in details the involvement of oxidative stress in tissue injury induced by SM and its mono-alkylating derivatives. Damage to macromolecules by ROS is well characterized and includes DNA base oxidation leading to interference in the replication and repair processes. ROS may cause lipid peroxidation which can generate highly reactive electrophilic lipid peroxidation end products; they can also oxidize proteins resulting in modification of their enzymatic and structural functions [61]. For instance, exposure of SKH-1 hairless mouse skin to the mono-functional mustard 2-chloroethyl ethyl sulfide (CEES) increased oxidation of dermal DNA and proteins [62]. Vesicants caused elevation in lipid peroxidation in mouse skin [62], lung [63] and human plasma [64].

The mechanism by which SM elicits oxidative stress may involve direct action, namely, decreasing intracellular antioxidants or suppressing activity of enzymes that produce or regenerate antioxidants. For instance, the tripeptide glutathione (GSH) that serves as an intracellular antioxidant is also a powerful nucleophile that reacts with the highly electrophilic ethylene episulfonium derivative of SM and its monochloroethyl analogs. Vesicant-induced decrease in GSH levels [63, 65–67] may cause a reduction in the antioxidant capacity of the cell and result in oxidative stress. The protective role of GSH is supported by the decreased mortality in mice treated with GSH after inhalation exposure to SM [63] and CEES [68]. This is corroborated by the protection conferred by *N*-acetylcysteine against CEES-induced

lung toxicity [68, 69]. An additional approach for protection against vesicant toxicity is to induce glutathione S-transferase (GST) and GSH synthesis enzymes via activation of the transcriptional nuclear factor erythroid 2-related factor 2 (Nrf2) [70]. Under basal unstimulated conditions, Nrf2 complexes with Keap1 in the cytosol where it is targeted for ubiquitination and proteolysis [71]. Upon oxidative stress signals or electrophilic agents, Nrf2 is released from the Keap-1, allowing for newly translated Nrf2 to translocate to the nucleus and elicit transcription of its target genes via binding to antioxidant response elements (ARE). Abel and coworkers [72–74] found that both sulforaphane and methyl-2-cyano-3,12-dioxooleana-1,9-dien-28-oate stimulated nuclear localization of Nrf2, induced expression of the glutamate cysteine ligase modifier (GCLM) subunit, elevated reduced GSH content and decreased CEES-induced cytotoxicity in human keratinocytes. Activation of the GSH system either by induction of the relevant enzymes or elevation of intracellular GSH may serve as one potential treatment against alkylating agents and oxidative stress.

An additional Nrf2-controlled system that mediates oxidative stress is thioredoxin/thioredoxin reductase [74]. SM and its analogs can induce oxidative stress by alteration of these enzymatic activities. For instance, thioredoxin reductase can be modified by CEES [75], which covalently binds to the selenocysteine residue of the enzyme. Inhibition of thioredoxin reductase has been demonstrated to deplete cells of reduced thioredoxin, a key player in cellular redox regulation. Both thioredoxin reductase and thioredoxin function as antioxidants and their inhibition by CEES can lead to oxidative stress [61].

An additional factor involved in cellular toxicity is nitric oxide (NO). In spite of being an important mediator of numerous physiological processes, excessive amounts may be toxic, particularly upon reaction with superoxide anion forming peroxynitrite, which is a strong oxidant and nitrating agent that triggers oxidative injury and tissue damage [61]. The NO generating enzymes, nitric oxide synthases, were reported to be modulated by SM or its analogs [76–80]. Furthermore, NOS inhibitors protected cell cultures from these vesicants [81–83]; however, *in vivo* studies with hairless guinea pigs did not show consistent protection against topical vapor challenge of SM [81].

### **19.2.4** Potential Antidotes for SM

In view the mechanisms of toxic action of SM, a variety of anti-inflammatory agents and radical scavengers have been proposed as countermeasures against its vesicating activity. Compound screening by the US Medical Chemical Defense Research Program presented a series of the most active compounds in the mouse ear swelling test including non-steroidal and steroidal anti-inflammatory drugs such as indomethacin, hydrocortisone, dexamethasone and olvanil for their antidotal activity [84]. A mixture of steroidal and non-steroidal anti-inflammatory agents showed efficacy in reducing skin injury caused by SM [58]. Scavengers like mercaptopyridine and mercaptopurine derivatives, dimercaprol, inhibitors of poly (ADP-ribose) polymerase and proteinases and, antioxidants such as trolox, quercetin and reduced GSH have also shown reduction in SM toxicity [63,73,84]. Topical treatment with iodine ointment was markedly effective against vesicant-induced skin injury in the haired guinea pig model. Post exposure treatment with a commercially available preparation of povidone iodine significantly reduced skin damage caused by various irritants such as SM, nitrogen mustard (mechlorethamine), cantharidine, divinylsulfone and iodoacetic acid [46]. Improved efficacy was observed with a novel iodine formulation that enabled a relatively long interval of 30 min between SM exposure and iodine application [47]. However, the beneficial effect of topical iodine was not limited to chemical injuries; povidone iodine significantly protected against heat burns in both animal models [48] and humans [85, 86]. The anti-inflammatory and counter-irritating activity of topical iodine is presumably attributed to induction of a nonapeptide, which demonstrated anti-inflammatory properties in a variety of experimental systems [87].

### **19.3 Summary and Future Aspects**

Despite the accumulating information on the mechanism of toxic action of SM and its derivatives, intensive research is needed to better explore the molecular aspects of the vesicating activity. As a result, novel and more targeted therapies may be developed as countermeasures for the irritating effects of SM. Due to the complexity of the mechanism of toxicity, a combination of compounds, each acting at different mechanism of action, may be the ultimate antidote against the vesicating activity of SM and other hazardous chemical and physical irritants.

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## Part III Special Topics

### Chapter 20 On the Biochemistry of Antioxidants: Current Aspects

Lars-Oliver Klotz

### 20.1 Introduction

In a toxicology and pharmacology context, reactive oxygen species (ROS) are frequently regarded as damaging by-products of xenobiotic metabolism, and antioxidants are the presumed balancing protective measures, interfering with oxidant action by quenching or scavenging them before they can do harm. However, this simple view fails to explain why large-scale antioxidant supplementation trials have not yielded many promising data so far (for a detailed discussion, see Chap. 21 by Wilhelm Stahl). The purpose of this chapter is to highlight some current aspects in antioxidant research rather than reiterate facts of antioxidant biochemistry that have been highlighted in previous chapters. For details on lowmolecular mass antioxidants and enzymatic antioxidants, the reader is referred to Chaps. 5, 9 and 21.

Here, antioxidant lines of defense and antioxidant principles beyond direct oxidant scavenging will be discussed, followed by a brief analysis of potentially adverse effects of compounds usually regarded as antioxidants.

### 20.2 Some Basics

Several "strategies of antioxidant defense" were pointed out by Sies [1], including prevention, interception, repair and adaptation (see Fig. 20.1). While *prevention* includes measures of averting the formation of ROS in the first place, *interception* 

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**Fig. 20.1 Antioxidant strategies**. Antioxidant strategies according to [1, 2, 6]. Oxidative modification of (or damage to) selected biomolecules that escape the protective mechanisms of prevention, interception and repair may elicit cellular signaling processes that can turn into protective adaptation processes or contribute to ROS toxicity. The modulation of cellular signaling cascades (*blue box*) is suggested as a novel antioxidant approach to channel ROS effects into the desired direction

refers to chemical neutralization (in its broadest sense) of a formed ROS by compounds that react with ROS. *Repair* mechanisms are a crucial line of defense in the cellular antioxidant network, and exist for oxidative DNA damage and oxidized protein. For example, there is base excision repair specific for oxidized guanine in DNA, or methionine sulfoxide reductases for the reduction of oxidized methinoyl residues in proteins (see Chap. 5 by Reeg and Grune), to name a few. Finally, *adaptation* to oxidative stress includes the modulation of gene expression by ROS to alter cellular levels of antioxidant proteins (including the aforementioned repair proteins). One interesting feature of ROS-induced adaptation is that the very damage to target molecules that antioxidants are supposed to prevent or revert may actually elicit signaling processes in exposed cells that may then result in adaptation (Fig. 20.1). Several such oxidative alterations of cellular target molecules were demonstrated to trigger signaling processes (see Chap. 8).

### 20.2.1 Application of the "Antioxidative Strategies" Concept

An example of the usefulness of the above concept was provided by Arteel et al. [2] for the strong oxidant and nitrating species, peroxynitrite, along the following lines. As peroxynitrite is generated by a nearly diffusion-controlled reaction of superoxide with nitrogen monoxide (for reviews on peroxynitrite biochemistry, see [3–5]), an inhibition of either NO or superoxide generation or facilitation of their decomposition prior to reaction would be equal to a *prevention* of peroxynitrite formation. This may be achieved by inhibition of NO synthases, inhibition of either NO or  $O_2^{-}$  generating oxidases, or by interception of either NO or  $O_2^{-}$  using appropriate enzymes or scavengers. Several peroxynitrite scavenger

molecules (besides endogenous peroxynitrite target molecules, that is) are available and although not absolutely specific for peroxynitrite, they may still contribute to interception of peroxynitrite. Examples are Mn- and Fe-porphyrins, selenocompounds, and others [2, 6]. Interestingly, some compounds were identified that do not fully scavenge peroxynitrite but interfere with a subset of its reactions: for example, epicatechin was demonstrated to preferably attenuate nitration rather than oxidation reactions of peroxynitrite [7, 8]. Repair of peroxynitrite-induced damage includes the above-mentioned general mechanisms: repair of oxidized and nitrated proteins and DNA, along the pathways outlined in Chaps. 5 and 6. Interestingly, while *oxidative* damage to proteins caused by peroxynitrite is efficiently recognized by the 20S proteasome [9], the exact mode of reversal of protein tyrosine nitration (a frequent alteration identified in tissues exposed to peroxynitrite), although described, is still unclear, and the nature of this "denitrase" activity is being investigated [10, 11]. Adaptation to an exposure to peroxynitrite occurs along the principles outlined in Chap. 8, i.e. by stimulation of stress-responsive signaling cascades, including growth factor receptor-dependent signaling, mitogen-activated protein kinases, and others [12–14].

### 20.2.2 How to Assess "Antioxidant Capacity"

In light of the broad definition of an "antioxidant" provided above, and of the obvious non-straightforward, web-like nature of cellular antioxidant strategies (and, of course, in an attempt to boil a set of multiple required assays down to just one) it appears desirable to find a way to assess an overall capability of a biological system such as a cell or a tissue to defend itself against oxidative stress. Such a tool would allow for a quick assessment not only of the "defense status" of a cell but would also aid in judging alterations of cellular antioxidant defenses in response to drugs, phytochemicals or any type of exposure. Several tools and assays for the determination of a total antioxidant capacity (TAC) were developed and do have their merit in defined chemical systems, but prove problematic if applied to biological systems, as pointed out by Sies [15]. In these assays, TAC is defined as the capability of a sample (tissue, cell lysate, food item, chemical, etc.) to scavenge a defined reactive molecule. TAC assays usually follow one of two general principles, i.e. they analyze how effectively a sample prevents the oxidation of a chemical probe induced by an oxidant specific to the assay (Fig. 20.2a) or they assess how well a sample directly reduces a chemical probe whose change in redox status comes with altered absorption or luminescence features (Fig. 20.2b). TRAP ("total peroxyl radical-trapping antioxidant parameter"), ORAC ("oxygen radical absorbance capacity"), and PCL (photochemiluminescence analysis of antioxidative capacity) assays all follow the first principle. Hydro- or lipophilic peroxyl radicals (TRAP, ORAC) or superoxide (PCL) are generated and the oxidation of a probe followed spectrophotometrically or by luminescence measurement. Any attenuation in oxidation of the probe that is caused by a sample under investigation would be set equal to the sample's TAC - sometimes using a known antioxidant



Fig. 20.2 Total antioxidant capacity assays: principles. See text for further information

molecule as a control. Examples for the second group of TAC assays include TEAC ("Trolox equivalent antioxidant capacity") or FRAP ("ferric ion reducing antioxidant power") assays that essentially analyze the capacity of a sample to reduce a radical generated *in situ* in the assay (TEAC, with Trolox as a standard antioxidant) or an Fe(III)-containing complex (FRAP).

As obvious from these brief descriptions, such assays simply cannot measure all types of antioxidant activity in one simple approach. Not only are the ROS whose quenching or scavenging is analyzed in these assays very specific, but also the respective probes are of course not reduced or oxidized equally well by all sorts of enzymes or chemicals. For example, it would appear improbable that intact superoxide dismutase, no matter what its concentration in a sample, reduces the above Fe(III) complex. Lastly, as outlined above, antioxidative strategies include mechanisms beyond interception that would therefore not be captured by TAC assays.

Considering these restrictions and problems, there currently seems to be no way around a classical approach of determining whether a cell is under oxidative stress and/or prepared to "anti-oxidatively" counter this stress. Such an approach would include the determination of (i) extent of actual oxidative damage (e.g. lipid peroxidation, protein modification, oxidative DNA damage), (ii) the concentrations or specific activities of non-enzymatic and enzymatic antioxidants, respectively, and (iii) the behavior of the system under defined oxidative stress conditions. Of course, it always helps to define the exact antioxidant parameter of interest and to confine experimental approaches accordingly.

### 20.2.3 Non-redox Activities of Antioxidants

The observation that nutrition rich in fruits and vegetables has beneficial effects at several levels has frequently been related to the action of antioxidants. This conclusion is obviously premature as countless other phytochemicals that are usually not considered classical (i.e. ROS scavenging) antioxidants are taken up in a fruit/vegetable-rich diet. Moreover, should any "antioxidant" compound indeed contribute to beneficial effects of a diet, it would still be questionable that these effects are due to their radical scavenging activity – rather than any other non-redox

effect. A major reason for this assumption is that *in vivo* concentrations of phytochemicals or metabolites usually achieved are insufficient to explain any major contribution to overall tissue radical scavenging activity (see [16, 17] and references therein).

Examples of such non-redox activities have been known for decades, including the pro-vitamin A properties of certain antioxidant carotenoids ( $\beta$ -carotene,  $\alpha$ -carotene,  $\gamma$ -carotene and  $\beta$ -cryptoxanthin) that may contribute to retinoid effects, or protein kinase C inhibition by tocopherol [18].

Further examples include kinase inhibition by flavonoids, from tyrosine kinase inhibition by the isoflavone, genistein [19], and MAPK inhibition by the flavone, apigenin [20], to the first synthetic inhibitor of the extracellular signal-regulated kinase (ERK)-1/-2 pathway, another flavone (2'-amino,-3'-methoxyflavone; PD98059) that targets MAPK/ERK kinase (MEK)-1 and MEK-2, the kinases upstream of ERK-1 and ERK-2 [21]. Except for the synthetic derivatives, kinase inhibitory activities of natural flavonoids are usually quite general and of moderate specificity, as they act as competitors of ATP, which is, of course, a substrate to all kinases.

Flavonoids are rather pleiotropic bioactive agents; in addition to kinase inhibitory properties of some, several flavonoids are phytoestrogens, i.e. stimulate estrogen receptor activity-dependent processes [22].

An example of flavonoid action on cellular signaling cascades and the potential impact on cell physiology is the effect of green tea flavonoids - epicatechin (EC), epigallocatechin, EC gallate, and epigallocatechin gallate (EGCG) (Fig. 20.3a) - on transcription factors of the forkhead box, class O (FoxO) family. FoxOs control the expression of genes involved in antioxidant defense and cell survival as well as fuel metabolism, and are negatively regulated by insulin. Green tea flavonoids were tested for their effect on FoxO activity in different cell types, such as human fibroblasts and human hepatoma cells (HepG2). Of these flavonoids, EGCG is of particular interest in cell culture and other in vitro studies because it is not only the major flavonoid in green tea [23] but also because in vivo a high percentage of consumed EGCG reaches the circulation in unmetabolised form [24, 25]. In these tested cells, phosphorylation, nuclear exclusion and inactivation of FoxOs was observed upon exposure to EGCG - similar to the effects elicited by insulin. Interestingly, this effect was found only at supraphysiological flavonoid concentrations of >10  $\mu$ M. H<sub>2</sub>O<sub>2</sub> was generated upon incubation of cells in the presence of EGCG and mediated insulin-like signaling via the serine/threonine kinase Akt to result in FoxO phosphorylation [26]. At lower concentrations of EGCG (1  $\mu$ M) that did not cause significant H<sub>2</sub>O<sub>2</sub> generation there was not only no effect on FoxO activity, but rather the opposite effect was elicited, i.e. stimulation of FoxO DNA binding and FoxO nuclear accumulation [26]. Therefore, two EGCG effects appear to compete – the prooxidative and insulin-like effect observed at high concentrations and the insulin-antagonistic effect observed at very low concentrations. EGCG, therefore, may serve as an example of a hormetic substance that does have an effect



**Fig. 20.3** Green tea flavonoids and FoxO signaling. Structures of green tea flavonoids (a) and of harmine (b). Stimulation of FoxO DNA binding and nuclear accumulation by epigallocatechin gallate (EGCG) and harmine is hypothesized to occur via inhibition of an inhibitor of FoxO proteins, "dual-specificity, tyrosine-phosphorylated and regulated kinase" (DYRK)-1A (c) (Taken from Ref. [70], with kind permission from Springer Science and Business Media)

at low concentrations which is actually inverted at higher concentrations. EGCG concentrations tested in these experiments are in a region of concentrations achievable *in vivo*, where approx. 0.2  $\mu$ M to approx. 5  $\mu$ M were detected in human serum after consumption of green tea or green tea extract [25, 27, 28].

Regarding the mechanism of action of EGCG that led to enhanced FoxO DNA binding and nuclear accumulation, it is currently hypothesized that the FoxO kinase, DYRK1A, may be a molecular target mediating the observed effects [26]: phosphorylation of FoxO transcription factors by DYRK1A attenuates FoxO-dependent transcriptional regulation [29], and DYRK1A, in turn, is very efficiently inhibited by EGCG [30]. In support of this hypothesis of DYRK1A being responsible for EGCG effects on FoxOs, a known inhibitor of DYRK1A, i.e. harmine (Fig. 20.3b), was demonstrated to have the same effect on FoxO activity as EGCG [26]. The mode of action of EGCG is hence hypothesized to be that of an inhibition of an endogenous inhibitor of the effector – to result in the effector's net stimulation (Fig. 20.3c).

In summary, so-called antioxidants may have beneficial effects irrespective and independent of their potential radical scavenging or redox activities.

### 20.3 Antioxidant Toxicity?

Can antioxidants be toxic? Considering not only the virtually omnipresent toxicology motto stating (and paraphrasing Paracelsus) that any compound, depending on its dose, may be a poison, but considering also the aforementioned mere variety in types of antioxidants and antioxidative strategies, the answer is, of course, yes. Interestingly, it has even become almost fashionable recently to claim that antioxidant supplementation may not only be devoid of benefits, but even toxic [31, 32]. Some intervention studies that provide a basis for these conclusions will be discussed in Chap. 21. At a molecular level, such adverse effects of antioxidants may be explained in many ways, some of which are outlined below.

### 20.3.1 Prevention of Essential or Beneficial ROS Effects by Antioxidants

Assuming that stimulation of a stress-responsive signaling cascade – e.g. by oxidative stress – has beneficial effects, e.g. in terms of inducing adaptation, it might be undesired to interrupt these processes by blocking the initial stress, i.e. by scavenging ROS. Such attenuation of adaptation was indeed observed in studies with rats and humans, where ascorbate supplementation decreased training efficiency, apparently due to preventing cellular adaptations to exercise [33, 34]. Similarly, exerciseinduced insulin sensitivity was decreased and the induction of ROS defense systems attenuated by vitamin C/vitamin E supplementation [35].

Another example of note is the potential link between antioxidant selenoenzymes and insulin signaling. Cytosolic glutathione peroxidase (GPx-1) is a selenoenzyme and major contributor to cellular reduction of hydrogen peroxide and other peroxides [36]. Interestingly, transgenic mice overexpressing GPx-1 developed insulin resistance and obesity [37] – features that have since also been identified in selenium feeding/supplementation studies [38]. As insulin signaling requires the generation of  $H_2O_2$  [39] (see also Chap. 8), both GPx and selenium supply, affecting GPx levels, are likely to interfere with insulin signaling, which was indeed demonstrated at a cellular level [40] (see Fig. 20.4a).

*Vice versa*, insulin controls the expression of the major plasma selenium transporter, selenoprotein P (SelP), which is required for selenium supply to extrahepatic tissues in order to allow for biosynthesis of selenium-dependent antioxidant enzymes, such as GPx [41, 42] (Fig. 20.4b): SelP expression is enhanced by FoxOs [43] and peroxisomal proliferator activated receptor-coactivator-1 $\alpha$  (PGC1 $\alpha$ ) [44], both of which are inhibited in insulin-exposed cells. Moreover, high SelP levels were found to be correlated with insulin resistance [45].



**Fig. 20.4 Selenium and insulin signaling**. (a) Signaling from insulin/insulin-like growth factor receptors (InsR, IGF1R) to the serine/threonine kinase Akt requires hydrogen peroxide formation. Scavenging  $H_2O_2 - e.g.$  by a glutathione peroxidase (GPx) – will interfere with proper signaling downstream of the insulin receptor. GPx levels are increased in cells exposed to selenocompounds or to selenoprotein P (SelP), which provides selenium to cells. (b) Insulin-induced activation of Akt will result in phosphorylation and inactivation of FoxOs. Selenoprotein P expression is controlled by FoxO transcription factors. (c) Hydrogen peroxide formation is required for insulin signaling. Mechanistically, this is currently thought to be through oxidative (but reversible) inactivation of negative regulators of insulin signaling, such as protein tyrosine phosphatases (PTP) or the lipid phosphatase PTEN

As discussed in Chap. 8, a mechanism for  $H_2O_2$  to affect insulin signaling is through inhibition of inhibitory phosphatases, such as protein tyrosine phosphatases (PTP), or the lipid phosphatase, PTEN (Fig. 20.4c).

From these data, it seems that selenium supplementation, by way of increasing SelP synthesis and release into circulation, could cause an enhanced generation of antioxidant selenoproteins in peripheral tissues, causing an interruption of insulin signaling, of carbohydrate metabolism and leading to symptoms of insulin resistance [46]. This would feed into the recent discussion linking high selenium intake to type II diabetes, which was based on epidemiological data surfacing in the late 2000s, suggesting that high plasma selenium is correlated with an increased chance of developing diabetes – a discussion that, upon addition of further studies and evaluation of all available epidemiological data, has slightly calmed down (see [47] for a recent review). Nevertheless, the effect of selenium and SelP on carbohydrate and lipid metabolism is obvious in cell culture studies

[46], and the identified control of SelP expression by insulin might thus be part of a regulatory circuit counteracting selenium saturation (and insulin resistance) of non-hepatic, peripheral tissues.

### 20.3.2 Antioxidants as Pro-oxidants

Depending on the redox status of the environment a redox-active compound may, in principle, react both ways, i.e. reduce or oxidize. This almost trivial statement explains how essential constituents of antioxidant systems can at the same time be pro-oxidants with adverse effects, if concentrations of these compounds are not properly controlled. Take iron and copper ions: these essential trace elements are components of antioxidative enzymes and defense systems, such as catalase and other heme peroxidases or Cu, Zn-superoxide dismutases. On the other hand, they may both contribute to the *generation* of ROS, e.g. through Fenton-type reactions of hydroperoxides with ferrous (Fe<sup>2+</sup>) or cuprous (Cu<sup>+</sup>) ions, resulting in the generation of hydroxyl or alkoxyl radicals. Also, these redox-active ions may undergo redox cycling to generate superoxide [48].

Similarly, certain "antioxidant" flavonoids facilitate the generation of ROS – a phenomenon described for such systems as brewed coffee – both in the cup and in urine after consumption [49, 50] – and also cell culture, where incubation of flavonoids in cell culture media – especially those rich in iron – results in significant concentrations of hydrogen peroxide [26, 51–53].

### 20.3.3 Adverse Non-redox Effects of Compounds Generally Perceived as Antioxidants

As multiple antioxidative strategies exist in tissues, the claim of a compound X being an antioxidant would have to be supported by the explanation of how this compound is an antioxidant. This explanation would have to answer whether X is an antioxidant only in cell-free TAC tests with no biological relevance whatsoever because it simply is not bioavailable. Or such an explanation could state that compound X is some bioavailable compound that – although it would not show up as antioxidant in TAC and other assays – in fact is essential to certain cellular antioxidative measures. Zinc ions, for example, are redox-inert in biological systems. Nevertheless,  $Zn^{2+}$  is an essential component of several enzymes involved in antioxidant defenses – at all levels, i.e. prevention/interception (Cu, Zn-superoxide dismutase), repair (e.g. DNA damage recognition and repair, for example through the Zn-containing transcription factor p53 or Zn-finger proteins in nucleotide excision repair) and adaptation (by stimulating metalregulatory transcription factor, MTF-1, or by stimulating stress-responsive antiapoptotic signaling; for review, see [54, 55]). Therefore, the frequent claim that Zn<sup>2+</sup> is an antioxidant carries at least some truth in that it contributes to cellular antioxidant defense systems. Despite its comparatively low overall toxicity [56], Zn, at high concentrations / doses, also has adverse effects – in part directly, such as neurotoxic effects [57], in part through secondary copper deficiency [56]. Like zinc, some compounds may be labeled "antioxidant" due to their indirect contribution to cellular antioxidant defense, e.g. by stimulation of cellular adaptation processes. Adaptation may occur through stimulation of Nrf2 signaling, which controls the expression of various protective enzymes (see Chaps. 8 and 9). However, in order to stimulate these adaptation processes, compounds need to have a certain reactivity in cells, e.g. alkylate thiols of crucial proteins – such as Keap-1, the central negative regulator of Nrf-2 signaling – and it is this very reactivity that may also elicit adverse effects. Accordingly, reports on biological effects of the consumption of phytochemicals with antioxidative properties vary. Prominent examples include glucosinolates from brassica vegetables, such as broccoli or kale: biological effects range from genotoxic and mutagenic [58, 59] to clearly chemoprotective [60]. Glucosinolate metabolites these effects are, at least in part, ascribed to are isothiocyanates and indole derivatives, stimulators of Nrf2 signaling and aryl hydrocarbon receptor (AhR)-dependent signaling, respectively [60].

Further potentially adverse non-redox effects of "antioxidants" may be exemplified referring to flavonoids and include (i) their aforementioned phytoestrogenic activity (both at the level of stimulating estrogen receptor activity and inhibiting endogenous estrogen metabolism), which may be also considered as disruptive of endogenous endocrine circuits [61] and (ii) their topoisomerase inhibitory activity [62, 63]. Topoisomerase poisoning may lead to accumulation of DNA damage; despite inhibiting topoisomerases, however, the DNA damaging effects of bioflavonoids appear to be comparatively weak [64].

Lastly, the adverse non-redox effect of compounds – even if stimulating potentially protective antioxidant adaptation reactions – may be due to the signaling pathway activated: even signaling effects generally perceived as beneficial or protective do of course have their undesired sides. For example, Nrf2 stimulation, if constitutive, may confer antitumor drug resistance [65, 66]. Similarly, FoxO transcription factors are modulated by ROS and xenobiotics [67–69], and FoxOs, in turn, modulate the expression of antioxidant proteins and of other proteins involved in stress response [43, 68]. This would render FoxO transcription factors excellent targets of chemoprevention, aiming at an upregulation of endogenous defense mechanisms against noxious stimuli. However, such an approach is based on the assumption that stimulation of FoxOs is beneficial – which, of course, cannot always be the case, as FoxO transcription factors may also stimulate the production of pro-apoptotic factors.

# 20.4 Conclusion: Modulation of Signaling as an Antioxidative Approach?

ROS-induced adaptation reactions are initiated by oxidative damage that has escaped the cellular repair machinery. Antioxidants acting to prevent this damage will deprive the cell of the potential to stimulate signaling processes that may result in an adaptive response supporting stress resistance. One might suggest, therefore, that a novel antioxidative approach might exploit the fact that signaling cascades are stimulated by oxidative stress and attempt to direct theses cascades to result in a desired outcome – using pharmacologic modulators of signaling cascades. In line with this, numerous nutritional and environmental chemicals with "antioxidative" or beneficial effects have very limited bioavailability and reach low *in vivo* concentrations. It is suggested that they may act as perceived antioxidants not by directly scavenging ROS, but rather in an indirect manner, i.e. by modulating cellular signaling processes – which would be achievable with only minute amounts of active agent.

Although several stress-induced signaling cascades mediating adaptive responses are known that may be suitable as potential targets for chemopreventive approaches (including cascades affecting Nrf2 or FoxO transcription factors), measures will have to be identified to direct signaling to a desired outcome. In parallel, some of the adverse consequences or side effects mentioned above that result from that very modulation of the signaling cascade of interest will have to be avoided.

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# Chapter 21 Prevention of Age-Related Diseases: Effects of Antioxidant Supplements

Wilhelm Stahl

## 21.1 Introduction

"Antioxidants fall from grace! The popular dietary components may not do any good, and may actually harm". This information was widely disseminated following an article on the home page of Newsweek in January 2011. The story refers to results of several meta-analyses and the outcome of some large-scale intervention trials which failed to demonstrate beneficial effects of supplementation with anti-oxidants for the prevention of major diseases such as cancer and cardiovascular disorders. It is the intention of the present article to illustrate the basic scientific concepts underlying the design of these studies, discuss the interpretation of the results and evaluate the impact of the outcome on future research in the field of dietary antioxidants. A number of compounds were investigated for disease preventing properties, including flavonoids, ubiquinone, selenium, thiols or plant extracts of a complex composition. But in a majority of the trials focus was on the popular antioxidants vitamins E and C and the provitamin A carotenoid  $\beta$ -carotene. Sufficient data for reliable meta-analyses were available for these compounds.

All substances are considered to be "classical" antioxidants and comparable from the biochemical mechanisms supposed to mediate health effects. However, most intervention studies included in the evaluation are different from design and thus difficult to compare. Supplements used were from various sources, different structure and applied over a wide dose range. In some of the studies mixtures of two or sometimes three different antioxidant compounds were applied not always with the single constituent as a control. Such differences in experimental detail are likely relevant for interpretation of single studies but will not be addressed generally in

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this paper. A detailed analysis of single intervention studies regarding design and outcome is beyond the scope of this article. Finally it should be noted that the focus here will be on cancer, cardiovascular diseases and cataract since the majority of data pertain to these disorders.

#### 21.2 Scientific Background

In order to understand and evaluate the design of the intervention studies mentioned above it is important to realize the scientific background underlying the development of the concepts. A major aspect was the interpretation of the principle of oxidative stress defined in the 90s as an "imbalance between oxidants and antioxidants in favor of the oxidants, potentially leading to damage" [84]. Reactive derivatives of molecular oxygen are formed in the human organism and the endogenous antioxidant defense system may be inadequate to scavenge them completely. Biologically important molecules are damaged by oxidation reactions resulting in impaired function or loss of activity [38]. Such damage may accumulate and contribute to the development or progression of degenerative diseases. Antioxidant defense may be fostered by increasing dietary (exogenous) antioxidants and preventive effects can be achieved [85].

Several major sources for the generation of reactive oxygen molecules were identified: leakage of the respiratory chain, free transition metal ions, UV-radiation, X-rays, redox-cycling compounds, or enzymatic redox processes. Generated molecules include either oxygen-centered radicals like the superoxide anion, peroxyl radicals and the hydroxyl radical or non-radical reactive intermediates, e.g. singlet oxygen, hydrogen peroxide and organic hydroperoxides. Such reactive oxygen species (ROS) are inevitable byproducts of aerobic life and the adaptation to oxygen-dependent energy supply [48, 83]. Due to their usually short half-lives in biological systems and limited technology it was and still is difficult to determine ROS (and the effects of antioxidants) directly in cells, tissues or complex organisms [4, 59, 97]. In-vitro data, although with inherent limitation, provide evidence that ROS are scavenged by dietary antioxidants [5, 44].

Vitamin C is a powerful water-soluble antioxidant of low toxicity present in high concentrations in many tissues. Upon radical scavenging ascorbate is oxidized to dehydro-ascorbate, which is enzymatically recycled. Ascorbate was shown to be effective against the superoxide radical anion, hydrogen peroxide, the hydroxyl radical, water-soluble peroxyl radicals and singlet oxygen. There is evidence from invitro studies that vitamin C regenerates tocopherol from the tocopheroxyl radical, a process allowing for the transport of a radical load from a lipophilic to an aqueous compartment where it is taken care of by efficient enzymatic defense systems [26, 32, 66]. It should be noted, however, that ascorbate may also act as a prooxidant and its major biological function is that of a cofactor of oxidoreductases [17].

The term "vitamin E" encompasses several structurally different compounds, basically tocopherols and tocotrienols, with  $\alpha$ -tocopherol as the most prominent in the human diet. The only naturally occurring form is the RRR optical isomer, but

several other stereoisomers are present in supplements prepared with synthetic  $\alpha$ -tocopherol. Vitamin E is thought to be the most efficient inhibitor of lipid oxidation, scavenging lipid peroxyl radicals in membranes and lipoproteins. The antioxidant activity of E vitamers is due to the redox properties of the chromane ring. Several vitamin E oxidation products have been described, some of which also exhibit antioxidant activity [19, 68]. A debate on the relevance of antioxidant properties in relation to the biological function of this vitamin is ongoing [6, 95].

β-Carotene and almost all other dietary carotenoids efficiently quench singlet molecular oxygen (<sup>1</sup>O<sub>2</sub>), excited triplet state molecules and inactivate peroxyl radicals. Singlet oxygen quenching by carotenoids involves the transfer of excitation energy from  ${}^{1}O_{2}$  to the carotenoid, resulting in ground state oxygen and an excited triplet state carotenoid. The energy is dissipated between the excited carotenoid and the surrounding solvent to yield the ground state carotenoid and thermal energy. In this type of physical quenching the carotenoid remains intact and can undergo further cycles of singlet oxygen quenching. The rate constants for the reaction are in the range of  $10^9 \text{ M}^{-1} \text{ sec}^{-1}$ , i.e. near diffusion control.  $\beta$ -Carotene is among the most efficient natural <sup>1</sup>O<sub>2</sub>-quenchers and its high quenching activity is attributed to the system of conjugated double bonds present in the core of the molecule [14, 53, 54, 90]. Prooxidant actions of carotenoids and other antioxidants have been addressed and a possible interference of antioxidant compounds with signaling pathways was discussed [72, 102]. Although the definition of oxidative stress and knowledge on its implication in cellular signaling developed further within the next decades, oxidative damage to DNA, lipid and proteins was still assumed to play a major role in the pathogenesis of degenerative diseases.

Dietary antioxidants are embedded in a network of antioxidant defense that comprises further small molecules such glutathione and powerful enzymes and proteins [21]. The importance and contribution of antioxidant vitamins within this network is a matter of debate also in context with the basic concept of intervention studies to foster antioxidant defense in order to prevent damage.

# 21.3 Concept

From a chemical point of view, almost all molecules present in tissues are prone to oxidative modification. The biopolymers, DNA and proteins, as well as polyunsaturated fatty acids and glucose as the major carbohydrate were at the center of research. In a reaction with ROS, the molecules are chemically modified, which leads to a loss of function or the generation of chemically reactive secondary products like epoxides, peroxides or aldehydes [77, 86].

Lipid peroxidation comprises a sequence of reactions initiated by the abstraction of a hydrogen atom, resulting in the oxidative deterioration of polyunsaturated fatty acids. It is characterized by the formation of lipid peroxyl radicals, which are sufficiently reactive to propagate a chain reaction with neighboring polyunsaturated fatty acids. Lipid peroxyl radicals and lipid hydroperoxides decompose into intermediates and end products, including malondialdehyde and various kinds of hydroxy-alkenals that are biologically active, toxic, or mutagenic. Aldehydes and epoxides are prone to react with functional groups of proteins or DNA and modify these macromolecules [30, 67].

Upon extended lipid peroxidation, cellular membranes are destroyed, leading to a loss of compartmentalization in cells and finally to cell death. Low density lipoproteins (LDL) are targets of lipid oxidation and, depending on the nature of the prooxidant, various modifications of the lipid core or of the protein portion (apolipoprotein B-100) may occur. According to the oxidative modification hypothesis the process of LDL oxidation is associated with atherogenesis, in particular the formation of atherosclerotic plaques [91]. Oxidized LDL particles exhibit atherogenic activities, including chemotaxis for T-lymphocytes or macrophages, inhibition of the motility of tissue macrophages, cytotoxicity towards cells of the arterial wall, or induction of proinflammatory genes. Oxidized LDL particles are substrates for the scavenger pathway in which foam cells are generated as a key event in the formation of atherosclerotic plaques. Although the chemical and biochemical mechanisms involved in the conversion of LDL to its pathogenic modification are not fully understood, lipid peroxidation is thought to play an important role. Vitamin E and carotenoids are efficient lipophilic antioxidants transported in the blood as constituents of lipoproteins. Thus, it was suggested that dietary supplementation with these compounds may improve the resistance of LDL against lipid oxidation and prevent or delay the formation of atherosclerotic lesions and prevent cardiovascular diseases [16, 46, 74, 92].

Mutagenesis and carcinogenesis are closely related processes where mutations in somatic cells initiate and drive the complex and multi-step process of cancer formation. The initial event of a mutation is the generation of damaged and/or modified DNA which occurs spontaneously or as a result of exposure to a mutagenic agent. ROS or products formed in reactions with ROS are mutagenic agents and may chemically modify DNA bases or generate DNA strand breaks. Although powerful enzymes efficiently repair most of the damage, some repair is incorrect or the presence of chemically modified DNA bases leads to incorrect replication, thus manifesting a mutation. Oxidized DNA bases have been identified and characterized after exposure of cells and tissues to prooxidant conditions. Several molecular mechanisms were postulated such as mismatch mutations due to the formation of 8-oxo-guanosine, a frequent oxidative modification of DNA. Consequently, it was suggested that dietary antioxidants may prevent oxidation of DNA, mutations and cancer [3, 23, 50, 76].

Proteins are multifunctional molecules and uncontrolled modification usually results in loss of function or impaired biological activity. Some functional groups in the side chain of amino acids are prone to oxidative modification, including cysteine, lysine, methionine and others. The biological effects of oxidative modifications on protein-dependent signaling are a current topic in oxidative stress research. Earlier studies addressed the impact of oxidative modifications on the function of structural proteins and long-term effects on specialized tissues. Some lens proteins persist with a long half-life and oxidative damage may accumulate over time. Crystallins, for example, contribute to the structural organization of the lens, which is important to maintain its transparency.  $\alpha$ -Crystallin is a small chaperone protein, which binds selectively to misfolded proteins to prevent them from aggregation, thus helping to maintain the optical clarity of the lens. Oxidative and other modifications may accumulate and influence transparency, finally leading to the formation of protein aggregates and cataract. Especially photooxidative stress has been suggested to play a major role in cataractogenesis and oxidatively modified proteins were isolated from diseased lenses. Water-soluble antioxidants such as vitamin C may prevent oxidation of lens proteins and protect against cataract or delay the onset of the disease [8, 93, 98].

Based on the concept of oxidative damage as an initial event in the pathogenesis of several degenerative disorders the intervention with high doses of dietary antioxidants was developed as a possibly cheap and efficient strategy of prevention or treatment and studied in a number of large-scale intervention trials.

### 21.4 Intervention Trials

Cardiovascular Diseases Early epidemiological studies provided evidence for an inverse association between plasma vitamin E and mortality from ischemic heart disease. Supplementation with vitamin E in female nurses was associated with a decreased risk for coronary heart diseases and similar results were reported from a study with male health professionals. Further studies also revealed an inverse association between the highest vs. lowest categories of vitamin E intake and the risk of coronary heart disease and mortality, fostering the idea of a beneficial effect of vitamin supplement use and ischemic heart disease [34, 51, 55, 62, 79]. Based on these apparently convincing data a number of randomized controlled trials (RCT) were initiated. However, until now the results have been disappointing. Several meta-analyses of RCT and systematic reviews of existing data did not support the claim [29, 96]. In a meta-analysis, 19 clinical trials with more than 135,000 participants were included. Here, vitamin E supplementation was associated with an elevated risk of high-dose vitamin E on total mortality [63]. Thus, there is currently no evidence to support the recommendation of vitamin E supplementation at high doses in the prevention of cardiovascular disorders. However, the contradiction between results from observational and randomized controlled trials is not resolved.

As with vitamin E, first evidence for a possible implication of carotenoids in the prevention of cardiovascular diseases was derived from studies that showed that higher intakes of fruit and vegetables rich in carotenoids were related to a decreased risk. However, despite the evidence from epidemiological studies randomized intervention trials failed to demonstrate a protective effect. In an early meta-analysis of 8 RCT of  $\beta$ -carotene vs. placebo,  $\beta$ -carotene supplementation was related to a small but statistically significant increase in cardiovascular diseases of about 10 %; also, overall mortality was increased in the verum group [96]. More recent meta-analysis

proved that  $\beta$ -carotene, alone or in combination with vitamin A and tocopherol, significantly increased overall mortality from ischemic heart disease [10, 11]. It was concluded that supplementation of  $\beta$ -carotene at high dose levels is not recommended. Again, the discrepancy between epidemiological data on the intake of a carotenoid-rich diet and supplementation is not resolved. Increasing the consumption of carotenoid rich fruit and vegetables is still recommended (e.g. 5-a-day campaign).

In a number of prospective studies, the role of vitamin C (dietary sources or supplements) on the incidence of cardiovascular disorders was studied. A pooled analysis of 9 cohorts showed that the intake of supplemental vitamin C (700 mg/d) was related to a lower incidence of about 25 % [52]. A meta-analysis including 15 studies, with more than 7,000 participants found that supplement use of vitamin C had no significant correlation with the risk for CHD [101].

Overall, there is no conclusive evidence to recommend the use of high doses of antioxidants for the prevention of CVD [65].

Cancer As with other degenerative diseases, the consumption of a diet rich in fruits and vegetables was associated with a lower incidence of several types of cancers [75, 76]. Because fruits and vegetables provide all types of antioxidant compounds and elevated levels of antioxidants in blood were correlated with a decreased risk for cancers several large intervention trials were initiated to prove this correlation. Among the first large scale intervention studies was the so called Linxian study performed in China, which included about 30,000 participants. In this study a decrease in cancer mortality was found compared to control in the group which received a combination of  $\beta$ -carotene, vitamin E and selenium [12, 56]. However, several other studies failed to confirm this result. No effect of a supplementation with  $\beta$ -carotene on cancer risk was revealed in the Physicians' Health Study (USA) with more than 22,000 male physicians, and cancer mortality was also not altered according to the results of the MRC/BHF heart protection study (UK) with 21,000 patients suffering from cardiovascular disease or diabetes and taking antioxidants (vitamin E, vitamin C and  $\beta$ -carotene) over a period of 5 years [40, 41]. No effect of β-carotene and vitamin E supplementation on cancer was also determined in the Women's Health Study (WHS) performed in the USA including about 40,000 female participants.

The Alpha-Tocopherol Beta-Carotene Trial (ATBC-study) was performed in Finland and included about 30,000 male smokers that were supplemented with tocopherol or tocopherol plus  $\beta$ -carotene. No decrease of lung cancer incidence was found but unexpectedly in the group that received  $\beta$ -carotene alone lung cancer risk was elevated by about 17 % [2, 94]. This unexpected result was confirmed by another study from USA, the " $\beta$ -Carotene Retinol Efficiency Trial" (CARET). Here about 18,000 smokers and asbestos workers ingested  $\beta$ -carotene and retinyl palmitate. After an interim analysis for the incidence for a risk of lung cancer the study was stopped [69, 70, 71].

Accordingly, no effect of supplementation with  $\beta$ -carotene was calculated in two meta-analysis including nine or 20 randomized trials, respectively. However, the

incidence of lung and stomach cancer was significantly elevated by intervention with the carotenoid [11].

In the French SU.VI.MAX study, a combination of  $\beta$ -carotene, vitamin E, vitamin C, selenium and zinc was applied. Here, a significant decrease in cancer incidence was found in men but not in women and the preventive effect was only found in male participants with a low status of  $\beta$ -carotene and vitamin C at the beginning [11, 42]. However, this result did not persist in the 5 year follow up [11, 43].

*Cataract* Basic research and observational studies suggest that dietary antioxidants including ascorbate, carotenoids or vitamin E may contribute to the protection of the lens against oxidative damage and thus interfere with the initiation and promotion of cataract [31]. Again, results from randomized, controlled intervention studies led to conflicting results [18]. In most cases, no statistically significant effects on clinical endpoints were observed. This result was confirmed by a recent meta analysis compiling data from nine intervention trials with more than 117,000 participants evaluating primary end points such as diagnosis of cataract or lens extraction due to cataract formation [60]. It was concluded that the recommendation of an intake of the above-mentioned antioxidants beyond daily allowances should be weighed carefully.

In contrast to supplementation studies, evidence still suggests that consuming more fruits and vegetables contributes to the prevention of diseases [13, 49].

## 21.5 Explanations

Although most of the large-scale intervention trials with antioxidants failed to show an effect on the incidence of cancer, CVD and cataract, there is still an unsolved contradiction to the results from observational studies showing that an increased intake of antioxidants with diet and elevated blood levels of antioxidants are related to a lower risk. The discussion on biochemical mechanisms underlying this controversy is ongoing and a number of experimental approaches for single compounds have been made. It is beyond the scope of this article to present all aspects in detail, however, there have been basic considerations why intervention trials failed or even showed adverse effects [24, 35, 61].

*Compounds* Most of the large-scale studies performed until now were focused on three major compounds with superior antioxidant properties,  $\beta$ -carotene,  $\alpha$ -tocopherol and ascorbate, alone or in combination with other dietary components. Due to limited resources, an array of other secondary plant constituents including further carotenoids, other E-vitamers, or selected polyphenols were not investigated. It was speculated that high levels of the selected major antioxidants in blood are just indicative of a high intake of fruit and vegetables in general and that the observed health effects are related to biological activities of other plant-based molecules [7, 99]. Those compounds may either act as antioxidants or reveal other biochemical mechanisms of action [47, 57]. Flavonoids may serve as an example

with possible (but debated) antioxidant activities but also selected pharmacological properties not related to antioxidant activity [45]. Epicatechin was shown to reveal vasodilatory effects. Indirect antioxidant activity has been attributed to compounds which stimulate secondary (enzymatic) defense systems against ROS [37]. In most of the studies either single compounds or combinations of a key component with 2-3 other antioxidants were used for supplementation. With dietary intervention (e.g. "5 a day"), however, a complex mixture of dietary constituents is applied and additionally macronutrients (carbohydrates, protein, fat) and fiber are provided. Especially fat and fiber affect the bioavailability of lipophilic antioxidants, as shown for carotenoids and vitamin E [15]. Some plant components including isothiocyanates (glucosinolates) or  $\alpha/\beta$ -unsaturated carboxy derivatives (chalcones) modulate the metabolic detoxification system and may influence metabolism and half-life of bioactive substances [22, 100]. In vitro studies provide evidence that antioxidants act synergistically. Mixtures of carotenoids exhibited a higher antioxidant activity than single compounds. Supra-additive effects were attributed to mixtures containing lycopene or lutein [39, 89]. It was speculated that the superior protection may be related to specific positioning of different carotenoids in membranes. Cooperative interaction of antioxidants was discussed regarding regeneration e.g. of tocopherol at the expense of vitamin C in relation to a translocation of the oxidative load from lipophilic to hydrophilic compartments [66].

Doses In most of the intervention trials discussed above high doses of the antioxidants were applied. Compared to the recommended dietary intake or amounts available from a normal diet doses by far exceeded physiological levels. In some of the studies the concentrations of the antioxidant in blood were up to 10-fold increased over normal. For example, see Table 21.1. In most  $\beta$ -carotene intervention trials mean  $\beta$ -carotene blood levels at baseline were around 0.3 to 0.5  $\mu$ M, which is in accordance with values reported for the general population. After supplementation,  $\beta$ -carotene dominated the pattern of dietary antioxidants and the organism was "flooded" with the compound. Adverse effects were observed in studies with the highest blood levels of  $\beta$ -carotene after supplementation; i.e. the ATBC (5.59 µmol/L) and CARET study (3.91 µmol/L). In the studies with no effects, blood levels were below those of the latter. Interestingly, in the Linxian study, which revealed preventive effects on cancer incidence, mean blood levels of  $\beta$ -carotene were quite low at the beginning and mean level at the end of the study was only 1.59 µM. Thus, it has been suggested that - as with many other compounds - there is an optimal level to achieve health benefits. This idea is fostered by in vitro findings which demonstrate that the antioxidant activity of carotenoids is dose-dependent and prooxidant effects are observed at high doses [28, 72, 87, 102]. The reasons are not well understood but likely related to the chemistry of antioxidants in the presence of oxygen. In vitro-studies show that under conditions of high oxygen tension carotenoids exhibit prooxidant activities. Increased markers of lipid oxidation (e.g. MDA) were determined when  $\beta$ -carotene was

	Blood level	Blood level	Dose	
Study	$\beta$ -carotene (µmol/L)	β-carotene (µmol/L)	β-carotene (mg/day)	Outcome
MRC/BHF HPS [40]	0.32 (control)	1.22	$20 \text{ mg }\beta$ -carotene	5 years; n >20,000
			+600 mg vitamin E	No effect on cancer incidence
			+200 mg vitamin C	
Linxian [12]	0.11	1.59	15 mg β-carotene	5 years; n >29,000
			+30 mg Vitamin E	Decreased cancer incidence
			+50 µg Selenium	
PHS [82]	0.57	2.19	50 mg β-carotene (every 2 days)	12 years; n >22,000
				No effect on cancer incidence
CARET [69,70]	0.32	3.91	30 mg mg β-carotene	4 years; n >18,000 smokers asbestos workers
			+25,000 IU Vitamin A (Retinylpalmitate)	Increased risk for lung cancer
ATBC [1] [2]	0.32	5.59	20 mg β-carotene	6 years; n >29,000 smokers
				Increased risk for lung cancer
SU.VI.MAX	0.75 (f)	1.71 (f)	6 mg mg β-carotene	7 years; n >13,000
[42]	0.46 (m)	1.00 (m)	+30 mg vitamin E	Decreased cancer incidence in men*
			+120 mg C	
			+20 mg Zn+100 μg Se	

Table 21.1 Blood levels of β-carotene (µmol/L) in intervention trials – effect on cancer incidence

\*Effect not confirmed in postintervention follow-up [43]

exposed to oxidizing conditions at high levels of oxygen. Reactions of the first carotenoid radical adduct with molecular oxygen are thought to be responsible for prooxidant properties under these conditions.

*Network* The antioxidant network comprises exogenous and endogenous lowmolecular weight compounds but also efficient enzymes scavenging peroxides and the superoxide radical. The activity of these enzymes is quite high and they are (to some extent) constitutively expressed. Their contribution to the overall antioxidant defense may have been underestimated and accordingly the importance of dietary antioxidants might have been overestimated [88]. In contrast to enzymes some dietary compounds are destroyed when acting as an antioxidant. Interaction of a carotenoid with a radical finally results in bleaching; i.e. degradation of the molecule and loss of the conjugated system of double bonds required for chemical reaction with a radical. Regeneration of vitamin E by vitamin C (see above) has not been demonstrated yet to be relevant in a living organism. At optimal doses dietary antioxidants may complete and support the basal defense but may also interfere with the system when they develop prooxidant properties at high dose levels (see above).

Signaling Increasing knowledge reveals the implication of reactive oxygen molecules like hydrogen peroxide in cellular signaling. Taking this into account, the term oxidative stress has been redefined as "an imbalance between oxidants and antioxidants in favor of the oxidants, leading to a disruption of redox signaling and/or molecular damage" [88]. Cellular redox sensors trigger gene expression or posttranslational modification of proteins and can be addressed by pro- and antioxidant reactants. An understanding of these processes for the situation in vivo is developing but yet far from being accomplished. However, it is obvious that antioxidants may interfere with redox signaling when the compounds are present in high amounts [20]. Interference might be due to undesired scavenging of signaling molecules preventing the formation of a gradient or oxidation of sensitizing functional groups in redox-regulated proteins. Recently, blood samples from the ATBC study were reanalyzed to determine metabolic profiles. The data suggest that cytochrome P450 enzymes of the phase I metabolizing system were induced, a mechanism that may play role in the biochemical events related to the increased cancer incidence [64].

*Hormesis* The term hormesis describes the concept that exposure of an organism to a low dose of a toxic agent stimulates defense systems and, in the long run, contributes to improved health or increased stress tolerance. It has been first described when epidemiological data revealed that low dose exposure to radioactive irradiation later increased the resistance against higher doses of X-rays [9, 33, 73]. In an oxidative stress and antioxidant defense context, the generation of reactive oxygen intermediates from mitochondria was suggested to play a similar role [80, 81]. The term mitohormesis (mitochondrial hormesis) was coined to describe an adaptive process related to the extension of lifespan or health-promoting effects of glucose restriction and physical exercise. It is beyond the scope of this article to discuss the idea in detail (see also Chap. 8 for further discussion). However, redox sensitive pathways require a basal oxidative load of a cell to modulate sensitive pathways with redox active molecules, and the application of large amounts of dietary antioxidants may therefore interfere.

*Concept* Despite a solid theory based on chemical, biochemical and molecular studies the role of oxidative stress in the pathogenesis of degenerative diseases has been challenged as a general concept. Especially the lack of direct evidence for the implication of ROS and the importance of ROS scavenging by dietary antioxidants are still debated.

At present also a generalized debate on the impact of population-wide diet changes in order to reduce cardiovascular disease and cancer has been initiated, and the evidence for dietary advice has been generally questioned. The effects of providing dietary advice to achieve sustained dietary changes or improved cardiovascular risk profile among healthy adults were assessed in a meta-analysis. The authors concluded that "dietary advice appears to be effective in bringing about modest beneficial changes in diet and cardiovascular risk factors over approximately 12 months, but longer-term effects are not known" [78].

#### 21.6 Biomarkers

Lack of direct evidence for the generation of ROS and the disappointing results from intervention studies led to the application of the biomarker concept adapted to the field of oxidative stress. This concept comprises the determination of suitable and valid markers indicating oxidative damage in target molecules. A series of markers and techniques have been established and evaluated in large inter-laboratory studies investigating DNA, lipids and proteins as target molecules. Although the biomarker concept has limitations and its applicability is controversially discussed, studies with suitable biomarkers as readouts are at present the basis for the acceptance of a health claim for antioxidant dietary constituents [25, 36, 58].

It is generally believed that significant oxidative modification of the target molecules (DNA, proteins, lipids) is potentially harmful and that a decrease in the extent of oxidative modifications may represent a beneficial physiological effect [27]. A valid marker should be able to measure accurately a specific oxidative modification of the biologically relevant target molecule. A number of valid markers have been identified, several supportive markers to foster evidence are also accepted. For substantiation of a health claim a biomarker of oxidative damage must be determined in human studies measuring its level in plasma, urine, blood cells, lipoproteins. The biomarker approach may be helpful to use and finally evaluate small size human intervention studies with dietary antioxidants to prove their activity. They may also provide a suitable tool to overcome problems related to heterogeneity in large-scale studies.

## 21.7 Outlook

The idea that a continuous supplementation with dietary antioxidants at high doses inhibits the development of degenerative diseases is not supported by most largescale intervention trials. Since the reasons are not yet clear, new approaches are required to test the general hypothesis that antioxidant constituents in the diet play a role in the health benefit associated with consumption of a selected diet (e.g. rich in fruit and vegetables). This implies research on questions related to the identification of the bioactive compounds and their mechanism of action. The adverse effects observed in some of the studies demand also for basic scientific work to identify underlying mechanisms of toxicity. Redox-dependent signaling plays an important role in the cellular processes, and disturbances in signaling impair biological functions. New methods to address these aspects have to be developed for application in human intervention studies. The available set of biomarkers must be refined and extended also for signaling aspects.

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# Chapter 22 The Neural Progenitor Cell (NPC) Niche in the Adult Brain Provides a Target for Neurotoxicity: A Putative Adverse Outcome Pathway for ROS-Induced NPC Dysfunction with Higher Sensitivity During Aging

**Ellen Fritsche** 

# 22.1 The AOP Concept in the Context of Risk Assessment Procedures

Hazard identification for the purpose of human risk assessment is still mainly performed *in vivo* in animals. However, due to the resource-intensity of this approach (time, money, space) there is only sufficient information on approx. 2–3 % of the 100,000 compounds currently present in consumer products [1]. This lack of consumer-relevant information has initiated the world-wide largest safety assessment approach for chemicals: the EU regulation REACH (Registration, Evaluation, Authorisation and Restriction of Chemicals). Generating data to comply with the REACH legislation will cost € 8.8 billion using today's mainly animal-based tests [2]. In addition to the excessive resource requirements for filling existing toxicological data gaps with animal tests, human hazard prediction by using animals is limited due to species differences in toxicokinetics and –dynamics [3]. For example, 40 % of the chemicals that irritated the skin of rabbits were found not to be irritants in the skin 'patch test' in humans [4] leading to exclusion of useful compounds. These limitations of present in vivo testing and ethical concerns with excessive performance of animal experiments coupled with the lack of data for thousands of chemicals in the human chemosphere has caused a paradigm shift in current toxicological testing strategies [5, 6]. This shift proposed a change from primarily *in vivo* animal studies to human-relevant in vitro assays, in vivo assays with lower organisms, and computational modelling for toxicity assessments. It is anticipated that

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such 'alternative' approaches cannot *per se* substitute whole organism responses to chemicals. Therefore, there is a current effort on both sides of the Atlantic to place results from alternative testing strategies into a framework, which facilitates understanding of complex biological systems and the toxicity pathways that result in adverse outcomes (AOs) [7, 8]. This framework is called the adverse outcome pathway (AOP) concept and provides a tool for a knowledge-based safety assessment that relies on understanding a molecular initiating event (MIE), in which a chemical interacts with a biological target, followed by a sequential series of measurable key events (KEs), which are cellular, anatomical and functional changes in biological processes, that ultimately result in an AO manifest in individual organisms' and populations' toxicity (Fig. 22.1).

Thereby, the MIE is the very first interaction of a compound with cellular macromolecules initiating consecutive KEs, which are in the end responsible for the AO. This could be e.g. binding to a receptor or direct interaction with other cellular proteins, lipids or ribonucleic acids. KEs in contrast are reactions of cells, tissues and organs towards an initiating stimulus like altered gene expression or modified cellular function. The AO in the end is defined as adversity on the organism and/or population level. To make this concept applicable, potential AOPs have to be posed into a quantitative framework relating exposure to the adverse outcome.

In support of the AOP concept, in 2012 the OECD launched the AOP Development Program. The OECD guidance document and template for developing and assessing AOPs aims to ensure consistency in approach and compliance with AOP standards related to content, structure and presentation [10]. This tool is applicable for safety assessment of chemicals as well as for risk assessment of other environmental exposure scenarios like ionizing and non-ionizing radiation and particulate matter. In the safety sciences, a number of institutions are involved in the evolution of risk assessment approaches: authorities (regulation), industry (characterization of toxicity), universities (mechanisms of action), and contract institutes (compilation, testing) [11]. The re-thinking process in the safety sciences favouring human-relevant methodologies parallels with technological achievements and causes accelerating increase in knowledge about mechanisms underlying adverse outcomes. This situation implies an urgent demand for appropriate communication between the different stakeholders and partners mentioned above. This was recently also recognized by regulatory agencies in Europe and North America [12].



Fig. 22.1 The Adverse Outcome Pathway (AOP) concept causally linking a molecular initiating event to adverse outcomes on the cellular, organ, organism and population level (Modified from [9])

## 22.2 AOPs for Neurotoxicity

The AOP concept had initially been developed for assessment of ecotoxicological hazards and risks [7]. Meanwhile, the application of this framework has been broadened to cover a few more exposure scenarios including skin sensitisation and domoic acid effects on neuronal signalling [8, 13]. AOP development e.g. for skin sensitisation is a relatively straightforward process due to the common chemical property of skin sensitizers: most of them are electrophilic compounds. Because each MIE triggers an individual AOP, scenarios with numerous MIEs prompt plentiful AOPs. In case of neurotoxicity, such a case is given. This is for one due to the broad range of physico-chemical properties that neurotoxicants possess ranging from metals to all kinds of receptor modulating compounds. Second, the brain offers a large variety of targets, which can be affected by noxae: endothelial cells, astrocytes, oligodendrocytes, neurons with the different neuronal subtypes expressing a variety of neuronal receptors/transporters, neural progenitor cells (NPCs) and microglia. These targets are not equally distributed throughout the brain, but certain proteins/receptors are expressed predominantly in certain brain areas. On the organ level, these structures form functional units, which can also be targets of compounds like the blood brain barrier (BBB), neuronal networks consisting of synapses formed by neuron-glia units, myelinated neurites and neuron-microglia interaction. Thereby, special attention has to be given towards susceptible life stages like development and aging. In addition, inter-species differences reported for the expression or function of some proteins in brain complicate the issue. For example, thyroid hormone (TH) transporters are expressed differently on the surface of mouse and humans brain cells leading to the creation of mouse disease models, which do not resemble human pathology [14]. As another case, TrkB (Tyrosine kinase receptor B) agonists cause opposite effects on food intake and body weight in primates and rodents [15]. Similar to these two examples, there is a general lack of understanding of the MIEs for most neurotoxins that are causally responsible for AOs at the different life stages. Although the relationship between developmental lead (Pb<sup>2+</sup>) exposure and adverse cognitive outcomes in children is well described [16], the initial molecular interactions between Pb<sup>2+</sup> molecules and cellular targets that are causatively linked to adverse cognitive outcomes, like loss in children's IQ, are still not well understood. Therefore it is of mutual interest to increase knowledge on molecular and cellular effects of chemicals causing AO of the nervous system. The AOP approach will help with this ambitious endeavour by first creating putative AOPs for neurotoxicity by extracting existing knowledge generated over the last decades from the available literature [17]. Second, knowledge gaps within putative AOPs have to be identified. These gaps will be filled by experimental data eventually allowing generation of full AOPs taking modified Bradford-Hill criteria [18] into consideration. Eventually, as biology does not follow a linear function, AOP networks will be created helping to understand molecular integration of initiating and key events within the nervous system at different levels of complexity. Publication of the AOP Wiki (http://aopwiki.org/) will greatly facilitate this approach by enabling eased international collaboration on individual AOPs via this Web platform.

#### 22.3 Putative AOP on ROS-Induced NPC Dysfunction

Adult neurogenesis of hippocampal neural progenitor cells (NPCs) takes place in human brains up to old age [19] and contributes to brain function in the adult mammal including humans [20, 21]. During the physiological process of aging, hippocampal NPC function declines [22–26] correlating with a decline in learning and memory tasks [23, 26–35]. Investigating adult neurogenesis in rodents *in vivo* has been very valuable for linking NPC function with AOs. However, the extent and the mechanisms responsible for decreasing neurogenesis with age between rodents and primates do not necessarily follow the same paths [27, 36] raising the need for studying specifically human signalling involved in age-related loss of NPC function.

Oxidative stress contributes to loss-of-function during NPC aging [37]. Thereby, the intracellular redox state seems to govern cell fate during differentiation as an oxidized intracellular environment favours glial over neuronal differentiation of subgranular zone (SGZ) neural stem cells [38]. Hence, increased ROS generation might influence NPC proliferation, differentiation and fate determination [37].

# 22.3.1 The Molecular Initiating Event (MIE)

The individual MIEs prompting this proposed AOP on reduction of adult neurogenesis are binding of redox cycling chemicals (R) to enzymes catalysing electron transport from NADH or NADPH to the chemical. These include NADPHcytochrome P-450 reductase [39], NADPH-cytochrome c reductase [40], the mitochondrial complex I (also known as NADH: ubiquinone oxidoreductase) [41, 42], NADH-cytochrome  $b_5$  reductase and NADH-quinone oxidoreductase (diaphorase) located on the outer mitochondrial membrane [43, 44]. Thereby a radical R<sup>•</sup> and the NAD(P)H oxidation products NAD(P)<sup>+</sup> are formed [43–45]. Amongst others, these processes take place at the cytosolic side of the outer mitochondrial membrane and thus may not directly involve or alter the mitochondrial electron transport chain [43, 44]. The radical R<sup>•</sup> causes non-enzymatic generation of the reactive oxygen species (ROS) superoxide, O<sub>2</sub><sup>--</sup>. Enzymatic detoxification of O<sub>2</sub><sup>--</sup> involves superoxide dismutase and glutathione peroxidase, thereby producing glutathione disulfide (GSSG) from glutathione (GSH) [46, 47]. Glutathione reductase then reconstitutes GSSG to reduced glutathione by forming NADP<sup>+</sup> (reviewed in [48, 49]). The mitochondrial enzyme nicotinamide nucleotide transhydrogenase (NNT) is able to reconstitute NADP<sup>+</sup> (directly formed via NADPH-dependent electron-donation to a chemical or indirectly as a result of GSSG reconstitution) to NADPH by generating NAD<sup>+</sup> [50]. Thus, NAD<sup>+</sup> is formed by two different mechanisms: as the MIE by direct chemical interference with NADH-dependent electron-donating enzymes and secondly by the first series of key events, i.e. ROS formation, detoxification and reconstitution of GSH. One example of such a redox-cycling chemical is paraquat (PQ). PQ directly interacts with NADH-cytochrome  $b_5$  reductase and NADH-quinone oxidoreductase, thereby accepting one electron from NADH reducing PQ<sup>2+</sup> to PQ<sup>++</sup> and forming NAD<sup>+</sup> [43–45, 48].

The multiple ROS effects on cells, tissues and organs depend on the amount of intracellular redox active species. While certain low levels of ROS produced by mitochondrial respiration function as 'physiological signalling molecules', excess of ROS induce macromolecular and thus cellular damage with potentially deathly consequences for the cell. ROS concentrations triggering this potential AOP are meant to be subcytotoxic, but function as signalling molecules by shifting the cellular redox state towards the oxidative side. Such ROS production occurs during aging in humans and experimental animals (reviewed in [37]) as well as in response to toxicant exposure [51–54] or radiation damage [55, 56]. Thus, aging poses a higher susceptibility to adverse effects of exogenous ROS due to raised basal intracellular levels.

# 22.3.2 Responses on the Cellular/Tissue Level that May Be an Adverse Outcome or Linked to the Final Adverse Outcome

One result of the MIE by redox-active chemicals is the formation of NAD<sup>+</sup>. This oxidation product is a necessary co-factor and activator for the histone deacetylase (HDAC), Sirt-1 [57, 58], the mammalian homologue of the yeast, drosophila and C. elegans Sir2 protein [59]. Due to the lack of a DNA binding domain, Sirt-1 cannot *per se* bind to DNA. It has to be recruited to target promoters by sequence-specific transcription factors to induce chromatin remodelling and regulate gene expression [60]. One of the transcription factors associating with Sirt-1 is the basic helix-loop-helix (bHLH) protein Hairy-enhancer of Split (Hes1) [61]. This transcriptional corepressor is expressed in neural stem/progenitor cells (NS/PCs) and prevents premature neuronal differentiation into DCX (double cortin)<sup>+</sup> cells by repressing activation of the pro-neuronal bHLH transcription factor Mash1 ([62]; reviewed by [63]). Redox state contributes to NS/PC proliferation and neuronal differentiation: oxidation-mediated *Mash-1* repression in NS/PCs is blocked in the absence of Sirt-1 or Hes-1 *in vitro* [38]. The signalling molecule linking redox state and Sirt-1-dependent repression of neuronal differentiation is probably NAD<sup>+</sup>.

# 22.3.3 Responses on the Organ Level that May Be an Adverse Outcome or Linked to the Final Adverse Outcome

Sirt-1 does not only determine differentiation fate *in vitro*, but also regulates the neurogenic potential of NS/PCs in the early postnatal as well as in the adult subventricular zone (SVZ) and adult hippocampus in vivo [38, 64]. In adult mouse SVZ and hippocampi, Sirt-1 knock down results in a significant increase in neuronal production, whereas Sirt-1 overexpression or activation by resveratrol, a potent chemical Sirt-1 activator, prevent adult neural precursors from differentiating into neurons [64]. In a similar way, neurogenesis is promoted by depletion of Hes-1 through inactivation of its regulator Notch in vivo [65]. A pro-oxidative state by systemic glutathione depletion decreases NS/PC proliferation and generation of young neurons and increases the number of GFAP<sup>+</sup> cells at the same time in the SVZ in a Sirt-1 dependent manner, demonstrating contribution of Sirt-1 to neural fate decision in the oxidative milieu ([38]; reviewed by [63]). One repression target of Sirt-1 is the pro-neural gene Mash-1 [62] and Mash-1 regulates neural versus glial fate of embryonic and adult NS/PC [66, 67]. During the aging process, oxidative damage occurs in the hippocampus of mice [68]. Feeding middle-aged mice with already impaired NS/PC proliferation and generation of DCX<sup>+</sup> young neurons with an NO-donating flurbiprofen derivative, which amongst others has antioxidative properties, restores these NS/PC functions almost to levels of young controls [69], suggesting causal involvement of oxidative stress in age-related decline of NS/ PC functions. These are related to altered wnt-signaling [69] and a crosstalk between Sirt-1- and wnt-signaling was reported in a different context earlier [70]. Whether this aging-related, oxidation state-dependent, wnt-mediated decline in NS/PC functions is determined by NAD+-dependent Sirt-1 activation needs further clarification.

# 22.3.4 Responses on the Organism Level that May Be the Final Adverse Outcome or Linked to the Final Adverse Outcome

The adverse outcome of impaired cognitive function that mirrors changes characteristic of aging is produced by decreased adult neurogenesis through waning NS/PC proliferation and/or generation of new, young neurons [23, 27, 29, 30, 34, 35]. This is supported by two lines of research: (i) Interventions that enhance or reduce hippocampal neurogenesis cause improved [23, 26, 28, 31–34], or impaired, agingcharacteristic [34, 35], cognitive functions, respectively. (ii) Creating an inducible transgenic strategy allowing specific ablation of adult-born hippocampal neurons in mice causes impairment of spatial relational memory in these animals [20]. Such spatial learning and memory impairment is also one phenotype of Sirt-1 knockout mice supporting the here presented concept that Sirt-1 is indeed involved in hippocampal-dependent cognitive functions [71]. The concept that oxidative stress indeed triggers the impaired adverse behavioural outcome is supported by the observation that feeding aged mice an antioxidative saffron diet improves learning and memory measured by a passive avoidance task [72].

#### 22.3.5 The Adverse Outcome in the Population

In humans, neurogenesis continues throughout life in the subgranular zone of the hippocampal dentate gyrus [37]. During the course of life, this generation of new neurons declines in rats [24], mice [23], monkeys [73] and humans [74, 75]. It is assumed, that aspects of age-related cognitive decline are related to reduced adult neurogenesis [37]. Due to the lack of methods for investigating the consequence of adult neurogenesis for cognitive function in humans most of such data has been derived from rodent studies. One recent approach for translating this information from rodents to humans was taken by Knoth et al. [76]. This group analysed human brain tissue across a broad age spectrum (1 year -100 years) and demonstrated an exponential decline in the number of cells in the dentate gyrus staining positive for doublecortin and several other surrogate markers of neurogenesis. It is suggested that this reduced neurogenesis might be due to a neural-glia switch during NS/PC differentiation [38]. Assuming similar functions of newborn neurons between species, this decline supports the notion that a decreased hippocampal function is responsible for cognitive decline also in humans. By current knowledge, such stem cell exhaustion belongs to the nine identified hallmarks of aging (reviewed by [77]). Thereby, oxidative stress is one of the main contributors to NS/PC aging [37]. Such age-related decline in NS/PC function can be accelerated by exogenous noxae, which increase the oxidative burden in the brain. In the human population, chemotherapy or gamma-irradiation for cancer treatment cause cognitive impairment probably due to compromised NC/PC function [78-80]. One discussed common mechanism of chemotherapy- or gamma-irradiation-induced cognitive changes is the generation of ROS [79, 81] and thus supports the here proposed AOP on the population level. Such accelerated cognitive decline poses a large financial and social burden on society. Whether besides cancer therapy also environmentally relevant compounds trigger the same AOP in humans is so far not known. However, accumulating data from animals and humans suggest that antioxidative strategies have the ability to improve cognition in the elderly [82].

## 22.3.6 Higher Sensitivity of NPCs Towards ROS in the Elderly

There are two major reasons why the elderly are suggested to be more sensitive towards chemical-induced reduced adult neurogenesis. For one, as indicated above, the neurogenic potential is *per se* diminished in the elderly. Attenuating a process,

which is already reduced to begin with, will thus have a greater implication on the functional outcome. This is depicted by treating young and aged mice with the neurotoxin MPTP (1-methyl-4- phenyl-1,2,3,6-tetrahydropyridine). While NS/PCs of the subventricular zone (SVZ) of aged mice proliferate less and show reduced differentiation into DCX<sup>+</sup> young neurons than those of young animals, this is significantly exacerbated by MPTP treatment, especially in the aged animals [69]. The mechanism of MPTP neurotoxicity is conveyed by induction of oxidative stress [83]. Oxidative stress is one of the main contributors to NS/PC aging [37]. Thus, the reduced antioxidative defence capacity via diminished function of a major antioxidant defence, Nrf2 (NF-E2-related factor 2, NFE2L2), observed in aging animals [84, 85] is likely the second reason for a higher susceptibility towards the attack of the NPC niche in the elderly. This assumption is supported by the observation that an antioxidant diet induced normalization of the Nrf2-dependent redox balance in the aging SVZ and reverses neurogenic impairment, NS/PC proliferation and differentiation into DCX<sup>+</sup> neurons. However, the causal relationship between Nrf2 function and NS/PC function still has to be drawn.

# 22.3.7 Utilization of AOPs for Neurotoxicity Testing

One reason why the OECD is currently supporting the AOP concept is because it might allow the interpretation of results from *in vitro* testing for regulatory decisionmaking. However, if this strategy will in the end be successful for the entity of different organs and endpoints of the human body has to undergo practical evaluation. Therefore, full AOPs have to be established and reliable methods have to be found, which are predictive for the identified endpoints. A special challenge thereby has to be tackled within the field of neurotoxicity. Neurotoxins act through a large variety of MIEs on an array of different cellular structures, which cause distinct clinical features of nervous system malfunctioning (reviewed in [86]). Thus, alternative test methods for neurotoxicity have to represent this large variety of structures. This can either be achieved by generating a high-throughput strategy for individual, 'simple' tests for individual MIEs. However, signal integration within neurons and glia as well as across different cell types is critical for the clinical outcome. Therefore, also more complex systems are needed, which allow signal integration on the next level of complexity. Neural 3D in vitro methods might be a solution for this need as they are organotypic cultures, contain neurons and glia cells [87, 88] and such 3D in vitro cultures are generally thought to bridge the gap between 2D in vitro methods and the organ in vivo [89]. Moreover, such more complex in vitro systems offer the possibility of investigating common endpoints (KEs) across different neurotoxicity AOPs. For example, cell migration is a necessary process during development of the central nervous system guided by multiple signalling pathways. As a 3D in vitro method neurospheres have the ability to mimic such neural migration in the dish. By inhibiting different signalling pathways known to be involved in neural cell migration, the inhibition of this process due to specific pathway intervention can be quantified [90]. Similar to this example, as indicated in the here described potential AOP, the adult NPC niche needs proliferating NS/PCs and their subsequent neuronal differentiation for adult learning and memory. Also multiple signalling pathways can compromise cellular proliferative capacities as well as neuronal differentiation. Therefore, common key events disturbing adult learning and memory are the inhibition of proliferation and/or differentiation, which could both be tested in neurospheres. If such an approach can reliably predict the various outcomes of neurotoxicants needs scientific evaluation.

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# Chapter 23 Oxygen Toxicity: From Cough to Convulsion

Marlon A. Medford and Claude A. Piantadosi

## 23.1 Introduction

...though pure dephlogisticated air might be very useful as a medicine, it might not be so proper for us in the usual healthy state of the body; for as a candle burns out much faster in dephlogisticated than common air, so we might, as may be said, live out too fast and the animal powers be too soon exhausted.... (Joseph Priestly 1775)

Oxygen first appeared in the earth's atmosphere 2.2 billion years ago when cyanobacteria, using the energy of sunlight to split water, excreted oxygen  $(O_2)$  into the biosphere. The rise in atmospheric oxygen placed enormous stress on simple organisms that had evolved in a reducing atmosphere. Their survival depended on the development of antioxidant defenses (aerobes) or the avoidance of oxygen (anaerobes). Higher aerobes have evolved not only to tolerate  $O_2$  but also to harness its redox potential through the evolution of iron- and copper-containing enzymes that reduce it to water, conserving energy as phosphorylated nucleotides such as ATP that drive function.

Early eukaryotes evolved mitochondria, perhaps from engulfed cyanobacteria capable of completely reducing  $O_2$  to water, resulting in the first major anti-oxidant defense [1]. The terminal mitochondrial electron acceptor, cytochrome *c* oxidase, has a very low Km for  $O_2$ , which limits the amount of  $O_2$  available to be converted

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to reactive oxygen species (ROS). And an aggregation of respiring cells, a high fixed  $O_2$  consumption rate, and a longer distance between cell and  $O_2$  atmosphere serves to lower the oxygen tension (PO<sub>2</sub>) in the tissue microenvironment.

In mammals, only lung cells are exposed to the high  $O_2$  concentrations in the atmosphere. Oxygen is transported across the alveolar barrier of the lungs to tissues at lower PO<sub>2</sub> where the PO<sub>2</sub> is a function of the rate of O<sub>2</sub> delivery (blood flow), the median diffusion distance from capillaries to cells and the rate of oxygen consumption. This staged lowering of PO<sub>2</sub>, or oxygen cascade, constitutes a key first line antioxidant defense. Mitochondria, which utilize 90 % of the oxygen consumed by mammalian cells [2], are capable of extracting O<sub>2</sub> at these low tensions. Although cytochrome *c* oxidase adds four electrons to O<sub>2</sub>, fully reducing it to water, the partial reduction of O<sub>2</sub> to ROS by the addition of one, two or three electrons (Fig. 23.1) occurs at other sites within the electron transport system. The rate of ROS production in mitochondria, cells, and tissues increases with increasing PO<sub>2</sub> [3]; for instance, when O<sub>2</sub> is added to the inhaled gas (normobaric hyperoxia). As a general



**Fig. 23.1** Formation of reactive oxygen species (ROS). Oxygen (O2) requires the addition of four electrons for its complete reduction to water. The addition of one, two or three electrons produces superoxide, hydrogen peroxide and hydroxyl radical, respectively. During hyperoxia, the presence of excess O2 in the tissues increases the probability of ROS formation

rule, oxygen toxicity occurs in a dose- and time-dependent manner when the inspired  $O_2$  percentage exceeds approximately 60 % at sea level (i.e. a fraction of inspired oxygen (FIO<sub>2</sub>) of 0.6) [4]. When inspired PO<sub>2</sub> is increased beyond 1 atm absolute (hyperbaric hyperoxia), tissue PO<sub>2</sub> rises profoundly, and the latency for O<sub>2</sub> toxicity is greatly shortened.

The toxic effects of  $O_2$  have been recognized since Joseph Priestly first purified oxygen in 1774, but Paul Bert first described nervous system oxygen toxicity in 1878 in larks exposed to hyperbaric conditions, and in 1899, Lorraine-Smith described pulmonary oxygen toxicity in birds and mice. In 1941, retinopathy of prematurity was discovered in neonates receiving normobaric hyperoxia. During the decades that followed, the use of purified  $O_2$  under both normobaric and hyperbaric conditions grew immensely due to its applications in critical care medicine, aeronautics, and diving and hyperbaric medicine. As its applications expanded, so has basic and applied research into its toxicities and how to avoid them. The rest of this chapter describes the mechanisms and variability of this toxicity and efforts in use to limit oxygen toxicity during practical exposures to hyperoxia. It focuses on therapeutic use of oxygen and does not cover endogenously generated mechanisms of oxidative damage.

#### 23.2 Definitions

**Hyperoxia** The presence of oxygen in air exceeding an FIO<sub>2</sub> of 0.21 ATA (21 % or 159 mmHg at sea level or 0.21 ATA and a barometric pressure of greater than 1.0 ATA (760 mmHg)). When hyperoxia is applied clinically in lung disease to prevent tissue hypoxia, it is called supplemental oxygen.

**Hyperbaric Oxygen (HBO<sub>2</sub>)** The delivery of pure oxygen (100 %) at an atmospheric pressure greater than sea level (760 mmHg). This is most commonly encountered in two scenarios: in undersea divers and in hyperbaric chambers.

**Oxidative Stress and Oxidative Damage** Oxidative stress is defined in biological systems by the production of ROS in excess of the available antioxidant capacity [5]. This may result from either an increase in ROS production or diminished antioxidant defenses. Excessive ROS can be generated not only by increased  $FIO_2$  [3], but by acute and chronic inflammation, ischemia-reperfusion (IR) syndromes and disruption of the anti-oxidant defenses [5]. Disturbances in antioxidant defense can result from direct enzyme damage, from mutations of genes encoding anti-oxidant enzymes (such as the superoxide dismutases), by depletion of essential dietary antioxidant micronutrients (such as zinc), by depletion of low molecular weight antioxidants or by deficiencies of vitamins C and E (ascorbate;  $\alpha$ -tocopherol). Oxidative stress induces damage to proteins, lipids and nucleic acids as well as adaptive responses that increase anti-oxidant enzyme synthesis and enhance cellular repair and proliferation. Oxidative tissue damage occurs when the anti-oxidant defense systems fail to adequately respond to oxidative stress, leading to cellular injury, damage to extracellular matrix, early senescence, and cell death. The key biological mechanisms are briefly described below.

# 23.3 ROS Production and Biological Targets in Hyperoxia

ROS include superoxide ( $O_2^{-}$ ), hydroxyl radical ('OH) and hydrogen peroxide ( $H_2O_2$ ), but oxygen itself is actually also a free radical since its outermost orbital contains two unpaired electrons in a state of parallel spin. This so-called ground state ( $O_2$ ) is the most stable form of oxygen. Although mitochondria account for most of the ROS production in cells, there are many  $O^2$  requiring enzymes, such as those of the P450 and NADPH oxidase systems, that also produce ROS endogenously. In 1954, Gerschmann and Gilbert first proposed that hyperoxia caused tissue damage because of free radical formation, similar to the effect of ionizing radiation [6]. Today it is clear that hyperoxia, through formation of ROS, chemically alters cellular macromolecules leading to alterations to signal transduction, to cell proliferation and to cell senescence, to genomic instability, and eventually to cell death [7, 8]. These events produce the tissue and organ system dysfunction observed in oxygen toxicity.

## 23.3.1 Nucleic Acids (DNA and RNA)

There has long been concern that prolonged exposure to hyperoxia could potentiate the risk of cancer because ROS are known to be mutagenic through attack on nucleic acids constituents such as dexoyribose and purine and pyrimdine bases. Oxidative damage causes DNA strand breakage, formation of a basic sites, 'alkali-labile sites' and oxidized bases [9, 10]. Thus ROS can cause point mutations, but generally do not lead to genetic deletions. In chromatin, DNA packaged with histones and other proteins is relatively resistant to ROS attack. Mitochondrial DNA, however, is more vulnerable to oxidative damage because it lacks histones and is located in close proximity to the sites of ROS production by the electron transport chain. Highly reactive ROS cause DNA damage when they are formed in proximity to oxidizable bases. For instance, guanine in 2'-deoxyguanosine moieties, when attacked by 'OH, produces 8-hydroxy-2'-deoxyguanosine (8-OHdG). 8-OHdG is a useful marker of oxidative DNA damage, and during oxidative stress, its levels increase several fold more in mitochondrial DNA than in nuclear DNA [5]. DNA fragmentation can also be detected and quantified by single cell gel electrophoresis (SCGE; comet assay) [11]. During HBO<sub>2</sub> therapy, DNA damage is rapidly repaired and is not cumulative. Moreover, adaptation occurs. When healthy subjects are exposed to repeated, daily HBO<sub>2</sub>, DNA damage is detected after the first, but not after subsequent treatments (Fig. 23.2). DNA repair is robust, in blood cells, beginning almost immediately



**Fig. 23.2** DNA migration in human leukocytes by comet assay following HBO<sub>2</sub> exposure. Blood samples analyzed before and after the first, third and fifth day of HBO<sub>2</sub>. DNA fragmentation is detectable only after the initial HBO<sub>2</sub> exposure (Adapted from Dennog et al. (1996), Ref. [11]) by permission of Oxford University Press

[11, 12] and completed within hours following  $HBO_2$  treatment [13]. Despite its capacity to damage DNA, there is no evidence to date that  $HBO_2$ -related DNA damage increases carcinogenesis [14].

## 23.3.2 Lipids

It has long been known that fats and oils stored for prolonged periods of time become rancid in a process that is arrested by the addition of antioxidant spices. This observation led eventually to the chemical understanding of lipid peroxidation, the oxidation of polyunsaturated fatty acids (PUFA). These fatty acids are especially vulnerable to oxidative attack owing to the presence of carbon-to-carbon double bonds in the fatty acid tails. Lipid peroxidation is initiated by highly reactive radicals such as 'OH, while radicals of lower reactivity such as superoxide and NO' cannot initiate lipid peroxidation. During hyperoxia, the hydroxyl radical ('OH) generated by Fenton chemistry abstracts H' from a fatty acid, forming a carbon radical, followed by propagation by peroxyl radical (ROO') formation in the presence of oxygen or other ROS. During hyperoxia, even relatively stable lipid peroxides will decompose in the presence of free transition metals (particularly iron), thus,
contributing to propagation of the lipid peroxidation chain reaction [15]. Iron chelators, such as desferrioxamine, inhibit this process, even more than do superoxide dismutase and catalase [16]. Oxidative damage to membrane PUFA and associated proteins compromise membrane fluidity, ion transport and enzyme activity causing cell and organelle dysfunction and ultimately autolysis [17]. Lung cells and erythrocytes are most vulnerable to lipid peroxidation during hyperoxia.

# 23.3.3 Protein

Susceptibility to protein oxidation and its biological implications depends on several factors [17, 18], such as the type of amino acid residue, its molecular position, the location of the protein, and the nature of the chemical attack. In particular, sulfurcontaining amino acids, such as cysteine and methionine, are vulnerable to oxidation. Oxidation interferes with protein functions including catalysis, receptor binding, and transport. As early as 1946, Haugaard showed that enzymes whose catalytic function depended on sulfhydryl groups were unusually sensitive to oxygen damage [19]. In the lung, the degree of inactivation of such enzymes is correlated with increasing PO<sub>2</sub>; by 5 ATA, reduced sulfhydryl groups become undetectable prior to the onset of injury [20, 21]. Proteins can be damaged directly by ROS or indirectly by isoketal products of lipid peroxidation, such as malondialdehyde (MDA) and 4-hydroxynonenal (HNE). These damaged proteins are eliminated by several processes, such as proteolytic degradation through lysosomal proteases, cytosolic and nuclear proteasome or mitochondrial proteases, as well as during autophagy. Heavily oxidized proteins that cannot be effectively removed by proteolysis are sequestered into insoluble, but less toxic clumps. In hyperoxic tissue injury, the persistence, for example, of oxidized lens proteins and neuronal membrane transporters manifests as cataracts and reduction in seizure thresholds, respectively [22-24].

## 23.3.4 Cell Death

Ultimately, irreparable hyperoxic damage to cellular constituents leads to cell death either by apoptosis or by necrosis. ROS initiate and propagate both pathways. Activation of apoptosis is a final tissue-protective pathway in the antioxidant defense and does not typically cause inflammation or tissue destruction [25, 26]. The presence of excess ROS can arrest apoptosis however by inactivating cysteine-aspartyl-specific-proteases (caspases) [27] forcing cell death by necrosis or by an intermediate pathway [5]. Necrotic cell death is generally more destructive, as cell disruption and spillage of cell contents into surrounding tissues activates inflammation, generating further ROS and releasing intracellular, nuclear and mitochondrial contents that propagate destruction of neighboring tissue. Not mutually exclusive, both apoptosis and necrosis coexist in hyperoxic lung injury [28].

## 23.4 Anti-oxidant Defense

The level and composition of the antioxidant defense systems vary with cell and tissue type and are maintained at intracellular locations where particularly detrimental biological oxidations occur [5]. The antioxidant defense comprises enzymes, free radical scavengers and sacrificial molecules, and repair/replacement mechanisms for damaged molecules. The most critical enzymes for ROS detoxification are the superoxide dismutases, catalase, and the glutathione peroxidase/reductase systems. The latter systems require NADPH and the pentose phosphate shunt (Fig. 23.3) [29].

There are also many endogenous and dietary free radical scavenger molecules, including water-soluble ascorbic acid and glutathione, the lipid soluble carotenoids (including pro-vitamin A carotenoids such as beta-carotene), tocopherols (vitamin E), and dietary flavonoids.

These antioxidant defense systems can be augmented through gene expression (antioxidant enzymes and glutathione biosynthesis) and dietary intake of antioxidant compounds (antioxidant (pro-) vitamins, flavonoids). As mentioned earlier, the mitochondrial electron transport chain (ETC) helps manage oxidative stress imposed by oxygen by reducing the molecule to water and deriving energy in the process; however, it too is a source of ROS during hyperoxia.



**Fig. 23.3** Main enzymatic antioxidant defenses that detoxify reactive oxygen species. Superoxide dismutase (SOD) converts superoxide to hydrogen peroxide ( $H_2O_2$ ), which is degraded to water by catalase and/or peroxidases (e.g. GPx).  $H_2O_2$  oxidizes reduced glutathione (GSH) to GSSG, which is recycled back to GSH by gluthathione reductase (GluRed) using reducing equivalents from NADPH. NADPH is continuously replenished by the pentose phosphate shunt. When the rate of  $H_2O_2$  production exceeds the rate of  $H_2O_2$  dissipation by the peroxidases, it may participate in Fenton reactions with transition metals (M) to generate highly toxic hydroxyl radical ('OH), resulting in attacks on nucleic acids, proteins and lipids

### 23.4.1 Antioxidant Enzymes

#### 23.4.1.1 Superoxide Dismutases

The discovery of superoxide dismutase (SODs) as a defense against an oxygen metabolite was the first scientific evidence that the free radical theory of oxygen toxicity might be valid [30]. The three types of mammalian SOD now identified all catalyze the conversion of superoxide to  $H_2O_2$  and  $O_2$ . They differ in their transition metal moieties and cellular locations. SOD-1 and -3 (copper-/zinc-SODs) are located in the cytosol and extracellular space, respectively, while SOD-2 (manganese-SOD) is found exclusively in mitochondria. The expression of SODs is induced during hyperoxia and is fundamental to reducing oxidative damage. Typically, rats exposed to 100 %  $O_2$  die within 60–72 h of exposure [31, 32] but, when exposed to a lower FIO<sub>2</sub> of 85 % over 7 days, they adapt to subsequent exposure to 100 %  $O_2$ . The lungs of these rats show increased SOD expression [31, 32]. Transgenic mice over-expressing both SOD-1 and SOD-2 are more resistant to oxygen toxicity than wild type controls. Likewise, SOD-2 knockout mice die quickly in hyperoxia [31, 32]. In baboons, exogenous SOD-2 administered via aerosol protects the lung against hyperoxia even though it remains outside the cells [33]. Extracellular SOD-3 within cerebral blood vessels plays an important role in regulating cerebral blood flow (CBF) through its interaction with nitric oxide (NO), an endogenous vasodilator. By scavenging superoxide, SOD-3 prevents peroxynitrite (ONOO<sup>-</sup>) formation, which impairs NO-mediated vascular relaxation. In acute hyperoxia, excess superoxide escapes SOD-3, resulting in loss of NO bioactivity and vasoconstriction [34].

Although protective in oxidative stress, SODs occasionally inadvertently catalyze reactions that are harmful to the cell. For instance, at millimolar  $H_2O_2$  concentrations, SOD-1 can catalyze 'OH formation [5]. This may contribute to the development of central nervous system (CNS) and pulmonary  $O_2$  toxicity under hyperbaric conditions.

#### 23.4.1.2 Catalase and Peroxidases

Catalase and other peroxidases remove  $H_2O_2$ , but catalase directly converts  $H_2O_2$  to water and  $O_2$ , whereas other peroxidases use  $H_2O_2$  to oxidize a substrate such as glutathione (GSH) or ascorbate. Glutathione peroxidases (GPx) utilize two reduced glutathione molecules as electron donors, reacting with  $H_2O_2$  to form glutathione disulfide (GSSG) and water. GSSG can be reduced back to GSH by glutathione reductase, consuming NADPH in the process. The NADPH for recycling is generated by the pentose phosphate shunt, where the rate-limiting enzyme, glucose-6-phosphate dehydrogenase (G6PD), is induced by hyperoxia, thereby increasing the capacity for glutathione turnover [35, 36]. Catalase is abundant in erythrocytes, where it removes the  $H_2O_2$  produced by auto-oxidation of hemoglobin. Since  $H_2O_2$  readily crosses cell membranes, erythrocytes act as a sink for  $H_2O_2$  produced elsewhere.

### 23.4.2 Radical Scavengers

#### 23.4.2.1 Glutathione

A substrate for GPx, glutathione is also a radical scavenger undergoing a range of chemical reactions. In its sacrificial role, the glutathione thiol group may be oxidized to a thiyl radical (GS<sup>\*</sup>) which can further react with GSH and oxygen to form superoxide; the latter is removed by SODs. Reduced glutathione also chelates copper ions, limiting 'OH production associated with spontaneous dismutation of superoxide. As an effective scavenger of RNS, reduced glutathione removes peroxynitrite and in the process is converted to S-nitroglutathione (GSNO<sub>2</sub>) and S-nitrosoglutathione (GSNO), limiting unwanted protein nitration [5].

#### 23.4.2.2 α-tocopherol

Vitamin E and  $\alpha$ -tocopherol are frequently used interchangeably in the literature, but vitamin E is a dietary term and one of its congeners is  $\alpha$ -tocopherol, a hydrophobic molecule that resides in the lipid milieu of cell membranes. It contains an aromatic ring that scavenges H<sub>2</sub>O<sub>2</sub> faster than it can react with membrane fatty acids and proteins [17]. Alpha-tocopherol is a potent inhibitor of lipid peroxidation. By reacting with the peroxyl radical it forms a stable  $\alpha$ -tocopheryl radical, terminating the fatty acid chain reaction [37]. This knowledge led to the proposition that supplemental vitamin E might protect against oxygen toxicity. Indeed, rats fed vitamin E have reduced lipid peroxidation and free radical damage to the retina after repeated exposure to hyperbaric oxygen [38]. However, the evidence for the use of supplemental vitamin E to protect the lungs in well-nourished humans is limited [39] and use of vitamin E as an antioxidant to protect against pulmonary oxygen toxicity has been largely abandoned [40].

#### 23.4.2.3 Ascorbic Acid

Ascorbic acid or vitamin C is a water-soluble vitamin that serves as a cofactor for several enzymes involved in collagen synthesis and in oxygen sensing. Ascorbate ion directly scavenges ROS and peroxyl radicals. It also participates in the recycling of other antioxidants, making it very important in systems like the lung that face continuous exposure to oxygen or other oxidants. As with vitamin E, ascorbate was proposed to be lung protective in hyperoxia, but in well-nourished individuals there is no evidence that ascorbate supplementation has any protective effect [39].



**Fig. 23.4** Exposure limits for signs and symptoms of  $O_2$  toxicity in humans vary with the organ system and the partial pressure of oxygen. The asymptotes for the pulmonary and CNS curves correspond to maximum safe exposures of ~0.6 and ~1.4 ATA respectively (Adapted from Lambertsen (1987), Ref. [103])

# 23.5 Tissue Toxicity

Ultimately,  $O_2$  is toxic to all tissues, but physiologically, elevated  $PO_2$  levels most affect the lungs and brain. At sea level, the lung is the main target of  $O_2$ toxicity owing to its direct exposure to elevated  $PO_2$  in inspired gas when supplemental oxygen is given due to the presence of impaired gas exchange. The brain and spinal cord are affected exclusively at hyperbaric  $O_2$  pressures. Pulmonary and central nervous system (CNS) oxygen toxicity, once considered separate entities with differing etiologies, are linked when HBO<sub>2</sub> produces excitotoxicity and  $O_2$ -seizures that cause a neurogenic pulmonary injury unique to hyperbaric hyperoxia (Fig. 23.4).

# 23.5.1 Lung

Pulmonary oxygen toxicity is characterized by the development of burning chest pain on deep inspiration, dry cough, and eventually dyspnea [41, 42]. These symptoms progress more rapidly at higher PO<sub>2</sub> levels. Breathing pure oxygen (1 ATA) causes chest soreness within 6 h, alveolar damage occurs by 24 h and progresses to acute respiratory distress syndrome by 72–96 h. At 2 to 3 ATA, patients develop symptoms by 3 h [43]. Symptoms of pulmonary O<sub>2</sub> toxicity are generally absent below 0.5 ATA but subclinical oxidative damage may still occur. At as little as 0.28 FIO<sub>2</sub>, lipid peroxidation, but without acute lung injury, can be detected [17, 44, 45].

Histologically, oxidative damage impairs pulmonary capillary endothelial function; proteins from blood plasma leak into the alveolar space. Type I alveolar cells are quite sensitive and easily damaged by hyperoxia. By contrast, surfactant-producing type II alveolar cells are relatively resistant and proliferate and replace type I cells. Surfactant, particularly dipalmitoyl-phosphatidylcholine, is largely resistant to hyperoxia although it is vulnerable to nitration [46]. To protect from oxidative stress caused by particles and toxins in air, lung tissue contains higher levels of antioxidants than plasma. When the lung alveolar-capillary barrier is injured by hyperoxia, plasma antioxidants such as ascorbate, urate, and albumin leak into the alveolar space to supplement the antioxidant pool. An additional antioxidant defense is provided by mucus rich in cysteine and disulfide bridges. ROS stimulate mucus production in airways, where it is a powerful scavenger of hydroxyl radical and peroxynitrite produced during hyperoxia [47].

Eventually, prolonged exposure to high PO<sub>2</sub> surpasses pulmonary antioxidant defenses causing demonstrable gas exchange and lung mechanical abnormalities on pulmonary function tests. During prolonged normobaric hyperoxia, gas exchange becomes significantly impaired and the rate of reversal is affected by duration of oxygen exposure [43, 48]. When PO<sub>2</sub> exceeds 1.5 ATA, reductions in vital capacity and expiratory flow rates are more rapid and profound, with rapid reversal after return to normoxia [49, 50]. Unlike lung mechanics, gas exchange abnormalities may require several weeks to resolve following O<sub>2</sub> exposure [51].

The magnitude of pulmonary mechanical changes and their relatively rapid reversal after HBO<sub>2</sub> exposure, suggests that neurotoxicity may be a contributing factor in acute pulmonary oxygen toxicity [49]. This was proposed by Demchenko and colleagues who showed that rats exposed to normobaric hyperoxia (1 ATA) and hyperbaric oxygen (2–3 ATA) developed differing pulmonary manifestations [52]. Lung injury during normobaric hyperoxia involves direct ROS attack on alveolar epithelium, whereas HBO<sub>2</sub>, particularly when accompanied by O<sub>2</sub>-seizures, cause more extensive lung microvascular injury. The hemodynamic basis of lung injury during HBO<sub>2</sub> toxicity is through NO-related modulation of the glutamate-GABA equilibrium that leads to increased sympathetic outflow, left ventricular dysfunction, and rapidly rising transpulmonary hydrostatic pressures [34, 52]. The pulmonary hypertension and extravasation of red cells and proteins into alveoli is similar to so-called neurogenic pulmonary edema and does not occur acutely in normobaric O<sub>2</sub> toxicity.

Pulmonary  $O_2$  toxicity can limit treatment of patients requiring prolonged  $O_2$  therapy, e.g. on mechanical ventilators or in HBO<sub>2</sub> therapy, such as those suffering decompression sickness, where potentially toxic levels of  $O_2$  exposure are needed to maintain the therapeutic effect. This  $O_2$  toxicity can be mitigated by using intermittent exposures to breathing gas containing less  $O_2$ , markedly improving the cumulative duration to which individuals can be exposed to higher  $O_2$  concentrations [53]. One interpretation of this effect is that the initiation of repair mechanisms is an important aspect of the anti-oxidant defense.



Fig. 23.5 Exercise hastens the onset of oxygen neurotoxicity in working divers at 50 fsw (2.52 ATA) (Adapted from Donald (1947), Ref. [54])

## 23.5.2 Central Nervous System (CNS)

Oxygen seizures in humans exposed to hyperbaric hyperoxia were described in 1947 by Donald [54]. The  $O_2$  convulsion is usually a sudden generalized tonic-clonic seizure, often with no prodromal phase. The tonic phase lasts for about 30 s followed by a clonic phase lasting a minute or longer during which the subject experiences apnea and hyperventilation followed by recovery over 5 to 30 min and a variable post-ictal course. There are no long term effects of these brief seizures [55] and no correlation with age, weight, gender, smoking or alcohol use [54]. There are large variations in seizure latency among subjects and within individuals from day to day, despite identical exposures, making the onset of convulsions difficult to predict. There may be preceding auras or premonitory symptoms in humans, but these are not consistent, nor are abnormalities on electroencephalogram (EEG) prior to the event. Exercise while under pressure does reduce the seizure threshold (Fig. 23.5) and is largely attributed to carbon dioxide (CO<sub>2</sub>) retention [54, 56]. Increased PCO<sub>2</sub> results in increased cerebral blood flow and delivery of  $O_2$  at toxic doses to the brain. Immersion in cold water is another predisposing factor [54] likely due to increased metabolic activity as a result of cold rather than to immersion [57]. CNS O<sub>2</sub> toxicity occurs exclusively in hyperbaric hyperoxia and may be a consequence of ROS injury to membrane ion transport proteins, inhibition of enzymes responsible for synthesis of key neurotransmitters and modulation of cerebral blood flow related to CO<sub>2</sub> production and NO metabolism.

#### 23.5.2.1 Carbon Dioxide

Carbon dioxide, through its central vasodilator effect, increases cerebral blood flow and predisposes to  $O_2$ -induced seizures [58, 59]. Rats breathing 60 mmHg  $CO_2$ exposed to HBO<sub>2</sub> at 4 ATA more rapidly develop seizures. When allowed to adapt to the same  $CO_2$  under normobaric conditions over 5 days, seizure latency is increased. This is consistent with prior observations that hyperoxia in the presence of acute hypercapnia results in a larger cerebral  $O_2$  exposure [60], an effect that is partially reversed following adaptation to chronic hypercapnia [61–63].

#### 23.5.2.2 Na<sup>+</sup>/K<sup>+</sup> ATPase Membrane Transporter

ROS can affect the regulation of ion channel gene expression and function [64]. The Na<sup>+</sup>/K<sup>+</sup> ATPase of neuronal plasma membrane maintains the electrochemical gradient necessary for neuronal function. Na<sup>+</sup>/K<sup>+</sup> ATPase thiol groups are attacked and inactivated by ROS [65]. At 4 ATA, the activity of Na<sup>+</sup>/K<sup>+</sup> ATPase decreases in the rat cortex up to 90 min prior to the onset of convulsions [22, 23]. While noteworthy, the significance of decreased cortical Na<sup>+</sup>/K<sup>+</sup> ATPase activity in causing the convulsions of O<sub>2</sub> toxicity has not been demonstrated.

#### 23.5.2.3 Glutamate and Gamma-aminobutyric Acid (GABA)

The inhibitory neurotransmitter  $\gamma$ -aminobutyric acid (GABA) is synthesized by enzymatic decarboxylation of L-glutamate by glutamic acid decarboxylase (GAD) [66]. GAD is inhibited by molecular O<sub>2</sub>, and the consequent decreases in GABA levels are associated with a predisposition to O<sub>2</sub>-induced seizures [67]. In rats exposed to 6 ATA, GABA levels decrease prior to the onset of convulsions, an effect reversible within 1 h after HBO<sub>2</sub> exposure. Rats treated with a GABA agonist prior to HBO<sub>2</sub> show prolonged seizure latency [68]. From several animal studies, a rapid decrease in GABA best correlates with the increased susceptibility to convulsions observed with increasing PO<sub>2</sub> [69], but GABA reduction itself is not sufficient, as the administration of radical scavengers, such as disulfiram, reduces GABA but delays seizure onset [70, 71], while some agents that increase cortical GABA (aminooxyacetic acid and hydrazinopropionic acid) hasten the onset, frequency and severity of convulsions [70]. Thus, decreasing GABA levels may also reflect underlying changes in neurotransmitter modulation [72, 73] and ion channel activity [74]. Although GABA is playing some important role in O<sub>2</sub>-induced seizures, the mechanism is not yet clear.

#### 23.5.2.4 Nitric Oxide

This endogenous vasodilator is produced constitutively by neuronal and endothelial nitric oxide synthase (NOS) from the substrates  $O_2$ , NADPH and L-arginine. Through its vasodilator effect, increased NO bioactivity hastens the onset of  $O_2$ -induced convulsions. When rats are treated with a phosphodiesterase-5 inhibitor to

block cyclic-GMP degradation and potentiate NO activity, time to onset of  $O_2$ induced seizures is reduced significantly [75]. Here, NO reverses the initial protective vasoconstriction response to hyperoxia, permitting toxic levels of  $O_2$  delivery to brain, leading to convulsions. Conversely, when NOS is inhibited, neuronal  $O_2$  toxicity is mitigated [76–79].

 $O_2$  concentration is linked to NO metabolism in a dose-dependent manner. As a rate limiting substrate for NOS [80] [81] increasing  $O_2$  concentration increases NO production and thus its vasodilator effect, but excess  $O_2$  and ROS promote RNS formation, which interferes with neurotransmitter synthesis and synaptic function while reducing the effective concentration of physiologically active NO. At 5 ATA, NO, reacting with superoxide to form peroxynitrite (ONOO<sup>-</sup>), nitrosylates GAD, reducing GABA synthesis and shifting the inhibitory-excitatory neurotransmitter equilibrium in favor of the latter, predisposing to neuronal excitation [75]. Peroxynitrite also reduces the inhibitory effect of GABA; the resulting disinhibition of sympathetic outflow overwhelms protective baroreflex-mediated cardiac vagal activity causing cardiac alterations, pulmonary hypertension, and consequent extravasation of erythrocytes and protein into alveoli [52, 75]. CNS and acute pulmonary  $O_2$  toxicity are therefore apparently uniquely linked through the modulation of central NO metabolism in hyperbaric hyperoxia (Fig. 23.6).



**Fig. 23.6** Neurogenic pulmonary injury occurs when HBO<sub>2</sub> modulation of NO metabolism leads to increased CBF and Glutamate-GABA dysequilibrium. Epileptiform discharges on EEG signal seizure onset with autonomic hyperactivation and cardiac LV dysfunction. Pulmonary hypertension rapidly develops with lung microvascular damage and leakage of red cells and proteins into alveoli (*CBF* cerebral blood flow, *NO* nitric oxide, *PV* pulmonary venous, *RVSP* right ventricular systolic pressure)

#### 23.5.2.5 Management

The management of CNS  $O_2$  toxicity is founded on the avoidance of unnecessarily high PO<sub>2</sub>. Exercising divers are limited to a maximum PO<sub>2</sub> of 1.4 to 1.6 ATA and resting patients in hyperbaric chambers generally do not breathe O<sub>2</sub> at pressures exceeding 3 ATA. The only definitive treatment of O<sub>2</sub> toxicity is to limit the O<sub>2</sub> exposure. In divers, O<sub>2</sub> convulsions can be lethal due to loss of the regulator and those individuals should be brought carefully to the surface to reduce the PO<sub>2</sub> and avoid drowning [82]. In a hyperbaric chamber, the hood or mask is removed, and once the seizure subsides, the chamber is depressurized to a PO<sub>2</sub> of less than 0.6 ATA [83]. The use of anticonvulsants has not gained widespread use due to the rarity of O<sub>2</sub> convulsions with modern protocols and to the difficulty in identifying at-risk individuals.

### 23.5.3 Eye

The components of the eye are vulnerable to ROS attack, giving rise to distinct clinical entities. Oxidative damage to the lens constituents causes myopia and cataracts and ROS-mediated alterations in retinal blood flow lead to peripheral visual field loss and the retinopathy of prematurity.

#### 23.5.3.1 Retinopathy of Prematurity

The retinopathy of prematurity (ROP) became widespread with the use of supplemental  $O_2$  in incubators. Hyperoxia stresses the retina due to the energy demands of neurotransmission and turnover of vision molecules [5]. Premature infants have underdeveloped antioxidant defenses and are incapable of tolerating hyperoxia, which arrests retinal vessel development. When returned to air, the retina releases angiogenic factors causing disorganized vessel regrowth; these lack structural integrity and bleeding leads to vascular fibrosis, which causes disproportionate traction on the retina, and retinal detachment and irreversible blindness. The National Cooperative Study (1954) recommended the curtailed use of  $O_2$  in incubators, which did much to decrease the severity of ROP, but did not prevent it, later giving rise to controversy about the role of hyperoxia as the sole cause of ROP [84]. To balance the risk of ROP versus hypoxia, the monitoring of blood  $O_2$  levels in premature infants and judicious use of supplemental  $O_2$  is necessary [85].

#### 23.5.3.2 Myopia

Hyperoxic myopia is a well-recognized, largely reversible, complication of HBO<sub>2</sub>. It results in a shift in focal length of the eye to near-sightedness and occurs during daily HBO<sub>2</sub> protocols of 2.0–2.5 ATA over several sessions. Refractive changes of the lens become noticeable to patients by 15–20 treatments and occur symmetrically

(average 0.5 to 1.0 diopters/month) [86, 87].  $O_2$  diffuses through the avascular cornea, from the atmosphere, increasing PO<sub>2</sub> in the aqueous humor [88]. In humans exposed to HBO<sub>2</sub> via hood delivery, where the eyes are exposed to pure oxygen, refractive changes were more pronounced than if O<sub>2</sub> was delivered by facemask alone [89], and susceptibility increases with patient age and medical conditions such as diabetes and pre-existing cataracts [24, 86]. Hyperoxic myopia typically resolves over 6–10 weeks following termination of HBO<sub>2</sub> therapy but can persist for up to 1 year [87, 89]. The condition is largely reversible and permanent changes to corrective lenses are not recommended in patients undergoing HBO<sub>2</sub> therapy.

#### 23.5.3.3 Cataract

Lens epithelial cells are readily damaged by ROS. The outward facing lens epithelial cells divide and differentiate into lens fibers that synthesize crystallins, the lens proteins responsible for near perfect transmission of light. The crystallins together with chaperones protect other lens proteins from thermal and oxidative insult. Lens fibers elongate, progressively lose their organelles and migrate toward the nucleus, pushing older damaged fibers centrally. Lacking organelles they are unable to synthesize new proteins or remove oxidized ones, so oxidative damage is cumulative [90-92]. Protein cross-linking and aggregation interferes with light transmission, causing clinically significant cataracts [24]. Progression of pre-existing cataracts will occur in about 80 % and the formation of new cataracts in under 50 % of individuals exposed to HBO<sub>2</sub> at 2.0–2.5 ATA for 60–90 min over 2–19 months (>150 sessions) [93]. A threshold of cumulative O<sub>2</sub> exposure beyond which clinically relevant damage to the lens occurs is not yet defined [94].

#### 23.5.3.4 Peripheral Vision

Reductions in peripheral vision in humans occur during exposures to  $PO_2$  in the hyperbaric range. Behnke (1935) first observed this in a man exposed to 3.5 ATA oxygen over 3.5 h who experienced near total blindness that was completely reversed within 50 min after the resumption of breathing normobaric air [95]. This was reproduced in larger series where it was shown that *central visual* functions, such as visual acuity and cortical visual evoked responses, are not affected during this process [54, 96, 97]. Decrements in peripheral vision are proportional to increasing  $PO_2$ , and provided that the HBO<sub>2</sub> exposure is not extended beyond complete visual extinction, it is fully reversible [97].

## 23.5.4 Red Blood Cell

The mammalian erythrocyte has specialized antioxidant defenses to protect it. The erythrocyte delivers bulk  $O_2$  bound to hemoglobin to tissues and thus functions in a highly oxidative environment where its cell membrane is vulnerable to oxidative

damage. RBCs contain high levels of SOD1 and catalase in order to cope with constant superoxide flux from oxyhemoglobin and with free iron (Fe<sup>2+</sup>) produced from hemoglobin breakdown. Superoxide and superoxide-derived ROS attack phosphatidyl-ethanolamine, reducing membrane fluidity and function leading to hemolysis. Erythrocytes, unable to synthesize lipids, must depend upon deacylationreacylation to recycle damaged membrane lipids, which becomes inefficient during oxidative stress. At 3 ATA, human erythrocytes show a 30 % reduction of [9,10 <sup>3</sup>H] oleic acid re-incorporation into membranes preceding hemolysis [98]. The extent of lipid peroxidation is time dependent; the more prolonged the O<sub>2</sub> exposure, the more significant the lipid peroxidation and the more likely hemolysis is to occur [99– 101]. Despite these effects, hemolysis is mild in individuals receiving HBO<sub>2</sub> [102] and does not cause anemia in individuals with no erythrocyte abnormalities.

### 23.6 Conclusions

Although oxygen is essential for aerobic life, as the inspired PO<sub>2</sub> increases, ROS are produced that attack cellular macromolecules, leading to cell and tissue injury and organ dysfunction. This is the basis of O<sub>2</sub> toxicity, which occurs across a spectrum of O<sub>2</sub> partial pressures, from as little as 0.6 ATA, which causes lung damage, to 1.6 ATA, where CNS O<sub>2</sub> toxicity occurs consistently. HBO<sub>2</sub> places additional oxidative stress on the lungs, CNS, and other organs beyond those achievable by normobaric hyperoxia due not only to increased ROS production, but to the physiological responses to the underlying oxidative damage. CNS O<sub>2</sub> toxicity and peripheral visual field loss are unique to hyperbaric hyperoxia and the pulmonary manifestations of HBO<sub>2</sub> toxicity differ from those seen in normobaric hyperoxia. Ultimately, O<sub>2</sub> toxicity is fatal and its prevention involves the judicious use of supplemental O<sub>2</sub>. The therapeutic safety of O<sub>2</sub> depends on understanding its toxicities and the measures needed to mitigate them.

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# Chapter 24 Oxidative Stress in Reproductive Toxicology

Yu-Guang Zhao and Lu Cai

## 24.1 Introduction

There is a saying that the reproductive system is among the most important systems in the entire body. Indeed, a species dies without the ability to reproduce. The reproductive system is a collection of organs that work together for the purpose of producing a new life. The reproductive system is composed of several organs, mainly defined for the external genitalia and internal organs, including gonads that produce gametes. A germ cell is any biological cell that gives rise to the gametes of an organism that reproduces sexually. Gamete is the cell that fuses with another cell during conception in organisms that reproduce sexually. Substances such as fluids, hormones, and pheromones are thus important to the effective functioning of the reproductive system. In many animals, the germ cells originate near the gut of an embryo and migrate to the developing gonads where they undergo two type cell divisions, mitosis and meiosis, followed by cellular differentiation into mature gametes, either eggs or sperm (http://en.wikipedia.org/wiki/Reproductive\_system; http://www.livescience.com/26741-reproductive-system.htm).

Reproductive biology is a field of study mainly involving the reproductive system and sex organs. Reproductive toxicology involves research on the impact of chemical and physical agents on the reproductive organs or on the reproduction process. Therefore, the impact of reproductive toxicology is related to reproductive

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endocrinology, infertility, reproductive physiology, and developmental biology. For instance, reproductive toxicity is the adverse effects of the toxic substances on sexual function and fertility in adult males and females, as well as developmental toxicity in the embryos and offspring [1].

Many drugs have effects on the human reproductive system: these may be desired (hormonal contraception), a minor unwanted side effect (many antidepressants) or a major public health problem (thalidomide). However, most studies of reproductive toxicity have focused on the reproductive effects of occupational or environmental exposure to chemicals. In fact, both consumption of alcohol and tobacco smoking are also known to be "toxic for reproduction". These substances may be specifically toxic for male or female reproductive organs and germ cells, but some of them may be similarly toxic to both genders. In this chapter, we will mainly discuss male reproductive toxicology, particularly toxic effects on male germ cells [1–3].

## 24.2 Testis, Spermatogenesis and Cell Death

## 24.2.1 Testis and Spermatogenesis

The testicle (also called testis, plural testes), as the male gonad in mammals, forms part of the male reproductive system. Testes are components of both the reproductive system and the endocrine system. Anatomically, the testes are contained in the scrotum and are composed of dense connective tissue containing around 300 internal compartments called lobules. Each of these lobules contains a number of highly coiled tiny tubules where the sperm is produced. Sperm travel through the testis from the tubules, through a network of ducts called the rete testis, to the epididymis. Testosterone is produced in cells located between the lobules. Therefore, the testes not only produce androgens, primarily testosterone, but most importantly generate sperm via spermatogenesis [4–6].

Spermatogenesis occurs within the seminiferous tubules of the testis. It is divided into three distinct phases:(a) spermatogonia proliferate, giving rise to spermatocytes; (b) spermatocytes go through two meiotic divisions, leading to the formation of spermatids; (c) spermatids go through extensive morphological remodeling, producing highly differentiated spermatozoa. In addition, spermatozoa continue to undergo a maturation process as they transit through various regions of the seminiferous epithelia within the seminiferous tubule. The seminiferous tubules are divided into discrete stages according to the development of spermatozoa [4–6]. For instance, the seminiferous tubules are divided into 12 stages in the mouse and 14 stages in the rat [4].

Germ cells at different developmental stages in the seminiferous epithelium possess their own distinct physiological features and respond differently to exogenous stimuli. The complex process of spermatogenesis is orchestrated by adjacent Sertoli cells that support the maturation process by providing nutrition, hormones, and other mediators [7–10]. Sertoli cells also maintain the architectural and functional integrity of the seminiferous epithelium by mediating phagocytosis of germ cells that have died in the vicinity, predominantly via apoptosis [4–6].

# 24.2.2 Apoptotic Death of Germ Cells

Apoptosis, also called programmed cell death, is a genetically programmed process that occurs during the development of many cell lineages. Apoptosis kills cells without damaging surrounding cells and tissues. Programmed apoptotic deletion of cells promotes the dynamic process of tissue development and also plays a critical role in tissue homeostasis to maintain the balance between cell death and cell proliferation in mature tissues [7, 10–12]. Apoptosis occurs within the seminiferous epithelia of the testis of many mammalian species [7–9, 13].

Apoptotic cell death of germ cells occurs under normal physiological conditions as an important mechanism to eliminate the germ cells with genomic abnormalities that spontaneously arise during spermatogenesis. In the below sections, several features of the apoptotic death of male germ cells are discussed briefly.

#### 24.2.2.1 Spontaneous Apoptotic Death of Germ Cells During Spermatogenesis

Spontaneous apoptosis of germ cells during spermatogenesis occurs in the absence of an outside apoptotic stimulus in many mammalian species [7, 9, 14], and has been thoroughly reviewed [14–19]. Apoptosis plays a critical role in eliminating overproduced, genetically abnormal, or accidentally-damaged germ cells. In rodents, as well as cats and rabbits, high levels of germ cell apoptosis are seen in spermatogonia and spermatocytes [14–18]. These deaths occur at the same time that spermatogonia undergo mitotic divisions and spermatocytes proceed through meiosis. By this means, apoptosis in the germ cell serves as a checkpoint to control and eliminate abnormal cells, and to provide a proper balance of somatic and germ cell numbers [7, 13, 18]. The homeostatic control for the balance between mitotic or meiotic cell division and apoptotic cell death in higher organisms is dependent upon signals received from appropriate growth or survival factors coinciding with checkpoints of the cell.

Apoptotic cell death occurs in a cell- and tubule-stage-specific manner during the differentiation process of spermatogenesis. This process is probably dependent on a number of factors, including the biological features of the different germ cell types, species and genetic strain differences within a given species, hormonal regulation, and age of the animal [14–19]. Effects of age on testicular cell apoptosis have been studied in mouse, rat, and hamster testes [19, 20]. All three species display apoptotic degeneration of damaged cells for unknown reasons during normal developmental processes. Koji and Hishikawa have systemically summarized the general features of germ cell apoptosis in normal testes of fetal, neonatal, and adult mice

examined by electron microscopy and TUNEL staining [16]. In general, young individuals showed a higher incidence of apoptotic cell death in the testis as compared to adults.

Germ cells at different stages of the seminiferous epithelium possess their own physiological features and respond differently to exogenous stimuli. To determine the stage specificity of TUNEL staining for apoptosis in the seminiferous epithelium, the seminiferous tubules were divided into four groups, i.e., I–IV, V–VII, VIII–X, and XI–XIV, according to the standards described by Leblond and Clermont [5] and by Russell et al [4], which include specific cell associations, the position of early and late spermatids within the seminiferous tubules in stages I (13.9 %), VII (18.1 %), VIII (9.4 %), and XII (10.1 %) together contribute to more than 50 % of the total. The TUNEL-stained germ cells were identified as spermatogonia and spermatocytes or as spermatids by their location in the seminiferous epithelium and by the features of neighboring cells.

Spontaneous germ cell apoptosis was detected mainly in premeiotic cells [13, 21, 22] in stages I–IV and XI–XIV [7, 9, 21–23]. During spermatogenesis, a self-defense system may be established so that the cells that develop spontaneous abnormalities are destined to die, thus preventing the transmission of abnormalities to the next cell generation. The spontaneous apoptosis of spermatocytes may not be related only to meiotic divisions because meiotic prophase is longer than mitotic prophase and there may be an extended time during which these cells are exposed to challenge by spontaneous insults. Genetic reassortment by the formation of a synaptonemal complex takes place in zygotene to early pachytene primary spermatocytes; synaptonemal complex anomalies may result in meiotic arrest or affect cell death [24, 25]. Therefore, spontaneous apoptosis in zygotene and early pachytene spermatocytes is likely to provide a defense system against the transmission of abnormal signals into the next cell population.

#### 24.2.2.2 Characterization of Apoptotic Death of Germ Cells

Allan et al. [26] have divided the process of male germ cell apoptotic death into three phases. These consist of (a) an early phase in which cells show margination of nuclear chromatin; (b) an intermediate phase in which phagocytosed apoptotic bodies are partly degraded; and (c) a late phase in which only debris of degraded apoptotic bodies is evident. The entire process of apoptosis is rapid and the morphological phase of apoptotic germ cells probably takes just a few minutes [9].

Apoptotic cell death in male germ cells has two features distinct from somatic cells. The classical morphology of apoptosis in somatic cells is defined by cellular shrinkage, condensation of chromatin and the cytoplasm, and chromatin fragmentation [7]. Although most apoptotic germ cells in the testis exhibit these typical features, some exhibit cellular swelling and decondensed, homogeneous chromatin [9]. In DNA gel electrophoresis, in addition to the expected band at around 185 bp, the presence of a band of about 90 bp is a unique feature of apoptosis in testicular germ

cells. This is because in male germ cells protamines, instead of histones, form the nucleosome particles that yield small lengths of DNA during DNA fragmentation [26].

#### 24.2.2.3 Methods for Detecting Apoptotic Cell Death of Testicular Germ Cells

There are several well-established assays for apoptosis that are applicable to male germ cells. Morphologic methods include microscopic visualization of structural alterations in the cytosol and examination of nuclear morphology and chromatin condensation. Several assays quantitate DNA fragmentation in apoptosis. DNA fragmentation is assayed in the DNA laddering assay by agarose or pulsed field gel electrophoresis [22]. DNA fragmentation is also assayed by TUNEL assay [14]. The flow cytometry measurement (FCM) assay quantitates the incidence of apoptosis by measuring the intensity of a sub G1 peak compared to peaks in other phases of the cell cycle with a DNA staining dye such as propidium iodide [27] or with combined use of Annexin V and propidium iodide [28, 29].

Each method to assess apoptosis has its own advantages and disadvantages. In situ morphologic methods of analysing testicular apoptosis within the seminiferous tubule are critically important because these methods permit us to visualize the stages of development that had been attained by the apoptotic cells at the time of death within the tubule (Fig. 24.1a). Different staining reagents including haematoxylin and eosin (H&E), TUNEL, toluidine blue, and acridine orange have been used for in situ studies [9, 22, 23, 26]. However, whereas the morphologic methods are essential to qualitative characterization of apoptotic cells within the testis, they do not reveal accurate quantitative information. Biochemical studies of apoptotic cell death permit mechanism studies and quantitative analyses. For instance, Western blotting analysis of apoptosis-related proteins is sensitive and quantitative assay for apoptotic cell death.

In addition, the DNA laddering assay can be both qualitative and quantitative for apoptotic cell death because it can not only inform whether there is a ladder or not, but also allows to be quantitatively compared among groups by analysing the laddering DNA contents with densitometry [14, 22, 30]. For the latter, a more sensitive assay has been established to utilize radioisotope to label fragmented DNA, by which small quantities of fragmented DNA can be detected [22, 31]. This procedure utilizes terminal transferase enzyme to uniformly add one molecule of [ $\alpha$  <sup>32</sup>P]-dideoxynucleotide to the 3'-end of DNA fragments. Following gel electrophoresis and autoradiographic analysis, the total amount of radiolabel incorporated into the low molecular weight DNA fraction can be quantitated and used to estimate the degree of apoptotic DNA fragmentation in any given sample [31]. Cyclophosphamide at a low-dose level induces apoptotic cell death of a small percentage of cells in a testicular tissue sample (Fig. 24.1a). Using this radioisotopic DNA laddering procedure it was possible to detect apoptotic cell death of a small number of cells (Fig. 24.1b). Although the DNA ladder and western blotting assays are good for



**Fig. 24.1** Apoptosis in germ cells detected by TUNEL staining and DNA fragmentation. (a) Adult male rats (3 months old) were treated with cyclophosphamide at 70 mg/kg. 12 h later the testes were stained by a modified TUNEL method, as described [22]. Color was developed with 0.05 % diaminobenzidine (DAB) and 0.5 % nickel chloride for 10 min. Testicular tubules were divided

quantitative demonstration of apoptotic cell death in tissues, these two methods do not reveal the localization of the apoptotic cells within the testicular tissue sample.

FCM permits the investigator to quantify the percentage of germ cell types that undergo apoptosis. Healthy germ cells in different stages of development differ in their DNA contents, and those that have undergone apoptosis can be distinguished from those that have not by virtue of their distinct DNA contents. As illustrated in Fig. 24.1c, the FCM DNA content distribution histograms of various germ cells from a whole testicular tissue sample are characterized by the presence of four distinct peaks: subhaploid peak (less than 1n); elongated and round spermatids (1n); diploid or the spermatogonia cells (2n) and tetraploid or primary spermatocytes (4n). The 2n peak also includes non-germ cells such as Sertoli and Leydig cells, which constitute about 3 % of the total cell population; and secondary spermatocytes, the frequency of which is less than the tetraploid population. The region between 2n and 4n peaks represents cells that are actively synthesizing DNA and are termed S-phase cells. The haploid region (1n) is further resolved into two distinct regions because of differential binding of the fluorescent dye. The elongated spermatids undergo greater compaction of the DNA and bind less dye than round spermatids, and therefore fall to the left of round spermatids. These cells are known as the subhaploid peak (less than 1n) while round spermatids bind more dye and represent the 1n peak.

Because of the inherent differences in DNA content in male germ cells at different stages of development, apoptotic cells cannot be identified by FCM analyses of testicular cells without prior isolation and separation of the different differentiated germ cells. This separation must be accomplished in a way that minimizes altering the distribution of the different cell types. We have used discontinuous density gradient centrifugation to separate different types of germ cells to perform FCM for detection of apoptotic cells in the mouse testes exposed to low dose radiation [27]. Experimental results showed that in spermatogonia, incidences of apoptotic cell death measured by FCM and TUNEL are slightly higher than those detected by H&E staining (Fig. 24.1c). In spermatocytes, the incidence of apoptotic cell death

**Fig. 24.1** (continued) into four groups of stages I–IV, V–VII, VIII–X, and XI–XIV, respectively. Apoptotic cells, stained black, are found in controls with a low incidence and in drug-treated animals with an increased incidence. (**b**) Apoptotic DNA fragmentation pattern of control were compared to CYP-treated testicular cells from rats. Assays were conducted using a modified method of 3'-end labeling with <sup>32</sup>PddATP. The molecular weight markers are in the lane labeled M, with sizes indicated in base pairs. Images are adapted from the author's previous work [22] with permission. (**c**) Detection of apoptosis by flow cytometry method (FCM). Principle of detection of apoptotic cells by FCM based on DNA contents of various germ cells. Left panel: FCM distribution of cell types as a function of ploidy. Right panel: pictorial representation of differentiated male germ cell types and their ploidies. (**d**) Quantitative comparison of apoptotic cell death detection methods for spermatogonia (left panel), and spermatocytes (right panel) as a function of LDR dosage at 12 h after LDR. Graphs compare data collected by TUNEL, H&E staining, and FCM methods. The results were presented as the mean ±SD and subjected to one-way ANOVA followed by Student's *t* test [27]. *Asterisk* indicates significant at p<0.05 compared to corresponding controls (0 groups); #, p<.05 compared to 100 or 200 mGy group. Results are adapted from the author's previous work [27]

detected by FCM is significantly higher than that detected by TUNEL and H&E staining methods (Fig. 24.1c). As we discussed above [27], this difference is due to contaminating spermatids in the spermatocyte population isolated by gradient centrifugation. We know that after the secondary spermatocytes complete meiosis II, newly-formed spermatids with a haploid DNA content (1n) would not change the cell size and shape immediately (Fig. 24.1a right panel, inside of the yellow oval). Therefore, the isolated spermatocyte fraction contained a proportion of these newly formed spermatids, indistinguishable from spermatocytes by their size and shape. However, because the peak with less than 2n DNA content would conventionally be scored by FCM as a peak of apoptotic cells, these new-formed spermatids would be counted as apoptotic by FCM in both control and radiation groups. Consequently, an artificially high apoptotic incidence of apoptosis will be scored by FCM compared to H&E staining and TUNEL assay (Fig. 24.1c) [27].

In addition, there was a unique method to identify the apoptotic death of testicular cell with a non-invasive approach using fluorescence labeled Annexin V [32]. This method can provide a unique opportunity to observe the dynamic in vivo apoptotic death of testicular cells without sacrificing animals even though such need may be very small [32]. In summary, because apoptosis in the testis is a dynamic process, no single method accurately quantifies germ cell apoptosis. Multiple approaches are required to accurately determine the incidence and phenotypic distribution of apoptosis in germ cells, dependent on the specific question to be addressed.

# 24.3 Oxidative Stress and Its Toxic Effects on Spermatogenesis

Spermatogenesis is an extremely active replicative process capable of generating approximately 1,000 sperm a second. The high rates of cell division inherent in this process imply correspondingly high rates of mitochondrial oxygen consumption by the germinal epithelium. However, the poor vascularization of the testes means that oxygen tensions in this tissue are low and that competition for this vital element within the testes is extremely intense. Because both spermatogenesis and Leydig cell steroidogenesis are vulnerable to oxidative stress, the low oxygen tension that characterizes this tissue may be an important component of the mechanisms by which the testes protects itself from free radical-mediated damage. ROS are the underlying mediator in a number of sperm toxicants. In the case of biological agents, it has also been possible to demonstrate a direct ability to induce ROS production via immediate pathogen action (e.g. via endotoxin release in the case of gram negative rods) [33].

The testes contain an elaborate array of antioxidant enzymes and free radical scavengers to protect the germ cells and Sertoli cells from oxidative stress. These antioxidant defense systems are very important because oxidative damage is currently regarded as the single most important cause of impaired testicular function underpinning the pathological consequences of a wide range of conditions from testicular torsion to diabetes and xenobiotic exposure [34]. As illustrated in Fig. 24.2, the fundamental biochemistry of these antioxidant enzymes involves the rapid conversion of superoxide anion ( $O_2^-$ ) to hydrogen peroxide ( $H_2O_2$ ) in the presence of superoxide dismutase in order to prevent the former from participating in the formation of highly pernicious hydroxyl radicals. The  $H_2O_2$  generated in this manner is a powerful membrane permeable oxidant in its own right that must be rapidly eliminated from the cell in order to prevent the induction of oxidative damage to lipids, proteins and DNA. The elimination of  $H_2O_2$  is either effected by catalase or glutathione peroxidase (predominating in the testes). Glutathione S-transferase, on the other hand, involves a large and complex family of proteins that catalyze the conjugation of reduced glutathione via the sulfhydryl group to electrophilic centers on a wide variety of substrates in preparation for excretion from the cell. This activity is critical in the detoxification of peroxidized lipids as well as the metabolism of xenobiotics [33].

Oxidative stress reflects an imbalance between the systemic manifestation of ROS and/or reactive nitrogen species (RNS) and tissue antioxidants. Although some ROS and/or RNS can act as cellular messengers, or affect sensitive molecules involved in redox signaling, ROS and/or RNS can be beneficial, as they are used by the immune system as a way to attack and kill pathogens [33]. Excess oxidants become involved in specific and non-specific reactions with nearby cellular components such as unsaturated lipids, proteins and DNA, consequently impairing normal cell processes. Therefore, just as oxidative stress has been implicated in many major diseases, including cardiovascular diseases, cancer, diabetes and brain disorders, it



**Fig. 24.2** Schematic illustration of the generation of ROS and RNS. Superoxide can be generated by specialized enzymes, such as the xanthine or NADPH oxidases, or as a by-product of cellular metabolism, particularly the mitochondrial electron transport chain. Superoxide dismutase (SOD) then converts the superoxide to hydrogen peroxide which is rapidly removed from the system. This is generally achieved by catalase or peroxidases, such as the glutathione peroxidases that use reduced glutathione (GSH) as the electron donor yielding glutathione disulfide (GSSG)

has also been incriminated as the major factor in the etiology of male reproductive toxicology [33].

A large number of independent clinical studies have demonstrated a correlative relationship between male infertility and evidence of oxidative stress in the ejaculate. Moreover, the literature reveals an abundance of experimental data in animal models demonstrating a causal relationship between the induction of oxidative stress in the testes and the impairment of male reproductive function. It is known that there are many factors capable of inducing oxidative stress in the testes. This also implies that testis is a vulnerable tissue that is both highly dependent on oxygen to drive spermatogenesis and yet highly susceptible to the toxic effects of reactive oxygen metabolites [34].

# 24.4 Apoptotic Death of Testicular Cells Induced by Oxidative Stress Conditions

In addition to the evidence mentioned above indicating spontaneous apoptotic death of testicular cells [7, 9, 14–19], they are also susceptible to apoptotic cell death induced by exposure to hyperthermia [35, 36], to chemotherapeutic agents such as cisplatin, etoposide, and cyclophosphamide [22, 37, 38], to chemical agents such as 2,5-hexanedione and 2-methoxyethanol in vivo [39–42], to radiation [27], and even in response to certain chronic diseases such as diabetes [28, 43, 44].

# 24.4.1 Anticancer Drugs

Doxorubicin (DOX) is an anthracycline antibiotic closely related to the natural product daunomycin. Like all anthracyclines, it works by intercalating DNA. It is commonly used in the treatment of a wide range of cancers including hematological malignancies, many types of carcinoma, and soft tissue sarcomas. For DOX, the most serious adverse effect is life-threatening heart damage, but it is also reported to be toxic for testis and male germ cells [45, 46]. Comparing the toxic effects of DOX on somatic and germ cells revealed that there was induction of chromosome damage in both somatic and germ cells, with the frequency of chromosome breakages peaking at 5 h or 1 day for the bone marrow and at 3 and 5 days for the testis after single injection of 3, 12 or 24 mg/kg of DOX. In long-term follow-up studies, DOX was found to induce germ cell death, resulting in a reduction in the numbers of spermatocytes and sperm from mice treated with the higher doses [45]. Eventually, testicular atrophy occurred. In mice treated with 3 mg/kg DOX, there was gradual recovery of spermatogenesis from 50 days onward [45]. When male rats were treated once with DOX at 3 mg/kg on either postnatal day 6, 16, 24, or 45 and then mating studies, sperm counts and assessment of pathological parameters were performed at the time of onset of reproductive capacity of the controls and for 12 weeks thereafter, the male reproductive toxicity of DOX was clearly dependent on the age at the time of treatment, being greatest for 6 day old animals and absent for 45 day old animals [46]. Although there was absence of acute testicular toxicity for 45 day old animals exposed to single a dose of DOX at the low level of 3 mg/kg, delayed and persistent testicular toxic effects could be observed in the animals exposed to multiple doses of DOX event at the lower level of 1 mg/kg [47, 48].

Two early studies investigated rat models to determine whether apoptosis is involved in DOX-induced testicular toxicity [49, 50]. In rats treated with DOX at 5 mg/kg [49], or 8 or 12 mg/kg [50], testes observed with TUNEL staining, suggested the involvement of apoptotic cell death in the toxic effect of DOX. The apoptotic effect of DOX was found also at specific stages of the seminiferous epithelial cycle. The most sensitive cell types were type A and intermediate spermatogonia [49, 50]. This may be related to the fact that premitotic DNA synthesis was more sensitive than premeiotic DNA synthesis to DOX inhibition [51].

Several prevention studies have demonstrated the effectiveness of antioxidants such as lipoic acid [52, 53], melatonin [54], taurine [55], the extract of Ginkgo biloba [56], doxycycline, an antibiotic with anti-oxidant properties [57], ginseng intestinal metabolite-I (GIM-I) [58], and fish omega-3 fatty acids [59] in reducing male germ cell death caused by DOX. These data suggest that the induction of male germ cell death by DOX is predominantly mediated by oxidative stress. Another study examining the protective effects of fish omega-3 (n-3) fatty acids on acute DOX-induced testicular apoptosis and oxidative damage found that acute DOX treatment caused severe damage such as disorganization and separation of germ cells, and pretreatment with fish n-3 fatty acids significantly preserved the normal spermatogenesis of mice exposed to acute DOX by decreasing germ cell apoptosis and oxidative stress [41].

## 24.4.2 Radiation

Male germ cells are highly sensitive to radiation-induced cell death. Dead cells are removed from the testicular tubules, leading to a decrease in the testis weight. However, if stem spermatogonia cells are not killed when exposed to small doses of radiation, these cells can proliferate continually to recover testicular weight at longer times after irradiation [7, 13, 18]. Sexually immature male rats (prenatal stage at 21 days) exposed to 0.5 Gy of  $\gamma$ -rays displayed a 45 % reduction of the testicular weight relative to control values when observed at 26 days after birth [60]. Adult animals (2 months of age) are less sensitive, displaying only about 25 % reduction in the testicular weight at 21 days after they were exposed to the same dose, 0.5 Gy of  $\gamma$ -rays [61]. Considering that the testicular weight is the final result of cell death during the acute phase and cell proliferation during the late phase, the testis weight of animals at the longer post-irradiation may have a greater contribution from proliferating cells than animals at the shorter post-irradiation time. Thus, the death of the testicular cells in the study with observation at 26 days post-irradiation may have more cell death originally in response to 0.5 Gy exposure [60] than that those observed at 21 days [61]. Therefore, although these previous observations were not performed under exactly the same experimental conditions, including species (mouse vs. rat), radiation dose rate and times after irradiation, these results indicate the high sensitivity of the testis of immature or young males [60–63].

Apoptosis induced by radiation is not only dose-dependent, but also cell-type and seminiferous-stage-specific. Hasegawa et al. detected germ cell apoptosis using light microscopy with H&E staining, electron microscopy and TUNEL analyses in 8-week-old C57BL/6 mice exposed to 0.5–5.0 Gy of whole body  $\gamma$ -rays (dose rate 1.69 Gy/min, [64, 65]). The numbers of abnormal spermatogonia detected by H&E and TUNEL positive staining reached a peak 12 h after irradiation and then declined. The total number of spermatogonia began to decline at 12 h. A4–B type spermatogonia at XII–I and I–IV stages and spermatocytes at proleptotene stage are the most sensitive to radiation-induced cell death, as measured by either TUNEL or H&E staining. There were rare TUNEL positive cells among spermatids, Sertoli cells and spermatocytes at VII–VIII stages in response to radiation at 0.5 or 5 Gy [27].

There are only a few studies on the apoptotic response of male germ cells to low dose radiation (<250 mGy low LET radiation). Exposure of mice to 100 mGy X-rays causes an increase in testis weight [60]. In theory, testis weight loss can reflect increased apoptosis or decreased rate of cell proliferation. Conversely, increased testis weight can reflect decreased apoptosis or increased proliferation. Moreno et al. have found that 0.1-0.5 Gy radiation induced both cell death and regeneration of germ cells. Therefore, when prenatal rats were exposed to 0.1 Gy of X-rays (i.e. LDR), LDR-stimulated regeneration of germ cells may be predominant, leading to an increased testis weight [60]. Lambrot et al. showed that there was neither apoptotic cell death nor germ cell proliferation in the human fetal testicular tissues exposed to 0.01 Gy (10 mGy). However, there were both apoptotic cell death and cell proliferation in the human fetal testicular tissues when exposed to 0.1 Gy of  $\gamma$ -rays [62]. In contrast, Otala et al. did not find an increase in testis weight when adult mice were also exposed to LDR (0.1 Gy [61]), suggesting the young animal has high proliferation potential in response to LDR as compared to adult individuals [60, 61].

Recently, Liu et al.[27] have used the TUNEL assay to observe the apoptotic effect of LDR at the dose range of 25–200 mGy of X-rays on germ cells of mice 6, 12, 18 and 24 h after radiation. Comparing results of TUNEL assay with H&E staining and the FCM assay for the apoptotic effect of 25–200 mGy of X-rays in spermatogonia and spermatocytes without distinguishing seminiferous stages at 12 h post-irradiation showed a significant increase in apoptotic cell death by TUNEL and FCM analyses of spermatogonia in response to 25–200 mGy of X-rays. However, the highest incidence of apoptotic cell death was found in the group of spermatogonia, especially at stages of I–VI and X–XII, in response to 75 mGy [27].

As compared to spermatogonia, spermatocytes showed a significant increase in apoptotic death detected by FCM, and slight increase detected by the TUNEL assay. However, the incidence of apoptotic cell death detected by both methods was highest in the group exposed to 75 mGy. In spermatogonia, increased apoptotic cell

death occurs 6–18 h after exposure to irradiation, and gradually decreases thereafter. Spermatogonia exhibit the maximal apoptotic response at same time (12 h) after exposed to LDR as they do after exposure to high dose radiation [64]. In spermatocytes, apoptosis transiently increases 12 h after exposure to 200 mGy of X-rays, but not to 100 mGy of X-rays; both in studies employed TUNEL and H&E staining [27, 64]. Taken together, these results suggest that exposure of adult mice to 25–200 mGy of X-rays induces a significant increase in apoptotic cell death with a maximal effect at 75 mGy.

Biological effects of ionizing radiation are related to its generation of various ROS and indirectly RNS [66]. Therefore, treatment with various antioxidants or antioxidant-like compounds often showed significant protection against radiation-induced testicular cells death. These antioxidants or antioxidant-like compounds include: melatonin [67], L-carnitine [68], and H2 (hydrogen) as a novel radioprotector without known toxic side effects [69, 70]. These studies strongly suggest a pivotal role for oxidative stress in radiation-induced apoptotic death of male germ cells or testicular cells.

## 24.4.3 Diabetes

As mentioned above, testicular cell death is often observed in the testis of individuals with chronic diseases such as diabetes. We reported in the year 2000, that diabetes induces apoptotic death of male germ cells and testicular damage in experimental diabetes induced with streptozotocin [71]. Later, several studies from the author's laboratory demonstrated the induction of male germ cell apoptosis by diabetes under different conditions.

Diabetes induces a significant increase in testicular apoptotic cell death predominantly in spermatogonia and spermatocytes in the testis of diabetic rats and mice, defined by the TUNEL assay [28, 44]. The induction of testicular cell death was associated with mitochondrial dysfunction because the Bax/Bcl-2 ratio as an index of mitochondrial cell death pathway significantly increased in the diabetic group compared to control [28, 44].

Oxidative stress and damage, detected by measuring malondialdehyde [28] and 4-hydroxy 2-nonenal [44], and protein nitration by measuring 3-nitrotyrosine [44] were significantly increased in the testes of diabetic rats and mice. The levels of testicular antioxidants such as catalase and superoxide dismutase were significantly decreased in diabetic rats [28]. One important finding in the study of Zhao et al. is the down-regulation of the transcription factor, nuclear factor-erythroid 2-related factor 2 (Nrf2), in the diabetic testis [44]. Nrf2 regulates basal and inducible transcription of genes encoding protective molecules against various oxidative stresses. Nrf2 plays a critical role in oxidative defense in the testis [72, 73]. Deletion of the Nrf2 gene caused an age-dependent testicular oxidative stress and disrupted spermatogenesis [73]. The significant down-regulation of Nrf2 may explain why multiple antioxidant expressions in the diabetic testis were low [28].

When N-acetylcysteine (NAC) was administered for the first month after the induction of diabetes, testicular apoptotic cell death was significantly reduced [28]. Because NAC is a precursor of glutathione that plays important role in preventing various oxidative damages, the administration of NAC for diabetic rats also significantly prevented the diabetes-induced testicular oxidative damage, measured by malondialdehyde and the depression of endogenous antioxidants such superoxide dismutase and catalase. It is known that both superoxide dismutase and catalase belong to Nrf2 downstream antioxidant targets. These results support the concept that oxidative damage plays a critical role in the induction of testicular cell death by diabetes. Thus, any agent that can up-regulate the endogenous level of antioxidants may afford a protective effect on diabetes-induced testicular cell death.

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# Chapter 25 Toxicogenomics-Based Assessment of Xenobiotic-Induced Oxidative Stress

Christine M. Karbowski, Melissa M. Martin, and Paul Nioi

## 25.1 Introduction

Drug-induced liver injury (DILI) represents a major obstacle during drug development to which numerous black box warnings and market withdrawals are attributed [1–4]. Retrospective analysis of terminated clinical development projects from 1992 to 2002 found that 43 %, 25 %, and 35 % of drugs in Phase I, II, or III, respectively, failed due to toxicological concerns [5]. Of the 16 drugs withdrawn during this period, 27 % were withdrawn due to hepatotoxicity [5]. A recent analysis of data from 2003 to 2011 reported that 31 % of drugs with applications under review for approval by the U.S. Food and Drug Administration were discontinued due to safety, however the nature of the safety reports was not analyzed [6].

Hepatotoxicants are often categorized as "intrinsic" toxicants, with dosedependent toxicities that are reproducible in animals, or "idiosyncratic" toxicants, characterized by infrequent occurrence, no clear dose relationship, and lack of reproducibility in animals [7]. While the mechanisms underlying DILI remain unknown, formation of chemically reactive metabolites and the resulting oxidative stress is considered to play a role in the mechanism of toxicity of both intrinsic and idiosyncratic hepatotoxicants [8]. Therefore, an extensive amount of research has focused on understanding drug-induced oxidative stress.

Cells contain multiple cellular stress response pathways to respond to distinct cellular insults such as inflammation, DNA damage, or heat shock, and which serve to repair and return cells to homeostasis [9]. The Nrf2 oxidative stress response is a critical, inducible cellular pathway which serves to counteract the cytotoxic effects of electrophilic reactive metabolites generated from xenobiotics and oxidative stress

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[8, 10]. Measurement of Nrf2 target genes serves as a surrogate indicator of pathway activation and, in turn, the presence of reactive metabolites and/or oxidative stress following xenobiotic exposure. However, while toxicogenomic studies have been key to identifying reactive metabolite and oxidative stress as a mechanism of druginduced hepatotoxicity, there are limitations with this approach. Specifically, activation of the Nrf2 oxidative stress response pathway, and downstream genes, does not necessarily equate to hepatotoxicity. This poses a challenge when using toxicogenomics as means of prospectively identifying drug candidates that are likely to induce reactive metabolite and/or oxidative stress mediated hepatotoxicity. This chapter will focus on the research leveraging the nuclear factor (erythroid-derived 2)-like 2 (Nrf2) oxidative stress response to identify drug-induced oxidative stress as a mechanism of hepatotoxicity, primarily due to intrinsic hepatotoxicants. Key studies that have established the utility of toxicogenomics in identification of Nrf2 activation as an indicator of xenobiotic-induced oxidative stress, with a focus on drug-induced toxicities, will be discussed. Furthermore, it will explore gaps that remain to be addressed, such as when observation of Nrf2 activation simply represents cellular adaptation and is not necessarily indicative of an adverse outcome.

# 25.2 Nrf2 Activation as a Response to Electrophilic and Oxidative Stress

Reduction of molecular oxygen produces oxidative species such as the superoxide anion, hydrogen peroxide, and the hydroxyl radical. Generation of such reactive oxygen species (ROS) can occur as a normal consequence of endogenous processes including oxidative phosphorylation, the inflammatory respiratory burst, cytochrome P450 metabolism, and peroxisome proliferation. ROS production can also occur due to exogenous sources including xenobiotics that undergo bioactivation leading to chemically reactive intermediates and metals that participate in the Fenton reaction [8, 9, 11–14]. The resulting reactive metabolites and oxidative stress can lead to disruption of critical cellular processes via oxidation of and/or covalent binding to DNA, proteins, and lipids, ultimately resulting in cellular damage and associated pathologies [14–18]. Cells maintain basal levels of antioxidant proteins and enzymes to counteract low levels of oxidative stress, while inducible response pathways exist to increase levels of these critical cellular defense molecules, when necessary [9, 19].

The Nrf2 oxidative stress response pathway is a critical, inducible cellular defense mechanism to counterbalance oxidative stress and maintain cellular redox homeostasis. Recent research suggests that there are multiple mechanisms by which the Nrf2 pathway is activated in response to reactive metabolites and oxidative stress. For a comprehensive overview of the mechanisms of Nrf2 pathway activation and regulation, readers are referred to a recent review [11]. In short, the current theory is that cysteine residues in the Kelch ECH associating protein 1 (Keap1) are modified in the presence of electrophiles, including electrophilic reactive metabolites

and oxidants, which results in disruption of proteasomal degradation of Nrf2 and the consequent increase in transcription of Nrf2 responsive genes. However, it should be noted that Keap-1 independent regulation through alterations in Nrf2 mRNA levels, intracellular localization, and post-translational modifications affecting stability are also proposed to play a role in Nrf2 activation, both during redox sensitive and insensitive conditions [11]. Nrf2 activation results in transcription of cytoprotective genes with an antioxidant response element (ARE). This array of Nrf2 responsive genes includes electrophile conjugating enzymes, antioxidant enzymes, genes regulating glutathione (GSH) levels, and the proteasome (Fig. 25.1; Table 25.1) [9, 11–14]. Activation of the Nrf2 pathway is also intimately tied to xenobiotic metabolism. Phase I metabolism of xenobiotics often leads to oxidant formation and is therefore closely coupled with Nrf2 activation and induction of Phase II detoxification genes [8, 13, 20]. Activation of this transcriptional response serves to restore cellular homeostasis and protect against cellular damage. However, when the levels of pro-oxidants in a cell overwhelm the defense systems, and there is an imbalance in redox homeostasis, adverse cellular events can result.

Disruption of the Nrf2 pathway has been shown to render organisms susceptible to electrophilic and oxidative cellular damage, while there is valid evidence that Nrf2 activation has protective effects. Nrf2 knockout mice demonstrate lower basal and/or inducible expression of xenobiotic metabolism and antioxidant genes in numerous tissues, including the liver [20-23], and also exhibit a greater susceptibility to xenobiotic-induced toxicities, including hepatotoxicity [15, 17, 24]. When treated with acetaminophen (APAP), Nrf2 knockout mice show greater hepatotoxicity than their wild type counterparts [15, 24]. This increased susceptibility is attributed to a reduced ability to restore glutathione levels and to conjugate and excrete APAP [15, 24]. Conversely, mice with hepatocyte-specific disruption of Keap1 demonstrate increased Nrf2 activation and are less susceptible to APAP-induced hepatotoxicity than their wild type counterparts [25]. Similarly, pharmacologic activation of the Nrf2 oxidative stress response is being explored from a therapeutic perspective for conditions in which oxidative stress is thought to play a role, such as cancer, neurodegenerative diseases, and autoimmune diseases [13]. Dimethyl fumarate (BG-12) is an approved multiple sclerosis drug which is proposed to activate Nrf2 through modification of a Keap1 cysteine residue [26], resulting in decreased oxidative stress and cytoprotective effects [27]. Therefore, the Nrf2 oxidative stress response represents a key tipping point in the balance of cellular homeostasis. Activation of this pathway likely indicates the presence of an electrophilic or oxidative stress, but is a necessary cytoprotective mechanism.

## 25.3 Toxicogenomics

The union of traditional toxicology with relatively new molecular profiling technologies, often termed 'omics technologies, has led to the emergence of the distinct discipline known as "toxicogenomics." Oligonucleotide microarrays are commonly


Fig. 25.1 Transcriptional Responses to Nrf2 Activation. Nrf2 activation results in binding of Nrf2 to the Antioxidant Response Element (ARE) in target genes which mediate various protective cellular processes

employed for such studies; however, the emergence of mainstream next generation sequencing platforms and the discovery of additional RNA species, such as microR-NAs, has expanded the field of toxicogenomics beyond traditional mRNA analysis [28–30]. The goal of toxicogenomics studies is to understand mechanisms of xenobiotic-induced toxicities by profiling gene expression changes following xenobiotic exposure [31, 32]. Therefore, toxicogenomics, and liver gene expression profiling in

**Table 25.1** Nrf2 Target genes (Reprinted from, Suzuki, T., H. Motohashi et al, Toward clinical application of the Keap1-Nrf2 pathway. Trends Pharmacol Sci, 2013. 34(6): p. 340–6, with Permission from Elsevier [13])

Function	Symbol	Name	
Synthesis and conjugation of glutathione	GCLC	Glutamate-cysteine ligase, catalytic subunit	
	GCLM	Glutamate-cysteine ligase, modifier subunit	
	GSR	Glutathione reductase	
	GSTA4	Glutathione S-transferase alpha 4	
	GSTM2	Glutathione S-transferase mu 2	
	GSTM3	Glutathione S-transferase mu 3	
	MGST2	Microsomal glutathione S-transferase 2	
Antioxidant	PRDX1	Peroxiredoxin 1	
	SRXN1	Sulfiredoxin 1	
	TXN	Thioredoxin	
	TXNRD1	Thioredoxin reductase 1	
Drug metabolizing	NQO1	NAD(P)H dehydrogenase, quinone 1	
enzymes and transporters	EPHX1	Epoxide hydrolase 1, microsomal (xenobiotic)	
	AOX1	Aldehyde oxidase 1	
	ABCB6	ATP-binding cassette, subfamily B (MDR/TAP), member 6	
	ABCC1	ATP-binding cassette, subfamily C (CFTR/MRP), member 1	
	ABCC5	ATP-binding cassette, subfamily C (CFTR/MRP), member 5	
	SLC25A25	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	
	SLC44A3	Solute carrier family 44, member 3	
	SLC48A1	Solute carrier family 48 (heme transporter), member 1	
	SLC7A11	Solute carrier family 7 (anionic amino acid transporter light chain, xc-system), member 11	
Metabolic enzymes	ТКТ	Transketolase	
	G6PD	Glucose-6-phosphate dehydrogenase	
	IDH1	Isocitrate dehydrogenase 1 (NADP+), soluble	
	ADO	2-Aminoethanethiol (cysteamine) dioxygenase	
	LPL	Lipoprotein lipase	
Heme and iron metabolism	HMOX1	Heme oxygenase (decycling) 1	
	BLVRB	Biliverdin reductase B [flavin reductase (NADPH)]	
	FECH	Ferrochelatase	
	FTH1	Ferritin, heavy polypeptide 1	
	FTL	Ferritin, light polypeptide	

(continued)

Function	Symbol	Name
Transcription factors	AHR	Aryl hydrocarbon receptor
	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha
	HES1	Hairy and enhancer of split 1
	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)
	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)
	RXRA	Retinoid X receptor, alpha
	YAF2	YY1 associated factor 2

Table 25.1 (continued)

particular, is often employed during drug discovery with the goal of reducing drug failure or shifting the occurrence of failure to earlier stages of development through identification, and mechanistic understanding, of drug-induced toxicities.

Global gene expression profiling has clear utility in elucidating mechanisms of toxicity, based on the fundamental concept that drug-induced toxicities are accompanied by gene expression changes mechanistically linked to the toxicity. Consequently, compounds sharing a similar mechanism of toxicity cause common alterations in gene expression [33]. In some cases, toxicogenomics studies are run prospectively in order to predict tissue injury or identify hazards that may not manifest until longer-duration and more resource-intensive toxicology studies are conducted to support clinical development. Toxicogenomics is complementary to assessment of traditional endpoints such as clinical and anatomic pathology and may allow for differentiation of compounds based on mechanism of toxicity. This can help support the selection of clinical candidates for subsequent testing and ultimately shift attrition earlier in drug discovery.

# 25.4 Utilizing Toxicogenomics to Understand Reactive Metabolite and Oxidative Stress Based Cellular Injury and Outcome

The liver plays a major role in energy and xenobiotic metabolism and is frequently exposed to high levels of xenobiotics through the portal vein. As a result, the liver has a high potential for exposure to ROS and reactive metabolites generated from xenobiotics. The resulting oxidative stress creates a particularly high risk for hepatotoxicity. This hepatotoxicity ultimately manifests in microscopic observations of tissue damage and/or clinical chemistry alterations such as increased aspartate aminotransferase (AST) or alanine aminotransferase (ALT). While these endpoints are critical to identify and monitor cellular damage, they are not specific to reactive metabolite exposure or oxidative stress, and represent the convergence of multiple mechanisms of toxicity. In other words, these traditional endpoints do not provide mechanistic information. Thus, toxicogenomics endpoints have been leveraged to fill the gap.

In the case of reactive metabolite and oxidative stress based mechanisms, the resulting activation of the Nrf2 response pathway is particularly well suited for toxicogenomic identification. A key feature of the Nrf2 oxidative stress response is the transcriptional activation of cytoprotective genes [13] which can be leveraged for toxicogenomic studies. Identification of the Nrf2 transcriptional cascade in toxicogenomic studies can indicate the presence of a reactive metabolite and/or oxidative stress, which is useful for hazard identification early in the drug development process. However, identification of the Nrf2 transcriptional cascade alone does not denote or predict the occurrence of toxicity. This pathway sits at the balance point between adaptive and adverse events. As previously discussed, Nrf2 activation is considered to be beneficial and has been demonstrated to have protective effects against reactive metabolites and oxidative stress. In theory, if the response pathway is successful, homeostasis will be restored and there will be cellular recovery. Therefore, toxicogenomic identification of Nrf2 activation can be considered a cellular response signature which provides critical information regarding the presence of a reactive metabolite and/or oxidative stress. However, the relevant question is whether or not there will be an adverse cellular outcome? The Nrf2 oxidative stress response signature, as currently defined, does not necessarily impart information regarding the downstream cellular outcome. Additional gene expression changes are necessary to provide context and evidence of the cellular outcome. For toxicogenomic studies one can envision a model where layers of gene expression changes exist, possibly over a time course, which contain pertinent evidence of the cellular response, Nrf2 activation in this case, and the cellular outcome (Fig. 25.2).

# 25.5 Establishing Toxicogenomics as a Means for Identification of Nrf2 Activation

Early studies proved instrumental in providing a clear link between Nrf2 pathway gene expression changes and xenobiotic-induced oxidative stress. These studies validated Nrf2 activation as a cellular response indicative of the presence of a reactive metabolite and/or oxidative stress. APAP-induced hepatotoxicity has been extensively studied as a model of a drug that causes hepatotoxicity through reactive metabolite and oxidative stress related mechanisms. Toxicogenomic analysis of rat livers following subtoxic doses of APAP (defined not to be associated with alterations in traditional microscopic or clinical chemistry parameters) identified increased expression of stress-related genes [34]. Phenotypic anchoring was then used to validate the oxidative stress gene expression signature observed following a subtoxic dose of APAP: accumulation of nitrotyrosine protein adducts, increased 8-hydroxy-deoxyguanosine, and glutathione depletion, were observed, providing evidence to support the occurrence of oxidative stress at this dose [35]. Nrf2 nuclear translocation and increased expression of the Nrf2 responsive genes which included heme oxygenase-1 (Hmox1), glutamate cysteine ligase catalytic subunit (Gclc), and epoxide hydrolase 1 (Ephx1) demonstrated the direct link between APAP treatment and activation of Nrf2 [36].



**Fig. 25.2** Layers of Toxicogenomic Signatures. Toxicogenomic assessment of Nrf2 activation highlights a cellular response to stress. This cellular response may result in cellular adaptation and recovery. However, in some cases, the protective response is not sufficient to allow for recovery and an adverse cellular outcome occurs. Therefore, assessment of the cellular outcome signature is also critical

Key studies from McMillian et al. demonstrated that toxicogenomic profiling in rat liver could be used to discriminate compounds which act primarily through reactive metabolites or direct oxidative stress from compounds which cause oxidative stress secondary to macrophage activation or peroxisome proliferation [37–39]. Furthermore, they demonstrated that the Nrf2 responsive genes in particular were unique to primary reactive metabolite and oxidative stressors [37–39]. Supervised analysis of a 12 compound training set of reactive metabolite/oxidative stressor compounds led to identification of 100 genes that were most significantly altered when compared to 85 other hepatotoxicants. Using this 100 gene set, 18 additional test set reactive metabolite/oxidative stressor compounds co-clustered with the original training set, and the reactive metabolite/oxidative stressors were discriminated from the other hepatotoxicants, including macrophage activators [38]. Multivariate analysis was then used to distill the gene list down to 25 genes which separated the reactive metabolite/oxidative stressors. This subset of

genes contained the Nrf2-responsive genes Ephx1, NAD(P)H dehydrogenase quinone 1 (Nqo1), glutathione-S-transferase, alpha type 2 (Gsta2), glutathione-Stransferase, mu 1 (Gstm1), and glutamate cysteine ligase, modifier subunit (Gclm) [38]. Not surprisingly, the macrophage activator signature comprised many acute phase response and immune system activation related genes as well as chaperone and endoplasmic reticulum stress related genes [39]. While macrophage activators are thought to cause oxidative stress in the liver, there were only 3 genes in common between the 100 most significant gene changes for the reactive metabolite/oxidative stressor and macrophage activator class. Interestingly, analysis of 36 genes which had been documented to be Nrf-2 regulated genes in mouse liver [40] led to a similar separation of reactive metabolite/oxidative stressors and macrophage activators [38]. These studies indicate that there are distinct transcriptional changes associated with different mechanisms of oxidative stress. Alterations in the Nrf2 responsive genes, in particular, are specific to compounds that act through a reactive metabolite/oxidative stress mechanism rather than macrophage activators or peroxisome proliferators.

These early studies from McMillian et al. were key in demonstrating that gene expression changes, including members of the Nrf2 transcriptional cascade, could be relatively specific to a distinct class of oxidative stressors. However, while the specific gene changes can discriminate reactive metabolite/oxidative stressors from macrophage activators and peroxisome proliferators, the relevant question of cellular outcome remains. The toxicants studied by McMillian et al. were chosen for the most part because they are relatively well-studied hepatotoxicants and there was a priori knowledge regarding the cellular outcome. However, when prospectively analyzing potential drug candidates, this knowledge of ultimate cellular response is lacking. Given the protective nature of the Nrf2 activation pathway, identification of increased transcriptional responses within this pathway does not dictate the occurrence of cellular toxicity. Therefore, when utilizing toxicogenomics to assess Nrf2 activation and the potential toxicity of new potential drug candidates, a greater understanding of the resulting cellular outcome is desirable.

## 25.6 Nrf2 Activation Does Not Necessarily Indicate Toxicity

We assembled a large compendium of liver gene expression data derived from both proprietary molecules and reference toxicants (~300 unique molecules in total). Mining of this toxicogenomics data supports the theory that Nrf2 activation does not necessarily indicate an adverse cellular outcome. Analysis of the state of the Nrf2 pathway (as defined by Ingenuity Pathway Analysis) in this liver dataset highlights that approximately one third of conditions (time-point and dose-level combination) have significant pathway scores for an Nrf2 oxidative stress response 24 h following a single dose. For a subset of ~135 reference toxicants, 69 compounds (123 conditions) demonstrated Nrf2 activation, as determined by a significant IPA pathway score, following single dose treatment. However, analysis of ALT levels as



**Fig. 25.3** ALT Levels of Reference Toxicants with Nrf2 Activation. ALT levels of reference toxicants that received a significant Nrf2 activation pathway level score 24 h following a single dose. ALT levels are shown following a single dose and 4, 8, 15, or 29 days of dosing. In most cases, 3 dose levels are shown. Each color represents a distinct reference toxicant. The *mid line* represents the mean of all vehicle treated control levels. The *upper and lower lines* represent +/–2-fold the mean of the vehicle treated control levels

an indicator of hepatotoxicity revealed that only 6 of these compounds had greater than a 2-fold increase in ALT at the same time point when compared to vehicle treated controls. Longer term treatment led to a greater number of compounds (21 total) with a 2-fold or larger increase in ALT, but the majority of compounds did not result in ALT increases (Fig. 25.3). Furthermore, of the 69 compounds with a significant score for Nrf2 activation following a single dose, only 45 continued to have a significant score following 4 days of treatment. Our experience with internal compounds is similar. These analyses support the idea that a deeper understanding of the resulting ultimate cellular response to drug treatment and subsequent oxidative stress is warranted.

# 25.7 Advancing the Understanding of Reactive Metabolite and Oxidative Stress Induced Cellular Outcome Through Toxicogenomics

Few toxicogenomics studies have attempted to identify gene expression signatures following Nrf2 activation and whether or not this translates to an adaptive or adverse effect. In the case of xenobiotic-induced oxidative stress in particular, the cellular balance between adaptive and adverse effects can be shifted by increasing

the dose and/or by chronic activation over a prolonged period [9]. Therefore, assessment of the time- and dose-dependency of gene expression changes following oxidative insult, along with phenotypic anchoring, is likely to uncover gene expression changes indicative of downstream cellular response. Recently, a toxicogenomics-based approach was used to investigate time-dependent gene alterations following exposure to different oxidants [41]. The goal was to understand the temporal nature of distinct mechanisms of oxidative stress from different species of ROS and to correlate these expression changes with oxidative stress markers. Analysis of menadione, tert-butyl hydroperoxide (TBH), and hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) treated HepG2 cells led to the identification of 136 genes that were commonly modified following exposure to all 3 oxidants. Cluster analysis of the 136 common genes highlighted that the compounds were similar at early time points but diverged over time. This set of 136 commonly altered genes contained documented Nrf2 responsive genes [13] such as GCLC, GCLM, glutathione reductase (GSR), sulfiredoxin 1 (SRXN1), and solute carrier family 7, member 11 (SLC7A11), and pathway analysis highlighted a significant alteration in the glutathione metabolism pathway, which comprises many Nrf2 responsive genes [41]. It should be noted that MetaCore, the pathway analysis tool used by the authors, does not have a distinct Nrf2 pathway for analysis. Rather, Nrf2 responsive genes are contained within other pathways such as the glutathione metabolism pathway. Further analysis of Nrf2 responsive genes highlighted that while members of this pathway were altered by all compounds, the nature of Nrf2 gene expression changes were not similar across the compounds. Menadione treatment resulted in an early, strong increase in expression of the Nrf2 gene (NFE2L2) and a decrease in expression of *KEAP1*, with a subsequent increase at later time points in expression of the Nrf2 responsive genes NQO1, GCLC, GCLM, and HMOX1 [41]. TBH treatment demonstrated a strong increase in expression of the same Nrf2 responsive genes but with no alteration in the Nrf2 gene, while H<sub>2</sub>O<sub>2</sub>, on the other hand, led to a decrease in the Nrf2 gene along with increased expression only of GCLM and GCLC [41]. STEM (Short Time-series Expression Miner) analysis was also used to determine genes that were co-regulated in a time-dependent manner. A similar temporal gene expression profile which contained the Nrf2 responsive genes GCLC, SRXN1, GCLM, and GSR was observed following menadione and TBH treatment. The lack of similarity in temporal gene expression profiles following treatment with H<sub>2</sub>O<sub>2</sub> highlights the potential for temporal differences in Nrf2 activation between compounds. The differences in Keap1 and Nrf2 gene changes over the time course were interesting as they may indicate compound specific effects on Nrf2 activation feedback mechanisms. Menadione and TBH in particular, demonstrated an initial decrease in KEAP1 expression followed by an increase, with menadione also demonstrating increased expression of the Nrf2 gene at most time points.  $H_2O_2$  on the other hand, did not have significant alterations in KEAP1 but did have decreased expression of the Nrf2 gene as time progressed. These subtle differences in key regulatory genes may provide valuable information regarding feedback mechanisms within the Nrf2 pathway which in turn could translate to cellular adaptability and downstream cellular consequences. They

highlight the valuable information that may be gleaned from assessing multiple time points following initial activation of the Nrf2 pathway. Therefore, while this study identifies early gene expression changes following oxidant exposure, it also begins to address the need to identify gene expression signatures beyond the initial cellular response activation. The authors pose that correlation of the compoundspecific gene expression temporal profiles with endpoints suggests that the temporal profiles are indicative of compound-specific cellular responses [41]. However, there are limitations to this study due to the use of an in vitro system which lacks critical elements of drug elimination and other cell types such as Kupffer cells which would be expected to influence cellular response. Extending this type of approach to future in vivo studies could be useful to systematically identify specific gene expression changes denoting of adaptive vs. adverse cellular responses to reactive metabolite and oxidative stress.

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# Chapter 26 Oxidative Stress Responses in Aquatic and Marine Fishes

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Oxidative stress can be defined as the deleterious cellular effects arising from the production of reactive oxygen species (ROS) beyond the capacity of antioxidant defense systems to detoxify them. ROS are reactive O<sub>2</sub>-based molecules including the superoxide anion radical  $(O_2^{-1})$ , the hydroxyl radical (OH), hydrogen peroxide  $(H_2O_2)$ , ozone  $(O_3)$  and singlet oxygen  $({}^1O_2)$ . The importance of oxidative stress and antioxidant defenses in human health and disease has been a major topic of research and clinical application for decades (see review by [1]). More recently, there has been an increasing appreciation for these phenomena in fishes, particularly in the context of pollution of freshwater and marine systems. This has spurred substantial research into a mechanistic understanding of oxidative stress in fishes. The mechanistic study of oxidative stress in fishes serves many purposes: (1) increase our understanding of the basic biochemical and molecular mechanisms related to oxidative stress in fish; (2) explore evolutionary adaptations to oxidative stress to inform our understanding in other vertebrate species, including humans; and (3) understand the impact of prooxidant environmental stressors on fish population health. Many xenobiotics induce the production of ROS by several biochemical mechanisms (Fig. 26.1) such as the impairment of membrane-bound electron transport (e.g., mitochondrial, microsomal electron transport), redox cycling, inactivation of antioxidant enzymes, depletion of free radical scavengers, photosensitization, and facilitation of Fenton reactions [2]. A number of reviews have been published that discuss the nature of ROS, mechanisms by which they are produced naturally and

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Fig. 26.1 An overview of ROS generation by redox cycling, key enzymatic antioxidant defenses, and cellular targets

via xenobiotics, antioxidant defense systems, cellular targets and organismal consequences [2, 3].

Many environmental chemicals of varying chemical classes have been shown to cause oxidative stress in marine and freshwater fishes. The severity of the oxidative stress can be influenced by temperature [4–6], salinity [7–9], and hypoxia [10–12]. It is unclear in many cases whether these stressors are acting synergistically or additively with xenobiotic chemicals since antioxidants and oxidative stress responses can be influenced by many environmental factors, including temperature [13–15], dissolved oxygen [16–19], salinity [20], and acidification [21]. A very interesting case is the notothenoid ice fish that have adapted to the cold, oxygen-rich waters of Antarctica through genomic loss or gene amplification [22, 23] and have a pronounced loss of heat shock response and a non-traditional battery of oxidative stress-responsive genes [24]. This suggests that they might be highly sensitive to the effects of oxidative stress or any other stressor that might promote oxidative stress [25]; therefore, questions arise regarding their ability to adapt to warming in the Antarctic and the increased environmental pollution via global transport mechanisms and expanding ecotourism.

The association of pesticide exposure and oxidative stress is well established for many environmentally-relevant agents, and their structural diversity leads to a spectrum of effects. For example, a number of pesticides have been shown to impact catalase activity [26–28], lipid peroxidation [29–31], and mitochondrial function [32–34]. A relatively recent and thorough review of pesticide-induced oxidative stress in fish was produced by Slaninova and coworkers [35].

Metals are known inducers of oxidative stress in many species of fish, promoting the formation of ROS through either redox cycling [36–38] or interaction with antioxidant defenses, especially with thiol-containing antioxidants and enzymes [39– 41]. Sevcikova et al. have published a thorough review of metals and oxidative stress in fish [42].

Aromatic hydrocarbons are found in nearly all aquatic environments around the globe. They are structurally diverse, but all are composed of one or more benzene rings. In general, aromatic hydrocarbons are metabolized in fish by Phase I enzymes (e.g., cytochrome P450s or epoxide hydrolase) to reactive intermediates that are substrates for conjugation by Phase II enzymes to create hydrophilic metabolites for excretion. As part of this metabolic process, reactive oxygen species are produced that lead to the induction of antioxidant enzymes and protective molecules [43–45]. Also, the metabolic products of PAHs include quinones that can generate ROS via redox cycling [46]. The toxicity of aromatic hydrocarbons can also be increased by exposure to UV light in the environment, which has been demonstrated in a number of fish species and life stages [47–49].

Microcystins are potent cyanobacterial toxins produced by *Microcystis spp.* during bloom events, and their effects on fish and other aquatic animals have been reviewed recently [50, 51]. In cultured fish cells, purified microcystin causes increases in lipid peroxidation and the expression of several antioxidant enzymes [52]. In many whole organism studies using fish, the exposures occur via the addition of cultured *Microcystis spp.* to the water in which the fish are being held. Under these conditions, there is also an increase in lipid peroxidation and the expression of several antioxidant enzymes with the liver being the most affected organ followed by kidney and gills [53]. A few studies have observed that *Microcystis spp.* exposure also inhibits protein serine/threonine phosphatase in liver that may initiate a metabolic response to the toxin (Olivares [54]). Interestingly, *Amado* et al. suggest that hyperphosphorylation linked to ROS is responsible for inducing and maintaining the antioxidant response to *Microcystis spp.* exposure [50]. The exact mechanistic linkages between oxidative stress, phosphorylation state and oxidative stress responses induced by *Microcystis spp.* remain to be determined.

## 26.1 Small Molecule Antioxidant Defenses

A number of small molecules have been shown to have a protective effect in fish under environmentally-induced oxidative stress. We will briefly discuss what are often considered the most important small molecules in the prevention of ROS-induced damage-glutathione, ascorbic acid (vitamin C), and tocopherol (vitamin E). Glutathione is considered the most important small molecule for cellular defense against ROS-induced damage. As observed in mammals, tissue glutathione levels are often depleted after short-term oxidant exposures but elevated after long-term exposures [3, 55, 56]. Glutathione-associated antioxidant enzymes-glutathione peroxidase, glutathione reductase, and glutathione S-transferase-(discussed below) are also critical for maintenance of normal cellular redox status and protection against ROS [2]. Non-glutathione small molecules are increasingly under scrutiny and evidence suggests they also play a critical role in protection against ROS. Ascorbic acid (vitamin C) levels are modulated by environmental chemicals [57, 58] and other environmental stressors including osmotic stress [20] and redox stress associated with air breathing [59]. Tissue ascorbic acid levels have been shown to protect against lipid peroxidation [60]. The majority of studies using fish to investigate the protective effect of tocopherol (vitamin E) are based on dietary supplementation, which can reduce oxidative stress-related biomarkers [61-63]. Environmental toxicants can modulate the levels of tocopheral which may influence ROS-induced damage [64, 65].

## 26.2 Antioxidant Transcriptional Response

Cellular homeostatic mechanisms have evolved to deal with low levels of oxidative stress through modulation of the basal cellular concentrations of glutathione and the transcription factor commonly known as NRF2 (HGNC approved name: nuclear factor, erythroid 2-like 2, symbol: NFE2L2). With elevated levels of oxidative stress, cells can adapt by up-regulation of networks of responsive proteins regulated by NRF2 or NFkB (Fig. 26.2). Most proteins whose expression is regulated by NRF2 activity function as cryoptotectants [66]. The cellular pool of NRF2 is regulated through binding to KEAP1 (kelch-like ECH-associated protein 1), which promotes NRF2 ubiquitination and limits protein half-life. Under oxidative stress conditions, ubiquitination of NRF2 is dramatically reduced and KEAP1 binding sites are rapidly saturated. This leads to an increase in free cytosolic NRF2, which acts as a redox probe and translocates to the nucleus under oxidative conditions [66]. In the nucleus, NRF2 dimerizes with small MAF proteins to up-regulate the transcription of numerous target genes via binding to antioxidant response elements (also known as electrophile response elements) [67].

NFkB is known to regulate proteins that are cryoprotectants and some that are pro-oxidant. While these two functions seem contradictory, the expression of NFkB target genes typically promotes cellular survival in response to numerous cellular stressors [68]. The canonical NFkB pathway is activated mostly under proinflammatory conditions. The NFKB1-RELA dimer is held inactive via interaction with IkB inhibitory proteins. Under oxidative stress conditions, IkB is phosphorylated and subsequently ubiquinated, which allows the NFKB1-RELA dimer to translocate to the nucleus and bind to NFkB binding sites [68].



**Fig. 26.2** Transcriptional activation in response to oxidative stress via NRF2 and NFkB pathways. Both pathways play a key role in the transcriptional responses to oxidative stress. Interestingly, the two pathways have been described as mutually stimulatory and inhibitory in an apparently celltypes specific manner

## 26.3 Antioxidant Enzymes and Protective Targets

These two pathways are largely responsible for transcriptional activation of gene products that protect the cell from oxidative stress-associated damage (Table 26.1). These proteins can be broadly described as antioxidant enzymes or protective targets. Antioxidant enzymes catalyze the elimination of reactive metabolic intermediates and ROS, or are important modulators of these processes. Enzymes such as superoxide dismutase and catalase act directly to detoxify the inorganic free radicals superoxide and hydrogen peroxide, respectively [69]. Enzymes such as glutathione S-transferase and UDP glucuronosyltransferases generally catalyze the conjugation of small molecules (glutathione and glucuronic acid, respectively) to reactive intermediates which makes them readily excretable [70, 71]. In contrast, the enzyme glutamate-cysteine ligase, which has a catalytic subunit (GCLC) and a modifier subunit (GCLM), is the rate-limiting enzyme in glutathione synthesis [72].

Activity	Gene name	Symbol
Glutathione biosynthesis	Glutamate-cysteine ligase, catalytic subunit	GCLC
	Glutamate-cysteine ligase, modifier subunit	GCLM
	Glutathione reductase	GSR
ROS detoxification	Glutathione peroxidase 1A	GPX1A
	Glutathione peroxidase 1B	GPX1B
	Superoxide dismutase 1, soluble	SOD1
	Superoxide dismutase 2, mitochondrial	SOD2
	Superoxide dismutase 3, extracellular a	SOD3A
	Superoxide dismutase 3, extracellular b	SOD3B
	Catalase	CAT
	Peroxiredoxin 1	PRDX1
	Peroxiredoxin 6	PRDX6
Metal binding	Thioredoxin	TXN
	Metallothionein 2	MT2
Glutathione S-transferase	Glutathione S-transferase M	GSTM
	Glutathione S-transferase M3 (brain)	GSTM3
	Glutathione S-transferase pi 1	GSTP1
	Glutathione S-transferase pi 2	GSTP2
	Microsomal glutathione S-transferase 1.1	MGST1.1
	Microsomal glutathione S-transferase 1.2	MGST1.2
	Microsomal glutathione S-transferase 2	MGST2
	Microsomal glutathione S-transferase 3	MGST3
UDP glucuronosyl	UDP glucuronosyltransferase 1 family, polypeptide A6	UGT1A6
transferase	UDP glucuronosyltransferase 2 family, polypeptide B1	UGT2B1
	UDP glucuronosyltransferase 2 family, polypeptide B5	UGT2B5
Reduction	NAD(P)H dehydrogenase, quinone 1	NQO1
	Aldo-keto reductase family 1, member A1A (aldehyde reductase)	AKR1A1a
	Aldo-keto reductase family 1, member A1b (aldehyde reductase)	AKR1A1B
Heme oxygenase	Heme oxygenase (decycling) 1a	HMOX1A
	Heme oxygenase (decycling) 1b	HMOX1B
Hydrolysis	Epoxide hydrolase 1, microsomal (xenobiotic)	EPHX
Iron transport	Ferritin, heavy polypeptide 1a	FTH1A
	Ferritin, heavy polypeptide 1b	FTH1B

 Table 26.1
 Selected antioxidant genes controlled by NRF2 and/or NFkB and identified in fish species

Proteins that function as protective targets can generally be considered ROS scavengers. Many members of the globin gene family (including myoglobin, neuro-globin, cytoglobin) are thought to play an important role in ROS scavenging and are prominent stress-responsive proteins in fish [73–75]. The globin X member of the gene family is found only in fishes and may either protect the lipids in cell membrane from oxidation or may act as a redox-sensing or signaling protein [76]. As in

other vertebrates, metallothioneins and thioredoxins are also important free radical scavengers [16, 77].

# 26.4 Adverse Outcome Pathways, Oxidative Stress, and the Health of Wild Fish Populations

The effects of oxidative stress can be measured and interpreted at the level of individual fish as correlations between biomarker activation and measured changes in physiology. However, when considering impacts on wildlife, it is the impacts at the population level that are most relevant. This relationship between molecular responses, individual health, and population effects are rarely straightforward or readily apparent. The Adverse Outcome Pathway (AOP) framework as defined by Ankley et al. [78] is an approach toward understanding the linkages from a molecular initiating event, through a series of biological processes, to an ultimate adverse outcome of relevance to human or ecological risk assessors (Fig. 26.3). This approach is based on the 2007 report by U.S. National Research Council (NRC) Committee on Toxicity Testing and Assessment of Environmental Agents that sought to transform toxicity testing and embrace newly-developed high-throughput and computational approaches focused on pathways to inform risks to humans (NRC 2007). One primary difference between the NRC approach and the AOP framework approach for ecotoxicology or public health is the focus on populationlevel effects in the AOP.

Oxidative stress and oxidative stress responses are a very important component of many AOPs; however, the nature of oxidative stress responses as homeostatic pathways precludes consideration as a defined AOP [79]. For example, oxidative stress is a key component of proposed AOPs for drug-induced cholestasis and chemical-induced liver fibrosis [80]. At this time, the role of oxidative stress in the initiation of specific disease or dysfunction processes (or AOPs) is rarely well-defined.



Fig. 26.3 Schematic of a generalized Adverse Outcome Pathway. Points where oxidative stress and subsequent and transcriptional responses play a role are indicated. The gray arrows indicate the multiplicity of cellular- and organ-level responses to oxidative stress. Biomarkers are commonly used to indicate (1) oxidative damage that initiates stress responses (e.g. lipid peroxidation, oxidative DNA damage, depleted glutathione levels) to indicate (2) processes that are initiated when homeostatic mechanisms are overwhelmed (e.g. apoptosis, necrosis)

There are numerous biomarkers of oxidative stress that include macromolecular damage (e.g., lipid peroxidation, oxidative DNA damage) or changes in expression levels of oxidative stress-responsive genes (Table 26.1). There is a substantial body of scientific literature that clearly connects toxicant exposure with the generation of oxidative stress and the expression or certain biomarkers. Enhancing our understanding of these linkages to disease and dysfunction will increase the certainty with which one can apply oxidative stress biomarkers to predict and assess the potential for adverse effects at the organism and population level.

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