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Arachidonate Remodeling and Inflammation

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Contents

List of contributors	vii
Preface	xi
<i>Alfred N. Fonteh</i> An outline of arachidonate remodeling and its biological significance	1
<i>Suzanne E. Barbour, Salma Al-Darmaki and Alex D. Manguikian</i> Phospholipase A ₂ and remodeling in inflammatory cells	13
<i>Chad R. Marion and Alfred N. Fonteh</i> Enzymatic and receptor mediated effects of secretory phospholipase A ₂ on the pathophysiology of inflammatory diseases	37
<i>Jesús Balsinde, Rebeca Pérez, Yolanda Sáez and María A. Balboa</i> Control of arachidonic acid levels in resting and activated U937 phagocytic cells by Ca ²⁺ -independent phospholipase A ₂	61
<i>Robert L. Wykle</i> Arachidonate remodeling and PAF synthesis in human neutrophils	73
<i>Allen M. McAlexander, Brooke J. Barham, Margaret Johnson and Alfred N. Fonteh</i> Control of long chain polyunsaturated fatty acid levels and the role of inhibitors of incorporation and remodeling on the biosynthesis of lipid mediators	89
<i>Massimo Triggiani, Giorgio Giannattasio, Francescopaolo Granata, Stefania Loffredo, Francesca W. Rossi, Salvatore Salzano and Gianni Marone</i> Remodeling of arachidonic acid in inflammatory cells of the human lung	115
<i>Royal D. Saunders and Nicolas G. Bazan</i> Arachidonate remodeling, platelet-activating factor signaling, and the inflammatory response in the central nervous system	131

Alfred N. Fonteh and Michael G. Harrington
Remodeling of arachidonate and other polyunsaturated fatty acids in
Alzheimer's disease 145

Charles N. Serhan and Nan Chiang
Lipoxins and resolvins: local mediators in endogenous anti-inflammation
and resolution 169

*Takayuki Sugiura, Seishi Kishimoto, Saori Oka, Maiko Gokoh
and Keizo Waku*
Metabolism and physiological significance of anandamide and
2-arachidonoylglycerol, endogenous cannabinoid receptor ligands 211

Index 239

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Preface

Arachidonic acid (AA) and other 20 or 22-carbon polyunsaturated fatty acids (PUFAs) are precursors of signaling molecules that are critical in disease processes and in regulating normal cell function. Remodeling is critical in homeostatic control and in dictating how PUFAs are converted to mediators. Thus, understanding remodeling will unravel better therapeutic targets for controlling inflammatory diseases.

The review chapters associate AA remodeling and the biosynthesis of mediators of inflammation or pain. By following the movement of AA rather than discussing a single enzyme and its product, the influence of upstream biosynthetic pathways on the formation of lipid mediators and interrelationship between all AA-derived mediators are examined in a comprehensive fashion. This approach innovates AA metabolism by describing new inhibitors, mode of action of these inhibitors and potentially efficacious targets not previously examined.

This volume is written by experts in the field to serve as a rich resource of knowledge for scientists and clinicians in academia, and researchers in the pharmaceutical industry involved in inflammation and pain research. Since AA is derived from essential fatty acids, this volume is also of interest to nutritionists.

July 2003

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An outline of arachidonate remodeling and its biological significance

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Introduction

Arachidonic acid (AA) is a member of the n-6 family of essential fatty acids. Mammals obtain AA directly from vegetable or animal oils or from successive elongation and desaturation of linoleic acid (LA, 18:2, n-6) by the liver (Fig. 1) [1, 2]. Once presented to cells, AA is rapidly incorporated into glycerolipids. This incorporation is initiated by the ATP-dependent conversion of AA to arachidonyl CoA by arachidonyl CoA synthetases [3–6]. AA CoA can then be incorporated into lyso phospholipids by CoA-dependent acyl transferases [7–10]. This initial incorporation of AA into phospholipids is directed mainly into 1-acyl-linked subclasses. Once in these early AA pools, arachidonate is continuously and selectively transferred to 1-ether-linked phospholipids by CoA-independent transacylase (CoA-IT) and CoA-dependent transferase activities present in cells [11–14]. This selective transfer of arachidonate from 1-acyl-linked to 1-ether-linked phospholipids likely accounts for the asymmetrical distribution of arachidonate within phospholipid subclasses such that arachidonate is greater in ether-linked subclasses than in 1-acyl-linked subclasses in many cell types [11, 13–17]. While the most characterized remodeling processes have involved mammalian cells, many studies have shown that remodeling occurs in other cell types and may be a universal phenomenon in which the distribution of AA is maintained within glycerolipid classes. In most studies, remodeling has been characterized as the transfer of AA from 1-acyl-2-AA-GPC to ether-linked phospholipids [16]. However, the initial pool of AA that is labeled may be different in many cell types or in different species. For example, in breast cancer cells, AA is initially incorporated into PI and then remodeled into PE while in amoeba; AA is rapidly incorporated into PE and remodeled into PC. Regardless of the initial entry pool for AA into a cell type, the eventual outcome of the remodeling process is a shift of AA to predominantly ether-linked or triglyceride pools for storage or for utilization in mediator formation [14, 18, 19].

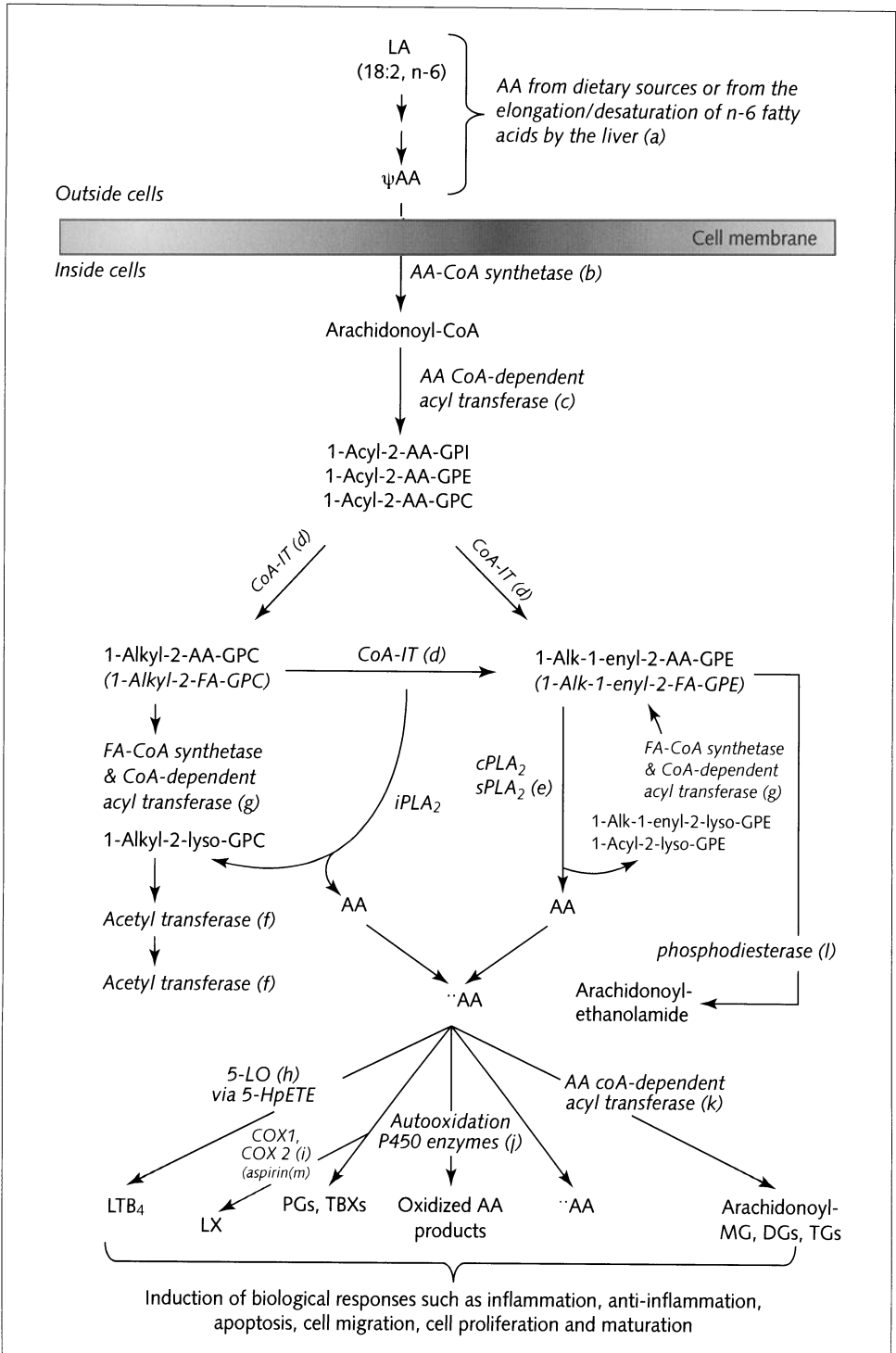
Pro-inflammatory lipid mediators

Under resting conditions, the incorporation and remodeling process is well controlled such that very low levels of free AA are found within cells. However, cellular activation is accompanied by a rapid increase in AA remodeling concomitant with a drastic increase in free AA and AA-derived products [5, 12]. AA is recognized as the major fatty acid precursor of an important class of lipid mediators that are collectively known as eicosanoids. This class of lipids that include leukotrienes, prostaglandins and thromboxanes has been shown to be important as intra- and extra-cellular mediators of cell function. Eicosanoids are produced by a series of enzymatic reactions. Various phospholipase A₂s (PLA₂) may initiate this process by releasing AA from the *sn*-2 position of glycerophospholipids [20–25]. Once released, free AA can induce biological responses in neighboring cells or may be converted to leukotrienes or prostaglandins by 5-lipoxygenases and cyclo-oxygenases, respectively [26–28]. AA that is not converted to eicosanoids can undergo auto-oxidation [29–31] to form bioactive lipids, or it can be rapidly re-esterified into membrane glycerolipids. Under conditions where cells are exposed to high concentrations of AA, there is a shift in the incorporation/remodeling pattern such that

Figure 1

Overview of AA remodeling, role in lipid mediator formation and its potential biological significance

*Free AA is obtained from vegetable or animal oils or from the elongation and/or desaturation of n-6 fatty acids by the liver (a). AA is converted to AA-CoA and incorporated into 1-acyl-linked phospholipid subclasses by AA-CoA synthetase (b) and AA-CoA-dependent acyl transferases (c), respectively. Under resting conditions, AA is gradually remodeled from 1-acyl-linked phospholipids to 1-ether-linked phospholipids by CoA-IT activity (d). During cell activation, the remodeling process is accelerated due to the formation of 1-alk-1enyl-2-lyso-GPE by PLA₂ (e). Enhanced remodeling is also accompanied by an increase in the formation of 1-alkyl-2-lyso-PAF, which is converted, to PAF by acetyl transferase (f). A combination of fatty acid CoA synthetases (FA-CoA synthetases) and acyl transferases acylate lyso phospholipid generated (g). Concomitantly, 5-LO utilizes free AA to form LTB₄ (h), or COX transforms AA to prostanoids and thromboxanes (i). P450 enzymes or autoxidation reactions also convert free AA to potent bioactive lipids (j). AA that is not utilized for mediator formation (AA**) is released from cells to act as a second messenger or to be reincorporated into the remodeling cycle. When there is an excess of free AA within cells, there is increase incorporation into monoglycerides (ligand of CB2 receptors), diglycerides and triglycerides (k). A CoA-, calcium- and ATP-independent transferase in combination with phosphodiesterase activity (l) is responsible for generating arachidonoyl ethanolamide (ligand of CB1 receptor). Changes in AA distribution within lipid classes and the formation of lipid mediators likely play important roles in inflammation, analgesia, cell maturation, apoptosis, cell migration and proliferation.*



AA does not only accumulate in glycerophospholipids, but is rapidly expanded in neutral lipids such as diglycerides and triglycerides [5, 19].

In addition to AA that is converted to bioactive metabolites, PLA₂s also generates lyso phospholipids that are the precursor of another important class of bioactive lipid known as platelet activating factor (PAF). Several studies suggest that CoA-IT and reacylation/deacylation reactions may play a crucial role in the formation of lyso phospholipids such as lyso-PAF (1-alkyl-2-lyso-GPC) when cells are activated [32–36]. CoA-IT catalyzes the selective transfer of arachidonate from 1-alkyl-2-arachidonoyl-GPC to 1-alk-1-enyl-2-AA-GPE acceptors thereby forming the PAF intermediate 1-alkyl-2-lyso-GPC (Fig. 1). Acetylation orchestrated by acetyl transferase converts this intermediate to PAF [35].

Anti-inflammatory lipid mediators

Serhan and colleagues have extensively characterized another class of AA-derived mediators, known as lipoxins (LX) [37]. LX are trihydroxytetraene-containing eicosanoids formed by a combination of various LO activities. Interestingly, aspirin has been shown to trigger the biosynthesis of LX and novel receptors for these mediators have been cloned and characterized [38–40]. Various stable analogues of LX have been synthesized and shown to inhibit chemotaxis, adhesion and transmigration of inflammatory cells in various animal models of inflammation [41]. Together, LX and RX are distinguished from other eicosanoids by having anti-inflammatory properties that can be harnessed for the treatment of many diseases.

In addition to AA-derived anti-inflammatory mediators, other long chain PUFAs have recently been shown to be precursors of novel mediators [42]. For example, human COX-2 has been shown to generate stereo specific-oxygenated products of eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA). EPA and DHA are n-3 fatty acids that are implicated in anti-inflammation. DHA, a major PUFA in brain and retina, is released from mainly phosphatidylethanolamine after cell activation and is then converted to novel docosatrienes by glial cells *via* various hydroxyperoxy-DHA and epoxide-containing intermediates [43]. Transcellular metabolism of 17-HDHA results in its conversion to resolvins. Docosanoids and resolvins regulate the resolution of the acute phase of inflammation in many animal models of inflammation [42, 43].

Conjugated AA species

Recently, new classes of AA-derived metabolites consisting of AA attached to ethanolamine, or to amino acids such as glycine, have been described in mammalian brain tissues [44].

Arachidonylethanolamide (also known as arachidonamide or anandamide) is the natural ligand of the cannabinoid CB1 receptor while lipoamino acids such as N-arachidonoyl glycine, N-arachidonoyl γ -aminobutyric acid and N-arachidonoyl-alanine lack affinity to CB1 receptors. Studies have shown that these widely distributed lipoamino acids have a physiological role in controlling analgesia [45, 46]. A novel calcium-, CoA- and ATP-independent pathway, which is highly selective for AA as the aliphatic constituent, is specific for ethanolamine as the polar group, catalyzes the synthesis of arachidonylethanolamide. Enzymes responsible for the synthesis of arachidonylethanolamide are located in brain microsomal and cytosolic fractions. Arachidonylethanolamide is formed either by the direct conjugation of AA to ethanolamine or by the combined activities of transacylase and phosphodiesterase. Initially, AA located in diarachidonoyl GPC is transferred to ethanolamine head group by transacylase. Subsequently, the arachidonylethanolamide is cleaved by phosphodiesterase activity to release it within brain tissues [44, 47]. Thus, the incorporation and remodeling of AA from specific phospholipid pools to PE or to specific membrane locations within the brain may be crucial in regulating the formation of arachidonylethanolamide and these important lipoamino acids. Another AA-derived molecule, arachidonoylglycerol has recently been shown to be the natural ligand of the cannabinoid CB2 receptor and is likely formed by acyl transferase-dependent mechanisms [48].

Oxidized phospholipids and novel pathways

The classical pathway for eicosanoid biosynthesis assumes that AA must be released by lipases and made available for oxygenation. However, recent studies show that prostanoids and related oxygenated compounds can be found acylated to phospholipids [49–53]. Moreover, prostanoids and related compounds can also be formed independent of enzyme activity *via* auto-oxidative pathways [54]. The oxidized lipids are very potent mediators of biological function and are implicated in many disease conditions.

PUFA-derived products and lipidomics

While the above outline has concentrated on the remodeling of AA and the generation of AA products, it is worthwhile noting that other PUFAs, especially those of 20 or 22 carbon chain length, can also be utilized for generating lipid mediators as has been demonstrated by Serhan and colleagues [42, 43, 55]. One can envisage various COX or LO-derived products of these PUFAs. Interestingly, these products can also be conjugated to various amino acids leading to the formation of new classes of mediators. These new structures have different biological activities based on the

affinities of the new compounds for novel receptors. The new field of structural elucidation of all lipids, recently termed lipidomics, will be advanced rapidly as new tools are being utilized for characterizing these new molecules. Of interest is the use of liquid chromatography coupled to electrospray ionization tandem mass spectrometry to identify over 500 molecular species of phospholipids [56], discover docosatrienes or to identify oxidized phospholipid species [52, 57]. A comprehensive determination of all lipid molecular species and oxidized products will be the backbone for a searchable database that will facilitate functional lipidomics. An understanding of the importance of lipids in diseases will be the basis for applied lipidomics where nutritional supplements can be used to control the signs and symptoms of diseases.

Summary

Overall, a critical look at AA metabolism suggests that it is a very complex process. First, AA levels are tightly controlled in resting cells by many enzyme activities. Secondly, AA is asymmetrically distributed between different phospholipid classes and subclasses. In most cells, the bulk of AA resides in ether-linked phospholipid subclasses. Thirdly, cellular activation or injury creates an imbalance in AA incorporation/remodeling leading to the release and buildup of free AA levels within cells. Under these conditions, the distribution of AA may be altered such that classes of glycerolipids that normally have low AA are substantially enriched with AA. Fourthly, cellular activation/injury is accompanied by rapid deacylation/reacylation of arachidonate within glycerolipid classes. These changes in arachidonate distribution are closely linked to pathological conditions. Fifthly, free AA is converted to bioactive lipid mediators. These mediators are implicated in inflammation, analgesia, apoptosis, cell migration, maturation and proliferation through processes linked to receptors, signaling pathways involving kinases and the activation of various transcription factors [14, 17, 45, 58–64]. Recent advances in technology are revealing that other PUFAs are remodeled in similar fashion as AA and can also be utilized in mediator formation. These important observations underscore the importance of the AA remodeling process in cell function. Details examining the critical roles of enzymes that regulate AA homeostasis (incorporation and remodeling) will be examined in detail in subsequent chapters of this book.

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Phospholipase A₂ and remodeling in inflammatory cells

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Acyl chain composition of glycerophospholipids

For many years, lipids were long thought to be merely the bricks and mortar that composed cell membranes. However, in the past 20 years it has become evident that these molecules are not merely passive building blocks but contain information that can be unleashed when they are metabolized upon cell activation. The signaling properties of specific glycerophospholipids and their metabolites highlight the importance of lipid composition in cell homeostasis. For example, phospholipid to sterol ratios are tightly maintained and the loss of these ratios is thought to contribute to foam cell death and the progression of atherosclerosis [1, 2]. Different cell types not only vary in the relative abundance of each phospholipid class, but also in the fatty acyl composition within each class of phospholipids [3, 4].

Glycerophospholipids consist of a glycerol backbone to which substituents are esterified (Fig. 1). The *sn*-3 carbon is occupied by a phosphate ester that in turn is associated with a polar alcohol (e.g., choline, ethanolamine, phosphorylated inositol). The glycerophospholipid class is determined by the polar alcohol at the *sn*-3 position (choline, ethanolamine, etc.). Long chain hydrocarbons (fatty acids) are esterified at the *sn*-1 and *sn*-2 carbons. Typically, the *sn*-1 carbon is occupied by a saturated fatty acid, while some phospholipid subclasses contain ether- or vinyl ether-linked hydrocarbons at the *sn*-1 position [3, 4]. In mammalian glycerophospholipids, the *sn*-1 acyl chain length is typically C-16 or C-18 [3, 4]. The acyl chain in the *sn*-2 position can vary tremendously, ranging from the minimal *sn*-2 acetyl moiety of platelet-activating factor (PAF) to acyl chain lengths that exceed 20 carbons. Although saturated fatty acids can occupy the *sn*-2 position of glycerophospholipids, this position is often enriched in long chain unsaturated species [3, 4]. Inflammatory cells (macrophages, neutrophils) in particular are noted for the prevalence of polyunsaturated fatty acids in the *sn*-2 position [3, 5]. The fatty acyl composition of the glycerophospholipids of inflammatory cells has important implications for the functioning of these cells, as some of these substituents (arachidonic acid, in particular) are precursors of bioactive lipids that regulate the inflammatory response [5, 6].

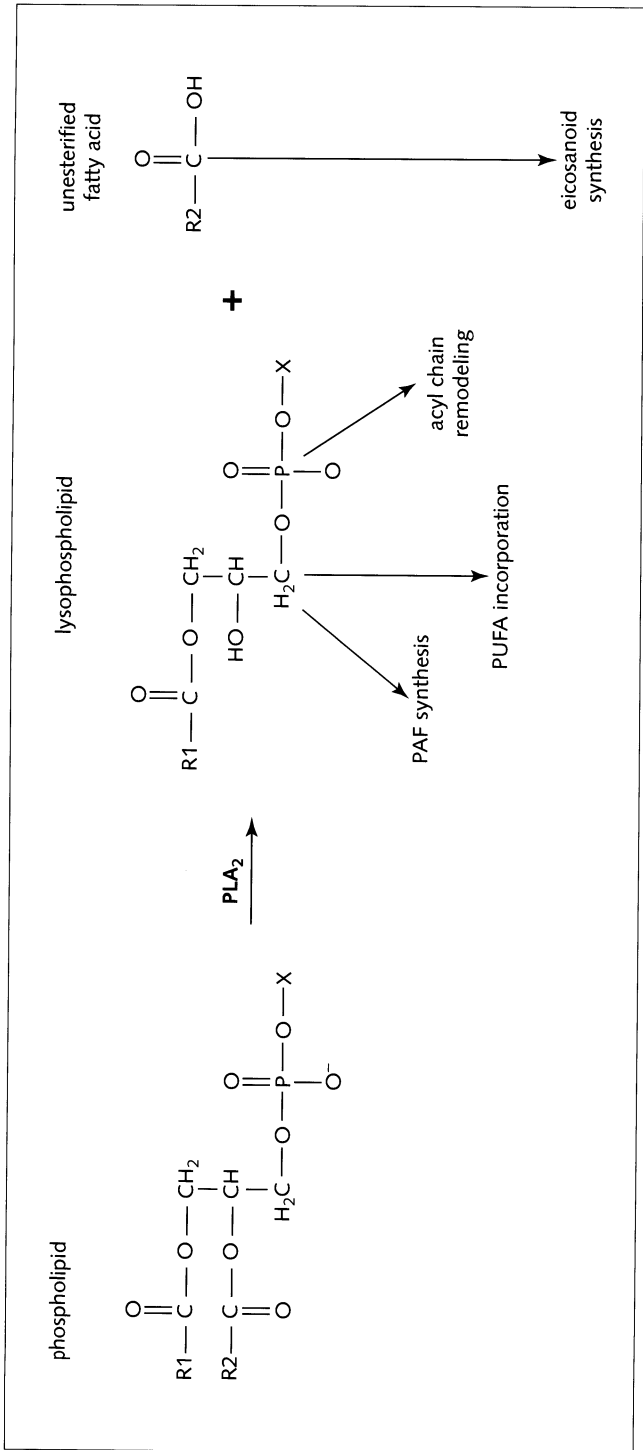


Figure 1

The phospholipase A₂ reaction and its effects on glycerophospholipid metabolism

The phospholipases A₂ (PLA₂) catalyze the hydrolysis of sn-2 acyl chains from glycerophospholipids, producing lysophospholipid and unesterified fatty acid as products. Oxygenated derivatives of one sn-2 fatty acid, arachidonic acid, promote the inflammatory response through their interactions with G protein coupled receptors. In addition, nuclear receptors for arachidonic acid metabolites have been associated with the regulation of cell cycle progression. The lysophospholipid product is associated with regulation of the acyl chain composition of glycerophospholipids as it is essential for both the initial incorporation of polyunsaturated fatty acids (PUFA) into glycerophospholipid and for acyl chain remodeling. In addition, lysophospholipid is involved in the synthesis of platelet-activating factor (PAF), another bioactive lipid.

The acyl chain composition of glycerophospholipids is determined both by the endogenous fatty acids that are produced by a cell and by exogenous fatty acids that are derived from the diet. Acyl chain composition is also determined by the specificity of the biosynthetic enzymes that generate glycerophospholipids. In mammalian cells in general, saturated and monounsaturated fatty acids are incorporated during the *de novo* synthesis of glycerophospholipids [3, 4]. However, the incorporation of long chain polyunsaturated fatty acids such as arachidonic acid occurs much later and is largely dependent on the Lands pathway [3, 4, 7, 8]. In the Lands pathway, the *sn*-2 acyl chain is hydrolyzed from intact glycerophospholipid generating a lysophospholipid acceptor for polyunsaturated fatty acid. Typically, the source of the polyunsaturated fatty acid is a coenzyme A (CoA) adduct in a reaction catalyzed by a CoA-dependent acyltransferase. Although none of these enzymes has yet been cloned or purified to homogeneity, it is clear that they exhibit acyl chain specificity [3–5, 9–11]. This acyl chain specificity is of particular importance in inflammatory cells in which acyltransferases with specificity for arachidonic acid (C20:4) and other long chain polyunsaturated fatty acids have been identified [12–14]. The substrate specificity of the acyltransferases in inflammatory cells also impinges on the observation that *sn*-2 acyl chains are not static, but are remodeled during the lifetime of the glycerol backbone. For example, arachidonic acid is initially incorporated into diacylphosphatidylcholine (PC) but over time is transferred into ether-linked species of PC and phosphatidylethanolamine (PE) [5, 14–17]. This process of fatty acid remodeling typically involves CoA-independent transacylases that transfer polyunsaturated acyl chains directly from intact PC to lysophosphatidylethanolamine (lysoPE), most likely through an enzyme-fatty acid intermediate [3, 4]. As a result of these reactions, the ether-linked subclasses of PE and PC in macrophages and neutrophils are enriched in polyunsaturated fatty acids [18–21]. As noted above, this enrichment has functional consequences for inflammatory cells, as it generates a pool of precursor for such bioactive lipids as the eicosanoids and platelet-activating factor (PAF).

The phospholipases A₂

Both the initial incorporation of polyunsaturated fatty acids into glycerophospholipids and their remodeling among phospholipid subclasses are dependent on sources of lysophospholipid [3–5]. The generation of these lysophospholipids is most closely associated with the phospholipase A₂ (PLA₂) family of enzymes [22, 23]. These enzymes are defined by their hydrolytic actions on the *sn*-2 carbonyl of glycerophospholipids. Although the PLA₂s vary in their substrate specificities, all of these enzymes generate lysophospholipids and unesterified fatty acids as the products of their reactions (see Fig. 1). As noted below, some of the PLA₂ enzymes also possess lysophospholipase activity and therefore can limit the accumulation of

Table 1: Families of phospholipase A₂ enzymes

Enzyme	M.W. (kDa)	Ca ²⁺ ?	Active site	Expression	Location	Regulation
sPLA ₂	14–18	mM	His-Asp	Inducible	Extracellular	Expression
cPLA ₂	85 (α)	μM	GLSGS	Constitutive	Cytosol	Ca ²⁺ , PO ₄ (α,β)
iPLA ₂	80	None	GxSxG	Constitutive	Cytosol	Oligomerization?

detergent-like lysophospholipids. In addition, as lysophospholipids serve as the initial acceptors for polyunsaturated fatty acids, the PLA₂s play important roles in determining the acyl chain composition of glycerophospholipids.

The PLA₂s vary tremendously in their primary, secondary, and tertiary structures, catalytic mechanisms, substrate specificities, subcellular localization, and regulatory mechanisms [22, 23]. To date, at least twelve PLA₂ family members have been identified and these enzymes are found in a diverse array of species ranging from bacteria and invertebrates to reptiles and mammals. The PLA₂s are typically grouped into three broad families of enzymes: the secreted or sPLA₂s, the cytosolic or cPLA₂s, and the calcium-independent or iPLA₂s (Tab. 1). As will be noted below, some of these monikers are rather unfortunate as they describe members of several families of PLA₂.

The sPLA₂s were the first family to be identified and studied intensely, in large part due to the accessibility of these enzymes [24]. As their name implies, the sPLA₂s are all secreted enzymes and are found in high concentrations in snake and bee venoms [23, 24]. In the late 1980s, it became apparent that mammalian cells also express sPLA₂s and that the expression and secretion of these enzymes are induced in inflammation [25–31]. The sPLA₂s are relatively small enzymes, ranging from ~12–18 kDa in molecular mass. A common structural characteristic shared by all of the sPLA₂s is the presence of multiple (5–8) disulfide bonds [23, 32, 33]. Thus, these enzymes have a rather rigid structure and are only active when sequestered away from the reducing environment of the cytosol. The catalytic activity of the sPLA₂s is strictly dependent on calcium at mM concentrations and this cation plays an essential role in the catalytic mechanisms of these enzymes. The association with calcium is mediated through the “calcium binding loop”, a glycine-rich stretch of amino acids [23, 24, 32]. The calcium ion has been shown to co-ordinate with the *sn*-3 phosphate and *sn*-2 carbonyl and thereby to stabilize the transition state of substrate in the active site of the sPLA₂ [34, 35]. The active site itself consists of a histidine-aspartic acid pair that participates in a charge relay system resulting in the polarization of a water molecule, the nucleophile that actually attacks the *sn*-2 carbonyl [34, 35]. The sPLA₂s show little specificity for the acyl chain in the *sn*-2 position, although some sPLA₂s appear to preferentially hydrolyze anionic phospho-

lipids [36–38]. Importantly, the expression of these enzymes is typically very low in resting cells but is induced upon activation with such pro-inflammatory stimuli as interleukin 1 (IL-1), interleukin-6 (IL-6), and bacterial lipopolysaccharides (LPS) [26, 39–43]. This regulatory mechanism impinges on the functioning of the sPLA₂s in the lipid metabolism of activated mammalian cells, in particular on their roles in the production of eicosanoids and other pro-inflammatory lipids.

The cPLA₂ family was initially named based on its localization in the cytosol of mammalian cells. This turns out to be a rather unfortunate choice, as it is now known that other PLA₂s (the iPLA₂s, in particular) are also localized to the cytosol [22, 23]. As a result, it has also been proposed that this family be called the calcium-dependent cytosolic PLA₂s. This choice is also inappropriate, as at least one cPLA₂ family member is known to be calcium-independent [44, 45]. Thus, cPLA₂ is a rather diverse class of enzymes that are grouped together based on rather loose structural homologies [22, 23]. The first family member to be described (and the best studied and understood) is the group IVA cPLA₂- α . Although the catalytic activity of this enzyme is calcium dependent, requiring μ M concentrations like the sPLA₂s, it has no structural homology and has a distinct catalytic mechanism. In fact, the catalytic mechanism of cPLA₂- α is more closely akin to that of general lipases, as an active site serine serves as the nucleophile that attacks the *sn*-2 carbonyl [46–48]. The calcium-dependence of cPLA₂- α is related to substrate binding. The enzyme has an N-terminal C2 domain and has been shown to translocate from cytosol to membrane (substrate) in a calcium-dependent manner [49–51]. Several lines of evidence indicate that cPLA₂- α activity is augmented when the enzyme is phosphorylated on serine 505, although there is some discrepancy regarding the kinases that mediate this phosphorylation, the relationship of phosphorylation to calcium dependence/translocation, and the physiological relevance of phosphorylation [52–57]. Together, the regulation of cPLA₂- α by calcium and phosphorylation suggest that this enzyme plays a role in the lipid metabolism of activated cells. This hypothesis is borne out by mounting evidence that the enzyme is activated in response to receptor-dependent stimuli and that it plays an essential role in the production of bioactive lipids by activated cells [58–64]. To this end, it is of interest that cPLA₂- α shows a preference for hydrolyzing arachidonic acid in the *sn*-2 position of glycerophospholipid and therefore contributes to eicosanoid production by inflammatory cells [65–67].

Two other cPLA₂ family members have been cloned, cPLA₂- β and cPLA₂- γ [44, 45]. Little is known about the regulatory mechanisms of these enzymes and they do not appear to be as widely expressed as is cPLA₂- α . However, we have demonstrated that cPLA₂- γ is most likely the isoform expressed by *Naegleria fowleri* amoebae, suggesting that this calcium-independent “paralog” may have important roles in the lipid metabolism of lower organisms [68].

Like cPLA₂, the iPLA₂ family consists of a diverse array of enzymes with the group VIA enzyme being the most intensively studied and understood [22, 23, 69].

As its name implies, the iPLA₂ family shows absolutely no requirement for calcium in its catalytic mechanism. Like cPLA₂, this family uses an active site serine as the nucleophile that attacks the *sn*-2 carbonyl and also acts as a lysophospholipase [70–75]. Unlike cPLA₂- α and cPLA₂- γ , the group VIA iPLA₂ shows little or no specificity for either the *sn*-2 fatty acid or head group of its substrate, although it has been suggested that some iPLA₂s preferentially hydrolyze plasmalogens [70, 71, 76]. A key feature that distinguishes iPLA₂ from the other two families is its regulatory mechanism, as this does not appear to be dependent on cell activation. Indeed, although ATP has been shown to “stabilize” iPLA₂ activity in cell homogenates, there is no evidence that this involves a phosphorylation event [70, 77]. Interestingly, the iPLA₂ pre-mRNA has been shown to undergo alternative splicing events that may impinge on the regulation of enzyme activity [78, 79]. In this regard, it is useful to consider the structure of iPLA₂ by dividing the protein roughly in half. The C-terminal portion of the protein contains the active site serine. Much of the N-terminal portion consists of a series of ankyrin repeats that are thought to mediate the oligomerization of iPLA₂ monomers into a ~320 kDa active homotetramer [70, 79]. Two iPLA₂ splice variants have been described that contain the N-terminal ankyrin repeats but lack the active site serine in the C-terminus [78,79] (see Fig. 2). When over expressed with the full length iPLA₂ (containing both ankyrin repeats and catalytic domain), the splice variant proteins suppress iPLA₂ activity, presumably by acting in a dominant negative fashion to inhibit the association of full length monomers into active tetramers [79]. These observations suggest that the catalytic activity of iPLA₂ may be regulated through alternative splicing. Indeed, our preliminary experiments indicate that the catalytic activity of iPLA₂ is cell cycle dependent and may correlate with the accumulation of splice variant proteins (Manguikian and Barbour, unpublished).

Regulation of glycerophospholipid composition by PLA₂s

As noted earlier, the glycerophospholipid composition of mammalian cell membranes is tightly controlled, both at the level of the phospholipid classes and the acyl chains esterified to the glycerol backbones of each class of glycerophospholipid. Recent studies indicate that the PLA₂s, in particular iPLA₂, may play major roles in the regulation of glycerophospholipid composition of mammalian cells. The involvement of iPLA₂ in these processes is consistent with the constitutive expression and regulatory mechanisms of this enzyme. Unlike the sPLA₂s or cPLA₂, iPLA₂ activity is not controlled by events associated with cell activation and hence this appears to be a homeostatic enzyme [22, 69]. In fact, iPLA₂ appears to play several roles in glycerophospholipid homeostasis, ranging from the regulation of phospholipid mass to the regulation of *sn*-2 acyl chain composition, to the accumulation of lipids for daughter cell membranes.

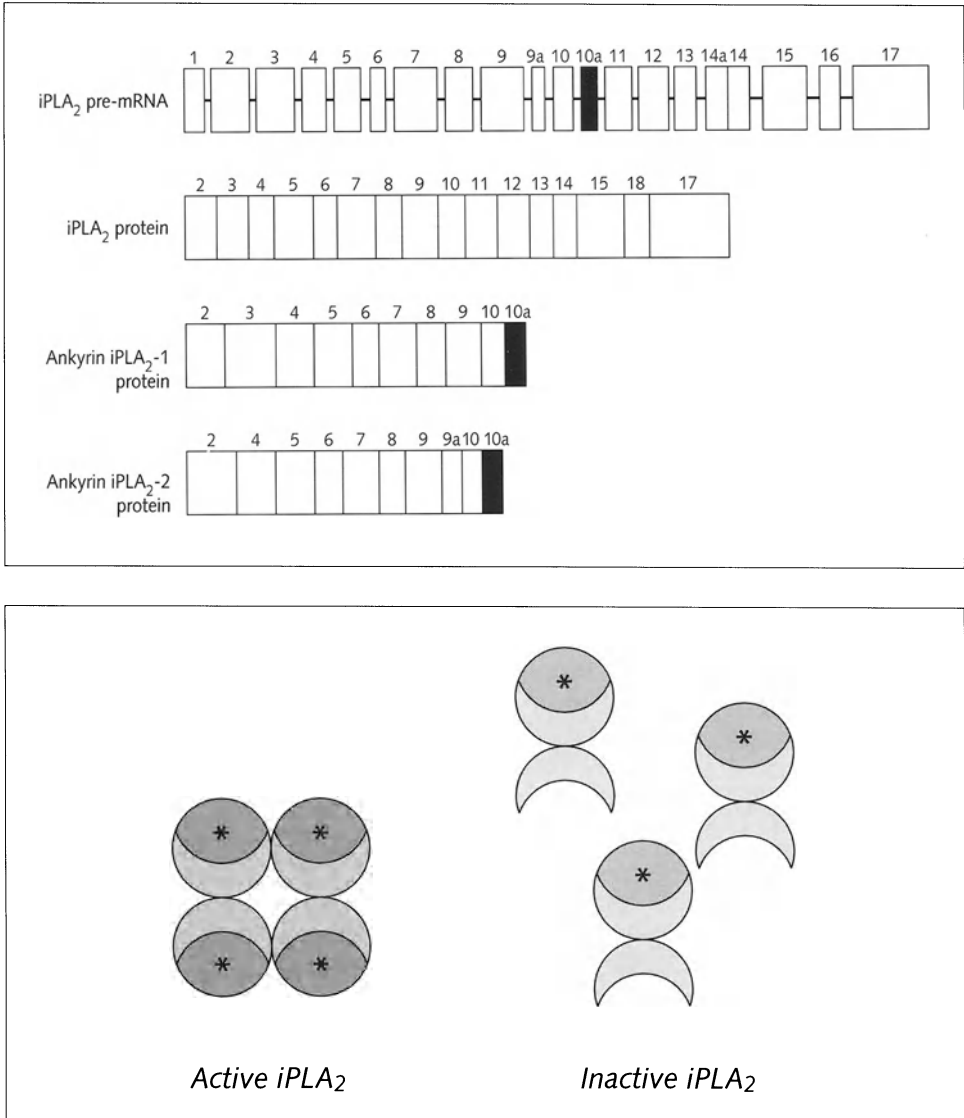


Figure 2

Regulation of iPLA₂ activity

The structure of the iPLA₂ gene is shown along with exon usage for catalytically active iPLA₂ and two splice variants (ankryin-iPLA₂-1 and ankryin-iPLA₂-2) that do not contain the active site and may inhibit iPLA₂ activity through a dominant negative mechanism.

Proposed models for catalytically active and inactive iPLA₂ are shown. The active enzyme is thought to be a homotetramer. The truncated splice variant proteins are proposed to interact with full length proteins through their N-terminal ankyrin repeats and block the formation of active tetramers.

The role of iPLA₂ in acyl chain composition has been most extensively studied by Balsinde et al. These investigators have used a selective inhibitor of iPLA₂, bromoenol lactone (BEL) and an antisense oligonucleotide strategy to study the enzyme in macrophage-like P388D₁ cells [80–82]. Like most other mammalian cells, macrophages do not incorporate arachidonic acid into phospholipids through *de novo* pathways, but rather rely on the Lands pathway to esterify arachidonic acid into existing glycerophospholipid backbones [3, 4]. Balsinde et al. showed that this initial incorporation of arachidonic acid was inhibited in cells with reduced iPLA₂ activity and/or expression, presumably because the enzyme was necessary to generate the lysophospholipid acceptor for arachidonyl-CoA. In macrophages, arachidonic acid is initially esterified into PC, but is rapidly remodeled into the various subclasses of PE and phosphatidylinositol (PI). Interestingly, neither the iPLA₂ inhibitor nor the antisense oligonucleotide had effects on this process. These data suggest that while iPLA₂ is essential for the initial incorporation of polyunsaturated fatty acids into macrophage phospholipids, it is not involved in remodeling *per se*. To date, the identity of the PLA₂ that generates the lysoPE acceptor for remodeled arachidonic acid remains unknown. Although it remains possible that remodeling is mediated by sPLA₂, cPLA₂, or one of the other known forms of iPLA₂, it is likely that this important process is mediated by an as yet undescribed form of PLA₂ [80].

In addition to its role in determining the acyl chain composition of glycerophospholipids, several recent studies have also implicated iPLA₂ in the regulation of phospholipid mass [83–85]. Most of these studies have focused on PC, the most abundant glycerophospholipid in mammalian cell membranes [86]. The initial studies were performed by Walkey and Cornell who showed that over expression of CTP – phosphocholine cytidyltransferase (CT), the rate limiting enzyme in PC synthesis – resulted in a compensatory increase in PC catabolism to maintain mass [87]. The increase in catabolism was associated with the accumulation of glycerophosphocholine, suggesting the involvement of a PLA₂. Baburina and Jackowski [83] subsequently over-expressed CT in a HeLa cell model and demonstrated that a suicide inhibitor of iPLA₂, bromoenol lactone (BEL), prevented the accumulation of glycerophosphocholine. Similarly, BEL treatment both induced PC accumulation in, and allowed the survival of, mutant Chinese hamster ovary (CHO) cells that could not synthesize PC [85]. Our laboratory extended these studies by demonstrating the induction of iPLA₂ protein in CHO cells that over expressed CT [84]. Importantly, this induction was specific for iPLA₂, as neither cPLA₂ or lysophospholipase activity was induced in the over-expressing cells. Conversely, iPLA₂ activity was suppressed in mutant MT58 cells that exhibited little CT activity, although the expression of the enzyme remained unchanged (Barbour, unpublished observation). Based on these studies, we propose that iPLA₂ is co-ordinately regulated with the activity of CT and other synthetic enzymes to maintain lipid homeostasis as is shown for PC in Figure 3. This model proposes that changes in glycerophospholipid synthesis are balanced by changes in iPLA₂ activity such that the mass of a given glycerophos-

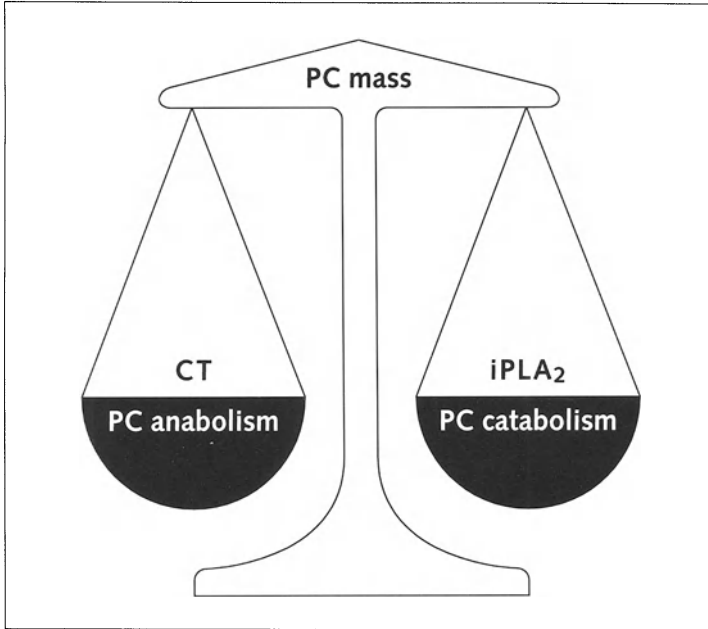


Figure 3

Proposed model for the regulation of glycerophospholipid mass

The model shown is based on phosphatidylcholine metabolism, but is thought to be applicable to other glycerophospholipids. The activities of enzymes involved in glycerophospholipid synthesis (for example, CT, CTP : phosphocholine cytidylyltransferase) are co-ordinately regulated with iPLA₂ activity so that glycerophospholipid mass remains balanced.

phospholipid remains relatively constant. This hypothesis is in accord with the observation that the ratios of glycerophospholipid species in mammalian cell membranes are tightly maintained [4, 12]. It should be noted that a recent report refutes this model and suggests that changes in iPLA₂ expression do not necessarily induce compensatory changes in PC synthesis [88]. While the experiments in this report were performed in transiently transfected COS cells, the proposed model is based on studies of phospholipid metabolism in stably transfected cells. Thus, it is possible that this discrepancy can be attributed to chronic *versus* acute alterations in phospholipid metabolism.

At least one circumstance exists in which homeostasis is not maintained: when lipids are accumulated during the cell cycle for daughter cell membranes. Several lines of evidence indicate that this accumulation occurs during S phase and is not the result of increased glycerophospholipid synthesis but rather a decrease in catabolism [89–94]. Preliminary experiments in our laboratory (Manguikian and Barbour, unpublished) and others [95] indicate that the accumulation of PC during S

phase may be mediated through a decline in iPLA₂ activity. Hence, iPLA₂ not only maintains lipid mass in resting cells, but also controls the accumulation of glycerophospholipids in cells that are actively dividing.

Relevance of lipid composition to the functioning of inflammatory cells

The glycerophospholipids of inflammatory cells such as macrophages and neutrophils are relatively enriched in arachidonic acid (C20:4) and other long chain polyunsaturated fatty acids [3, 5]. This fatty acyl composition almost certainly has important implications for the physicochemical properties of membranes in these cells, as polyunsaturated fatty acids tend to increase membrane fluidity [96–99]. It is also possible that the degree of unsaturation may contribute to the formation of lipid rafts, discrete areas of the plasma membrane that are enriched in sphingolipids, cholesterol, and signaling proteins [100]. Apart from these physical effects, the enrichment of polyunsaturated fatty acids also provides macrophages and neutrophils with raw materials necessary for producing bioactive lipids associated with inflammation. Among these bioactive lipids are the eicosanoids (oxygenated derivatives of arachidonic acid) and platelet-activating factor (PAF), a derivative of PC. Inflammatory cells not only produce these bioactive lipids, but they respond to them as well, typically through G protein coupled receptors.

Two pathways for the synthesis of PAF have been described, a *de novo* pathway and a pathway that is dependent on acyl chain remodeling. The remodeling pathway is thought to be the most relevant in inflammatory cells [3, 5, 15, 17 101–104]. The goal of the remodeling pathway is to generate the PAF precursor 1-O-alkyl-2-lyso-*sn*-glycero-3-phosphocholine (lyso-PAF), a substrate for the CoA-dependent acetyltransferase that generates PAF [101]. A prerequisite for this goal is the removal of the acyl chain at the *sn*-2 position of 1-O-alkyl-PC. This is accomplished, at least in part, through transfer of the acyl chain in a reaction catalyzed by coenzyme A independent transacylase (CoAIT). The CoAIT reaction requires a lyso-PE acceptor and it is thought that this substrate is generated through the actions of a PLA₂.

This mechanism was implicated in early studies in human mesangial cells and HL60 granulocytes (a human neutrophil model) in which inhibitors of sPLA₂ (p-bromophenacyl bromide, mepacrine) were shown to inhibit the synthesis of PAF [64, 105]. The role of sPLA₂ in PAF synthesis was later supported in a variety of primary cell types (human monocytes, PMN, and endothelial cells, for example) treated with scalaradial or SB203347, specific inhibitors of sPLA₂ [106–108]. In contrast, arachidonyltrifluoromethyl ketone (AACOCF₃) and methyl arachidonyl fluorophosphonate (MAFP), inhibitors of cPLA₂ and iPLA₂ have no effect on PAF synthesis by human monocytes, alveolar macrophages, or vascular endothelial growth factor- (VEGF-) stimulated endothelial cells [107–110]. Furthermore, anti-

sense oligonucleotides against cPLA₂ have been shown to suppress expression of the enzyme and the production of prostanoids but have no effect on the synthesis of PAF [107, 109]. Conversely, PAF synthesis is induced when U937 monocytes are treated with recombinant human sPLA₂ while cPLA₂ has no such effect [107]. Together, these data indicate that although sPLA₂ and cPLA₂ are both able to produce lyso-PE, the sPLA₂ reaction is more relevant for PAF synthesis. These observations are somewhat surprising given that PE is enriched in arachidonic acid, that arachidonic acid release is typically observed in concert with PAF production, and that cPLA₂ has been shown to selectively hydrolyze arachidonate containing glycerophospholipids [65–67]. It is possible that the pool of lyso-PE generated by cPLA₂ is rapidly reacylated with long chain fatty acids and therefore is not available as a substrate for CoAIT. Alternatively, the lyso-PE generated by cPLA₂ may be rapidly converted to glycerophosphocholine by the inherent lysophospholipase activity of the enzyme [74, 75]. There is at least one cell type in which cPLA₂ activity may contribute to the synthesis of PAF. We have recently reported that monocyte-derived dendritic cells synthesize large amounts of PAF [111] and our preliminary experiments indicate that this may be related to the high levels of cPLA₂ activity that are exhibited by these cells (Al-Darmaki and Barbour, unpublished).

As the sPLA₂ inhibitors do not target specific sPLA₂ isoforms, it is not known if the production of lyso-PE for PAF synthesis is mediated by specific sPLA₂s. At least one isoform of sPLA₂, the group IIa enzyme preferentially hydrolyzes PE and this may be relevant to the production of lyso-PE for PAF synthesis [36–38]. However monocytes express primarily the group V sPLA₂ [112], suggesting that this may be the relevant isoform for PAF synthesis. Another cautionary note regarding the role of PLA₂ in PAF synthesis regards endothelial cells. A recent report [113] suggests that thrombin-stimulated endothelial cells produce PAF in an iPLA₂-dependent manner. However, the production of PAF by VEGF stimulated endothelial cells is not inhibited by bromoenol lactone (BEL), a specific inhibitor of iPLA₂ [108]. Taken together, existing data are consistent with a role for PLA₂ in the acyl chain remodeling that precedes PAF synthesis, although the specific PLA₂s involved may vary with different cell types and stimuli.

The production of PAF by inflammatory cells is typically accompanied by the production of eicosanoids, oxygenated derivatives of arachidonic acid [3, 5, 101]. The two major families of eicosanoids, prostaglandins and leukotrienes, are produced through the addition of molecular oxygen to arachidonic acid (C20:4) in reactions catalyzed by the cyclooxygenase and lipoxygenase enzymes, respectively. Receptor-dependent stimulation of inflammatory cells induces eicosanoids that then modulate cell behavior and biological responses through their binding to G protein coupled receptors (GPCR) [114, 115]. For example, activated macrophages produce PGE₂, a bioactive lipid that induces such diverse responses as the production of Th2 cytokines, interferon- γ production, bone resorption, and the production of IgG2 antibodies [116–119]. It has been proposed that the rate-limiting step in the pro-

duction of both families of eicosanoids is the release of arachidonic acid from intact phospholipids by a PLA₂ [120,121]. However, it can also be argued that the limiting step is the initial incorporation of arachidonic acid into glycerophospholipid pools, as this is clearly a prerequisite for arachidonate release. As noted above, this incorporation is mediated through the Lands pathway and involves the reacylation of lysophospholipid [3–5]. In macrophages, iPLA₂ activity is essential for generation of the lysophospholipid acceptor for arachidonyl-CoA [80–82]. Although most studies indicate that the release of arachidonic acid from glycerophospholipids of activated cells is mediated by either sPLA₂ or cPLA₂, iPLA₂ has been implicated in these reactions as well [58, 69, 122–124]. Thus, iPLA₂ may play two distinct roles in eicosanoid production by inflammatory cells: the initial incorporation of arachidonate into glycerophospholipid and its release upon cell activation. Interestingly, although iPLA₂ is involved in the release of arachidonic acid by activated pancreatic islet cells, it is not required for the initial incorporation into phospholipids [125–127]. This again suggests that the roles of the various PLA₂s in acyl chain remodeling may be cell type specific.

For many years, it has been known that the eicosanoids can regulate cell behavior by binding to GPCR in the plasma membrane [114, 115]. More recently, intracellular receptors for the eicosanoids have been identified. These receptors, the peroxisome proliferator-activated receptors, PPAR, are DNA binding proteins that, when bound to ligand, translocate to the nucleus and regulate gene expression [128–130]. Three families of PPAR have been described and each family of receptors binds a different spectrum of bioactive lipids or lipophilic drugs. For example, PPAR- α is the target of the fibrate class of hypolipidemic drugs and has been shown to regulate fatty acid metabolism [131, 132]. Endogenous ligands of PPAR- α include linolenic acid and 8S-HETE [128–130]. The biological function of the PPAR- β/δ subtype remains somewhat debatable, although this receptor has also been shown to bind linolenic acid [128–130]. A variety of functions have been ascribed to PPAR- γ , including the regulation of adipogenesis and antagonism of the inflammatory response [133]. Most recently, the ligation of PPAR- γ has been linked to cell cycle arrest through a novel mechanism that explains a large body of data [134].

For many years it has been known that exogenous prostanoids induce growth arrest in a variety of tumor cell types. Specifically, prostaglandin A₂ (PGA₂), prostaglandin D₂ (PGD₂), and 15-deoxy- $\Delta^{12,14}$ prostaglandin J₂ (PGJ₂) have been shown to arrest cells at the border of G1 and S phases [134–140]. This growth arrest has been linked to reduced expression of cyclin D and cdk4 proteins and the induction of p21, a cdk inhibitor [134, 135]. However the molecular mechanism of prostanoid-induced growth arrest has remained elusive until recently. Using MCF 7 breast carcinoma cells as a model, Wang et al. recently demonstrated that PGD₂ and PGJ₂ suppress cyclin D1 expression through their association with PPAR- γ [134]. In these experiments, ligated PPAR- γ was shown to recruit p300 away from a critical c-Fos binding site in the cyclin D1 promoter and thereby suppress transcription of the

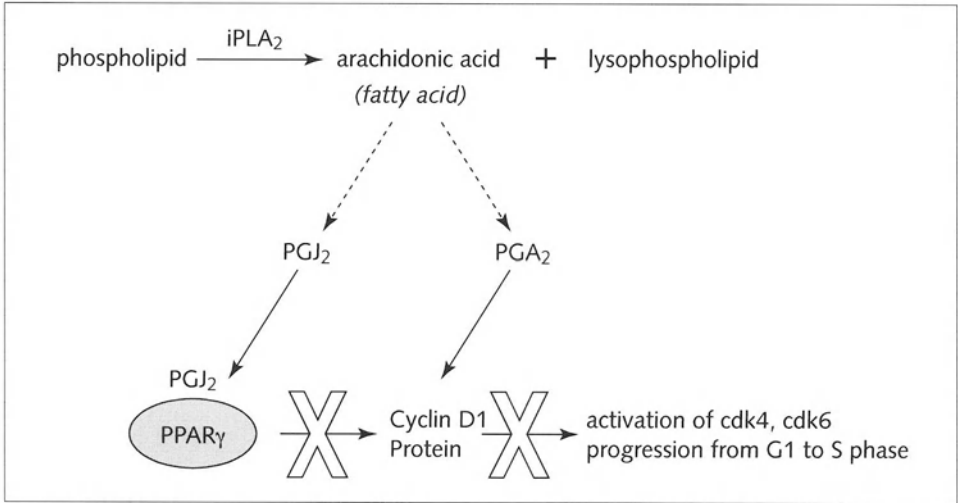


Figure 4

Regulation of cell cycle progression by derivatives of arachidonic acid

Once arachidonic acid has been released from glycerophospholipids by iPLA₂, it can be converted into oxygenated derivatives such as prostaglandin A₂ (PGA₂) and 15-deoxy- $\Delta^{12,14}$ prostaglandin J₂ (15-deoxy PGJ₂). These bioactive lipids are known to down-regulate the expression of cyclin D1 and other proteins that are essential for progression from G1 to S phase and thereby to limit cell cycle progression.

gene. Together, these data suggest that a cell's ability to generate prostanoids can have a major impact on its ability to proliferate. As prostanoids are derived from arachidonic acid, this in turn suggests that cell growth and viability are linked to the acyl chain composition of glycerophospholipid. We have recently demonstrated that the catalytic activity of iPLA₂ (the PLA₂ that provides the lysophospholipid acceptor for the initial incorporation of arachidonic acid into glycerophospholipid) exhibits cell cycle dependence and is lowest at the border of G1 and S phase (Manguikian and Barbour, unpublished). Our work is consistent with a recently published study in human T-cells [141]. In contrast, other phospholipases (e.g., cPLA₂) do not exhibit cell cycle dependent activity. We predict that loss of iPLA₂ activity during G1 results in reduced levels of endogenous prostanoids and that this in turn facilitates entry into S phase (see Fig. 4). There are at least two potential roles for iPLA₂ in this regard, as it can both modulate the amount of arachidonic acid in glycerophospholipids and release incorporated arachidonic acid from glycerophospholipids, thereby regulating the amount of substrate available for the synthesis of PGJ₂, PGA₂, and other prostanoids. Thus, iPLA₂ regulation may be essential for cell cycle progression.

Conclusion and perspectives for the future

For many years, it has been known that the distribution of fatty acids among glycerophospholipid species is tightly controlled and is maintained in a cell type specific manner. Recently, it has become clear that this regulation is essential not only for maintaining membrane structure and fluidity, but also to control the way that cells interact with their environments. This is of special significance for inflammatory cells such as macrophages and neutrophils as these cells produce a battery of bioactive lipids and are also capable of responding to these molecules in ways that dramatically affect the host immune response. Among these bioactive lipids are oxygenated derivatives of arachidonic acid and platelet-activating factor (PAF). Acyl chain remodeling is essential for production of both of these classes of bioactive lipids. This process is dependent on the activities of various forms of PLA₂, the family of hydrolases that generate lysophospholipid acceptors for acyl chain remodeling. Hence, identification of the specific forms of PLA₂ involved in remodeling and a clearer understanding of their catalytic mechanisms and regulation may facilitate the development of novel strategies to control inflammatory cells and the bioactive lipids that they produce. In addition, as some derivatives of arachidonic acid have been implicated in the regulation of cell cycle progression, such studies may also provide insights into novel mechanisms to control the proliferation of transformed cells.

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Enzymatic and receptor mediated effects of secretory phospholipase A₂ on the pathophysiology of inflammatory diseases

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Overview of phospholipases

Phospholipases A₂ are enzymes that share the common attribute to hydrolyze fatty acids from the *sn*-2 position of glycerol phospholipids [1–3]. Groups I, II, V and X PLA₂ are four sets of enzymes in a highly conserved family of secreted PLA₂ found in mammals [4–14]. Other non-secreted PLA₂ enzymes include group IV, cytosolic PLA₂ (cPLA₂) [15–17], group VI, calcium-independent PLA₂ (iPLA₂) [18–22] and groups VII and VIII, selective acetyl hydrolases [23–28]. The secretory family of enzymes has a number of features that distinguish them from other PLA₂ families including a relatively low molecular weight (~ 14 kDa), high disulfide bond content and a requirement for relatively high concentrations of calcium for maximal activation [29, 30]. In contrast, cytosolic enzymes are generally higher molecular weight proteins and require no calcium or very low calcium concentrations for optimal activation [18, 22]. Many sPLA₂ isotypes are synthesized as proenzymes that contain a signal peptide sequence that facilitates its release from cells. sPLA₂ isotypes have been studied extensively in mammals and in snake venoms, yet there is no clear understanding of their physiological and pathophysiological roles. Inspection of numerous publications dealing with sPLA₂s reveals that they have potential to mediate a wide range of biological activities including:

- 1) Producers of AA that contributes to eicosanoid formation [31–36];
- 2) Generation of lysophospholipids that contribute to electrophysiologic alteration that lead to arrhythmogenesis in the heart or altered airway permeability and surfactant properties in the lung [37–48];
- 3) Potent antibacterial effects and implications in viral infections [49–54];
- 4) Key components in glycerophospholipid digestion [55];
- 5) Serum markers and potential regulators of severe illnesses such as sepsis, shock, organ injury and pancreatitis, all of which are linked to the development of adult respiratory distress syndrome or multiple organ failure [56–75];

- 6) Regulators of platelet aggregation in hemorrhagic diseases [76–78];
- 7) Prevention of apoptosis of inflammatory cells and initiators of cell proliferation in several cancer cell lines [79–82];
- 8) A potent modifying locus in intestinal tumorigenesis in mice that is absent in human [83];
- 9) Pro-inflammatory components in diseases such as rheumatoid arthritis and asthma [84–93].

This overwhelming list of biological activities and diseases raises deep-seated questions as to whether sPLA₂ cause or is merely associated with the aforesaid effects. It also raises questions about molecular mechanisms that this family of enzymes could influence in order to control such a wide range of biological activities.

Role of sPLA₂ on cell function and animal physiology

With the milieu of so many potential biological activities, inhibitors, antibodies, antisense oligonucleotides and genetic models have been used to better define the essential processes induced by sPLA₂ secretion into sites of inflammation [94–105]. While some inhibitors, antibodies and antisense oligonucleotides have been developed that block sPLA₂ activity and inflammatory processes, the lack of selectivity among these reagents against different sPLA₂ isotypes make data interpretation ambiguous. Various genetic models have been discovered or developed in order to address the complex issue of the role sPLA₂ isotypes may play in diseases [106–111]. For example, peritoneal macrophages from mice with targeted gene disruption of group IV cPLA₂ show a marked reduction in their capacity to synthesize leukotriene B₄ (LTB₄), leukotriene C₄ (LTC₄), prostaglandin E₂ (PGE₂) and platelet-activating factor (PAF) [111]. These animals have attenuation in pulmonary responses and hyper-responsiveness after allergen challenge. In terms of sPLA₂, Nevalainen and colleagues designed experiments where transgenic mice expressed more than eighty fold more group II PLA₂ in most tissues including liver, lung, kidney and skin than non-transgenic littermates. Histopathological analysis of these animals revealed a disorder in skin consisting of hyperkeratosis, epidermal and adrenectral hypoplasia [112]. Chronic hypoplasia and hyperkeratosis observed in these animals is similar to that seen in a variety of skin disorders including human psoriasis. Certain mouse strains (C57BL/6, 129, A/J, C58 and P/J) have been shown to have a natural disruption of group IIA PLA₂ gene [106]. Thus, these strains are deficient in functional group IIA PLA₂ and have been used to determine the need for this enzyme in cell function. Interestingly, mast cells obtained from PLA₂g2a^{+/+} and PLA₂g2a^{-/-} mice both contained sPLA₂ activity and release similar quantities of AA upon antigen stimulation. Studies using these animals and antisense oligonucleotides reveal that group V sPLA₂, and not IIA, is likely an important sPLA₂ iso-

type in mast cell immune activation [113]. Similar studies using antisense oligonucleotide specific for group V PLA₂ in macrophages also demonstrated that group V PLA₂ has an important role in extracellular AA release after endotoxin and PAF stimulation [114]. Fonteh and colleagues have also shown that cells over-expressing group IIA PLA₂ and group V PLA₂ release more AA than mock-transfected cells [115]. Together, these studies show that various sPLA₂ isotypes can induce AA release from a variety of inflammatory cells.

Cytokine-like effects of sPLA₂ in inflammatory diseases

sPLA₂ may contribute to the pathogenesis of an inflammatory disease such as asthma in one of the following ways. First, sPLA₂ may induce lipid mediator formation. Second, sPLA₂ may induce degranulation of inflammatory cells leading to the release of preformed mediators such as histamine. Third, sPLA₂ may induce the synthesis of inflammatory cytokines. Our data show that sPLA₂ can also induce the formation of cytokines that prevent mast cells from undergoing apoptosis, thus preventing the resolution of inflammation. These potential effects of sPLA₂ summarized in Figure 1 and discussed in detail below can have significant ramifications in the management of inflammatory diseases.

Eicosanoid biosynthesis

Although the existence of sPLA₂ receptors has been recognized for several years, few studies have focused on the significance of receptor occupancy or the signaling mechanisms associated with receptor occupancy and how these events manifest themselves in inflammatory disease processes. Early work on sPLA₂ receptors focused on the neurotoxic effects of snake venom sPLA₂ acting through high affinity for sPLA₂ receptors. It has been speculated that somewhere along the evolution of sPLA₂, the mannose receptor may have been duplicated to accommodate other forms of and other functions of sPLA₂. These sPLA₂ receptors and their agonists (sPLA₂) regulate events in inflammatory cells that are critical to the pathogenesis of diseases such as asthma. Thus, sPLA₂ isotypes can act through their receptors in both autocrine and cytokine-like fashion. For example, mast cells contain and release group V PLA₂ during antigen activation and our data reveal that mast cells contain plasma membrane receptors and respond to receptor occupancy by sPLA₂ [116, 117]. A sPLA₂ receptor pathway could clarify several studies in the literature. For example, Arm and colleagues have shown that there are two phases of prostaglandin production in cultured mast cells that are primed with *c-kit* ligand and stimulated with antigen [118, 119]. AA is supplied for the first phase of prostanoids synthesis by cPLA₂ activation and AA for the second phase is provided by sPLA₂. It has

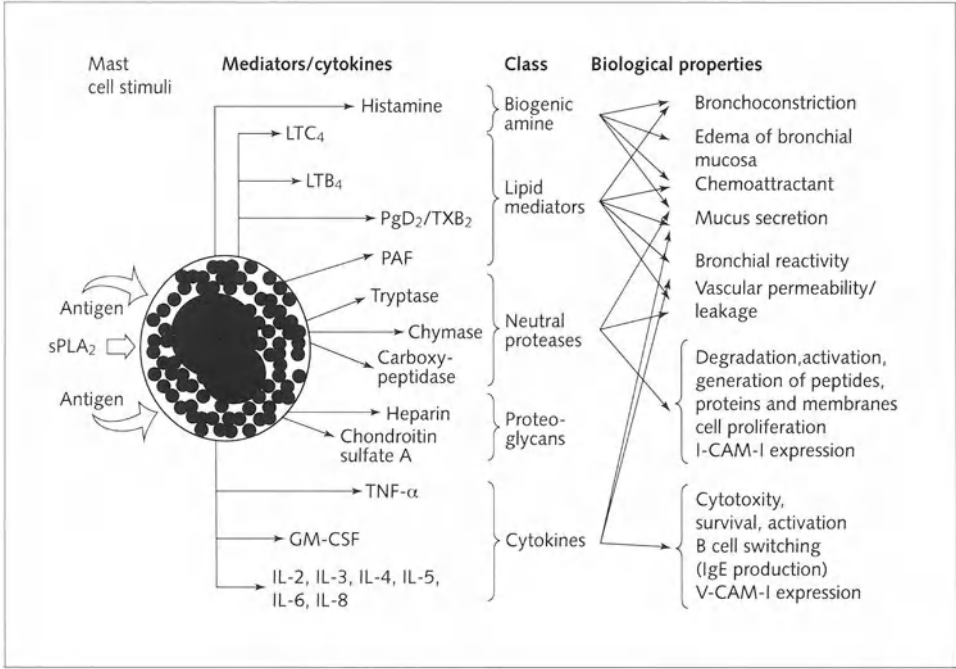


Figure 1

Stimulation of mast cells by sPLA₂, formation of mediators and their biological properties
 sPLA₂ receptor occupancy results in the activation of mast cells. Mediators released include preformed biogenic amines (histamine), newly formed lipid mediators of inflammation (leukotrienes (LTC₄, LTB₄), prostaglandins (PGD₂), thromboxane (TXB₂) and platelet activating factor (PAF)), neutral proteases, proteoglycans and cytokines. These mediators induce various biological functions that are linked to disease processes.

been proposed that sPLA₂ hydrolyzes AA from membrane phospholipids to supply the substrate for PGD₂ biosynthesis. Fonteh and colleagues have provided evidence that sPLA₂ binds to cell surface receptors on mast cells that may initiate subsequent activation of cPLA₂, cyclo-oxygenase and lipoxygenase enzymes needed for AA release, prostaglandin formation and leukotriene biosynthesis, respectively [115, 116]. sPLA₂ also could have cytokine-like roles in that it could be released from one cell type and subsequently act on a variety of other cells types expressing sPLA₂ receptors. For example, it is well documented that high levels of sPLA₂ are found in serum of patients with sepsis, shock, organ injury or pancreatitis. Tools for studying these diseases suggest that group IIA sPLA₂ is involved. However, many of these studies used antibodies that are non-specific recognizing group IIA, V and X PLA₂. Thus, it is not clear which of the various sPLA₂ isotypes play a role in these diseases.

We have postulated that sPLA₂ isotypes released from mast cells after antigen challenge are found in sites of inflammation and these sPLA₂ isotypes induce lipid mediator formation or influence the recruitment and function of cells that participate in airway diseases. A study by Reddy and colleagues showing that mast cells can provide sPLA₂ to fibroblasts for prostaglandin production supports this postulation [120]. Cells other than mast cells can also provide sPLA₂ in airways. For example, using an enzyme-linked immunoassay specific for groups IIA and V PLA₂, has shown that human eosinophils have approximately 14-fold more of the enzymes than human neutrophils and this activity is released very rapidly upon cell activation [121]. In a related study, Hundley and colleagues have shown that sPLA₂ is released from human basophils and likely participates in leukotriene generation [122]. Thus, there is also potential for sPLA₂ from eosinophils or basophils to have both autocrine and cytokine effects in airway disease by inducing the formation of eicosanoids.

Degranulation of inflammatory cells

In addition to eicosanoid production, sPLA₂ has been shown to induce degranulation of several cells. Fonteh and colleagues showed that incubation of mast cells with different sPLA₂ isotypes resulted in the release of histamine. Likewise Triggiani and colleagues have duplicated these mast cell studies using macrophages, monocytes and eosinophils [123–125]. Their studies show that sPLA₂ induce the release of β -glucuronidase and the production of IL-6, IL-8, IL-12 and TNF- α by these cells. They conclude that this process is mediated *via* the mannose receptor and another receptor based on experiments showing that sPLA₂ isotypes are not cytotoxic to macrophages that were used in their studies. Together, these studies suggest that sPLA₂ may induce immune and inflammatory responses in cells by inducing exocytosis resulting in the release of mediators such as histamine and cytokines. Mast cells and macrophages also contain other proteases, which are released by activated inflammatory cells [126–129]. Induction of the release of these can result in bronchoconstriction, edema of the bronchial mucosa, chemoattraction, mucus secretion, vascular permeability and leakage, cell proliferation and expression of adhesion molecules (Fig. 1). Together, these biological properties constitute events related to inflammatory diseases of the airway.

Induction of cytokine formation

An important observation in mast cells, macrophages, monocytes and eosinophils incubated with sPLA₂ is that these cells while releasing AA still remain viable, indicating that these enzymes are not cytotoxic to these cells. This paradoxical effect can

be explained by the fact that sPLA₂ acts on receptors to induce processes that prevent apoptosis. For example, sPLA₂ acting on sPLA₂ receptors may activate mitogen-activated protein kinase (MAP kinase) and this process may result in the biosynthesis of cytokines, which prevent apoptosis. We confirmed this process by showing that incubation of bone marrow-derived mast cells with low concentrations of sPLA₂ resulted in the induction of IL-3 release into supernatant fluids. Only sPLA₂ isotypes that induced IL-3 production prevent apoptosis of mast cells [130]. A similar study showed that some sPLA₂ isotypes induce IL-6, IL-8, IL-12 and TNF- α formation by other inflammatory cells [123–125]. In addition to preventing apoptosis, cytokines induced by sPLA₂ also induce several biological effects including bronchial reactivity, chemoattraction, and activation of other inflammatory cells and the induction of adhesion molecules. Prevention of apoptosis of inflammatory cells such as mast cells and macrophages keep these cells longer in the site of inflammation and thus prevent quick resolution of the inflammatory process.

Mechanisms that account for the biologic functions of sPLA₂

sPLA₂ receptors

To date, most of the biological activities of sPLA₂ have been attributed to its capacity to hydrolyze membrane phospholipids. However, several of the biological functions described above cannot be easily reconciled with enzymatic activity alone. For example, intradermal injection of inactivated sPLA₂ causes similar phenotypic changes in skin to those observed when the fully active enzyme was injected [131]. Similarly, others have shown that the physiologic action of sPLA₂ is not due to hydrolytic activity [125, 132]. We have demonstrated that very low concentrations of sPLA₂ (low nanomolar levels) of certain sPLA₂ isotypes induce AA release, histamine release, and proliferation of some cells and enhance the survival of other cells in a receptor-mediated fashion [82]. Our studies also show that sPLA₂'s cause the selective release of AA and not other more abundant fatty acids from cells that express sPLA₂ receptors [115]. In contrast, cells that do not express sPLA₂ receptors do not selectively release AA when incubated with low amounts of sPLA₂.

Recently, different subtypes of membrane receptors for sPLA₂ have been identified in a variety of cells by determining their affinities for various types of sPLA₂. Arita and colleagues described the existence of a specific receptor family termed PLA₂-I receptor that is abundant in brain and several other tissues and has high affinity for the binding of pancreatic-type PLA₂ [133–136]. More recently, receptors have been divided into two classes termed N-type receptors (neuronal) or M-type receptor (muscle). Lambeau and colleagues report that a major difference between N-type and M-type receptors is their capacity to bind group III PLA₂ from bee venom [137, 138]. N-type receptor associates very tightly with both pancreatic

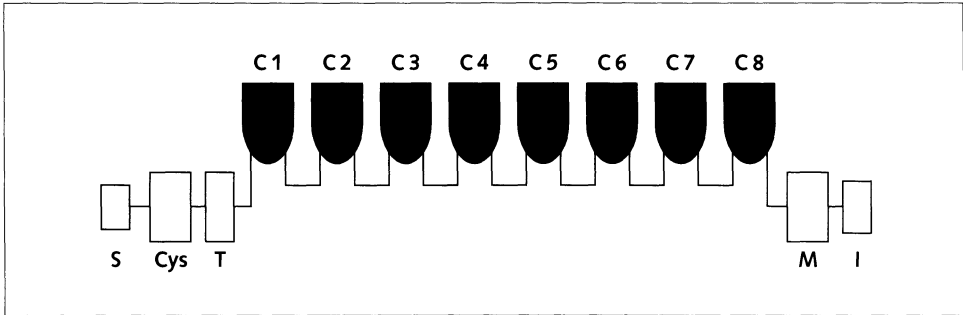


Figure 2

Domain organization of the sPLA₂ receptor

S, signal sequence; Cys, cysteine-rich domain; T, fibronectin type repeat; C1–C8, carbohydrate-like domain; M, membrane spanning domain; I, intracellular region

sPLA₂ and bee venom group III PLA₂ while rabbit muscle M-type receptor tightly binds human synovial fluid group II PLA₂ but does not bind bee venom sPLA₂. Our studies show that bee venom sPLA₂ at extremely low concentrations induced the selective release of AA from mast cells suggesting that this mast cell line expresses a protein that is similar if not identical to N-type receptors. Both membrane and plasma bound sPLA₂ receptors have been described [139]. The plasma bound sPLA₂ receptors seem to prevent the LPS-induced inflammatory process by binding sPLA₂ and thus preventing septic shock during bacterial infections [140].

Despite the fact that these receptor subtypes show somewhat different sPLA₂ binding profiles, their amino acid sequences are strikingly similar with as much as 82% homology. Additionally, the sequences of the cloned sPLA₂ receptor is homologous to that of the macrophage mannose receptor and DEC-205, suggesting that these proteins constitute a new family of membrane proteins [137]. The sPLA₂ receptor is composed of an N-terminal cysteine rich domain (Cys) a fibronectin-like type II domain (T), eight carbohydrate recognition domains (C1–C8), a membrane spanning domain (M) and an intracellular tail (I) (Fig. 2). sPLA₂ is thought to bind to the M-type receptor *via* the carbohydrate domains (particular C5) [137]. Although occupancy of the sPLA₂ receptor has been suggested to enhance cell survival, proliferation, cell migration, much remains to be learned about the molecular events and physiological ramifications of sPLA₂ receptor activation.

Hydrolytic activity of sPLA₂

In addition to receptor binding, the hydrolytic activity of PLA₂ may also play an important role in releasing fatty acids from cells. There are several distinct features

that distinguish receptor-mediated effects of sPLA₂ from enzymatic activity. First, whereas sPLA₂ receptor-mediated release is specific for AA [35, 115, 116], hydrolytic activity releases other more abundant fatty acids and degrades phospholipids [141]. Various reports have shown more release of oleic acid than AA in cells where hydrolytic activity is the major mechanism of action. Secondly, very low levels of sPLA₂ (nanomolar amounts) are required for receptor-mediated release of AA. In contrast, 1,000 fold more sPLA₂ is needed to release fatty acids by hydrolytic activity. Thirdly, disruption of cell membrane is not required for receptor-mediated AA release, while perturbation of cellular membranes is needed for hydrolytic activity [79, 130, 142]. Disruption of cell membranes or loss of membranes phospholipid asymmetry is usually accomplished using cell-activating agents such as ionophore and thrombin in the case of platelets or antigen in the case of mast cells [143, 144]. Additionally, there is alteration in membrane asymmetry when cells are undergoing apoptosis. A combination of disruptive agents and sPLA₂ treatment, or treatment of apoptotic cells, usually results in enhanced fatty acid mobilization. Fourthly, sPLA₂ receptor-mediated AA release is predominantly from the phosphatidylethanolamine pool whereas hydrolytic release favors phosphatidylcholine [35, 145, 146]. As shown in Figure 3, very low amounts of sPLA₂ (0.1 nM) induce the selective formation of lysophosphatidylethanolamine from [³H]-ethanolamine-labeled mast cells while higher concentrations (100 nM) are required to significantly form lysophosphatidylcholine from [³H]-choline labeled mast cells. It is important to note that the receptor-mediated release from a pool of phospholipid that is usually found within the inner bilayer of cell membranes will only be possible if there is recruitment of another lipase activity within cells. Importantly, it is worth noting that the profile of AA release in mast cells incubated with sPLA₂ (receptor-mediated) is similar to that of IgE-receptor mediated release of AA. Finally, sPLA₂-receptor mediated processes may lead to enhanced cell survival or cell proliferation while hydrolysis inevitably results in cell death as a result of lysis of cell membranes. Similarities between receptor-mediated and hydrolytic activity revolve around the fact that both processes release AA from phospholipid pools and also form lysophospholipids. These lysophospholipids can be acetylated to form PAF or can act as mediators of several processes in cells [147–149]. Thus, AA and lysophospholipids released by hydrolytic action of sPLA₂ can be converted to eicosanoid or PAF, respectively and these lipid mediators can then induce several biological effects at sites of inflammation.

sPLA₂ receptor-mediated signaling pathways

Although several sPLA₂ binding proteins have been described in various mammalian cells, little is currently known about signaling events that are initiated once sPLA₂ isotypes or mannose receptors are occupied by ligands. Although little is known about binding of group I PLA₂ to N-type receptors, it is clear that calcium is not

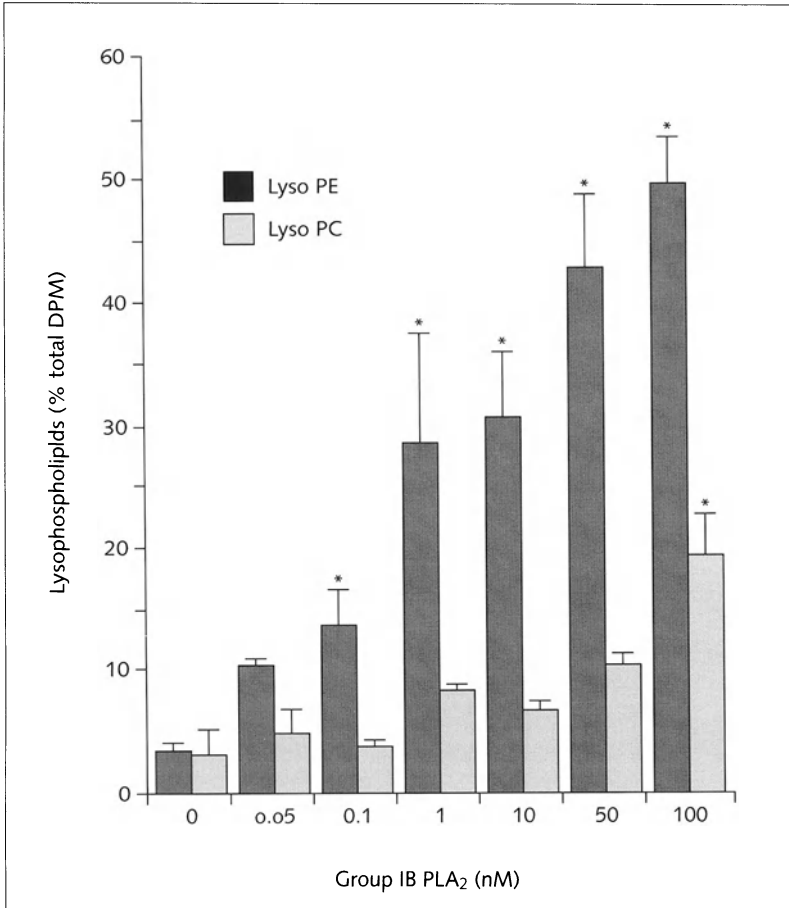


Figure 3

Mobilization of lysophospholipids by group IB PLA₂

Mast cells labeled with [³H]-ethanolamine or [³H]-choline are incubated with increasing concentrations of group IB sPLA₂. Lysophosphatidylethanolamine (Lyso PE) and lysophosphatidylcholine (Lyso PC) were isolated using thin layer chromatography and radioactivity in these lipid species determined using lipid scintillation counting (*p < 0.05).

required, while calcium is required for the mannose receptor. Mannose receptor occupancy is linked with tyrosine phosphorylation while sPLA₂ receptors have been recently shown to mediate cell proliferation and AA release by MAP kinase activation [116, 150]. Demonstration of sPLA₂ receptor function as opposed to catalytic action is based on studies using catalytically inactive sPLA₂ or ligands of sPLA₂ receptors that are devoid of hydrolytic activity. In these studies, catalytically inactive sPLA₂ induced the selective release of AA from mast cells and prevented apop-

tosis of these same cells when they were cultured in cytokine-depleted cell culture medium. Likewise, a ligand of the mannose receptor, *p*-amino-phenyl-D-mannopyranoside BSA (APDM-BSA) is shown to induce AA release from mast cells and to compete with sPLA₂ in this process. Binding studies also show that only sPLA₂ isoforms that selectively induce AA release can compete with each other for specific binding. Interestingly, APDM-BSA does not prevent mast cells from undergoing apoptosis. This suggests that there are at least two sPLA₂ receptor subtypes in mast cells, one that is linked to AA release (binds APDM-BSA) and another that prevents apoptosis. Alternatively, there are multiple signaling pathways in mast cells activated differentially likely due to difference in receptor affinity of the different ligands. These signaling events are reviewed below.

In receptor-mediated AA release, another lipase activity must be recruited if sPLA₂ activity is not required. As described above, AA is mobilized from phospholipid pools (mainly PE) that are normally found within cells. Therefore, an ideal PLA₂ that can release this AA pool is the hormonally regulated cytosolic PLA₂ (cPLA₂). cPLA₂ is translocated to a membrane location in response to an increase in cytosolic calcium and activated by phosphorylation of serine 505 or other phosphorylation sites by MAP kinases [151–154]. The extracellular signal-regulated kinase (ERKs, p42/p44) initially was thought to be the major kinases responsible for cPLA₂ phosphorylation. However, recent studies suggest that p38 kinase pathway, which can be activated by environmental stresses and inflammatory cytokines, may also phosphorylate/activate cPLA₂. In stimulated platelets, inhibitors of p38 kinase have been shown to prevent cPLA₂ activation while these same inhibitors indicate that ERKs and not p38 kinase may activate cPLA₂ in other cell types [155, 156]. Wykle and colleagues have shown in human neutrophils that both ERKs and p38 kinases are important in cPLA₂ activation depending on the stimuli used. Fonteh and colleagues have also shown that tyrosine kinase inhibitors attenuate sPLA₂-induced cPLA₂ and Ras activation [116]. Since Ras activation is upstream of MAP kinase activation, we have proposed the signaling pathway depicted in Figure 4A for cPLA₂ recruitment and AA release after sPLA₂ receptor occupancy. We have proposed that the sPLA₂ receptor is similar to other protein tyrosine kinase (PTK) receptors that may have an intrinsic kinase activity or may be able to recruit kinases from cytosol upon ligand binding. Once tyrosine kinases are activated, a sequence of events including Ras, ERKs or p38 activation lead to the phosphorylation and translocation of cPLA₂ from cytosol to membranes [116]. This results in the mobilization of AA that is utilized for eicosanoid formation (Fig. 4A). It is likely that the c-Jun pathway may also be linked to cPLA₂ activation. As the tools become available for studying and discriminating between the various signaling pathways, it will become clearer whether c-Jun kinases phosphorylate cPLA₂ and induce AA release from cells.

The high affinity IgE receptor is a well-characterized membrane bound protein that belongs to the multi-chain system of receptors involved in hypersensitivity reac-

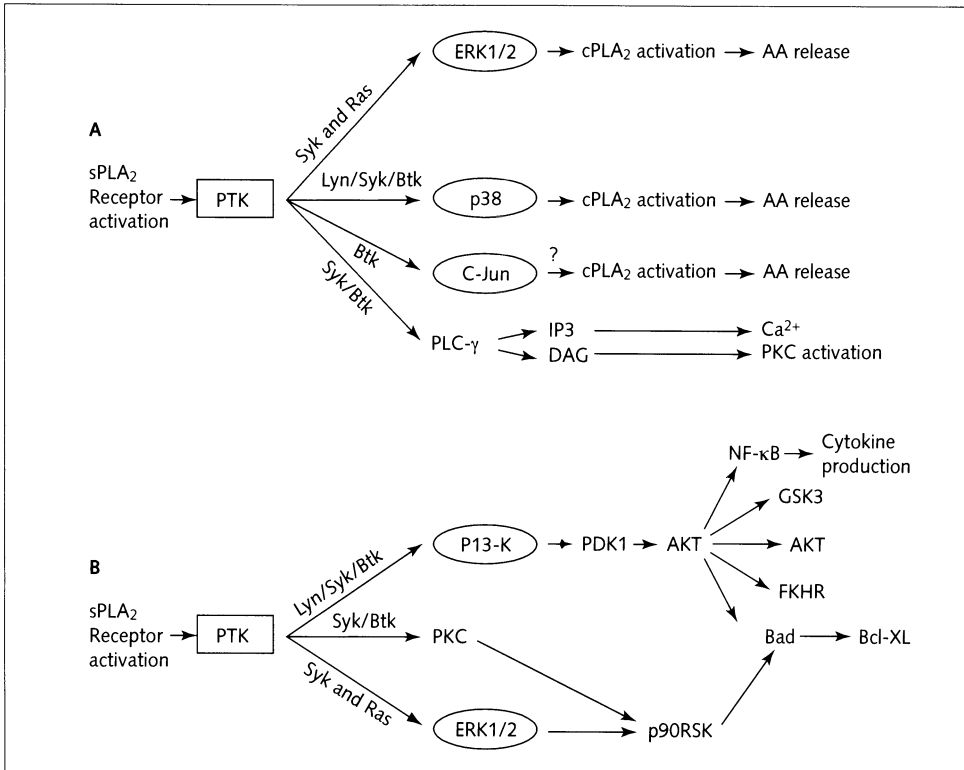


Figure 4

sPLA₂-receptor mediated signaling pathways

A) Cytosolic PLA₂ activation. Binding of sPLA₂ to its receptors results in the activation of kinase pathways (protein tyrosine kinase (PTK), tyrosine kinases (Syk, Syk and Btk), MAP kinases (ERK1/2, p38, c-Jun)). These kinases activate cytosolic phospholipase A₂ (cPLA₂) via phosphorylation of various amino acid residues. Activated cPLA₂ translocates to membrane fraction of cells and releases AA that is used for eicosanoid biosynthesis. Other second messengers (DAG and Ca²⁺) are also initiated via PLCγ.

B) Anti-apoptotic signaling pathways. sPLA₂ binds to its receptors and activates kinase pathways (phosphoinositide 3-kinase (PI3-K), phosphatidylinositol dependent kinase (PDK, glycogen synthase kinase (GSK)), transcription factors (nuclear factor kappa B (NF-κB) and anti-apoptotic proteins such as Bad. Activation of these pathways prevents apoptosis of cells and/or induces cell growth and differentiation.

tions [157]. These receptors lack intrinsic tyrosine kinase activity and so have to recruit cytoplasmic tyrosine kinase that phosphorylates the receptor at sites known as immunoreceptor tyrosine-based activation motifs (ITAMs). Phosphorylation of ITAMs results in protein tyrosine kinase activation. Three major PTKs have been

described in mast cells including Lyn, Syk and Burton's tyrosine kinase (Btk) that are upstream of the three subfamilies of MAK kinases (ERKs, p38 and c-Jun NH₂ terminal kinases) [158–160]. Activation of PTKs and their respective downstream MAP kinases result in cPLA₂ activation and the formation of pro-inflammatory mediators described above. Another group of mast cell receptors characterized by *kit*, have intrinsic tyrosine kinase activity and are involved in mast cell survival and proliferation [160, 161]. Similar to *kit*, the high affinity nerve growth factor (NGF, 165 kDa) receptor autophosphorylates tyrosine residues to activate multiple downstream effectors including PLC γ , MAP kinases and phosphoinositide-3-kinase (PI3-K/Akt). Of the many signaling pathways influenced by *kit* and NGF, the PI3-K/Akt pathway has been implicated in mast cell survival and growth. PI3-K is a dual kinase consisting of an 85 kDa regulatory unit and a 110 kDa catalytic unit. PI3-K adds a phosphate molecule specifically to the 3 position of the inositol ring of phosphatidylinositols resulting in the formation of products that have been implicated in survival, proliferation or cell migration. There are striking similarities between *kit*, NGF and the sPLA₂ receptor when one examines mast cell survival. First, the cloned sPLA₂ receptor (180 kDa) has one membrane-spanning domain, as does the NGF receptor. Secondly, NGF prevents apoptosis of mast cells, as does sPLA₂ isotypes that bind specifically to sPLA₂ receptors. Thirdly, NGF activates PI3-K/Akt pathway. We have shown that PI3-K specific inhibitors reverse the anti-apoptotic effects observed in mast cells incubated with very low levels of sPLA₂. Moreover, sPLA₂ also induce Akt phosphorylation in mast cells while inhibitors of nuclear factor kappa B (NF- κ B) are shown to prevent sPLA₂ effects on mast cells. Both active and catalytically inactive sPLA₂ induce IL-3 production from mast cells and NF- κ B inhibitors reverse this property of sPLA₂ [130]. Taken together, these data show that sPLA₂ produce IL-3 by activating the PTK/PI3-K/Akt/NF- κ B pathway. Similarly antigen-stimulated mast cells have been shown to produce cytokines *via* PTK/PI3-K/Akt/NF- κ B activation.

Conclusions

The first step in designing new pharmaceutical agents is the identification of a candidate target. Elucidation of all biological properties of the identified target plays a crucial role in conceptualizing new strategies for selectively blocking disease-related events.

The above review examines sPLA₂ from mast cells as a candidate ligand and sPLA₂ receptor as a potential target responsible for important biological functions linking sPLA₂ to inflammatory diseases. To our knowledge, the concept that sPLA₂ receptors play an important role in inflammatory diseases is novel and potentially interesting to pursue in the development of agents to avert allergic and inflammatory reactions associated with these diseases.

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Control of arachidonic acid levels in resting and activated U937 phagocytic cells by Ca^{2+} -independent phospholipase A_2

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Phospholipase A_2 regulation of arachidonic acid levels

Availability of free arachidonic acid (AA) is widely recognized as a rate-limiting step in the formation of prostaglandins. This fatty acid is an intermediate of a reacylation/deacylation cycle of membrane phospholipids, the so-called Lands pathway, in which the fatty acid is cleaved from phospholipid by phospholipase A_2 s (PLA_2) and reincorporated by acyltransferases. Whereas in resting cells reacylation dominates, in stimulated cells the dominant reaction is the PLA_2 -mediated deacylation. Nevertheless, increased AA reacylation during cellular activation is still very significant, as manifested by the fact that only a minor portion of the free AA released by PLA_2 is converted into eicosanoids, the remainder being effectively incorporated back into phospholipids.

Phagocytic cells generally contain multiple PLA_2 s [1, 2]. Thus the challenge in recent years has been both to identify these PLA_2 s and to clarify their roles in AA metabolism. A general mechanism for PLA_2 -regulated AA metabolism in resting and activated cells has emerged from the studies by several laboratories [3, 4], and involves participation of all three major classes of PLA_2 , namely cPLA_2 (cytosolic PLA_2), iPLA_2 (Ca^{2+} independent PLA_2) and sPLA_2 (secreted PLA_2) (Fig. 1).

In resting conditions, iPLA_2 accounts for most of the PLA_2 activity of cells. iPLA_2 is therefore the dominant PLA_2 involved in the liberation of fatty acids, including AA, during the continuous recycling of membrane phospholipids that takes place under these conditions. Since, as indicated above, the rate of AA release by iPLA_2 is lesser than the rate of its reacylation back into phospholipids, no net accumulation of free fatty acid occurs. Stimulation of the cells by receptor agonists results in the activation of cPLA_2 , which then becomes the dominant PLA_2 involved in AA release. Under these conditions, the rate of AA release clearly exceeds that of reincorporation into phospholipids; hence net accumulation of AA occurs that is followed by its conversion into different oxygenated compounds, collectively called the eicosanoids.

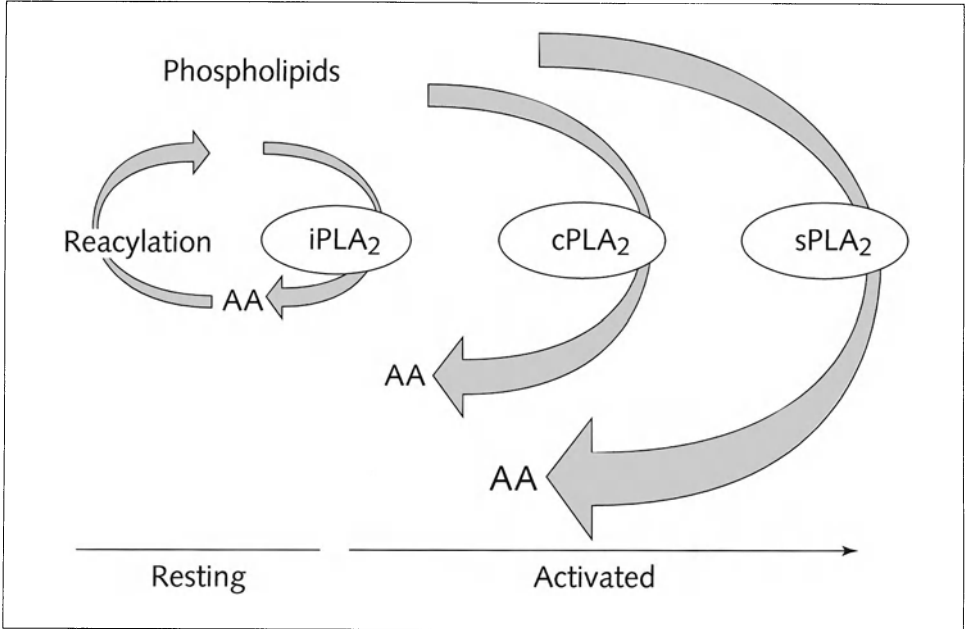


Figure 1
 PLA₂ regulation of AA release.

During long-term AA mobilization responses, i.e., those that are typical from immunoinflammatory cells such as macrophages or mast cells, the inducible sPLA₂ also participates in the process, thereby creating an amplification loop that results in a greatly enhanced release of AA for eicosanoid synthesis. At these stages, the contribution of sPLA₂ to overall AA release often exceeds that of cPLA₂. The sPLA₂ acts not only upon the cells that synthesized it but also upon surrounding cells, which allows for efficient propagation of the inflammatory response (Fig. 1).

Within the framework of the model depicted in Figure 1, recent studies have further explored the involvement of other PLA₂s in addition to iPLA₂ in *housekeeping* phospholipid and fatty acid remodeling. Possible iPLA₂-roles in inflammatory signaling distinct from receptor-regulated AA metabolism have also been investigated. These are discussed in the following sections.

Production of lysophospholipid acceptors for AA incorporation and remodeling into phospholipids

Unlike saturated fatty acids, AA at physiologically relevant nanomolar levels does not generally enter cellular phospholipids *via* direct acylation of glycerol phos-

phate/dihydroxyacetone phosphate or lysophosphatidic acid (i.e., the *de novo* pathway) but rather does it at later stage, *via* direct acylation of pre-existing lysophospholipid acceptors (the Lands pathway). Since lysophospholipids are produced by the hydrolytic action of (PLA₂ on phospholipids, this class of enzymes necessarily plays a key role in AA incorporation into phospholipids. Initial incorporation of AA into phospholipids takes place primarily into phosphatidylcholine (PC); hence the lysophospholipid acceptor utilized is lysophosphatidylcholine (lysoPC) [5]. In many cells, the steady-state levels of lysoPC appear to be maintained by the continuing action of Ca²⁺-independent group VI phospholipase A₂ (iPLA₂) on cellular phospholipids [6]. Thus, a decrease in the activity of the iPLA₂ frequently results in the diminished production of lysoPC and hence in the inhibition of AA incorporation into phospholipids.

Once the AA has been incorporated into PC by the action of CoA-dependent acyltransferases, it is then transferred to certain lysophospholipids, particularly the ethanolamine lysophospholipids (lysoPE) in a process that generally takes several hours, and is governed by the enzyme CoA-independent transacylase (CoA-IT) [5]. Thus, for the efficient incorporation of AA into phospholipids, two kinds of lysophospholipid acceptors should be readily available in the cell (Fig. 2).

Earlier studies on the initial incorporation of AA into the phospholipids of murine macrophages demonstrated that the process was essentially Ca²⁺-independent [7]. This suggested that the PLA₂ activity responsible for generating lysophospholipid acceptors for AA incorporation would correspond to that of an iPLA₂-like enzyme [7]. Such an activity was later identified to belong to the group VI PLA₂ in studies carried out with murine P388D₁ macrophages [8, 9]. These findings were later extended by other authors to different cellular systems, such as human neutrophils [10], rat submandibular ductal cells [11], and rat uterine stromal cells [12].

Importantly, the contribution of group VI iPLA₂ to maintaining the lysophospholipid pool that facilitates AA incorporation appears to largely depend on cell type. Based on studies of iPLA₂ inhibition by the selective inhibitor bromoenol lactone (BEL), the iPLA₂ contribution ranges from ~90% in rat submandibular ductal cells [11], to 50–60 in phagocytic cells [8–10], and to only 20–25% in rat uterine stromal cells [12]. It follows from these findings that, in addition to the contribution of group VI PLA₂ to the cellular lysophospholipid pools, the cells may possess other mechanisms to generate and maintain the appropriate levels of lysophospholipid acceptors.

The above notion was highlighted by a recent report in rat pancreatic islets [13], where iPLA₂-inhibition by BEL does not result in diminished AA incorporation into phospholipids. Nevertheless, group VI PLA₂ is estimated to contribute to at least 20% of the very high steady-state lysophospholipid levels in pancreatic islets, indicating that the enzyme possesses significant *housekeeping* activity in islets as well. Since rat pancreatic islets maintain cellular lysophospholipid levels at high levels, it is very likely that the amount of lysophospholipid present in these cells after BEL

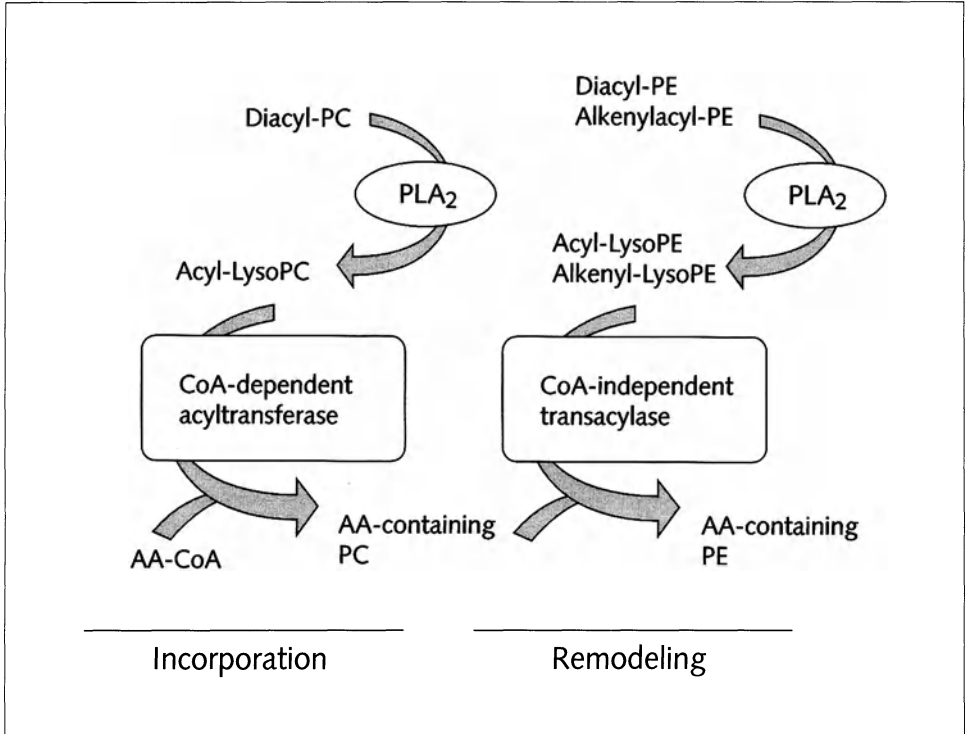


Figure 2

AA incorporation into and remodeling within phospholipids.

treatment is still high enough to account for a normal rate of AA incorporation into phospholipids. In support of this contention, recent studies on AA incorporation utilizing cells over-expressing group VI PLA₂ have demonstrated that the excess amount of lysophospholipid produced under those conditions does not serve to increase the rate of fatty acid incorporation [14]. Collectively, these findings have suggested that, while a threshold level of lysophospholipid seems necessary to support AA incorporation into phospholipids, increasing cellular lysophospholipid above that threshold level does not increase the rate of AA incorporation. Thus other factor(s) in addition to lysophospholipid availability limit AA incorporation into phospholipid.

We have recently employed the U937 cell line as a system model to study the enzymes involved in generating and maintaining the lysophospholipid threshold level that is necessary for fatty acid incorporation into phospholipids. These cells differentiate into macrophage-like cells when treated with phorbol esters such as phorbol myristate acetate (PMA). U937 cells express group IV PLA₂ (also known as

cPLA₂) and group VI PLA₂ (generally referred to as iPLA₂) but not any of the AA-releasing sPLA₂s, including group IIA, IID, V and X (Balboa, Sáez, Pérez and Balsinde, unpublished observations).

AA incorporation into phospholipids of both resting and ConA-activated PMA-differentiated U937 cells exhibits features that are fully similar to those of other phagocytic cells such as P388D₁ macrophages and neutrophils [8–10], i.e., it is Ca²⁺-independent and BEL-inhibitable. Interestingly, BEL reduces AA incorporation only partially, suggesting again the existence of Ca²⁺-independent pathway(s) for AA incorporation into phospholipids that do not involve the BEL-sensitive group VI PLA₂ [15].

Parallel studies comparing the features of AA incorporation to those of eicosapentaenoic acid (C20:5, ω-3; EPA), show that the two fatty acids compete with each other for incorporation into the phospholipids of resting cells. Thus, AA and EPA share a common pathway for incorporation into phospholipids in resting cells. Since EPA incorporation is not affected by BEL, this common pathway must also be insensitive to BEL [15]. This situation contrasts with the one seen in ConA-activated cells, where AA and EPA do not compete with each other. Unlike AA, EPA incorporation into phospholipid is sensitive to cPLA₂ inhibitors in ConA-activated cells [15]. Thus, it seems that the increased lysophospholipid availability produced as a consequence of stimulus-induced cPLA₂ activation plays a role in EPA incorporation. In accord with this idea, the PE pools appear to be preferential targets for cPLA₂ phospholipolysis in stimulated phagocytes [16, 17], and PE is the phospholipid class to which EPA preferentially incorporates [15]. Thus, cPLA₂ would provide an additional supply of lysoPE acceptors to be used by EPA but not by AA, and the existence of such an alternative route for EPA incorporation may explain why in the activated cells EPA does not compete with AA.

After the initial incorporation of AA mostly into PC, a slow transfer of the fatty acid occurs toward PE in most cell types. These changes have been well documented in other cell systems and reflect the remodeling action of the enzyme CoA-IT on cellular phospholipids [5]. A PLA₂ is strikingly involved in the CoA-IT-driven remodeling reactions by providing the lysoPE acceptors utilized in the transacylation reaction [5].

The nature of such a PLA₂ has recently been investigated in U937 macrophages [15] and peripheral T lymphocytes [18] by measuring the transfer of AA from PC to PE in the presence of different PLA₂ inhibitors. Inhibitors of cPLA₂ (methyl arachidonyl fluorophosphonate), iPLA₂ (BEL) and sPLA₂ (LY311727), all fail to exert any detectable effect on the transfer of AA from PE to PC in either cell type. These findings suggest that the PLA₂ involved in this pathway might not be any of the previously identified PLA₂s. The Ca²⁺-independent nature of the response suggests the involvement of an iPLA₂-like activity different from the group VI enzyme. It should be noted that the aforementioned experiments are reported to be carried out at inhibitor doses that completely ablate the corresponding PLA₂ activity [15,

18]. That excludes the possibility that residual PLA₂ activity in the presence of any of these inhibitors might provide enough lysoPE to accommodate substrate needs of CoA-IT.

Unlike other macrophage-like cells such as P388D₁ cells [8], PMA-differentiated U937 cells exhibit a significant iPLA₂ activity component that is resistant to BEL [15, 19]. This component is more evident when PE is used as a substrate for the assay [15]. It is very intriguing to speculate with the possibility that such an activity is the one generating lysoPC and lysoPE acceptors for incorporation into and remodeling among phospholipids under conditions where all other known PLA₂s are not involved. Purification and characterization of this novel iPLA₂ activity seems important to further clarify the mechanisms responsible for lysophospholipid level maintenance in resting and activated phagocytes.

The intracellular level of lysophosphatidylcholine as a regulatory signal for phagocyte secretion

As a part of their surveillance functions in the immune system, monocytes/macrophages secrete large amounts of the bactericidal enzyme lysozyme to the extracellular medium. Lysozyme degrades bacterial cell walls of Gram-positive bacteria and the chitinous components of fungal cell walls. The enzyme occurs in many body fluids such as tears, saliva or mucus, and is produced and secreted by phagocytic cells and a variety of cells of epithelial origin. Stimuli that induce lysozyme secretion from phagocytic cells also induce the PLA₂-mediated mobilization of free AA. Thus the question arises as to whether these two phenomena are causally related.

Studies with cPLA₂ knock-out mice have unambiguously demonstrated that this is the key enzyme in stimulus-induced AA mobilization [20, 21]. In keeping with these data, countless articles in the scientific literature have shown that inhibition of cPLA₂ results in greatly diminished AA release responses. The classical method for studying the involvement of cPLA₂ in a given cellular response is to use chemical inhibitors that are reasonably selective for this enzyme. While some of these studies may be flawed by the use of inhibitors that are actually not that selective for cPLA₂ [22], recent studies have described new chemical inhibitors of cPLA₂ with improved potency and specificity. These are pyrrophenone [23] and related compounds [24]. Inhibition by pyrrophenone of pure cPLA₂, as measured in an *in vitro* assay, is over two orders of magnitude more potent than that for other PLA₂ types [23]. Importantly, much of this selectivity is retained in assays utilizing cell homogenates as the source of enzyme [24, 25], implying that pyrrophenone may indeed constitute an excellent tool to study the involvement of cPLA₂ in cell function. For example, in U937 cells pyrrophenone completely inhibits stimulus-induced AA release at concentrations well below 1 μM [25], and at this concentration no effect is seen on either iPLA₂ or sPLA₂ [26].

Despite its potent effects on AA mobilization, pyrrophenone does not exert any effect on lysozyme secretion in activated U937 cells, indicating that cPLA₂ has no role in this process. However, lysozyme secretion is impaired by BEL, which suggests the involvement of iPLA₂ [27]. Such an involvement has been confirmed by anti-sense oligonucleotide inhibition experiments, which selectively target the iPLA₂ [27]

The low lysoPC level found in iPLA₂-deficient cells appears to be related to the diminished capacity of these cells to secrete lysozyme, since exogenous supplementation of lysoPC fully restores the response. Other putative PLA₂ products such as exogenous AA and other fatty acids fail to restore lysozyme secretion in the U937 cells deficient in iPLA₂ activity [27]. This suggests that stimulus-triggered increases in free AA levels have no role in regulating lysozyme secretion. Since in activated U937 cells AA mobilization appears to be under the control of cPLA₂, these results are fully consistent with the aforementioned studies showing that cPLA₂ inhibition by pyrrophenone has no effect on lysozyme release.

cPLA₂ activation transiently elevates cellular lysoPC levels in activated phagocytic cells [28]. Since cPLA₂ plays no discernible role in lysozyme release, it is the steady-state level of lysoPC (iPLA₂-mediated), not the transient increase in lysoPC that occurs as a consequence of cellular activation (cPLA₂-mediated), which is important for lysozyme secretion. In agreement with these observations, exogenous lysoPC in the absence of PMA neither triggers secretion on its own nor increases the secretory response of cells containing normal iPLA₂ levels (and hence, exhibiting normal steady-state lysoPC levels) [27].

Recently two important cellular functions that, like enzyme secretion, require profound membrane rearrangement have also been suggested to involve participation of the iPLA₂. These are chemotaxis [29], and cell spreading [30]. Coincident with the aforementioned studies on lysozyme secretion, it is the constitutive activity of the iPLA₂ that was found to be necessary to sustain both of these functions. In addition, in these studies the contribution of the iPLA₂ was dissociated from cPLA₂ activation [29, 30]. Altogether these findings underscore the importance of iPLA₂ in regulating processes that require changes in membrane phospholipid homeostasis and provide support to the idea that iPLA₂ and cPLA₂ play separate and often unique roles in inflammatory cell signaling.

iPLA₂-derived products and oxidative stress

Phagocytic cells produce reactive oxygen intermediates such as superoxide anion and hydrogen peroxide in response to a variety of agonists. While the production of these oxygen metabolites plays an important role in cellular signaling and host defense, their uncontrolled production may constitute a serious pathophysiological factor for a wide variety of vascular-based disorders. Oxidative damage is often associated with AA mobilization from cells from the vascular system, such as

endothelial cells, smooth muscle cells, platelets and phagocytes. Reactive oxygen intermediates enhance AA release and prostaglandin production in different cell systems, but the molecular mechanism responsible for these effects appears to vary from cell to cell. PLA₂ activation has been pointed out as the most likely mechanism for AA mobilization in vascular smooth muscle cells, stromal cells, and striatal neurons exposed to H₂O₂ [31–34]. In other systems however, diminished AA incorporation into phospholipids, not PLA₂ activation, has been suggested to be the event responsible for free AA accumulation [35, 36].

Our recent data in U937 cells have established a novel mechanism for AA mobilization in phagocytic cells under an oxidative stress that involves participation of iPLA₂ rather than of cPLA₂ [25]. In these cells, H₂O₂ is able to induce a delayed AA mobilization response with a kinetics that strongly contrasts with the response of the cells to Con A, which is mediated by cPLA₂ and hence shows the typical saturation kinetics that is expected from a highly regulated cellular response such as AA release. The response to H₂O₂ however, is inhibited by BEL and by specific iPLA₂ antisense oligonucleotides [25].

Importantly, H₂O₂ treatment of the U937 cells does not increase the iPLA₂ specific activity of the cells, as measured by different *in vitro* assays, indicating that a stable activation of the iPLA₂ (e.g., phosphorylation) is not the mechanism for H₂O₂-mediated AA release in U937 cells. When membranes from H₂O₂-treated cells are used in the assay, the iPLA₂ activity measured is significantly higher than that found in membranes from otherwise unstimulated cells. Therefore, treating the cells with H₂O₂ results in facilitated iPLA₂ attack on membrane phospholipids. Since membranes from H₂O₂-treated cells contain significantly higher amounts of lipid peroxides than membranes from untreated cells [25], these findings suggest that lipid hydrolysis by iPLA₂ occurs more readily in H₂O₂-treated cells because of changes in the physical state of membrane substrates, which may result, at least in part, from lipid peroxide accumulation.

Taken together, the above findings have suggested a model for fatty acid mobilization in H₂O₂-treated cells whereby the oxidant induces lipid oxidation, which results in accumulation of lipid peroxides at the membrane. These lipid peroxides destabilize the membrane and render it more susceptible to iPLA₂ attack, which results in increased liberation of fatty acids. An important aspect of the above model is that this fatty acid release appears to occur in the absence of cPLA₂ activation, which underscores the apparent lack of a regulated signaling component in the process. Still, a mechanism such as this one may be very relevant under pathophysiological conditions such as oxidative stress, where increased iPLA₂ activity may account for a significant phospholipid hydrolysis before cellular homeostasis is re-established.

Analysis of the AA metabolites produced after exposure of the cells to H₂O₂ reveals a significant production of prostaglandins, particularly the pro-inflammatory prostaglandins E₂ and D₂. This may suggest that an immediate biological conse-

quence of H₂O₂-induced AA release is to generate mediators that propagate and/or amplify the oxidative injury. However, unmetabolized free AA is, by far and large, the main compound released into the medium after exposure to H₂O₂, which raises the possibility that its metabolism to eicosanoid mediators might not be its actual fate or, at least, not the only one. Thus, further studies will be needed to address the biological roles of H₂O₂-mediated release of unmetabolized AA in phagocytic cells.

Another aspect that remains unknown is whether iPLA₂, in addition to its house-keeping role in U937 cells and phagocytic cells in general, also plays some role in regulated phospholipid hydrolysis in phagocytic cells. The fact that multiple splice variants of iPLA₂ exist in some cells and that other iPLA₂s distinct from the “classical” group VI enzyme have recently been described [6], suggest the possibility that iPLA₂ may be subject to complex regulatory mechanisms that differ among cell types. Two recent reports utilizing cells over-expressing group VI PLA₂ have shown the enzyme to be responsive to Ca²⁺ ionophore in HEK293 cells [37] and to glucose plus cAMP-elevating agents in INS-1 insulinoma cells [38], thus suggesting that the enzyme might be capable of playing some signaling roles in cells.

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Arachidonate remodeling and PAF synthesis in human neutrophils

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Introduction

Both AA-derived eicosanoids and platelet activating factor (PAF) serve important physiological functions, but also participate in pathological developments [1–4]. The metabolism and actions of PAF, arachidonic acid (AA), and AA-derived eicosanoids are closely linked in neutrophils, indeed they can be derived from the same phospholipid precursor, 1-O-alkyl-2-AA-GPC (sn-glycero-3-phosphocholine). Neutrophils play a major role in host defense and inflammation and many studies have focused on neutrophil signaling systems and pharmacological intervention in these systems. Since neutrophils are terminally differentiated cells and can be maintained for only short periods of time after their isolation, molecular approaches for their study have been limited. In addition, many of the enzymes that are responsible for PAF and AA metabolism, except for cPLA₂ (85 kDa cytosolic phospholipase A₂) and 5-lipoxygenase, are membrane proteins and have not been isolated. Thus much of our knowledge of the lipid metabolism and lipid-mediated signaling has been obtained through the study of crude systems and intact cells. This review attempts to summarize the work of my colleagues and me in this area and closely related work of others. Our understanding of neutrophil signaling draws on numerous studies of other cells and tissues largely beyond the scope of this review but generally acknowledged in the primary literature cited.

Human neutrophils contain high levels of ether-linked phospholipids enriched in arachidonate

At the time we began our studies of AA and PAF metabolism in neutrophils, two biosynthetic pathways for the formation of PAF had been found, a remodeling pathway in which lyso PAF derived from membrane lipids could be acetylated by an acetyltransferase to form PAF [5] and a *de novo* route which converted an acetylated alkyl diglyceride to PAF *via* a CDP-choline cholinephosphotransferase-catalyzed reaction [6]. We examined human neutrophils to determine if they contained enough 1-O-

alkyl-2-acyl-GPC to support PAF synthesis by the remodeling pathway and conducted experiments to see if we could find evidence for the *de novo* pathway.

We were surprised to find that almost half of the cholined-containing phosphoglyceride class (PC) was comprised of the 1-O-alkyl ether-linked subclass [7]. In addition, we found that two-thirds of the ethanolamine-containing phosphoglyceride class (PE) was 1-O-alk-1'-enyl linked (plasmalogen). Thus the ether-linked phospholipids are major components of the neutrophil membranes. Eosinophils were found to contain even higher levels of the 1-O-alkyl and plasmalogen subclasses comprising 70 mol% of PC and 75 mol% of PE, respectively [8]. It is clear these cells contain far more 1-O-alkyl-2-acyl-GPC than needed to support PAF synthesis by the remodeling pathway. Since the ether bonds are not hydrolyzed by phospholipases it is possible the ether-linked subclasses help stabilize neutrophil membranes when the cells leave the blood stream to invade other tissues. The high plasmalogen content might also help protect against reactive oxygen species [9], which are actively produced by the cells particularly during the oxidative burst that is initiated to kill invading organisms.

In studies of the ether lipid content of neutrophil lipids, Mueller and co-workers [10] found that although AA comprised only 7% of all fatty acyl chains found in the PC fraction, 63% of this amount was found as 1-O-alkyl-2-AA-GPC. The PE contained much greater levels of AA comprising 27% of the acyl chains; 80% of this amount was found as 1-O-alk-1'-enyl-2-AA-GPE (1-O-alk-1'-enyl-2-arachidonoyl-sn-glycero-3-phosphoethanolamine). Chilton and Connell [11] observed a similar distribution of AA in human neutrophils based on mass spectral analysis. Similar enrichment of AA in the ether linked subclasses of rat neutrophils was reported by Ramesha and Pickett [12]. The subcellular distribution of the ether-linked phospholipid classes and AA distribution was examined by MacDonald and Sprecher [13] who found that the subclass composition was markedly uniform throughout the subcellular membrane fractions yet the major pool of AA was localized in intracellular membranes. Our laboratory made very similar observations (Venable and Wykle, unpublished).

A number of studies have shown that when the diets of rats [14], monkeys [15] or humans [16–18] are supplemented with a fish oil diet containing eicosapentaenoic acid (EPA), the EPA is incorporated in a pattern almost identical to that of AA. Thus it is enriched in the ether-linked subclasses and is released from these pools upon stimulation of the cells. The incorporation of gammalinolenic acid into human neutrophils has also been examined [19]. Since the n-3 fatty acids yield less active lipoxygenase products, the substitution of EPA or other polyunsaturated fatty acids could importantly affect eicosanoid responses in inflammation [16].

These studies have revealed that human neutrophils contain high levels of ether-linked phospholipids in their membranes and that these subclasses are enriched in AA. The ethanolamine plasmalogen fraction contains by far the greatest pool of AA in the cells and donate the most free AA upon stimulation [11].

Co-synthesis of PAF and eicosanoids

It was early recognized that the same stimuli which elicit eicosanoids also elicit synthesis of PAF. PAF and the eicosanoids have overlapping activities and act synergistically to promote cell function [20, 21]. The formation of lyso PAF from 1-O-alkyl-2-acyl-GPC in the remodeling pathway of PAF synthesis requires the removal of the 2-acyl chain by a phospholipase A₂ (PLA₂) or transacylase reaction, a reaction which also requires formation of a lysophospholipid acceptor by a PLA₂ reaction. It was at first puzzling why no [¹⁴C] lysophospholipid was observed in stimulated neutrophils labeled with [³H] AA in the *sn*-2 position and [¹⁴C] stearate in the *sn*-1 position of PC, even though [³H] AA release was seen [22]. This was subsequently explained by the finding from the labeling studies that [³H] AA and [¹⁴C] stearate are not found in the same molecules; [³H] AA is in molecules containing unlabeled stearate in the *sn*-1 position while stearate-labeled PC species contain oleate and linoleate but not AA in the *sn*-2 position. Thus the specific release of [³H] AA releases only unlabeled lyso PC. In further studies [³H] AA was shown to be incorporated into seven molecular species of PC, 1-O-alkyl ether-linked species and 1-acyl-linked species [23]. A similar pattern of incorporation was observed employing mass spectroscopy [24, 25]. These studies revealed that 1-O-alkyl-2-AA-GPC is actively formed in neutrophils and provided evidence that it could yield 1-O-alkyl-2-lyso-GPC (lyso PAF) through the AA-specific action of PLA₂.

One of our most striking discoveries was the finding that when human neutrophils are exposed to PAF labeled in the 1-O-alkyl chain, 1-O-[³H]hexadecyl-2-acetyl-GPC, the cells rapidly remove the acetate and reacylate the [³H]lyso PAF in a highly specific manner with AA accounting for approximately 90% of the added acyl chains [26, 27]. Similarly exogenous [³H]lyso PAF was also rapidly taken up and acylated with AA [26–28]. This observation provided a labeling approach to specifically label the neutrophils with 1-O-[³H]alkyl-2-AA-GPC and only traces of other labeled products. Using neutrophils labeled in such a manner we were able to show directly that the arachidonate-containing species, 1-O-alkyl-2-AA-GPC is readily converted to PAF upon stimulation [28]. Thus the same precursor can yield both PAF and AA products. Similar conclusions were drawn from studies of macrophages by Albert and Synder [29]. In the acylation of lyso PAF, we found that neutrophils from monkeys on a fish oil diet substituted EPA for AA in the acylation of lyso-PAF in the same ratio of EPA:AA as found in the cells [15]. Again, it appears EPA from fish oil may interact in a centrally important pathway.

Evidence that the arachidonate-containing molecular species, 1-O-alkyl-2-AA-GPC is the obligate precursor of PAF was obtained from studies of HL60 cells grown in essential fatty acid-deficient media and differentiated into neutrophil-like granulocytes [30]. The cells grown in essential fatty acid-deficient media could not make PAF unless they were supplemented with AA or other polyunsaturated fatty acids [30]. Rat neutrophils that were 90% depleted of AA synthesized 85% less PAF than con-

trol cells containing normal levels of AA [31, 32]. Much of the AA was replaced by eicosatrienoate (20:3) but the 20:3-containing 1-O-alkyl-2-acyl-GPC did not serve as a precursor of PAF, indicating a highly specific deacylation reaction is required [33].

Molecular species of PAF and related products synthesized by stimulated neutrophils

Although there are reports of the production of highly selective molecular species of PAF by human neutrophils, our laboratory observed several molecular species of PAF labeled by acetate formed upon fMLP stimulation, with the 16:0 (39%) species being the major product followed by 18:1 (22%), 18:0 (15%) and other minor alkyl-linked species [34]. In addition, 1-acyl-2-acetyl-GPC was produced and accounted for approximately 12–15% of the acetate-labeled products; the 1-acyl-2-acetyl-GPC also accounted for the major PAF-like products synthesized by other cells [35]. The molecular species of acetate-labeled products was significantly different from the alkyl chain composition of the PC fraction and more closely followed the AA-linked species. Pinckard and co-workers [36] also observed five molecular species of PAF as detected by reverse phase high performance liquid chromatography coupled with rabbit platelet aggregation assays; only one species was identified by mass spectroscopy, the 16:0 species.

1-Acyl-2-acetyl-GPC containing a 1-acyl linkage rather than ether linkage, which is at least a hundred-fold less active than the ether-linked species [37] is formed in a number of cells. Its predominance appears to reflect the arachidonate-containing species of PC. If cells, such as endothelial cells, contain low levels of 1-O-alkyl-2-AA-GPC and more 1-acyl-2-AA-GPC the acetylated product will be predominantly 1-acyl-2-acetyl-GPC as shown by Chilton and co-workers. The function of this product is not clear but it may be able to act synergistically with other agonists to elicit responses.

In addition to choline-containing acetate species, neutrophils produce an acetate-containing 1-O-alk-1'-enyl-2-acetyl-GPE (ethanolamine plasmalogen) upon stimulation [38]. The production of this compound is not surprising since large amounts of 1-O-alk-1'-enyl-2-lyso-GPE accumulates in stimulated neutrophils and reflects the high levels of AA found as 1-O-alk-1-enyl-2-AA-GPE. Upon stimulation of human neutrophils, the arachidonate-containing species of PE are selectively hydrolyzed [39].

Arachidonic acid incorporation into phospholipids and remodeling

As in many other cells and tissues [40–42], radiolabeled AA given to neutrophils is first incorporated primarily into diacyl-GPC and phosphatidylinositol (PI) and grad-

ually transferred to 1-O-alkyl-2-AA-GPC and the ethanolamine plasmalogen, 1-O-alk-1'-enyl-2-AA-GPE [24, 43]. At higher concentrations, much of the exogenous AA is initially incorporated into triglyceride. It is generally agreed that exogenous AA is initially incorporated by a Land's cycle-type mechanism by which arachidonic acid is first converted to CoA-AA and then incorporated into 1-acyl-2-lyso-GPC and PI by a CoA-dependent acyltransferase reaction. However, the ultimate disposition of the AA into the ether-linked pools is catalyzed by a CoA-independent transacylase (CoA-IT)-catalyzed reaction [41, 44–48]. The CoA-IT is an intrinsic membrane protein that is highly specific for polyunsaturated fatty chains especially AA and EPA [15, 41, 42, 44, 48, 49]. It has no metal ion requirements or requirement for ATP. The enzyme was concluded in one study to be activated by TNF- α , but we were unable to confirm the activation of the enzyme in neutrophils [50]. The assay systems for measuring CoA-IT activity are quite complex and may explain these discrepant results; we now believe the CoA-IT is constitutatively active and specifically transfers AA to lysophospholipids and that its activity is dependent only on the appearance of an appropriate lysophospholipid acceptor. We found that the CoA-IT has a preference for 1-O-alk'-enyl-2-lyso-GPE, which could explain the enrichment of AA found in the ethanolamine-containing plasmalogen subclass [51]. However the enzyme also readily transfers AA to 1-acyl-2-lyso-GPC and 1-O-alkyl-2-lyso-GPC. It seems likely that the CoA-IT acts in synchrony with the Ca²⁺-independent PLA₂ and the low molecular weight secreted PLA₂ to achieve the pattern of AA distribution observed in intact neutrophils.

A number of intriguing questions surround the role and action of CoA-IT. The high specificity of the enzyme for AA is maintained in isolated membrane fractions which readily convert trace amounts of lyso PAF, 1-O-alkyl-2-lyso-GPC, to 1-O-alkyl-2-AA-GPC. The membrane fractions even more readily convert 1-O-alk-1'-enyl-2-lyso-GPE to 1-O-alkyl-1'-enyl-2-AA-GPE. In these reactions the membranes supply the AA but what is the origin of the AA transferred? Also the transfer of AA from one molecular species of phospholipid to a lysophospholipid only generates another lysophospholipid. When 1-O-alkyl-2-lyso-GPC is formed by CoA-IT, some of it is converted to PAF by acetylation; more is likely reacylated by acyl-CoA-dependent mechanisms. Many PLA₂'s and lysophospholipases exhibit transacylase activity. This raises the possibility that CoA-IT with the help of chaperon proteins, or under certain conditions could act as a PLA₂ and release free AA by transferring the enzyme-bound AA to water, rather than to a lysophospholipid acceptor; to our knowledge no evidence for such an action has been found. However, the CoA-IT activity observed under optimal enzymatic assay conditions is much greater than any cellular PLA₂ activity we have observed. The CoA-IT clearly has the ability to cleave AA from phospholipids donors. Are the transferase and acylase sites of the enzyme the same? It should be possible to answer many of these questions once the structure of the enzyme is determined. Its purification from membranes has been problematic, in part because both donor and acceptor phospholipid substrates are

required and the effects of detergents on the interactions of the enzyme and substrates are unknown. We have speculated that CoA-IT might be related to lysolecithin:cholesterol acyltransferase (LCAT).

CoA-IT is clearly one of the most important enzymes in the remodeling of AA from diacyl-linked species to the ether-linked phospholipids and PE, and may also be a key enzyme in the synthesis of PAF as discussed below. Since the equilibration of labeled AA with endogenous pools requires many hours, studies of AA release based on short-period labeling can yield very misleading results that do not agree even closely with results based on mass. Thus the PE fraction of neutrophil phospholipids is poorly labeled by exogenous AA within the time constraints of these labile cells and most observed loss of AA-label upon stimulation of prelabeled cells is from the highly labeled PC and phosphatidylinositol classes, whereas mass determinations reveal that far more AA is lost from the PE plasmalogen fraction [11], which contains little labeled AA.

The shift over time of AA from the diacyl-GPC into 1-O-alkyl-2-AA-GPC and 1-O-alk-1'-enl-2-AA-GPE appears to provide an exciting tool for examining the subcellular movement of AA among organelles as well as the metabolic pools giving rise to 5-HETE, LTB₄ and other eicosanoids. Thus by double labeling the cells by first incubating them for 30 to 60 minutes with [¹⁴C] AA, then washing the cells followed by a five minute pulse labeling with [³H] AA, one should be able to observe a higher ³H:¹⁴C ratio in the more rapidly labeled pools and a lower ratio in the more slowly labeled pools such as 1-O-alkyl-2-AA-GPC and PE. Upon stimulation of the doubly labeled cells the ³H:¹⁴C ratio of products such as 5-HETE and LTB₄ might reflect and reveal the pool of origin. By cooling the cells, isolating subcellular fractions, and determining their ³H:¹⁴C ratio it might be possible to follow the movement of the exogenous AA among the subcellular fractions. Although we obtained promising results using this approach, a number of problems make interpretation of such data difficult. One of the problems is the rapid labeling of phosphatidylinositol and release of labeled AA from that pool upon stimulation. In addition the subcellular pools appear to be labeled very rapidly. Further, refinement of this approach might yet shed light on the role of various AA pools of neutrophils. The approach has been used in other cells.

Stimulated release of AA and PAF synthesis

Synthesis of PAF and release of AA

The *de novo* pathway of PAF synthesis, which is dependent in the final step on a specific dithiotheitol insensitive CDP-choline cholinephospho-photransferase to convert 1-O-alkyl-2-acetyl-*sn*-glyceryl to PAF [6]. This pathway does not appear to be a significant route of PAF synthesis in neutrophils or other inflammatory cells.

Since the ether bond is derived from a fatty alcohol, hexadecanol e.g., should be incorporated into PAF in a 1:1 molar ratio with acetate to form 16:0 PAF. We observed the synthesis of 1-O-alkyl-2-acyl-*sn*-glycerophosphate from [¹⁴C] hexadecanol but no species containing a 2-acetyl moiety [52]. One study concluded that holine from CDP-choline can be incorporated into PAF upon treatment with PMA [53], but further confirmation of this finding and its mechanism of incorporation have not been reported. Since studies have not shown the direct incorporation of fatty alcohol into PAF, it is possible that the *de novo* pathway could be initiated by PLA₂ and lysophospholipase D acting on 1-O-alkyl-2-lyso-GPC to generate 1-O-alkyl-2-lyso-*sn*-glycero-3-phosphate that could then be acetylated and yield PAF. However, we have been unable to detect lysophospholipase D in neutrophils. Overall, it does not appear the *de novo* pathway is responsible for PAF synthesis in stimulated neutrophils. On the other hand, the remodeling pathway has been conclusively demonstrated.

Although the remodeling pathway of PAF synthesis is firmly established, what is less clear is the relative contributions of a direct route of synthesis initiated by PLA₂ acting directly on 1-O-alkyl-2-AA-GPC to generate lyso PAF, and an indirect route in which PLA₂ first acts on ethanolamine plasmalogen to generate 1-O-alk-1'-enyl-2-lyso-GPE which then serves as an acceptor for the transfer of AA from 1-O-alkyl-2-AA-GPC by the CoA-independent transacylase (CoA-IT) to generate lyso PAF. We believe both pathways are likely operative in stimulated neutrophils. The acetyl-CoA:lyso PAF acetyltransferase responsible for the conversion of lyso PAF to PAF prefers 1-O-alkyl-2-lyso-GPC as a substrate but can also accept 1-acyl-2-lyso-GPC [5]; the same enzyme may be able to form the 1-O-alk-1'-enyl-2-acetyl-GPE observed [38]; however, Lee and coworkers [54] found evidence that a transacetylase which transfers acetate from PAF to 1-O-alk-1'-enyl-2-lyso-GPE is more active in the synthesis of the PE-derived product. In support of an indirect route of PAF synthesis:

- 1) CoA-IT is highly specific for AA
- 2) an accumulation of 1-O-alk-1'-enyl-2-lyso-GPE and its acetylated derivative is observed upon stimulation of the cells;
- 3) the bulk of AA released upon stimulation is derived from the ethanolamine plasmalogen;
- 4) a loss of specificity for AA in the reacylation of lyso PAF is observed and explained by the buildup of 1-O-alk-1'-enyl-2-lyso-GPE which competes as an acceptor for AA in the CoA-IT reaction [3];
- 5) and the indirect route can be demonstrated in an enzymatic system or permeabilized neutrophils [55].

In support of the direct route, the 85 kDa cytosolic PLA₂, cPLA₂ can readily be shown to act directly on 1-O-alkyl-2-AA-GPC to generate lyso PAF and is also high-

ly specific for AA. The direct route thus yields the concomitant release of AA and lyso PAF, which can be converted to PAF. cPLA₂ is widely believed to be the PLA₂ responsible for initiating PAF synthesis in neutrophils. Some of the strongest evidence for such a role comes from studies of cells derived from cPLA₂-knockout mice, which lose the ability to synthesize PAF [56]. Low molecular weight secreted PLA₂, sPLA₂, could also play a role [57, 58] but might be acting through its receptors to activate cPLA₂ [59]. The relative importance of the direct and indirect routes has been difficult to determine; it should be noted that both routes require the action of a PLA₂. The sPLA₂ is not specific for AA, but by generating an ethanolamine acceptor for CoA-IT could lead to the specific release of AA from the PC class. We observed a selective loss of AA-containing species of PE based on measuring the molecular species of PE in stimulated and unstimulated neutrophils, a finding that appears to favor hydrolysis by an AA-selective PLA₂ such as cPLA₂ [39].

The cPLA₂ has been extensively studied in many cells [60]. Its activity in neutrophils was earlier difficult to demonstrate since the cells contain high levels of proteases that rapidly destroy its activity when the cells are disrupted. The activity of the enzyme is recovered when cells are disrupted in buffer containing a mixture of protease inhibitors [61]. The properties of cPLA₂ and its movement from the cytosol to membranes in the presence of Ca²⁺ and upon phosphorylation has been well documented; see [60] for review. Phosphorylation has recently been shown not to be required for movement to the membranes [60]. The enzyme was thought earlier to migrate largely to the nuclear membrane but is now found to move to membranes throughout the cells based on studies of Leslie and co-workers [62].

Once AA is released, much remains as free arachidonic acid, which likely acts as a mediator itself, e.g., possibly serving to translocate protein kinase C to membranes and assist its activation. The free AA is also converted to eicosanoids largely leukotriene B₄ (LTB₄) and 5-hydroxyeicosatetraenoic acid (5-HETE), both important mediators of inflammation. The 5-HETE can be oxidized to the 5-keto compound, 5-oxo-EETE [63]. The 5-HETE can also be reincorporated into phospholipids.

PAF and the eicosanoids are not only synthesized in concert, they act synergistically to elicit responses. The mediators serve to signal both other neutrophils and an array of other cells including endothelial cells that participate in the inflammatory process. Early studies of PAF revealed that although PAF alone can elicit the degranulation response of neutrophils, the same response can be obtained with 100-fold lower concentrations of PAF in the presence of 5-HETE. In more recent studies, 5-oxo-EETE was found to profoundly potentiate the activity of cytokines in neutrophils [64] and of PAF in eosinophils [65]. The findings suggest that 5-oxo-EETE produced by neutrophils may increase the responses of eosinophils to other stimuli and thus plays a major role in inflammation.

Neutrophils exposed to certain agents that do not themselves elicit AA release become more responsive (primed) to subsequent exposure to agonists that do. The

mechanisms of priming are still poorly understood. In studies to compare the priming ability of diacyl diglycerides, which activate protein kinase C and 1-O-alkyl-2-acyl diglycerides, which do not activate protein kinase C, both diglycerides primed neutrophils to release markedly more AA in response to the chemotactic peptide fMLP [66, 67]. However, one of the most interesting findings was that priming with the diacyl diglyceride resulted in the further conversion of the released AA to 5-HETE and LTB₄ whereas no conversion of the released AA to lipoxygenase products was observed when the cells were primed with the alkyl acyl diglyceride. Subsequent studies revealed that while the diacyl diglyceride activates cPLA₂, the ether species does not [68] but rather involves the mobilization of low molecular weight sPLA₂ [57]. The lack of conversion to 5-HETE and LTB₄ in the cells primed by the ether-linked diglyceride might result from lack of activation of the lipoxygenase, or release of AA from a pool not accessible to the lipoxygenase, or from other parameters.

Activation of PAF synthesizing enzymes

The key enzymes in the synthesis of PAF and the mobilization of arachidonate are the acetyltransferase, which converts lyso PAF to PAF by transferring an acetyl group from acetyl-CoA, the 85 kDa cPLA₂, which specifically hydrolyzes AA from phospholipids, and the CoA-independent transacylase (CoA-IT), which allows the formation of 1-O-alk-1'-enyl-2-lyso-GPE to trigger lyso PAF formation by transferring AA from 1-O-alkyl-2-AA-GPC to the lyso plasmalogen acceptor, a reaction that is highly specific for AA and can generate lyso PAF without releasing free arachidonic acid. A role for sPLA₂ or the Ca²⁺-independent phospholipase A₂ (iPLA₂) has not been ruled out. We have been unable to demonstrate activation of CoA-IT as discussed above; the appearance of a lysophospholipid acceptor apparently is sufficient to trigger action of the enzyme to remove and transfer AA. On the other hand, activation of cPLA₂ has long been recognized and widely studied as recently reviewed [60, 69] while the rapid activation (30 seconds) of the acetyltransferase (four- to ten-fold basal activity) upon stimulation was early recognized in a number of cell types [70–74].

The exact signaling pathways responsible for activation of the cPLA₂ and the acetyltransferase have been difficult to pinpoint because of the extensive cross-talk between systems; e.g., protein kinase C activation can result in activation of ERK and p38 MAP kinases. Thus activation responses due to a protein kinase C activator such as PMA yet dependent on the direct action of a MAP kinase may be blocked by protein kinase C inhibitors due to the cross-talk.

We recently carried out a series of studies that indicate the ERK's and p38 kinase play a central role in the regulation of PAF synthesis in human neutrophils [50, 75]. We further examined the priming of the cells by alkylacylglycerol and diacylglycerol

[68] and found that the diacyl diglyceride activated the p42 and p44 MAP kinases along with cPLA₂, whereas the alkyl diglyceride, which did not activate protein kinase C, did not activate MAP kinases on cPLA₂. These studies provided support for the phosphorylation of cPLA₂ by ERK's linked to activation by protein kinase C. Many studies of neutrophil stimulation have employed the Ca²⁺ ionophore A23187; we recently found that the ionophore closely mimics physiological stimuli in the activation of MAP kinase and enzyme activities [50]. In further studies [50], the stimulated phosphorylation and activation of cPLA₂ was found to be reduced both by SB203580, a p38 MAP kinase inhibitor and by the MEK inhibitor PD98059 which blocks activation of the ERK's; cPLA₂ activity was suppressed below unstimulated levels when a combination of both inhibitors was used. On the other hand the acetyltransferase activation was blocked by the p38 inhibitor but not by the ERK inhibitor [75]. We also demonstrated using membrane fractions that active recombinant p38 increased the acetyltransferase to the maximal level observed with TNF- α . However, recombinant ERK's did not activate the enzyme [75]. We have found as reported by others [76, 77] that both the recombinant p38 and ERK's can phosphorylate and activate recombinant cPLA₂.

These findings support a scheme by which both ERK's and p38 MAP kinase phosphorylate and activate cPLA₂ whereas only p38 activates the acetyltransferase.

Overall, a complex network of signaling pathways have now been revealed in human neutrophils linking PAF and AA metabolism through signaling by ERK's, p38 kinase and protein kinase C. More definitive studies can be carried out once the structures and genes for the acetyltransferase and CoA-IT have been determined. The earlier studies have shown that the metabolism of PAF and AA and their actions are very closely linked and constitute an important signaling system for neutrophils and other inflammatory cells as well as endothelial cells.

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Control of long chain polyunsaturated fatty acid levels and the role of inhibitors of incorporation and remodeling on the biosynthesis of lipid mediators

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Overview of AA and PUFA metabolism

AA and 20–22 carbon PUFAs play a number of roles in mammalian physiology [1–7]. These fatty acids serve as structural components of cellular membranes; as signaling molecules; and as precursors of mediators of inflammation, pain, cellular differentiation and cell growth [8–13]. Thus, their levels in mammalian systems are more tightly controlled than those of saturated fatty acids, which appear to primarily serve a structural role.

There are several levels of control of long chain PUFA levels. Mammalian cells lack Δ -9 desaturase and cannot readily convert the more readily available oleic acid to PUFAs. PUFAs of the n-6 or n-3 families are obtained from the diet, mainly from plant oils and marine oils and are thus considered essential fatty acids (EFA) [14, 15]. In addition to dietary sources, elongation/desaturation of precursors also controls levels of long chain PUFAs. These precursors, linoleic acid (LA, 18:2, n-6), and α -linolenic acid (ALNA, 18:3, n-3), for n-6 and n-3 pathways, respectively, are sequentially elongated and desaturated by mitochondrial enzymes to form AA and other 20–22 carbon PUFAs [14, 16–21]. Once PUFAs are obtained from the diet or synthesized, they are rapidly incorporated into glycerolipids and transported between organs in plasma associated with fatty acid binding proteins and lipoproteins. Cellular activation or pathophysiological conditions result in the release of PUFAs by lipases [22–24]. Enzyme-mediated oxygenation or auto-oxidative processes generate potent inflammatory mediators from AA and other PUFAs [12, 25–39]. Thus, PUFAs are implicated in human diseases such as rheumatoid arthritis, cardiovascular dysfunction, tumor growth and metastasis, diabetic neuropathy, cirrhosis of the liver, as well as Alzheimer's disease and other neurological disorders [33, 40–48].

Dietary sources of fatty acids and mechanism of action

Human breast milk is a rich source of EFAs such as gamma linolenic acid (GLA, 18:3, n-6) and low amounts are found in meats [5, 49–51]. High levels are found in plants, marine and fungal oils, mainly as components of triglycerides [52–54]. Major sources of GLA include primrose oil, where GLA is mainly acylated at the *sn*-3 position of triglycerides, blackcurrant seed oil with acylation at the *sn*-3 position, borage oil (*sn*-2 position) and fungal oils (*sn*-2 and *sn*-3 positions). Because of the importance of GLA in physiology and pathophysiology, many biotechnological approaches have been undertaken to engineer plants or unicellular organisms to produce GLA [54, 55]. For example, transgenic tobacco plants expressing Δ -6 desaturase or bacteria or yeast mutants have been designed for enhanced GLA production [54, 56–58]. GLA may act to ameliorate the symptoms of a number of diseases due to its capacity to modify lipid composition of cells and its role in the synthesis of anti-inflammatory lipid mediators [59–65]. Following GLA supplementation, there is an increase in the levels of the elongase product, dihomo gamma linolenic acid (DGLA) within inflammatory cells such as neutrophils, without a corresponding increase in the desaturase product, AA. However, there is a significant increase in AA content of serum, which may be detrimental in chronic disease conditions [62, 64]. A combination of elongase inhibitors or substrate competitors or feed back inhibitors may prevent such a build-up of AA within serum, while maintaining the positive attributes of GLA supplements. Elongated GLA is rapidly incorporated into cellular membranes and these reside in the same cellular glycerophospholipid pools, as does AA. Thus, they are equally utilized for the biosynthesis of eicosanoids by lipoxygenases (LO) and cyclo-oxygenase (COX) activities. The incorporation of elongase products into phospholipids is mediated by ligases and CoA-dependent acyl transferases, while remodeling within lipid pools is mediated by CoA-dependent and independent transacylases. Upon cell activation due to disease processes, phospholipases A₂ (PLA₂) may release DGLA, which is a substrate of COX and LO enzymes. Similar to GLA metabolism, fatty acids from the n-3 pathways can also be elongated to form eicosapentaenoic acid (EPA, Fig. 1) and subsequently incorporated/remodeled within glycerophospholipids using similar enzymatic activities. These metabolic pathways compete with AA metabolism because similar enzyme activities are involved. Thus, supplementation of human diets with GLA or EPA may result in a decrease in the formation of pro-inflammatory mediators such as LTB₄ and platelet activating factor formed during the rapid remodeling and reacylation of lipids. In addition to competing with AA, DGLA and EPA are converted to eicosanoids (1- or 3-series of prostanoids and 3- or 5 series of leukotrienes, respectively) that are either anti-inflammatory in nature or thousands of folds less active than AA-derived eicosanoids (2-series prostanoids and 4 series leukotrienes). Supplementation of human diets with GLA has been shown to reduce the signs and symptoms of chronic inflammatory diseases [42, 43, 46, 52, 66–74]. Being a pre-

cursor of AA, it is counter intuitive that GLA supplementation results in a decrease in pro-inflammatory lipid mediator biosynthesis; however, studies using neutrophils from subjects fed with GLA supplements have shown decreased LTB₄ and PAF biosynthesis [64]. Recent *in vitro* and *in vivo* studies have shown that human neutrophils do not express Δ -5-desaturase activity; thus, dietary GLA supplementation leads to the accumulation of DGLA, rather than AA, in cellular glycerolipids [62]. Levels of GLA, other n-6 fatty acids, and n-3 PUFAs available to cells after ingestion of nutraceuticals will likely be determined by pharmacokinetic parameters, stereo-specificity of lipases that release free fatty acids from triglycerides and the levels of free fatty acids that are controlled by rapid acylation and remodeling processes. Together, various studies reveal that the conversion of AA precursors by endogenous elongase activity to AA structural analogues such as DGLA or EPA can be an effective strategy for controlling the biosynthesis of mediators of inflammation.

Enzyme activities that control AA and PUFA levels

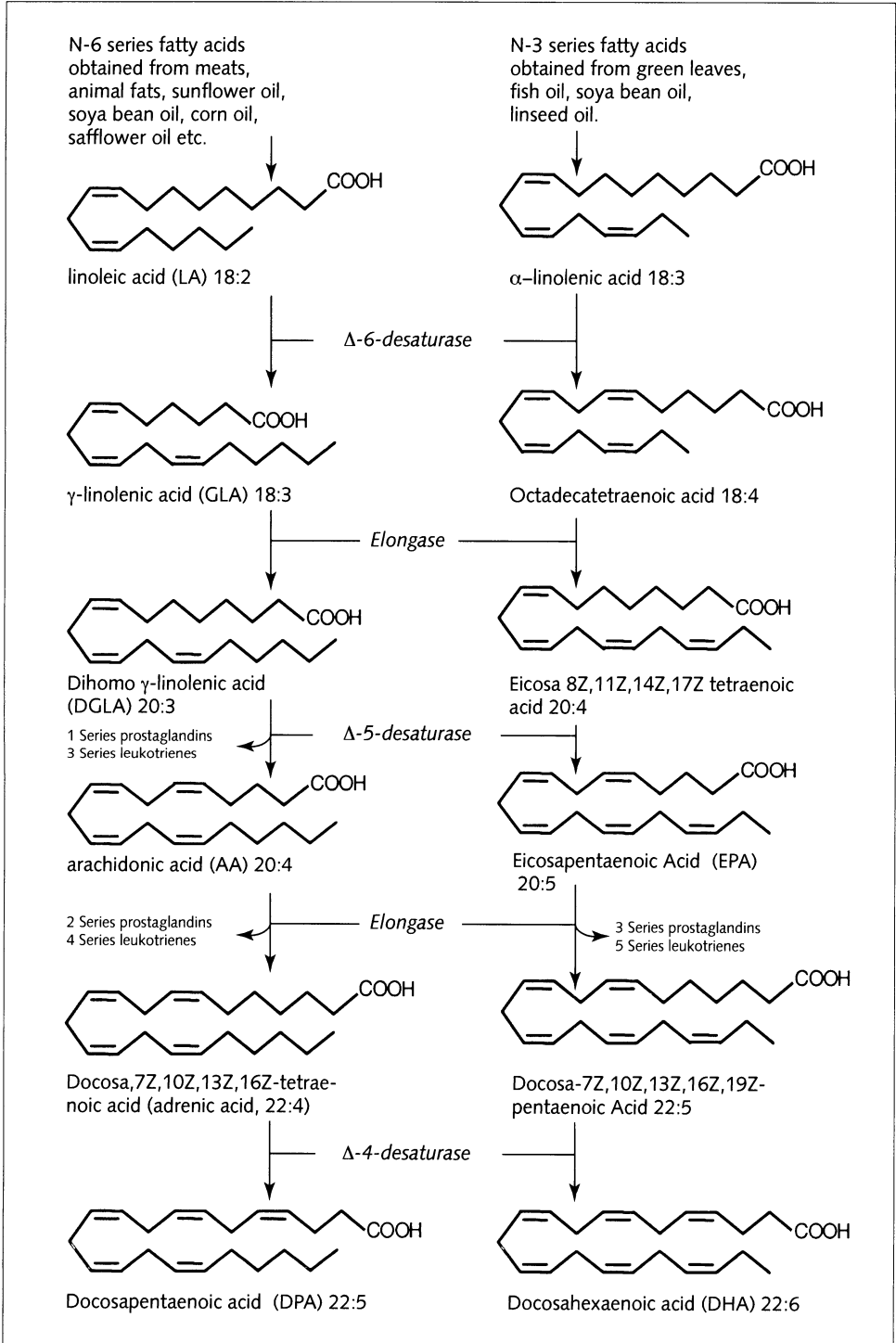
The synthesis of 20 and 22 carbon PUFAs

Long chain PUFAs, which serve as eicosanoid precursors, may be obtained either through the diet or by elongation and desaturation of 18 carbon fatty acids (Fig. 1). Sprecher has also proposed that 22 carbon fatty acids are formed in mammalian systems by 2 elongation of 20 carbon fatty acids followed by a Δ -6 desaturation reaction and retro conversion [75, 76]. Deficient retroconversion of 22:6 (n-3) to 20:5 (n-3) has been demonstrated in fibroblasts from subjects with Zellweger Syndrome, suggesting a defect in β -oxidation and peroxisomal function [77, 78].

AA (20:4, n-6) and DHA (22:6, n-3) are major acyl components of membrane phospholipids [79]. The brain, especially non-myelin membranes, is very rich in AA and DHA. Dietary deficiency in precursors of AA and DHA has been shown to reduce their levels in the central nervous system, resulting in altered learning behavior and impaired visual function. In addition to dietary levels, free levels of these fatty acids may also be influenced by oxidation for energy, and their distribution and transport determined by acylation into phospholipids, triglycerides and cholesterol esters. Thus key enzymes responsible for controlling levels of these PUFA include elongase, desaturase, acyl CoA-synthetase and acyl CoA transferases.

Elongase enzymes

Elongations of 18 carbon fatty acids, combined with desaturation (discussed below), generate 20 and 22 carbon fatty acids. Elongase activity converts GLA (18:3 to n-6) to DGLA (20:3, n-6) and also AA (20:4, n-6) to docosatetraenoic acid (DTA,



22:4, n-6). Similarly, elongase converts stearidonic acid (SDA, 18:4 n-3) to eicosatetraenoic acid (20:4, n-3) and EPA (20:5 n-3) to docosapentaenoic acid (DPA, 22:5 n-3) (Fig. 1). While our understanding of the importance of elongation of fatty acids is advanced in unicellular organisms and plants, knowledge of the biochemical properties of elongase enzymes in animals is limited because these enzymes have only recently been cloned from animal sources. Human elongase (ELOVL5) uses monounsaturated and PUFA as substrates [80]. Two cDNA clones with 56.4% and 58% amino acid identity to ELOVL5 encoding a 296 amino acid peptide have recently been expressed in yeast and shown to elongate 20 and 22 carbon fatty acids [80, 81]. Studies using various other cloning and expression strategies have been applied to bacteria, yeast and plants to provide the following mechanistic details about elongases [82–85]. The elongation process is thought to be a four-step process involving condensation of malonyl-CoA with acyl-CoA to form carbon dioxide and an elongated β -ketoacyl-CoA. This first reaction catalyzed by β -ketoacyl CoA synthase is substrate specific and rate limiting. This condensation reaction is then followed by reduction to β -hydroxyacyl-CoA, dehydration to form enoyl-CoA and a final reduction to form acyl CoA.

Desaturase enzymes

Since 20 and 22 carbon PUFAs are synthesized from LA (18:3, n-6) and ALNA (18:3, n-3), the synthesis or ingestion of these precursors dictates the availability of these 20 and 22 carbon PUFAs. Sequential elongation and desaturation of precursors by enzymes are key events in the synthetic pathways. Three desaturation enzymes are involved in this process (Fig. 1). These include a Δ -6 desaturase that converts 18:2 (n-6) or 18:3 (n-3) to 18:3 (n-6) and 18:4 (n-3), respectively, a Δ -5 desaturase that converts 20:3 (n-6) or 20:4 (n-3) to 20:4 (n-6) and 20:5 (n-3), respectively and a Δ -4 desaturase that converts 22:4 (n-6) or 22:5 (n-3) to 22:4 (n-6) and 22:6 (n-3), respectively. Desaturases are complexes consisting of NADPH-cytochrome b5 reductase, cytochrome b5 and Δ -5 or Δ -6 enzymes [57, 86–92]. The liver contains high levels of desaturases and is the site for the synthesis of most

Figure 1

Elongation and desaturation of n-6 and n-3 fatty acids.

LA (18:2, n-6) and ALNA (18:3, n-3) are precursors for long chain PUFA synthesis by elongase and desaturase activities. PUFAs are incorporated into phospholipids and subsequently utilized for the synthesis of prostanoids designated series 1, series 2 or series 3 from DGLA, AA and EPA, respectively. Leukotrienes generated from these same fatty acids are designated series 3, 4 and 5, respectively.

PUFAs [87, 93, 94]. Human lung, brain and heart have recently been shown to contain comparable levels of Δ -5 desaturase, while very low but detectable enzyme expression is described in other tissues. Δ -6 is comparatively more abundant in most tissues than Δ -5 desaturase, although age-related or nutritional-regulated processes may alter this balance. Human Δ -5 and Δ -6 enzymes have recently been cloned [87, 88, 95, 96]. These genes are located on chromosome 11, have 75% nucleotide homology and 61% amino acid homology. Δ -5 is a single transcript of ~ 4.4 kb (444 amino acid peptide) while Δ -6 is 3.4 kb transcript. Δ -5 desaturase has two membrane-spanning domains characteristic of membrane anchored proteins, three histidine-rich regions suspected for heme iron binding and contain cytochrome b5 domain at the N terminus. In PUFA biosynthesis, Δ -6 is considered the rate-limiting step in the pathway (Fig. 1). It is still controversial whether there are specific desaturases for n-3 and n-6 pathways. Studies using the enzyme inhibitor, N-ethyl maleimide showed differential inhibition of n-6 product formation, suggesting that there may be different desaturases specific for these pathways [97]. However, expression of cloned enzymes has shown that the same activity is responsible for both pathways [87]. Several studies have implicated regulation of desaturase activities on dietary intake of various fatty acids and on hormonal levels. For example, when animals are fed an EFA deficient diet, Δ -6 and Δ -5 activities increase. Similarly, supplementation of animal diets with n-6 or n-3 fatty acids reduces Δ -6 and Δ -5 desaturase activities [20, 98, 99]. In contrast, supplementation of diets with oleic acid (18:1, n-9) does not affect desaturase activity. While the biochemical mechanisms that account for these dietary regulations have not been determined, it is possible that these enzymes share a regulatory sequence due to their localization and reverse sequence orientation on the same chromosome. These desaturases are also located on a chromosome that has been implicated in obesity, raising the possibility that these activities have pathologic importance. Further evidence for the involvement of desaturases in diseases is provided by studies showing that Δ -6 activity is induced by peroxisome proliferators and by insulin administration to diabetic animals [100–102]. As described above, 20 and 22 carbon PUFAs are implicated in many biological processes such as brain development, cognition, reproduction, inflammation, homeostasis, and pain [95, 101, 103, 104]. Δ -6 desaturase abnormalities have been described in brain autopsy samples from subjects with Alzheimer's disease, where there is elevated LA and a corresponding reduction in 20:4 (n-6), 22:4 (n-6) and 22:6 (n-3) [103]. Desaturases may influence these events and diseases by generating signaling molecules that control gene expression and influence lipid metabolism, thermogenesis and cell differentiation.

Supplementation studies show that in brain astrocytes, the rate of DHA synthesis is limited by elongation [105]. Addition of ALNA or EPA to these cells resulted in a decrease in 22:5 (n-3) and 22:6 (n-3) synthesis, whereas supplementation with LA (18:2, n-6) did not affect 22:5 (n-3) synthesis. Astrocytes also secrete cholesterol esters and phosphatidylethanolamine (PE) containing AA and DHA. Similar studies

by Laposata and colleagues used a fibrosarcoma cell line deficient in EFA to show the importance of elongation and desaturation in PUFA synthesis [20]. During n-6 fatty acid supplementation, these cells synthesize EPA *via* elongation while n-3 fatty acid supplementation results in a decrease in the desaturation of GLNA to AA and decrease in AA elongation to 22:4 (n-6). Interestingly, these supplementation strategies also shifted the majority of EPA from phospholipids to triglycerides. These supplementation strategies also resulted in the formation of series 1, 2 or 3 prostanoids. Together, these studies show that there is co-ordinate regulation of n-3 and n-6 pathways by modulation of elongation and desaturation activities. These pathways are also important in directing the distribution of PUFAs into glycerolipids and in directing the types of eicosanoids that are formed.

Incorporation of PUFAs into phospholipids

20 and 22 carbon PUFAs obtained from the diet or through elongase and desaturase reactions are preferentially incorporated into phospholipids. The incorporation process involves PUFA activation by acyl CoA synthetase also known as ligase, followed by acyl CoA transfer into glycerophospholipids.

Acyl CoA synthetase (ACS)

ACS catalyzes the reaction of a long chain carboxylic acid with ATP and CoA to form acyl-CoA, AMP and diphosphate. The enzyme acts on a variety of saturated and unsaturated fatty acids but enzymes from different tissues show differences in specificity. The enzyme from the liver acts on C6–C20 fatty acids while the enzyme from the brain acts on fatty acids with up to 24 carbons [106, 107]. ACS has been purified from many sources and Majerus and colleagues have described isoforms that are specific for AA [108–110]. Five ACSs have been cloned in mammalian tissues and their expression has helped elucidate substrate requirement and cellular distribution of these enzymes [111–116]. ACS2 and ACS3 mRNA are expressed in brain but not in liver, while ACS4 and ACS5 mRNA are expressed in steroid producing cells and intestines. ACS4 is a 75 kDa protein that is modified by translation and shows various changes in its expression during brain development [117]. ACS1 and ACS5 show very broad substrate specificity while ACS4 has marked preference for AA and EPA. Likewise, ACS3 has been shown to be AA specific and to be expressed in brain and heart tissues. ACS belongs to a super family of enzymes with two luciferase-like regions, an AMP and fatty acid binding sites located in both luciferase-like regions. ACS1, 2 and 3 have 60% amino acid identity but may be independently regulated by diet and hormones [118, 119]. Once formed by ACS, fatty acyl CoA may be metabolized *via* β -oxidation, used for glycerolipid synthesis,

elongated or desaturated, used for synthesis of cholesterol esters, protein acylation or may serve as signaling molecules [120, 121]. Long chain ACS is linked to several pathologic conditions including X-linked adrenoleukodystrophy and polymorphism of the ACS gene is linked to risk factors of hypertriglyceridemia, visceral obesity and hypertension [122–124] and is deleted in a family with Alport syndrome, alliptocytosis and mental retardation [115, 116, 118, 122, 125–129].

CoA-dependent acyl transferase

Once acyl CoAs are formed, they are rapidly incorporated into glycerolipids by CoA-dependent acyl transferase (Fig. 2). Two major forms of acyl transferases synthesize phosphatidic acid by sequentially adding acyl CoA to glycerol-3-phosphate (Kennedy pathway) [130, 131]. In addition, acylation of lysophospholipids described by Lands and colleagues utilizes acyl CoAs [132–134]. In these acylation reactions, selectivity depends on whether the acyl CoA is saturated or unsaturated, the concentration of the acceptor molecules and the types of bond at the *sn*-1 position of lysophospholipid acceptors. This selectivity distinguishes *de novo* synthesis from the incorporation of low AA amounts into glycerolipids. Studies using human cells have shown that very low free levels of 20 and 22 carbon PUFAs are present under resting conditions [135]. ACS and CoA acyl transferase activities play the crucial role of controlling these levels by activating and rapidly incorporating fatty acids into glycerophospholipids.

Transacylase

Both CoA-DT and CoA-IT move acyl groups between phospholipid pools. Due to the selectivity of these activities, they play major roles in asymmetrically distributing fatty acids in phospholipid subclasses. CoA-DT transfers fatty acids from one phospholipid to another utilizing an acyl CoA and lysophospholipid intermediate. Waku and colleagues have demonstrated that the preferred substrates for CoA-DT are AA, LA and SA [136–140]. The major activity that transfers 20- and 22-carbon fatty acids between phospholipid subclasses is known as CoA-independent transacylase (CoA-IT). CoA-IT is specific in transferring these fatty acids from mainly diacyl phospholipid donors to 1-alkyl- or 1-alk-1-enyl-linked lysophospholipid acceptors and does not require a cofactor (CoA) or ATP for its activity [141–143]. Thus, CoA-IT is responsible for the fact that the majority of 20- and 22-carbon PUFAs are found in ether-linked phospholipids and not in the early ester-linked phospholipids in which they are initially synthesized. The main acceptors are 1-alkyl-2-lyso glycerophosphocholine or 1-alk-1-enyl-2-lyso glycerophosphoethanolamine (Fig. 2). CoA-IT thus generates the major precursor of platelet activating factor. CoA-IT is a

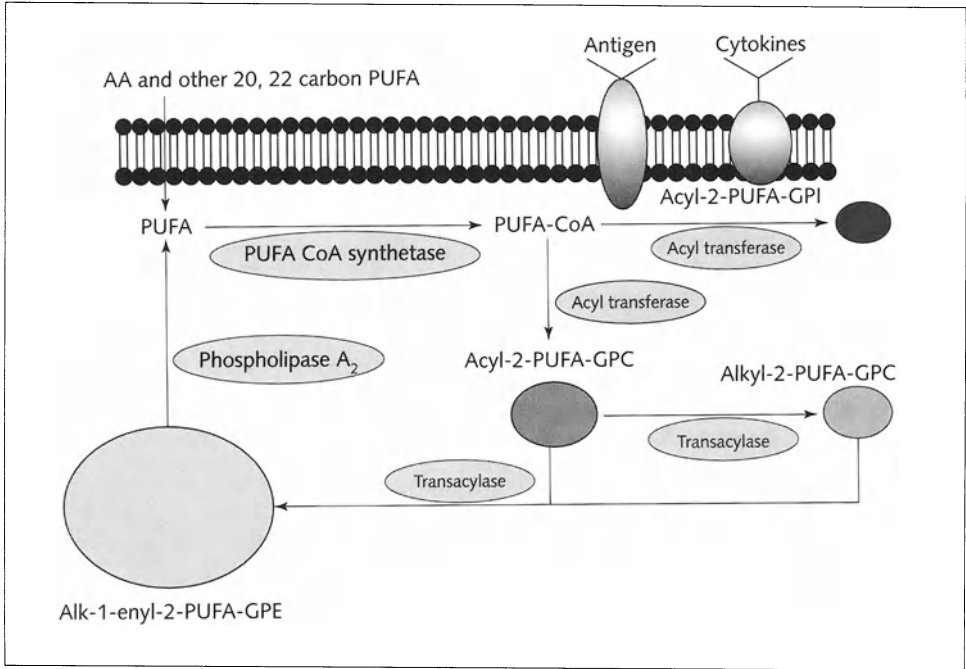


Figure 2

Remodeling of AA in inflammatory cells

AA and other PUFAs presented to mast cells or human neutrophils are rapidly incorporated into 1-acyl-linked glycerophospholipids, (1-acyl-2-PUFA-GPC and 1-acyl-2-PUFA-GPI). Transacylase activity transfers AA to ether-linked phospholipid subclasses (1-alk-1-enyl-2-PUFA-GPE and 1-alkyl-2-PUFA-GPC). This remodeling process is completed by the slow release of AA from these major ether pools and is enhanced when these cells are activated by antigen, cytokines or bacterial peptides such as FMLP or endotoxins.

membrane bound enzyme that has not been purified or cloned. However, gel filtration studies and native gel electrophoresis data suggest that CoA-IT is a ~ 60 kDa protein that is found in great quantities in microsomal fractions [144]. Various biochemical and pharmacological approaches have been utilized to gain a comprehensive insight into CoA-IT activity and function. Using radiolabeled assays or mass spectroscopic experiments, we have identified specific phospholipid subclasses and molecular species that are donors or acceptors of PUFAs during the remodeling process in neutrophils or mast cells [142]. Importantly, these studies have also shown how PUFAs get incorporated into inflammatory cells and get remodeled between phospholipid subclasses [145, 146]. Further evidence lending credence to these biochemical studies comes from experiments in which CoA-IT inhibitors block the movement of AA between phospholipid subclasses (discussed below).

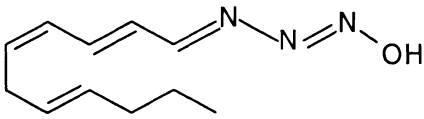
Role of inhibitors in modulating PUFA levels

PUFA levels may be manipulated through dietary control or through inhibition of specific enzymes that maintain PUFA homeostasis. Currently, advances have been limited to inhibitors of desaturases, ligases and CoA-IT. Needleman and colleagues used a Δ -6 desaturase inhibitor (SC-26196) that was shown to increase LA levels, concomitant with a decrease in AA and DHA levels in mice [147, 148]. Interestingly, the decrease in AA was specific for PC, PI and cholesterol esters and not for PS, PI or triglycerides, and the molecular species formed were determined by the fatty acids at the *sn*-1 position of the phospholipid. These studies suggest that phospholipid remodeling mediated by Δ -6 desaturase is important in *de novo* synthesis of glycerolipids and cholesterol esters.

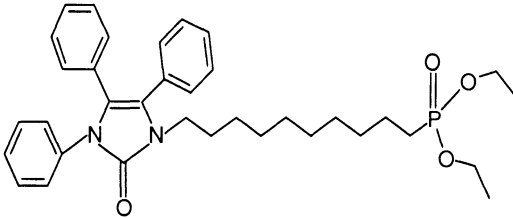
Similar to desaturase and elongase, inhibitors of acyl CoA-synthetase activity have the potential of influencing PUFA biosynthesis. Various inhibitors have been used to show the importance of ACS in fatty acid metabolism and in disease processes. Of these inhibitors, products of the Streptomycin species known as triacsin (Fig. 3A) have been shown to be very potent ACS inhibitors (Tab. 1) [113, 149–152]. In addition to triacsin, structurally related compounds having an N-hydroxytriazone moiety (WS-1228) that are known hypotensive vasodilators inhibit ACS activity. These inhibitors show that there are different ACSs in cells that show different selectivity by inhibiting the activation of some fatty acids. Additionally, inhibitor studies show that there are likely different acyl CoA pools in different cells. Importantly, triacsin interferes with PAF formation, suggesting that it blocks reacylation by enhancing the supply of lysoPAF [136]. Triacsin blocks *de novo* synthesis of triglycerides and phospholipids but not the reacylation of lysophospholipids or the synthesis of cholesterol [151]. In some cells, triacsin inhibits OA incorporation without affecting AA and controls fatty acid distribution into glycerolipids during neuronal outgrowth [127]. In addition to triacsin, the potent antidiabetic agents, thiazolidinedione drugs (triglitazones) achieve their pharmacologic effects in part by direct interaction with ACS4, independent of PPAR- γ [113]. Similar to triacsin, triglitazones inhibit long chain fatty acid incorporation into cellular lipids. Medium chain ACS is also inhibited by quinolone antimicrobial agents and by non-steroidal anti-inflammatory agents [153].

Inhibitors of AA-remodeling

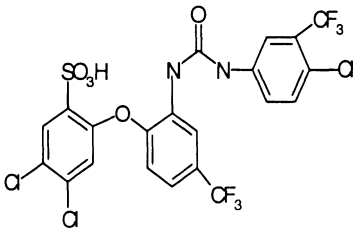
Ether lipids play a prominent role in cell biology especially in inflammation, cancer biology and in CNS pathophysiology. As described above, AA is transferred from 1-acyl-linked phospholipids to 1-ether-linked phospholipids, leading to the latter class containing most of the mass of cellular AA. Inflammatory cells such as mast cells, macrophages or neutrophils contain high amounts of ether-linked phospholipids



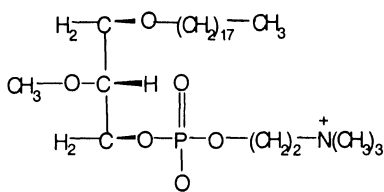
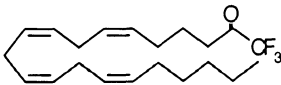
A) 2E, 4E, 7E-Undecatriene-1-triazene (Triacsin)



B) Diethyl 7-(3,4,5-triphenyl-2-oxo-2,3-dihydroimidazole-1-yl)heptane phosphonate (SK&F 98625)



C) 2-[2-(3-chloro-3-(trifluoromethyl)phenyl)ureido]-4-(trifluoromethylphenoxy)-4,5-dichlorobenzenesulfonic acid (SK&F 45905)

D) 1-O-Octadecyl-2-O-methyl-*sn*-glycero-3-phosphorylcholine (ET-18-OCH3)

E) Arachidonoyltrifluoromethyl ketone

Figure 3
Inhibitors of AA or PUFA metabolism.

Table 1 - Inhibitors of AA incorporation and remodeling

Inhibitor	Enzyme	IC ₅₀	Refs.
Triacsin A	ACS	17–18 μ M	[152]
Triacsin C		4–10 μ M	
SK&F 98625	CoA-IT CoA-D transferase PLA ₂	< 11 μ M 50 μ M > 50 μ M	[142]
SK&F 45906	CoA-IT CoA-D transferase PLA ₂	< 20 μ M 35 μ M ND	[142]
ET-18-O-OCH ₃	CoA-IT	0.5 μ M	[159]
AACOFC ₃	ACS CoA-IT cPLA ₂ sPLA ₂ iPLA ₂	~ 5 μ M 3 μ M > 10 μ M ND ND	[160]

ND denotes not determined.

that are rich in arachidonate. These ether lipids provide most of the AA that is released by stimulated cells. As well as providing lyso PAF that is acetylated to form PAF, radiolabel studies show that ether lipids provide the majority of AA that is used for eicosanoid biosynthesis [135, 146, 154]. Laposata has provided additional evidence for a role of ether lipids in eicosanoid and PAF formation by demonstrating that depletion of AA in ether lipids reduces eicosanoid and PAF formation [155]. Because 1-alkyl-2-AA-GPC is the common precursor for LTB₄ and PAF, inhibitors of the formation of this precursor are likely to have significant anti-inflammatory properties. One approach that has been investigated by Winkler and colleagues is the inhibition of the transfer of AA from 1-acyl-linked phospholipids to 1-ether-linked phospholipids [142, 156–159]. CoA-IT has been the major focus on the development of various inhibitors described below.

Diethyl 7-(3,4,5-triphenyl-2-oxo-2,3-dihydro-imidazole-1-yl) heptane phosphonate (SK&F 98625, Figs 3B and C) 2-[2-(3-4chloro-3 (trifloromethyl) phenyl) ureido]-4-(trifluoromethylphenoxy)-4,5-dichlorobenzenesulfonic acid (SK&F 45905, Fig. 3C)-SK&F 98625 and SK&F 45905 are two inhibitors of CoA-IT

which were developed with the assumption that the mechanism of action of CoA-IT resembled that of acyl transferases such as LCAT or ACAT and that the inhibitor should have the capacity to recognize similar substrates as PLA₂s [142]. Thus, analogues of ACAT inhibitors (SK&F 98625) and a PLA₂ inhibitor (SK&F 45905) have shown great promise as inhibitors of CoA-IT (Figs. 3B and 3C). These inhibitors block the movement of AA from 1-acyl-linked phospholipids to 1-ether-linked phospholipids in cell-free and whole cell assays with IC₅₀ < 20 μM (Tab. 1), 3–5-fold lower than their IC₅₀s for inhibition of PLA₂ or other transferases. CoA-IT inhibition produces a decrease in PAF and LTB₄ biosynthesis, concomitant with an increase in intracellular and extracellular free AA levels [157, 161]. Inhibition of lipid mediator biosynthesis likely accounts for the anti-inflammatory effects of these compounds in animal models of inflammation, while the build-up of free AA may account for induction of cancer cell apoptosis by these same compounds [143, 145, 159, 162, 163]. While none of the above inhibitors have been clinically developed, they have revealed several critical aspects about levels of control of lipid mediator biosynthesis and the potential of targeting specific enzymes for therapeutic benefits.

1-O-Octadecyl-2-O-methyl-*sn*-glycer-3-phosphorylcholine (ET-18-OCH₃)

ET-18-OCH₃ (Fig. 3D) is an ether lipid that has been shown to induce apoptosis of cancer cells and to display a range of other biological properties. In addition to its inhibitory effects on kinases, ET-18-OCH₃ has been shown by Winkler and colleagues to be a potent inhibitor of CoA-IT (IC₅₀ = 0.5 μM) [159].

Arachidonoyl trifluoromethyl ketone (AACOCF₃)

AACOCH₃ (Fig. 3E) has been extensively used as a specific slow binding inhibitor of cPLA₂ or iPLA₂ in mixed micelle assays [164]. However, other studies have shown that AACOCF₃ is a very non-specific inhibitor of many enzyme activities including CoA-IT (IC₅₀ = 3 μM), 5-LO (90% inhibition by 10 μM) and anandamide amidase, which is completely inhibited by 7.5 μM [160]. Higher concentrations of AACOCF₃ inhibited all AA-metabolic processes, including the incorporation of AA into cellular phospholipid pools. The implications of AACOCF₃ inhibition of CoA-IT have been many fold. First, treatment of human neutrophils with < 10 μM resulted in the inhibition of LTB₄ and PAF formation without significant effects on AA release, suggesting that there are distinct arachidonate pools within inflammatory cells; one of which is destined for PAF and LTB₄ formation and is linked to the CoA-IT-mediated formation of the common precursor 1-alkly-2-AA-GPC. A second revealing aspect of these studies is that AA release alone is not sufficient for lipid mediator biosynthesis. It requires the incorporation of AA into specific AA pools,

accompanied by the remodeling of AA into ether-linked phospholipid pools for lipid mediators to be formed. Thus, remodeling may not only be needed to maintain membrane structure, but may be an essential process that transfers AA to specific membrane regions such the endoplasmic reticulum where it is further metabolized by 5-LO.

Conclusion

AA is an EFA derived from the diet or synthesized by the liver or brain cells using LA as the major precursor. LA is sequentially elongated and desaturated to form AA. AA is incorporated into cellular lipids by CoA-dependent enzymes and then remodeled within various phospholipid subclasses and molecular species by transacylases. Specific inhibitors of the aforementioned enzyme activities can be used to control AA levels. These inhibitors have been shown to alter the distribution of AA within cellular pools in inflammatory cells and to influence the biosynthesis of lipid mediators. Thus, use of combinatorial chemistry and structure-activity relationships of existing inhibitors, will likely result in the discovery of new and potent classes of anti-inflammatory agents. These inhibitors will be beneficial in controlling inflammatory diseases such as arthritis and asthma. In addition to specific inhibitors, nutraceuticals are becoming an essential component of the health management regimen of many people in industrialized countries. Examination of fatty acid supplements shows that some diets may have dangerous side effects due to the build up of AA levels in serum. Therefore, it is important that biochemical modifications and all key enzymes responsible for controlling AA be studied in order to avoid any detrimental side effects. Biochemical side effects may be avoided by using combinations of fatty acids in dietary supplements or specific inhibitors of key enzymes. Dissecting how AA and other PUFA pools are altered in various diseases provides pathophysiologic mechanisms that will be the basis of future therapeutic design or the design of efficacious dietary supplements.

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Remodeling of arachidonic acid in inflammatory cells of the human lung

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Introduction

Arachidonic acid (AA) is a key molecule in the modulation of several pathophysiological events in mammalian cells, including gene expression, membrane signal transduction, cell differentiation and apoptosis, exocytosis and generation of eicosanoids [1–4]. It has been now convincingly demonstrated that the intracellular levels of free AA within mammalian cells are crucial for most of these events and, therefore, they are carefully regulated by complex biochemical reactions [5, 6]. These reactions are catalyzed by enzymes involved in both AA mobilization and re-esterification into the storage sites and transfer from one intracellular pool to another [7, 8].

Under normal circumstances, AA is stored within different phospholipid and neutral lipid pools. The distribution of AA in the lipid pools of the cell is a highly dynamic phenomenon that may follow routes different from cell to cell and in the same cell exposed to various conditions [9, 10]. The changes in the distribution of AA within the glycerolipid pools have been referred to as remodeling. In the last ten years a large body of evidence has accumulated indicating that remodeling of AA between lipid pools is an important mechanism to regulate the intracellular levels of free and esterified AA and to determine the quantities of AA that can be mobilized at any time from the storage pools [11–13].

The rate and extent of AA remodeling is strongly influenced by the stage of maturation and differentiation of the cell and by its state of activation [14–17]. Increasing evidence also suggests that AA remodeling may be biochemically or pharmacologically modulated and that this type of intervention has relevant and complex effects on a variety of intracellular processes [18–21].

AA metabolism is a crucial biochemical event in cells involved in inflammatory and immune responses. In both humans and experimental animals, inflammatory cells contain relatively large quantities of esterified AA that is utilized primarily for the production of prostaglandins, thromboxanes, leukotrienes and other metabo-

lites involved in inflammation [22, 23]. In addition, AA in inflammatory cells has been implicated in the degranulation process leading to the release of preformed mediators [4, 24, 25], in the production of cytokines and chemokines [26–28], activation of respiratory burst [1, 29], chemotaxis and phagocytosis [2, 30] as well as in the survival of cells recruited at sites of inflammation [13, 31].

Arachidonic acid pools in human inflammatory cells

The bulk of AA in human inflammatory cells under resting conditions is esterified into various phospholipid pools [6]. Data obtained with cells isolated from peripheral blood of healthy donors including neutrophils [32–34] and eosinophils [35] show that the majority of AA in unstimulated cells is esterified in phosphatidylethanolamine (PE), followed by phosphatidylcholine (PC), phosphatidylinositol (PI) and phosphatidylserine (PS). In these cells a small percentage of the total cellular AA (1–5%) is usually associated with neutral lipid pools, primarily triglycerides (TG), diglycerides (DG) and cholesterol esters [36, 37]. Most of the AA in resting inflammatory cells isolated from blood is esterified into the 1-alkyl and the 1-alk-1'-enyl (plasmalogen) subclasses of PE and the 1-alkyl subclasses of PC [32, 33].

The distribution of AA in inflammatory cells resident within tissues, i.e., the lung or the gastrointestinal tract, is to some extent different from that of inflammatory cells circulating in the blood. For example, mast cells purified from the human lung contain approximately 50% of the total cellular AA esterified into TG [38]. Similarly, macrophages isolated from the lung or the peritoneal cavity contain 10–25% of AA associated with TG [39, 40].

Major differences also exist in the distribution of AA within phospholipid pools between tissue and blood inflammatory cells. For example, the majority of AA in mast cells purified from the human lung or skin is esterified into 1-acyl-PC and 1-acyl-PE [41, 42], making these, and not the 1-ether-linked, the major AA-containing phospholipid subclasses. As previously mentioned, it is believed that the distribution of AA into glycerolipid pools may to some extent dictate the quality and quantity of eicosanoid produced upon cell activation [32, 43, 44]. Several studies have shown that some classes and subclasses of membrane phospholipids represent preferential substrates for PLA₂s [31, 45]. In other words, certain intracellular pools of AA are predominantly involved in the production of eicosanoids whereas others may represent primarily storage pools [39, 43]. A good correlation between the amount of AA in certain phospholipid pools (1-ether-linked) and products (eicosanoids) has been demonstrated in several inflammatory cells such as neutrophils, eosinophils, macrophages and mast cells [43, 44, 46, 47]. In particular, only AA derived from the 1-alkyl subclasses of phosphatidylcholine and phosphatidylethanolamine has been closely linked to eicosanoid synthesis. In contrast, AA derived from other classes of phospholipids (phosphatidylinositol and phos-

phatidylserine) or from the 1-acyl subclass of phosphatidylcholine and phosphatidylethanolamine may be preferentially secreted as free AA or may remain inside the cell functioning as a second messenger.

Remodeling of arachidonic acid in inflammatory cells migrating to the lung

The possibility of comparing cells in a relatively resting state (isolated from blood) with those retrieved by bronchoalveolar lavage (BAL) in patients with inflammatory diseases of the lung offered a great opportunity to explore AA remodeling and changes in lipid mediator synthesis induced by the cell recruitment in an inflamed tissue.

In initial studies we compared the total cellular content and the distribution of endogenous AA in the glycerolipid classes of neutrophils isolated from peripheral blood or from the BAL of patients with adult respiratory distress syndrome (ARDS), an acute and severe inflammation of the lung with extensive neutrophilic infiltration [36]. Neutrophils from the BAL of ARDS patients contain an amount of total AA almost four times higher than that found in neutrophils from peripheral blood of the same patients (4.3 ± 1.2 versus 1.3 ± 0.4 nmol/ 10^6 cells). The major difference between the distribution of AA in the glycerolipid classes between neutrophils from peripheral blood and those from the BAL of ARDS patients is the accumulation of large quantities of AA in TG [36]. BAL neutrophils contain a pool of AA associated with TG that is almost ten-fold larger than that in resting blood neutrophils. AA in TG accounted for $28.7 \pm 7.9\%$ versus $3.1 \pm 1.2\%$ of total cellular AA in BAL and peripheral blood neutrophils, respectively. In addition, a smaller but significant increase in the percentage of AA esterified in PC can be detected in BAL neutrophils. The percentage of AA in PE, which is the major pool in blood neutrophils, is reduced by 30% in BAL neutrophils. These data indicate that there is a significant increase in the total cellular content of AA and a major remodeling of AA within glycerolipid pools in human neutrophils migrating from the blood to the lung and the alveolar space. In particular a large pool of AA in TG is constituted in neutrophils entering the inflamed lung *in vivo* [48].

A similar observation has been made in human eosinophils. Blood eosinophils from normal donors contain 3–5% of AA into the TG pool [38]. However, when the eosinophils are isolated from the blood of patients with hypereosinophilic syndromes, they are found to contain up to 30% of AA esterified into TG [36]. This observation suggests that in inflammatory cells, such as eosinophils and neutrophils activated in the blood or recruited in the lung during an inflammatory response, there is a remodeling of AA pools, with an increase of AA associated with the TG pool.

Subsequent studies suggested that the pool of AA associated with TG may be located in the lipid bodies, non-membrane-bound cytoplasmic organelles whose

function is unknown [49]. Lipid bodies are abundant in human lung macrophages and mast cells, but they are very few in resting blood neutrophils and eosinophils [49, 50]. However, there is a dramatic increase in the number of lipid bodies in neutrophils and eosinophils isolated from the BAL of ARDS and asthmatic patients, respectively [36]. In these cells the increase in the number of lipid bodies correlates significantly with the accumulation of AA in the TG pool [36].

The remodeling of AA pools observed in the cells isolated *ex vivo* can be reproduced *in vitro*. For example, peripheral blood neutrophils from normal donors significantly increase their TG pool of AA and the number of lipid bodies when incubated with high concentrations of exogenous AA [37]. Similarly, eosinophils from normal donors acquire the same characteristics of the eosinophils recruited in the airways of asthmatic patients when they are cultured with GM-CSF for 24 hrs in the presence of exogenous AA [38, 46]. In these experimental conditions, both neutrophils and eosinophils acquire the morphologic features of “hypodense” cells, similar to those found in BAL eosinophils and macrophages of asthmatic patients. Taken together, these observations suggest that a large increase in the amount of AA occurs in cells recruited in an inflammatory area, such as the eosinophils and the neutrophils in the lungs of asthmatics and of patients with ARDS, respectively. This increase is mostly due to the expansion of the TG pool, which presumably functions as a large reservoir for AA.

Remodeling of arachidonic acid into TG pool induced by cell differentiation and maturation in the lung

The aforementioned studies have shown that TG may be the largest arachidonate-containing pool in certain inflammatory cells. For example, mast cells isolated from the human lung contain up to 50% of endogenous AA esterified in TG [38]. Other cells such as macrophages, eosinophils, monocytes, endothelial cells and muscular cells contain 5–30% of the total cellular AA associated with TG [38, 39, 51, 52]. The large variability in the AA content of the TG pool from cell to cell is in contrast with the relatively constant distribution of this fatty acid within the phospholipid pools.

The reasons for the wide variation in the TG pool of AA are not known. Like other pools of AA, that associated with TG is a dynamic pool and its size can greatly change under various conditions. For example, accumulation of AA in TG occurs in neutrophils when they are recruited into an inflammatory area *in vivo* [36]. This phenomenon can be reproduced *in vitro* by incubating neutrophils or HL-60 cells with high concentration of exogenous AA [36, 53, 54]. Antigen-induced activation of murine mast cells or ionophore-induced activation of human macrophages results in a transient increase in the AA content of the TG pool [14, 39]. These data suggest that the AA pool in TG is not constitutive but it may be induced by different

stimuli. Understanding the cellular events that are able to promote the accumulation of AA into the TG pool may provide important information on the mechanisms regulating AA processing in inflammatory cells.

Previous works have consistently shown that little or no store of AA in TG is found in immature and/or actively proliferating cell lines. For example, in contrast with mature tissue mast cells, bone marrow-derived mast cells (BMMC) have little or no AA esterified in TG [14]. This observation led to the hypothesis that cellular differentiation and/or inhibition of cell proliferation may induce AA accumulation into the TG pool. We have tested this hypothesis in the human promonocytic cell line U937, an experimental model used to explore the biochemical modifications associated with cell differentiation. U937 can be differentiated into macrophage-like cells upon exposure to such diverse agents as IFN- γ , phorbol esters, retinoic acid (RetAc) and dimethylsulfoxide [55–57]. Differentiation of U937 is associated with inhibition of cell proliferation and with the acquisition of morphological and surface markers typical of mature macrophages [58].

In our experiments, differentiation of U937 into macrophages was achieved by incubation with RetAc, PMA, or both, either in the presence or in the absence of exogenous AA supplementation.

Incubation of AA with PMA or with PMA plus RetAc, but not with the AA supplement alone, blocked U937 proliferation and induced the expression of CD23, a marker of mature macrophages [59].

In addition, differentiation of U937 with PMA induced a significant increase in the total cellular content of AA from 0.9 ± 0.2 to 1.4 ± 0.4 nmoles/ 10^6 cells. This accumulation of AA was further enhanced in U937 incubated with PMA plus RetAc (to 1.7 ± 0.6 nmoles/ 10^6 cells). When differentiation of U937 with PMA plus RetAc occurred in the presence of the AA supplement, the total cellular content of AA reached 2.4 ± 0.9 nmoles/ 10^6 cells. Figure 1 shows the effect of U937 differentiation on the amount of AA into the major glycerolipid classes. Undifferentiated U937 contain AA esterified mostly in PE and to a lesser extent in PC and PI/PS. An average of $3.3 \pm 1.8\%$ of the total AA is associated with neutral lipids, 95% of which is esterified into TG. Exposure of U937 to PMA results in a significant increase in the percentage of AA associated with TG ($8.1 \pm 2.8\%$ of total cellular AA). When U937 are incubated with RetAc plus PMA, accumulation of AA into TG is higher than in U937 exposed to PMA alone ($11.0 \pm 4.6\%$). Finally, differentiation of U937 with RetAc plus PMA in the presence of AA supplement results in the esterification of $18.8 \pm 6.9\%$ of cellular AA into TG.

While the changes in the percentage of AA esterified into TG are the most striking, a significant increase in the percentage of AA esterified in PC is also observed in cells differentiated in the presence of exogenous AA (Fig. 1)

The increase in the TG pool of AA in differentiated U937 is due to an increase in the mass size of TG rather than to the substitution of other fatty acids stored in TG with AA. In fact, the mass amount of TG, expressed as $\mu\text{g}/10^6$ cells, increased

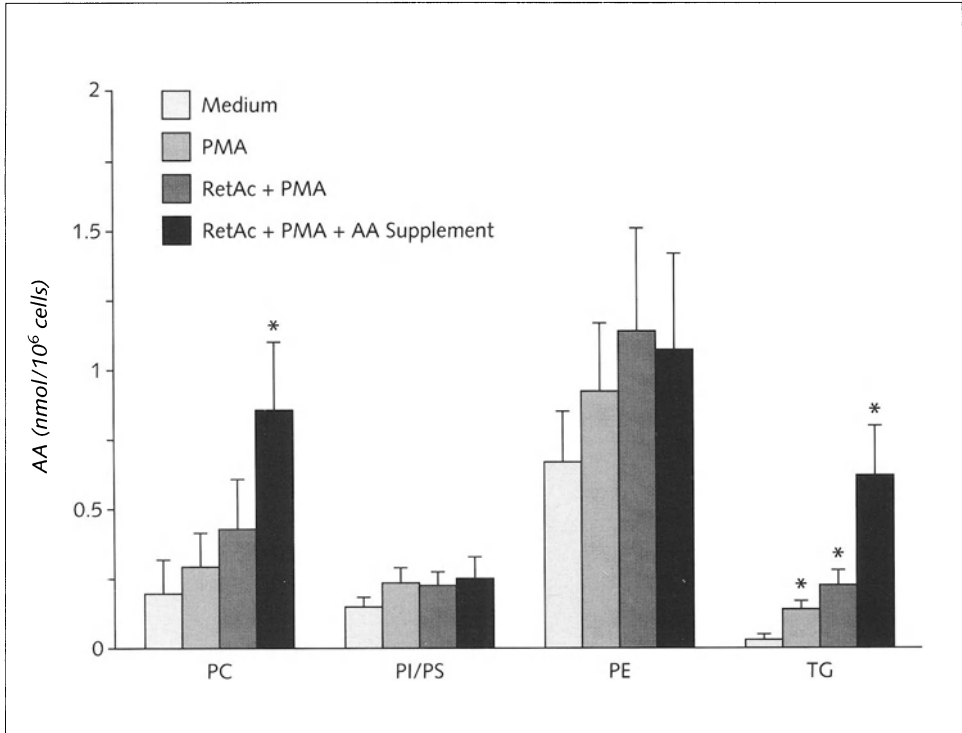


Figure 1

Distribution of AA in the glycerolipid classes of undifferentiated and differentiated U937. U937 were incubated for 96 hrs in medium alone, in the presence of PMA, RetAc and PMA or RetAc and PMA, with an AA supplement (10 μ M). At the end of incubation, the lipids were extracted and AA was determined in each pool by NICI-GC/MS. The data are expressed as nmoles of AA/ 10^6 cells and are the mean \pm SE of five experiments.

* $p < 0.05$ versus medium

from 0.78 ± 0.26 to 1.82 ± 0.56 and to 2.35 ± 0.68 , respectively, in undifferentiated, PMA and RetAc plus PMA differentiated cells. These findings suggest that the accumulation of AA into TG during differentiation of U937 is mostly due to the mass expansion of the TG pool.

Previous findings in the human neutrophil suggested that an increase in the total cellular content of AA is a major factor leading to AA accumulation in the TG pool [36]. The observation that AA supplement enhances the remodeling into the TG pool induced by cell differentiation further supports this hypothesis. To confirm the relationship between the total cellular content of AA and the amount of AA esterified in TG, we used mass spectrometry to determine the amount of endogenous AA (total and TG-associated) in U937 at various stages of differentiation induced by

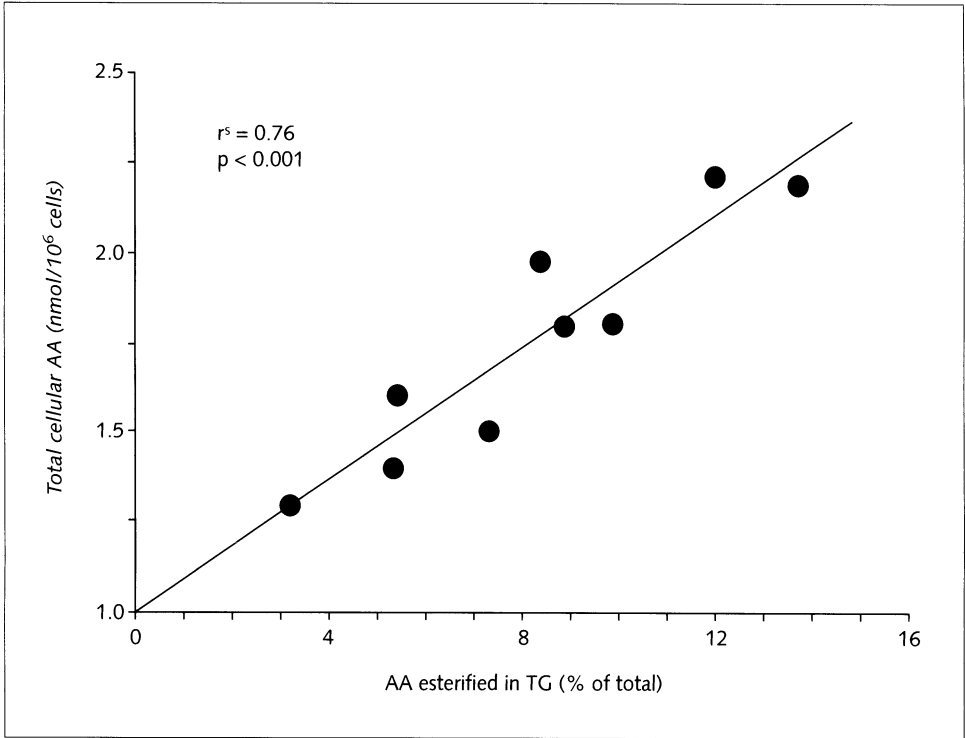


Figure 2

Correlation between the total cellular AA content and the percentage of AA esterified in TG in U937 at different stages of differentiation

U937 were incubated for 48–96 hrs in the presence of RetAc + PMA. At different time points the cells were harvested and the lipids were extracted. TG were isolated by TLC and endogenous AA was liberated by alkaline hydrolysis. Total cellular AA and AA associated with TG were determined by NICI-GC/MS. The data are obtained with three different preparations of U937.

RetAc plus PMA. A significant correlation can be found between the total cellular content of AA and the percentage of AA associated with TG in U937 at different stages of differentiation (Fig. 2).

This result suggested that accumulation of AA in the TG pool could be related to an increase in the capacity of differentiated U937 cells to incorporate exogenous AA. To test this, control and U937 exposed to RetAc, PMA or RetAc plus PMA for 96 hrs were incubated with radiolabeled AA (10^{-9} M) for another 12 hrs. Differentiation with PMA significantly increased the capacity of U937 to take up exogenous AA and this effect was increased up to 2.5-fold in U937 differentiated in the presence of the AA supplement.

Lipid bodies are non-membrane-bound cytoplasmic organelles detectable in most mammalian cells [49] by fluorescent staining with Nile red [60]. Indirect evidence suggests that these organelles may be the subcellular location of the TG pool of AA in human inflammatory cells [61]. Figure 3 shows the flow cytometry scan of Nile red-stained U937 after 96 hrs incubation with PMA or RetAc plus PMA. Incubation with PMA, but not with RetAc alone, increases the fluorescence intensity of U937 compared to control cells. Incubation with RetAc plus PMA further increases cell fluorescence compared to cells incubated with PMA alone. Direct microscope counting [62] and flow cytometry gave comparable results both indicating that differentiation of U937 with PMA or with RetAc plus PMA increased the number of cytoplasmic lipid bodies. This observation further supports the hypothesis that lipid bodies may be the cellular repository for the *de novo* formed TG pool.

Arachidonic acid pools in different populations of human lung macrophages

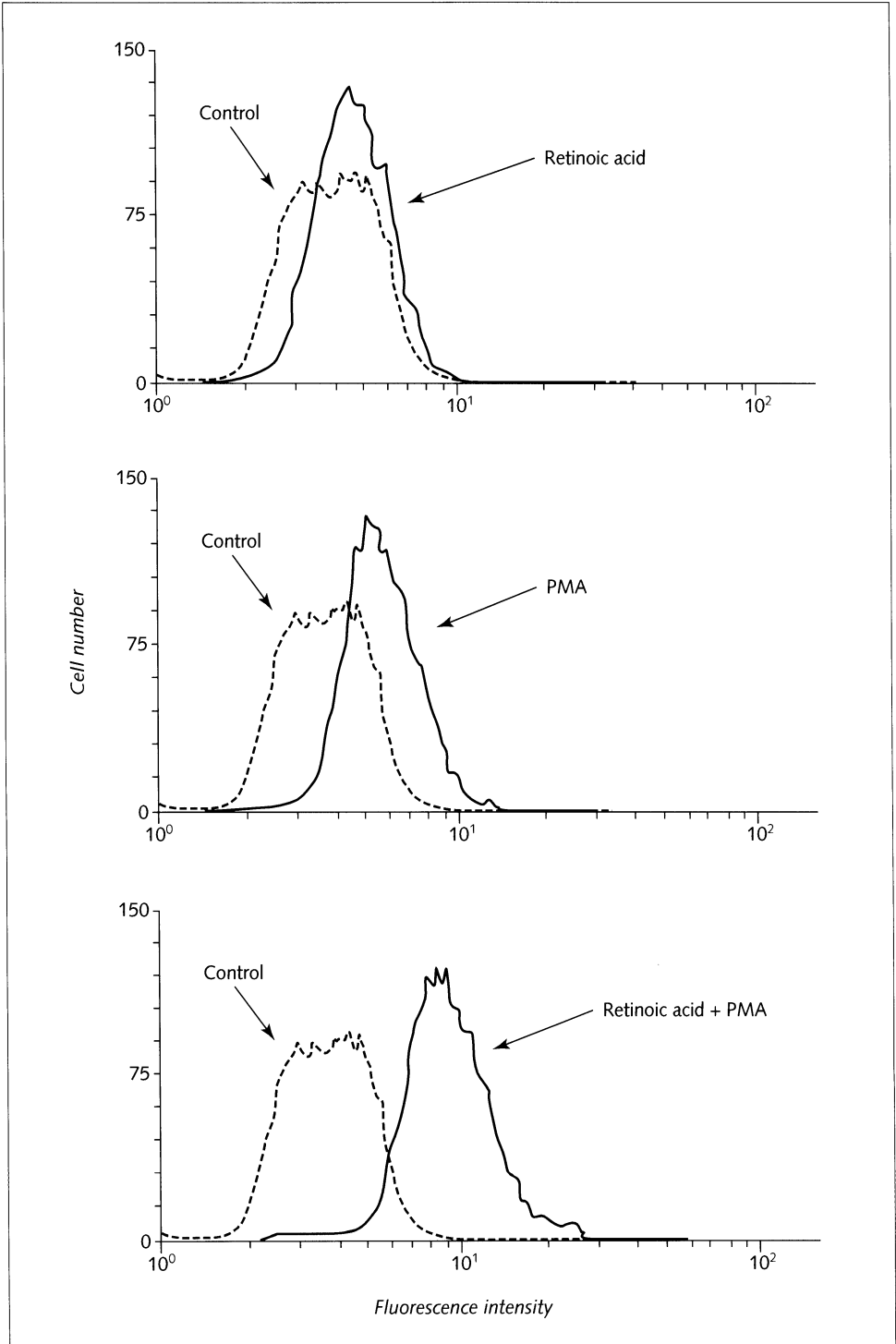
The above mentioned observations indicated that activation of inflammatory cells, e.g., by recruitment into an inflammatory area, or their differentiation and maturation may lead to significant changes in AA distribution within intracellular pools. The recent identification of different populations of macrophages in the human lung has been a timely occasion to confirm this hypothesis.

Centrifugation over density gradients of cells obtained by mechanical or enzymatic dispersion of the human lung tissue has been largely used to enrich the macrophage population. This procedure consistently yields two fractions of macrophages clearly distinct by their cell density. High density macrophages (HDM) have density comprised between 1.065 and 1.078 and account for two-thirds of the total macrophages in the human lung. Low density macrophages (LDM) have density between 1.039 and 1.052 and constitute the remaining one-third of the total lung macrophages [63]. LDM also have a larger area and diameter and appear highly vacuolated as compared to HDM. The two macrophage populations differ significantly in their expression of surface markers and in the production of cytokines

Figure 3

FACS scan of lipid bodies-associated fluorescence in undifferentiated and differentiated U937

U937 were incubated for 96 hrs in medium alone or in the presence of RetAc (10 nM), PMA (10 ng/ml) or both. At the end of the incubation, the cells were washed and incubated with Nile red. The cells were then washed and fluorescence was measured by flow cytometry. Fluorescence intensity units are indicated as a log scale on the abscissa. Each panel reports the peak fluorescence of undifferentiated cells for comparison.



in response to physiologic stimuli. HDM predominantly express co-stimulatory molecules (CD40 and CD86) whereas LDM express predominantly activation markers (CD63 and CD64). In addition, HDM are highly responsive to lipopolysaccharide and histamine, producing large quantities of IL-10 and IL-12. In contrast, LDM are stimulated more effectively than HDM by secretory PLA₂ (group IA, IB, II and X) [64] and by opsonized zymosan and they release mostly IL-6 and TNF- α .

We have recently initiated to explore the AA distribution into the lipid pools of HDM and LDM. HDM and LDM do not differ significantly in their total AA cellular content. However, LDM contain significantly higher percentage of AA esterified into TG (22% *versus* 10%) and a larger proportion of AA esterified into 1-acyl-PC and 1-acyl-PE as compared to HDM. The HDM population contains the majority of AA into 1-alk-1'-enyl-PE and 1-alkyl-PC. LDM also show a significantly higher number of cytoplasmatic lipid bodies per cell as compared to HDM (12 ± 5 *versus* 5 ± 3) (Triggiani et al., unpublished observations).

The mechanisms underlying the development of two subpopulations of macrophages in the human lung are presently unclear. Preliminary evidence suggests that the hypodense (LDM) cells may represent more mature macrophages in a pre-activated state, whereas HDM may be less mature cells more recently entered into the lung. This hypothesis is supported by the observation that HDM display several morphological, functional and biochemical features, including the AA distribution, similar to those of blood monocytes, the circulating precursor of tissue macrophages. These observations lend further support to the concept that maturation of the cells and/or their activation induced in the lung by local micro-environmental factors induces a profound remodeling of intracellular AA pools and the accumulation of AA into TG.

Biochemical functions of the triglyceride pool of arachidonic acid in inflammatory cells

While the role of the phospholipid pools as a source of AA for eicosanoid synthesis has been extensively studied, very little is known on the function of the TG pool, either constitutively present or induced by cell activation or differentiation. It has been clearly shown that TG are not substrates for PLA₂s [37, 39]. To address the role of TG as a source of AA in stimulated cells we have performed experiments in lung macrophages stimulated with the PMA or with the Ca²⁺ ionophore A23187. AA is released primarily from PC and PI in macrophages stimulated with PMA and from PC and PE in macrophages stimulated with A23187 [40]. In contrast to phospholipids, the amount of AA in the TG pool significantly increased at the early time points during cell activation induced by either PMA or A23187. These results suggest that TG do not act as a source of AA but rather as a pool to reincorporate AA released from phospholipids.

The rapid reacylation of free AA into TG in stimulated macrophages suggests at least two hypotheses. First, TG may act as a reacylation pool during the early phase of cell activation and thus contribute to maintain low intracellular concentrations of free AA. As mentioned before, free AA is a second messenger involved in the regulation of several cell functions and its intracellular concentrations must be closely regulated at any time during cell activation. A second hypothesis is that enzymes responsible for the transfer of AA into TG [54] are activated in stimulated cells as a mechanism to prevent excessive AA mobilization and depletion of this fatty acid. Should this be the case, the rapid reacylation of free AA into TG may be an important factor to limit the amount of AA available for the biosynthesis of eicosanoids. The hypothesis that TG are not an immediate source of AA for eicosanoid synthesis is confirmed by the data of Johnson et al. in the human neutrophils [37]. These cells supplemented in culture with exogenous AA to induce the accumulation of AA into TG produce the same amount of leukotrienes as the un-supplemented cells [37]. In addition, differential labeling of the endogenous pools of AA indicate that, even in neutrophils with a large TG pool of AA, the vast majority of AA converted to eicosanoids derives from the phospholipid pools.

Even though the TG may not be a direct source of AA during cell activation, this pool may still be important in the long-term regulation of cellular levels of AA. Experiments performed with human macrophages in which the cells were allowed to recover after stimulation, clearly demonstrate that, when the stimulus is removed, AA is progressively transferred from TG to phospholipids [39]. Therefore, among several possibilities, TG may be a late source of AA required to support eicosanoid biosynthesis once the phospholipid pools have been partially depleted. Alternatively, cell activation may in the delayed phase accelerate the transfer of AA from TG to phospholipids, a process normally occurring in resting cells [11]. The latter may be an important mechanism by which the cells may refill the early releasable phospholipid pools with AA.

Although these observations do not conclusively define the function of the TG pool, they indicate that phospholipid and TG pools have distinct biochemical roles in the release of AA in stimulated inflammatory cells. While phospholipid pools appear to be the major source of AA for immediate eicosanoid biosynthesis, the TG pool may play a crucial role to regulate intracellular levels of free AA and to maintain an adequate supply of AA to the phospholipid pools during the delayed phase of cell activation.

Closing remarks

Remodeling of AA within intracellular pools of inflammatory cells is gaining increasing attention as an important regulatory mechanism of several cell functions. The dynamic distribution of this fatty acid into long-term storage or rapidly-releas-

ing pools has been shown to modulate profoundly not only the pro-inflammatory potential of the cell but also its life cycle and differentiation programs.

An interesting observation that is emerged in the last decade is that human inflammatory cells may constitutively contain or build-up, under certain circumstances, a large pool of AA associated with TG. This is an expandable, high-capacity pool presumably located into cytoplasmic lipid bodies. Exposure of the cells to high concentrations of exogenous AA or to certain cytokines and growth factors as well as their activation by pro-inflammatory stimuli can induce the mass expansion of and the accumulation of AA into the TG pool. Formation of the TG pool may be also associated with the acquisition of a differentiated or hypodense cell phenotype.

The biochemical functions of the TG pool of AA in inflammatory cells are not yet defined. This pool is not an immediate source of AA in stimulated cells and it may rather function as a recapture pool for AA mobilized from phospholipids. Understanding the mechanisms involved in the TG pool formation and the definition of its role in the AA remodeling may open new perspectives in the modulation of eicosanoid synthesis and in the biochemical regulation of inflammatory responses in human diseases.

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Arachidonate remodeling, platelet-activating factor signaling, and the inflammatory response in the central nervous system

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Introduction

Arachidonate remodeling is a very prevalent process in cells of the central nervous system. As in other organs, there are a wide variety of phospholipid molecular species that display active arachidonate remodeling. In neurons, these events contribute to the maintenance of excitable membrane properties by providing a fluid environment for proteins to perform their functions. In addition, arachidonate remodeling allows the controlled release of free arachidonic acid. This fatty acid is a messenger in itself, and also serves as a precursor to a wide variety of biologically-active messengers, the eicosanoids. Recently, several novel messengers derived from arachidonic acid have been identified in addition to the well known prostaglandins. These new messengers include the endocannabinoids, which elicit potent modulatory actions in the nervous system. Overall, arachidonate remodeling in the nervous system is clearly engaged in cell function.

In the nervous system there is a very close relationship between arachidonate remodeling and inflammation. Ischemia promotes the rapid and selective release of brain free arachidonic acid [1]. This effect results in a major imbalance in arachidonate-remodeling pathways by enhancing the free arachidonic acid pool. This tells us that injury is critical in setting into motion this imbalance. Seizures and neurodegenerative diseases including Alzheimer's disease involve profound alterations in arachidonate remodeling [2, 3].

Platelet-activating factor

Although platelet-activating factor (PAF, 1-O-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine) was originally described as an inducer of platelet aggregation, it is now recognized as a physiologic mediator in synaptic plasticity. In addition, PAF is accumulated in neuronal degeneration that results from the activation of the injury

/inflammatory response. The synthesis and turnover of PAF are components of the “remodeling” of arachidonic acid-containing choline plasmalogens [4] (Fig. 1).

There are three routes for the synthesis of PAF. The nervous system contains alkyl-arachidonoyl-GPC, the PAF precursor, a very minor component of membrane phospholipids. This pool of choline-containing phospholipids is characterized by a high concentration of arachidonate (or docosahexaenoate) in the *sn*-2 position. Most of our current knowledge is on the arachidonate-containing PAF precursor. Arachidonate is hydrolyzed from the *sn*-2 position of alkyl-acyl GPC by phospholipase A₂, and then replaced with an acetyl group by an acetyltransferase. Other major routes of PAF synthesis in the brain may be a *de novo* pathway by the transfer of choline to alkylacetyl glycerol *via* cholinephosphotransferase or by a coenzyme-A-independent route [5]. There is an additional pathway for PAF formation that is particularly important during central nervous system (CNS) injury. After oxidative injury, fragmentation of *sn*-2 PUFA (mainly arachidonate and docosahexaenoate) of some species of phosphatidylcholine phospholipids can result in the formation of molecules with PAF-like activity. The presence of a shorter-chain peroxidated fatty acid at the C-2 position is recognized by the PAF receptor. The release of PUFA from the PAF precursor also generates bioactive molecules, such as leukotrienes, which may act as neuronal second messengers or as pro-inflammatory mediators.

PAF is an important modulator of neural function, but its over-production plays a role in neural dysfunction. Although PAF at relatively high concentrations may disrupt neural function by perturbing membrane function [6, 7], it is also a highly bioactive molecule.

Cellular responses to PAF

Phospholipase A₂ (PLA₂) releases arachidonic acid or docosahexaenoic acid [8]. These PUFA may be metabolized by one of several cyclooxygenase (COX) enzymes into other bioactive lipids (see below). The remaining lyso-lipid (1-O-alkyl-2-lyso-*sn*-glycero-3-phosphocholine or lyso-PAF) is acetylated, producing the bioactive PAF.

PAF binds to high- and low-affinity receptors in several cell types, including platelets, basophils, and lung tissue [9]. PAF attains high concentrations in the hippocampus in response to injury [10]. In addition to seven transmembrane domain receptor on the cell surface (including the synapse), high-affinity intracellular binding sites are present [11]. Moreover, a diversity of K_m parameters for PAF-receptor binding suggests heterogeneity of PAF-binding sites in the nervous system.

The synthesis of PAF results in physiologic responses in cells, including Ca²⁺ mobilization [12], activation of protein kinase [13], accumulation of arachidonic acid [14], and modulation of gene expression [15, 16]. This multiplicity of cellular responses to PAF is not surprising, considering that the PAF receptor belongs to the

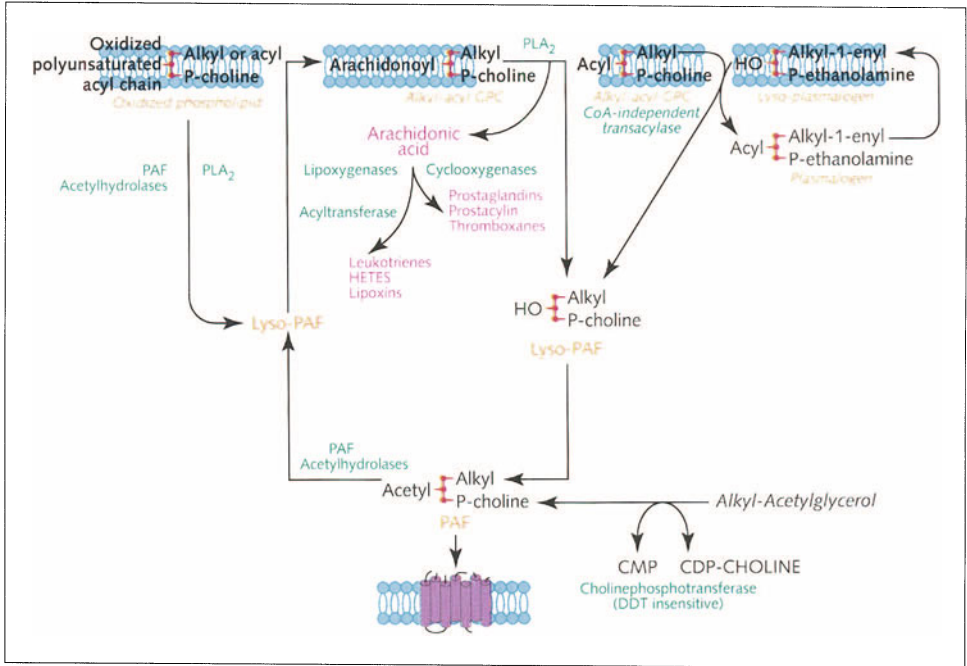


Figure 1

Platelet-activating factor (PAF) synthesis and degradation

The remodeling pathway or "PAF cycle" leads from the membrane phospholipid PAF precursor, alkyl-acyl (usually arachidonoyl)-glycerophosphorylcholine (GPC, on the left) to the biologically active PAF (at right), and includes the production of lyso-PAF, which is generated from the PAF precursor alkyl-acyl-GPC either directly by the action of phospholipase A₂, or by the transfer of the sn-2 acyl moiety to a lyso-plasmalogen (top), which is itself mobilized from membrane plasmalogen by phospholipase action. The de novo route of PAF synthesis (upper right) involves the direct transfer of a choline moiety to alkyl-acetyl-glycerol. Note that PAF acetylhydrolase (bottom) inactivates all PAF molecules, regardless of their biosynthetic route, and additionally inactivates oxidatively damaged phospholipids (shorter peroxidated acyl group at C₂) that possess biological activity at the PAF receptor.

family of receptors linked to the G-protein [17]. PAF may elicit cellular responses by activating phospholipase C (PLC), with the resultant hydrolyzing of PIP₂. In an *in vitro* model using [³H]-inositol-labeled platelets, a four- to five-fold increase in IP₃ and IP₂ was observed within five seconds of treatment with PAF [18]. The response was independent of extracellular [Ca²⁺] and was inhibited by the PAF antagonist CV 3988, indicating direct activation of PLC by the binding of PAF to its receptor.

As a consequence of PLC activation, the increase in intracellular [Ca²⁺] may activate PLA₂. PLA₂ is also activated during the same time course that PAF synthesis

occurs *via* the remodeling pathway. Several studies indicate that PAF antagonists effectively block the rise in intracellular $[Ca^{2+}]$. For example, in platelets a PAF antagonist decreases the PAF-induced rise in intracellular Ca^{2+} [9].

When the plasma membrane-bound PLC is activated, a series of intracellular events occur, which are involved in the pathologic changes during brain ischemia and seizures [19]. Triazolobenzodiazepines (alprazolam and triazolam) and some benzodiazepines antagonize PAF effects [20]. Because PLC and PLA_2 activities are elevated in brain undergoing ischemia [4, 19], investigators have targeted the PAF receptor as a potential site for the reduction of the progression of damage after CNS injury.

The PAF antagonist BN 50739 prevents postischemic hypoperfusion and edema formation in rabbit spinal cord [21]. PAF antagonists restore cerebral blood flow and also enhance survival during the post-ischemic phase [22, 23]. The mechanisms of protection by PAF antagonists have been studied in several models. Post-treatment with BN 52021 reduced free fatty acid (FFA) and diacylglycerol accumulation after ischemic injury, and pre-treatment with BN 52021 reduced FFA release following ischemic injury in mouse brain, although minuscule effect on PIP_2 hydrolysis was observed [24]. However, in this study the investigators reported no significant reduction in FFA accumulation and PLC activation after electroconvulsive shock (ECS).

PAF receptor antagonists also have proved beneficial in neuronal recovery as measured by electrophysiologic parameters [25]. In this study, a PAF receptor antagonist of the neolignan family, kadsurenone, enhanced neuronal recovery as measured by cortical somatosensory evoked potential. The protective effect appeared to be independent of effects on platelet aggregation, as evidenced by ^{111}I -labeled platelet distribution, which was the same in control and kadsurenone-treated brain. Thus, PAF antagonists may improve post-ischemic recovery by mechanisms separate from prevention of platelet aggregation. Histologic examination showed that CA1 hippocampal neurons in rats are protected from ischemic damage by the PAF antagonist ginkgolide B [26].

PAF receptor antagonists elicit neuroprotection in a rodent model of brain ischemia-reperfusion [27], suggesting that PAF may work at the synapse. In this study, the accumulation of free polyunsaturated fatty acids following ischemia was decreased by the PAF antagonists, which also restored cerebral blood flow [27]. Polyunsaturated fatty acid release accompanying ischemia probably results from synaptic phospholipase(s) A_2 activity [28]. The same PAF antagonist that was neuroprotective in ischemia-reperfusion also selectively displaced radiolabeled PAF binding in synaptic membranes [11]. For this reason, the synaptic membrane binding site was proposed to modulate glutamate neurotransmitter release [29]. Moreover, intracellular PAF-binding sites isolated from a microsomal fraction were distinct from synaptic membrane sites with regard to their responses to several antagonists [11]. At the time of those studies, PAF was already known to activate early-response

genes [15, 30, 31]; therefore the intracellular receptor was proposed to be the signaling linkage to gene expression. Cloning of the seven transmembrane domain PAF receptor [17, 32, 33] and the discovery of specific PAF receptor-mediated Ca^{2+} influx into neurons [34] has shed more light on neural PAF signaling. In studies of long-term potentiation in hippocampal neurons isolated from PAF-receptor-deficient mice, both incidence and size of LTP, defined as increased excitatory postsynaptic potentials, were decreased in the knockout mice, as compared to wild-type mice, and PAF-receptor antagonists reduced LTP in wild-type mice, but not in PAF-receptor knockout mice. These results lend additional support to the hypothesis that PAF is involved in hippocampal synaptic plasticity [35]. The intracellular PAF receptors have been more extensively characterized in subsequent studies that have identified one form in endosomes [36] and another in the nuclear membrane [37]. Both intracellular forms of the receptor may actually be components of the intracellular microsomal form that was previously described [11]. We now know that the PAF seven transmembrane domain receptor is expressed in neurons, astrocytes, and microglia, as well as endothelial cells. It is still unclear whether the intracellular PAF receptor(s) differ in molecular structure from, or instead are an intracellular state of, the cell-surface PAF seven transmembrane domain receptor. We do not yet know whether the cell-surface PAF receptor internalizes, or whether a cell-surface PAF receptor destined to insertion in the membrane is already active. If that is the case, does PAF itself internalize to access either of these intracellular PAF-receptor forms? Two possible mechanisms might explain the role of PAF in gene transcription:

1. The cell-surface receptor triggers the signaling cascade, or;
2. The intracellular form establishes interactions with specific kinases/phosphatases or transcription factors with or without specific scaffolding proteins.

In pathologic conditions involving oxidative stress such as ischemia or seizures, the rates of PAF synthesis and degradation that maintain a modulated PAF pool size become mismatched and PAF concentration increases to where it becomes a pro-inflammatory messenger and mediator of neurotoxicity. In this capacity PAF activates COX-2 expression [38], expression of several early-response genes that encode transcription factors [15, 30], apoptosis, and polymorphonuclear leukocyte (PMN) adhesion to microvessels [39], which has critical consequences for cell survival. Leukocyte infiltration mediates neural injury in head trauma, stroke, spinal cord injury, and other diseases and enhances the synthesis and release of IL-6, IL-8, IL-10, TNF- α , and of other mediators of the inflammatory response. PAF binding to its receptor activates phospholipases and results in additional PAF synthesis, along with that of prostaglandins and leukotrienes. While overall, PAF is a potent neuronal injury messenger, it also plays a prominent role in astrocytes and in microglial cells. Although many of these actions have been studied in non-neural cells they are assumed to occur in the nervous system as well.

In summary, excessive PAF promotes neuronal damage, and PAF-receptor antagonists elicit neuroprotection in various models of neural injury [21, 23, 25–27, 40].

Phospholipase A₂, arachidonate metabolism, and gene expression

Synaptic membrane-bound phospholipases play a key role in neuronal plasticity in long-term potentiation, which is a model of learning and memory [41, 42]. However, during seizures, ischemia, trauma, and neurodegeneration, these signaling mechanisms are overstimulated and lead to excitotoxic brain damage [1, 43]. Thus, during acute neuronal stimulation by excitatory glutamatergic neurotransmission, the balance of levels of mediators of neuronal plasticity and injury determines whether the neurons recover or become damaged.

PLA₂ enzymes are classified into three types: calcium-dependent PLA₂ (cPLA₂ or type IV), calcium-independent (iPLA₂ or type VI), and low-molecular-weight secretory PLA₂ (sPLA₂) [44]. cPLA₂ displays a high selectivity for phospholipids containing PUFA in the *sn*-2 position. The regulation of cPLA₂ activity by agonists that increase cytosolic Ca²⁺ involves translocation of the enzyme from the cytosolic compartment to the nuclear membrane or the endoplasmic reticulum, where phospholipids are hydrolyzed, thus releasing PUFA, mainly arachidonic and docosahexaenoic acids [45]. Two important enzymes, the inducible cyclooxygenase-2 (COX-2) and lipoxygenase (LOX), are located in the nuclear membrane and metabolize the PUFA into prostaglandins (PGs) and leukotrienes (LTs).

Several observations indicate that PGs, synthesized through the COX-2 pathway, play a pivotal role in neuropathology. In the brain, COX-2 is constitutively expressed, mainly in the cortex and hippocampus [46, 47]. Not only has the COX-2 pathway been implicated in neuronal plasticity, but expression of the enzyme is also induced during cerebral ischemia and seizures [19, 48]. Inhibition of COX-2 activity prevents ischemia and NMDA-induced cell death [49, 50].

Arachidonate and COX-2 gene expression

Because COX-2 activity is involved in neuronal death after CNS injury, the regulation of expression of the COX-2 gene is an important event in the utilization of free arachidonic acid during the activation of the remodeling pathway. Nuclear factor (NF)- κ B is a DNA-binding protein that controls the transcription of the COX-2 gene. NF- κ B binds to at least two sites in the mouse, rat, and human COX-2 gene proximal promoter [51, 52]. The human gene encoding for expression of COX-2 may be involved in the pathology of slower-onset neurodegeneration, such as in Alzheimer's disease (AD) [53]. Examination of nuclear protein extracts taken from aging control and AD-affected brain neocortical nuclei revealed a significant corre-

lation between the levels of NF- κ B-DNA binding and the production of COX-2 RNA. This study provided evidence linking NF- κ B-DNA binding to up-regulation of transcription of the gene coding for COX-2. In addition, oxidative stress due to exposure of reactive oxygen species (ROS) contributes to neuronal death during aging, disease, and injury [54], and there is a link between exposure of neurons to ROS and NF- κ B activation [55, 56].

Glutamate receptor signaling, sPLA₂, arachidonate, and COX-2 expression

Brain ischemia and seizures promote PAF accumulation that contributes to further glutamate release and COX-2 transcription, both of which increase neuronal cell damage and death. The interplay between PAF accumulation, EAA receptor activation, and a secretory PLA₂ are an additional factor. For example in hippocampal neurons, stimulation of the NMDA receptor by PAF activates several mitogen-activated protein (MAP) kinases, including c-JUN NH₂-terminal kinase (JNK), p38, and extracellular signal-regulated kinase (ERK). The hexazepine BN50730 (an intracellular PAF receptor antagonist) inhibits both NMDA-stimulated MAP kinases and neuronal cell death [57].

When sPLA₂ or glutamate was injected into the right striatum of male Wistar rats, there was a dose-dependent response in terms of neurologic abnormalities and tissue damage. When low levels (10–20 pmol) of sPLA₂ or glutamate (2.5 μ mol) were injected into the striatum, no neurologic abnormalities or tissue damage occurred. However, when 20 pmol sPLA₂ and 2.5 μ mol glutamate were co-injected, the animals became apathetic for several hours after injection and then displayed circling toward the side of injection in the following days [58]. The animals that were co-injected displayed extensive histologic damage in the right hemisphere, and in several rats the damage extended into the contralateral hemisphere. Thus, the investigators demonstrated a synergistic excitotoxic action *in vivo* exerted by sPLA₂ and glutamate.

Although the synergism of neuronal damage between sPLA₂ and glutamate is dramatic, it is noteworthy that the two may act by different but overlapping mechanisms. In primary cortical neuron cultures, sPLA₂ and glutamate display the same synergy in eliciting neuronal cell death as demonstrated *in vivo* [59]. In this study, ³H-arachidonic acid (AA)-labeled cultures were treated with mildly toxic doses of sPLA₂ and glutamate. Glutamate treatment resulted in the release of AA predominantly from phosphatidylethanolamine (PE), whereas sPLA₂ treatment resulted in AA release from phosphatidylcholine (PC). Co-treatment with sPLA₂ and glutamate resulted in a greater degradation in both PE and PC, although the NMDA antagonist MK-801 blocked only the glutamate effects. Therefore, the neurotoxicity induced by glutamate and sPLA₂, although synergistic, involves the hydrolysis of different phospholipid pools. In addition, both sPLA₂ and glutamate induce COX-

2 expression, although during different time intervals [60]. In this study, the expression of COX-2 in rat striatum was examined using *in situ* hybridization and immunohistochemistry. Injection of sPLA₂ induced COX-2 expression (4 hrs after injection), whereas glutamate induced COX-2 expression within 2 hrs after injection. This time differential suggests separate signaling mechanisms for sPLA₂ and glutamate. In addition, recent observations [61] indicate that sPLA₂ affects neuronal responses to glutamate through the opening of Ca²⁺ channels, which provides more evidence that sPLA₂, by releasing AA, is central in CNS pathology following injury.

Conclusions

PAF is a potent inducer of platelet aggregation, but the specific PAF receptors present on neurons may cause neuronal cell damage when over-activated by excessive PAF production. Because there are multiple pathways for PAF synthesis in the brain, the PAF receptor has been targeted for intervention in conditions of CNS degeneration, including traumatic injury and slower-onset degeneration such as Alzheimer's disease. In fact, the synthesis of PAF initiates several mechanisms leading to neuronal damage including:

1. The release of arachidonic acid that is metabolized *via* specific enzymes into the inflammatory compounds prostaglandins and leukotrienes. PGs and LTs also contribute to circulatory abnormalities and infiltration of blood cells that exacerbate CNS injury. Eicosanoids can also counteract the inflammatory response, such as lipoxins [62]. We have relatively scarce information regarding anti-inflammatory regulation by eicosanoids in brain.
2. The synthesis of PAF results in Ca²⁺ mobilization within neurons resulting in the activation of enzymes (particularly phospholipases A₂) leading to further action on arachidonate remodeling.
3. The release of PAF during CNS injury increases glutamate release and expression of the COX-2 gene. This in turn activates synthesis of eicosanoids.
4. PAF accumulation is related to excitatory amino acid receptor activation as well as the activation of sPLA₂. Glutamate and sPLA₂ are synergistic in causing neuronal cell damage [58]. These studies provide evidence that PAF can potentiate damage through more than one pathway, and that arachidonate remodeling is involved [63].

One of the conclusions from these studies is that therapeutic interventions may be possible to prevent PAF damage to neurons. In particular, novel PAF antagonists enhance neuronal survival after CNS injury. There is widespread signaling disruption during CNS injury that contributes to neuronal damage. PAF antagonism, how-

ever, provides an effective target to modulate multiple pro-inflammatory pathways, and as a consequence, neuroprotection.

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Remodeling of arachidonate and other polyunsaturated fatty acids in Alzheimer's disease

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Overview of AD

AD is the most common dementia, afflicting millions in developed countries [1]. AD is a neurodegenerative process characterized by irreversible destruction of the neocortex leading to impairment of memory and cognitive function, language deterioration, poor judgment, indifferent attitude, but preserved motor function. An estimated 7% of people above 65 years old have AD and its prevalence is expected to increase as better medical science increase life expectancy [1]. Although AD is the most characterized dementia, no effective treatments are available for controlling this debilitating disease. Definitive diagnosis of AD is made at autopsy. The pathogenic characteristics of AD include the cleavage of β -amyloid precursor protein (β APP) to form neurotoxic β -amyloid (β A) peptides that are two amino acids longer than normal, and an aggregated insoluble polymer of β A that forms senile plaques [2, 3]. Enzymes known as secretases mediate processing of β APP. In addition to plaques, the formation of intraneuronal tau pathology yielding widespread deposits of argyrophilic neurofibrillary tangles (NFT) is typical in AD. In addition to plaque formation, enhancement of inflammatory responses in the brain mediated by neurotoxic peptides is characteristic of AD. These peptides and inflammatory cytokines (IL-1, IL-6, and TNF- α) are implicated in the activation of glial cells and astrocytes [4].

The major risk factors associated with AD include genes, head trauma, environmental and demographic factors [5–8]. Four major genetic loci are associated with AD. These include APP, two presenilins and apolipoprotein E (apoE) [9, 10]. Mutations of APP are linked to early onset AD mainly as a result of increased formation of the plaque component of β A peptides. Various studies have shown that β A addition to cultures result in cell death [11–13]. Additionally, β A peptides can also induce activation of glial cells [14–16]. Induction of neuronal cell death and abnormal activation of cells are plausible mechanisms of action of β A. Mutations in the presenilin genes PS1 and PS2, implicated in early onset familial AD, cause abnormal

β APP processing with resultant overproduction of neurotoxic βA_{1-42} and related peptides [17, 18]. Various apoE alleles are found in humans, however, individuals homozygous for apoE4 are 3–4 times more likely to have AD [19, 20]. ApoE is linked to high-density lipoprotein (HDL) in plasma and cerebrospinal fluid (CSF) and functions mainly to provide lipids to cells. Unfortunately at this time, much less is known of the unique distribution, transport and biochemistry of CSF and brain apolipoproteins compared to the plasma. ApoE affects lipid transport, neurite growth *via* low density lipoprotein (LDL) receptors and processes critical to neurodegeneration [19]. ApoE forms are extensively O-glycosylated and glycation changes to apoE alter LDL and VLDL binding that can change specific receptor binding of these complexes [21, 22]. Furthermore, the increase in advanced glycation end products that occur in AD co-localize with ApoE4, linking this phenotype with the plaque deposition in AD [23–26].

In addition to genetic predisposition, repeated head trauma may contribute to early onset of AD, perhaps by creating a dysfunctional blood brain barrier (BBB) [6]. Changes in BBB may allow environmental agents (organic solvent, heavy cigarette smoking, industrial toxins, transition metals, Al, Fe) more access to the brain leading to higher incidences of AD [6, 7, 27–36]. Finally, demographic factors (age, gender, race, co-morbid conditions, especially cerebrovascular insults) may play important roles in AD [8, 35, 37]. While AD has been shown to be age-dependent, only small gender differences have been documented [38]. Overall, biochemical knowledge on the interplay of these contributing factors in AD pathogenesis is still limited.

Brain lipids

Lipids comprise approximately 50 percent of the dry matter of the brain and play important roles in brain function (signaling molecules, inducers of chemotaxis, pro- and anti-inflammatory mediator formation, ion channel, receptor and membrane functions and an energy source). Major cerebral lipids (also found in lesser quantities in other organs) include cholesterol and cholesterol esters, glycerolipids, sphingolipids and ceramide. Apart from water, cholesterol is greater than any other single constituent in the brain comprising 4–5% by mass. The most abundant form is free cholesterol that may be linked to other lipids or proteins. The fatty acid constituents of cholesterol esters are oleic, palmitic, palmitoleic, and arachidonic acids. Levels of these esters are altered in autopsied AD brain with a significant decrease in unsaturated fatty acids [39, 40]. Cholesterol levels are controlled by its synthesis, transport and metabolism. For example, higher activities of cholesterol ester hydrolyase increase cholesterol levels, while lecithin cholesterol acyl transferase (LCAT) controls the reverse transport of cholesterol [41–43]. Conversion of cholesterol to esters or hydroxylation are critical events in AD pathology. Not surprisingly, levels

of 24 hydroxy cholesterol in CSF or plasma are very good correlates of AD pathology [44, 45]. Only trace amounts of free fatty acids are found in the brain and CSF, while most fatty acids are acylated into glycerides and their levels and distribution within glycerolipids and brain regions are altered in diseased conditions [46–51]. The brain is rich in very long chain polyunsaturated fatty acids (PUFA) obtained from dietary sources or synthesized from precursors by brain cells. Our data show that CSF contains various enzymes involved in PUFA binding, transport and degradation [52]. Significant levels of the prostanoid metabolites, $\text{PGF}_{2\alpha}$ (100–500 pg/ml) and 6-keto $\text{PGF}_{1\alpha}$ (100 pg/ml) are found in CSF and these levels are increased many-fold in pAD and other head traumas [53–56]. Compared to plasma, the CSF contains less total lipid (400–800 mg/100 ml compared to 1–2 mg/100 ml) [57]. The distribution of lipids varies in brain regions or within cells. Certain membrane fractions are enriched with unsaturated fatty acids or with plasmalogen-linked phospholipids. Unsaturated fatty acids acylated onto phospholipids in myelin are mainly oleic acid while nerve endings contain mainly arachidonic acid (AA, 20:4, n-6) and docosahexaenoic acid (22:6, n-3) [57].

In the brain, turnover in lipids varies according to their precursor. The fastest phospholipid turnover occurs in phosphatidic acid (PA) and phosphatidylinositol (PI). In addition to the biosynthesis of phospholipids, there is rapid turnover of fatty acyl constituents. Changes in acyl constituents likely reflect function of fatty acids in the brain. Defects in lipid metabolism are enhanced in neurological disorders including AD. Various catabolic enzymes including phospholipases A_2 (PLA_2) and anabolic enzymes such as lysophospholipid acyltransferase that recycles lysophospholipids into intact glycerophospholipids and glycerophosphocholine phosphodiesterase are decreased in AD brain regions. Enzymes involved in *de novo* synthesis (ethanolamine kinase, choline kinase) are normal or just slightly altered in AD [57].

Biosynthesis and sources of AA and other PUFAs

Fatty acids are important in mammalian systems, being the structural elements of cell membranes, a source of energy and they provide signaling molecules that control cell growth, development, ion channel function and cell death. Most saturated and monounsaturated fatty acids are obtained from dietary sources or can be synthesized by fatty acid synthetic machinery. However, precursors of PUFAs that are needed for regular functioning of cells can only be derived from dietary sources. These fatty acids are known as essential fatty acids (EFA). The two major classes of essential fatty acids are the n-6, derived from linoleic acid (LA) and the n-3 derived from α -linolenic acid (ALNA). A series of desaturation ($\Delta 6$ - and $\Delta 5$ -desaturase) and elongase enzymes convert LA and ALNA to longer chain PUFAs (Fig. 1) [58]. The major PUFAs found in brain are arachidonic acid (AA, 20:4, n-6), docosahexaenoic acid (DHA, 22:6, n-3) and eicosapentaenoic acid (EPA, 20:5, n-3). DHA and EPA

can also be derived from fish oils [59]. AA is the major substrate for the production of lipid mediators of inflammation. Evidence for a major role of PUFAs in brain physiology are provided by studies showing their enhanced elongation and desaturation during myelination. *In vitro* studies show that cerebral microvascular endothelium and astrocytes can produce DHA and AA *via* elongase and desaturase activities [60]. In contrast, neurons cannot produce PUFAs but get enriched with PUFAs if they are co-cultured with astrocytes and endothelial cells. In addition to synthetic pathways for PUFA, the brain may also obtain dietary PUFA *via* fatty acid binding proteins. Little is known of the plasma/CSF/brain differences in sources of PUFA. For example, does the brain obtain all PUFAs from the plasma or is there substantial *de novo* synthesis of PUFAs by the brain? Do PUFAs from the plasma diffuse into the brain or is there active transport through receptor-mediated processes? Is the PUFA transport mechanism similar to that of cholesterol utilizing lipoproteins (HDL and LDL) and their receptors? Is there a preference for n-6 or n-3 fatty acid biosynthesis by astrocytes? Are all apolipoprotein species found in the brain involved in PUFA transport? These important questions are being addressed as our knowledge about apolipoproteins is increased. For example, it is now known that various apolipoproteins present in CSF are composed of phospholipids that contain PUFA [19] and brain DHA is suggested to be important in brain development, plasma membrane composition, neuroplasticity, aging, neuronal ion channels and in signal transduction [61].

The major biochemical processes involved in AA metabolism and their potential to influence AD are summarized in Figure 1. Very low levels of free PUFA are maintained in mammalian cells. Free PUFAs in plasma are closely associated with lipoproteins, albumin or fatty acid binding proteins. Once presented to mammalian cells, PUFAs are rapidly converted to acyl CoAs by synthetases [62]. PUFA acyl CoAs are rapidly incorporated into glycerolipids by CoA dependent enzymes [63, 64]. This initial incorporation is accompanied by remodeling of PUFA into ether-linked plasmalogen lipid pools that comprise the major repository of PUFA in the brain. The remodeling and release of PUFA from glycerolipids is important in maintaining homeostasis and in regulating cell function [65–69].

Uptake and transport of PUFAs

PUFAs and other major brain lipids such as cholesterol are transported in plasma bound to lipoproteins (presumably also in CSF, but this is not confirmed). PUFAs are activated by synthetases and then incorporated into glycerolipids or cholesterol esters by CoA dependent acyl transferases. Once obtained from the diet, fatty acids are presented to cellular tissues as complexes associated with binding proteins, albumin or apolipoproteins. Upon contact with cells, proteins with high affinity for PUFAs (fatty acid translocase or fatty acid binding protein (FABP) mediate dissoci-

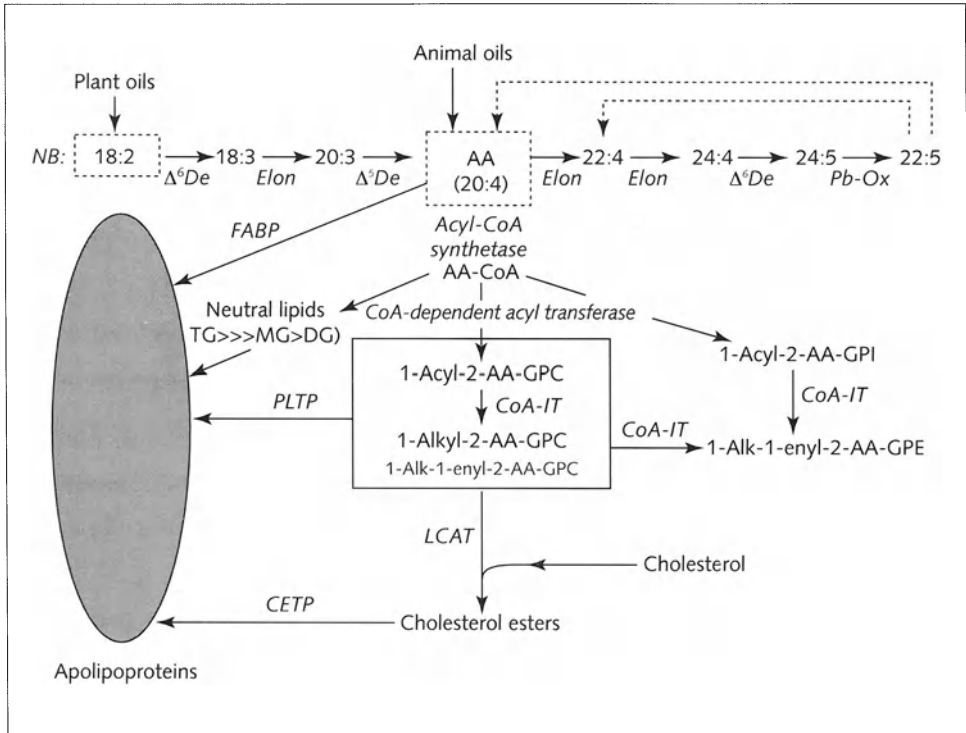


Figure 1

AA metabolism

AA is obtained from the diet or from elongation/desaturation of LA (18:2, n-6) or retro conversion of other longer chain PUFAs. AA is converted to AA-CoA by acyl CoA synthetase and is rapidly incorporated into cellular lipids by acyl transferase activity. AA in phospholipids is remodeled from 1-acyl-linked to 1-alkyl- or 1-alk-1-enyl-linked phospholipid classes by transacylases. Cholesterol esters are also formed by LCAT that is associated with apo-A1 from HDL. Various fatty acid binding proteins (FABP), phospholipid transport proteins (PLTP) and cholesterol ester transfer proteins are coupled with cells or lipoproteins and albumin to deliver lipids to tissues.

ation of these complexes. Flip-flop of fatty acids across the lipid bilayer is associated with cytosolic FABP or with caveolin-1 containing vesicles known as caveolae. Caveolae deliver lipids to subcellular organelles. The transport of fatty acids may be accompanied by activation by acyl CoA synthetase and targeting to specific membranes controlled by anchoring to phospholipid bilayers.

Edmond has suggested that there is selective uptake of essential PUFA by the brain based on studies showing that linoleic acid (18:2, n-6) enters the brain while oleic acid (18:1, n-9), cholesterol and other non-essential fatty acids do not enter the

brain [70]. Capillary networks composed of endothelial cells have receptors for lipoproteins but do not use LDL-cholesterol. The recent discovery of a transmembrane monocarboxylic acid transporter (MCT) and fatty acid transport proteins (FATPs) that are positioned at the inner luminal membrane allow essential PUFAs to be transported into the brain [70].

In addition to esterification to glycerolipids, PUFAs are also acylated into cholesterol and are similarly transported bound to lipoproteins. Low-density lipoprotein (LDL) transports cholesterol from the liver to peripheral tissues while HDL transports cholesterol from the periphery to the liver for excretion as bile salts [71–74]. HDL is a macromolecule made up mainly of phospholipids, cholesterol and little triglycerides complexed to apolipoproteins. The major apolipoprotein in HDL is apoA-1 which is synthesized and secreted by the liver. Nascent HDL containing apoA-1 interacts with cells to acquire cholesterol and phospholipids. Properties and functions of HDL include promotion of cellular cholesterol efflux, reverse cholesterol transport, antioxidation (protects LDL from oxidation), anti-inflammation (induces nitric oxide) and anti-coagulation properties. HDL also transports cholesterol to steroidogenic tissues where it is used as the major precursor for the synthesis of steroid hormones. Cholesterol esters are also transferred to apoB-1 containing lipoproteins in exchange for triglycerides through the action of cholesterol ester transfer protein (CETP). The transport of cholesterol from tissues to the liver is commonly referred to as “reverse transport” and is linked to an enzyme known as lecithin cholesterol acyl transferase (LCAT) [42].

LCAT catalyzes the transfer of a fatty acid from lecithin (phosphatidylcholine) to cholesterol to form cholesterol esters and lysophosphatidylcholine (LPC) (Fig. 1). The reaction takes place on the surface of high-density lipoprotein (HDL) in several steps including interfacial binding to HDL and activation of LCAT by apo-A1, PC binding, acyl enzyme formation, release of LPC, cholesterol binding and is terminated by the release of cholesterol ester and LCAT. In addition to cholesterol, LCAT can also esterify steroid hormones such as pregnenolone and dehydroepiandrosterone and has been shown to convert 25-hydroxycholesterol, an AD marker, to diester by acylating carbon 3 and carbon 27 [75–77]. LCAT can also use phosphatidylethanolamine as a fatty acyl donor but has no reactivity towards phosphatidylserine or diacylglycerol. LCAT also transesterifies and hydrolyzes platelet-activating factor and oxidized PC molecules containing short chain fatty acids at the *sn*-2 position. LCAT is a 49–60 kDa glycoprotein consisting of β sheets and α -helical elements that was first identified in the late 1960s by Glomset [78]. The human LCAT gene located on chromosome 16 was first cloned by McLean and colleagues [79, 80] and subsequently chemically sequenced in 1987 [81, 82]. The 416 amino acids sequence has four heterogeneous N-glycosylation sites and six cysteine residues with two disulfide bonds that are implicated in lipoprotein binding but not in enzyme activation. An Asp-His-Ser catalytic triad catalyzes the transesterification reaction. Conversion of cholesterol to esters results in the removal of cholesterol

from the surface of HDL concomitant with the accumulation cholesterol esters in the core of HDL. This process promotes the flux of more cholesterol from cell membranes into HDL and the HDL particle grows in size as more esters are transported to the HDL core. LCAT is synthesized mainly by liver cells and circulates in association with lipoproteins. The brain also produces LCAT and low levels of LCAT have also been found in CSF amounting to 2.2% of the activity in plasma. However, the function of LCAT in the brain has not been determined. In animals with LCAT deficiency, cholesterol and cholesterol esters accumulate in tissues and blood cells. This accumulation alters cell and lipoprotein structure and function resulting in familial LCAT deficiency or Fish eye disease [42, 83, 84].

Several studies have implicated cholesterol homeostasis with AD pathology. Cholesterol reducing drugs have no effect or very modest effect on LCAT expression. However, various substrates and fatty acids can influence LCAT expression or activity. For example, supplementation with LA increases LCAT activity while DHA reduces LCAT activity. Other evidence that LCAT is involved in cholesterol metabolism is derived mainly from transgenic animal studies. Transgenic mice over-expressing LCAT and fed with cholesterol increased apoE-containing cholesterol esters in HDL1 particles [85]. Over-expression of LCAT also delays the catabolism of apoA-1 while deficiency results in reduction in HDL-c and apoA-1. Positive correlation between LCAT activity or mass and HDL-c has been established [86]. Together, these studies show that LCAT is an important enzyme in regulating cholesterol and fatty acid levels as well as in controlling the biosynthesis of steroid hormones.

Degradation of brain lipids

Once AA and other PUFAs are acylated into glycerolipids of the brain, they can be degraded by enzyme-catalyzed processes or by auto-catalyzed oxidative processes. These processes generate potent mediators of inflammation and cytotoxic lipid radicals that are implicated in AD pathology.

Release of PUFA from lipids

Pro-inflammatory microglia, reactive astrocytes and their associated cytokines and chemokines are linked to the mobilization of PUFAs as an integral part of the inflammatory process [87]. The release of PUFAs is mediated by cellular and secretory lipases. Secretory phospholipase A₂ (sPLA₂) has the ability to hydrolyze HDL phospholipids. Inducible oxidoreductase enzymes and cytosolic phospholipase A₂ (cPLA₂) are strongly activated during brain trauma, epilepsy and AD [88]. Properties of secretory PLA₂ and intracellular PLA₂ are reviewed in the chapters by Bar-

bour et al., Marion and Fonteh, and Balsinde et al., in this volume. Lipoprotein lipase (LPL) hydrolyzes triglycerides resulting in enhanced transfer of lipids from apolipoproteins to HDL. LPL is an extracellular enzyme that enables tissues to import fatty acids from triacylglyceride-rich lipoproteins. LPL occurs in all tissues including the brain where its function is not known. LPL activity is high in newborn brain and this activity increases during postnatal development. The hippocampus shows the highest LPL activity where levels are 5–11-fold higher than other sections of the brain.

Generation of lipid mediators

Cyclo-oxygenase (COX) also known as prostaglandin H synthase (PGHS) catalyzes the conversion of arachidonic acid (AA) to prostaglandin H_2 (PGH₂), an intermediate in the synthesis of prostaglandins (PGE₂, PGF_{2 α} , PGD₂, PGI₂), and thromboxane A₂ (TXB₂) [89]. mRNA and protein levels of one COX isoform (COX-2) have been shown to be induced by endotoxin and inflammatory cytokines in brain astrocytes and glial cells [90]. COX can also convert other PUFAs into oxidized lipids; however, AA is the best substrate. COX has two different enzymatic activities: the formation of PGG₂ from oxygen and AA by a cyclo-oxygenase; the reduction of PGG₂ to PGH₂ catalyzed by hydroperoxidase. The COX intermediate PGH₂ is the substrate for terminal synthases that convert it to PGD₂ (PGDS), PGE₂ (PGES), TXB₂ (TBXS) and PGI₂ (PGIS) [91] (Fig. 2). Induction of COX-2 plays an important role in inflammatory disease by increasing the formation of these lipid mediators. NSAIDs prevent the formation of lipid mediators of inflammation by inhibiting COX activity [92]. Our data show an increase of PGDS in CSF of AD subjects [93] and studies by Bazan's group show the induction of COX-2 mRNA in the brain of AD subjects [87]. Likewise Morrow and colleagues have shown an increase in PGE₂ levels in CSF from pAD subjects compared to controls [54]. Post-mortem brain studies also show neuronal COX-2 content to be an indicator of early AD dementia [94]. Together with data showing the induction of cPLA₂ that releases AA from membrane lipids, these data suggest that pro-inflammatory lipid mediator pathways may play a role in the pathogenesis of AD. In addition to COX-derived products, PUFAs may also be converted to leukotrienes by the lipoxygenase (LO) pathways [95, 96]. Very little is known about LO pathways in the brain. However, various studies have shown that brain cells express LO [97, 98]. Any changes in levels of these products in AD compared with "controls" will suggest a role of LO-derived products in disease. Finally, PUFAs are also substrates of cytochrome P450 (CYP) enzymes [99]. These enzymes convert PUFAs such as AA to conjugated dienols, ω -terminal hydroxylated alcohols and cis-epoxyeicosatrienoic acids (EETs) [100]. These compounds have been shown to regulate cellular proliferation, inflammation and to be involved in many signaling pathways.

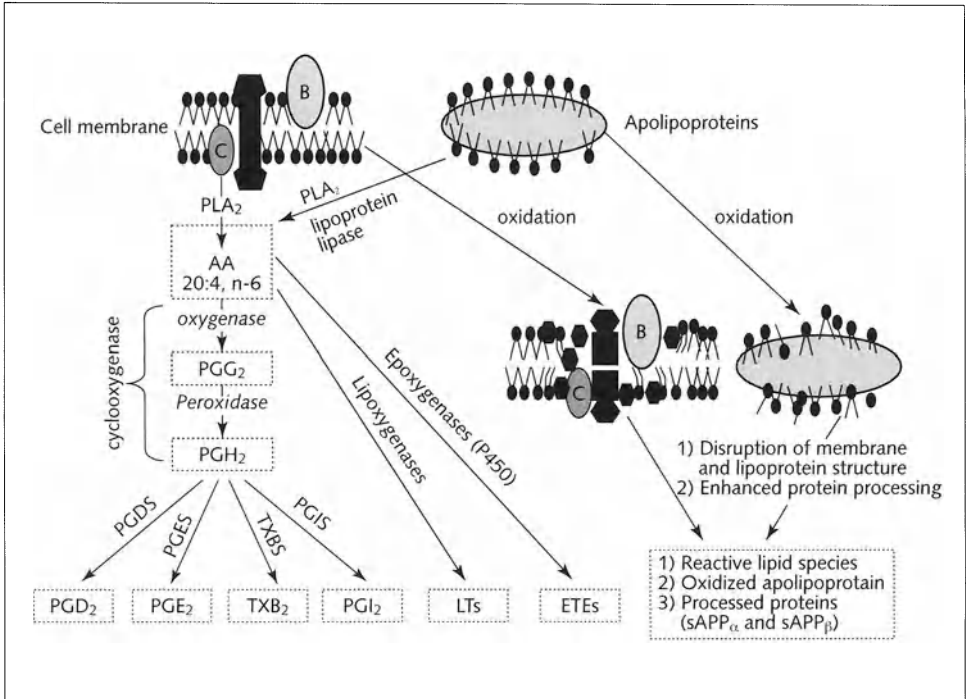


Figure 2

Formation of mediators of inflammation and membrane perturbation in AD

AA in phospholipid membranes or in lipoproteins is mobilized by PLA₂ or lipoprotein lipase activity, respectively. Release of fatty acid from cellular membranes or from lipoproteins disturbs their structure and function. In addition to lipases, autooxidation of PUFAs generates reactive phospholipid species that also destroy membrane integrity. Free AA is converted to lipid mediators of inflammation by various oxygenases and the perturbed cellular membrane exposes amyloid precursor proteins (A) to secretases (B and C), making them more susceptible to the amyloidogenic processing. Generation of lipid mediators of inflammation coupled with the destruction of cellular membranes may result in apoptosis of brain cells and the propagation of AD pathology that is typified by increased amyloid peptide cleavage and deposition of plaques in the brain.

Similar to LO products, little is known about the production of CYP products in the brain. However, oxidized EETs have been shown conjugated to phospholipids and these could potentially alter lipoprotein and cell membrane structure and function (Fig. 2), but this is not established for plasma or brain. HDL lipoproteins in patients with dementia showed reduced AA (20:4, n-6) compared to normal controls, likely due to enhanced degradation by enzymes or increased auto peroxidation [101].

Auto-oxidation of PUFAs

Since PUFAs are important in cell membrane structure and function, they can play a role in AD in one of three ways. First, PUFA are essential in brain physiology. Therefore any change in their composition or their distribution in the brain or in the blood cells is likely to have pathophysiological ramifications. A second role of PUFAs in AD reflects their inflammatory properties. In the context of an inflammatory process, PUFAs may be mobilized from cells by lipases [102]. Free PUFAs can be reduced and oxidized by enzymes to form inflammatory products. This inflammatory process is enhanced in AD compared to normal subjects. Thirdly, a decrease in the antioxidant defense system will result in the autooxidation of PUFAs. This auto oxidative process is catalyzed by free radicals and results in the formation of cytotoxic aldehyde products, isoprostanes and oxidized lipoproteins. Montine and colleagues have done extensive studies, which suggest that there is increased oxidative damage, and enhanced lipid peroxidation of PUFA rich lipids in AD brain tissues [54, 104–106]. The following pieces of evidence are cited as evidence:

- 1) Lipoproteins from AD extracellular fluid are more vulnerable to oxidation than controls.
- 2) ApoE is a major apolipoprotein in the CNS that is implicated in lipid transport and receptor-mediated regulation of lipid metabolism. Inheritance of the apoE4 allele is the strongest known genetic risk factor for sporadic AD.
- 3) ApoE isoforms may influence cellular distribution of peroxidation products in the brain by influencing lipoprotein trafficking and lipid oxidation and the convergence of these processes contributes to neurodegeneration in AD brain.
- 4) Mass spectrometric data show that there is enhanced formation of reactive products of auto-oxidized PUFAs known as isoprostanes [54, 104–106].

Similar to the enzyme-catalyzed breakdown of PUFA-containing lipids, auto-oxidized lipids perturb the cellular structure of cell membranes and lipoproteins leading to dysfunction of these entities and thence AD pathology. Oxidation of PUFAs that are components of lipids that make up lipoproteins may alter lipoprotein function and increase its reactivity towards brain cells (Fig. 2). Autopsy studies and analyses of spinal fluids show that AA and DHA are oxidized to F₂ and F₃ series isoprostanes, respectively in the brain of AD subjects [107–111]. Theoretically, lipid changes would enormously influence many of the hallmarks of Alzheimer's disease (AD). Most prominently, a lipid-depleted plasma membrane would ease production of deadly βA_{1-42} , since a secretase would more easily access a longer stretch of the peptide chain as it protrudes from a shrunken lipid bilayer [101, 103]. Amyloidogenic processing of proteins will generate cytotoxic peptides and result in the formation of protein plaques. Likewise, the exposure of nerve cells to oxidative break-

down products of PUFA or peptide fragment may induce neurodegeneration *via* apoptosis.

Other oxidative processes and AD

The loss of an electron by a compound is known as oxidation. Chemical species known as free radicals initiate oxidation of macromolecules in biological systems. Free radicals contain an unpaired electron and are thus very reactive because they can gain electrons from other molecules. Molecules that donate their electrons are known as oxidizing agents. In cells, cellular metabolism and exposure to environmental factors result in free radical generation. The most common free radicals are superoxide (O_2^-), hydroxyl (OH_2^{\cdot}) and nitric oxide (NO) [112–114]. Molecules such as hydrogen peroxide (H_2O_2) and peroxyxynitrate ($ONOO^-$) readily generate free radicals through various chemical reactions. Reactive oxygen species (ROS) is a general term for all free radicals and related molecules. Regular metabolic process such as the formation of excitatory amino acids and neurotransmitters produce ROS. For example, activation of glial cells results in enhanced production of NO *via* five-electron oxidation of L-arginine [115, 116]. NO synthase (NOS) mediates NO production. Because these compounds can cause oxidative damage to lipids, proteins and DNA, cells tightly control production of ROS. An imbalance in ROS production and inability to defend against them is known as oxidative stress.

Because of the ability of ROS to cause cell injury, oxidative stress is now considered to play a major role in the pathogenesis of AD [117]. Cells control ROS using an antioxidant defense system. The major components of this system are enzymes (superoxide dismutase (SOD), catalase, glutathione peroxidase) that destroy ROS, low molecular weight antioxidants (glutathione, tocopherol, ascorbic acid, retinoic acid, melatonin, uric acid, and lipoic acid), cofactors such as coenzyme Q₁₀, precursors of antioxidants (acetylcysteine, caretenoids) and natural plant compounds such as flavonoids [118–120]. Recent studies have shown that amyloid peptides may also have anti-oxidative properties leading to speculations that their occurrence in AD may be the result of the body mounting a defense against ROS produced by activated microglial cells [121]. However, most links between oxidative stress and AD have not been biochemically proven in human subjects. Since their double bonds make them more susceptible to oxidation, a decrease in oxidant defense will destroy PUFAs. Such destruction of PUFA in the brain will result in altered membrane structure and nerve function. One implication of such a membrane change is to contribute to the abnormal cleavage of βA : a lipid-damaged cell membrane might enable greater access by secretases, to a more proximal region of $\beta A P P$ and this mechanism may participate in the increased production of amyloid fragments. Oxidized PUFA are also cytotoxic and can induce nerve cell death [122]. Various studies showing an increase in lipid peroxidation in AD suggest that

the destruction of PUFA may be one mechanism by which oxidative stress is linked to the pathogenesis of AD.

Role of metals and trace elements in the oxidation of PUFAs

Metals and trace elements play important roles in PUFA metabolism. Metals and elements enter the body through food and diet or from respiration. Metals are important cofactors or components involved in antioxidant defense mechanisms. For example, activation of SOD requires copper and zinc [123–125]. Zinc plays an essential biochemical role in participating in the synthesis/degradation of macromolecules including lipids. Copper is widely distributed in metalloproteins/enzymes and is a major component of respiration. It is an essential component of erythrocytes and plasma where it is mostly bound to caeruloplasmin and closely linked to iron metabolism. Selenium is a constituent of glutathione peroxidase that is a component of the antioxidant defense system of the body [126, 127]. Molybdenum, manganese and vanadium are also activators of several enzymes while vanadium plays a role in lipid metabolism [128]. Other metals are known to be neurotoxic (aluminum, lead, cadmium, mercury) and are implicated in AD etiopathogenesis through mechanisms that are not well defined [31, 129–133]. While no biological function has been attributed to aluminum, it is known to interact and reduce the absorption of calcium, iron, manganese and phosphorus [134]. Therefore, any neurological or neurobehavioral effects of aluminum may be due to the alteration of the metabolism of other metals. In addition to being components of enzymes, metals can also serve as scavengers that prevent free radical formation. While trace amounts of elements can be protective, higher levels or alterations in homeostatic control of metals may induce the formation of free radicals that would destroy PUFA.

Clinical trials

There is presently no cure for AD and no treatment to prevent the gradual progression of the disease. However, remedial medication may help symptoms and make patients more comfortable by controlling sleeplessness, agitation, wandering, anxiety, and depression. For example, in the early or middle stages of AD, tacrine may alleviate some cognitive symptoms and acetylcholinesterase inhibitors (donepezil) and rivastigmine) are prescribed for the treatment of mild to moderate dementia related to AD. Various clinical trials have examined the effects of NSAIDs, antioxidants, and metal chelators on AD development [135–138]. Most of these studies are based on circumstantial evidence or on mouse studies that cannot be duplicated in human subjects. Epidemiological and longitudinal studies have identified a reduced

risk for AD in patients (<70 yrs) previously treated with NSAIDs for non-CNS afflictions such as arthritis [139]. Prospective clinical studies targeting COX-2 are now using more specific inhibitors to avoid gastrointestinal side effects that limited initial trials [140]. However, this new generation of COX-2 inhibitors may also have detrimental side effects because they inhibit a whole spectrum of prostanoids needed for normal physiologic actions of organs (heart, kidney) [141–143]. In addition to COX inhibition, mouse studies have shown that NSAIDs also inhibit secretases, thus preventing β A formation [144]. *In vitro* studies also suggest that NSAIDs may directly scavenge superoxide [145]. The overall effects are to prevent inflammation and oxidative damage. Our studies also show that preventing the conversion of PUFAs to lipid mediators by NSAIDs results in the increase of free PUFA levels in cells and a shift in their distribution in glycerolipids subclasses [146]. An understanding of specific pathways and mechanisms will enable us to design interventions that may lessen AD progression and reduce the side effects of current therapy.

Similar to the NSAID studies, vitamins B1, B12, C, E, folate, choline, magnesium, DHA, phosphatidylserine, DHEA, NADH, acetyl-L-carnitine, melatonin and *Ginkgo Biloba* extract supplements have been administered to AD patients without clear biochemical rationales [147–149]. Thus, while minor beneficial outcomes have been reported in some of these studies, it is difficult to scientifically evaluate these approaches without mechanism-based data. Lipids and their products are associated with nearly all of these agents and baseline lipid biochemistry will allow predictions of lipid altering substances. Furthermore, baseline studies will then enable appropriate monitoring of any treatments.

Conclusions and implications

A biochemical baseline for lipid composition and metabolism in the brain, CSF and plasma, including post-translational modifications, will likely predict candidate lipid markers for early diagnosis of AD, determine which patients might respond to specific treatments and lead to a better understanding of the underlying pathophysiology of AD. There may be a need to replenish PUFA in adult brain using dietary manipulations or identify enzymes that destroy PUFAs in AD in order to direct effort to selectively inhibit specific pathways. Determining whether a decrease in PUFA biosynthesis and transport or whether enhanced oxidation accounts for the decrease in PUFA in the adult brain will better define the use of antioxidants as remedies for AD progression and provide assays to monitor their efficacy. It might turn out that agents that cross the blood brain barrier are needed to control PUFA levels in brain. Alternatively, agents that control PUFA levels in plasma may be sufficient in maintaining physiologic levels of PUFA or preventing their destruction. A combination of dietary manipulation with enzyme inhibitors or antioxidants may be required for effective control of PUFA levels in the adult brain. Future studies are

needed to validate all enzyme inhibitors and nutraceuticals approaches that are presently used for AD management.

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Lipoxins and resolvins: Local mediators in endogenous anti-inflammation and resolution

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Introduction

Since the early concepts on the importance of the phagocyte in the host defense and inflammation as introduced by Metnivos more than 100 years ago (for which he was awarded the Nobel prize) the focus of research in inflammation was maintained with the credo – elucidate the chemical mediators that could cause/mediate the cardinal signs of inflammation – heat, redness, swelling, pain and loss of function. Inflammation initially involves the recognition of self and non-self by leukocytes. It is now clear that a diverse range of endogenous chemical mediators control these events and orchestrate the host response [1]. These small chemical signals regulate leukocyte traffic as well as the cardinal signs of inflammation. It is well established that the classic eicosanoids such as prostaglandins (PG) and leukotrienes (LT) play important roles and exert a wide range of actions in responses of interest in inflammation [2]. In recent years, the scope and range of chemical mediators identified has expanded considerably [1] to include novel lipid mediators, many new cytokines and chemokines, gases (i.e., nitric oxide and carbon monoxide), and reactive oxygen species as well as new roles for nucleotides as mediators such as adenosine [3–5] and the most recently uncovered of this class, namely inosine monophosphate (IMP), that also regulates neutrophil (PMN) trafficking [6].

A body of evidence demonstrated that endogenous mediators are generated to dampen the host response and orchestrate resolution [1, 7, 8]. In this regard, the lipoxins (LX) were the first to be identified and recognized as endogenous anti-inflammatory lipid mediators relevant in resolution in that they can function as “braking signals” or chalone in inflammation (Fig. 1) [9]. It is of particular interest that aspirin (ASA), a widely used non-steroidal anti-inflammatory drug with many beneficial properties [10] in addition to its well-appreciated ability to inhibit PG [11], also triggers the endogenous generation of 15-epimeric LX, termed aspirin-triggered LX (ATL). This occurs *via* acetylation of cyclooxygenase (COX)-2 at sites of inflammation *in vivo* [12] (*vide infra*) that carry anti-inflammatory and anti-pro-

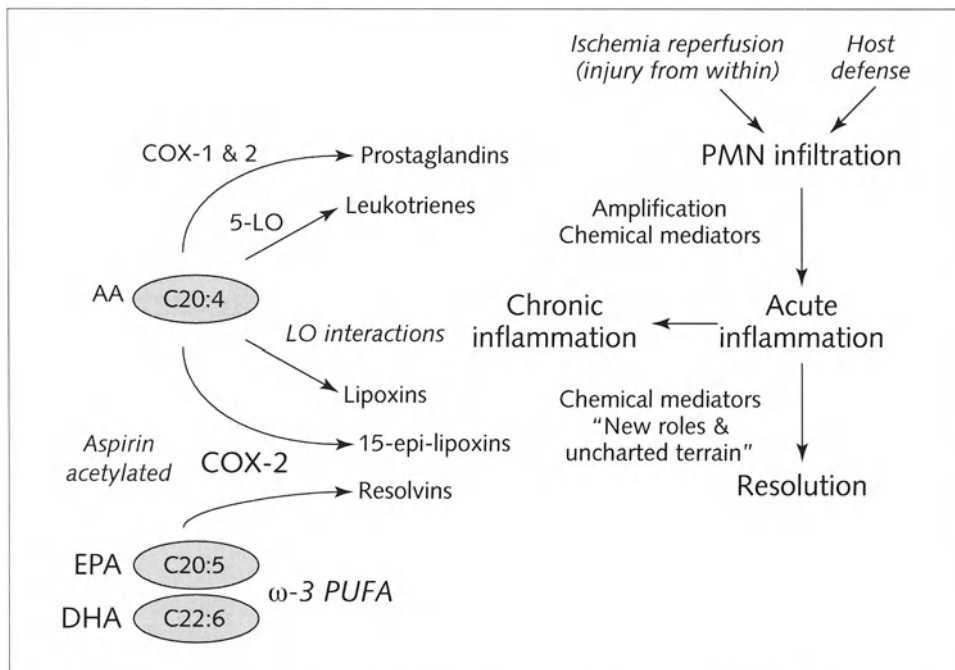


Figure 1

Resolution circuits in inflammation: Novel lipid mediators

During cell-cell interactions, lipid-derived mediators can be amplified (e.g., PG and LT) to enhance the actions of signal molecules, or braking signals (e.g., LX, ATL and resolvins) that can be generated via cell-cell interactions to limit further PMN recruitment and promote resolution.

liferative actions [13, 14]. This is a previously unappreciated and novel mechanism of drug action that has intriguing implications for targeted drug design. But more importantly, they help to further illustrate the importance of endogenous generation of lipid mediators with anti-inflammatory properties.

As a class, LX, ATL and their analogs possess physiologic, pathophysiologic and pharmacological actions in several target tissues. Each action of lipoxins is stereoselective in that changes in potencies accompany double bond isomerization and change in alcohol chirality (R or S) at key positions, as well as selective dehydrogenation of alcohols and reduction of double bonds. The self-limited impact of LX in the local micro-environment suggests that they contribute to resolution of injury sites and/or resolve inflammatory loci by regulating further recruitment of PMN and stimulating monocyte migration to promote healing and remodeling. LXA₄ stimu-

lates rapid lipid remodeling within seconds and releases arachidonic acid within PMN but without oxygenation, which is sensitive to pertussis toxin (PTX) treatment [15, 16]; findings that pointed to the involvement of a G protein-coupled receptor (GPCR) in the actions of LX on human leukocytes. This specific GPCR was identified and cloned in human and mouse, and denoted LXA₄ receptor (ALX). Together, they were identified as the first cloned lipoxygenase (LO)-derived eicosanoid receptors.

The traditional approach to develop anti-inflammatory drugs, as in other human conditions amenable to pharmacologic interventions, is the use of biosynthesis inhibitors and receptor antagonists of pro-inflammatory mediators, which indeed have enjoyed both considerable clinical and commercial successes [1, 17], but are not without significant unwanted side effects [18–20]. Hence, the emergence of endogenous pathways and cellular mechanisms involved in counter-regulation of responses that can lead to tissue injury and acute inflammation not only charts relatively unappreciated sides of human biology [21, 22], but also provides an opportunity to explore new therapeutic approaches based on these novel endogenous mechanisms that may reduce the possibilities for unwanted toxic side effects and help control inflammation with a high degree of precision.

Biosynthesis of lipoxins and aspirin-triggered lipoxins

Transcellular biosynthesis of LXs: The role of cell-cell interactions

Formation of LXs are promoted during platelet-leukocyte interactions and/or platelet-leukocyte micro-aggregates [23] by transcellular conversion of the leukocyte 5-lipoxygenase (LO) epoxide product LTA₄ (Fig. 2, right side). Once thought to be solely an intracellular intermediate in LT production, it is now clear that LTA₄ released by activated leukocytes is available for enzymatic conversion by neighboring cell types [5, 24]. When platelets are adherent, their 12-LO converts LTA₄ to lipoxin A₄ and B₄. For a review and mechanistic details with recombinant 12-LO, see [22]. Hence it is important to note that human platelets, which do not produce LX on their own, become a major source of LX, given their abundance *in vivo* and their highly active 12-LO.

The second classical pathway for LX production is initiated by 15-LO (Fig. 2, left side) in airway epithelial cells, monocytes or eosinophils, which up-regulate their 15-LO when exposed to cytokines such as IL-4 or IL-13 [25, 26]. The 15-LO, by definition, inserts molecular oxygen at the carbon 15 position of, for example, arachidonic acid, in the “S” configuration. When these cell types are activated, they generate and release 15S-HETE, which is rapidly taken up and converted by PMN to LX *via* the action of their 5-LO. This event not only leads to LX biosynthesis, but also “turns off” LT formation.

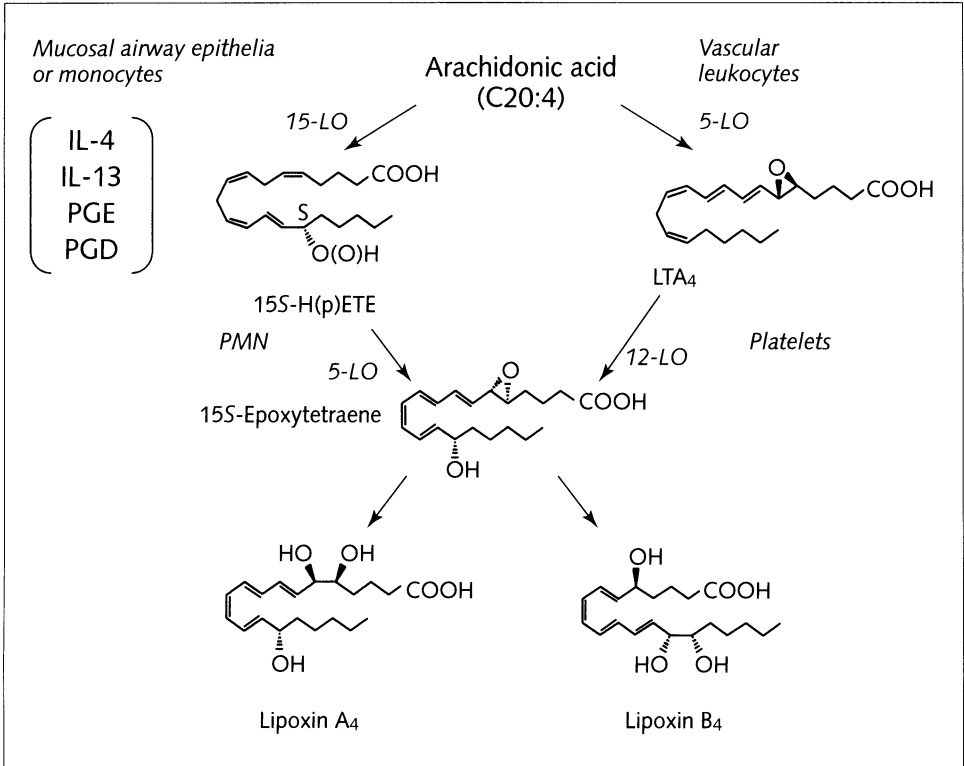


Figure 2

Transcellular lipoxin biosynthesis

During cell-cell interactions, lipoxins can be amplified by transcellular biosynthesis via the interactions of two or more cell types. Two main pathways appear to be used in human cells and tissues to generate LX. This event also blocks LT formation and therefore regulates leukocytes.

Biosynthesis of aspirin-triggered lipoxins via aspirin-acetylated COX-2

We sought evidence for alternate explanations for ASA's therapeutic actions because many beneficial new actions have been documented in recent clinical studies. These new potential therapeutic indicators for ASA include decreasing incidence of lung, colon, and breast cancer (reviewed by Levy [27]), and prevention of cardiovascular diseases [28]. Inhibition of cyclo-oxygenase and biosynthesis of prostaglandins can account for many of ASA's therapeutic properties [29]; however, its ability to regulate neutrophil-mediated inflammation or cell proliferation remains of interest. Along these lines, we uncovered a new action of aspirin that involves COX-2-bear-

ing cells such as vascular endothelial cells or epithelial cells and their co-activation with PMN (Fig. 3). Hence, inflammatory stimuli (i.e., TNF- α , LPS, etc.) induce COX-2 to generate 15R-HETE when ASA is administered [13]. This intermediate carries a carbon-15 alcohol in the R configuration that is rapidly converted by 5-LO in activated PMN to 15 epimeric-LX, or LX that carry their 15 position alcohol in the R configuration [22] rather than 15S native LX, which in humans can result from LO:LO interaction. 5-LO conversion of 15R-HETE also results in inhibition of LT biosynthesis [14]. 15R-HETE is a major product of arachidonic acid in several cell types when COX-2 is up-regulated after acetylation by ASA. Thus, it is possible that aspirin can regulate the *in vivo* production of LT by 15R-HETE conversion to 15-epi-LX, and 15-epi-LX can in turn also regulate the cellular actions of LT.

LXB₄ is a positional isomer of LXA₄, carrying alcohol groups at carbon 5S, 14R, and 15S positions, instead of the C-5S, 6R, and 15S positions present in LXA₄. Aspirin-triggered LXB₄ carries a 15R alcohol, hence 15-epi-LXB₄. Although LXA₄ and LXB₄ show similar activities in some biologic systems [30], in many others each shows distinct actions ([31] and reviewed in [22]). 15-epi-LXB₄, for example, is a more potent inhibitor of cell proliferation than LXA₄ or 15-epi-LXA₄ [22].

Generation of LXA₄ and 15-epi-LXA₄ in animal models and in human diseases

LXA₄ is produced *in vivo* during the course of inflammation such as in an experimental immune complex glomerulonephritis model [32, 33] and in pleural exudate upon allergen challenge in rats [34]. Also, endogenous LXA₄ was also produced in ischemic lungs and elevated by reperfusion in a hind limb ischemia reperfusion model [35]. A recent report demonstrated that LXA₄ is generated during microbial infection reported in a *T. gondii*-exposed murine model [36, 37] as well as in a murine model of asthma [38]. In addition, LXA₄ is formed in rat brain and elevated in focal cerebral ischemia [39]. In human subjects, a reduction and alteration in LX generation was found in patients with chronic liver disease [40] and chronic myelogenous leukemia [41–45]. These diseases contrast with recent findings that LXA₄ production is up-regulated in localized juvenile periodontitis [46] and mild asthma [47], as well as following atherosclerotic plaque rupture [48], and with nasal polyps [49].

Recently, using a newly developed specific enzyme-linked immunosorbent assay (ELISA) method and liquid chromatography tandem mass spectrometry (LC-MS-MS) system [12], 15-epi-LXA₄ could be detected *in vivo*. For examples, 15-epi-LXA₄ was generated in murine peritonitis [12] and murine dorsal air-pouches [50], and also was detected in rat kidney [33] and liver [51] in an aspirin-dependent manner. Along these lines, it was reported that ASA rapidly up-regulates COX-2 expression in the stomach and causes a significant increase in gastric 15-epi-LXA₄ pro-

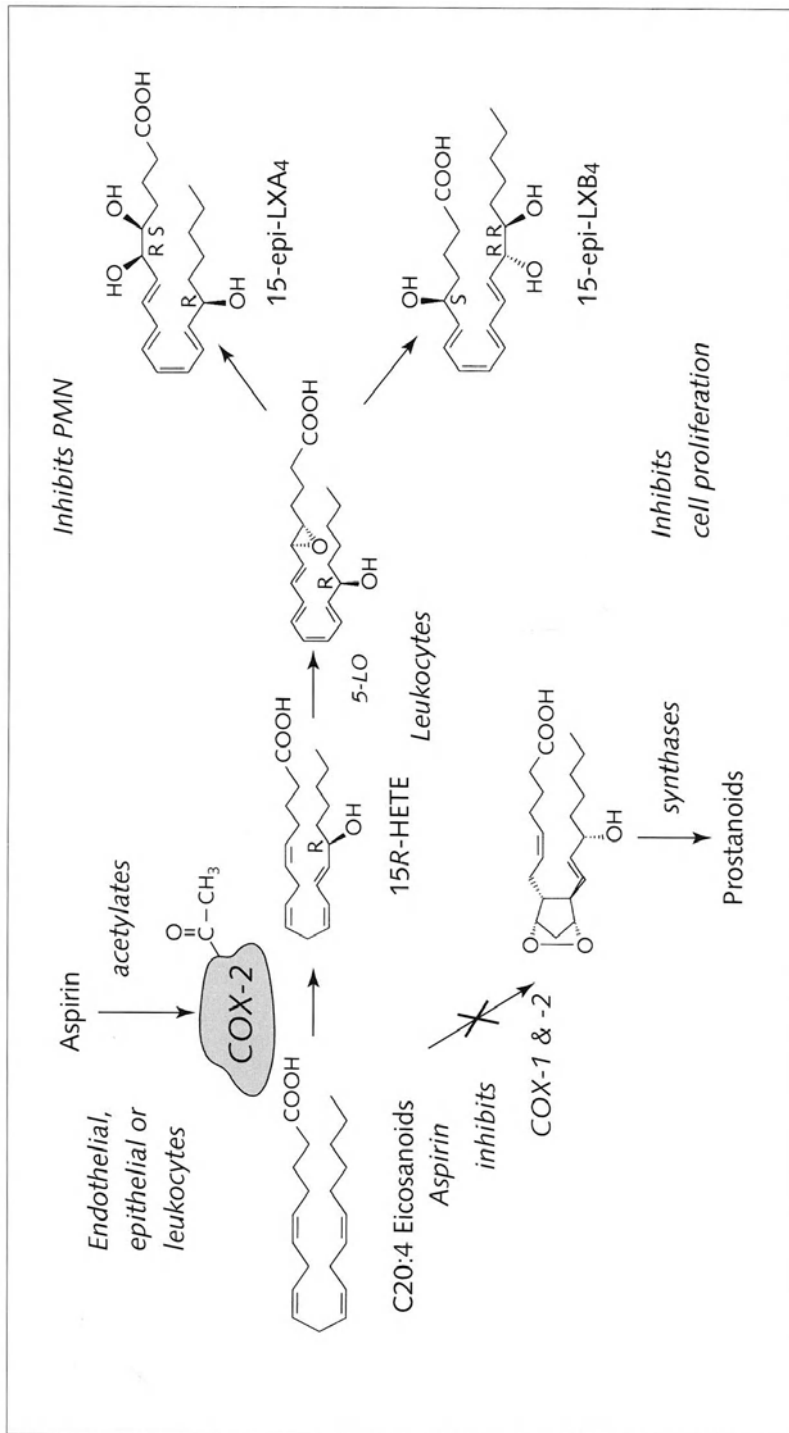


Figure 3

Generation of aspirin-triggered lipid mediators

15-epi-LXs are generated when COX-2 is up-regulated and acetylated by ASA. Irreversible acetylation of COX-2 by aspirin changes the enzyme's product from prostaglandin intermediate to precursors of ATL. The acetylated COX-2 remains catalytically active to generate 15R-HETE.

Table 1 - Lipoxin A₄ and human diseases

Organ/System	Impact <i>in vivo</i>	Refs.
Hematologic	Defect in LX production with cells from chronic myeloid leukemia patients in blast crisis	[42]
	LX stimulate nuclear form of PKC in erythroleukemia cells	[121]
	Formation of LX by granulocytes from eosinophilic donors	[122]
Cardiovascular	Angioplasty-induced plaque rupture triggers LX formation	[48]
Dermatologic	LXA ₄ regulates delayed hypersensitive reactions in skin	[123]
Pulmonary	LXA ₄ detected in bronchoalveolar lavage fluids from patients with pulmonary disease and asthma	[124]
	Production of LX by nasal polyps and bronchial tissue	[49]
	LXA ₄ inhalation shifts and reduces LTC ₄ -induced contraction in asthmatic patients	[125]
	Aspirin-intolerant asthmatics display a lower biosynthetic capacity than aspirin-tolerant patients	[53]
	LXA ₄ inhibits IL-8 release by monocytes from asthma patients	[47]
Hepatic	LX generation decreased in cirrhotic patients	[40]
Rheumatoid arthritis	LX levels increase with recovery	[126]
Oral	LXA ₄ production is up-regulated in localized juvenile periodontitis	[46]

duction in rats [52]. These methods (e.g., LC/MS/MS and ELISA) were used to evaluate ATL and LXA₄ formation in ASA-tolerant and ASA-intolerant asthmatics and their relation to leukotriene C₄. Of interest, the ASA-tolerant subjects generated both LX and ATL, but the ASA-intolerant patients proved to have a diminished capacity to generate ATL and LX upon ASA challenge [53]. The lower levels of these potentially protective mediators could contribute to the pathobiology of this chronic disorder in that the disease state is not only characterized by the overproduction of pro-inflammatory mediators but the loss or reduction in LX and ATL that may keep inflammation in check. Together, this result indicates that alterations in LX and ATL levels may be linked to the pathophysiology of several human diseases and may display local organ-specific functions that stand apart from their roles in inflammation and within local inflammatory lesions (Tab. 1).

Stable analogs of LXA₄ and 15-epi-LXA₄ resist rapid metabolic inactivation

Enzymatic inactivation of LXs: Structure requirements for LXA₄ anti-inflammatory actions

As other autacoids, lipoxins are rapidly generated in response to stimuli, act locally and then are rapidly enzymatically inactivated. The major route of LX inactivation is through dehydrogenation by monocytes that convert LXA₄ to 15-oxo-LXA₄, followed by specific reduction of the double bond adjacent to the ketone [21]. 15-hydroxy/oxo-eicosanoid oxidoreductase (15-PGDH) catalyzes the oxidation of LXA₄ to 15-oxo-LXA₄ (Fig. 4). This compound is biologically inactive and is further converted to 13,14-dihydro-15-oxo-LXA₄ by the action of LXA₄/PGE 13,14-reductase/LTB₄ 12-hydroxydehydrogenase (PGR/LTB₄DH). Moreover, reduction of the 15-oxo-group by 15-PGDH yields 13,14-dihydro-LXA₄, revealing an additional catalytic activity for this enzyme [54]. LXB₄ can also be dehydrogenated by 15-PGDH at carbon-5 to produce 5-oxo-LXB₄, therefore sharing a common route of inactivation [55]. It has recently been shown that 15-oxo-LXA₄ is also produced from LXA₄ in mouse whole blood [56] suggesting that the mouse shares with the human a common pathway for LXA₄ inactivation.

Each action of lipoxins is stereo-selective in that changes in potencies accompany double bond isomerization and change in alcohol chirality (R or S) at key positions as well as selective dehydrogenation of alcohols and reduction of double bonds. For example, the 15-hydroxyl group is important for anti-inflammatory properties since aspirin-triggered LXA₄ (15R-LXA₄) with the 15-hydroxyl group in the R-configuration as well as 15(R/S)-methyl-LXA₄ have been established in several experimental settings to be more potent than native LXA₄ (15S-LXA₄) *in vitro* and *in vivo* [57, 58]. Also, both 15-oxo-LXA₄ [54] and 15-deoxy-LXA₄ [21] are biologically inactive in inhibiting superoxide anion generation and transmigration in PMN, respectively. The 13,14-double bond is important since 13,14-dihydro-LXA₄ proved to be inactive in inhibiting superoxide anion generation [54]. These pharmacophores for LX's anti-inflammatory action are also required for their interaction with ALX since these biologically inactive isomers (e.g., 15-oxo-LXA₄, 15-deoxy-LXA₄ and 13,14-dihydro-LXA₄) did not bind to ALX, whereas the active ones (e.g., 15R-LXA₄ and 15(R/S)-methyl-LXA₄) give specific binding to ALX, as demonstrated by specific [³H]-LXA₄ binding (see Fig. 5).

Design of stable analogs of LXA₄ and 15-epi-LXA₄

Since LXs are rapidly transformed and inactivated by monocytes, and, potentially, other cells *in vivo*, it was highly desirable to design LX analogs that could resist this form of metabolism, maintain their structural integrity, and potentially enhance

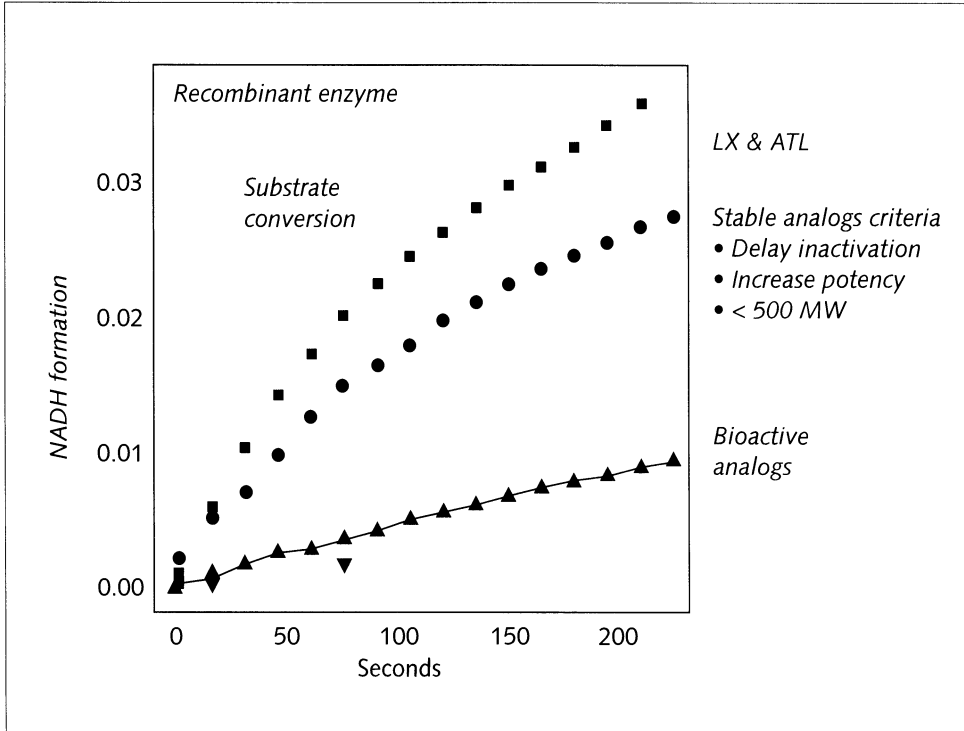
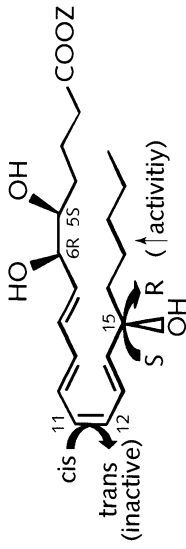


Figure 4

LX and ATL stable analogs resist rapid inactivation

The initial step in LXA_4 inactivation is dehydrogenation of the 15-hydroxyl group, catalyzed by 15-hydroxy prostaglandin dehydrogenase (15-PGDH). Metabolic stable analogs of both LXA_4 and 15-*epi*- LXA_4 were designed to resist rapid inactivation at carbon 15 as well as the ω -end of the molecule.

beneficial bioactions. LX analogs were constructed with specific modifications of the native structures of LXA_4 and LXB_4 , such as the addition of methyl groups on carbon-15 and carbon-5 of LXA_4 and LXB_4 structures, respectively, to block dehydrogenation by 15-PGDH. For example, 15(R/S)-methyl- LXA_4 is a racemic stable analog of both LXA_4 and 15-*epi*- LXA_4 . Additional analogs of LXA_4 were synthesized with a phenoxy group bonded to carbon-16 and replacing the ω -end of the molecule. This design permits 16-phenoxy- LXA_4 to resist potential ω -oxidation and to be protected from dehydrogenation *in vivo*. Fluoride was added to the para-position of the phenoxy ring to make 16-(para-fluoro)-phenoxy- LXA_4 to hinder degradation of the phenoxy ring. The aspirin-triggered 15-*epi* counterpart of 16-(para-fluoro)-phenoxy- LXA_4 , namely 15-*epi*-16-(para-fluoro)-phenoxy- LXA_4 , was



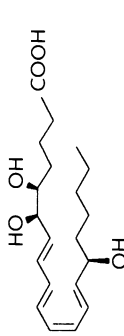
Compounds compete with [³H]-LXA₄:

LXA₄: (Z = H) and methyl ester (Z = CH₃)

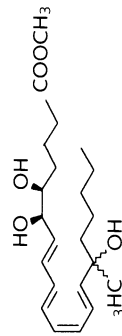
DO NOT compete (at equal molar levels):

- 6(S)-LXA₄
- 11-trans-LXA₄
- 15-deoxy-LXA₄

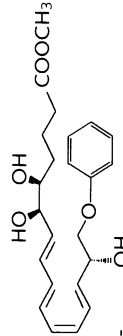
• 15-epi-LXA₄



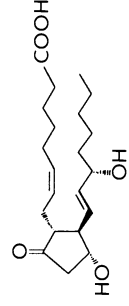
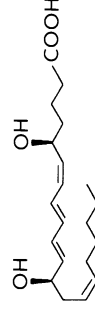
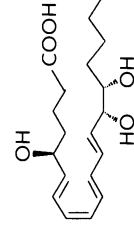
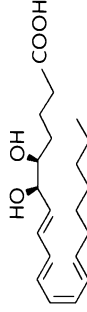
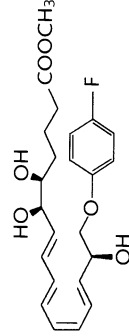
• 15(R/S)-methyl-LXA₄



• 16-phenoxy-LXA₄



• 15-epi-16-(para-fluoro)-phenoxy-LXA₄



• LXB₄

• LTB₄

• PGE₂

also synthesized. These modifications not only prolong the half-life of the compounds in blood but also enhance their bioavailabilities as well as bioactivities (Fig. 4) [56].

When compared to the native LXs, the ATLs are less effectively converted *in vitro* to their 15-oxo-metabolite [21]. This indicates that the dehydrogenation step is highly stereo-specific and suggests that, when ATLs are generated *in vivo*, their biologic half-life is increased by about two-fold greater than that of native LXA₄, thereby enhancing their ability to evoke bioactions. Hence, biologically stable analogs of LX and ATL can be engineered to enhance their bioactions, which suggests that they are useful tools, and offers leads for developing novel therapeutic modalities. These analogs proved to be active and also interact directly with ALX (Fig. 5).

Biological properties of LX and ATL

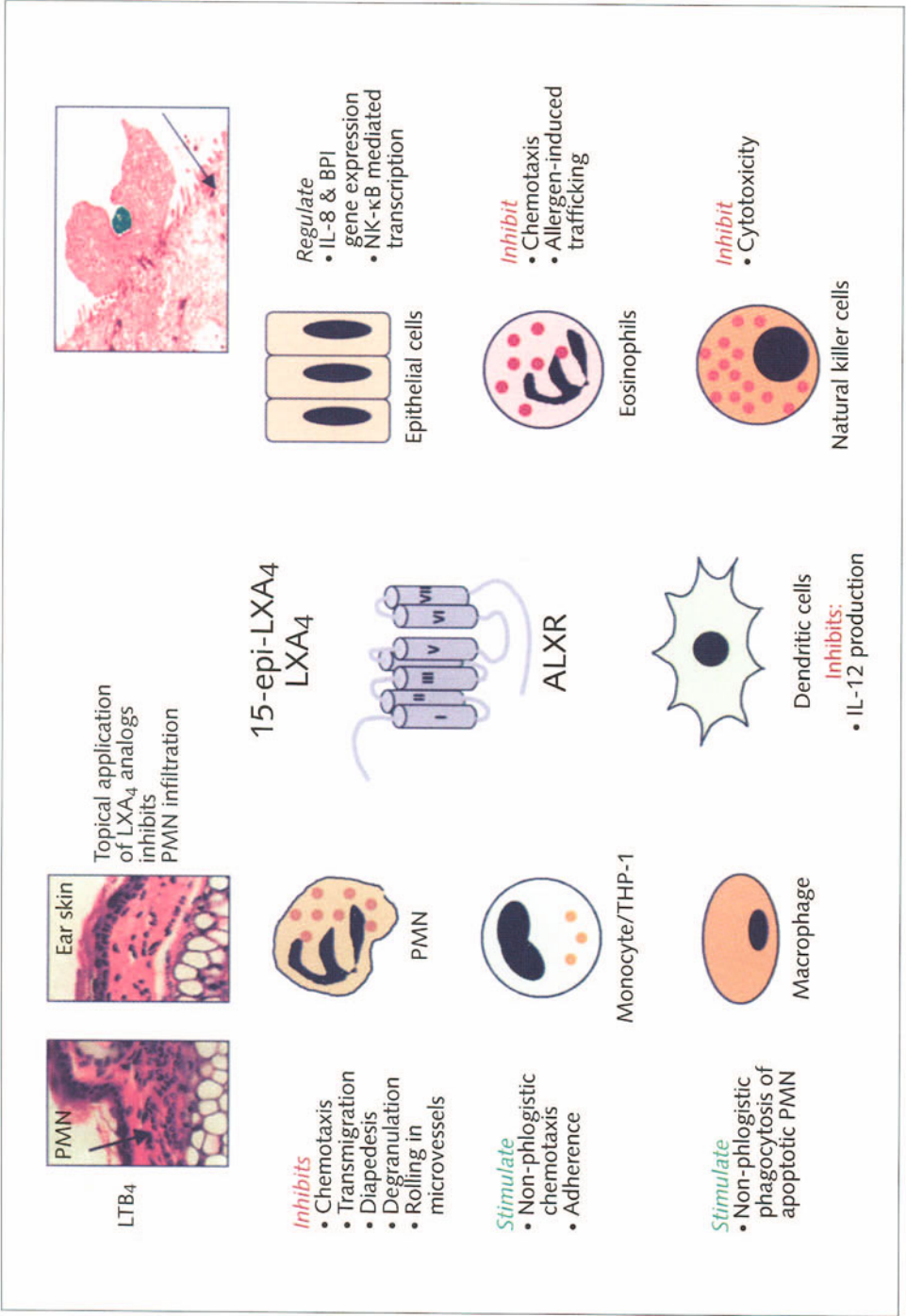
Actions of LX and ATL *in vitro*

LXA₄ and ATL display counter-regulatory roles in various cell types *in vitro* (Fig. 6, Tabs. 2 and 3). With human peripheral blood leukocytes (Tab. 2), LXA₄ inhibits both isolated PMN and eosinophil chemotaxis *in vitro* in the nanomolar range [59, 60] and blocks human natural killer (NK) cell cytotoxicity in a stereo-selective fashion [22] as well as stimulate myeloid bone marrow-derived progenitors [45]. In cell-cell interaction systems, LXA₄ inhibits PMN transmigration across both endothelial and epithelial monolayers [30, 61] *via* actions on both cell types (i.e., PMN and endothelial cells, PMN and epithelial cells). LXA₄ stimulates chemotaxis and adherence in monocytes but no apparent “pro-inflammatory” responses of these cells *in vitro* or *in vivo*, findings that may relate to the recruitment of monocytes to sites of

Figure 5

Ligand binding specificity of human ALX

LXA₄ interaction with ALX is highly stereo-specific, that is the 5*S*, 6*R*-orientation of the two hydroxyl groups as well as 11-*cis* double bond conformation are essential for bioactions. 15-*epi*-LXA₄ (an aspirin-triggered lipoxin, ATL) carries a C-15 alcohol at the *R* configuration, opposite to the *S* configuration in native LXA₄, and was shown to have higher potency than native LXA₄ in certain bioassays. In 15(*R/S*)-methyl-LXA₄, hydrogen at C-15 was replaced by a methyl group as a racemate at C-15. 16-phenoxy-LXA₄ has a phenoxy group at C-16. These compounds, which are more resistant to rapid dehydrogenation by 15-PGDH than native LXA₄, compete with [³H]-LXA₄ specific binding on PMN as well as recombinant ALX and are potent inhibitors for PMN functions *in vitro* and *in vivo*.



wound healing and clearance. Indeed, LX and ATL stimulate the uptake of apoptotic PMN by macrophages in a non-phlogistic fashion [62].

With human enterocytes and fibroblast, LXA₄ regulates pro-inflammatory cytokine release as well as gene expression (see below). These counter-regulatory actions are initiated *via* unique cell surface receptors on leukocytes and enterocytes as well as fibroblasts. In hepatocytes, ATL significantly reduces PPAR α and cytokine-induced neutrophil chemo-attractant (CINC)-1 [63]. With other cell types such as endothelium and mesangial cells, LXA₄ evokes bioactions and interacts with a subclass of peptido-LT receptors (CysLT1) [reviewed recently in Ref. 22]. The leukocyte receptors are physiologically and pharmacologically distinct and evoke selective actions on each type of leukocyte tested to date.

Actions of LX and ATL *in vivo*

The metabolically stable analogs of LX and ATL have been examined in various experimental animal models and summarized in Table 4.

Acute inflammation

In dermal inflammation, these LX stable analogues when applied topically to mouse ears inhibit both PMN infiltration and vascular permeability changes in a concentration-dependent fashion [57, 58]. Also, the fluorinated analog of ATL, denoted ATLa, at levels as low as ~24 nmol/mouse, potently inhibited TNF- α -induced leukocyte recruitment into the dorsal air-pouch [56]. Inhibition was evident by either local intra-air-pouch delivery (~77% inhibition) or *via* systemic delivery by intravenous injection (~85% inhibition) and proved more potent than local delivery of ASA. Recently, using a thioglycollate-induced peritonitis, ATL analogs were shown to rapidly promote macrophage phagocytosis of apoptotic PMN, supporting a role for LXs as pro-resolution signals in inflammation [64].

Figure 6

LXA₄ actions via ALX in leukocytes and enterocytes

Actions of LXA₄ in leukocytes (reviewed in [22]) and human epithelial cells [74, 102]. (Upper left panel) Ear biopsies: Inhibition of LTB₄-induced PMN infiltration into mouse ear by topical application of LXA₄ analogs in acute skin inflammation [58]. PMN is indicated by an arrow. (Upper right panel) Photomicrograph: Internalization of Salmonella typhimurium (shown in green) by intestinal epithelium (indicated by an arrow). In response to this gastrointestinal pathogen, intestinal epithelium secretes chemokines, which promote neutrophil infiltration. This chemokine (IL-8) secretion can be down-regulated by LXA₄ analogs.

Table 2 - Lipoxin A₄ and ATL on myeloid cells

Cell type/tissue	Action	Refs.
Whole blood	Down-regulate CD11/CD18, prevent shedding of L-selectin and reduce peroxynitrite generation on PMN, monocytes and lymphocytes	[98, 127]
Neutrophils	Inhibit chemotaxis, adherence and transmigration Inhibit PMN-epithelial and endothelial cell interactions Block superoxide anion generation Inhibit CD11b/CD18 expression and IP ₃ formation Inhibit peroxynitrite generation Attenuate AP-1 and NF-κB accumulation and inhibit IL-8 gene expression	[21, 59] [30, 61] [97] [15, 93]; [98] [98]
Monocytes	Stimulate chemotaxis and adhesion to laminin without increase in cytotoxicity Inhibit peroxynitrite generation Inhibit IL-8 release by cells obtained from asthma patients	[82] [98] [47]
Macrophages	Stimulate non-phlogistic phagocytosis of apoptotic PMN	[62, 64]
Dendritic cells	Inhibit IL-12 production	[36, 37]
Eosinophils	Inhibit migration/chemotaxis	[65]
NK cells	Block cytotoxicity	[128]
Myeloid progenitors	Stimulate myeloid bone marrow-derived progenitors	[45]

Table 3 - Actions of lipoxin A₄ and ATL on resident cell types

Cell type/tissue	Action	Refs.
Enterocytes	Inhibit TNF-α-induced IL-8 expression and release Inhibit <i>Salmonella typhimurium</i> -induced IL-8	[74] [102]
Fibroblasts	Inhibit IL-1β-induced IL-6, IL-8 and MMP-3 production	[83]
Endothelia (HUVEC)	Stimulate protein kinase C-dependent prostacyclin formation Block P-selectin expression	[129] [68]
Mesangial cells	Inhibit LTD ₄ -induced proliferation	[108]
Pulmonary artery	Induce relaxation and reverses pre-contraction by PGF ₂ or endothelin-1	[130]
Hepatocytes	Reduce PPARα and CINC-1 levels	[63]
Bronchi	Relaxation after pre-contraction by blocking peptido-leukotrienes in human airway	[125]

Table 4 - Actions of lipoxin A₄ and ATL in vivo in disease models

System	Model	Action	Refs.
Acute inflammation (mouse)	Peritonitis	Promote macrophage phagocytosis of PMN	[64]
	Dorsal air pouch	Inhibit TNF- α -induced PMN infiltration	[56]
	Dermal inflammation	Inhibit LTB ₄ induced PMN infiltration into ear skin	[58]
Lung (mouse)	Asthma	Inhibit airway hyper-responsiveness and pulmonary inflammation	[38]
	Ischemia and reperfusion	Inhibit PMN infiltration into lungs	[35]
Kidney (rat)	Glomerulonephritis	Antagonize the effects of LTC ₄ and LTD ₄	[139]
	Ischemia and reperfusion	Reduce PMN infiltration and is protective against acute renal failure	[69]
Microbial infection	<i>T. gondii</i> infection (mouse)	Stun and block dendritic cell migration and IL-12 production	[36, 37]
	<i>A. costaricensis</i> infection (rat)	Shorten the duration of pleural exudation	[34]
Endothelium (mouse)	Granuloma	Reduce angiogenic phenotype	[71]
Eye (rabbit)		Lower intraocular pressure	[72, 73]
Gastrointestinal tract	Colitis (mouse)	Attenuate induction of pro-inflammatory gene expression and reduce severity of DSS-induced colitis	[70]
	Aspirin-induced gastric damage (rat)	Reduce the severity of gastric damage and suppress aspirin-induced leukocyte adherence	[52]

Lung (endogenous versus exogenous stimuli)

Since LXA₄ and ATL selectively regulate leukocyte responses, they were tested in BLT1 transgenic mice that give dramatically increased PMN trafficking to lungs after hind limb ischemia-reperfusion. Despite excessive PMN recruitment in BLT1 transgenic mice, intravenous injection of ATL sharply diminished reperfusion-initiated PMN trafficking to lungs, revealing a novel protective role for LX and ATL in stress responses that have applications in perioperative medicine [35]. With exogenous allergen challenge in a murine model of asthma, LXA₄ biosynthesis and ALX

expression was increased. Transgenic expression of human ALX leads to significant inhibition of pulmonary inflammation and eicosanoid-initiated eosinophil infiltration. Administration of a stable analog of ATL blocks both airway hyper-responsiveness and pulmonary inflammation, highlighting a unique counter-regulatory role for LX in airway responses [38]. Along these lines, LXA₄/ATL analogues dramatically blocked allergic pleural eosinophil influx on allergen-induced eosinophilic pleurisy in sensitized rats [65].

Kidney

LXA₄ and ATL display physiological and pathophysiological roles in kidney including regulation of renal functions by increasing glomerular filtration rate and renal plasma flow rate [66, 67]. LXA₄ also antagonizes the effects of LTC₄ and LTD₄ on the glomerular microcirculation [139]. In ischemic acute renal failure, ATL stable analog shows functional and morphologic protection and reduces PMN infiltration. In addition, ATL-treated mice also display increased renal mRNA levels for suppressors of cytokine signaling (SOCS)-1 and SOCS-2 [69].

Gastrointestinal tract

During aspirin-induced gastric damage in rats, LXA₄ exhibits potent protective action on gastric mucosa by reducing the severity of gastric damage and suppressing aspirin-induced leukocyte adherence [52]. Also, ATL is protective in intestinal inflammation in a mouse model of dextran sodium sulfate-induced colitis. Oral administration of ATL analog (10 µg/day) significantly reduced the weight loss, hematochezia and mortality that characterize DSS-induced colitis [70].

Microbial infection

In *Angiostrongylus costaricensis* infected rats, two stable LXA₄ analogues did not alter the magnitude of pleural exudation response, but clearly shortened its duration. These results indicate that the early resolution of allergic pleural edema observed during *A. costaricensis* infection coincided with a selective local eosinophilia and seemed to be mediated by COX-2-derived PGE₂ and LXA₄ [34]. Along these lines, ATL stable analog shows reduced splenic dendritic cell mobilization and IL-12 response in *T. gondii*-infected mice, demonstrating a novel role for LXs in regulating pro-inflammatory responses during microbial infection [36, 37].

Endothelium

ATL analog inhibits endothelial cell proliferation and VEGF-induced endothelial cell chemotaxis. In a granuloma *in vivo* model of inflammatory angiogenesis, ATL treatment (10 µg/mouse) reduces the angiogenic phenotype, as assessed by both vascular casting and fluorescence. Together, these results identify a novel and potent previously unappreciated action of ATL in angiogenesis [71].

Eye

Both LXA₄ and LXB₄ and their stable analogs lower intraocular pressure in rabbits and that may underlie their role in the physiology of ocular pressure regulation within the eye [72, 73]. In human eye tissues, the receptor ALX is indeed present and appears to be associated with corneal epithelial cells [74].

Cell surface receptors for LXA₄ and ATL

Human and mouse ALX: Molecular cloning, receptor expression and up-regulation

The specific LXA₄ binding sites were first characterized on human PMN that are likely to mediate many of its selective actions on these cells [75]. Intact PMN demonstrate specific and reversible [11, 12-³H]-LXA₄ [described in 76] binding (K_d ~0.5 nM and B_{max} ~1,830 sites/PMN), which is modulated by guanosine stable analogs. These LXA₄ binding sites are inducible in promyelocytic lineage (HL-60) cells exposed to differentiating agents (e.g., retinoic acid, DMSO and PMA) and confer LXA₄-stimulated phospholipase activation [77]. Together, these findings provided further evidence that LXA₄ interacts with specific membrane-associated receptors on human leukocytes that belong to the classical GPCR. Based on our finding that functional LXA₄ receptors are inducible in HL-60 cells, several putative receptor cDNAs that are also induced within this temporal frame, cloned earlier from myeloid lineages and designated orphans [78, 79], were systematically examined for their ability to specifically bind and signal with LXA₄.

One of the orphans (denoted previously as pIN114, also known as FPRL1 and FPR2) when transfected into Chinese hamster ovary (CHO) cells displays specific [³H]-LXA₄ binding with high affinity (K_d =1.7 nM) and demonstrated selectivity when compared to LXB₄, LTB₄, LTD₄ and PGE₂ (Fig. 5) [80]. These transfected CHO cells transmit signal with LXA₄, activating both GTPase and the release of arachidonic acid (C20:4) from membrane phospholipid, indicating that this cDNA encodes a functional receptor for LXA₄ in myeloid cells (Tab. 5). The mouse LXA₄

Table 5 - Lipoxin A₄ and ATL signal transduction with human ALX

Cell type	LXA ₄ and ATL-evoked signal transduction	Kinase associated	Gene expression
HL-60 (differentiated)	PLD activation (lipid remodeling)	protein kinase C (staurosporine sensitive)	
PMN	PLD activation GTPase activity C20:4 release PIPP signal (↑PSDP accumulation) (with second signal) No increase of cAMP and proton efflux Weak [Ca ²⁺] _i	tyrosine kinase (genistein sensitive)	Inhibit IL-8 mRNA expression Up-regulate NAB1
Monocyte	Increase of [Ca ²⁺] _i (PTX sensitive) No increase of cAMP and proton efflux		
Enterocyte	No proton efflux		Reduce IL-8 mRNA level Reduce NF-κB mediated transcription activation Regulate bactericidal/permeability-increasing protein (BPI)
Synovial fibroblast	PLD activation Inhibit NF-κB binding		Stimulate tissue inhibitor of metalloproteinase (TIMP)-1 and TIMP-2 transcription

receptor cDNA was cloned from a spleen cDNA library and displays specific [³H]-LXA₄ binding and LXA₄-initiated GTPase activity when transfected into CHO cells [58]. The human and mouse LXA₄ receptors represented the first cloned LO-derived eicosanoid receptors.

Both human [80] and mouse [58] ALX cDNA contain an open reading frame of 1051 nucleotides, which encode a protein of 351 amino acids. Northern blot analysis demonstrated that ALX mRNA is ~1.4 Kb in both human and mouse [58]. Chromosome mapping revealed that the gene encoding ALX [80] is located on chro-

mosome 19q [81], denoted as FPRH1 in this early report of the orphan receptor. Northern blot analysis of multiple murine tissues demonstrated that ALX mRNA is most abundant in PMN, spleen and lung with lesser amounts in heart and liver [58]. In the absence of disease, the pattern is similar in human tissues. In humans, ALX mRNA is also abundant in PMN, followed by spleen, lung, placenta and liver [58, 80].

To date, ALX is identified by function and direct actions, and cloned in both human and mouse PMN [58, 80], human monocytes [82] and human enterocytes [74], as well as synovial fibroblasts [83]. In human PMN, results of subcellular fractionation experiments revealed that [^3H]-LXA₄ binding sites are associated with plasma membrane and endoplasmic reticulum (42.1%) and granule (34.5%) as well as nuclear-enriched fractions (23.3%), a distribution distinct from [^3H]-LTB₄ binding [75]. The finding that LXA₄ blocks both PAF and fMLP-stimulated eosinophil chemotaxis [60] suggests that functional ALX is also present on eosinophils. In human enterocytes, ALX is present in crypt and brush border colonic epithelial cells [74].

Retinoic acid, PMA and DMSO, which lead to granulocytic phenotypes in HL-60 cells, induce a ~3–5-fold increase in the expression of ALX as monitored by specific [^3H]-LXA₄ binding [77] (see Tab. 5). Also, ALX transcription is dramatically up-regulated by cytokines in human enterocytes, with lymphocyte-derived IL-13 and interferon (IFN)- γ being most potent, followed by IL-4 and IL-6. IL-1 β and LPS also showed moderate induction of ALX mRNA [74]. In view of the cytokine regulation of ALX, it is likely that the expression of these receptors will change dramatically in disease states, which in turn, might attenuate mucosal inflammatory and allergic responses.

Structure-function relationships of ALX

ALX belongs to the GPCR superfamily characterized by seven putative transmembrane segments (TMS) with N-terminus on the extracellular side of the membrane and C-terminus on the intracellular side [84]. The overall homology between human and mouse ALXs is 76% in nucleotide sequence and 73% in deduced amino acid [58]. An especially high homology is evident for their second intracellular loop (100%) and between their sixth TMS (97%) followed by the second, third and seventh TMS as well as the first extracellular loop (87–89%), suggesting essential roles for these regions in ligand recognition and G protein coupling. Molecular evolution analysis (Fig. 7) suggests that ALX is only distantly related to prostanoid receptors and belongs to the cluster of chemoattractive peptide receptors exemplified by fMLP, C5a and IL-8 receptors [85] and now known to also include BLTs as well as the recently cloned cysteinyl-leukotriene receptors (CysLTs). BLT1 was obtained from human HL-60 cells [86] and mouse eosinophils [87] and found to share an overall

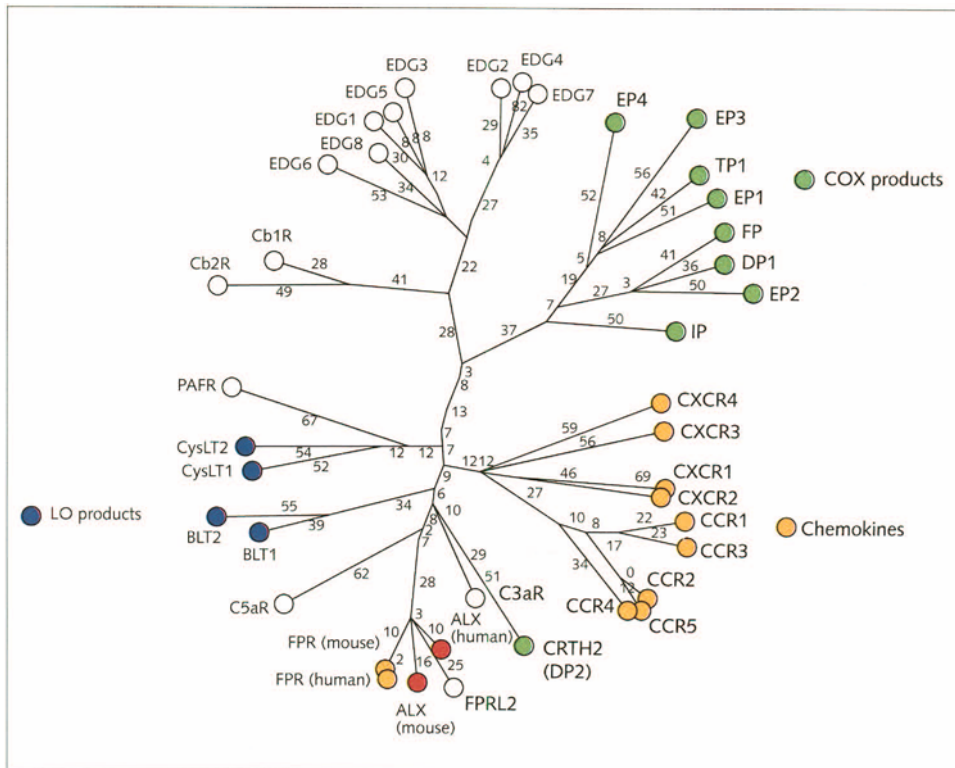


Figure 7

Phylogenetic tree of GPCRs for chemokines and lipid mediators

This tree is constructed with deduced amino acid sequences of human eicosanoid and chemokine receptors using the "All-All Program" at the Computational Biochemistry Server at ETHZ (<http://cbgr.inf.ethz.ch/Server/AllAll.html>).

Abbreviations: TP, thromboxane A₂ receptor; DP, prostaglandin D₂ receptor; EP1, EP2, EP3, EP4, subtypes of prostaglandin E₂ receptor; FP, prostaglandin F₂ receptor; IP, prostacyclin receptor; Cb1R, Cb2R, cannabinoid receptors; ALXR, lipoxin A₄ receptor and BLT, leukotriene B₄ receptor. BLT, CXCR-4 and CCR-5 were identified as co-receptors for HIV-1 entry.

~30% homology with ALX in deduced amino acid sequences. High homologous region (~46%) is present within the second transmembrane segments in both ALX and BLT1 with the amino acid sequence LNLALAD. Prostanoids interact with their receptors *via* carboxyl group interacting with an arginine residue within the seventh transmembrane segment [88]. Neither ALX nor BLT1 share this Arg (in 7th transmembrane segment) requirement [80, 86], yet both ligands contain COOH, which at physiological pH could present as a counter-anion. Together, these findings fur-

ther provide evidence that the origin of receptors for LT and LX is distinct from that of receptors for prostanoids.

Several conserved motifs and amino acid residues important for post-translational modification are found in ALX. For example, conserved N-glycosylation sites are present on Asn-4 and Asn-179 of human ALX and N-glycosylation was shown to be important for ligand specificity of this receptor [89]. Site-directed mutagenesis study demonstrates that Ser-236, Ser-237 and Tyr-302 are essential for human ALX phosphorylation and signaling [90]. In addition, the NPXXY motif in the TMS-7, which plays a role in receptor desensitization and/or resensitization [91], and DRY motif in the TMS-3 that is essential for β -arrestin binding and G protein activation [92] are also present in ALX, suggesting a conserved mechanism in regulation of ALX signaling.

Ligand binding specificity: peptide and lipid ligands

ALX is stereo-selective for its eicosanoid-based ligands. Intact human PMN and retinoic acid-differentiated HL-60 cells demonstrate specific and reversible [3 H]-LXA₄ binding with Kds \sim 0.5 and \sim 0.6 nM, respectively [75, 77]. Several isomers of LXA₄ tested, namely 11-trans-LXA₄, 6S-LXA₄ and LXB₄, did not compete for these recognition sites, consistent with their functional responses in these systems. Results from Scatchard analyses indicate that [3 H]-LXA₄ binds PMN granule membrane-enriched fractions with comparable Kd (0.8 nM) but with a larger B_{max} (4.1×10^{-11} M) than plasma membrane fractions (Kd = 0.7 nM, B_{max} = 2.1×10^{-11} M) [80]. Hence, it appears that additional receptors can be mobilized by granule fusion to the plasma membrane of PMN. [3 H]-LXA₄ specific binding is stereo-selective, since LTB₄, LXB₄, 6S-LXA₄, 11-trans-LXA₄ or SKF104353 (a CysLT1 antagonist) does not compete for [3 H]-LXA₄ in human PMN. Human and mouse ALX cDNA, each transfected into CHO cells, display specific binding with [3 H]-LXA₄, with Kd values of 1.7 nM [80] and 1.5 nM [58], respectively. Human ALX-transfected CHO cells were also tested for binding with other eicosanoids, including LXB₄, LTD₄, LTB₄ and PGE₂. Only LTD₄ shows competition with [3 H]-LXA₄ binding, giving a K_i of 80 nM [80].

It is of interest to note that, although ALX shares \sim 70% homology with FPR, ALX binds [3 H]-fMLP with only low affinity (Kd \sim 5 μ M) and proves to be selective for LXA₄ by three log orders of magnitude [93]. More recently, it was reported that certain peptides/proteins can also interact with ALX in *in vitro* and *in vivo* settings (Tab. 6). For examples, MHC binding peptide (a potent necrotactic peptide derived from NADH dehydrogenase subunit 1 from mitochondria) directly binds to human ALX and evokes PMN chemotaxis that is inhibited by ATL analog [89]; it also stimulates macrophage phagocytosis of PMN [64]. In addition, naturally produced cleaved form (i.e., D2D3(88–274)) of urokinase-type plasminogen activator

Table 6 - Comparison of LXs versus potential peptide ligands for human ALX

Ligand	Binding and signaling	Bioaction	EC ₅₀
LXA ₄ and ATLa	See Table 5 for details	Inhibit PMN See Table 2, 3 and 4 for details	~ 1 nM
MHC peptide [64, 89]	Displace [³ H]-LXA ₄ binding	Induce PMN chemotaxis Induce phagocytosis of apoptotic PMN	~ 1 nM
SAA [131]	Partially displace [³ H]-LXA ₄ binding Ca ²⁺ mobilization Activate ERK-1/2 and P38	Induce PMN and monocyte chemotaxis Induce IL-8 and TNF- α secretion Induce NF- κ B and IL-8 gene expression	~ 100 nM
uPAR (aa 88–274) fragment [94]	Direct [¹²⁵ I]-peptide binding Activate Hck tyrosine kinase	Induce PMN and monocyte chemotaxis	~ 5 pM
Annexin 1 and derived peptides [50]	Direct [¹²⁵ I]-peptide binding	Inhibit PMN infiltration into murine dorsal air pouches	~ 1 μ M
HIV-1 gp120 peptides (F and V3 peptides) [132]	Ca ²⁺ mobilization	Induce chemotaxis Down-regulate CCR5 and CXCR4	~ 1–10 μ M
HIV-1 gp41 peptides (T21 and N36 peptides) [133]	Ca ²⁺ mobilization	Induces chemotaxis	~ 0.1–10 μ M
Amyloid β ₄₂ [134]	Ca ²⁺ mobilization	Induces chemotaxis	~ 1 μ M
LL-37 [135]	Ca ²⁺ mobilization	Induces chemotaxis	~ 1 μ M
Hp (2–20)		Induce PMN chemotaxis	~ 0.3 μ M
<i>H. pylori</i> peptide [136]		Up-regulate integrins (Mac-1) Activate NADPH oxidase	
Prion (aa 106–126) [137]		Induces chemotaxis in monocytes	~ 25 μ M
MMK-1 [64, 89]	Evoke proton efflux Displace [³ H]-LXA ₄ binding	Induce PMN chemotaxis Evoke PMN infiltration into murine dorsal air pouches Induces phagocytosis of apoptotic PMN	~ 1 nM
WKYMVm [138]	Ca ²⁺ mobilization phosphoinositide hydrolysis	Induces chemotaxis Down-regulates CCR5 and CXCR4 Stimulates superoxide generation Enhances monocyte survival by inhibiting caspase-3 activity	~ 1 pM

(uPAR) directly binds to ALX and is a unique endogenous chemotactic agonist for ALX providing the first direct link between the fibrinolytic machinery and the inflammatory response [94]. These endogenously generated peptides evoke their bioaction *via* ALX in the subnanomolar range.

We recently reported that glucocorticoid-induced annexin 1 (ANXA1)-derived peptides (e.g., Ac2-26) are generated *in vivo* and act at the ALX to halt PMN diapedesis. These peptides specifically interact directly with recombinant human ALX, demonstrated by radioligand binding and function as well as immunoprecipitation of PMN receptors. In addition, the combination of both ATL and ANXA1-derived peptides limited PMN infiltration and reduced production of inflammatory mediators in murine dorsal air pouches [50]. These results demonstrate spatial and temporal separation in endogenous lipid and peptide anti-inflammatory circuits where both ATL and specific ANXA1-derived peptides act at ALX to down-regulate PMN recruitment to inflammatory loci.

Along these lines, additional peptides in the micromolar range can also interact with ALX in some *in vitro* model systems [95] including HIV envelope peptides (e.g., T21, N36, V3 and F peptides) and bacterial-derived peptides (e.g., Hp2-20 from *H. pylori*), as well as host-derived peptides (e.g., SAA, PrP106-126 and A β). These findings are summarized in Table 6. The functional role(s) of these peptides in human biology, pertaining to their ability to activate FPRL-1/ALX, albeit at μ M levels, remains of interest.

These new findings suggest that small peptides as well as bioactive lipids can function as ligands for the same receptor, however with different affinity and/or distinct interaction sites within the receptor and separate intracellular signaling depending on the cell type and model system. Hence, it appears likely that the intracellular protein interactions following ligand-receptor binding are different for peptide *versus* lipid ligands of this receptor because different conformations of the ligand-receptors are likely to be formed. Taken together, the finding that specific LXA₄-related structures and certain peptides interact with this receptor may reflect the need for multi-recognition and receptor redundancies in the immune system.

Signal transduction of ALX

PMN *versus* monocytes

The intracellular signaling cascade of ALX appears to be highly cell type-specific. For example, in human PMN, LXA₄ stimulates rapid lipid remodeling (within seconds) with release of arachidonic acid that is evoked *via* PTX-sensitive G proteins [16] without formation of either LT or PG. Only a modest Ca²⁺ mobilization was observed. Also, LXA₄ was reported to block intracellular generation of IP3 [15] as well as Ca²⁺ mobilization in response to other stimuli [59]. In human peripheral blood monocytes

and cultured THP-1 cells, LXA₄ triggers intracellular Ca²⁺ release and adherence to laminin [82, 96]. Thus, different intracellular signaling pathways are present in PMN *versus* monocytes despite identical receptor sequences (see Tab. 5). It is of interest that Ca²⁺ is not the second messenger for LX actions in monocytes, since LXA₄-stimulated monocyte adherence to laminin is not dependent on a LX-stimulated increase in [Ca²⁺]_i. The EC₅₀ value for LXA₄-stimulated increase in [Ca²⁺]_i is > 100 nM in monocytes, which is more than two log orders of magnitude higher than that required for LXA₄-stimulated adherence (EC₅₀ < 1 nM). In view of G-protein coupling events in monocytes, both Ca²⁺ mobilization and adherence are PTX-sensitive. This indicates that receptor coupling in monocytes and PMN is similar to this point, although there could be different PTX-sensitive G-protein subtypes that couple to the intracellular domains of the receptors and diverge downstream in the signal transduction pathways leading to chemotaxis of monocytes and inhibition of PMN.

Novel anti-inflammatory signaling (not just desensitization)

Recently, additional results from this laboratory indicated that, with PMN, ALX interaction with LX and ATL analogs regulates a newly described polyisoprenyl phosphate (PIPP) signaling pathway [97]. ALX activation reverses LTB₄-initiated polyisoprenyl phosphate remodeling, leading to accumulation of presqualene diphosphate (PSDP), a potent negative intracellular signal in PMN which inhibits recombinant PLD and superoxide anion generation. Along these lines, LXA₄ reduces peroxynitrite formation and thus can oppose peroxynitrite signaling in leukocytes [98]. Recently findings by Maderna et al. [99] demonstrated that LXs induces cytoskeleton reorganization and an increase in membrane-associated RhoA GTPase as well as RhoA activity in monocytes and macrophages *via* inhibition of cAMP, revealing a potential mechanism of LXs in promoting resolution.

In retinoic acid-differentiated HL-60 cells, LXA₄ stimulated PLD activation that is staurosporine sensitive, suggesting the involvement of PKC in signal transduction in these cells [77]. It was also demonstrated that LXA₄ blocks LTB₄ or fMLP-stimulated PMN transmigration or adhesion by regulation of β₂ integrin-dependent PMN adhesion [93]. This modulatory action is partially reversed by prior exposure to genistein, a tyrosine kinase inhibitor [30].

ALX regulate pro-inflammatory gene expression

Leukocytes

Using differential display RT-PCR, a subset of genes was identified that was selectively up-regulated upon short exposure of PMN to ATL_a. Among them, a tran-

scriptional co-repressor NAB1 identified previously as a glucocorticoid-responsive gene in hamster smooth muscle cells was further investigated and also found to be up-regulated by ATLa in murine lung vascular smooth muscle *in vivo* [100]. These findings provide evidence for rapid transcriptional induction of a cassette of genes *via* an ATLa-stimulated G protein-coupled receptor pathway.

In addition, ATLa attenuates nuclear accumulation of activator protein- α and NF- κ B in both PMN and monocytes and inhibits IL-8 mRNA expression [98].

Epithelial cells

Microarray analysis reveals that epithelial cells of wide origin (oral, pulmonary, and gastrointestinal mucosa) express bactericidal/permeability-increasing protein (BPI), an antibacterial and endotoxin-neutralizing molecule and that is transcriptionally regulated by ATL. A BPI-neutralizing anti-serum revealed that surface BPI blocks endotoxin-mediated signaling in epithelia and kills *Salmonella typhimurium* [101]. These studies identify a previously unappreciated “molecular shield” for protection of mucosal surfaces against Gram-negative bacteria and their endotoxin. Along these lines, in human enterocytes, ALX activation by LXA₄ and LX analogs diminishes *Salmonella typhimurium*-induced IL-8 transcription [102]. The reduction of IL-8 mRNA level parallels decrements in IL-8 secretion, indicating that in these cells ALX’s mechanism of action for blocking this chemokine is at the gene transcriptional level. In an effort to elucidate the mechanism by which these lipid mediators modulate cellular pro-inflammatory programs, global epithelial gene expression was surveyed using microarray analysis. ATL analog pretreatment attenuates induction of approximately 50% of *Salmonella typhimurium*-induced gene expression [70]. A major subset of genes whose induction was reduced by ATL analog pretreatment is regulated by NF- κ B, suggesting that ATL analog was influencing the activity of this transcription factor. Nanomolar concentrations of ATL analog reduced NF- κ B-mediated transcriptional activation in an ALX dependent manner and inhibited induced degradation of I κ B α .

Resident cell types

In human synovial fibroblasts, LXA₄ inhibits IL-1 β responses with reduction of IL-6 and IL-8 synthesis and prevented IL-1 β -induced MMP-3 synthesis at nanomolar concentrations [83]. Also, LXA₄ induces a two-fold increase of tissue inhibitor of metalloproteinase (TIMP)-1 and an approximately three-fold increase of TIMP-2 protein levels that is abrogated by pretreatment with LXA₄ receptor antiserum. LXA₄-induced changes of IL-6 and TIMP were accompanied by parallel changes in mRNA levels. These findings suggest that LXA₄ may be involved in a negative feed-

back loop opposing inflammatory cytokine-induced activation of synovial fibroblasts. In addition, LXA₄ induces tissue factor activity by increasing its mRNA level in EC304 cells (non-endothelial parenchymal cells) *via* a PTX-sensitive and PKC-dependent mechanism [103]. The ability of LXA₄ to induce tissue factor is an intriguing result. Its physiological role remains to be established in relation to LX generation and proximity to tissue factor releasing cells *in vivo*.

Additional sites of action for LX and ATL – CysLTs

In several tissues and cell types other than leukocytes, results from pharmacological experiments indicate that LXA₄ acts *via* interacting with a subclass of peptido-LT receptors (CysLT₁) as a partial agonist to mediate its actions [75, 104]. Along these lines, both LTC₄ and LXA₄, albeit at high concentrations (> 1 μM), induce contractions of guinea pig lung parenchyma and release of thromboxane A₂ that is sensitive to CysLT₁-receptor antagonists [105], which is not likely to be a physiologic action of LXA₄. In certain cell types, LXA₄ (in the nanomolar range) blocks LTD₄ actions, and in this regard blocks specific [³H]-LTD₄ binding to mesangial cells [104] and human umbilical vein endothelial cells (HUVEC) [58, 77]. HUVEC specifically bind [³H]-LXA₄ at a K_d of 11 nM, which can be inhibited by LTD₄ and SKF104353 [77]. Therefore, it appears that LXA₄ interacts with at least two classes of cell surface receptors, one specific for LXA₄, which is present on leukocytes and enterocytes (ALX), the other shared by LTD₄, which is present on HUVEC and mesangial cells (CysLT₁). Along these lines, an inducible CysLT₁ was recently identified and cloned from HUVEC [106].

Recombinant CysLT₁ receptor gave stereo-specific binding with both [³H]-LTD₄ and a novel labeled mimetic of ATL ([³H]-ATLa) that was displaced with LTD₄ and ATLa (~IC₅₀ 0.2–0.9 nM), and not with a biologically inactive ATL/LX isomer. In sharp contrast, LTD₄ was an ineffective competitive ligand for recombinant ALX with [³H]-ATLa. Endogenous murine CysLT₁ receptors also gave specific [³H]-ATLa binding that was displaced with essentially equal affinity by LTD₄ or ATLa. Systemic ATLa proved to be a potent inhibitor (> 50%) of CysLT₁-mediated vascular leakage in murine skin (200 μg/kg) in addition to its ability to block PMN recruitment to dorsal air-pouch (4 μg/kg). These results indicate that ATL and LTD₄ bind and compete with equal affinity at CysLT₁, providing a molecular basis for ATL serving as a local damper of both vascular CysLT₁ signals as well as ALX-regulated PMN traffic [106].

In human renal mesangial cells, LXA₄ inhibits PDGF and LTD₄-stimulated proliferation *via* regulation of PDGFRβ [107]. Also, LXA₄ stimulates MAP kinase superfamily *via* two distinct receptors: one *via* a PTX-sensitive G protein, leading to p38 activation, and the other *via* a PTX-insensitive G protein, leading to ERK activation [108]. Also, LXA₄ modulates MAP kinase activities on mesangial cells in a

PTX-insensitive manner [109], suggesting the presence of additional novel LXA₄ receptor subtypes and/or signaling pathways in these cells.

LXs and ATL exhibit unique molecular mechanism in anti-inflammation

LXA₄, ATL and their stable analogs activate ALX, which then modulates PMN responses *in vitro*, such as chemotaxis, transmigration, adhesion, degranulation, cytokine release and functions, as well as inhibit PMN recruitment in several murine models. For example, ATL analog inhibits TNF- α -initiated PMN infiltration in murine dorsal air-pouch [56] and LTB₄-induced PMN influx during dermal inflammation [58] as well as PMN-mediated second organ injury [35]. When compared to other eicosanoids of COX, LO and p450 products reported in the literature to display potential anti-inflammatory properties, LXs and ATL stand apart both in mechanism and amount range for action. For example, PGE₂ reduced the antigen response [110] and inhibited macrophage phagocytosis [111], presumably *via* increasing intracellular cAMP levels, which in turn inhibits MAPK activation by stimulating PKA-dependent phosphorylation of Raf-1 [112]. In contrast, LXA₄ does not give significant increase of cAMP levels in PMN [96]. In addition, cyclopentenone prostaglandins such as 15-deoxy- $\Delta^{12,14}$ -PGJ₂, in relatively high amounts, give anti-inflammatory action in adjuvant-induced arthritis in rats [113]. However, it appears that 15-deoxy- $\Delta^{12,14}$ -PGJ₂ acts *via* mechanisms that are independent of cell surface GPCRs [114, 115]. To date, LXA₄ and ATL are the only lipid mediators that possess anti-inflammatory and pro-resolution properties acting in the nanomolar range, since they regulate leukocyte trafficking and contribute to the early resolution.

Resolvins: The novel omega-3 PUFA derived endogenous local autacoids in anti-inflammation and pro-resolution

A recent report demonstrates that inflammatory exudates from mice treated with omega-3 polyunsaturated fatty acid (PUFA) and aspirin (ASA) generate a novel array of bioactive lipid signals (Fig. 8) [116]. Human endothelial cells with up-regulated COX-2 treated with ASA converted C20:5 omega-3 PUFA, namely eicosapentaenoic acid (EPA), to 18R-hydroxyeicosapentaenoic acid (HEPE) and 15R-HEPE. Each was used by PMN to generate separate classes of novel trihydroxy-containing mediators, including 5-series 15R-LX(5) and 5,12,18R-triHEPE. These new compounds proved to be potent inhibitors of human PMN transendothelial migration and infiltration *in vivo* (ATL analogue > 5,12,18R-triHEPE > 18R-HEPE) (Fig. 9). Acetaminophen and indomethacin also permitted 18R-HEPE and 15R-HEPE generation with recombinant COX-2 as well as omega-5 and omega-

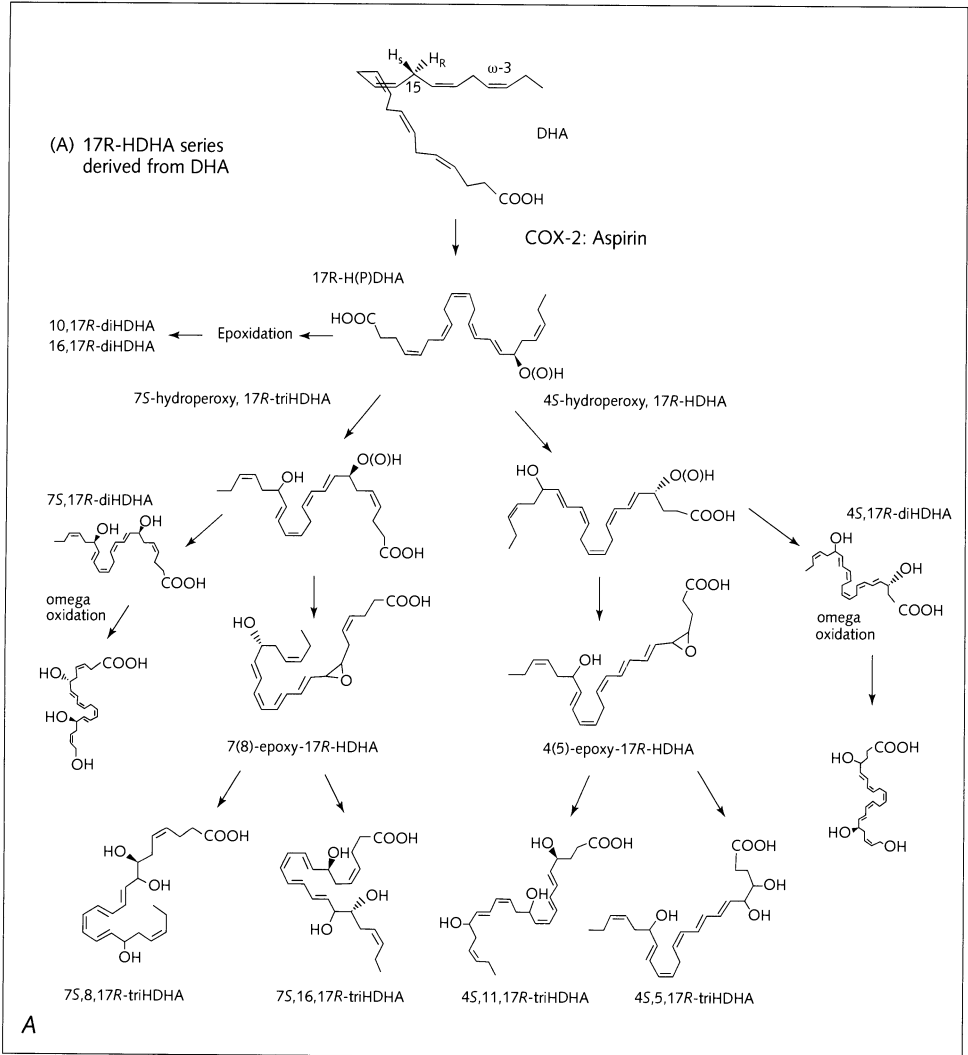
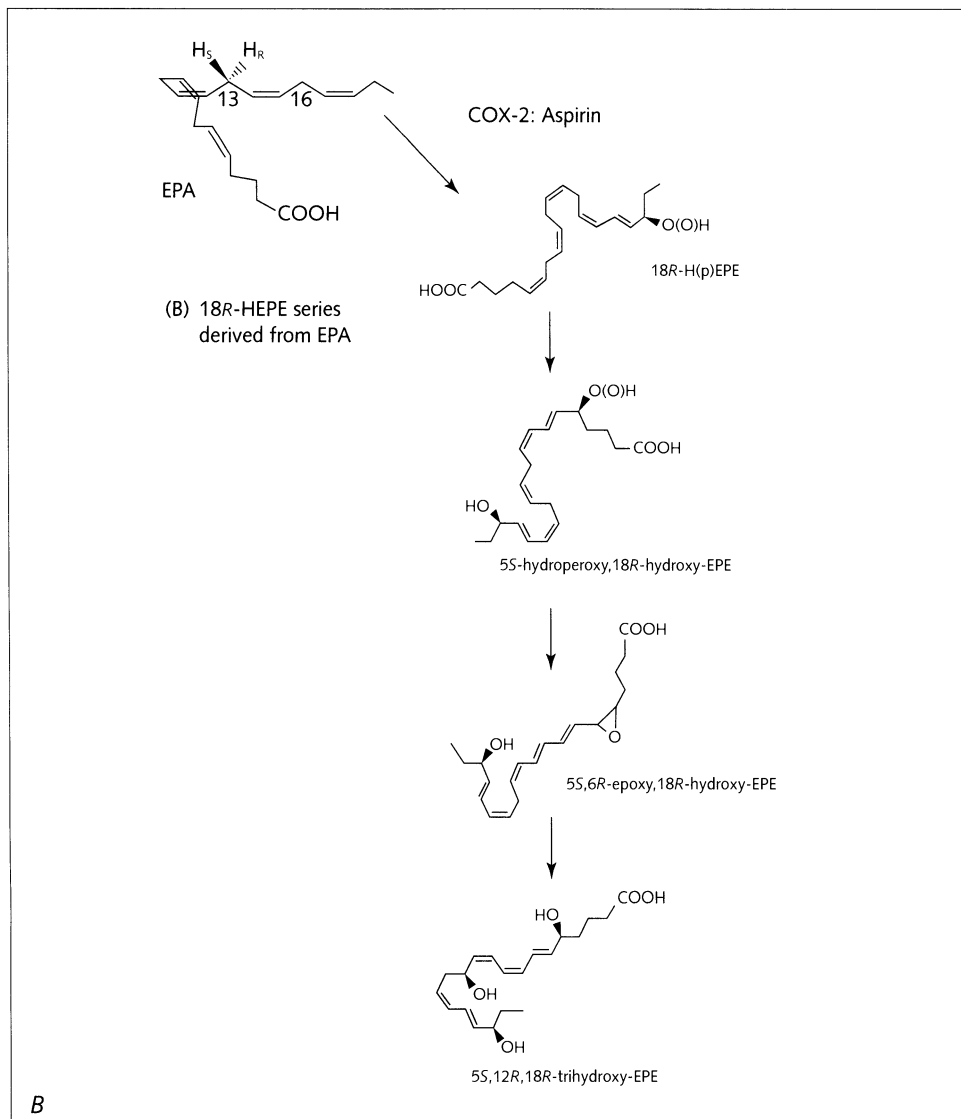


Figure 8

Proposed biosynthetic scheme for resolvins

Interactions of omega-3 polyunsaturated fatty acids (ω -3 PUFA) with aspirin (ASA)-acetylated COX-2 generate novel arrays of bioactive compounds, which inhibits PMN transmigration in vitro and inflammation in vivo. A prototypic oxygenation with DHA (panel A) and EPA (panel B) is depicted as an omega-3-containing fatty acid.

9 oxygenations of other fatty acids that act on hematologic cells. These findings establish new transcellular routes for producing arrays of bioactive lipid mediators



via COX-2-non-steroidal anti-inflammatory drug-dependent oxygenations and cell-cell interactions that impact micro-inflammation. The generation of these and related compounds provides a novel mechanism(s) for the therapeutic benefits of omega-3 dietary supplementation, which may be important in inflammation, neoplasia, and vascular diseases.

Along these lines, lipidomic analysis of exudates obtained in the resolution phase from mice treated with ASA and docosahexaenoic acid (DHA) (C22:6) produced a novel family of bioactive 17*R*-hydroxy-containing di- and tri-hydroxy-docosanoids

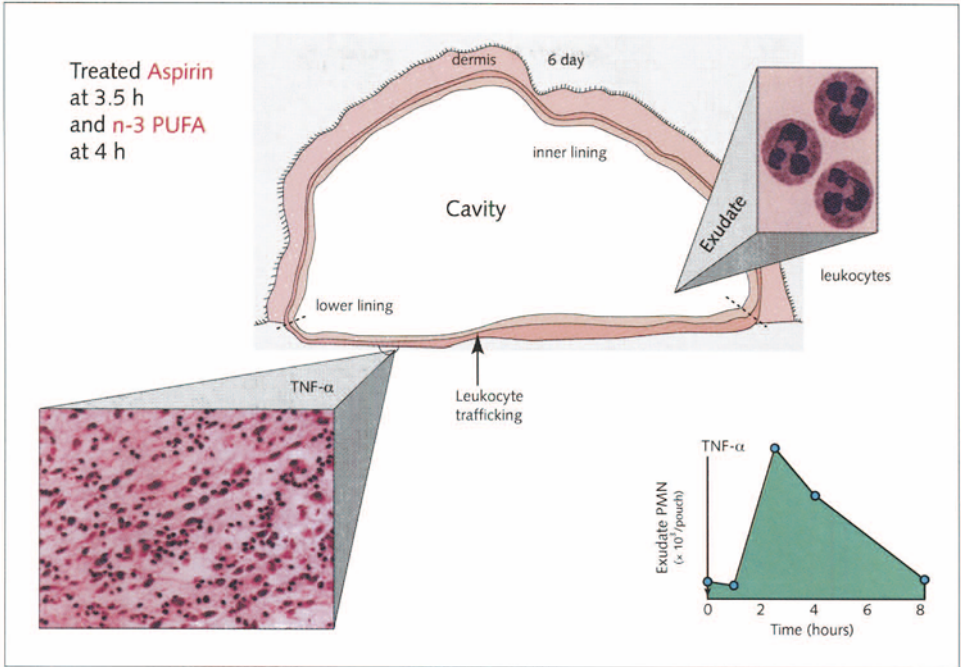


Figure 9

Murine dorsal air pouch

The 6-day murine dorsal air-pouch is characterized by the presence of a nascent lining that encloses the air cavity. TNF- α induces leukocyte infiltration, predominantly PMN, which is inhibited by iv injection of aspirin and ω -3 PUFA (25–60%).

[117]. Murine brain treated with aspirin produced endogenous 17R-hydroxydocosahexaenoic acid, as did human microglial cells. Human COX-2 converted DHA to 13-hydroxy-DHA that switched with ASA to 17R-HDHA, which also proved a major route in hypoxic endothelial cells. Human neutrophils transformed COX-2-ASA-derived 17R-hydroxy-DHA into two sets of novel di- and tri-hydroxy products; one initiated *via* oxygenation at carbon 7 and the other at carbon 4. These compounds inhibited (IC₅₀ approximately 50 pM) microglial cell cytokine expression and *in vivo* dermal inflammation and peritonitis at nanogram doses, reducing leukocytic exudates by 40–80%. These results indicate that exudates, vascular cells, leukocytes and neural cells treated with aspirin convert DHA to a novel 17R-hydroxy series of docosanoids that are potent regulators. Together, these biosynthetic pathways utilize omega-3 DHA and EPA during multicellular events in resolution to produce a family of protective compounds, i.e., resolvins, which enhance pro-resolution status.

Summary

Lipoxins are the trihydroxy-tetraene-containing eicosanoids that are primarily generated by cell-cell interactions *via* transcellular biosynthesis that serve as local endogenous anti-inflammatory mediators. These “stop signals” in inflammation and other related processes may be involved in switching the cellular response from additional PMN recruitment toward monocytes (in a non-phlogistic fashion) that could lead to resolution of the inflammatory response and/or promotion of repair and healing. Aspirin impinges on this homeostatic system and evokes the endogenous biosynthesis of the carbon 15 epimers of lipoxins, namely aspirin-triggered-lipoxins, which mimic the bioactions of native LX in several biological systems and can thus modulate in part the beneficial actions of ASA in humans. The activation of a LX biosynthetic circuit *in vivo* requires up-regulation of key enzymes by cytokines such as IL-4 and IL-13 that also control the expression of the receptor ALX [74]. Moreover, both the temporal and spatial components in LX formation and actions are important determinants in their bio-impact during an acute inflammatory reaction [118]. In this regard, generation of lipid (i.e., ATL) *versus* protein (i.e., ANXA1) mediators during the host inflammatory response displays different time courses. This temporal difference suggests that ALX/FPRL1 could regulate PMN by interacting with each class of ligands within specific phases of the inflammatory response.

LXA₄ elicits biological actions *via* at least two main classes of receptor systems known to date: (1) ALX on leukocytes and enterocytes, and (2) a shared CysLT1 subtype on endothelial and mesangial cells.

ALX belongs to the classical G-protein-coupled receptors (GPCR) and was identified in mammalian tissues and characterized using direct evidence obtained with specific [³H]-LXA₄ binding and activation of functional responses with LXA₄. ALX is the first cloned lipoxygenase-derived eicosanoid receptor. ALX and BLT are more akin to chemokine receptors in their deduced amino acid sequences than the currently known prostanoid receptors. The signaling pathways and bioactions of ALX are cell type-specific. In agreement with *in vitro* results, ALX agonists, namely LXA₄ and 15-epi-LXA₄ as well as their stable analogs, are topically active in inhibiting PMN infiltration and vascular permeability during murine dermal inflammation. In addition, it appears that LX also display organ-specific actions in addition to host defense and immune roles such as in the eye, kidney, lung, oral and GI tract and within bone marrow progenitors, possibly involving stem cells. The development of these relatively few synthetic stable analogs has already provided valuable tools to evaluate the biological roles, significance and pharmacological actions of ALX as well as provided a novel means to selective therapies for inflammatory diseases.

The relationship between LX generation and current NSAID therapies is more intertwined than currently appreciated [119] in that aspirin inhibits COX-1 and converts COX-2 into an ASA-triggered lipid mediator-generating system that produces an array of novel endogenous local autacoids from dietary omega-3 PUFA;

some of which display potent anti-inflammatory or anti-neutrophil recruitment activity [116, 117] as well as impinge on the role of these compounds in resolution and thus termed resolvins. Hence, it is not surprising that others have recently found a protective action for COX-2 in cardiovascular disease [120]. Together with the LXs and 15-epi-LXs, the identification of these novel endogenous anti-inflammatory lipid mediators [116] gives us new avenues of approach in considering therapeutics for inflammation, cardiovascular diseases and cancer.

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Metabolism and physiological significance of anandamide and 2-arachidonoylglycerol, endogenous cannabinoid receptor ligands

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Introduction

Arachidonic acid is known to be metabolized into a number of bioactive eicosanoids such as prostaglandins, thromboxanes, leukotrienes, lipoxins and mono- and dihydroxyeicosatetraenoic acids. It is well known that these bioactive eicosanoids are involved in diverse physiological and pathophysiological processes in mammalian tissues. In the last decade of the 20th century, two remarkable derivatives of arachidonic acid, i.e., N-arachidonylethanolamine (anandamide) and 2-arachidonoylglycerol (2-AG) (Fig. 1) were reported to be new members of the bioactive lipids. Anandamide and 2-AG have unique structural characteristic in that they contain an intact arachidonoyl moiety in their molecules, thus differing from other eicosanoids. Both anandamide and 2-AG have been shown to act as endogenous cannabinoid receptor ligands. In this review, we focused on anandamide and 2-AG and described the metabolism and possible physiological significance of these molecules in mammalian tissues and cells including inflammatory cells and immune competent cells.

Cannabinoid receptors

Marijuana has been used as a traditional medicine and a pleasure-inducing drug for thousands of years around the world, especially in Asia. In the 1960s, Gaoni and Mechoulam [1] demonstrated that Δ^9 -tetrahydrocannabinol (Δ^9 -THC) (Fig. 1) is the major psychoactive ingredient of marijuana. Δ^9 -THC is known to exert a variety of pharmacological effects on experimental animals and humans. For example, the administration of Δ^9 -THC induces reduced spontaneous motor activity, immobility, analgesia, heightened sensory awareness, euphoria, hypothermia and impairment of short-term memory [2]. Δ^9 -THC is also known to exert profound effects in various biological systems other than in the nervous system such as the suppression of immune responses. The mechanisms of these actions of Δ^9 -THC, however, remained

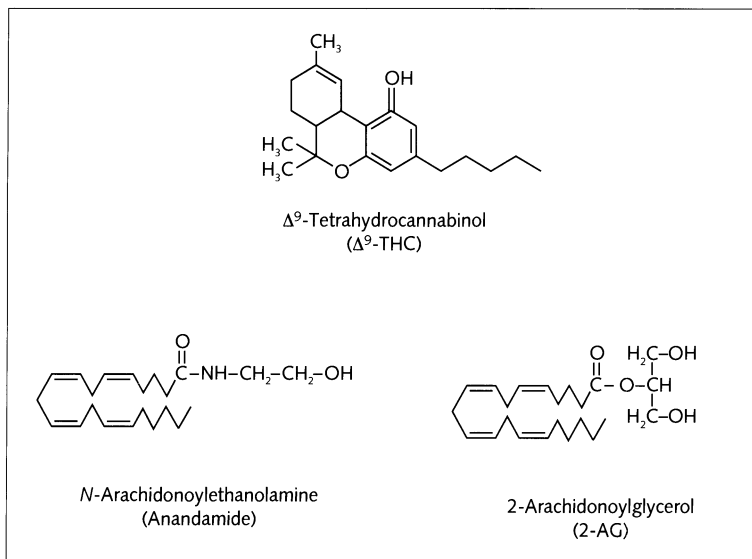


Figure 1
 Chemical structures of Δ^9 -tetrahydrocannabinol (Δ^9 -THC), N-arachidonylethanolamine (anandamide) and 2-arachidonoylglycerol (2-AG)

unclear until recently. The occurrence of specific binding site(s) for cannabinoids has been postulated based on the observation that (-)- Δ^9 -THC exhibited potent pharmacological activities whereas its stereoisomer (+)- Δ^9 -THC was far less potent. However, binding experiments of radiolabeled cannabinoids were unsuccessful until the late 1980s due to their highly lipophilic properties.

In 1988, Devane et al. [3] succeeded in showing the occurrence of specific binding sites for cannabinoids in rat brain synaptosomes using a radiolabeled synthetic cannabinoid, [3 H]CP55940. The K_d was 133 pM and the B_{max} was 1.85 pmol/mg protein. Finally, Matsuda et al. [4] cloned a cDNA encoding a cannabinoid receptor (CB1 receptor) from a rat brain cDNA library in 1990. The CB1 receptor is present in various mammalian tissues, especially in the nervous tissues, and is assumed to be involved in the attenuation of neurotransmission [5]. The CB1 receptor is a seven-transmembrane, G protein-coupled receptor, and contains 472 (human) or 473 (rat) amino acids. It is noteworthy that the whole-brain cannabinoid receptor density is similar to the whole-brain densities of receptors for glutamate and GABA [6]. Indeed, the CB1 receptor is one of the most abundant G protein-coupled receptors expressed in the brain. Among the various brain regions, the CB1 receptor is especially abundant in the substantia nigra, globus pallidus, molecular layer of the cerebellum, hippocampus and cerebral cortex. The CB1 receptor is assumed to be involved in the regulation of cognition, memory and motor activity [5].

In 1993, Munro et al. [7] cloned a cDNA encoding another type of cannabinoid receptor (CB2 receptor) from an HL-60 cell cDNA library. The CB2 receptor is also a seven-transmembrane, G protein-coupled receptor, and consists of 360 amino acid residues. The CB1 receptor and the CB2 receptor share a 44% overall identity (68% identity for the transmembrane domains). The CB2 receptor is abundantly present in various lymphoid tissues such as the marginal zone of the spleen, the cortex of the lymph nodes and the nodular corona of Peyer's patches [6], and is expressed in various types of leukocytes with a rank order of B lymphocytes > natural killer cells > monocytes/macrophages > polymorphonuclear leukocytes > T8 lymphocytes > T4 lymphocytes [8–10]. The CB2 receptor is assumed to participate in the regulation of inflammatory reactions and immune responses [6, 8–10], although the details of the physiological functions of the CB2 receptor still remain to be clarified.

The mechanisms of the diverse actions of the natural and synthetic cannabinoids have not yet been fully elucidated. However, it has been assumed that various cannabinoids including Δ^9 -THC exert their biological activities mainly by acting on these cannabinoid receptors (CB1 and CB2) although there remains the possibility that non-CB1 and non-CB2 binding sites for the cannabinoids exist in mammalian tissues.

Identification of endogenous cannabinoid receptor ligands

The discovery of the specific receptors for cannabinoids prompted the search for endogenous ligand(s). In 1992, Devane et al. [11] isolated anandamide from pig brain as the first endogenous cannabinoid receptor ligand. They demonstrated that anandamide binds to the brain cannabinoid receptor ($K_i = 52$ nM) and inhibits the mouse twitch response. Anandamide also induces the inhibition of the voltage-gated Ca^{2+} channels, the activation of an inwardly rectifying K^+ current, the stimulation of [^{35}S]GTP γ S binding to G proteins, the activation of mitogen-activated protein kinase (MAP kinase) and the neural form of focal adhesion kinase, the inhibition of neurotransmitter release, the inhibition of long-term potentiation in hippocampal slices, the impairment of memory, reduced spontaneous motor activities, immobility, hypothermia, analgesia, vasodilation, hypotension, bradycardia, the growth inhibition of human breast and prostate cancer cells and the inhibition of the sperm acrosome reaction [5, 12–16]. It should be noted, however, that anandamide acted as a partial agonist in some cases [16]. It is curious that an endogenous natural ligand acts as a partial agonist at its own receptor; natural ligands usually act as full agonists. Therefore, it seems unlikely that anandamide acts as an endogenous cannabinoid receptor agonist with significant physiological importance, although this still remains a controversial subject.

In addition to acting as an endogenous cannabinoid receptor ligand, anandamide was shown to act as an endogenous ligand for an ion channel-type vanil-

loid receptor (VR1 receptor). Moreover, anandamide can also bind to several other types of ion channels. Therefore, it seems possible that some of the anandamide effects mentioned above are mediated through receptors or binding sites other than the cannabinoid receptors. It is necessary to keep this in mind when interpreting the experimental results concerning the biological activities of anandamide.

On the other hand, in the mid-1990s, we isolated 2-AG, a unique molecular species of monoacylglycerol, from rat brain, and found that it acts as an endogenous cannabinoid receptor ligand [17, 18]. Independently and concurrently, Mechoulam et al. [19] also isolated 2-AG from the canine gut. It has been shown that 2-AG binds to the cannabinoid receptors (CB1 and CB2), and exhibits several cannabimimetic activities *in vitro* and *in vivo* [5, 12–16, 18–21]. Despite its possible physiological significance, however, much less attention has been paid to 2-AG compared with anandamide until recently. Indeed, the physiological significance of 2-AG has very often been overlooked. Unequivocally, 2-AG is a quite noticeable molecule from a variety of viewpoints. We have focused on 2-AG and intensively investigated the biological activities and physiological roles of 2-AG since 1995.

In 1996, we found by chance that 2-AG induces a rapid transient increase in the intracellular free Ca^{2+} concentrations ($[\text{Ca}^{2+}]_i$) in neuroblastoma x glioma hybrid NG108-15 cells expressing the CB1 receptor [22–24]. We confirmed that the response induced by 2-AG was blocked by pretreatment of the cells with SR141716A, a cannabinoid CB1 receptor-specific antagonist, indicating that the response induced by 2-AG was mediated through the CB1 receptor [22, 24]. 2-AG-induced Ca^{2+} transients were also observed in promyelocytic HL-60 cells expressing the CB2 receptor [25]. We confirmed that the response was abolished by pretreatment of the cells with SR144528, a cannabinoid CB2 receptor-specific antagonist, indicating that the response induced by 2-AG was mediated through the CB2 receptor [25]. Free arachidonic acid failed to exhibit any agonistic activity in either case, indicating that arachidonic acid that may be generated from 2-AG during incubation is not involved in the response. We also confirmed that the pretreatment of the cells with indomethacin, a cyclo-oxygenase inhibitor, or nordihydroguaiaretic acid, a lipoxygenase inhibitor, did not affect the response, suggesting that arachidonic acid metabolites are not involved.

We then examined the mechanism underlying the rapid transient increase in $[\text{Ca}^{2+}]_i$ induced by 2-AG. We found that pretreatment of the cells with pertussis toxin abolished the response induced by 2-AG, indicating that Gi/Go is involved in the response. We also found that pretreatment of the cells with U73122, a phospholipase C inhibitor abrogated the response induced by 2-AG, whereas pretreatment of the cells with U73343, an inactive analog of U73122, did not affect the response [23], suggesting that phospholipase C is involved in the response induced by 2-AG. We assumed that the 2-AG-induced rapid transient increase in $[\text{Ca}^{2+}]_i$ involves:

- 1) 2-AG binding to the cannabinoid receptors (CB1 and CB2) followed by
- 2) activation of Gi/Go, and
- 3) the liberated $\beta\gamma$ subunit of Gi/Go then stimulates phospholipase C β to enhance the production of inositol 1,4,5-trisphosphate, thereby increasing $[Ca^{2+}]_i$.

We next investigated in detail the structure-activity relationship of 2-AG and other cannabinoid receptor ligands using NG108-15 cells (for the CB1 receptor) and HL-60 cells (for the CB2 receptor). We found that an ether-linked analog of 2-AG (2-AG ether) possesses substantial biological activity, indicating that the structure of 2-AG itself, but not its metabolite, is actually recognized by the receptor molecules (CB1 and CB2) [24, 25]. In contrast to 2-AG, anandamide was found to act as a weak partial agonist toward either the CB1 receptor or the CB2 receptor. The activity of Δ^9 -THC, a major psychoactive constituent of marijuana, was also low [23, 25]. We further examined the activities of various 2-AG analogs as well as classical and synthetic cannabinoids. The activities of the monoacylglycerols containing various saturated, monoenoic and dienoic fatty acids were almost inactive. 1(3)-AG, the positional isomers of 2-AG, exhibited appreciable agonistic activities, yet their activities were much lower than those of 2-AG. Among the various naturally occurring analogs, 2-AG acted as the most efficacious agonist toward both types of cannabinoid receptors (CB1 and CB2) [22–25]. This has also been confirmed by several investigators [26–28]. We proposed that 2-AG, but not anandamide, is the intrinsic natural ligand for the cannabinoid receptors (CB1 and CB2) and both receptors are originally and primarily 2-AG receptors [20, 21, 23–25].

Recently, Hanus et al. [29] reported that 2-AG ether is present in pig brain. They described that 2-AG ether is the third endogenous cannabinoid receptor ligand (they called it “noladin ether”). Fezza et al. [30] also reported that a small amount of 2-AG ether is present in rat brain. We examined in detail whether 2-AG ether is actually present in the brain. However, we did not detect any appreciable amounts of the 2-AG ether in the brains of various mammalian species such as mouse, rat, hamster, guinea pig, and pig (<0.2 pmol/g tissue, if at all present) (S. Oka and T. Sugiura, unpublished results). The ether bond is known to be located exclusively at the 1-position of the glycerol backbone in mammalian tissues [31–33]. It is questionable whether 2-AG ether is a naturally-occurring molecule and acts as an endogenous ligand for the cannabinoid receptors.

Tissue levels of endogenous cannabinoid receptor ligands

Previously, Schmid and co-workers [34] estimated the levels of the N-acylethanolamines including anandamide by GC/MS. They detected anandamide in the brains of several animal species. The levels of anandamide in the sheep brain were negligible, whereas low levels were found in the pig and cow brain (17 and

10 pmol/g tissue, respectively). These values were, however, significantly lower than the levels of anandamide in the pig brain (370 pmol/g tissue) reported by Devane et al. [11]. The exact reason for this difference is uncertain. However, it is possible that a considerable amount of anandamide was generated during the postmortem period in the latter case. Schmid and co-workers [34] demonstrated that the levels of anandamide in isolated pig brain were dramatically augmented when kept at ambient temperature. The generation of anandamide in the brain during the postmortem period was also reported by Kempe et al. [35] and Felder et al. [36]. We detected a small amount of anandamide in fresh rat brain (4.3 pmol/g tissue), which accounts for only 0.7% of the total N-acylethanolamine [37]. The predominant species of N-acylethanolamine detected in the rat brain were the N-16:0 and N-18:0 species.

The levels of anandamide in the brains of various mammalian species have also been studied by a number of investigators (reviewed in [21]). The levels of anandamide in the rat brain were 3.37–15 pmol/g tissue and those in mouse brain were 10–15 pmol/g tissue. The level of anandamide was variable depending on the physiological and pathophysiological conditions of the brains. Di Marzo et al. [38] reported that the levels of anandamide in the hypothalamus markedly decreased following the administration of leptin. On the other hand, Giuffrida et al. [39] reported that D2-like dopamine receptor activation evokes the release of anandamide in the dorsal striatum of freely moving rats. Recently, Baker et al. [40] reported that the levels of anandamide in the brain and spinal cord were elevated in spastic mice with chronic relapsing experimental allergic encephalomyelitis.

Anandamide was detected in various peripheral tissues as well (reviewed in [21]), such as the bovine retina (64 pmol/g tissue), the human heart (10 pmol/g tissue), human spleen (15 pmol/g tissue), rat heart (21.2–126 pmol/g tissue), rat liver (19.7–77.1 pmol/g tissue), rat kidney (8–164 pmol/g tissue, 0.32–0.35 pmol/ μ mol lipid P), rat spleen (6 pmol/g tissue, 0.34 pmol/ μ mol lipid P), rat thymus (40.6–137 pmol/g tissue), rat testis (2.9–43.5 pmol/g tissue, 0.25–0.31 pmol/ μ mol P), mouse uterus (2215–20982 pmol/g tissue), rat skin (23 pmol/g tissue, 49 pmol/g tissue), and rat paw skin (0.69 pmol/mg of extracted lipids). Schmid et al. [41] reported that mouse peritoneal macrophages contain a small amount of anandamide (0.25 pmol/ μ mol lipid P). Anandamide was also detected in rat plasma collected by decapitation (144 pmol/ml) or by cardiac puncture (3.1 pmol/ml) and in the sera from normal donors (4 pmol/ml) and patients with endotoxin shock (18 pmol/ml) (reviewed in [21]). On the other hand, Yang et al. [42] described that the levels of anandamide in the rat brain, spleen, testis, liver, lung and heart were below the levels of quantification achievable (<0.1 pmol/mg protein).

The available information as to the tissue levels of 2-AG is still limited. Mechoulam et al. [19] detected 2-AG in the canine gut, although they did not quantify it. We detected 3.25 nmol/g tissue of arachidonoylglycerols (2-AG plus 1(3)-AG) [18] and 3.36 nmol/g tissue of 2-AG in rat brain [43]. The level of 2-AG in the brains obtained from rats sacrificed in liquid nitrogen was 0.23 nmol/g tissue [44].

Stella et al. [45] also detected 4.0 nmol/g tissue of 2-AG in the rat brain. Bisogno et al. [46] examined the levels of 2-AG in various brain regions. 2-AG was also detected in the peripheral nervous system. Huang et al. [47] reported that 2-AG is present in the rat sciatic nerve (0.052 nmol/g tissue), lumbar spinal cord (0.432 nmol/g tissue) and lumbar dorsal root ganglion (0.370 nmol/g tissue). 2-AG was also detected in the rat retina (2.97 nmol/g tissue) and bovine retina (1.63 nmol/g tissue). We further estimated the levels of 2-AG in several rat tissues [43]. The levels of 2-AG in the rat liver, spleen, lung, kidney and plasma were 1.15 nmol/g tissue, 1.17 nmol/g tissue, 0.78 nmol/g tissue, 0.98 nmol/g tissue and 0.012 nmol/ml, respectively. The tissue levels of 2-AG in rats have also been reported by Schmid and co-workers [48]: 13.04-6.19 pmol/ μ mol lipid P (kidney), 3.21-3.05 pmol/ μ mol lipid P (testis), 10.94 pmol/ μ mol lipid P (heart), 29.03 pmol/ μ mol lipid P (spleen) and 5.05 pmol/ μ mol lipid P (liver). 2-AG was also detected in the sera from normal donors (10 pmol/ml) and patients with endotoxin shock (30 pmol/ml) and in human milk (0.33 μ g/ml) and rat paw skin (51.1 pmol/mg of extracted lipids) (reviewed in [21]).

Noticeably, the levels of 2-AG in the brain changed following several treatments of experimental animals. We found that the amount of 2-AG in rat brain was significantly augmented following decapitation [49]. Di Marzo et al. [50] demonstrated that the levels of 2-AG in the globus pallidus were augmented in reserpine-treated rats. Baker et al. [40] demonstrated that the levels of 2-AG in the brain and spinal cord were elevated in spastic mice with chronic relapsing experimental allergic encephalomyelitis. Interestingly, the levels of 2-AG as well as anandamide in the rat hypothalamus were significantly reduced in mice injected with leptin compared with the control [38], suggesting that these endogenous cannabinoid receptor ligands are involved in the regulation of appetite.

Biosynthesis and degradation of endogenous cannabinoid receptor ligands

Evidence is gradually accumulating that anandamide is produced in relatively small amounts in a variety of tissues and cells upon stimulation. Di Marzo et al. [51] demonstrated that rat brain neurons generated anandamide when stimulated with ionomycin or several membrane-depolarizing agents such as kainate, high K^+ and 4-aminopyridine. Di Marzo et al. also demonstrated that anandamide was produced in ionomycin-treated J774 macrophages [52, 53], ionomycin-treated RBL-2H3 cells [53] and phospholipase D-treated N18TG2 neuroblastoma cells [52]. Hansen and co-workers [54] investigated whether N-acylethanolamine is produced in glutamate- or A23187-stimulated mouse cortical neurons in culture. They showed that the generation of N-acylethanolamine takes place in stimulated cells prelabeled with [3 H] ethanolamine, although they could not detect the generation of anandamide when the cells were prelabeled with [3 H] arachidonic acid. Later, they detected the formation of [14 C] anandamide in NaN_3 -treated neurons [55]. The generation of anan-

damide was also observed in ionomycin-stimulated rat macrophages [56], LPS-, platelet-activating factor- and Δ^9 -THC-stimulated RAW264.7 mouse macrophages [57], veratridine-, 4-aminopyridine- and A23187-stimulated SK-N-SH neuroblastoma cells [58] and in the periaqueductal gray region of the rat brain following electrical stimulation and the subcutaneous injection of formalin [59]. On the other hand, we found that the level of anandamide was augmented in inflamed rat testis, although the augmentation of the levels of saturated and monoenoic species was much more prominent [60]. Kuwae et al. [61] also demonstrated the generation of anandamide as well as other molecular species of N-acylethanolamine in mouse peritoneal macrophages in culture supplemented with ethanolamine.

Anandamide can be enzymatically formed *via* two independent synthetic pathways (Fig. 2) (reviewed in [21]). One is the direct N-acylation of ethanolamine and the other is transacylase-phosphodiesterase-mediated synthesis (Schmid's pathway). The first pathway is catalyzed by the reverse reaction of an anandamide amidohydrolase/fatty acid amide hydrolase [62–64], suggesting that the formation of anandamide *via* this pathway may not be physiologically relevant, yet there remains the possibility that a significant amount of anandamide can be formed *via* this pathway if high concentrations of arachidonic acid and ethanolamine are co-localized at some sites within the cell. The second pathway (Schmid's pathway) is the formation of anandamide from pre-existing N-arachidonoyl phosphatidylethanolamine (PE) through the action of a phosphodiesterase. This enzyme reaction has been assumed to be the major synthetic route for various N-acylethanolamines such as N-palmitoyl- and N-stearoyl-ethanolamine [65]. Several investigators have demonstrated that anandamide can be formed from N-arachidonoyl PE through the action of a phosphodiesterase [37, 51]. This is probably the major synthetic pathway for anandamide in various mammalian tissues. Nevertheless, this pathway does not appear to be able to generate a large amount of anandamide, because the tissue level of N-arachidonoyl PE is usually very low. The reason for this is that N-arachidonoyl PE is synthesized from PE and arachidonic acid, esterified at the 1-position of the glycerophospholipids through the action of a transacylase [37, 66]. It should be noted that the level of arachidonic acid esterified at the 1-position of glycerophospholipids is usually very low. The absence of efficient synthetic pathways for anandamide coincides with the observation that the tissue levels of anandamide are generally low (in the order of pmol/g tissue) except in a few cases [21].

The degradation of anandamide is catalyzed by two separate types of anandamide amidohydrolase/fatty acid amide hydrolases; the optimal pH of one isoform is 8.5–10 [67] and the optimal pH of the other is 5 [68]. The gene encoding the first enzyme protein has already been cloned by Cravatt et al. [69]. The second enzyme identified and purified by Ueda et al. [68] is less sensitive to several inhibitors than the first anandamide amide hydrolase/fatty acid amide hydrolase having the optimal pH of 8.5–9 and efficiently degraded N-palmitoylethanolamine. The role allotment of these two types of anandamide amidohydrolase/fatty acid amide hydrolase

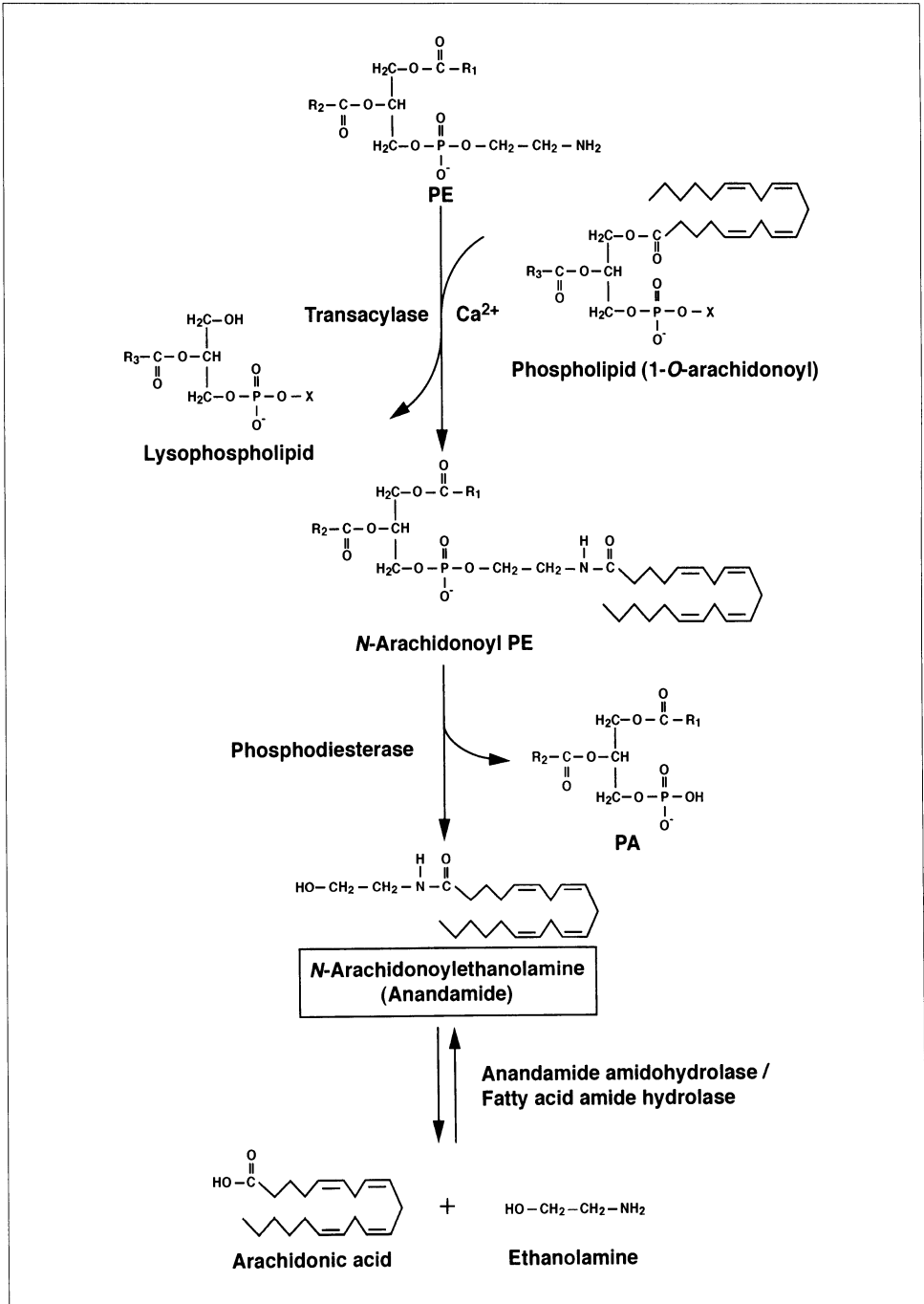


Figure 2
Biosynthesis and degradation of anandamide

remains to be clarified. The anandamide amidohydrolase/fatty acid amide hydrolase is capable of producing anandamide if the concentrations of arachidonic acid and ethanolamine are high enough as already described.

In contrast to anandamide, 2-AG is present in relatively large amounts in various mammalian tissues (the order of nmol/g tissue) [20, 21]. Noticeably, the levels of 2-AG were rapidly elevated in tissues and cells following stimulation [20, 21]. In addition, it is noteworthy that a significant portion of newly formed 2-AG can be released from stimulated cells [20, 21]. These characteristics appear to be favorable in acting as an intercellular mediator derived from stimulated cells.

The first description in the literature concerning the generation of arachidonoylglycerols in stimulated tissues and cells was that in thrombin-stimulated platelets reported by Prescott and Majerus in 1983 [70]. Later, the generation of arachidonoylglycerols in platelet-derived growth factor-stimulated Swiss 3T3 cells [71] and in bradykinin-stimulated rat dorsal ganglion neurons [72] was also demonstrated. However, at that time, the physiological significance of 2-AG as an endogenous cannabinoid receptor ligand was unknown. The generation of 2-AG as an endogenous cannabinoid receptor ligand was first described in ionomycin-stimulated N18TG2 cells [73], and in electrically stimulated rat hippocampal slices and ionomycin-stimulated neurons [45]. We also investigated the generation of 2-AG and found that the rapid generation of 2-AG occurs in the rat brain homogenate during incubation in the presence of Ca^{2+} (T. Sugiura and S. Oka, unpublished results) and in thrombin- or A23187-stimulated human umbilical vein endothelial cells [74]. Furthermore, we recently found that the levels of 2-AG in the rat brain were dramatically elevated (six-fold) following the intraperitoneal injection of picrotoxinin, a central nervous system stimulant [44]. In this case, the generation of monoacylglycerols other than arachidonoylglycerols was negligible or very small. The generation of 2-AG was also observed in the carbachol-treated rat aorta [75] and ethanol-treated cerebellar granule neurons in culture [76]. Several types of blood cells or inflammatory cells produce 2-AG upon stimulation such as in LPS-stimulated rat platelets [77], LPS-stimulated rat macrophages and LPS- or ionomycin-stimulated J774 macrophage-like cells [78] and platelet-activating factor-stimulated human platelets and P388D1 macrophage-like cells [79].

There are several possible metabolic routes for the generation of 2-AG in mammalian tissues. Previously, we described that 2-AG can be formed from arachidonic acid-enriched membrane phospholipids, such as inositol phospholipids, through the combined actions of phospholipase C and diacylglycerol lipase or through the combined actions of phospholipase A₁ and phospholipase C (Fig. 3) [18, 20, 21]. The first pathway, involving the rapid hydrolysis of inositol phospholipids by phospholipase C and subsequent hydrolysis of the resultant diacylglycerol by diacylglycerol lipase, was described two decades ago by Prescott and Majerus as a degradation pathway for arachidonic acid-containing diacylglycerol in platelets [70]. Stella et al. [45] demonstrated that these enzyme activities are involved in the ionomycin-

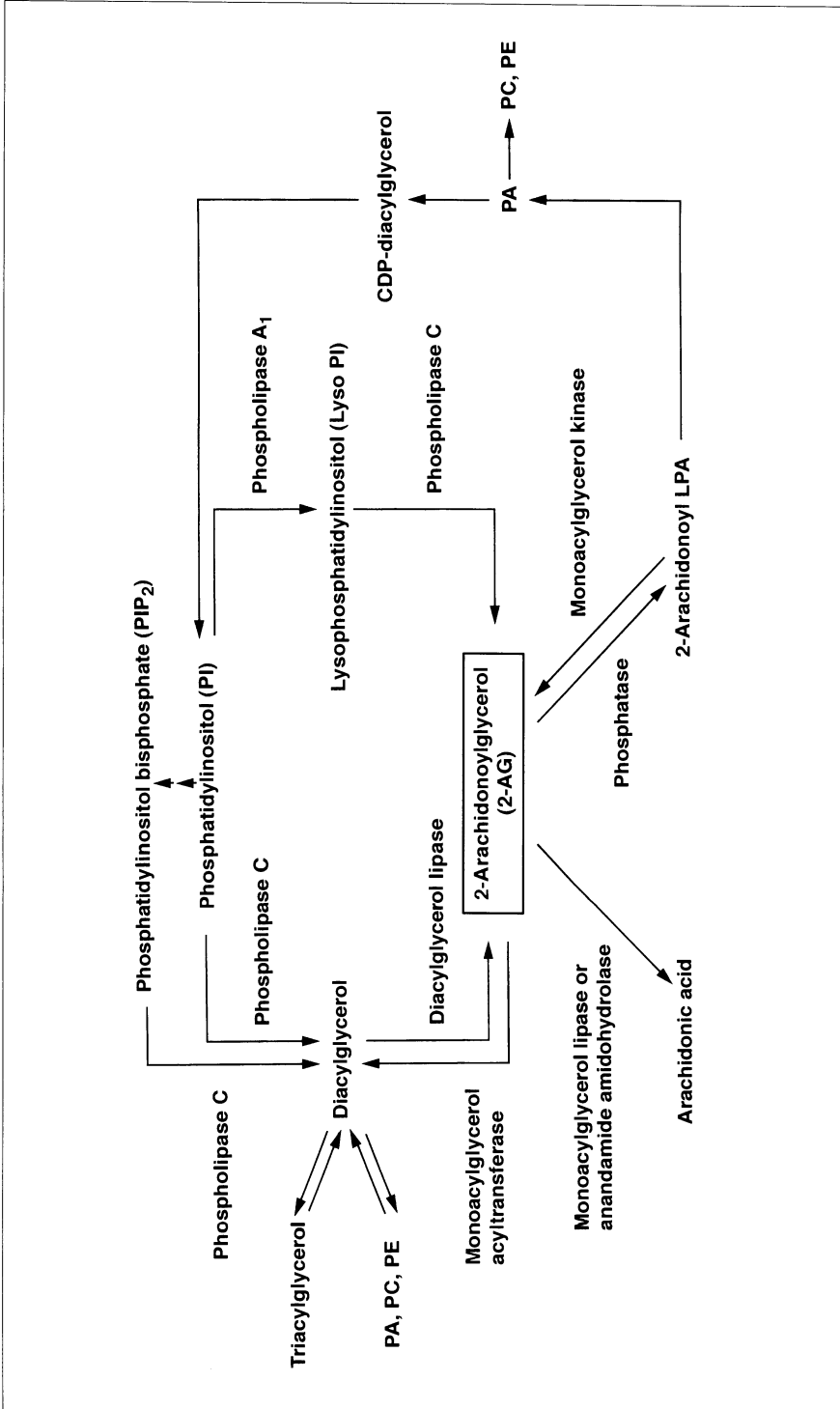


Figure 3
Biosynthesis and degradation of 2-AG

induced generation of 2-AG in cultured neurons using metabolic inhibitors. Recently, we confirmed that this pathway is important for the depolarization-induced generation of 2-AG in rat brain synaptosomes (T. Sugiura and S. Oka, unpublished results).

The second pathway involves the hydrolysis of phosphatidylinositol (PI) by phospholipase A₁ and the hydrolysis of the resultant lysoPI by a specific phospholipase C. Noticeably, lysoPI-specific phospholipase C is distinct from the various types of phospholipase Cs which act on other inositol phospholipids, and is localized in the synaptosomes [80]. Therefore, it is possible that this unique enzyme may also be involved in the generation of 2-AG in synapses. In addition to these two pathways, there are several possible routes for the generation of 2-AG, such as the generation from 2-arachidonoyl LPA [81] or 2-arachidonoyl PA [82]. We obtained evidence that a substantial amount of 2-arachidonoyl LPA is present in rat brain and that the formation of 2-AG from 2-arachidonoyl LPA takes place in the rat brain homogenate [81]. The biosynthetic pathways for 2-AG appear to differ, depending on the types of tissues and cells, and the types of stimuli. A full understanding of the mechanism and regulation of the biosynthesis of 2-AG awaits further investigations.

As for the degradation of 2-AG, 2-AG is metabolized by monoacylglycerol lipase similar to other monoacylglycerols [83]. In addition to this, several investigators have demonstrated that anandamide amidohydrolase/fatty acid amide hydrolase is also able to metabolize 2-AG [84, 85]. A part of 2-AG may be degraded by anandamide amidohydrolase/fatty acid amide hydrolase in some cases.

Physiological roles of endogenous cannabinoid receptor ligands in the nervous system

Anandamide was the first endogenous cannabinoid receptor ligand to be found. To date, it has been established that anandamide possesses strong binding activity toward the cannabinoid receptors and exhibits a variety of cannabimimetic activities *in vitro* and *in vivo* [5, 12–16]. However, evidence has gradually accumulated recently against the physiological significance of anandamide as the natural ligand for the cannabinoid receptors:

- 1) The levels of anandamide in tissues are usually low except in a few cases.
- 2) No selective and efficient synthetic pathway for anandamide has hitherto been found.
- 3) Anandamide, as well as Δ^9 -THC, acted as a partial agonist at least in some cases.

Among them, the final issue is particularly important, because it is unusual that an endogenous natural ligand acts as a partial agonist at its own receptor. Hence, it is questionable whether anandamide actually serves as an endogenous cannabinoid

receptor ligand of great physiological significance in living animals. Recently, Zygmunt et al. [86] demonstrated that anandamide is a potent agonist of the vanilloid receptor. Anandamide is also known to regulate the background K⁺ channel TASK-1 and several other ion channels [21, 87, 88]. It is possible that the physiological significance of anandamide may exist in its being an endogenous ligand of the receptor(s) other than the cannabinoid receptors or as a modulator of ion channels. Alternatively, there may exist some other unknown physiological functions of anandamide. In any case, further studies are necessary to clarify the exact physiological significance and functions of anandamide.

2-AG was the second endogenous cannabinoid receptor ligand to be discovered and was found to act as a full agonist at the cannabinoid CB1 receptor abundantly expressed in the nervous system. Noticeably, 2-AG can be rapidly and selectively produced from a variety of cells upon stimulation. The tissue levels of 2-AG are usually markedly higher than those of anandamide. In contrast to anandamide, 2-AG does not bind to the vanilloid receptor. Based on these observations, we have proposed that 2-AG is the intrinsic natural ligand for the cannabinoid CB1 receptor, and the cannabinoid CB1 receptor is originally and primarily a 2-AG receptor [20, 21, 23–25].

2-AG is present in relatively high amounts in mammalian brains; it seems unlikely that 2-AG induces psychedelic reactions such as heightened sensory awareness, dissociation of ideas, errors in judgment of time and space and hallucinations in living animals. Recently, we obtained evidence that a substantial amount of 2-AG was generated and released from depolarized rat brain synaptosomes (T. Sugiura and S. Oka, unpublished results). We also found that the treatment of the synaptosomes with SR141716A, a cannabinoid CB1 receptor-specific antagonist, enhanced the release of glutamate upon depolarization (T. Sugiura and S. Oka, unpublished results). These results strongly suggest that the endogenous ligand of the cannabinoid CB1 receptor, that is, 2-AG, plays an essential role in the attenuation of neurotransmission. We proposed that the physiological role of 2-AG in the synapse is as follows: 2-AG is generated through increased phospholipid metabolism, especially inositol phospholipid breakdown, at the presynapses and/or postsynapses during accelerated synaptic transmission. 2-AG is rapidly released from the neuronal cells to the synaptic cleft, because 2-AG is a membrane-permeable molecule. The released 2-AG then binds to the cannabinoid CB1 receptor mainly expressed in the presynapse, and suppresses neuronal excitation through inhibiting Ca²⁺ channels or activating K⁺ channels, thereby diminishing subsequent neurotransmitter release (Fig. 4) [20, 21].

Such a negative feedback regulation mechanism should be effective in calming stimulated neurons after excitation. The 2-AG- and cannabinoid CB1 receptor-dependent negative feedback regulation of neurotransmission would be of great physiological significance, because sustained activation of neuronal cells is known to cause cell exhaustion and may lead to neuronal cell death. 2-AG probably plays

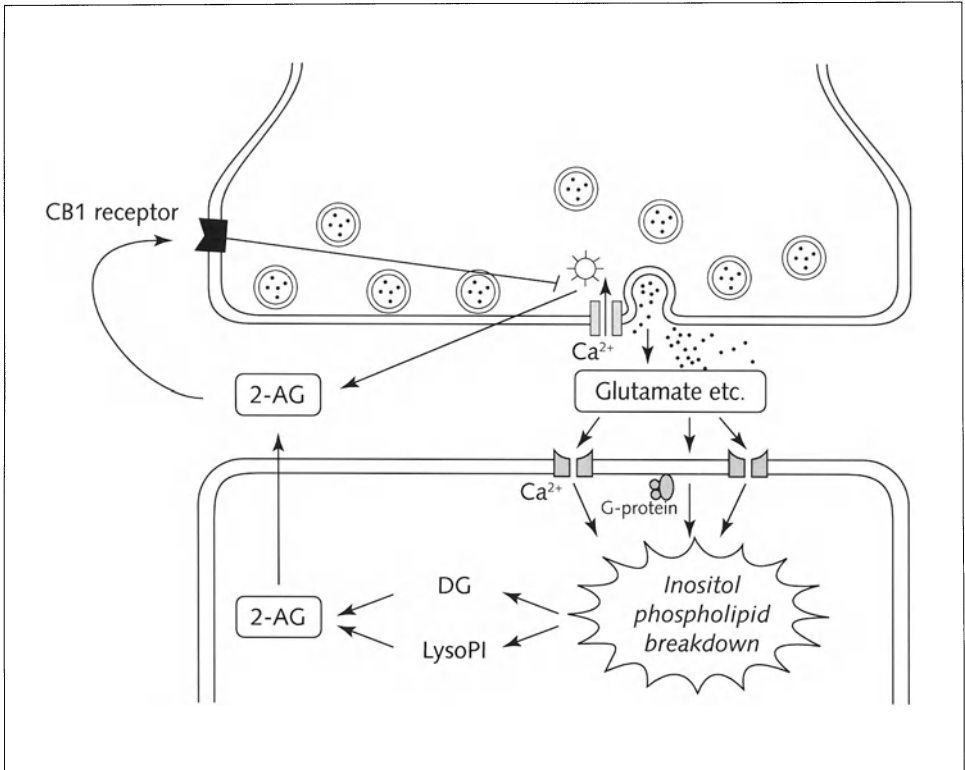


Figure 4

Physiological significance of the cannabinoid CB1 receptor and 2-AG in the synapse

such an important regulatory role in the neurotransmission in cooperation with other inhibitory neurotransmitters and neuromodulators such as GABA and adenosine *in vivo*. As for 2-AG in the brain, Stella et al. [45] demonstrated that 2-AG suppresses long-term potentiation in rat hippocampal slices, and Ameri and Simmet [89] reported that 2-AG reduces neuronal excitability in rat hippocampal slices. Panikashvili et al. [90] also recently proposed the protective role of 2-AG in the brain. On the other hand, Δ^9 -THC, the major psychoactive constituent of marijuana, is a partial agonist of the cannabinoid CB1 receptor. It is possible that Δ^9 -THC interferes with the actions of the physiological ligand 2-AG, thereby inducing several pharmacological effects such as altered perception and hallucination.

Recently, several investigators have reported that the endogenous cannabinoid receptor ligand derived from the postsynapse is the effector molecule of the depolarization-induced suppression (DSE) [91–93]. Based on our previous experimental results on 2-AG in the nervous system as previously mentioned, we considered that

the cannabimimetic molecules involved in this response is 2-AG. Unlike anandamide, 2-AG has long been outside the limelight until recently. 2-AG is now in the spotlight. Details of the physiological functions and the regulation of the biosynthesis, degradation, release and re-uptake of 2-AG in synapses will be clarified in the near future.

Physiological roles of endogenous cannabinoid receptor ligands during inflammation and immune response

The cannabinoid CB2 receptor is abundantly expressed in various types of inflammatory cells and immune cells such as natural killer cells, B lymphocytes and macrophages [6, 8–10], suggesting that its endogenous ligand plays an important role in the regulation of inflammation and immune response. Previously, we found that the structure of 2-AG is strictly recognized by the CB2 receptor [23–25]. 2-AG acted as the most efficacious agonist among the various structural analogs; 2-AG acted as a full agonist at the CB2 receptor whereas anandamide acted as a weak partial agonist. Gonsiorek et al. [27] also demonstrated that 2-AG is a full agonist and anandamide is a partial agonist using the membrane fraction of the Sf9 cells transfected with the human CB2 receptor cDNA. These observations strongly suggest that 2-AG, and not anandamide, is the true endogenous ligand for the cannabinoid CB2 receptor as in the case of the CB1 receptor [20, 21].

Only limited information is thus far available concerning the biological activities of 2-AG toward inflammatory cells and immune cells. Previously, Lee et al. [94] reported that 2-AG affects lymphocyte proliferation. Ouyang et al. [95] also demonstrated that 2-AG suppresses the IL-2 gene expression in murine T lymphocytes through down-regulation of the nuclear factor. Very recently, Chang et al. [96] demonstrated that 2-AG inhibited the production of IL-6 in J774 macrophage-like cells. However, it remains unclear whether these effects of 2-AG are mediated through the cannabinoid receptor. On the other hand, we recently found that 2-AG induces the rapid phosphorylation and activation of the p42/44 MAP kinase in HL-60 cells [97]. 2-AG-induced activation of the p42/44 MAP kinase was abolished when the cells were pretreated with either SR144528 or PTX, indicating that the response was mediated through the CB2 receptor and Gi/Go. CP55940, a synthetic cannabinoid, also induced the activation of the p42/44 MAP kinase, whereas only a slight activation of the p42/44 MAP kinase was observed with anandamide. In addition to the p42/44 MAP kinase, we found that rapid phosphorylation of the p38 MAP kinase and c-Jun N-terminal kinase takes place in 2-AG-stimulated HL-60 cells (Fig. 5). A similar 2-AG-induced activation of the p38 MAP kinase and c-Jun N-terminal kinase has also been reported by several investigators [98, 99].

Recently, we found that 2-AG induces the migration of HL-60 cells differentiated into macrophage-like cells (Fig. 6). The 2-AG-induced migration of HL-60 cells

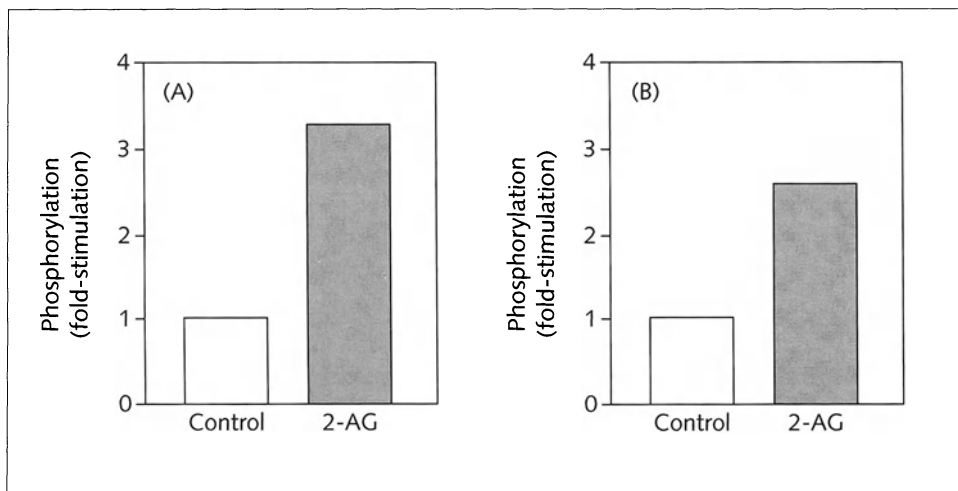


Figure 5

2-AG-induced phosphorylation of p38 MAP kinase and c-Jun N-terminal kinase in HL-60 cells

HL-60 cells were incubated in the presence or absence of 1 μ M 2-AG for 30 min. The phosphorylation of p38 MAP kinase (A) and c-Jun N-terminal kinase (B) was determined by Western blotting. The data are the means of two determinations.

was markedly reduced when the cells were pretreated with either SR144528 or PTX (S. Kishimoto, M. Gokoh and T. Sugiura, unpublished results), suggesting that the migration was mediated through the CB2 receptor and Gi/Go as in the cases of Ca²⁺ transients [25] and the activation of the p42/44 MAP kinase [97]. Arachidonic acid and its metabolites are not involved in the 2-AG-induced migration, because free arachidonic acid was not capable of inducing the migration. This was also confirmed by the fact that 2-AG ether, a metabolically stable analog of 2-AG, was able to induce the migration (S. Kishimoto, M. Gokoh and T. Sugiura, unpublished results), although its activity was significantly weak compared with that of 2-AG. The migration of HL-60 cells induced by 2-AG was assumed to mainly involve chemotaxis rather than chemokinesis. In contrast to 2-AG, anandamide did not exhibit appreciable activity to induce the migration. Recently, Jorda et al. [100] also demonstrated that 2-AG induces the migration of mouse splenocytes and several myeloid cells.

Previously, Gallily et al. [101] reported that 2-AG suppresses the production of the tumor-necrosis factor α (TNF- α) in LPS-stimulated mouse macrophages *in vitro* and in LPS-administered mice *in vivo*, although whether these effects of 2-AG are mediated through the CB2 receptor is uncertain. On the other hand, we found that

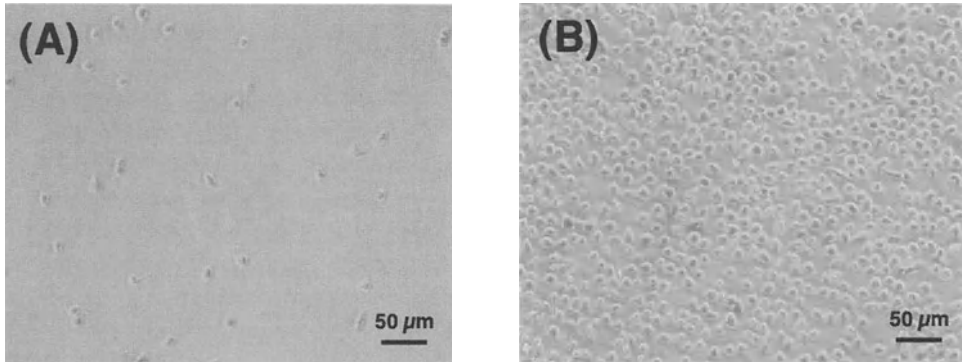


Figure 6

2-AG-induced migration of HL-60 cells differentiated into macrophage-like cells

The migration of HL-60 cells differentiated into macrophage-like cells (in the upper compartment) in response to $1 \mu\text{M}$ 2-AG (in the lower compartment) was examined using Costar Transwells (pore size, $5 \mu\text{m}$) and 24-well culture plates. Cells were incubated in an atmosphere of 5% CO_2 and 95% air for 4 h. (A), cells migrated from the upper compartment to the lower compartment in the presence of vehicle alone; (B), cells migrated from the upper compartment to the lower compartment in the presence of $1 \mu\text{M}$ 2-AG. The magnification was $\times 200$.

the addition of 2-AG to HL-60 cells enhanced the production of chemokines such as IL-8 and MCP-1 through a CB2 receptor- and Gi/Go-dependent mechanism (S. Kishimoto and T. Sugiura, unpublished results). CP55940 also caused the accelerated production of IL-8 and MCP-1. Meanwhile, anandamide as well as the free arachidonic acid failed to induce the augmented production of chemokines. Based on the experimental results concerning cell migration and chemokine production, we propose that 2-AG has a positive rather than negative role during inflammatory reactions and immune responses (Fig. 7).

It is well known that Δ^9 -THC affects inflammatory reactions and immune response *in vivo* [8–10, 102]. For example, orally administered Δ^9 -THC exhibited anti-inflammatory activity in rat paws injected with several stimulants such as carrageenan [103], although contradictory results have been reported as well [104]. The administration of Δ^9 -THC to experimental animals has also been shown to result in a decreased resistance to viral and bacterial infection [8–10, 102]. The impairment of cell-mediated immunity has been assumed to be involved in the decreased resistance to microorganisms. A number of investigators have already demonstrated that Δ^9 -THC suppresses several cellular functions of inflammatory cells and immune cells such as phagocytosis, antigen presentation, cytotoxicity, pro-

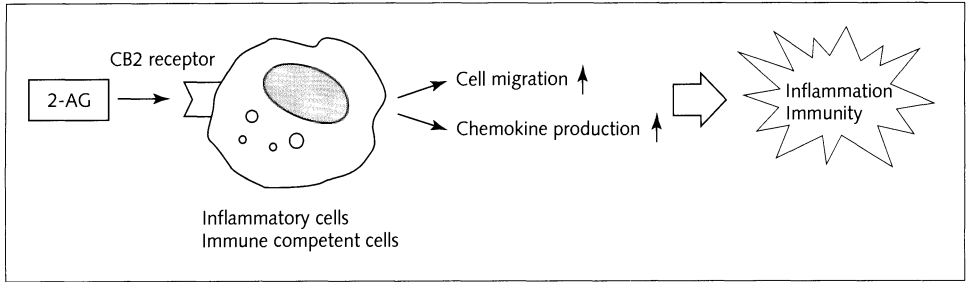


Figure 7

Physiological significance of the cannabinoid CB2 receptor and 2-AG during inflammation and immune response

duction of nitric oxide and cytokines such as TNF- α and mitogen-induced blastogenesis *in vitro* [8–10, 102], although the required concentrations are relatively high. The mechanism by which Δ^9 -THC suppresses inflammatory cell and immune cell functions has not been fully elucidated. It has been assumed that the effects of Δ^9 -THC are partly mediated by the cannabinoid receptors (CB2 and CB1) and partly by cannabinoid receptor-independent mechanisms. Previously, we demonstrated that Δ^9 -THC is a weak partial agonist of the cannabinoid CB2 receptor [25]. Bayewitch et al. [105] also reported that Δ^9 -THC acted as an antagonist toward the CB2 receptor. Therefore, it is possible that Δ^9 -THC interferes with the actions of the physiological ligand 2-AG thereby causing suppression or inhibition of several functions of inflammatory cells and immune competent cells at least in some cases.

Previously, it has been demonstrated that low concentrations of cannabinoids such as CP55940 induce the augmented production of chemokines such as IL-8 and MCP-1 in HL-60 cells [106]. Δ^9 -THC was also found to elicit the accelerated production of several cytokines such as IL-4 and IL-10 [107]. On the other hand, Berdyshev et al. [108] reported that micromolar concentrations of Δ^9 -THC induce the increased production of TNF- α , IL-6 and IL-8 in LPS-stimulated human peripheral blood mononuclear cells. These results are generally consistent with our experimental results on the stimulative effects of 2-AG on chemokine production as previously mentioned. Noticeably, low concentrations of CP55940 were shown to induce the proliferation [109] and differentiation [110] of B lymphocytes. This strongly suggests that the cannabinoid receptors are involved in the regulation of the functions of B lymphocytes and humoral immunity. Recently, Iwamura et al. [111] reported that JTE-907, a CB2 receptor antagonist/inverse agonist, inhibited inflammation in the paw evoked by the injection of carrageenan in mice. A similar effect was observed with SR144528 [111], suggesting close involvement and mandatory roles of the cannabinoid receptors in inflammation reaction. It is thus clear that the

endogenous ligand of the cannabinoid receptors (we are assuming that it is 2-AG) plays important positive roles during the course of inflammation and immune response, although details still remain to be determined. Further studies are necessary for a thorough elucidation of the physiological and pathophysiological significances of the cannabinoid receptor and its endogenous ligand 2-AG in the immune system. Such studies would be quite helpful to better understand the precise regulatory mechanisms of inflammation and immune homeostasis.

Concluding remarks

The cannabinoid receptors (CB1 and CB2) and their endogenous ligands, especially 2-AG, are assumed to play essential roles in the nervous system and the immune system as addressed in this review, although subsequent intensive studies are indispensable for a comprehensive understanding. In addition to this, the cannabinoid receptor system is also suggested to play important roles in other biological systems such as the cardiovascular system [112, 113] and the reproductive system [114, 115]. However, sufficient information has not yet been accumulated as to this issue and details still remain rather obscure. Apparently, the cannabinoid receptors and their endogenous ligands are attractive targets for new drug development such as anti-inflammation drugs, yet the research is just beginning. Thus, future studies on the cannabinoid receptors and their endogenous ligands will open promising new areas in the biological and biomedical sciences.

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Index

- AA pool 78
- ACAT 101
- acetyl-CoA:lyso PAF acetyltransferase 79
- acetylhydrolase 37
- acetyltransferase 2, 79–82
- acetyltransferase activation 82
- 1-acyl-2-acetyl-GPC 76
- acyl chain remodeling 24
- acyl CoA 77, 91, 93, 95, 149
- acyl CoA synthetase (ACS) 91, 95, 149
- acyl CoA transferase 91
- acyl-CoA-dependent mechanism 77
- adult respiratory distress syndrome (ARDS) 117
- airway hyperresponsiveness 184
- β -amyloid precursor protein 145
- anandamide 211, 218
- anandamide amidohydrolase/fatty acid amide hydrolases 211, 218
- ankyrin repeats 18
- annexin 1 191
- anti-inflammatory signaling 192, 195
- apolipoprotein 145, 148
- apolipoprotein E (apoE) 145
- apoptosis 46, 101, 135
- 2-arachidonoyl LPA 222
- arachidonoyl trifluoromethyl ketone 101
- arachidonoylethanolamide 5
- arachidonoylglycerol 5, 211, 220
- 2-arachidonoylglycerol (2-AG) 211
- arachidonyl-CoA 20
- arachidonyl-CoA synthetase 1
- aspirin-induced gastric damage 184
- aspirin-triggered lipoxin 169, 181
- aspirin-triggered LXA₄ (15R-LXA₄) 176
- astrocyte 94, 148, 151
- astrocyte cell 148
- ATL 169, 181
- auto-catalyzed oxidative process 151
- auto-oxidized PUFA 154
- bactericidal/permeability-increasing protein (BPI) 193
- bioactive lipid mediators 6
- blood brain barrier (BBB) 146
- brain astrocyte 94
- brain cell 102
- bromoenol lactone (BEL) 20, 23, 63
- bronchoalveolar lavage (BAL) 117
- C2 domain 17
- CB1 receptor 212, 223
- CB1 receptor-specific antagonist 223
- CB2 receptor 213, 228
- CB2 receptor antagonist 228
- cell cycle 21, 25
- cell differentiation 115
- cell surface receptor 185
- ceramide 146
- cerebrospinal fluid (CSF) 146
- chemoattractant peptide receptor 187
- chemotaxis, of monocytes 192
- cholesterol 94, 98, 146, 150
- cholesterol esters 94, 146
- cis-epoxyicosatrienoic acid 152

- c-Jun N-terminal kinase 225
CoA-dependent acyl transferase 1, 15, 63, 90, 96, 148
CoA-dependent transacylase 90
CoA-independent transacylase (CoA-IT) 1, 15, 22, 23, 63, 65, 77, 79, 81, 90, 96
cofactor, metals as 155
corneal epithelial cell 185
COX-2 173
CP55940 228
cPLA₂ 16, 17, 22–24, 38, 47, 65, 73, 79–82
cPLA₂-knockout mouse 80
85 kDa cPLA₂ 79, 81
CTP-phosphocholine cytidyltransferase (CT) 20
cyclo-oxygenase (COX) 2, 23, 40, 132, 152, 173
cyclopentenone prostaglandins 195
cysteinyl-leukotriene receptor 187
cytochrome P450 152
cytokine 39, 116, 151
cytoplasmic tyrosine kinase 47
cytosolic phospholipase A2 16, 17, 22–24, 38, 47, 65, 73, 79–82, 151
85 kDa cytosolic PLA₂ 79, 81
- deacylation/reacylation of arachidonate 6
15-deoxy- $\Delta^{12,14}$ prostaglandin J₂ (PGJ₂) 24, 25
15-deoxy-LXA₄ 176
dermal inflammation 181, 195
desaturase 89, 91, 147
desaturation 91, 93
diacylglycerol 150, 220
diacylglycerol lipase 220
dietary supplement 102
differentiated U937 65, 119
dihomo γ -linoleic acid (DGLA) 90, 92
dihomo γ -linolenic acid (DGLA), within inflammatory cells such as neutrophils 90
13,14-dihydro-15-oxo-LXA₄ 176
docosahexaenoic acid 4, 92, 147
docosanoid 198
- efficacy of antioxidants 157
eicosanoid 2, 15, 22–24, 37, 47, 61, 62, 90, 100, 186
eicosanoid biosynthesis 47, 62, 100
eicosanoid receptor 186
eicosapentaenoic acid (EPA) 4, 65, 74, 75, 90, 92, 147
elongase 91
elongation 91, 93
elongation and desaturation of 18 carbon fatty acids 91
endocannabinoid 131, 211
endogenous cannabinoid receptor ligands 211
endothelial cell 148
eosinophil 41, 116, 184
eosinophilic pleurisy 184
ERK 81, 82
essential fatty acid (EFA) 1, 89, 147
ethanolamine 217
ethanolamine plasmalogen 76, 79
ether lipid 101
ether-linked phospholipid 6, 98, 102
ether-linked phospholipid pool 102
ether-linked phospholipid subclasses 6
ether-linked plasmalogen lipid pool 148
- fatty acid binding protein (FABP) 149
fatty acid synthetase 2
fatty acids, increased liberation 68
FPR 189
free fatty acid, accumulation of 61
free radical 155
- G protein-coupled receptor (GPCR) 171, 185, 187
gastric damage, aspirin-induced 184
gene expression 136
glutamate 137
glycerolipids 96, 146
glycerophosphocholine 147
glycerophospholipid 13, 18, 147

- glycerophospholipid homeostasis 18
glycogen synthase kinase (GSK) 47
G-protein 133
group IIA PLA₂ 38
group IV cPLA₂ 38
group V sPLA₂ 38
- H₂O₂-mediated release, of unmetabolized AA 69
high density lipoprotein (HDL) 146
high density macrophage (HDM) 122
histamine 39
HL-60 cells 228
homeostasis (AA incorporation and remodeling) 6
host defense 169
housekeeping activity 63
housekeeping phospholipid and fatty acid remodeling 62
housekeeping role 69
human basophil 41
human eosinophil 41
human neutrophil 41
human promonocytic cell line U937 119
5-hydroxyeicosatetraenoic acid (5-HETE) 80, 81
hypereosinophilic syndrome 117
hypodense cell 118
- IL-8 181, 228
IL-8 secretion 181
incorporation of AA 63–65
inflammatory angiogenesis 185
inflammatory cell 13, 22, 23, 62, 67
inflammatory disease 90
inflammatory response 62, 187
inflammatory signaling 62, 67
inhibitors of cPLA₂ 65
intestinal inflammation 184
iPLA₂ 16, 18–22, 24, 25, 68
ischemia 131, 173, 183
ischemia reperfusion 173, 183
- kinases, signaling pathways 6
- Lands pathway 15, 20, 61, 63
lecithin (phosphatidylcholine) 150
lecithin cholesterol acyl transferase (LCAT) 101, 146
leukotriene 2, 40, 80, 81, 90, 132, 152
leukotriene B₄ (LTB₄) 80, 81
linoleic acid (LA) 89, 92, 149
α-linolenic acid 89, 92
γ-linolenic acid 90, 92
lipase 91, 154
lipid body 117
lipid classes 2
lipid hydrolysis by iPLA₂ 68
lipid marker 157
lipid mediators 169
lipid oxidation 68
lipid peroxide 68
lipid peroxide accumulation 68
lipid radicals 151
lipidomics 5
lipidomic analysis 198
lipoamino acid 5
lipoprotein 146, 153, 154
lipoprotein lipase 153
lipoprotein (LDL) receptor 146
lipoxin (LX) 4, 169, 181
lipoxygenase (LO) 2, 23, 40, 152
localized juvenile periodontitis 173
low-density macrophage (LDM) 122
low-density lipoprotein 150
LTB₄ 100
LTB₄-induced PMN 181
lung 116
LXA₄ analogs in acute skin inflammation 181
LXA₄ receptor 171, 185
LXA₄/PGE 13,14-reductase/LTB₄ 12-hydroxydehydrogenase (PGR/LTB₄DH) 176
[³H]-LXA₄ 176
lysoPC 44, 63, 66, 67
lysoPC level 67

- lysoPE 44, 63, 65, 66
lysophosphatidylcholine 44, 63, 66, 67
lysophosphatidylethanolamine 44, 63, 65, 66
lysophospholipase D 79
lysophospholipid 15, 37, 44, 63–66, 77, 96, 98, 147
lysophospholipid acceptors 63, 96
lysophospholipid acyltransferase 147
lysophospholipid availability, increased 65
lysophospholipid level 63, 64, 66
lysophospholipid level maintenance, in resting and activated phagocytes 66
lysophospholipid, AA incorporation into 64, 65
lysophospholipid, cellular 64
- macrophage 13, 22, 23, 41, 63, 65, 116, 122, 181, 195
macrophage phagocytosis 181, 195
mannose receptor 46
marijuana 211
mast cell 41, 48, 116
MCP-1 228
membrane phospholipid homeostasis 67
metal 155
15(R/S)-methyl-LXA₄ 176
MHC binding peptide 189
microbial infection 184
microglial cell 198
mitogen-activated protein kinase (MAP kinase) 42, 81, 82, 225, 226
mobilization, of AA 62
molecular species of PAF 76
molecular species of phospholipids 6
monoacylglycerol 220
monoacylglycerol lipase 220
monocyte 41, 192
M-type receptor 42
mucosal inflammatory response 187
murine P388D1 macrophage 63
myeloid lineage 185
- NAB1 193
N-acylethanolamines 215
N-arachidonoyl phosphatidylethanolamine (PE) 218
N-arachidonoylethanolamine (anandamide) 211
neuronal cell death 145
neutrophil 13, 22, 90, 116
NF- κ B 48, 193
N-glycosylation 189
nitric oxide (NO) 155
NSAID 156
N-type receptor 42
nutraceuticals 157
nutritional supplements 6
- obligate precursor of PAF 75
 β -oxidation 91
 ω -oxidation 177
oxidation of macromolecules 155
oxidative damage 157
oxidized phospholipid species 6
5-oxo-ETE 80
15-oxo-LXA₄ 176
1-O-alk'-enyl-2-lyso-GPE 77
1-O-alk-1'-enyl-2-acetyl-GPE (ethanolamine plasmalogen) 76, 79
1-O-alkyl-2-AA-GPC 73, 75
1-O-[³H]alkyl-2-AA-GPC 75
1-O-alkyl-2-acyl diglycerides 81
- p38 MAP kinase 81, 82, 225
p42/44 MAP kinase 226
P388D1 cell 66
P388D1 macrophage 65
PAF 4, 13, 22, 23, 73–76, 78, 90, 96, 100, 131, 134
PAF antagonist 134
PAF synthesis, *de novo* pathway 78
PC 20
peptido-LT receptor 181, 194
peroxisome proliferator-activated receptors (PPAR) 24

- PGES 152
PGIS 152
phagocytic cells 61
phosphatidylethanolamine (PE) 44, 94, 218
phosphatidylinositol 48
phosphatidylserine 150
phosphoinositide-3-kinase 48
phospholipase A₂ (PLA₂) 14–16, 18–25, 37–39,
61, 63, 68, 90, 132
phospholipase C (PLC) 133
phospholipid classes and subclasses 1, 6, 97
phospholipid hydrolysis 68, 69
phosphorylation of serine 505 46
phosphorylation of various amino acid residues
47
plasmalogen 74, 79, 147, 148
plasmalogen-linked phospholipids 147
platelet activating factor (PAF) 4, 13, 22, 23,
73–76, 78, 90, 96, 100, 131, 134
PMA-differentiated U937 cells 66
PMN transmigration 179
polyisoprenyl phosphate (PIPP) 192
polymorphonuclear leukocyte (PMN) 135,
179
polyunsaturated fatty acids (PUFA) 4, 94, 145,
147, 154, 157, 195
polyunsaturated fatty acids biosynthesis 94, 157
PPAR- γ 24
priming 81
pro-inflammatory mediators 48
promyelocytic lineage 185
pro-resolution 181, 195
pro-resolution signals 181
prostaglandin 2, 24, 25, 40, 61, 152
prostaglandin H synthase 152
prostanoid 95, 187
prostanoid receptor 187
protein kinase C 81
protein tyrosine kinase 47
pulmonary inflammation 184
pyrrophenone 66
reactive oxygen species (ROS) 155
reacylation 61
recycling of membrane phospholipids 61
AA release of AA 61, 62, 66
remodeling pathway of PAF synthesis 75
resolvin 195
reverse cholesterol transport 150
Schmid's pathway 218
second organ injury 195
skin inflammation 181
sphingolipids 146
sPLA₂ 16, 22–24, 39, 42
sPLA₂ receptor 39, 42
SR141716A 223
SR144528 225
stearidonic acid (SDA) 93
stimulus-induced AA release 66
superoxide 155
superoxide dismutase (SOD) 155
supplementation of animal diets with n-6 or
n-3 fatty acids 94
symptoms of diseases 6
synovial fibroblast 193
synthase 152
TBXS 152
 Δ^9 -tetrahydrocannabinol 211
thromboxane 2
Toxoplasma gondii 173, 184
transacetylase 79
transacylase 96
transcellular biosynthesis 171
triacsin 98
triglyceride (TG) 98, 116
tyrosine kinase 46, 47
tyrosine phosphorylation 45
U937 65, 66, 119
VEGF 185