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# Macrophage Biology and Activation

Edited by S.W. Russell and S. Gordon

With 42 Figures



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# Preface

The amazing world of the mononuclear phagocyte keeps expanding at a pace that, in current vernacular, is truly awesome. As a result, maintaining currency with the latest developments and controversies that pertain to this cell type is becoming increasingly difficult. Hopefully, what is contained in this volume will be of help in this regard.

The topics have been selected to provide an overview of subject areas that either have recently become much better understood or are ones that, in our opinion, hold the promise of new levels of understanding as they are developed in the future. The scope of what is included ranges from how these cells develop, through the means that are used to regulate them, to the roles that they have in different tissues and in a variety of infectious diseases.

In closing these brief introductory remarks, we want to thank the contributors to this volume, especially those who helped make our job easier by meeting their deadlines, and our coordinator at Springer-Verlag, Ms. Marga Botsch.

STEPHEN W. RUSSELL and SIAMON GORDON

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# Antigen Markers of Macrophage Differentiation in Murine Tissues

S. GORDON, L. LAWSON, S. RABINOWITZ, P. R. CROCKER, L. MORRIS, and V. H. PERRY

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# **1** Introduction

Cell-restricted membrane antigens have made it possible to map the distribution of mature macrophages in many murine tissues. Monoclonal antibodies (mAbs) have been used to define the appearance of macrophages dusing foetal and postnatal development, to establish the anatomic relationships between macrophages and other cells in the normal and diseased adult, and to investigate cellular modulation and heterogeneity within different microenvironments. Current studies have illustrated the complex differentiation pathway of mononuclear phagocytes in vivo and have raised questions concerning the mechanisms that determine monocyte entry, migration and fate within tissues. Macrophages constitute a major, widely dispersed system of cells that regulate homeostasis in the normal host and respond to tissue injury by contributing essential functions

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Table 1. N	Aembrane glycoprote	ein antigens u	ised to define macrophage distribution a	and heterogeneity in murine tissues	
Antigen (Ag)	Antibody (Ab)	MW (kDa)	Tissue distribution	Comments	References
F4/80	Rat mAb Rabbit polyclonal	~ 150	Mature macrophages	Down-regulated in T-cell dependent areas. Polyclonal Ab is cytotoxic and cross-reacts with rat Ag.	Austryn and Gorbon 1981 Starkey et al. 1987 Dri and Crocker, unpublished
CR <sub>3</sub>	Rat mAb M1/70 5C6	150/90	PMNs, macrophages and NK cells Heterogeneity on macrophages in tissues	Leucocyte integrin. Both mAbs block iC <sub>3</sub> b binding site; only 5C6 blocks adhesion in vitro and in vivo.	SPRINGER et al. 1979 BELLER et al. 1982 Rosen and Gorbon 1987
7/4	Rat mAb	~ 40	PMNs and activated macrophages	Polymorphic, useful for PMN depletion, e.g. in bone marrow.	Hirsch and Gorbon 1983 Tree, Hirsch and Rabinowitz, unpublished
Sialoadhe	sin Rat mAb SER-4 Rabbit polyclonal	185	Stromal macrophages	Macrophage lectin for sialylated structures. Expression modulated by homologous plasma/serum inducer.	Crocker and Gorbon 1989 Crocker, unpublished
FA.11	Rat mAb FA.11	85–90	Macrophage and dendritic cell endosome membrane	Differential glycosylation (WGA binding) in exudate macrophages	Rabinowitz et al. 1991; Rabinowitz, pa SiLva, MiLon, Steinwan and Austryn, unpublished

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during inflammation and repair. In this review we consider several membrane marker antigens which have proved useful in studying the life history and biologic properties of macrophages, and relate immunochemical studies on antigen expression to lineage analysis and macrophage differentiation in vivo. We restrict our discussion to the mouse, in which it is possible to manipulate the system in its entirety. Where known, properties of macrophages in other species are broadly similar.

#### 2 Antigen Markers

In this section we summarise the properties of antigens which we have used to study macrophage populations in situ and in vitro. Table 1 lists features that are relevant to their use as markers. Other mAbs that have been used to characterise murine macrophages will be referred to in the text. Details of antigen expression will be described and illustrated below and our standard protocol for immunocytochemical analysis is given in an appendix.

#### 2.1 F4/80

Knowledge of the presence of mature macrophages in murine tissues derives mainly from studies with mAbs and monospecific polyclonal antibodies directed against the macrophage-specific plasma membrane differentiation antigen F4/80. The epitope defined by a rat mAb isolated by AUSTYN and GORDON (1981) proved stable to perfusion-fixation, thus permitting HUME, PERRY and others to identify macrophages in a variety of tissues (for earlier reviews see HUME and GORDON 1985; PERRY and GORDON 1988). Subsequently DRI (unpublished observations) used affinity purified F4/80 antigen to raise a potent polyclonal antiserum that reacts with additional epitopes on the F4/80 molecule. This monospecific reagent enhances the detection of macrophage plasma membrane within tissues (LAWSON et al. 1990). The F4/80 antigen is a single chain glycoprotein which displays microheterogeneity on Western blot analysis of lysates prepared from various tissues and cell lines. The molecule has been purified (STARKEY et al. 1987) but not yet cloned and its function is unknown. Expression of F4/80 by peritoneal macrophages is down-regulated by inflammatory stimuli, which induce the recruitment of immature cells, by short-term adhesion in cell culture and by exposure to lymphokines, especially interferon- $\gamma$ (GORDON et al. 1986a). However, the F4/80 antigen can be readily detected on macrophages by immunocytochemistry after all these treatments. The labelling pattern in isolated macrophages is mainly (>80%) at the plasma membrane and is uniform over the cell surface, although F4/80 antigen expression is concentrated in ruffles and at the edge of spreading cells.

## 2.2 Complement Receptor, Type 3 (CR<sub>3</sub>)

The M1/70 mAb originally described by SPRINGER et al. (1979) reacts with the  $\alpha$  chain of this member of the  $\beta$ 2 leucocyte integrin family (SPRINGER 1990) and was subsequently found to inhibit binding of iC<sub>3</sub>b-coated sheep erythrocytes to leucocytes (BELLER et al. 1982). Whilst strongly expressed on polymorphonuclear leucocytes (PMNs), circulating monocytes and NK cells, CR<sub>3</sub> expression is variable on tissue macrophages (LEE et al. 1986; CROCKER and GORDON 1985). Another mAb raised by ROSEN and GORDON (1987) to inhibit adhesion of peritoneal macrophages to artificial substrata such as bacteriologic plastic also reacts with CR<sub>3</sub>. This reagent blocks iC<sub>3</sub>b binding activity and in addition is a potent inhibitor of myelomonocytic adhesion to inflamed endothelium in vivo (ROSEN and GORDON 1990a), unlike M1/70. In contrast with its modulation in vivo, expression of CR<sub>3</sub> is relatively constant on isolated macrophages in culture and is predominantly at the plasma membrane, although it is detectable in endosomes after endocytosis (ROSEN, unpublished).

#### 2.3 7/4

The polymorphic myelomonocytic antigen 7/4 is expressed at high levels on PMNs (HIRSCH and GORDON 1983), but is absent on resident tissue macrophages. Monocytes and immune-activated macrophages express low levels of antigen (TREE, RABINOWITZ and HIRSCH, unpublished). The 40-kDa antigen is stable to perfusion fixation and Western blotting (RABINOWITZ, unpublished), but has not been characterised further. mAb 7/4 has been useful as a depleting agent for myeloid cells in bone marrow (BERTONCELLO et al. 1989) and to enrich for undifferentiated 7/4-negative haemopoietic precursor cells, in combination with other lineage-restricted reagents (IKUTA et al. 1990; ZSEBO et al. 1990).

### 2.4 Sialoadhesin(SER)

Stromal macrophages express a lectin-like receptor that binds sialylated glycoconjugates on sheep erythrocytes (SER) (CROCKER and GORDON 1986) and other erythroid model systems (COCKER et al. 1991). Ligands for this receptor are also present on developing murine myeloid cells (CROCKER, MORRIS and GORDON, unpublished). Activity of the receptor, now termed sialoadhesin, can be induced on non-stromal peritoneal macrophages by cultivation in homologous serum (CROCKER et al. 1988a). This made it possible for CROCKER and GORDON (1989) to raise a specific inhibitory mAb, SER-4, and, after purification of the receptor by affinity chromatography, to raise a further panel of mAbs, and a monospecific polyclonal antibody (CROCKER, MCWILLIAM and GORDON, unpublished). The sialoadhesin molecule is a single chain glycoprotein which is mainly expressed on the plasma membrane, where it mediates binding but not ingestion of

attached cells. In situ, SER antigen is concentrated at points of contact between bone marrow stromal macrophages and myeloid, but not erythroid cells (CROCKER et al. 1990). A distinct divalent cation-dependent receptor for adherent erythroblasts (EbR) is expressed by stromal macrophages in foetal (MORRIS et al. 1988a) and adult tissues (MORRIS et al. 1991), but has not been defined immunochemically.

#### 2.5 FA.11

The mAb FA.11 isolated by SMITH and KOCH (1987) reacts with an intracellular membrane glycoprotein that is more widely expressed by tissue macrophages than is F4/80 (RABINOWITZ, PERRY and LAWSON, unpublished). It is also present on lymphoid dendritic cells (RABINOWITZ, MILON, STEINMAN, AUSTYN and GORDON, unpublished), but it is more tissue restricted than a family of lysosomal glycoproteins, present in many cell types, to which it may be related (DA SILVA and ROSEN, unpublished). Exudate (elicited and activated) but not resident peritoneal macrophages express a glycoform that binds wheat germ agglutinin through terminal sialic acid residues (RABINOWITZ et al. 1991a). The FA.11 molecule consists of a core polypeptide, recognised by the FA.11 mAb, and is heterogeneous as a result of extensive N and O glycosylation. Although it can be detected in the plasma membrane, the bulk of labelling in macrophages is within the prelysosomal compartment and phagolysosomes and FA.11 reactivity is absent from terminal lysosomes (RABINOWITZ et al. 1991b). The FA.11 antigen is present in resident and exudate macrophages, but its level of expression, as well as of glycosylation, is enhanced by endocytic stimuli (RABINOWITZ et al. 1991a; DA SILVA, unpublished).

#### **3 Distribution and Turnover of Macrophages**

#### 3.1 Ontogeny

The ontogeny of macrophages during development was largely unknown before the introduction of antigen markers. It is now clear from studies with F4/80 (MORRIS et al. 1991b) that macrophages are among the earliest haemopoietic cells to appear in the embryo (Fig. 1). Macrophages are abundant during mid and late gestation in most organs and are likely to play an important role in organogenesis and tissue remodelling. HUME, PERRY and others first used mAb F4/80 to follow recruitment of monocytes from blood to the developing nervous system at the time of natural death of neurons and their axons, before and after birth (Fig. 2) (HUME et al. 1983a; PERRY et al. 1985). Recruited cells phagocytose neuronal debris and differentiate into progressively more arborised microglia to



Fig. 1 (cont.)







**Fig. 2.** Macrophages in the developing brain. F4/80 demonstrates invading "amoeboid microglia" (solid arrowhead) alongside ramified cells (open arrowhead) similar to resident microglia, in the septum of a 1-day-old mouse. Scale bar 200 μm; cresyl violet counterstain. (Prepared by L. Lawson)

**Fig. 1 a–i.** Macrophage ontogeny in lymphohaemopoietic organs. F4/80 labelling of murine tissues as described. See MorRis et al. (1991b) for further details. During development, F4/80<sup>+</sup> monocytes and macrophages appear sequentially in yolk sac, liver, spleen and bone marrow and in non-lymphoid organs such as skin. **a** Yolk sac, day 10. F4/80<sup>+</sup> cells are found in small vessels and in interstitium, but are not associated with abundant erythroblasts in haemopoietic islands. **b–d** *Liver*: **b** Rounded F4/80<sup>+</sup> monocytes and early stellate macrophages appear in foetal liver (day 10) before local erythropoiesis is established; **c** stellate macrophages are found at peak levels in mainly erythropoietic islands by day 15; **d** by 3 days postnatally, haemopoiesis wanes and some sinus-lining F4/80 labelled macrophages resemble Kupffer cells. **e–g** *Spleen*: **e** day 12, earliest F4/80<sup>+</sup> macrophages are abundant in red pulp but are excluded from developing white pulp, which is rich in lymphoid cells. **h** *3-day newborn femur.* Stromal F4/80<sup>+</sup> macrophages have appeared at centre of haemopoietic cell clusters. **i** *3-day newborn skin.* Stellate F4/80<sup>+</sup> cells in developing epidermis resemble Langerhans cells. Labelled macrophages are also abundant in dermis

form a mosaic network of cells within the retina. Similar cell populations are recruited throughout the developing central and peripheral nervous system.

Subsequently, MORRIS et al. (1991b) studied the presence of F4/80<sup>+</sup> cells in the early embryo with special reference to haemopoietic tissues, mesenchyme and other developing organs. F4/80<sup>+</sup> cells appear in the yolk sac together with erythroid cells at day 9–10, although it is known from unpublished studies by SHIA that F4/80-negative precursors of mature macrophages, (Granulocytemacrophage colony-forming units, GM-CFUc) can be detected in suspensions of embryos by day 5. In yolk sac, primitive erythroid cells and F4/80<sup>+</sup> macrophages are not physically associated in haemopoietic cell clusters, as in more mature tissues (CROCKER et al. 1988b). From day 10 haemopoietic activity shifts to the foetal liver, where a rapidly expanding population of F4/80<sup>+</sup> stromal macrophages is found in erythroblastic islands. Monocytes and more differentiated, definitive erythroid cells produced in foetal liver sinusoids seed developing organs and mesenchymal tissues widely from day 10, presumably via newly formed blood vessels which develop at the same time.

After peak levels of haemopoietic activity are reached in the liver at day 14, the spleen (high levels at day 17) and bone marrow (from day 19) become active in turn. Erythroblastic islands disappear from liver later in gestation and during further postnatal development, and sinus-lining hepatic macrophages assume the appearance of Kupffer cells. A striking feature of haemopoiesis in the foetus is the relative absence of granulocyte production in foetal liver at day 14, and myelopoiesis only becomes prominent in spleen and bone marrow during late gestation. Lymphocytes in spleen and thymus also develop late in foetal life and expansion of secondary lymphoid organs occurs mostly during the early weeks of postnatal development.

The F4/80 antigen serves as a sensitive, specific marker for mature macrophages in foetal tissues throughout gestation. By contrast, the sialoadhesin antigen (SER) appears later in development and is restricted to subpopulations of F4/80<sup>+</sup> macrophages in lymphohaemopoietic tissues (MORRIS et al. 1992). The sialoadhesin receptor was first identified by CROCKER and GORDON (1986) on mature macrophages present in adult bone marrow clusters in situ and in vitro. Immunochemical and rosetting studies with the inhibitory mAb, SER-4, have shown that sialoadhesin is not expressed by day 14 foetal liver macrophages although these F4/80<sup>+</sup> cells express the distinct divalent cationdependent receptor for erythroblasts (EbR) which appears to be the major adhesion receptor involved in erythroblast island formation (MORRIS et al. 1991a). Sialoadhesin appears on stromal macrophages in developing lymphohaemopoietic organs from  $\sim$  day 17, at the time of myelopoiesis, and the striking pattern of strongly SER-labelled cells observed within the marginal metallophil zone of adult spleen (CROCKER and GORDON 1989) appears 2-4 weeks postnatally, in parallel with development of lymphoid cells and white pulp.

These studies have established that different macrophage- and subsetspecific antigens are regulated independently during development. Stromal macrophages in foetal liver, spleen and bone marrow are likely to regulate adhesion, growth and differentiation of various haemopoietic cells, although the role of different haemagglutinins and the nature of the ligands and haemopoietic cellular interactions remain to be defined. The non-haemopoietic functions of macrophages in the foetus are obscure, apart from a possible role in remodelling of the nervous system. Foetal macrophages express characteristic endocytic receptors such as FcR (CLINE and MOORE 1972) and proliferate vigorously in response to autocrine and paracrine stimuli. It is likely that they are an important source of growth factors for a range of other cell types during development (see chapter by RAPPOLEE and WERB elsewhere in this volume).

#### 3.2 Normal Adult

After the distribution of blood monocytes to many tissues during development, recruitment of haematogenous cells continues throughout adult life. Their entry, lifespan and rate of turnover vary in different tissues (for review see GORDON 1986). Enhanced recruitment of monocytes in response to inflammatory and infectious stimuli depends largely on production within the bone marrow. However, some resident tissue macrophage populations turn over independently, e.g. in lung, and are renewed by local proliferation. Macrophages are able to persist as relatively long-lived cells in tissues such as the adult nervous system, or migrate from peripheral sites such as skin and gut to lymph nodes, where they become trapped. It is often difficult to distinguish newly recruited from resident tissue cells since adaptation of monocytes and macrophages to each specialised microenvironment makes it impossible to use morphologic or antigenic markers by themselves to draw such a distinction. Antigen markers can be combined with labels for DNA synthesis to trace the kinetics of tissue entry. Haemopoietic reconstitution of x-irradiated animals has been used to trace the life history of macrophages, and the Y chromosome may provide a useful marker to distinguish macrophages of donor male origin from recipient female cells (PERRY and LAWSON, unpublished). Recently, fluorescent hydrophobic dyes such as dil (1.1' dioctadecyl 3,3,3',3' tetra methyl indocarbocyanine perchlorate) have proved useful for exvivo labelling of peritoneal macrophages before adoptive transfer to recipient animals (ROSEN and GORDON 1990b). Dil-labelled peritoneal macrophages can be used as surrogate monocytes since they migrate from blood to specialised regions of spleen as well as to lungs and liver in unstimulated animals, and are recruited into peritoneal exudates. After transfer to the peritoneal cavity, labelled resident peritoneal macrophages (RPM) migrate rapidly to regional draining lymph nodes (ROSEN and HUGHES, unpublished).

Antigen markers have helped to identify macrophages in tissues, but differences in regional expression of antigens reveal considerable heterogeneity of cell phenotype. We first describe the distribution of F4/80-labelled cells in tissues and then note variations in marker expression revealed by the use of SER-4, FA.11 and CR<sub>3</sub>. Figure 3 summarises the antigen phenotype of resident macrophages in various tissues, as described below.



Fig. 3. Schematic representation of differentiation of tissue macrophages and lymphoid dendritic cells in adult mouse. Diagram shows antigen phenotype and pathways of proven (solid line arrows) or presumed (broken line arrows) precursor cells

#### 3.2.1 Expression of Antigen Markers by Tissue Macrophages

#### 3.2.1.1 F4/80

A detailed description of F4/80<sup>+</sup> cells in normal murine tissues has been given in a series of immunocytochemical studies (summarised by HUME and GORDON 1985). Examples of the varied morphology and cellular associations of resident macrophages in adult lymphohaemopoietic organs and brain are illustrated in Figs. 4–6. Quantitative analysis of antigen levels in different tissues is broadly in agreement with the immunocytochemical findings (LEE et al. 1985). Substantial populations of sinusoidal and interstitial  $F4/80^+$  cells are found in liver (Kupffer cells), red pulp of spleen, bone marrow stroma (within haemopoietic cell clusters) and subcapsular regions of lymph nodes (HUME et al. 1983b). Thymus and T lymphocyte-dependent regions (white pulp of spleen and lymph nodes, Peyer's patches) are conspicuously free of F4/80 label whereas other mAbs reveal macrophage subpopulations at these sites (RABINOWITZ et al. 1991a). Populations of F4/80<sup>+</sup> cells are present throughout the lamina propria of the gastrointestinal tract, in epidermis (Langerhans cells) as well as in subcutaneous tissues (HUME et al. 1984a), and in the parenchyma of the nervous system (LAWSON et al. 1990). Delicately arborised F4/80<sup>+</sup> cells are found regularly dispersed within epithelium (Langerhans cells) and in the brain (microglia), whereas other stellate cells with shorter plasma membrane processes are present beneath the basement membrane of epithelial cells in small intestine and in renal medulla (HUME and GORDON 1983).

The airway, a major portal of entry to the body, contains a population of rounded alveolar macrophages which express F4/80 only weakly (HUME and GORDON 1985; GORDON, unpublished). F4/80<sup>+</sup> macrophages are ubiquitous in connective tissues but are absent within bone and cartilage matrix (HUME et al. 1984b) and infrequent in normal muscle and heart (GORDON, unpublished). Interstitial or sinusoidal F4/80<sup>+</sup> cells can be readily detected in several endocrine organs (testis, ovary, adrenal, pituitary) whereas they are sparse in normal pancreatic islets and thyroid (HUME et al. 1984c; HUTCHINGS et al. 1990; Pow et al. 1989). In the ovary, F4/80 labelling has revealed striking changes in macrophage number and morphology during the reproductive cycle (HUME et al. 1984c), and in posterior pituitary F4/80 labelled microglia selectively endocytose terminals of neuroendocrine cells containing oxytocin/vasopressin (Pow et al. 1989), suggestive of functional responses to hormonal stimulation.

F4/80 labelling has revealed considerable heterogeneity among macrophages in and outside the brain and made it possible for LAWSON et al (1990) to prepare a map of the distribution and morphology of microglia in the adult murine CNS (compare Figs. 5 and 6). Microglia form a network of F4/80<sup>+</sup> plasma membrane processes throughout white and grey matter; the morphology of F4/80<sup>+</sup> cells varies in different regions of the parenchyma, and distinguishes microglia from other macrophage populations in the choroid plexus and leptomeninges. F4/80 antigen is expressed at high levels on







**Fig. 4 a–h.** Macrophages in adult murine lymphohaemopoletic tissues exhibit varied phenotype and cellular associations. **a, b** *Liver*. Kupffer cells are relatively large and have simple stellate morphology. Hepatocytes and endothelial cells are F4/80 negative, **c, d** *Bone marrow*. Stromal macrophages in haemopoletic clusters express both F4/80 (**c**) and SER-4 antigen (**d**), whereas monocytes are only labelled by F4/80. Stromal macrophages are finely branched and contact developing erythroid and myeloid cells. **e** *Spleen*. F4/80 labels red pulp macrophages intensely, but not white pulp. SER-4 expression is intense in marginal matallophil zone, weak in red pulp and absent in white pulp (**f**). **g** *Skin*. The cytoplasm is drawn out into many fine processes with keratinocytes, shown by nuclear counterstain. **h** *Small intestine*. Macrophages are found throughout the lamina propria in gut, forming an almost continuous core within villi. Macrophages lie beneath epithelium, often enveloping capillaries and lymphatics.



**Fig. 5A–F.** Camera lucida drawings from F4/80 stained coronal sections of mouse brain: **A** cortex; **B** subfornical organ; **C** corpus callosum; **D** basal ganglia; **E** leptomeninges; **F** choroid plexus. Macrophages of the adult central nervous system vary in morphology and antigenic phenotype according to their location. Those lying outside the blood brain barrier (**B**, **E**, **F**) tend to be simpler stellate cells. Cells within the parenchyma are extensively arborised, with a radial pattern if they occur in grey matter (**A**, **D**) or a longitudinal one if in white matter (**C**). SER and CD4 antigens are down-regulated on these cells

microglia, whereas several other antigens (e.g. leucocyte common antigen,  $CD_4$ ) are down-regulated once cells pass through the blood-brain barrier (PERRY and GORDON 1987, 1991), as discussed further below.

In summary, F4/80 has proved to be a reliable and specific marker for the presence of macrophages in many adult tissues apart from specialised T cell-dependent regions and the alveolar space. F4/80 labelling has defined the association of tissue macrophages with endothelial, epithelial and other cell types, and has made it possible to begin to reconstruct the migration and differentiation of monocytes and macrophages in different compartments of the body.

#### 3.2.1.2 Sialoadhesin (SER)

The SER antigen is restricted to selected tissue macrophages in lymphohaemopoietic organs and scattered macrophages elsewhere (CROCKER and GORDON



**Fig. 6 a–c.** Microglia (resident macrophages) are numerous, ubiquitous but heterogeneous in their distribution and morphology in the normal adult mouse brain. **a** Mouse hippocampus stained with F4/80 shows the large amount of microglial membrane present and its heterogeneous distribution. *Scale bar* 500  $\mu$ m; *HF*, hippocampal formation; *fi*, fimbria. **b**, **c** Detail of microglial morphology in hippocampus (**b**) and fimbria (**c**). *Scale bars* 60  $\mu$ m, no counterstain

1989). Strongly SER<sup>+</sup> stellate macrophages are found in bone marrow stroma (where F4/80 but not SER mAb also labels developing monocytes), in a characteristic region of the spleen (marginal metallophil zone), where F4/80 is weak or absent, and in subcapsular stroma in lymph nodes. Weaker SER labelling is observed on Kupffer cells and spleen red pulp macrophages which are strongly F4/80<sup>+</sup>. Conversely, F4/80-poor alveolar macrophages can express sialoadhesin (CROCKER, MCWILLIAM and GORDON, unpublished). One reason for

differential expression of sialoadhesin is its dependence on exogenous inducer protein(s) which are present in normal mouse plasma and lymph (CROCKER et al. 1988a; MCWILLIAM and TREE, unpublished). Mouse serum contains similar levels of inducer activity to that found in plasma, and there is species restriction with regard to inducer source and target. Although the inducer proteins have not been characterised, exposure to plasma is correlated with sialoadhesin expression in vivo. In the central nervous system, for example, the SER antigen is absent where microglia are shielded from contact with plasma by the bloodbrain barrier. Microglia in circumventricular organs outside the blood-brain barrier are exposed to plasma proteins and express sialoadhesin; leakage of plasma proteins after injury to the nervous system also enhances SER antigen expression on microglia (PERRY et al. 1992). Monocytes and other SER-poor macrophages can be induced to express high levels of SER in vitro, although cells vary in the rate and extent of induction. Preliminary studies (MCWILLIAM and TREE, unpublished) indicate that cytokines, including interferons and interleukin-4, modulate sialoadhesin expression. These findings indicate that macrophage sialoadhesin is regulated by a complex network of signals that link immune responses and haemopoiesis. Although the role of sialoadhesin in haemopoietic cell interactions is not understood, its distinctive regulation in adult and foetal tissues makes it a valuable marker of specialised macrophages.

#### 3.2.1.3 FA.11

The FA.11 mAb reacts more broadly in tissues than F4/80 and is a candidate pan-macrophage reagent. However, since its expression is mostly intracellular, it is less satisfactory than mAbs that react with plasma membrane markers. FA.11 labels most of the cells which express F4/80 antigen in tissues, although some resident macrophage populations such as microglia are labelled lightly (LAWSON, unpublished), possibly reflecting down-regulation of endocytic activity in these cells. In contrast with F4/80 and sialoadhesin, FA.11 also reacts with scattered macrophage-like cells in T lymphocyte-dependent regions in spleen white pulp (RABINOWITZ et al. 1991a). Its labelling of dendritic and related cells in tissues will be discussed further below. Alveolar macrophages, another population which expresses low levels of F4/80, are strongly FA.11<sup>+</sup> (RABINOWITZ and CROCKER, unpublished). The distribution of FA.11 antigen therefore reflects endocytic stimulation, and its presence could provide a possible marker of macrophage activity in situ.

#### 3.2.1.4 CR<sub>3</sub>

Whilst the role of CR<sub>3</sub> in induced myelomonocytic recruitment has been studied in a variety of murine models of inflammation, as discussed below, expression on normal murine tissue macrophages is heterogeneous (FLOTTE et al. 1983). CR<sub>3</sub> and the other leucocyte integrins that share a common  $\beta_2$  chain, LFA-1 and p150/95, are regulated independently. Non-leucocyte integrins have been poorly characterised in murine tissues because of lack of suitable reagents, but monocytes and macrophages in other species are known to interact with fibronectin, fibrinogen, laminin and vitronectin (BEVILACQUA et al. 1981; BROWN and GOODWIN 1988; GRESHAM et al. 1989; SHAW et al. 1990; KRISANSEN et al. 1990).

Several anti-murine CR<sub>3</sub> mAbs label peritoneal macrophages and microglia. However, other major tissue macrophage populations, including Kupffer cells (LEE et al. 1985, 1986) and bone marrow stromal macrophages (CROCKER and GORDON 1985), express low levels of CR<sub>3</sub>. Alveolar macrophages lack CR<sub>3</sub> (Blusse van OUD ALBLAS and VAN FURTH 1979; GORDON, unpublished) but express high levels of LFA-1 (CROCKER, unpublished), a marker enhanced by macrophage activation (STRAUSMAN et al. 1986). In spleen, CR<sub>3</sub> is mainly present on PMNs in red pulp, but marginal zone macrophages are also labelled. The expression of p150/95 in murine tissues may provide a marker for lymphoid dendritic and related cells in spleen, as described below. Expression of the  $\alpha$  chains of leucocyte  $\beta_2$  integrins is therefore differentially regulated by their microenvironment in situ; CR<sub>3</sub> expression is rapidly up-regulated once CR<sub>3</sub>-negative macrophages are isolated from tissues and maintained in culture.

#### 3.3 Elicited and Activated Macrophages

Entry, accumulation and turnover of macrophages are markedly enhanced by many forms of tissue injury, inflammation and repair, including metabolic and neoplastic diseases. Plasma membrane molecules contribute to, and serve as useful markers of, many of the functional changes of macrophages involved in these processes. It is convenient to distinguish between exudate macrophages elicited by immunologically non-specific inflammatory stimuli and cells that are activated to display enhanced microbicidal and cytocidal properties by the actions of antigen-stimulated T lymphocytes (EZEKOWITZ and GORDON 1984). Both types of recruited cell also express common properties that distinguish them from resident macrophage populations in the peritoneal cavity and elsewhere (GORDON et al. 1988a). However, responses of macrophages in different tissues to local and systemic stimuli vary considerably and result in phenotypic heterogeneity that is difficult to interpret in regard to mechanism or functional significance (GORDON et al. 1988b).

Several broad generalisations can be made in this regard. Induced recruitment of monocytes following microbial infection and other forms of tissue injury is often accompanied by that of other myeloid cells, especially PMNs (myelomonocytic responses), whereas many forms of CNS injury, viral infection or malignancy recruit monocytes with T lymphocytes (mononuclear responses). Macrophages play a central role in initiating, perpetuating and resolving inflammation through their extensive repertoire of specific plasma membrane receptors (GORDON et al. 1988b) and secretory products (RAPPOLEE

and WERB 1991). However, it is not always clear to what extent these activities are mediated by resident macrophages already present in tissues, or by newly recruited monocytes. Resident macrophages in liver, spleen and bone marrow, for example, express plasma membrane receptors for sugar-specific recognition of foreign agents, but there is little information on the ability of these cells, possibly involved in first-line interactions with invading organisms, to produce monokines and other chemotactic and vasoactive mediators of inflammation. Resident tissue macrophages may be refractory to stimuli such as lipopolysaccharide (LPS), and host defence depends on rapid mobilization of blood monocytes that can be induced to release cytotoxic molecules (LEPAY et al. 1985a, b).

Surface receptors play a key role in macrophage production, migration and interactions with cellular and humoral ligands. The leucocyte integrin  $CR_3$  is known to be essential for induced myelomonocytic recruitment in response to a wide range of inflammatory stimuli (ROSEN and GORDON 1990a). The anti- $CR_3$  mAb 5C6 is a potent inhibitor of myelomonocytic cell adhesion to inflamed endothelium after non-specific stimulation (thioglycollate broth, LPS) and acute listerial infection (ROSEN et al. 1989) and partially inhibits monocyte recruitment in T cell-dependent delayed-type hypersensitivity (ROSEN et al. 1988) and autoimmune islet cell damage in non-obese diabetic mice (HUTCHINGS et al. 1990) However, other murine models of infection (e.g. BCG, PLASMODIUM yoelii) are resistant to 5C6 mAb (ROSEN, unpublished) and presumably involve  $CR_3$ -independent pathways of monocyte recruitment.

Once recruited cells arrive at a site of inflammation they undergo discrete stages of further differentiation before becoming fully activated, reflected by complex alterations of phenotype. For example, in a relatively simple model of inflammation, monocytes can be recruited to the peritoneal cavity of mice by local injection of biogel polyacrylamide beads (FAUVE et al. 1983; RABINOWITZ, unpublished; STEIN and GORDON 1991). These are too large to be ingested, but evoke the influx of macrophages which can be stimulated further by lymphokines or a phagocytic trigger to release high levels of tumour necrosis factor  $\alpha$  (TNF- $\alpha$ ), a characteristic property of immunologically activated as well as of thioglycollate-broth elicited macrophages (STEIN and GORDON 1991). Plasma membrane receptors for mannosylated ligands (MFR) or for Fc regions of lgG are efficient triggers for secretion of a range of mediators by primed macrophages, whereas CR<sub>3</sub> and other membrane antigens are inert in this regard (reviewed by GORDON et al. 1988b).

How useful are antigen markers in characterising the functional state of excudate macrophages in different local microenvironments? Several antigens are retained on recruited monocytes and/or induced in exudate macrophages, irrespective of the site at which the cells localise (LEE et al. 1986). These include F4/80, which is also present on Kupffer cells, and CR<sub>3</sub>, 7/4 and la (MHC class II), which are expressed mainly by recruited macrophages, for example in BCG-induced liver granulomata (Fig. 7) (RABINOWITZ, unpublished) Scattered cells in liver sinusoids which express these antigens in infected animals represent newly





**Fig. 7 a–e**. Heterogeneous expression of antigens by macrophages in murine liver during granuloma formation. Sections were labelled at the peak of the inflammatory response (day 10) after intravenous injection of bacille Calmette-Guérin (BCG) (RABINOWITZ, unpublished). **a**, **b** Low and high power views. F4/80 antibody labels all macrophages in granulomata, as well as Kupffer cells and trafficking monocytes in sinusoids. **c–e** Low, intermediate and high power views. Antibody 7/4 labels a subpopulation of activated macrophages in granulomata, as well as monocytes and neutrophils in blood vessels and sinusoids. Kupffer cells lining sinusoids are unlabelled

recruited migrating cells. In tissues such as liver (LEE et al. 1986) and the CNS (ANDERSSON et al. 1991) it becomes increasingly difficult to distinguish newly recruited monocytes that adopt the characteristic phenotype of macrophages in each microenvironment from resident cells that have been reactivated by local inflammation to express previously down-regulated markers.

It has also proved difficult to distinguish immunologically activated macrophages (i.e. those recruited cells which display an enhanced capacity to kill intracellular pathogens) from non-cytocidal exudate macrophages by antigen marker analysis in situ. Cytokines produced by macrophages themselves, by activated T lymphocytes or by other cells are potent modulators of the macrophage phenotype. There is little information on the effects of locally produced cytokines on antigen expression at sites of immune and inflammatory reactions and on the range of cellular targets induced. Interferon- $\gamma$ , for example, is a major, although not unique, inducer of la in lymphokine-activated macrophages. The 7/4 antigen is expressed by BCG-activated macrophages in situ; however, it is not inducible in vitro by interferon-y alone, but only in combination with other T cell dependent and other growth factors (TREE, unpublished; MAUDSLEY et al. 1991). la (MUNRO et al. 1989) and an intracellular antigen (IP10) induced in macrophages by interferon- $\gamma$  are also widely expressed in neighbouring endothelial and epithelial cells (KAPLAN et al. 1987). Immunomodulatory agents which deactivate macrophages in situ include glucocorticoids, transforming growth factor  $\beta$  (DING et al. 1990) and interferon- $\alpha/\beta$ (EZEKOWITZ et al. 1986). The profile of antigen markers expressed by macrophages therefore varies considerably at different stages of an inflammatory or immune process.

At present there are surprisingly few antigen markers available to assess macrophage functional status in situ, in spite of many attempts to produce such reagents. Further studies are needed to correlate antigen expression with changes in secretory repertoire (respiratory burst, TNF etc.) and to define the link between cell differentiation and activation more clearly. Cellular antigens could prove useful in analysing the effects of chemotactic and phagocytic stimuli, cytokines and hormones on macrophages if more discriminating mAbs were isolated and antigen expression correlated more precisely with function.

#### 4 Relationship of Macrophages to Cells of Related Lineages

Several cell types derived from bone marrow progenitors pass through the blood at some stage of their life history and express macrophage-like characteristics in tissues. Antigen markers have been of great value in distinguishing cells of clearly different haemopoietic lineages, but the relationship of macrophages (the cells of the mononuclear phagocyte system) to other cells of bone marrow origin such as lymphoid dendritic cells (LDCs) and osteoclasts remains unclear. LDCs belong to an ill-defined group of specialised accessory cells that include veiled, interdigitating and Langerhans cells (for reviews see AUSTYN 1987; MAC-PHERSON 1989). Isolated LDCs are uniquely potent in presenting antigen to T lymphocytes to initiate primary immune responses (STEINMAN et al. 1986). Macrophages and B lymphocytes also serve as accessory cells in secondary immune responses, but lack the ability to stimulate naive T lymphocytes efficiently. Dendritic cells are found mainly in lymphoid organs, although not necessarily in the same sites as macrophages, and both cell types can be present in epithelia. LDCs migrate through blood as well as lymph (AUSTYN 1989; LARSEN et al. 1990), and may recirculate from peripheral lymphoid organs, unlike macrophages. Both cell types express common markers during part of their life history and it is not clear whether, or at what stage, these lineages have separated from each other. Similarly, the mature osteoclasts of bone derive from circulating mononuclear cells (for review see CHAMBERS 1989), but it is not known whether they are distinct from monocytes. Recent studies to characterise these various cells in tissues and in culture have provided insights into their specialisation without resolving the question of their interrelationship. Antigen marker expression will be considered in the context of their other properties and of general methods of lineage analysis.

In principle, precursor-product relationships can be established for particular cell types by examining the progeny of suitably marked progenitor cells in vivo and in vitro. One difficulty has been the lack of defined culture systems to grow and maintain cells with the appropriate phenotype, another the shortage of specific markers. Although macrophages adapt readily to cell culture, they do not necessarily retain or remain able to acquire a specialised tissue phenotype. especially when derived from proliferating precursors. Studies on the stromal markers sialoadhesin and EbR have demonstrated the deficiencies of cell lines and standard culture systems in maintaining macrophage differentiation in vivo (MCWILLIAM and FRASER, unpublished). Lineage analysis of these macrophagerelated cells has proved difficult in vitro. It has not been possible to generate LDCs from haemopoietic progenitor cells in culture although cells of the LDC phenotype have been derived from isolated Langerhans cells, as discussed further below. Osteoclasts can be generated in small numbers as part of multilineage colonies derived from bone marrow or spleen progenitors (HATTERSLEY, KERBY and CHAMBERS, 1991; UDAGAWA et al. 1989; KURIHARA et al. 1991; KERBY et al. 1991). Stromal fibroblasts are required, as well as multispecific growth factors, and osteoclasts are often found in these cultures with macrophages, which proliferate more vigorously (KODAMA et al. 1991b). Tumourderived or transformed haemopoietic cell lines may provide alternative precursors for clonal analysis to primary sources in foetal liver, bone marrow or spleen, but have not yet contributed to the elucidation of this problem.

It might be thought that expression of plasma membrane receptors for lineage-restricted growth factors could provide ideal markers to distinguish macrophages from their close relatives. For example, receptors for CSF-1 (c-*fms*) mediate monocytic differentiation when primary precursors (see chapter by STANLEY in this volume) or undifferentiated myeloid cell lines (PIERCE et al. 1990; WU et al. 1990) are treated with CSF-1 in vitro. However, analysis of CSF-1 receptor expression on tissue macrophages, osteoclasts and LDCs is sketchy. Expression of CSF-1 receptors in situ is not restricted to macrophages, but is found on trophoblast epithelium, and receptor expression on macrophages is subject to down-regulation.

Recent studies with osteopetrotic mice, which display deficient osteoclast function, provide evidence that CSF-1 is essential for development of osteoclasts

(WIKTOR-JEDRZEJCZAK et al. 1990; YOSHIDA et al. 1990). Homozygote *op/op* mice carry a mutation in CSF-1 and in the adult contain reduced numbers of blood monocytes and selected tissue macrophages (FELIX et al. 1990a). Some of these deficiencies can be corrected by exogenous CSF-1 (KODAMA et al. 1991a; FELIX et al. 1990b). The role of CSF-1 in LDC differentiation has not been defined. Receptors for GM-CSF are also not sufficiently selective for fine lineage resolution. Apart from various myeloid cells, there is evidence that dendritic cells respond to this factor in cell culture (KOCH et al. 1990). Other receptors for known cytokines are often broadly distributed on haemopoietic and non-haemopoietic cells.

At present analysis of lineage depends on antigen markers and phenotypic properties of cells that have been studied in situ, or after isolation from various tissues. Interpretation of these studies should take into account the differentiation, migration and modulation of cells within different microenvironments. The problem of variability of cellular phenotype can be illustrated by considering the properties of LDCs and Langerhans cells (LENZ et al. 1989). Isolated LDCs lack F4/80, but constitutively express high levels of la and are potent stimulators of a mixed leucocyte reaction (MLR) when cocultivated with resting, allogeneic T lymphocytes. Earlier attempts to identify these cells in situ were handicapped by lack of dendritic cell-specific markers suitable for immunocytochemistry. Recent studies have reported that dendritic interdigitating cells in mouse spleen express a p150/95 integrin (METLAY et al. 1990) which is less widely expressed on other tissue macrophages than in man (HOGG et al. 1986), and which may therefore be a selective marker for murine LDCs. A possible relationship between altered integrin expression and induced migration of Langerhans cells and LDCs has not been reported.

Langerhans cells are widely distributed in the epidermis and in other complex epithelia and express properties which link them to tissue macrophages and LDCs. They contain morphologically distinct Birbeck granules and have been implicated in antigen responses in skin and in draining lymph nodes, to which they migrate. Langerhans cells express F4/80 and other plasma membrane antigens in a characteristic pattern of regularly spaced stellate cells surrounded by keratinocytes. When isolated from epidermal sheets, Langerhans cells lose F4/80 antigen, but acquire enhanced MLR activity in culture (SCHULER and STEINMAN 1985). GM-CSF improves survival of Langerhans cells in vitro (WITMER-PACK et al. 1987), but the cells do not retain F4/80, unlike macrophages derived from bone marrow precursors in the same culture medium. These findings are compatible with the hypothesis that Langerhans cells mature into functional LDCs.

Expression of the FA.11 antigen provides further evidence that LDCs and macrophages are related cells. FA.11 labelling is restricted to macrophages and dendritic cells (RABINOWITZ, MILON, STEINMAN and AUSTYN, unpublished), unlike other endosomal/lysosomal membrane glycoproteins which are more widely distributed in haemopoietic and non-haemopoietic cells (DA SILVA, LAWSON and ROSEN, unpublished). The FA.11 antigen is found in solitary granules in dendritic

cells, perhaps reflecting a rudimentary or specialised vacuolar apparatus, compared with its distribution in macrophages, which contain numerous FA.11<sup>+</sup> vesicles in their cytoplasm. Recent studies have confirmed that endocytic organelles become reduced when Langerhans cells are isolated from epidermis and differentiate into LDC-like cells in culture (STÖSSEL et al. 1990).

Osteoclasts lack F4/80 antigen, unlike macrophages on adjacent periosteal or endosteal surfaces in bone (HUME et al. 1984b), but express other leucocyte antigens (ATHANASOU et al. 1987). Although macrophages are potent catabolic cells able to degrade a range of connective tissue elements, including fragments of ingested bone, only true osteoclasts excavate intact bone by local secretion. Bone resorption is inhibited by calcitonin and osteoclasts express abundant receptors for calcitonin (NICHOLSON et al. 1986; TAYLOR et al. 1989). Giant cell formation is uninformative in distinguishing between osteoclasts, which can be mononuclear, and macrophages, which are often multinucleated, the extent of polykaryocytosis depending on the species. Osteoclasts and macrophages share a H<sup>+</sup> electrogenic vacuolar proton pump, but it is not known whether endosomal antigens such as FA.11 are present in both cell types.

These studies indicate that there is considerable overlap among these different lineages. Improved cell-restricted marker antigen would be helpful in defining in vivo precursors, branch points and possible interconversions among these cells, and their migration pathway within tissues.

#### **5 Antigens and Macrophage Heterogeneity**

We have demonstrated that macrophages and related cells are constitutively present in different compartments of the body, that they migrate via blood and lymph and that they undergo complex changes in phenotype in different tissues even in the absence of inflammation. The induced recruitment of blood monocytes as a result of inflammation and injury brings cells from a common pool to tissue environments in which extrinsic and local factors further modulate the macrophage phenotype.

Mature macrophages interact with most other cell types in the body, including endothelium, epithelium, fibroblasts, lymphohaemopoietic and neuroendocine cells. These cells and extracellular matrix influence expression of antigens and secretory products by macrophages within each microenvironment. Regional specialisation in macrophage biosynthetic activity can be detected by in situ hybridisation for mRNA products such as lysozyme (CHUNG et al. 1988), TNF- $\alpha$  (KESHAV et al. 1991) and other monokines. Does the extensive heterogeneity of cell phenotype reflect a single major lineage of mononuclear phagocytes or are there subsets of macrophages, perhaps analogous to the diversity of T lymphocytes? To what extent can cell differentiation and modulation within tissues account for current knowledge of macrophage heterogeneity and how successfully can we replicate in culture the unique phenotype expressed by macrophage populations in situ?

Antigen markers can be used to follow modulation of mature macrophages directly after adoptive transfer to different sites in the body. The effects on macrophage antigen expression of specialised microenvironments in spleen, liver and lung, for example, can be studied by introducing suitably marked cells via different routes in the intact animal. A more general method is to use mAbs directed against various plasma membrane antigens to separate progenitor cells from mature haemopoietic cells in bone marrow, foetal liver or spleen, and to study their progeny. This approach has been little used to analyse macrophage differentiation in vivo, but was used by HIRSCH et al. (1981) to examine expression of F4/80 during macrophage differentiation in cell culture. Bone marrow progenitors were sorted on the basis of F4/80 labelling and incubated with L cell conditioned medium as a source of CSF-1. FACS analysis showed that GM-CFUc lack F4/80, which first appeared on immature promonocytes at the time cells became adherent. Studies with anti  $CR_3$  and 7/4 mAbs (HIRSCH and GORDON, unpublished) indicate that, as expected for myelomonocytic markers, these antigens are expressed earlier than F4/80 on GM presursors that form clusters of both macrophages and PMNs in the presence of GM-CSF. Since SER and FA.11 are not expressed by PMNs, they are probably also acquired after these lineages separate. Monocytes and less mature stages of macrophage development express FA.11 (MILON and GORDON, unpublished), but not SER. F4/80 expression is weak and variable on monocytes so that it is difficult to use this marker to study blood mononuclear cell heterogeneity by fluorescence sorting experiments. Moreover, the yield of blood monocytes from the mouse is small and these cells have a more limited proliferative capacity than progenitor cells.

In addition to relating antigen expression to cell maturity, it is possible to study clonal heterogeneity in CSF-supplemented cultures. Bone marrow CFUc cultivated in L cell-conditioned medium yielded colonies in which all macro-phages in all colonies expressed F4/80 uniformly (HIRSCH et al. 1981). In other studies, the activation marker la was induced on all independent colonies, although variable numbers of macrophages in each colony expressed this antigen. Early studies in which only a limited range of precursors, CSFs and antigen markers were examined, failed to reveal clonal heterogeneity among mononuclear phagocytes, and the conclusion was drawn that we are dealing with a single cell lineage. Similar further clonal studies are needed with specific markers and functional assays for LDCs and osteoclasts.

Several variables need to be taken into account to perform this type of analysis. It is necessary to define the role of cell growth in influencing expression of a stable specialised phenotype. Clonal analysis might also bring to light a requirement for another cell type (macrophage or fibroblast) which could play an accessory role in haemopoietic cell differentiation. Improved culture systems are needed to study relationships among macrophages, LDCs and osteoclasts, and among mononuclear phagocytes, such as stromal macrophages, alveolar macrophages and Langerhans cells which display a tissue-specific phenotype. In particular, are different cell phenotypes stable or interconvertible, can they be modulated during a proliferative phase or only once cells become terminally differentiated? A related requirement is to define the environmental factors which regulate the phenotype of these cells in situ. Expression of markers such as CR<sub>2</sub> and sialoadhesin on macrophages is tightly controlled in different tissues, but regulation is lost or only partly reproduced in present culture systems. Although some of the variables that regulate marker expression in vivo have been identified, such as the plasma inducer of sialoadhesin, other modulating factors in the microenvironment such as the role of extracellular matrix require further study. The extensive down-regulation of antigens and other markers in highly differentiated macrophages such as resident microglia cannot be reproduced in vitro. This may result from inhibitory interactions with specialised cells in brain parenchyma (neurons, other glia) acting through macrophage surface receptors, or from the absence of elements found outside the CNS. The role of foreign antigens, LPS and other exogenous agents in modulating macrophage differentiation in tissues should also be borne in mind.

The lymphohaemopoietic system provides a variety of model systems to study the interplay between pluripotent stem cells and specific cytokines that regulate their growth and differentiation. Bipotential precursors for macrophages and granulocytes have been of particular interest in defining events that accompany commitment to specialised lineages. The heterogeneity of tissue macrophages and closely related cells, as discussed here, offers a unique opportunity to study modulation and differentiation of mature cells, and the interplay of environmental signals and intracellular events that regulate cellspecific functions. Development and characterisation of well-defined antigens should provide markers to analyse the mechanisms by which macrophage diversity is generated.

#### 6 Conclusion

The combined use of antigen markers and in situ hybridisation has delineated the life history of macrophages and their functions in tissues. The distribution of cells has been followed during development, and through adult life, in the steady state and in response to physiologic changes and pathologic perturbations. The F4/80 mAb provides a tool to map cell distribution, to identify microheterogeneity among macrophages within a single organ, and to reveal accumulation of newly recruited monocytes at sites of injury and their adaptation within a specific tissue environment. F4/80 antigen expression is absent on macrophages, defined by other marker antigens, in specialised regions of lymphoid organs. The FA.11 antigen is more widely expressed on macrophages and on LDCs and is responsive to endocytic stimuli. The sialoadhesin (SER) receptor marks a subpopulation of stromal macrophages in lymphohaemopoietic tissues which
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are involved in non-phagocytic, possibly trophic, cellular interactions. Antigen markers have revealed adaptations and novel functions of macrophages, and have provided tools to manipulate their migration and behaviour in tissues. Membrane antigens combined with other marker molecules make it possible to study the role of these versatile cells in a wide range of disease processes, and provide model systems to study fundamental questions of cellular differentiation.

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# Appendix

Immunohistochemistry with F4/80 mAb (adapted from HUME et al. 1983b; PERRY et al. 1985). Method is based on the biotin-avidin-peroxidase method of HSU et al. (1981).

### Reagents

a) F4/80 hybridoma supernatant can be purchased from:

UK:	Serotec 22 Bankside Station Approach Kidlington Oxford OX5 1JE	Tel: UK 0867579941 Fax: UK 086753899	
USA:	Bioproducts for Science Inc. PO Box 29176 Indiana 46229	Tel: (317) 894 7536 Fax: (317) 894 4473	
Japan:	Dai Nipon Pharmaceuticals Co. Ltd.		

Japan: Dai Nipon Pharmaceuticais Co. Ltd. 6–8 Doshomachi 2-Chome Chuo Ku Osaka 541

Use 1:20 in phosphate-buffered saline (PBS)

- b) Biotinylated rabbit anti-rat IgG, preferably adsorbed to remove crossreactivity with mouse IgG, 1:100 (Vector Laboratories Ltd. 16 Wulfric Square, Bretton, Peterborough, Cambridgeshire, UK).
- c) 1% normal rabbit serum (Vector Laboratories Ltd).
- d) Detection complex (Elite ABC; Vector Laboratories Ltd), 2 drops of each reagent in 5 ml PBS. This needs to be made up at least 30 min before use, but should not be kept longer than 72 h.

e) Chromogen (DAB)

0.125 g diaminobenzidine tetrahydrochloride
0.2 g imidazole (optional)
250 ml 0.1 M phosphate buffer, pH 7.2
125 µl 30% hydrogen peroxide, added just before use.

#### Methods

- 1. Dewax wax sections and take to water. Thaw frozen sections and ensure they are thoroughly dry.
- 2. Wash sections in PBS for ca. 10 min to remove embedding medium.
- 3. Incubate with 1% normal rabbit serum for 30 min at room temperature, in a humidity chamber. Do not allow any reagents to dry on sections.
- 4. Remove excess serum and incubate with F4/80 mAb for 60 min at room temperature.
- 5. Wash sections in PBS; at least  $2 \times 10$ -min washes are desirable.
- 6. Incubate in biotinylated secondary antiserum for 45 min.
- 7. Wash sections (at least  $2 \times 10$  min).
- 8. To quench endogenous peroxidase activity, place sections in 0.3% hydrogen peroxide in methanol (alternatively 96% alcohol) for 20 min.
- 9. Wash sections  $(2 \times 10 \text{ min})$ .
- 10. Incubate in Elite ABC for 45 min at room temperature.
- 11. Wash well (at least  $2 \times 10$  min, preferably 3 washes).
- 12. React in DAB, observing the progress of the reaction. If often takes only around 20-30 s.
- 13. Wash well in PBS or 0.1 M phosphate buffer.
- 14. The DAB reaction product may be intensified by incubation in 0.01% osmium tetroxide in 0.1 M phosphate buffer for about 30 s, followed by careful washing.
- 15. Counterstain as required, dehydrate and mount sections.

### Notes

- The commonest cause of failure of F4/80 staining is poor fixation of the tissue. We routinely use 2% paraformaldehyde, lysine, periodate (PLP) perfusion-fixed material (MCLEAN and NAKANE 1974) with or without 0.05%-0.1% glutaraldehyde for use with mAb F4/80, ensuring that the final pH is 7-7.4. The antigen is also stable to 0.5% buffered glutaraldehyde for use with mAb F4/80, Carnoy's fixative or acid alcohol. Buffered paraformaldehyde, Karnovsky's fixative and picric acid are not satisfactory fixatives.
- 2. F4/80 staining may be carried out on fixed frozen sections or on material embedded in paraffin or polyester wax. Morphologic preservation is better with wax-embedded material but there may be some loss of antigen during prolonged infiltration steps with paraffin wax at 60 °C.

3. It may be necessary to extend the incubation time for the primary antibody or to increase its concentration.

The perfusion fixation protocol has been successfully used with the other mAbs described, although the appropriate antibody concentration and incubation time have to be determined for each. For intracellular antigens such as FA.11 it may be necessary to extend the incubation time with mAb.

- 4. 0.1% Triton X-100 may be added to wash buffers, to improve washing and render sections more wettable. It is also useful for enhancing penel of mAbs directed at intracellular antigen.
- 5. An alternative method for carrying out colour reaction is to use glucose oxidase and glucose to generate  $H_2O_2$ :

To 250 ml 0.1 M phosphate buffer add:—0.125 g DAB

 $-0.4 \text{ g} \beta$ -D-glucose

—0.08 g NH<sub>4</sub>Cl

—A few mg glucose oxidase

Incubate sections with this mixture and observe progress of reaction. It takes about 8–10 min with 10  $\mu M$  sections depending on the amount of enzyme added.

A similar principle may be applied to the quenching of endogenous peroxidase activity. In this case a few mg glucose oxidase are added to 0.1 M phosphate buffer containing 1 mM sodium azide and 10 mM glucose. Sections are incubated with this mixture for 15 min at 37 °C with shaking.

6. Negative controls, where the primary antibody is replaced with diluted normal serum, PBS or irrelevant antibody should be included with each batch of experimental slides. Causes of false positive reactions include the presence of melanin, endogenous peroxidase activity, endogenous biotin, non-specific binding of the primary antibody (including binding by its Fc moiety) and cross-reactivity of the secondary antibody between rat and mouse IgG which may be present in the tissue.

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# Macrophages in the Uterus and Placenta

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# **1** Introduction

Macrophages are abundant in the mesenchymal and connective tissue stroma of the cycling and pregnant uterus, and constitute a significant proportion of the villous or labyrinthine mesenchymal cells in the human and murid placenta. In other contexts, the activities of these multifunctional cells are strongly influenced by regulatory molecules such as steroid hormones, polypeptide growth factors, and bioactive lipids. All of these are present at particularly high concentrations in the pregnant uterus and placenta. Thus, uterine and placental macrophages stimulated by endogenous factors could contribute to the complex cellular and molecular interactions that result in successful pregnancy.

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This article will focus on uterine and placental macrophages in the human, mouse, and rat species, in which placentation displays some similarities and considerable experimentation has been done. Studies are presented that document the preferred locations of these cells in uterine and placental compartments, explore chemoattractants, describe differentiation and activation in resident cells, and suggest some specific uterine and placental macrophage functions that might contribute to the success of pregnancy. The discussion will conclude with a commentary on our findings in the colony stimulating factor-1 (CSF-1)-less, macrophage-deficient osteopetrotic (op/op) mouse, which illustrate for the first time that a specific hormone-dependent uterine growth factor, CSF-1, has a major influence on the properties of macrophages in the uterus.

## 2 Anatomic Arrangements of Uterine and Placental Tissues and Hormonal Influences

In mammals, the uterus comprises two distinct layers of tissue, the endometrium and the myometrium, as shown for rats in Fig. 1a. The endometrium is composed of a single layer of epithelial cells forming the uterine lumen and leading to glands that ramify through the supporting mesenchymal stroma. The myometrium is composed of circular and longitudinal muscle layers interspersed with connective tissue stroma. In the mesometrial region of rat and mouse uterus, the stromal area between the longitudinal and circular muscles is termed the mesometrial triangle, the region in which the metrial gland arises during pregnancy.

In humans, rats, and mice, implantation of the blastocyst is accompanied by differentiation of adjacent endometrial stromal cells into decidual cells, as shown for rats in Fig. 1b. In humans, decidualization also takes place in the cycling uterus. During pregnancy in all three species, decidual cells form the maternal cellular component of the maternal–fetal interface. The fetal component of this interface comprises tropoblast cells, which arise from the trophectoderm layer of the blastocyst to form the placenta, the position of which is shown for rats in Fig. 1c. The inner cell mass of the blastocyst contributes cells to the underlying placental mesenchyme that is contiguous with the cord, to the membranes that surround the embryo, and to the embryo. Although the anatomic arrangements of the placental cell layers are not identical, hemochordial placentation, where maternal blood circulates through the placenta in direct contact with trophoblast cells, is common to humans, rats, and mice. The murids have therefore been used extensively for experimental purposes.

In the cycling or pseudopregnant uterus, fluctuating levels of estrogens and progesterone cause dramatic changes in the uterine endometrium. These include proliferation of the uterine epithelial cells in response to estradiol-17- $\beta(E_2)$ , differentiation stimulated by progesterone, and altered production of



**Fig. 1 a–c.** Anatomic compartments of the rat virgin uterus (**a**), and the pregnant uterus at days 7 (**b**) and 12 (**c**) of gestation. The figures are oriented such that the mesometrial region is at the top and the antimesometrial region is at the bottom. The positions of the blastocyst within the lumen (day 7) and the embryo (day 12) are shown. *CM*, circular muscle of the myometrium; *DB*, decidua basalis; *DC*, decidua capsularis; *EM*, stroma of the endometrium; *GC*, giant trophoblast cell layer of the placenta; *L*, lumen; *LEp*, luminal epithelium; *LM*, longitudinal muscle of the myometrium; *MG*, metrial gland; *MT*, mesometrial triangle; *P*, placenta; *PDZ*, primary decidual zone; *SZD*, secondary decidual zone. (CHEN et al. 1991)

polypeptide growth factors (POLLARD 1990). In the endometrial stroma, progesterone sensitizes the cells to respond to  $E_2$  by proliferation (MARTIN et al. 1973; TABIBZADEH 1990), and cyclic changes in proportions of stromal cells expressing specific hematopoietic cell markers have been noted (KING et al. 1989; LAGUENS et al. 1990). In humans, estrogen and progesterone concentrations remain high during pregnancy. In rat and mouse uterus, whilst progesterone levels are high, the estrogen levels only reach high concentrations late in pregnancy. New hormones such as chorionic gonadotropin (in humans), placental prolactins, luteotropins, and prolactin-like molecules are also synthesized in the decidua and placenta.

Alterations in cellular behavior observed in the cycling and pregnant uterus in response to steroid hormones may be an indirect effect of these hormones on the synthesis or release of locally acting growth factors and bioactive lipids (HILL 1989; BRIGSTOCK et al. 1989; POLLARD 1990; SIMMEN and SIMMEN 1991). For example, in mice, stimulation of uterine epithelial cells by ovarian hormones induces synthesis of CSF-1 (BARTOCCI et al. 1986; POLLARD et al. 1987; ROTH and STANLEY, this volume), a growth factor for macrophages (TUSHINSKI et al. 1982; BOOCOCK et al. 1989) that is targeted, in addition to macrophages, to both decidual cells and trophoblast in the pregnant uterus (MULLER et al. 1983; REGENSTREIF and ROSSANT 1989; ARCECI et al. 1989; POLLARD 1990). Other uterine growth factors that give indications of ovarian hormone regulation, but are less well documented than CSF-1, are transforming growth factor- $\beta$ 1 (TGF- $\beta$ 1) (TAMADA et al. 1990) and tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) (YELAVARTHI et al. 1991), molecules with pleiotropic effects on the growth and differentiation of cells, including macrophages (RIZZINO 1988; SPORN and ROBERTS 1989; BEUTLER and CERAMI 1989).

Hormonally stimulated epithelial–mesenchymal cell interactions have been identified in the uterus and other tissues (CUNHA et al. 1983). Macrophages are abundant in the connective tissue and mesenchymal stroma of the cycling and pregnant uterus (NICOL 1935; TACHI et al. 1981), and populate the mesenchyme of the placental villi, particularly in humans (MOSKALEWSKI et al. 1974, 1975; FOX 1978). Uterine and placental macrophages are therefore likely to be participants in these epithelial–mesenchymal cell interactions. Their products could influence developmental events in the uterus, placenta, and, possibly, the embryo (TACHI et al. 1981; HUNT 1989a, 1990; SOKOL et al. 1990).

## **3 Uterine Macrophages**

Migration of blood monocytes into the uterus is increased during pregnancy and the cells home to specific anatomic compartments, where residency stimulates differentiation into phenotypically distinct subpopulations, and local conditions induce the expression of activation-associated markers. Uterine macrophages seem to have multiple functions, many of which are related to their secretory products. (Table 1)

## 3.1 Distribution and Chemotaxis

The anatomic locations of macrophages are highly predictable in both the cycling and the pregnant uterus. In the virgin mouse uterus, macrophages are distributed throughout the endometrium. A recent study suggests the proximity to the epithelial cell layer may be related to stage of the cycle (DE and WOOD 1990). In the myometrium, the cells are present in the connective tissue stroma and are closely associated with the serous membrane (HUNT et al. 1985). Quantitative studies on rat macrophages in situ show that macrophages account for approximately 10% of the total cells in virgin rat endometrium, and 5% of the cells in the myometrium (YELAVARTHI et al. 1991).

Uterine macrophages	
Phagocytosis	Tachi et al. 1981 (rat) RedLine et al. 1990 (mouse)
Immunoregulation	HUNT et al. 1984b (mouse) TawFik et al. 1986a, b (mouse) MATTHEWS and SEARLE 1987 (mouse) LALA et al. 1988 (human) OKSENBERG et al. 1988 (human)
Growth factors	
CSF-1	Not documented
TGF-β1	IAMADA et al. 1990 (mouse)"
1 NF-02	FELAVARTHI Et al. 1991 (Fat) Hu et al. 1992 (monocutes, human)
IL-6	Тавівzаден et al. 1988 (human) <sup>a</sup>
Tissue remodeling	Not documented
Placental macrophages	
Phagocytosis	Fox 1978 (human)
	Loke et al. 1982 (human)
Immunostimulation	Hunt et al. 1984a (human)
Growth factors	
CSF-1	Daiter et al. 1992 (human) <sup>a</sup>
TGF-β1	Not documented
INF-α	CHEN et al. 1991 (human)"
IL-1	FLYNN ET AL 1982 (NUMAN)
IL-6	Not documented

Table 1. Potential functions of uterine and placental macrophages

<sup>a</sup> The results of the these studies provide circumstantial evidence that mononuclear phagocytes are sources of the particular uterine and placental polypeptide growth factors

Studies on dispersed cells show that the proportion of uterine cells bearing macrophage markers doubles during pregnancy (HUNT et al. 1985), and immunocytochemical analysis of rat tissues indicates the same (YELAVARTHI et al. 1991). In early gestation tissues, the distribution of macrophages in the myometrium and nondecidualized endometrial stroma is unchanged. However, where decidualization takes place in the stroma immediately surrounding the blastocyst (Fig. 1b), the macrophages are redistributed. There are virtually no cells bearing the usual macrophage-specific markers in the rat (TACHI et al. 1981; YELAVARTHI et al. 1991) or mouse (POLLARD et al. 1991a) primary decidual zone. Instead, macrophages are relegated to the nondecidualized endometrium immediately beneath the circular muscle of the myometrium. Exclusion of macrophages from the decidua basalis continues into late stages of pregnancy (REDLINE and LU 1988, 1989; YELAVARTHI et al. 1991). Mouse decidual substratum is apparently not conducive to macrophage migration, which could account for the lack of these cells in late gestation decidua (REDLINE et al. 1990).

At mid to late stages of pregnancy, macrophages remain abundant in the myometrium [15%–20% of the total cells in the rat (YELAVARTHI et al. 1991)].

Macrophages account for 10–20% of the cells in the rat metrial gland, a specialized structure in the mesometrial triangle (Fig. 1b, c) that is not present in human tissues, whereas they are scarcer in this compartment in mice (PARR et al. 1990).

The population densities of uterine macrophages as a function of the menstrual cycle have not been determined with certainty in human tissues because of the obvious difficulties in obtaining normal tissues, and the size of the uterus, which could cause sampling errors. Although marker studies indicate that the relative proportions of bone marrow-derived cells in the endometrial stroma fluctuate during the cycle (KING et al. 1989; LAGUENS et al. 1990), the proportions of macrophages seem to remain stable (KING et al. 1989). Macrophages are present in the cycling and pregnant human myometrium (KHONG 1987) and, during pregnancy, in the decidua. Unlike the situation in mice and rats, macrophages are among the bone marrow-derived cells that are most common in the human decidua, being found near the implantation site (KABAWAT et al. 1985) and in close proximity to trophoblast cells at both early and late stages of pregnancy (LESSIN et al. 1988; BULMER et al. 1988, 1989; HUNT 1989b).

Concentration gradients of chemotactic factors, discussed below, might dictate the final anatomic locations of monocytes migrating into the pregnant uterus. Synergistic interactions among some of these factors, CSF-1 and TNF- $\alpha$ for example (BRANCH et al. 1989), could also stimulate in situ proliferation. In mice, there is clear evidence that migration of blood leukocytes into the uterus is hormonally regulated (FINN and POPE 1986). An influx of leukocytes into the immature uterus in response to exogenously administered estrogens has been documented in rats, and monocytes constitute a significant proportion of the migrating cells (ZHENG et al. 1988). Pregnancy hormones such as progesterone may be directly chemotactic for monocytes (YANG et al. 1989) or might stimulate the production of factors that influence their migration (FINN and POPE 1986). This latter pathway seems more likely given the fact that at least one chemotactic molecule, CSF-1 (WANG et al. 1988), is hormonally regulated (BARTOCCI et al. 1986; POLLARD et al. 1987), and uterine levels of this factor increase markedly from day 1 of mouse pregnancy (POLLARD et al. 1987; POLLARD, unpublished data). Other potential chemoattractants are TGF- $\beta$ 1, TNF- $\alpha$ , and colony stimulating factor for granulocytes and macrophages (GM-CSF) (WAHL et al. 1987; MING et al. 1987; WANG et al. 1987), all of which are present in higher concentrations in the pregnant than in the cycling uterus (TAMADA et al. 1990; CHEN et al. 1991; YELAVARTHI et al. 1991; ROBERTSON and SEAMARK 1990) and might be stimulated by ovarian or other hormones. However, no studies have as yet documented directly that higher levels of any of these growth factors stimulate monocyte migration into the uterus.

### 3.2 Differentiation

Monoclonal antibodies to rat macrophages, ED1 and ED2 (DIJKSTRA et al. 1985; SMINIA and JEURISSEN 1986), have been instrumental in subdividing rat uterine



**Fig. 2 a,b.** Subpopulations of macrophages in the rat mesometrial myometrium at day 12 of gestation identified with the mouse monoclonal antibodies ED1 and ED2 (Bioproducts for Science). The tissue was fixed in an alcohol-based fixative (OmniFix, Xenetics Biomedical). **a** ED1<sup>+</sup> cells; **b** ED2<sup>+</sup> cells. Arrows mark some of the positive cells. Note that ED1<sup>+</sup> cells are small and round whereas ED2<sup>+</sup> cells are larger and highly vacuolated. x 313

macrophages into two categories, small round cells that closely resemble monocytes (ED1<sup>+</sup> cells) and fully differentiated, highly vacuolated tissue macrophages (ED2<sup>+</sup> cells) (Fig. 2). Studies on ED1<sup>+</sup> and ED2<sup>+</sup> subpopulations in the pregnant rat uterus show that ED1<sup>+</sup> cells are more common in the undecidualized endometrial stroma than ED2<sup>+</sup> cells, and that the few macrophages that are found in the decidua express only this marker (YELAVARTH) et al. 1991). ED1<sup>+</sup> and ED2<sup>+</sup> cells are present in approximately equal numbers in the metrial gland whereas the myometrial stroma contains predominantly ED2<sup>+</sup> cells. TACHI and TACHI (1989) have shown that ED1<sup>+</sup> and ED2<sup>+</sup> cells secrete different patterns of bioactive lipids. Thus, the ED1<sup>+</sup> and ED2<sup>+</sup> cells in the uterus might function differently. Differentiated subpopulations have not been identified in the mouse uterus-only a polyclonal reagent and the antimacrophage monoclonal antibody F4/80 (HUME et al. 1983), which marks a 150-kDa glycoprotein present on a proportion of bone marrow cells, monocytes, and macrophages (STARKEY et al. 1987), have been used (HUNT et al. 1985; REDLINE and LU 1988, PARR et al. 1990; POLLARD et al. 1991a).

There have not as yet been any studies on specific differentiationassociated macrophage markers expressed by the cells in the human uterus through the course of gestation. However, we have noted that the monoclonal antibody 63D3 binds to different macrophage subpopulations in the decidua adjacent to the chorion membrane than does the monoclonal antibody OKM1, which identifies C3 receptors (HUNT, unpublished data), and others have reported similar findings with different antimacrophage reagents (BULMER and JOHNSON1985).

Colony stimulating factor-1, GM-CSF, and TNF-α are major candidates for the factors that cause differentiation of new arrivals into morphologically and functionally distinct uterine tissue macrophages. These factors, found in the uterus, decidua, and placenta (BARTOCCI et al. 1986; ROBERTSON and SEAMARK 1990; CRAINIE et al. 1990; YELAVARTHI et al. 1991; CHEN et al. 1991), can influence macrophage maturation (TUSHINSKI et al. 1982; BOOCOCK et al. 1989; BRANCH et al. 1989).

## 3.3 Activation

Approximately half of the rat and mouse uterine macrophages express class II major histocompatibility (Ia) antigens (HUNT et al. 1985; HEAD and GAEDE 1986; REDLINE and LU 1988), a marker that is strongly associated with activation, and nearly all human decidual macrophages are class II HLA-D positive (LESSIN et al. 1988; BULMER et al. 1988). This is in contrast to the  $\sim 10\%$  of blood monocytes that are la positive in all of these species.

Although subclasses of Ia antigens have not been identified on rat or mouse uterine macrophages, in first trimester human tissues the decidual macrophages express only HLA-DR whereas during the second trimester and throughout the balance of pregnancy, the cells exhibit both HLA-DR and HLA-DQ (LESSIN et al.



**Fig. 3 a, b.** Macrophages in human term placenta and extraembryonic membranes. **a** Paraformaldehyde-fixed first trimester placenta stained with a mouse monoclonal antimacrophage reagent from ENZO Diagnostics, clone HAM56. Positive cells are present in the villous stroma. x 313. **b** A section of frozen term extraembryonic membranes stained with a monoclonal antibody to HLA-DR (clone 243, Becton–Dickinson) shows activated macrophages in the decidua and the mesenchymal stroma between the amnion and chorion (*arrows*). *A*, amnion membrane: *C*, chorion membrane; *D*, decidua. x 125

1988). Figure 3 shows HLA-DR-positive macrophages in the decidua adjacent to the chorion membrane component of the term extraplacental membranes.

Interferons (IFN), well-described modulators of macrophage activation (RUSSELL and PACE 1987), are likely to be among the endogenous molecules that stimulate uterine macrophages. IFNs are present in both mouse (FOWLER et al. 1980) and human (CHARD et al. 1986; CHARD 1989) tissues; trophoblast cells produce type I IFN in response to double-stranded RNA (TOTH et al. 1990), and both type I and type II IFN have been identified in human trophoblast cells (BULMER et al. 1990).

Macrophages are also activated by endotoxins, which are present when tissues are infected with gram-negative bacteria. This causes increased rates of transcription and subsequent elaboration of various proteins and biologically active lipids such as interleukin-1 (IL-1) (DINARALLO 1988), TNF- $\alpha$  (BEUTLER et al. 1985), TGF- $\beta$  (ASSOIAN et al. 1987), and prostaglandin E<sub>2</sub> (PGE<sub>2</sub>) (ADEREM et al. 1986). Concentrations of some of these factors, particularly PGE<sub>2</sub>, IL-1, interleukin-6 (IL-6), and TNF- $\alpha$  (ROMERO et al. 1987, 1989a, b, 1990), are higher in cases of preterm delivery associated with infection. In vitro, endotoxin stimulates TNF- $\alpha$  synthesis by decidua (CASEY et al. 1989). Such high concentrations of polypeptide growth factors might affect placental cell functions by altering DNA synthesis (HUNT et al. 1989) or the expression of membrane proteins (HUNT et al. 1990) by trophoblast cells, and prostaglandins might induce premature contractions in the uterus (OKAZAKI et al. 1981; MCGREGOR et al. 1988). Thus endotoxin-stimulated uterine macrophages may bear some of the responsibility for early pregnancy termination in cases of infection (HUNT 1989a).

Although many uterine macrophages are in a state that is associated with enhanced phagocytosis, increased antigen-presenting ability, increased cytotoxic potential, and enhanced synthesis of polypeptide growth factors and bioactive lipids (NATHAN 1987), the ability of the activated macrophages to perform specific tasks may be influenced by endogenous cytokines. For example, TGF- $\beta$ 1, which is present in the uterus (TAMADA et al. 1990), has been shown to diminish intracellular killing of parasites while having little effect on tumor cell killing (NELSON et al. 1991).

## **3.4 Potential Functions**

Functional studies on uterine macrophages suggest that these cells contribute in a variety of ways to survival of the embryo. Of particular note, the cells appear to serve as immunoregulators, defenders against microbial invasion, and sources of growth factors (Table 1).

#### 3.4.1 Immunosuppression, Antigen Presentation, and Phagocytosis

It has long been recognized that grafts to the pregnant uterus enjoy prolonged survival in comparison to grafts in other locations (BEER and BILLINGHAM 1974).

This immunosuppressive environment is believed to be mediated by soluble substances, and to aid in protection of the semiallogeneic fetus by preventing colonization of the uterus by potentially harmful maternal antifetal cytotoxic lymphocytes (HUNT et al. 1984b, 1991). Mouse uterine macrophages synthesize high levels of PGE<sub>2</sub> (TAWFIK et al. 1986a, b; MATTHEWS and SEARLE 1987), which inhibits lymphocyte proliferation by modulating interleukin-2 synthesis and receptor expression (CHOUAIB et al. 1985). In human tissues, both macrophages and decidual cells produce PGE<sub>2</sub> (PARHAR et al. LALA et al. 1988). PGE<sub>2</sub>-mediated immunosuppression might be augmented by the TGF- $\beta$ 2-like substance that has been identified as a product of small mouse uterine cells (CLARK et al. 1988), by TGF- $\beta$ 1 (WAHL et al. 1988; TAMADA et al. 1990), or by TNF- $\alpha$  (UMEDA et al. 1983; YELAVARTHI et al. 1991; CHEN et al. 1991). Complexities in factor interaction cannot be underestimated. For example, PGE<sub>2</sub> modulates macrophage synthesis of TNF- $\alpha$  (RENZ et al. 1988).

Efficient presentation of antigens to T lymphocytes, an initial step in the sequence of events that leads to clonal expansion and development of an immune response, seems not to be accomplished by uterine macrophages in situ, despite their display of class II MHC antigens. For example, chemical denaturation is required for antibody stimulation by a hapten-adjuvant preparation administered into the uterus but not other tissues (LANDE 1986). Although the male-specific H–Y antigen stimulates cytotoxic T lymphocytes in the spleen and lymph nodes when systemically administered, multiple inseminations of male cells at natural mating do not prime cytotoxic cells (HANCOCK and FARUKI 1986). Evidence has been presented which suggests that human decidual accessory cells exposed to fetal cells may, in fact, stimulate suppressor T cells (OKSENBERG et al. 1988). On balance, therefore, the evidence favors an immunosuppressive rather than immunostimulatory role for uterine macrophages.

A third protective function of uterine macrophages, phagocytosis of debris and microbial invaders, is well documented in situ in rats (TACHI and TACHI 1981). Of particular interest is a study showing that in mice infected with *Listeria monocytogenes*, the uterine macrophages contain the organisms (REDLINE and LU 1988). Interestingly, these investigators have postulated that vulnerability of the placenta to infection by *Listeria* is due to the lack of macrophages in the mouse decidua, which, by virtue of their phagocytic capacity, would have otherwise constituted an effective barrier to transmission.

#### 3.4.2 Growth Factors

The particular contributions of macrophages to uterine growth factor networks have been difficult to dissect. The cells are not morphologically distinct from other types of stromal cells, and selective harvesting of tissue macrophages could easily alter their patterns of gene expression (TANIGUCHI 1988). Thus, much of the evidence for growth factor production cited below is indirect and circumstantial. Further complexities have been introduced by the finding that,

during pregnancy, other types of uterine and placental cells are sites of synthesis of many factors that have been traditionally associated with macrophages.

Members of the TGF- $\beta$  family are well-documented regulatory molecules (SPORN and ROBERTS 1989; WAHL et al. 1989) that have pleiotropic effects on cell differentiation, influence formation of extracellular matrix (RIZZINO 1988), and are known to play a major role in mouse embryonic development (HEINE et al. 1987). Although activated macrophages synthesize TGF- $\beta$ 1 (Assolan et al. 1987), in the postimplantation mouse uterus TGF- $\beta$ 1 originates primarily with epithelial and decidual cells (TAMADA et al. 1990). Results in this study also indicated that endometrial stromal cells, which might be macrophages, contained TGF- $\beta$ 1 mRNA. Correlation of transcription and translation of the TGF- $\beta$ 1 gene by specific cells in the human uterus has not yet been accomplished, although the factor has been purified from human placenta (FROLIK et al. 1983).

Interleukin-6 is another example of a growth factor that has been identified as a product of macrophages (VAN DAMME et al. 1988; KATO et al. 1990; VAN SNICK 1990). In the human cycling uterus, this factor is synthesized by unidentified, undifferentiated endometrial stromal cells, some of which might be macrophage precursors, and induces IL-1 synthesis by macrophages (TABIBZADEH et al. 1988). In mouse decidua, IL-6 mRNA has been localized by in situ hybridization to the cords of endothelial cells that line the maternal blood spaces, and has been postulated to influence angiogenesis (MOTRO et al. 1990).

A third growth factor that arises from activated macrophages is TNF- $\alpha$ (BEUTLER et al. 1985). While originally this factor was described as an inhibitor of tumor cell proliferation produced by activated macrophages (SUGARMAN et al. 1985), recent studies suggest that low levels of TNF- $\alpha$  in normal tissues may contribute to cellular renewal (ULICH et al. 1989), which might be accomplished in part by stimulation of other growth factors (KAUSHANSKY et al. 1988), and that TNF- $\alpha$  is produced by a number of cell types (ROBBINS et al. 1987; KESHAV et al. 1990; BARATH et al. 1990). In both rats and humans, TNF- $\alpha$  is present in the uterus throughout gestation (YELAVARTHI et al. 1991; CHEN et al. 1991). Data collected in a rat model show that although epithelial and decidual cells are the most abundant TNF-a mRNA-containing cells in the uterus, cells in the myometrial connective tissue that resemble macrophages by morphology also contain specific messages (YELAVARTHI et al. 1991). Interestingly, only the nonmacrophages contain high levels of the protein. Thus, macrophages in the rat myometrium may be similar to tumor-infiltrating macrophages, which transcribe this gene but do not translate the messages into protein (BEISSERT et al. 1989). In early gestation human tissues, TNF- $\alpha$  mRNA and protein are found in epithelial and decidual cells, and, late in gestation, in cells that reside near the chorion membrane that resemble macrophages by morphology and anatomic location (CHEN et al. 1991). TNF- $\alpha$  is contained in human amniotic fluid and is produced by human uterine and placental cells in vitro (JAATTELA et al. 1988).

The growth factor IL-1, which has overlapping functions and synergistic interactions with TNF- $\alpha$  (LE and VILCEK 1987; ELIAS et al. 1987; DINARELLO 1988; AKIRA et al. 1990), is present in human amniotic fluid (TAMATANI et al. 1988), and

IL-1 mRNA-positive cells have been reported in the mouse endometrium (TAKACS et al. 1988). Recent immunocytochemical studies in our laboratory (Hu et al. 1992) that used two sets of polyclonal antibodies to the two species of IL-1, IL-1 $\alpha$  and IL-1 $\beta$ , indicated that although maternal leukocytes in human first trimester and term tissues contained the proteins, staining intensities were higher with antibodies to the latter than to the former. Double-labeling experiments showed that the IL-1-positive blood leukocytes were monocytes, cells that are well-documented sources of IL-1 with a preference for synthesizing IL-1 $\beta$  (BEESLEY et al. 1990). Although IL-1 $\alpha$ -positive cells were present in decidua, these may have been infiltrating extravillous cytotrophoblastic cells rather than maternal cells.

In mice, CSF-1, which is synthesized exclusively in the uterine epithelium in response to E<sub>2</sub> and progesterone, peaks on day 14 of pregnancy (BARTOCCI et al. 1986; POLLARD et al. 1987; REGENSTREIF and ROSSANT 1989; ARCECI et al. 1989; POLLARD 1990; POLLARD et al. 1991B; ROTH and STANLEY, this volume). Recent studies in our laboratory (DAITER et al. 1992) show that human tissues are similar to mice in many respects; uterine epithelium is the major source of CSF-1 in both the cycling and the pregnant human uterus, CSF-1 mRNA appears to be hormonally regulated in the cycling uterus, and CSF-1 concentrations in the endometrium increase with the onset of pregnancy. However, in contrast to the findings in mice, human endometrial CSF-1 concentrations are highest in the first trimester and decline as gestation progresses to term. Although there is no evidence at present that murine macrophages are capable of synthesizing CSF-1, human macrophages produce this substance (RAMBALDI et al. 1987), and the possibility that uterine macrophages in human endometrium contribute a portion of the CSF-1 has not been eliminated.

Macrophage-derived growth factors may be most influential in specific uterine microenvironments because the effects of polypeptide growth factors are highly concentration dependent. The observations accumulated to date on the spatial relationships between macrophages and other types of uterine cells suggest that in humans, rats, and mice myometrial macrophages have ample opportunity for tissue-specific effects, whereas there may be species differences in the ability of macrophages to influence decidual and placental cells.

#### 3.4.3 Other Functions

The paragraphs above describe some studies that have led to a better understanding of the contributions of uterine macrophages to protection from cytotoxic lymphocytes, to defense against microbial invasion, and to growth factor production. Macrophages might have other critical functions; NATHAN (1987) lists 13 categories of macrophage products. Among these are complement components and coagulation factors, various enzymes including plasminogen activator and collagenase, and proteins such as fibronectin that compose extracellular matrix. Uterine macrophages have not been examined specifically for production of any of these molecules, yet some might be highly important. To take just one example, in the myometrium, where the cells are consistently present in the connective tissue stroma and are closely associated with the serosa, proteolytic enzymes such as collagenase and plasminogen activator could be useful for tissue remodeling during uterine expansion and post-partum involution. As with other uterine macrophage products, synthesis of these enzymes would probably be influenced by endogenous growth factors, collagenase by uterine TNF- $\alpha$ (DAYER et al. 1985), and plasminogen activator by CSF-1 (HAMILTON et al. 1980) and GM-CSF (EVANS et al. 1989). Plasminogen activator enzyme activity is also stimulated by colony stimulating factor for granulocytes (KOJIMA et al. 1989), and receptors for this factor have been identified in the human placenta (UZUMAKI et al. 1989).

## **4 Placental Macrophages**

Patterns of distribution and activation markers have now been identified for fetal placental macrophages, and a few potential functions for the cells have been described (Table 1). These studies indicate that macrophages gradually mature in the placenta until, at parturition, they are sensitive to activation signals and are capable of performing some of the functions that have been attributed to macrophages in adult tissues.

## 4.1 Distribution and Marker Expression

Eearly gestation human placental villous stroma contains large, highly vacuolated Hofbauer cells (Fox 1978), which are one morphologic form of fetal placental macrophages. These were, until the development of monoclonal antibodies that could identify cells that are less distinct by morphology, considered to be the only macrophage-like cells in the human placenta. However, in 1975, MOSKALEWSKI, PTAK, and CZARNIK showed that human placentae contain many Fc receptorpositive cells, and further studies verified the mononuclear phagocyte lineage of many of these cells (WOOD et al. 1978). Human fetal placental macrophages have now been tested extensively by immunohistology (BULMER and JOHNSON 1984; GOLDSTEIN et al. 1988; MUES et al. 1989). The morphologic characteristics of these cells in first trimester placental villous stroma are shown in Fig. 3a. In term placentas, stromal macrophages appear slightly smaller and are often marginated to the capillary endothelium (HUNT, unpublished data)

Cells bearing macrophage markers increase in density in the placental villous stroma as gestation progresses, and the cells gradually develop HLA-D activation antigens (LESSIN et al. 1988; BULMER et al. 1988). The same is true of fetal macrophages in the mesenchymal stroma between the amnion and chorion membrane, as shown in Fig. 3b.

Although macrophages can be identified by immunohistology in term mouse placentae (WOOD 1980), and are also present in dispersed cell suspensions from this tissue (MOSKALEWSKI et al. 1974; MATTHEWS et al. 1985), early gestation murid placentae seem to contain few macrophages. Immunohistologic studies in rats indicate that macrophage antigen-positive cells are rare in the fetally derived components of early- to mid-gestation placentae, whereas near parturition, positive cells can be identified in the chorioallantoic plate at the base of the placenta (HUNT, unpublished data). The rat experiments show that embryo-derived macrophages in the placenta bear only the marker for monocyte/macrophages, EDI, and that the cells only occasionally express detectable levels of class II MHC antigens.

It is entirely possible that many more macrophages are present in the human placental villous mesenchyme and the rat and mouse labyrinthine placenta than can be identified, particularly at early stages of gestation, because of their gradual development of lineage-specific markers. The studies have been reported at this date would also indicate that fetally derived murid macrophages in extraembryonic tissues are less numerous and develop their markers more slowly than do their counterparts, despite the presence of high concentrations of CSF-1 (BARTOCCI et al. 1986).

### 4.2 Potential Functions

Placental macrophages in situ often contain phagocytosed material (Fox 1978), and in vitro they participate in both immune and nonimmune phagocytosis (LOKE et al. 1982). These cells are therefore likely to supplement the activities of uterine macrophages, providing additional protection from microbial invasion. It is worthy of note that many of the organisms that are transmitted from the mother to the fetus are intracellular parasites such as *Listeria, Toxoplasma*, and viruses (KLEIN, and REMINGTON 1990). The role that macrophages might play in the transmission of HIV-1 from the mother to the embryo is a current cause for concern (LEWIS et al. 1990).

Although it is not known whether fetal placental macrophages contribute to the immunosuppressive environment during pregnancy, other functions have been postulated for the cells. Macrophages taken from term human placentae bear both class I and class II major histocompatibility antigens, and are capable of stimulating maternal lymphocyte proliferation (HUNT et al. 1984a). Because of the close proximity of the fetal placental macrophages to the maternal circulation, these cells might provide the immunogenic stimulus for the antibodies to paternal class I and class II antigens that are common in pregnant women (VAN ROOD et al. 1958). Human fetal placental macrophages have been postulated to protect the fetus from these potentially harmful antibodies by phagocytosing immune complexes (WOOD and KING 1982).

As with uterine macrophages, fetally derived placental macrophages could be important sources of polypeptide growth factors. Recent studies in our laboratory have shown that although placental stromal cells in human first trimester tissues do not contain TNF- $\alpha$  mRNA, similar cells in term placentae are strongly positive when tested by in situ hybridization (CHEN et al. 1991). The positive cells are probably macrophages, which constitute approximately 25% of the stromal cells (HUNT et al. 1984a). Biologically active IL-1 has been reported as a product of macrophages harvested from human term placentae (FLYNN et al. 1982). Recent immunocytochemical experiments in our laboratory (HU et al. 1992) have shown that in both first trimester and term human placentas, mesenchymal cells contain immunoreactive IL-1 $\alpha$  and that fetal leukocytes in the blood vessels of term placentas contain IL-1 $\beta$ . Double labeling studies showed that many of these IL-1-positive cells were of mononuclear phagocyte lineage. CSF-1 is a product of villous mesenchymal cells in second trimester human placentas, suggesting that this growth factor might also be synthesized by fetal placental macrophages (DAITER et al. 1992). Thus, the data collected to date indicate that human fetal placental macrophages are sources of several of the polypeptide growth factors that have been identified as products of the same types of cells in adult tissues.

As in the uterus, other types of cells in the placenta synthesize growth factors that are usually associated with macrophages. These include IL-1, IL-6, CSF-1, and TNF- $\alpha$ , all of which have been localized to trophoblast cells in human, rat, or mouse placentas (MAIN et al. 1987; KAMEDA et al. 1990; MEAGHER et al. 1990; YELAVARTHI et al. 1991; CHEN et al. 1991; DAITER et al. 1992; HU et al. 1992). New tools consisting of monoclonal antibodies that specifically recognize human fetally derived placental macrophages and can be used to harvest the cells (NASH et al. 1989) should allow the performance of experiments that might shed further light on the functions of these cells.

## 5 Experiments in the Macrophage-Deficient Osteopetrotic Mouse Model System

The experiments described above have led to speculation that hormones influence growth factor production by uterine cells which, in turn, influences uterine macrophage population density, distribution, differentiation, and performance of differentiated cell functions. The osteopetrotic (*op/op*) mouse provides an opportunity to study regulation of uterine macrophages by a single growth factor, CSF-1. In the *op/op* mouse, an inactivating mulation in the CSF-1 gene results in the total absence of CSF-1 (YOSHIDA et al. 1990; WIKTOR-JEDRZEJCZAK et al. 1990). As a consequence these mice have less than one-tenth the normal number of bone marrow cells, greatly reduced numbers of blood monocytes, and severe deficiencies in the proportions of peripheral macrophages in locations such as the pleural and peritoneal cavities (WITKOR-JEDRZEJCZAK et al. 1982, 1990).

Experiments in this model system have shown that hormonally regulated uterine epithelial cell CSF-1 regulates the density and properties of mouse uterine macrophages, a relationship that was established by comparing F4/80-positive macrophages in the cycling and pregnant uteri of homozygous (op/op) and heterozygous (op/+) mice (POLLARD et al. 1991a). The observations were as follows: (a) the cycling uterus in op/op mice demonstrated a virtual absence of F4/80-positive cells whereas positive cells were, as expected, abundant in the endometrium, myometrium, and mesometrial triangle of op/+ mice (Fig. 4a, b); (b) early postimplantation op/op mouse tissues (gestation days 7 and 8) contained macrophages, but fewer than the same tissues from op/+ mice; (c)



**Fig. 4 a–d.** Macrophages are abundant in the uterus of an op/+ mouse (**a**) but are virtually absent from the uterus of an op/op mouse (**b**) × 40. **c,d** Macrophages in the myometrial stroma of an op/+ mouse uterus (**c**) and an op/op uterus. (**d**) At day 7 of gestation. Note that positive cells in the op/+ uterus are large and have cytoplasmic extensions whereas the cells in op/op myometrium are smaller and rounded. x 626. Cryostat sections of paraformaldehyde-fixed (**a** and **b**) or acetone-fixed (**c** and **d**) frozen tissues were stained using the anti-mouse macrophage reagent F4/80

the macrophages in the early gestation op/op tissues remained small and round, whereas, those in the op/+ tissues gave clear morphologic evidence of spreading (Fig. 4c, d); (d) the macrophages gradually disappeared in op/oputeri until, at day 14 of gestation, few macrophages could be identified in F4/80 stains of the op/op uterus; in contrast, numerous positive cells were present in the myometrium of op/+ mouse tissues at the same stage.

Although these data demonstrate clearly that CSF-1 is required for maintenance and differentiation of uterine macrophages during mouse pregnancy, it seems reasonable to conclude from our observations that some molecule other than CSF-1 that is present in the post-implantation tissues of the *op/op* mice influences monocyte chemotaxis. However, the chemoattractant has less effect than CSF-1 on induction of differentiation. If macrophage spreading, as has been shown with macrophage adherence (HASKILL et al. 1988), influences transcription of their growth factor genes and proto-oncogenes, this failure could have important ramifications in pregnancy. GM-CSF, which is chemotactic for monocytes (WANG et al. 1987), may be a suitable candidate for (one of) the replacement factor(s). ROBERTSON and SEAMARK (1990) have shown that synthesis of GM-CSF by mouse uterine epithelial cells is initiated on day 1 of pregnancy, seemingly stimulated by the presence of seminal vesical fluid, and that GM-CSF production remains at high levels through day 10 pregnancy.



**Fig. 5.** A schematic representation of the potential influences of ovarian hormone-stimulated, epithelial cell-derived CSF-1 and other cytokines on uterine macrophage chemotaxis, differentiation, and growth factor synthesis. Pathways for reciprocal influences on uterine epithelium and modulation of placental cells by products of differentiated macrophages are indicated

GM-CSF or other natural replacement factors are not entirely successful in overcoming the CSF-1 deficiency. In the *op/op* mice, pregnancy is severely compromised and even in those embryos that proceed to term the development of the extraembryonic tissue appears retarded, thus confirming a causal role for CSF-1 in gestation. Systemic reconstitution of the mice with human recombinant CSF-1 during pregnancy fails to restore fertility (WIKTOR-JEDRZEJCZAK et al. 1991), suggesting that local production of CSF-1 is required for normal fertility.

All of the functions of uterine CSF-1 are not known, but it is clear that along with trophoblasts and decidual cells, uterine macrophages are targets for this molecule. Figure 5 shows a potential pathway for CSF-1 and other cytokine influences on uterine macrophage density, differentiation, and factor production. Appropriate manipulation of the *op/op* mice should provide a unique opportunity to study the regulation and functions of macrophages in pregnancy.

### 6 Conclusions

Macrophages are recruited to the uterus during pregnancy, are present in the placenta, and are likely to perform important pregnancy-associated functions. These appear to include immunoregulation, phagocytosis, and growth factor production. When evaluating the potential functions of uterine and placental macrophages, however, it is appropriate to recognize that: (a) other types of uterine and placental cells are, particularly during pregnancy, capable of synthesizing some factors that are traditionally associated with macrophages, and (b) some macrophage functions are probably assumed by other cell types when conditions disallow normal proportions of macrophages in the uterus and placenta.

The studies cited in this article indicate that highly complex interactions take place among pregnancy hormones, polypeptide growth factors, and macrophages in the uterus and placenta. Causal relationships are best illustrated for CSF-1, where experiments in the *op/op* mouse model show that this hormonally stimulated polypeptide growth factor is responsible in large part for uterine macrophage chemotaxis and differentiation, and, in all likelihood, their synthesis of other factors that promote pregnancy.

Note added in press. Three new reports have been added to the literature since the writing of this article. One describes rat placental macrophages [van Oostveen DC, van den Berg TK, Damoiseaux JGMC, van Rees EP (1992) Macrophage subpopulations and reticulum cells in rat placenta. Cell Tissue Res, in press], a second documents macrophages in preimplantation rat uterus [Kachkache M, Acker GM, Chaouat G, Noun A, Garabedian M (1991) Hormonal and local factors control the immunohistochemical distribution of immunocytes in the rat uterus before conceptus implantation: effects of ovariectomy, Fallopian tube section, and injection. Biol Reprod 45:860–868], and a third describes macrophages in mouse uterus [De M, Wood GW (1991) Analysis of the number and distribution of macrophages, lymphocytes and granulocytes in the mouse uterus from implantation through parturition. J Leukocyte Biol 50:381–392].

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# Urokinase-Catalyzed Plasminogen Activation at the Monocyte/Macrophage Cell Surface: A Localized and Regulated Proteolytic System

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## **1** Introduction

In the adult organism, monocytes and macrophages are among the few cell types that can migrate within and between body compartments. To do so, they must have the capacity to clear for themselves a path through the macromolecular barriers of basement membranes and other extracellular matrices. This requires the controlled and localized degradation of matrix proteins by extracellular proteases. Mononuclear phagocytes can produce a number of such enzymes, including collagenolytic, elastinolytic, and gelatinolytic hydrolases (TAKEMURA and WERB 1984). Because they can, directly or indirectly, catalyze the degradation of most components of extracellular matrices, plasminogen activators (PAs) are thought to play a key role in the proteolytic events that accompany the migration of a wide variety of cell types, during ontogeny as well as in pathologic circumstances. Monocytes and macrophages can produce PAs, and the regulation of their PA-dependent proteolytic activity has been a focus of attention in recent years. The findings of a number of investigators converge to suggest that the expression of PA activity is a tightly controlled phenotypic property of human and murine mononuclear phagocytes, and that multiple mechanisms act concurrently to achieve the exquisitely focused and

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M-CSF

IFN - Y

TNF-α IL-1

**Fig. 1.** In vitro modulation of the PA activity of mouse macrophages. Peritoneal macrophages from thioglycollate-induced exudates were plated at low density, treated for 16 h with different cytokines (M-CSF, 100 U/ml; IFN- $\gamma$ , 20 U/ml; TNF- $\alpha$ ; 10 ng/ml, IL-1, 100 U/ml) and overlaid with a substrate mixture containing plasminogen and casein (VASSALLI et al. 1985). The picture was taken under dark ground illumination: plaques represent zones of substrate lysis around individual cells

regulated generation of plasmin precisely where and when it is needed to allow cell migration in the context of inflammatory reactions.

Hormones and cytokines play a particularly important role in the regulation of PA activity in many cell types, including fibroblasts, endothelial cells, ovarian granulosa cells, Sertoli cells, and mammary epithelial cells (DANØ et al. 1985; SAKSELA 1985; MOSCATELLI and RIFKIN 1988; SAKSELA and RIFKIN 1988). Similarly, the PA activity of cultured mouse peritoneal macrophages can be readily altered as a function of the cytokine balance in the macrophage environment (Fig. 1): Macrophages embedded in a layer of casein degrade the substrate in their immediate vicinity through the generation of plasmin from its inactive precursor plasminogen; this proteolytic activity is enhanced in the presence of the macrophage-activating cytokine interferon- $\gamma$  (IFN- $\gamma$ ), and decreased in the presence of the macrophage growth factor M-CSF. It is evident that such regulation can dramatically alter the extent of extracellular substrate degradation and this suggests that a clear and complete understanding of the physiologic and pharmacologic control of the macrophage PA system could be of great help in the therapeutic management of inflammatory reactions and their associated tissue destruction. The mechanisms involved in controlling plasmin generation by monocytes/macrophages have been, at least in part, elucidated, and this review will summarize the roles of the PAs themselves, of PA inhibitors, and of a plasma membrane binding site specific for the urokinasetype PA.

## **2** Plasminogen Activators

Plasminogen activators are serine proteases of tryptic specificity. Their major macromolecular substrate is the zymogen plasminogen; other proteins, such

as fibrinogen (WEITZ et al. 1988) and fibronectin (GOLD et al. 1989), can be directly cleaved by PAs, although this occurs only at very high enzyme to substrate ratios, and thus may not be of physiologic relevance except under particular circumstances. Plasminogen is abundant in plasma and in most extracellular fluids and constitutes a reservoir of broad spectrum proteolytic activity that can be recruited by PA-catalyzed conversion of the single-chain zymogen to the two-chain tryptic protease plasmin. Since plasmin appears to be required for the activation of a metalloprotease cascade that leads to the generation of active collagenase (WERB et al. 1977), for instance, PAs could play a key role in catalyzing extracellular proteolysis.

In all mammalian species explored to date, two PAs have been identified: urokinase-type PA (uPA) and tissue-type PA(tPA). They are the products of distinct genes and differ in certain aspects of their catalytic and binding properties. The single-chain form of uPA is a zymogen with no (or very little) activity (pro-uPA) (PETERSEN et al. 1988); both uPA and pro-uPA bind to a cell surface receptor that localizes plasmin generation to the immediate cell environment (see below). By contrast, tPA is active both as a single- and as a two-chain enzyme (although there are differences in the catalytic properties of the two forms of tPA); tPA binds to components of extracellular matrices, in particular fibrin (HOYLAERTS et al. 1982) but also fibronectin and laminin (SALONEN et al. 1984, 1985). The available evidence suggests that tPA-catalyzed proteolysis is preferentially involved in the maintenance of fluidity of the extracellular milieu. while uPA plays a role in the cell surface proteolysis necessary for cell migration. However, it is clear that this tentative model is a simplification. Indeed, in at least one case, the same cell type produces a different PA in two different species (CANIPARI et al. 1987). In addition, abundant uPA is produced by cells that are not in a process of migration (epithelial cells of the nephron and of the male genital tract, for instance) (LARSSON et al. 1984; HUARTE et al. 1987). Finally, plasma membrane binding sites for tPA have also been identified (HAJJAR et al. 1987; BARNATHAN et al. 1988). It should also be noted here that PAs have not been associated with the traffic of lymphocytes, which are endowed with remarkable migratory properties.

## **3 Monocytes and Macrophages Produce Plasminogen Activators**

In the early 1970s, studies on the production of proteases by cells in culture led to the identification of the PA-plasmin system as a widespread mechanism used by many different cell types to catalyze extracellular proteolysis (REICH 1978). UNKELESS and co-workers (1974) described the production of a PA by mouse peritoneal macrophages and human monocytes, and demonstrated that production of this enzyme could vary dramatically as a function of the
state of the cells: Macrophages from thioglycollate-elicited peritoneal exudates produced high levels of PA activity as compared to resident noninflammatory macrophages; also, certain populations of "in vivo primed" macrophages [e.g., after injection of lipopolysaccharide (LPS)] could be triggered in vitro to produce high levels of enzyme, for instance by phagocytosis of latex particles (GORDON et al. 1974).

The idea that PA production by macrophages could be a marker for one stage in the life cycle of these cells, i.e., in the early phases of their participation in inflammatory reactions, received support from further studies on the modulation of enzyme production in vitro and in vivo. A striking observation in this context was the inhibition of PA production by inflammatory macrophages under the influence of anti-inflammatory glucocorticoids (VASSALLI et al. 1976); similarly, increased enzyme production by macrophages exposed to products of activated T lymphocytes suggested that PAs could be a marker of macrophage "activation" (KLIMETZEK and SORG 1977; NOGUEIRA et al. 1977; VASSALLI and REICH 1977; GORDON et al. 1978). Thus, high levels of PA production appear to be a hallmark of murine inflammatory peritoneal macrophages. At this time only a few studies have attempted to determine whether this is true for other macrophage populations; in view of the difficulties inherent to the assay of PAs in tissue extracts, in particular because of the presence of PA inhibitors, assays that do not rely on the catalytic evaluation of PA amounts (i.e., immunoassays or determination of mRNA levels) should be the tools for such a study.

The types of PAs produced by mature human and murine monocytes/macrophages have been identified using immunologic techniques and nucleic acid hybridization. Most studies that have investigated this issue have shown that these cells usually produce exclusively uPA (VASSALLI et al. 1984; SAKSELA et al. 1985; COLLART et al. 1987). The enzyme appears to be secreted as a single-chain zymogen, the physiologic activation of which is still poorly understood; in vitro, it can be achieved by plasmin or plasma kallikrein (WUN et al. 1982a; ICHINOSE et al. 1986). The culture medium of certain leukemic cell lines has been reported to contain two-chain active enzyme, a result which suggests that these cells can produce a pro-uPA activator (STEPHENS et al. 1988). It is also possible that, in the presence of plasminogen, the intrinsic activity of single-chain tPA could initiate a uPA-dependent cascade (VIHKO et al. 1989).

Interestingly, tPA production has been observed in cultures of granulocyte/macrophage progenitors, and the switch to uPA production was proposed to be an index of cell differentiation (WILSON and FRANCIS 1987); in this context, the poor response to chemotherapy of patients with acute myeloblastic leukemia whose cells secrete tPA (WILSON et al. 1983) supports the notion that tPA is a marker of early monocyte precursors. Recently, new light has been shed on this issue by the observation that human peripheral blood monocytes, in addition to uPA, also produce tPA in response to LPS or interleukin-4 (IL-4) (HART et al. 1989a, b). It is intriguing that, under certain conditions, these cells can produce both enzymes; the identification of their respective roles is a challenge for future work. At this time, bone marrow-derived and peritoneal mouse macrophages have not been found to produce tPA, but circulating mouse monocytes have not been explored.

Given that uPA production is a marker of the activation state of at least certain macrophage populations, what are the molecular mechanisms that account for the large differences in enzyme activity between noninflammatory (resident) and exudate peritoneal macrophages? Nuclear run-on experiments that assay the transcriptional activity of the uPA gene show that this is markedly higher in thioglycollate-elicited than in resident macrophages (Fig. 2; see also COLLART et al. 1986). A comparable difference in the steady state levels of uPA mRNA between the two populations (Fig. 3) confirms that the modulation of uPA activity is, at least in part, due to changes in uPA gene transcription. Analyses of uPA gene transcription and mRNA levels in bone marrow-derived macrophages indicate that these cells are, in terms of uPA gene expression, similar to inflammatory exudate cells (Figs. 2, 3). In the context of such comparative studies between different populations of mouse macrophages, it is important to note that guite marked differences in absolute levels of uPA mRNA have been noted between different preparations of "inflammatory" (COLLART et al. 1987) or "resident" macrophages. This may be due to the difficulty inherent in achieving an inflammatory response of similar intensity from one experiment to the next, and in obtaining cells from animals completely



**Fig. 2.** Run-on transcription in isolated nuclei. Nuclei were prepared from mouse bone marrow-derived macrophages (WOHLWEND et al. 1987b) or thioglycollate-elicited or resident peritoneal macrophages (Collart et al. 1986, 1987). Run-on transcription was performed as described by Collart et al. (1987). The two PAI-2 DNAs used are from the 5' (lower dot, nucleotides 1–815) and the 3' (upper dot, nucleotides 810–1245) regions of the human cDNA (SCHLEUNING et al. 1987)



## 1) BONE MARROW-derived macrophages

# 2) THIOGLYCOLLATE-elicited peritoneal macrophages

## 3) **RESIDENT** peritoneal macrophages

Fig. 3. Northern blot analysis of total cellular RNA. Total RNA was prepared from mouse bone marrow-derived macrophages (WOHLWEND et al. 1987b), thioglycollate-elicited or resident peritoneal macrophages (Collart et al. 1987). Murine uPA (Belin et al. 1985; Collart et al. 1987) and human PAI-2 (SCHLEUNING et al. 1987; Belin et al. 1989) cRNA probes were prepared and used as described by Busso et al. (1986)

devoid of a peritoneal reaction. Macrophage uPA levels are very sensitive indices of the "activation" state of the cells and may vary from one preparation to the next; despite this variation, inflammatory cells obtained following intraperitoneal injection of thioglycollate broth always have at least ten fold higher levels (10–50 molecules per cell) of uPA mRNA than their resident counterparts obtained from uninjected animals.

In vitro pharmacologic studies have reinforced the notion that changes in uPA gene transcription play an important part in the modulation of uPA production. Those agents that had previously been shown to decrease macrophage uPA activity, such as glucocorticoids or compounds that raise intracellular cAMP levels, caused a decrease in uPA transcription and mRNA levels; similarly, agents that increase uPA production, such as lectins or IFN- $\gamma$  (VASSALLI et al. 1977; VASSALLI and REICH 1977), appear to do so through an effect on transcription of the gene (COLLART et al. 1987). A comparison with the changes in the transcription rates of other genes for macrophage-secreted proteins [e.g., tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) and IL-1] in response to these agents suggests that the control of uPA production is quite distinct and hence supports the hypothesis that uPA production is a marker for a specific stage of macrophage activation. Interestingly, changes in uPA transcription were

	PA	uPA		PAI-2	
	Activity	Enzyme	mRNA	Serpin	mRNA
IFN-γ	+	+	+	_	
Con A	+	+	+	=	n.d.
PMA	+	+	+	+	+
Endocytosis	+	+	n.d.	=	n.d.
1,25-VIT D <sub>3</sub>	+	+	+	_	
LPS	_	_		+	+
M-CSF		=	=	+	+
cAMP	_	_		+	+
Glucocorticoids	_				
Retinoids		_	_	n.d.	n.d.
IL-4	+	tPA+	tPA mRNA+	n.d.	n.d.

Table 1. Agents that modulate in vitro the PA activity of mononuclear phagocytes<sup>a</sup>

+, increase; =, no effect; -, decrease; n.d., not determined

<sup>a</sup> Agents for which only overall changes in PA activity have been reported are not included. For references, see the text.

found to be preceded by opposite changes in c-*fos* mRNA levels, suggesting a possible role for the c-*fos* gene product in the modulation of uPA gene expression (COLLART et al. 1987). In addition, protein synthesis inhibitors have been found to cause a rapid and transient induction of uPA mRNA synthesis (COLLART et al. 1986), suggesting the existence of short-lived repressors of uPA gene transcription.

To summarize the data that relate to the control of macrophage PA activity, we can say that, in most cases where this has been studied, there is a good correlation between changes in PA production and in uPA gene transcription or uPA mRNA levels (Table 1). A striking exception, however, is the effect of the macrophage growth factor M-CSF: while M-CSF decreases macrophage PA activity (Fig. 1), it does not affect the steady state level of uPA mRNA in these cells, at least at early times (Fig. 4). A probable solution to this apparent paradox will be discussed below: M-CSF induces the production of a PA-specific inhibitor (PAI) by mouse peritoneal macrophages. Further studies of the effects of M-CSF will be of interest, since stimulation of PA activity in cultures of peritoneal and bone marrow-derived macrophages has also been observed (HAMILTON et al. 1980; HUME and GORDON 1984). Finally, it should also be noted that some agents (i.e., LPS and cAMP) cause both a decrease in uPA transcription and an increase in PAI production, thus causing a profound decrease in uPA activity through combined effects. The mechanisms of increased uPA production in response to phagocytosis (GORDON et al. 1974; SCHNYDER and BAGGIOLINI 1978). endocytosis (FALCONE and FERENC 1988; FALCONE 1989), or 1,25-dihydroxyvitamin D<sub>3</sub> (GYETKO et al. 1988) and of decreased uPA production in the presence of retinoids or auranofin (VASSALLI et al. 1976; LISON et al. 1989) have not been investigated; changes in mRNA translation or stability could account for some of these effects.



- 1) Control
- **2) LPS (4h; 1 \mu g/ml)**
- 3) M-CSF (4h; 20 U/ml)

Fig. 4. Northern blot analysis of total cellular RNA. Thioglycollate-elicited murine peritoneal macrophages were incubated as indicated. Total RNA was prepared and analyzed as for Fig. 3

# 4 Monocytes and Macrophages Produce A Plasminogen Activator-Specific Inhibitor

Control of protease activity by macromolecular inhibitors is a physiologically important mechanism to avoid the damage that can be caused by excessive proteolysis. A demonstration of this is provided by the progressive destruction of lung elastic tissue in patients deficient in  $\alpha_1$ -protease inhibitor, an elastase inhibitor (HUBER and CARRELL 1989). Antiproteases amount to some 10% of total plasma proteins, and production in tissues may also contribute to the local proteolytic balance.

Monocytes and macrophages have been shown to produce different antiproteases, including  $\alpha_1$ -protease inhibitor and the broad spectrum inhibitor  $\alpha_2$ -macroglobulin (GANTER et al. 1989). A search for antiproteases directed against PAs has revealed the production by these cells of a PA-specific inhibitor: addition of uPA to medium from cultures of mouse peritoneal macrophages or human peripheral blood monocytes resulted in an inhibition of enzyme activity (KLIMETZEK and SORG 1979; CHAPMAN et al. 1982; GOLDER and STEPHENS 1983; VASSALLI et al. 1984; CHAPMAN and STONE 1985a; KOPITAR et al. 1985; WOHLWEND et al. 1987b). A number of cell lines from the mononuclear phagocyte lineage were also found to produce such an inhibitor. Biochemical purification from cultures of human U937 cells resulted in the isolation of a PA-specific antiprotease (KRUITHOF et al. 1986), similar to a uPA inhibitor that had originally been identified in human placenta (KAWANO et al. 1968). This "placental-type" PAI was named PAI-2, and was shown to be a member of the family of serine proteases inhibitors, the serpins (CARRELL and TRAVIS 1985). Two other serpins with specificity for arginine-proteases and high affinity for PAs have also been identified: PAI-1, originally identified in cultures of endothelial cells (LOSKUTOFF et al. 1983), and protease nexin 1 (PN-1), a fibroblast and glial cell product that also inhibits thrombin (BAKER et al. 1980; GLOOR et al. 1986). PAI-2 appears to be the predominant PA inhibitor produced by mononuclear phagocytes; PAI-1 has been detected in two human monocytic cell lines (WOHLWEND et al. 1987a; LUND et al. 1988). PAI-2 inhibits most efficiently uPA (second order rate constant  $5 \times 10^7 \text{ M}^{-1} \text{ s}^{-1}$ , and also reacts with two-chain tPA ( $10^5 \text{ M}^{-1} \text{ s}^{-1}$ ); it does not react with pro-uPA, nor with single-chain tPA, plasmin, or thrombin (KRUITHOF et al. 1986). Besides mononuclear phagocytes, PAI-2 has been reported in human placenta (syncytiotrophoblasts) (ÅSTEDT et al. 1986; FEINBERG et al. 1989), keratinocytes (HASHIMOTO et al. 1989), and endothelial cells (WEBB et al. 1987).

Cloning and sequencing of the human (SCHLEUNING et al. 1987; WEBB et al. 1987; YE et al. 1987; ANTALIS et al. 1988) and murine (BELIN et al. 1989) PAI-2 cDNAs and of the human PAI-2 gene (YE et al. 1989) confirmed that this inhibitor belongs to the serpin gene family, which also includes, in addition to PAI-1 and PN-1,  $\alpha_1$ -protease inhibitor,  $\alpha_2$ -antiplasmin, antithrombin-III, and other proteins with no known antiprotease function, such as ovalbumin, angiotensinogen, and cortisol-binding globulin (see HUBER and CARRELL 1989 for a recent review). Gene sequence comparisons reveal quite extensive divergence between members of the serpin family, and the similarity between mammalian PAI-2 and avian ovalbumin suggests that the two genes are closely related (YE et al. 1987, 1989).

Like other serpins, PAI-2 forms 1:1 complexes with its target proteases; these complexes are not dissociated in the presence of detergents such as SDS. Using preparations of radiolabeled enzyme, e.g., <sup>125</sup>I-uPA, the presence of PAI-2 can be demonstrated by gel electrophoresis: free radiolabeled enzyme can be separated from PAI-2-complexed enzyme, and, given excess enzyme, this also allows quantitation of PAI-2. Using this electrophoretic assay, two forms of PAI-2 were identified in cultures of human and murine monocytes/ macrophages (WOHLWEND et al. 1987a, b): one form, of  $M_r$  40000, accumulates in the cell, where it appears to be stored in the cytosol; another form, of  $M_r$ 55 000-60 000, is glycosylated and preferentially secreted. These two forms of PAI-2 are functionally and immunologically indistinguishable, and enzymatic removal of the polysaccharide portion of secreted PAI-2 yields a protein that comigrates with the cytosolic inhibitor. Thus these two forms differ only in the extent of their glycosylation (WOHLWEND et al. 1987a, b; GENTON et al. 1987; YE et al. 1988). Of newly synthesized PAI-2 molecules, approximately one-half remain in the cytosol, where they are stable for many hours, while the other half enter the secretory pathway and rapidly leave the cell. Cytosolic PAI-2 represents an abundant store of the inhibitor: the amount of nonglycosylated PAI-2 in the cell is comparable to the amount of glycosylated inhibitor that can be secreted over a 24-h period. Whether the cytosolic inhibitor can be released through a post-translational translocation process that does not involve cell death, or whether it is only released under conditions of cell suffering or apoptosis, is not known. Interestingly, monocytes/macrophages also contain in their cytosol other proteins that are believed to act following their release in the extracellular milieu, i.e., the cytokine IL-1 (SINGER et al. 1988) and elastase inhibitors (REMOLD-O'DONNELL et al. 1989; POTEMPA et al. 1988); it is possible that their mechanisms of release are similar. Alternatively, cytosolic PAI-2 may have an intracellular function, although neither serine proteases nor enzymes of specificity comparable to that of the PAs have been identified in the cytosol.

Interestingly, the two forms of PAI-2 are encoded by a single mRNA (BELIN et al. 1989). Indeed, only one PAI-2 mRNA can be detected by Northern blot hybridization and by RNase protection, and transfection of a PAI-2 cDNA leads to the synthesis of both forms of the protein. In vitro translation of the mRNA transcript of a PAI-2 cDNA in the presence of microsomal membranes yields the two topologically distinct forms of the inhibitor: a membrane-enclosed and a "cytosolic" product. In this context, it is noteworthy that translation of the two forms of PAI-2 initiates at the same AUG, and that the secreted form is released without removal of the putative signal peptide (YE et al. 1988). The latter observation is reminiscent of ovalbumin secretion, which also occurs without removal of the N-terminal region of the protein; it may be relevant that ovalbumin is the closest serpin relative of PAI-2.

Taken together, the available information on PAI-2 indicates that the inhibitor is secreted through a process of cotranslational, but facultative, translocation. To our knowledge such a situation has not been described previously. Other proteins that are distributed bi-topologically to the cytosol and the extracellular milieu, such as yeast invertase (CARLSON et al. 1983) and mammalian gelsolin (Kwiatkowski et al. 1988), are translated from distinct mRNAs, one of which encodes a signal peptide. Another mechanism to achieve bitopological distribution is illustrated by secreted and nuclear rat prostatic probasins, which result from alternate translational initiation on a bifunctional mRNA (SPENCE et al. 1989). The unusual mechanism of PAI-2 partition may be related to structural features of its N-terminal region: this region (amino acids 1-22) contains, in addition to a hydrophobic stretch, two negatively charged residues near the N-terminus, and two asparagines within the hydrophobic core. It is striking that these features, which have not been found in other secreted proteins, are conserved between human and murine PAI-2 (BELIN et al. 1989); it thus seems unlikely that PAI-2 is simply a secreted protein which is translocated with poor efficiency, and a possible role for the bitopological distribution of this powerful protease inhibitor will be discussed below.

The production of PAI-2 varies dramatically between different mouse macrophage populations (WOHLWEND et al. 1987b). While PAI-2 is essentially undetectable in cultures of bone marrow-derived macrophages, it is abundant in resident peritoneal macrophages. Peritoneal exudate macrophages induced

by injection of thioglycollate broth contain very little PAI-2; the inhibitor detected in the latter cultures is probably that produced by a preexisting subpopulation of "resident" macrophages. These differences in PAI-2 production can be accounted for by remarkably different rates of transcription of the PAI-2 gene (Fig. 2) and steady state levels of PAI-2 mRNA (Fig. 3); in fact, of those genes whose transcription rates we have compared, PAI-2 is that which differs the most between the resident and the inflammatory exudate macrophage populations (Fig. 2).

In vitro studies have identified some of the agents which may be responsible for controlling macrophage PAI-2 production (Table 1). Culture of peritoneal macrophages in the presence of LPS (CHAPMAN et al. 1982), of the phorbol ester phorbol myristate acetate (PMA), of agents which raise intracellular cAMP levels, or of M-CSF (WOHLWEND et al. 1987b) results in increased PAI-2 production, and in correspondingly increased steady state levels of PAI-2 mRNA (Fig. 4). It remains to be determined whether these changes in PAI-2 mRNA levels are due to changes in transcription of the gene or in message stability; PAI-2 mRNA contains in its 3' untranslated region structural determinants (AU-rich sequences) which have been shown to be responsible for instability of other mRNAs (SHAW and KAMEN 1986). Interestingly, in the context of the overall regulation of the macrophage PA system, IFN- $\gamma$ , which increases uPA production, does not affect PAI-2 while glucocorticoids, which decrease the production of uPA, also decrease that of PAI-2 (WOHLWEND et al. 1987b).

Less is known about modulation of PAI-2 production in human monocytes/ macrophages. PMA (GENTON et al. 1987; SCHLEUNING et al. 1987; WEBB et al. 1987; WOHLWEND et al. 1987a; YE et al. 1987), LPS (CHAPMAN and STONE 1985b; SCHWARTZ et al. 1988), muramyl dipeptide (STEPHENS et al. 1985), and infection by dengue virus (KRISHNAMURTHI et al. 1989) increase PAI-2 levels in monocytes or related cell lines, while 1,25-dihydroxyvitamin D<sub>3</sub> decreases PAI-2 production by U937 cells (GYETKO et al. 1988). Mononuclear phagocytes cultured from blood, peritoneal cavity, bone marrow, or alveolar lavage, but not those prepared from the colonic mucosa, have been shown to produce PAI-2 (CHAPMAN and STONE 1985b; STEPHENS et al. 1985).

While the available evidence does not allow a complete understanding of the role of PAI-2 in the biology of mononuclear phagocytes, it is reasonable to speculate that it may be required to control uPA-catalyzed proteolysis at certain stages of the inflammatory reaction. Monocyte uPA is thought to be necessary for migration of these cells from the blood into the tissues, and it may perhaps also play a part in removal of fibrin clots. However, fibrin also constitutes a transitory scaffold that helps the reconstitution of an appropriate extracellular matrix following tissue damage, and premature or excessive fibrin degradation would clearly be detrimental to the healing process. Once in the tissue, perhaps under the influence of locally produced cytokines such as M-CSF, monocytes/macrophages could start producing PAI-2 and thereby contribute to the delicate protease–antiprotease balance within the extracellular matrix. In this view, release of the large stores of cytosolic PAI-2 could play an 76 J.-D. Vassalli et al.

important part in limiting plasmin-mediated tissue destruction, even if the local conditions lead to some macrophage lethality.

# 5 A Plasma Membrane Binding Site for Urokinase-type Plasminogen Activator

The elucidation of the primary structure of uPA (GÜNZLER et al. 1982) revealed an unexpected characteristic of this protein: the presence, in its N-terminal region, of a domain with substantial homology to epidermal growth factor (EGF) and transforming growth factor  $\alpha$  (TGF $\alpha$ ). This suggested that this growth factor-like domain might dictate the binding of uPA to a receptor site on the surface of certain cells, and that, if this was the case, uPA could function as a cell surface-associated enzyme. Exploration of this hypothesis led to the discovery of a binding site for the  $M_r$  55 000 form of uPA on human monocytes and monocyte-like U937 cells (VASSALLI et al. 1985; STOPPELLI et al. 1985). A K<sub>d</sub> of approximately 10<sup>-10</sup> M, i.e., in the range of the concentration of pro-uPA



**Fig. 5.** Species-specific binding of uPA to a cell surface receptor. Murine resident peritoneal macrophages (WOHLWEND et al. 1987b) and human peripheral blood monocytes (VASSALLI et al. 1985) were prepared and plated at low cell density as described. Where indicated, cells were preincubated in the presence of a synthetic peptide corresponding to part of the growth factor-like domain of murine uPA (BELIN et al. 1985; APPELLA et al. 1987) ( $10^{-6}$ M, 15 min). They were then incubated for 45 min in the presence of equivalent catalytic amounts of human or murine uPA (0.6 Ploug unit/ml, approximately  $10^{-10}$ M), washed, and analyzed for PA activity as for Fig. 1

in blood plasma (TISSOT et al. 1982; WUN et al. 1982b), and a number of 60 000 sites per cell were calculated for U937 cells. This receptor was found to be specific for uPA, in that other proteins with similar domains, including tPA and EGF, did not compete for uPA binding (VASSALLI et al. 1985).

The uPA receptor can bind both the active enzyme and its zymogen pro-uPA (CUBELLIS et al. 1986). Binding occurs through the noncatalytic A chain of the enzyme (VASSALLI et al. 1985; STOPPELLI et al. 1985), and, in confirmation of the above-mentioned hypothesis, involves the growth factor-like domain of the molecule (APPELLA et al. 1987). Bound pro-uPA can be activated by plasmin (CUBELLIS et al. 1986), and the bound enzyme is catalytically active (VASSALLI et al. 1985) (Fig. 5). Thus, while pro-uPA is a secreted protein, its subsequent binding to a high affinity cell surface receptor localizes the enzyme to the plasma membrane; this probably accounts for previous reports describing membrane-associated forms of uPA (SOLOMON et al. 1980; CHAPMAN et al. 1982; LEMAIRE et al. 1983). Binding of uPA clearly contributes to limit the activity of the uPA-plasmin system to the close environment of the cell. It is clear that such a proteolytic system could operate to catalyze the focal lysis of extracellular substrates, in an optimal configuration to facilitate cell migration. In this context, it is interesting to note that immunochemical studies on human fibroblasts and fibrosarcoma cell cultures have demonstrated the presence of uPA at sites of attachment of the cells to the substratum, and its codistribution with the cytoskeletal component vinculin (PÖLLÄNEN et al. 1988; HÉBERT and BAKER 1988).

The biochemical characterization of the uPA receptor has shown that it behaves as an integral membrane protein (ESTREICHER et al. 1989) and that it comprises at least one carbohydrate-containing  $M_r$  55 000 polypeptide chain (NIELSEN et al. 1988). Binding, detergent partitioning, and chemical cross-linking studies have revealed the presence of uPA receptors with similar properties on human cells other than mononuclear phagocytes, for instance fibroblasts, polymorphonuclear leukocytes, or endothelial cells (BAJPAI and BAKER 1985; MILES and PLOW 1987; MILES et al. 1988). Studies in other species have been hampered by the species specificity of uPA binding (ESTREICHER et al 1989) and the limited availability of purified homologous uPAs. However, utilizing a catalytic assay, the presence of a receptor for murine uPA on mouse peritoneal macrophages and the species specificity of the interaction can be demonstrated (Fig. 5): addition of homologous uPA to human and murine monocytes/macrophages results in their acquisition of cell-associated PA activity, while the heterologous enzyme does not bind. The specificity is further demonstrated by the use of a synthetic peptide corresponding to a part of the growth factor-like domain of mouse uPA [mouse Ala<sup>20</sup>-uPA(13-33)] (APPELLA et al. 1987). This peptide markedly inhibits the binding of murine uPA to murine macrophages, but it does not affect the binding of human uPA to human cells. The observed species specificity of binding can probably be explained by the structural differences between human and murine uPAs within the growth factor-like domains of the molecules (ESTREICHER et al. 1989).

In addition to localizing plasminogen activation to the immediate vicinity of the cell surface, binding of uPA (or pro-uPA) to its plasma membrane receptor could change the catalytic specificity or efficiency of the enzyme, or convert the single-chain protein to an active enzyme. Such studies are not easy to perform, since they require that the activity of soluble and immobilized molecules be compared in quantitative terms. Despite these difficulties, a 16-fold acceleration of the activation of cell-bound plasminogen (see below) by cell-bound prouPA was observed in cultures of monocyte-like U937 cells (ELLIS et al. 1989). This could be accounted for by an increase in the rate of feedback activation of pro-uPA by cell-bound plasmin. Since such a potentiation was not observed in the presence of 6-aminohexanoic acid, which prevents cellular binding of plasminogen, or of the amino-terminal fragment of uPA, which prevents binding of pro-uPA, it appears that binding does not alter the activity or specificity of the individual molecules, but rather acts by increasing their rate of reaction, probably through a receptor-mediated concentration effect on the cell surface. This interesting study illustrates how the assembly of the components of the PA-plasmin system on the plasma membrane, through binding to their respective receptors, could dramatically favor proteolysis in the close cellular environment.

It has previously been suggested that receptor-bound uPA may be protected from rapid inhibition by antiproteases (BLASI et al. 1987). However, recent studies have shown that the rates of uPA inactivation by PAI-1 (CUBELLIS et al. 1989) or PAI-2 (KIRCHHEIMER and REMOLD 1989; ESTREICHER et al., submitted for publication)<sup>1</sup> (for footnote see p. 79) are not markedly different whether the enzyme is bound or free in solution. Thus, the receptor does not shield uPA from its specific inhibitors, and the controlled production and secretion of PAI-2 can play an important part in modulating plasminogen activation at the cell surface. Nevertheless, it will be of interest to compare the rates of plasmin formation in the presence and absence of PAIs, using the U937 cell system with cell-bound and soluble zymogens, as described above.

The affinity, density, and distribution of the uPA receptor are all subject to modulation. Differentiation of U937 monocyte-like cells in response to PMA leads to a marked increase in receptor number and a decrease in binding affinity (STOPPELLI et al. 1985; PICONE et al. 1989). A comparable modulation has been reported for HeLa cells exposed to PMA or to the growth factor EGF (ESTREICHER et al. 1989). The mechanisms responsible for these changes have not been elucidated, although a change in the extent of receptor glycosylation appears to accompany the change in affinity (PICONE et al. 1989). The biologic relevance of these changes is not clear. The K<sub>d</sub> value for the high affinity state of the receptor is close to the concentration of pro-uPA in plasma; at this concentration, the net result of the PMA effect would be only a small increase in receptor-bound uPA. Higher concentrations of uPA may prevail in the close environment of uPA-producing cells in tissues; under these conditions, a large increase in the amount of membrane-bound uPA could be achieved. Other studies have reported an increase in uPA receptor number, with no change in binding affinity, for U937 cells (LU et al. 1988) and peripheral blood monocytes

(KIRCHHEIMER et al. 1988) exposed to IFN- $\gamma$  or to IFN- $\gamma$  and TNF- $\alpha$ , respectively. Finally, the polarization of uPA receptor distribution on monocytes and U937 cells placed in a chemotactic gradient (ESTREICHER et al., submitted for publication)<sup>1</sup> suggests an additional dimension in the modulation of receptor expression and provides further evidence in favor of the hypothesis that the receptor can serve to focus plasmin generation to the leading edge of migrating cells.

### 6 Binding of Plasminogen to the Cell Surface

The discovery of plasminogen-binding sites on cells that also bear uPA receptors, including human monocytes and U937 cells, has added a new dimension to the concept of a cell surface system of PA-catalyzed extracellular proteolysis (HAJJAR et al. 1986; PLOW et al. 1986; MILES et al. 1988). The K<sub>d</sub> value for plasminogen binding is approximately  $10^{-6}$  M, i.e., close to its plasma concentration ( $2 \times 10^{-6}$  M), and a large fraction of the 200 000 plasminogen binding can be inhibited by 6-aminohexanoic acid, indicating that the lysine-binding sites present on the plasminogen kringles may be involved. The nature of the plasminogen receptor has not been elucidated, but recent data suggest a possible role for gangliosides (MILES et al. 1989).

Studies summarized above (ELLIS et al. 1989) have shown that coexpression of uPA and plasminogen receptors on the same cells facilitates pro-uPA activation, thus significantly accelerating the generation of plasmin. Most importantly perhaps, like fibrin-bound plasmin, cell-bound plasmin appears to be protected from inhibition by  $\alpha_2$ -antiplasmin, a highly effective inhibitor of soluble plasmin. Although the precise mechanism of this protection is not known, it may rely on the fact that the lysine-binding sites of cell surface-bound plasmin are occupied; indeed, the interaction of soluble plasmin with  $\alpha_2$ -antiplasmin involves both the lysine-binding sites on the non-catalytic part of the enzyme and the active site. In any event, it is clear that the combined effects of accelerated plasmin generation and prolonged plasmin action through resistence to inhibition should result in a highly effective cell surface-bound proteolytic system (STEPHENS et al. 1989). Future studies of plasminogen-binding sites on other cells of the mononuclear phagocyte lineage, such as murine peritoneal macrophages, should be of considerable interest in further evaluating the role of this cell surface catalytic cascade in extracellular proteolysis.

<sup>&</sup>lt;sup>1</sup> Note added in proof: The paper by Estreicher et al. that had been quoted as "submitted for publication" has been published. Estreicher A, Muhlhauser J, Carpentier J-L, Orci L, Vassalli J-D (1990) The receptor for urokinase-type plasminogen activator polarizes expression of the protease to the leading edge of migrating monocytes and promotes degradation of enzyme inhibitor complexes. J Cell Biol 111: 783–792





### 7 A Powerful Cell Surface Proteolytic System

The large body of information that has been summarized here converges to indicate that uPA could be a key determinant of a very powerful and highly regulated proteolytic system at the surface of mononuclear phagocytes, at certain stages of the inflammatory process. Plasmin generated at the level of the monocyte/macrophage plasma membrane could catalyze the degradation of fibrin, and also, either directly or indirectly through the activation of zymogens to the metalloproteases, that of collagen, elastin, and other components of extracellular matrices such as laminin and fibronectin (Fig. 6) (CHAPMAN et al. 1984). It is striking that uPA production has been associated with a number of situations where cell migration is required (trophoblast cells during embryo implantation, keratinocytes in reepithelializing wounds, endothelial cells during angiogenesis, malignant cells) (SAPPINO et al. 1989; GRØNDAHL-HANSEN et al. 1988; PEPPER et al. 1987; MIGNATTI et al. 1989; DANØ et al. 1985). Moreover, a direct role for uPA activity has been demonstrated in extracellular matrix invasion by tumor and endothelial cells (MIGNATTI et al. 1986, 1989; OSSOWSKI 1988a), and receptor-bound uPA has been shown to enhance tumor cell invasiveness (Ossowski 1988b). Hence, although this has not as yet been directly tested, it is reasonable to envision that the PA-plasmin system could be essential for the migration of monocytes and macrophages.

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# **Macrophage-Derived Growth Factors**

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# **1** Introduction

In the early decades of the twentieth century biologists sought to grow cells in culture. Clotted blood was found to contain molecules that accomplished this purpose (CARREL 1912), but only later did biochemists seek to purify these molecules. By the middle of the century, biochemists and biologists sought to explain neonatal eye opening in mice in molecular terms (COHEN 1987; LEVI-MONTALCINI 1987). Each of these goals ultimately led to the isolation of single species of molecules called growth factors by using in vitro or in vivo bioassays for growth and a biochemical algorithm for isolation. Epidermal growth factor

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(EGF), nerve growth factor (NGF), platelet-derived growth factor (PDGF), transforming growth factor- $\beta$  (TGF- $\beta$ ), interleukin-1 (IL-1), and macrophage colony-stimulating factor (M-CSF, or CSF-1) were isolated and directly sequenced or molecularly cloned (based on partial sequences) by these means in the 1970s and early 1980s. The production of transformed foci of cells by introduction of fragments of cloned transcripts or genes from tumors also produced a subclass of oncogenes that turned out to be growth factors [c-sis, or PDGF-B chain, and Kaposi's sarcoma-fibroblast growth factor (kFGF, or FGF-4)]. Most recently, the formation of tumors in vivo after random integration of a highly active viral promoter upstream of cellular genes has produced the int-1 and int-2 (also known as FGF-3) growth factors. Finally, after the founding member of a growth factor family is identified with a bioassay, low-stringency cDNA library screens and polymerase chain reaction can be used to complete the family (JAKOWLEW et al. 1988; HEBERT et al. 1990). All growth factors are operationally isolated and defined by their ability to cause growth, but may also act as nonmitogenic inflammatory factors.

Growth factors have a number of hallmarks. First, they are generally secreted and therefore act on nearby cells in a paracrine or autocrine fashion (ROSS and VOGEL 1978). Some growth factors may exit cells slowly (e.g. IL-1, M-CSF) or on cell death (basic and acidic forms of FGF), but all enter the extracellular milieu. Other growth factors have a membrane-bound form (e.g., IL-1, M-CSF, TGF- $\alpha$ , and EGF), but these growth factors also act locally between cells. The second hallmark of growth factors is that they tend to act in localized areas either within a cell (ROSS and VOGEL 1978; ROSS et al. 1986; DEUEL 1987) or within a few cell distances [as seen with NGF in pancreatic innervation (EDWARDS et al. 1989)]. Third, growth factors are generally not stored inside the cell (exceptions are PDGF and TGF- $\beta$  in the platelet) but are highly inducible at the level of transcription (IL-1), translation [TGF- $\beta$ , tumor necrosis factor (TNF)- $\alpha$ , IL-1] and post-translational activation (TGF- $\beta$ ). Fourth, since these molecules are extremely powerful, they are tightly regulated at the various levels of production. They are unstable at the transcriptional level because of an AUUUA motif in the 3' untranslated area of many growth factor transcripts [c-sis/PDGF, IL-1, IL-2, and granulocyte-macrophage colony-stimulating factor (GM-CSF) (SHAW and KAMEN 1986)], and at post-translational levels. PDGF and TGF- $\beta$  are both inactivated by a macrophage product,  $\alpha_2$ -macroglobulin (DANIELPOUR and SPORN 1990; ROBERTS and SPORN 1990). In addition, the mediators of the growth factors (e.g., prostaglandins induced by PDGF or IL-1) have been demonstrated to negatively regulate the transcription of the inducing growth factor (KUNKEL et al. 1986; DANIEL et al. 1987). Fifth, growth factors are pleiotropic, acting as secretagogues, chemoattractants, and differentiation factors. Finally, growth factors act on the target cell through a transmembrane receptor. Some growth factors allosterically activate protein kinase activity on the cytosolic end of the receptor and trigger an amplified cascade of events within the target cell that lead to the pleiotropic events described. In some cases the growth factor receptor does not have intrinsic kinase activity but





activates other kinases within the cell (e.g., TNF- $\alpha$ , IL-1, IL-6, GM-CSF, IL-2 receptors).

The number of growth factors and growth factor families has grown enormously within the last decade (Tables 1–13). The central interest of intercellular control of growth in abnormal circumstances, such as tumor formation, and in normal embryogenesis and postnatal growth as well as wound healing has led to the discovery of several major families of growth factors: PDGF (which currently has four members), FGF (seven members), EGF (five members), TGF- $\beta$ (five members in one subgroup, eight in another), insulin-like growth factors (four members), and immediate-response-gene growth factors KC/JE/PF-4 (15 members). There are a number of single-member growth factor "families" (Table 13), but for each founder growth factor, molecular biologic techniques are likely to identify several homologous family members, as they have for several of the growth factor families (JAKOWLEW et al. 1988; HEBERT et al. 1990). It is not clear whether these homologous factors are strong growth inducers or whether they induce other effects, such as inflammation. The current list of 80 growth factors may expand to several hundred in the next decade.

A case in point is the increase in the number of growth factors known to be synthesized by the macrophage. In the early 1980s IL-1 was the first growth factor to be isolated and cloned from macrophages. IL-1 is now known to be produced by many cells in smaller amounts than in macrophages. It is also pleiotropic in its functions (Tables 1–3). Since then, approximately 30 growth factors have been detected in macrophages (Table 4). Only about 15 growth factors have been found that are not synthesized by macrophages. Undoubtedly, these numbers will also increase rapidly in coming years (Tables 5–13).

A challenge for those who study the differentiation, production, and function of macrophages is to understand these processes in terms of the production and function of growth factors. In this chapter we will examine the current knowledge of macrophage function in terms of growth factor production and function. We will first examine the macrophage-derived growth factors as structurally or functionally related families. We will then examine negative modulation of growth factors. Finally, we will examine several specific models that are partially understood: inflammation, wound healing, nerve regeneration, the immune response, and hematopoiesis (Fig. 1).

## 2 Growth Factors Produced by Macrophages

### 2.1 Growth Factors Functionally Related to IL-1

Interleukin-1 $\alpha$ , IL-1 $\beta$ , TNF- $\alpha$ , IL-6, and leukemia inhibitory factor/differentiationinhibiting activity (LIF/DIA) are macrophage-derived growth factors with overlapping effects (Table 5). They are functionally but not structurally related. IL-1 $\alpha$ and IL-1 $\beta$  were the first growth factors purified, cloned, and sequenced from macrophages (AURON et al. 1984). IL-1 $\alpha$  and IL-1 $\beta$  arise from two distinct genes in a variety of cell types and act on two distinct receptors expressed in many cell types (Table 1). The IL-1 receptors exist in high-affinity and low-affinity forms (K<sub>d</sub> of 5–10 pM and 200–400 pM, respectively) (DINARELLO 1989), which bind to both IL-1 $\alpha$  and IL-1 $\beta$ . It is not clear what functional differences these receptors have. One of these receptors has been cloned and, like the IL-2 and IL-6 receptors, has no intrinsic enzymatic activity but associates with other plasmalemmal proteins to transduce signals. The IL-1 receptor is in the immunoglobulin superfamily (as are the PDGF  $\alpha/\beta$ , M-CSF, and FGF receptors). Its number varies from 200 to 20 000 per cell, which is low compared with the 10<sup>5</sup> copies of PDGF and EGF receptor per fibroblast but is similar to the number of GM-CSF receptors per cell (METCALF 1985).

Interleukin-1 has the longest molecular history of macrophage-derived growth factors and a correspondingly large body of knowledge about its endocrine, paracrine and autocrine effects (Tables 2, 3). IL-6 has biologic responses that broadly overlap those of IL-1; its receptor is also widely distributed, has been cloned and resembles the IL-1 receptor in that it lacks enzymatic

Agents stimulating	g IL-1 productio	n		
IL-1	LPS	LTD <sub>4</sub>	Zymosan	Adherence
TGF-β1	LTC₄	Muramyl dipeptide	IFN-α <sup>a</sup>	PMA
TNF-α	C5a	Silica	IFN-γ <sup>a</sup>	Urate crystals
Producer cell type	es			
Macrophages	Kupffer cells	Keratinocytes	Microglial cells	B cells
Endothelial cells	Fibroblasts	Mesangial cells	Astrocytes	Natural killer cells

Table 1.	Regulation	of IL-1	(modified	from	RAPPOLEE	and	Werb	1988)
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<sup>a</sup> GERRARD et al. (1987)

IFN, interferon; LTC, leukotriene C; PMA, phorbol 12-myristate 13-acetate

<i>T cells</i> Cytotoxic T cell generation IL-2 receptor induction LFA-1 induction	Chemoattractant MEL-14	Comitogen IL-2 ligand induction
<i>B cells</i> Chemoattractant LFA-1 induction	Comitogen MEL-14	Maturation inducer
Natural killer cells Cytotoxicity inducer	IL-2 receptor inducer	
Macrophages Cytotoxicity inducer PGE <sub>2</sub> inducer TNF-α inducer MIP-1 inducer IL-1RA inducer	Reactive oxygen inducer IFN- $\beta_2$ inducer MIP-2 inducer IL-8 inducer	Chemoattractant IL-1 inducer Thromboxane $\beta_2$ inducer JE inducer

 Table 2. Effects of IL-1 on immune and hematopoietic cells (modified from RAPPOLEE and WERB 1983)

IL-1RA, IL-1 receptor antagonist

Fibroblast and synovial cells PGE <sub>2</sub> inducer PI inducer GM-CSF inducer Stromelysin inducer PDGF-A chain/mitosis	Collagenase inducer Hyaluronate inducer IL-1 inducer Proliferation	IFN-β1/β2 inducer Class II MHC inducer
<i>Bone</i> Resorption		
Cartilage Proteoglycan synthesis suppressor		Metalloproteinase inducer
Endothelial cells Procoagulant activity inducer PAF, PGF <sub>2</sub> , PGI <sub>2</sub> inducer Antiocoagulant activity suppressor	PA suppressor PAI inducer GM-CSF, G-CSF, M-CSF inducer	IL-1 inducer Adherence of T and B cells, PMNs, macrophages
Systemic changes Drowsiness Acute-phase response inducer (C3, factor B, haptoglobin, fibrinogen)	Shock Iron decrease (due to lactoferrin secretion)	Glucocorticoid induction Fever (reset hypothalamic set point)
Schwann cells NGF inducer		
Basophils and mast cells Histamine release <sup>a</sup>		
Megakaryocytes Proliferation <sup>b</sup>		
<sup>a</sup> Suppananian and Bray (1987)		

Table 3.	Effects of IL-1	on connective tissue and other c	ells (modified fro	m Rappolee and Werb 1988)
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<sup>a</sup> SUBRAMANIAN and BRAY (1987) <sup>b</sup> WILLIAMS and MORRISSEY (1989)

PA, plasminogen activator; PAI, plasminogen activator inhibitor; PG, prostaglandin; PI, phosphatidyl inositol turnover

activity and is a member of the immunoglobulin superfamily (SIMS et al. 1988; KISHIMOTO 1989; BAUER et al. 1989; BEAGLEY et al. 1989). LIF/DIA was cloned recently as both an embryonic stem cell differentiation-inhibiting factor and a leukemia-inhibiting factor that causes differentiation. It is similar to TNF- $\alpha$ , IL-1, and IL-6 in its stimulation of acute-phase reactants in liver (BAUMANN and WONG 1989). Its major biologic activites most closely resemble those of IL-6 (MOREAU et al. 1988; ABE et al. 1989).

Tumor necrosis factor- $\alpha$  is another macrophage-derived growth factor with a distinct, recently cloned, receptor, which is widely distributed and mediates biologic responses that broadly overlap those of IL-1 (OLD 1985; BEUTLER and CERAMI 1988; DINARELLO 1989; SMITH et al. 1990; SCHALL et al. 1990). It induces fever, the acute-phase response, T and B cell activation, fibroblast proliferation, collagen synthesis, and many other effects. Several of these effects require a higher concentration of TNF- $\alpha$  than IL-1 (one to two orders of magnitude). IL-1

Growth factor	Reference	Growth Factor	Reference
Polypeptide produc	ction by macrophages		
IL-1α	а		
IL-1β	а	MIP-1α	а
IL-1 receptor	а	MIP-1 $\beta$	а
IL-1 receptor	а	JE	Koerner et al. 1987;
antagonist			INTRONA et al. 1987
PDGF-A	а	Mig (monokine	Farber 1990
PDGF-B/c-sis	а	induced by IFN-γ)	
PDGF-related	а	IL-6	а
Vascular	а	M-CSF	а
permeability factor			
		KC	Koerner et al. 1987; INTRONA et al. 1987
		IP-10	a
TGE-B1	а	IP-8	a
TGF-B2	a	MIP-2	a
Activin	ERAMAA et al 1990		a
	ENAMAA EL AI. 1990		
Miscellaneous		TGF-α	RAPPOLEE et al. 1988
		bFGF	Baird et al. 1985
TNF-α	а	IGF-I	RAPPOLEE et al. 1988
GM-CSF	а	Defensins	Ganz et al. 1989
G-CSF	а	Thymosin	а
LIF/DIA	а	Bombesin	WIEDERMANN et al. 1986
Frythropoietin	BICH et al. 1982	ACTH	SMITH et al. 1986
Lijimopolotin	PAUL et al. 1984	Fibronectin	ALITALO et al. 1980
Polypentide growth	factors not produced by m	acrophages	
NGE	BARPOLEE Unpublished	II -10	3
	data		a
EGF	RAPPOLEE et al. 1988	Neuroleukin	а
IL-2	а	IGF-II	RAPPOLEE, unpublished data
IL-3	а	Insulin	RAPPOLEE, unpublished
IL-4	а	TNF- $\beta$	a
IL-5	а	IFN-γ	a
IL-7	а	,	
Other regulatory pr	oducts produced by macro	ohages	
PGE <sub>2</sub>	a	Respiratory burst	а
Acidic isoferritin	BROXMEYER et al. 1985	products	
Nitric oxide	STUEHR and NATHAN 1989	Nitrates	а

Table 4. Macrophage-derived growth factors and regulatory molecules

<sup>a</sup> References from RAPPOLEE and WERB (1988) or in Tables 5-11. Structurally related genes are grouped between horizontal lines

ACTH, adrenocorticotropic hormone; IFN, interferon

is distinct from TNF- $\alpha$  in that it affects stem cells in the bone marrow (hemopoietin activity), whereas TNF- $\alpha$  suppresses colony formation (DINARELLO 1989). On the other hand, TNF- $\alpha$  is more powerful in inducing vascular shock, possibly by its greater effect in inducing capillary leak syndrome. Biologic responses, such as enhanced motility of endothelial cells in sprouting capillaries, may

Table 5. Growth fa	actors functionally	related to IL-1						
Growth	Synthesis by	Induction	Specific	mRNA		Protein		Reference
lacior	macrophages			Size (kb)	AUUUA instability sequence	Precursor amino acid number	Mature peptide (kDa)	
IL-1α	+	LPS	Cell surface form	2.0	+	271	27	Lomepico et al. 1984; March et al 1985
IL-1β	+	LPS	Cell surface form	1.3	+	269	33	стал. 1985; Максн et al. 1985; Grav et al. 1986
IL-1 receptor antagonist	+	LPS GM-CSF		0.T	I	177	25	EISENBERG et al. 1990; CARTER et al. 1990
TNF-a	+	LPS	Cell surface form	2.0	+	157	17	PENNICA et al. 1985; Wang et al. 1985; Second et al. 1987
TNF- <i>β</i>	ł			155	+	177	18	Semon et al. 1987
IL-6/IFN- <i>B</i> 2	+	Adherence		<del>د</del> ن	+	211	21	HIRANO et al. 1986; ZILBERSTEIN et al. 1986; VAN SNICK et al. 1988; TANABE
LIF/DIA	+	LPS		1.8/4.0	+	202	45	ет аг. 1900 Монел∪ et al. 1988; Селяпис et al. 1988; Үамамоя। et al. 1989

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increase the sensitivity of the TNF- $\alpha$  receptor (GERLACH et al. 1989). TNF- $\alpha$  also has a larger array of targets for inducing DNA fragmentation and concomitant cell death (BEUTLER and CERAMI 1988). TNF- $\alpha$  and IL-1 have similar effects on the major cells in the inflammatory response, inducing respiratory oxidative burst, chemotaxis, and adhesion in polymorphonuclear leukocytes (PMNs); production of granulocyte colony-stimulating factor (G-CSF), IL-6, and GM-CSF and procoagulants and adhesion in endothelial cells; production of multiple growth factors [G-CSF, GM-CSF, M-CSF, IL-1, TNF- $\alpha$ , IL-6, macrophage inflammatory protein (MIP)-1, MIP-2, and IL-8], chemotaxis, and adhesion in macrophages; and proliferation, growth factor, and extracellular matrix molecule expression in fibroblasts (CAVENDER et al. 1986; MUNKER et al. 1986; BEUTLER and CERAMI 1988; DINARELLO 1989; see also references in Tables 2 and 3). TNF- $\alpha$  induces IL-1 and IL-6 in vitro and in vivo (BROUCKAERT et al. 1989; DINARELLO 1989; FONG et al. 1989).

The control of adhesion molecules on interacting blood cells and endothelial cells by TNF- $\alpha$  and IL-1 is becoming clearer. The constitutive expression of MEL-14, an adhesion molecule for normal recirculating leukocytes and lymphocytes that is required for diapedesis by peritoneal exudate cells, is downregulated by TNF- $\alpha$  and IL-1 rapidly (within minutes), whereas Mac-1/gp155/90 inflammatory adhesion molecules and intercellular cell adhesion molecules (ICAM) in PMNs and macrophages and ICAM and endothelial leukocyte adhesion molecules (ELAM-1) in endothelial cells are up-regulated more slowly (4 h) (GAMBLE et al. 1985; SCHLEIMER and RUTLEDGE 1986; NAWROTH et al. 1986; DOHERTY et al. 1987; BEUTLER and CERAMI 1988; KISHIMOTO et al. 1989). It is speculated that the shedding of MEL-14 may prevent activated leukocytes from entering normal lymphoid tissue, or it may be a required step in diapedesis as leukocytes disconnect from their initial binding to the activated endothelial cells of the vessel wall (BEVILACQUA et al. 1986, 1989; BRETT et al. 1989). The interaction molecule for ELAM-1 on leukocytes is not known (POBER and COTRAN 1990). ICAM on endothelial cells and Mac-1/gp155/90 on leukocytes are also upregulated within 4 h but decay hours after ELAM-1, perhaps mediating immediate and long-range adhesion. This coordinate temporal expression parallels the autocrine effects of growth factors on stimulation of macrophages.

### 2.2 Immediate-Response-Gene Growth Factors

The founders of the two groups of inflammatory response genes (group 1: KC, MIP-2, IL-8, and PF-4; group 2: JE and MIP-1 $\alpha$ , $\beta$ ) were originally cloned as response genes to PDGF (JE and KC) and interferon- $\gamma$  (IP-10) (STILES 1983; LUSTER et al. 1985; DEUEL 1987; ROLLINS et al. 1988; KAWAHARA and DEUEL 1989; OQUENDO et al. 1989; STOECKLE and BARKER 1990). It is interesting to note that the PDGF-inducible genes JE and KC were recently found to be much more highly induced by IL-1 (HALL et al. 1989). IL-8 (also called neutrophil activity protein-1/monocyte-derived neutrophil chemotactic factor/T cell chemotactic

Table 6. Immediate	-response-gene c	prowth factor fam	hily					
Growth	Synthesis by	Induction	Specific	mRNA		Protein		Reference
tactor	macrophages		broperiles	Size	AUUUA	Precursor	Mature	
				(kb)	instability sequence	amino acid number	peptide (kDa)	
JE/monocyte chemoat-	+	LPS	Heparin binding	4.5	+	148	16.3	Rollins et al. 1988; Kawahara and
tractant protein-1								DEUEL 1989; YOSHIMURA et al.
-								1989
MIP-1a/LD78	+	LPS	Heparin binding	0.8	+	92	8.0	DAVATELIS et al.
								1989; Kwon and
								WEISSMAN 1989
MIP-18	+	I PS	Heparin binding	0.65	+	109	8.0	SHERRY et al. 1988;
<i>d</i> 1 11101	_	i						Brown et al. 1989
TCA-3				0.65	I	92		Burn et al. 1987
M-CSF	+	Adherence	Transmembrane	2.3/3.8/4.5	+	$118 \times 2$	70.0	Kawasaki et al. 1985;
00	-							RAJAVASHISTH et al.
								1987
9 	4	Adherence		1.3	Ŧ	211	21.0	YAMASAKI et al. 1988;
Ę	_							VAN SNICK et al.
								1988
IL-2	I			1.1	+	153	15-17	TANIGUCHI et al.
1								1983; Үокота
								et al. 1985

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IFN-α (4–10 members)	+	LPS		1.0/2.8/5.5	+	189/190	20, 29–35, 35–40	SHAW et al. 1983; EPSTEIN et al.
KC/Gro/MGSA	+	LPS		0.0	+	106	10.2	1990 Richmonb et al. 1988: Oouenbo
PF-4	+	LPS	Heparin binding	0.7/2.1/5.0	+	105	10.0	et al. 1989 DeueL et al. 1977;
β-TG/CTAP-III IP-10	+	IFN-γ	Heparin binding	1.2	+	81/85 98	8.0 20.0	Doi et al. 1987 Begg et al. 1978 Luster et al. 1985; Vangura and
IL-8/NAP-1/ MDNCF/310-C	+	LPS	Heparin binding	1.0	+	72	8.0	FARBER 1989 SCHMID and WEISSMAN 1987;
MIP-2 Mig monokine induced by allEN	+ +	LPS IFN-y	Heparin binding	1.6	+	126	6.0 14.5	иилі в ана в ан 1988 Woupe et al. 1989 Farber 1990

LD, leukocyte-derived; MGSA, melanocyte growth-stimulating activity; TCA, T cell activator; *β*-TG, *β*-thromboglobulin

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factor), MIP-2, and MIP-1 $\alpha$ , $\beta$  have been purified on the basis of biologic assays for inflammation and cloned from N-terminal sequences of the purified protein (DAVATELIS et al. 1988; SHERRY et al. 1988; MUKAIDA et al. 1989; STRIETER et al. 1989; WOLPE et al. 1989). The two groups are related by sequence homology, intron/exon conservation, and biologic function (Table 6).

Many of the factors reach high mRNA and protein concentrations quickly after exposure of macrophages and other cells to inflammatory stimuli (DEUEL 1987; see also Fig. 2). Therefore, these factors are available from multiple cell sources early in the inflammatory response or after trauma. They may also have roles in wound healing, nerve regeneration, delayed-type hypersensitivity, and other macrophage-mediated pathophysiologic events. As with the more highly characterized macrophage-derived growth factors (IL-1, TNF- $\alpha$ , and IL-6), these factors have common targets and effects: PMN chemoattraction (PF-4, IL-8, MIP-2, MIP-1 $\alpha$ , $\beta$ ), pyrogenesis (MIP-1 $\alpha$ , $\beta$ ), and macrophage chemoattraction (JE).

 $MIP-1 \alpha, \beta$ . MIP-1  $\alpha$  and MIP-1 $\beta$  were cloned from protein sequences obtained from a lipopolysaccharide (LPS)-stimulated macrophage cell line. They are 69 amino acid residue heparin-binding polypeptides that induce neutrophil chemotaxis and cytotoxicity. MIP mRNA is induced 1 h after LPS stimulation and continues at high levels for 16 h before decreasing at 24 h. MIP-1 $\alpha$  is a pyrogen and, 1 h after injection, induces a fast, monophasic fever that is not prostaglandin dependent and is therefore distinct from fever induced by TNF- $\alpha$ , IL-1, interferon- $\alpha$ , and perhaps IL-6 (DAVATELIS et al. 1989). MIP-1 $\alpha$ 



**Fig. 2.** The kinetics of RNA induction after addition of LPS. Note that various species and tissues were the sources of macrophages, and various types of LPS were used in the experiments. The interleukin receptor antagonist was stimulated by adhesion of macrophages to IgG. References: TNF- $\alpha$ , IL-1 $\alpha$ , SCALES et al. 1989; IL-1 receptor antagonist, EISENBERG et al. 1990; JE, KC, INTRONA et al. 1987; CSF-1, BECKER et al. 1989; LEE et al. 1990; GM-CSF, THORENS et al. 1987; LEE et al. 1990; IGF-I, NAGAOKA et al. 1990b; TGF- $\alpha$ , RAPPOLEE et al. 1988; TGE- $\beta$ , ASSOIAN et al. 1987; IL-6, NAVARRO et al. 1989; NORTHEMANN et al. 1989; PDGF-B, NAGAOKA et al. 1990a

also regulates the differentiation of macrophage precursors, but MIP-1 $\beta$  does not (GRAHAM et al. 1990).

*MIP-2.* MIP-2, a 6-kDa heparin-binding polypeptide, is induced by LPS in macrophages. It is a chemoattractant for PMNs but does not activate them for a respiratory burst. It is most closely related to the KC gene and is in the family of genes related to PF-4 (WOLPE et al. 1989). MIP-1 and MIP-2 also modulate in vitro granulopoiesis and monocytopoiesis (BROXMEYER et al. 1989).

*IL-8.* IL-8 is an 8-kDa heparin-binding polypeptide induced in LPS-stimulated macrophages. It is a chemoattractant and respiratory burst activator in neutrophils and causes leukotriene production by neutrophils but also appears to be important in the attraction of T cells to the sites of delayed-type hypersensitivity (MATSUSHIMA et al. 1989; SCHRÖDER 1989). IL-8 is not, however, a mitogen or comitogen for thymocytes. IL-1 and TNF- $\alpha$  induce IL-8 in macrophages, fibroblasts, and endothelial cells (MATSUSHIMA et al. 1988). Interestingly, IL-8 is not a chemoattractant for monocytes and does not amplify the macrophage response by increasing ingression of macrophages (MATSUSHIMA et al. 1989). It is closely related to the platelet  $\alpha$ -granule protein  $\beta$ -thromboglobulin/CTAP-III.

*PF-4.* PF-4 is a small polypeptide (76 amino acid residues) that is induced by PDGF in fibroblasts and delivered to wounds in large quantites by degranulation of platelet  $\alpha$ -granules. Serum contains only nanogram quantities of PDGF, but up to 20 µg/ml of PF-4. It is a neutrophil chemoattractant and is thought to modulate megakaryopoiesis, and it is anti-angiogenic (DEUEL et al. 1981; DEUEL 1987; OQUENDO et al. 1989; MAIONE et al. 1990).

JE. JE is a 148 amino acid polypeptide induced by interferon- $\gamma$  and IL-1 in macrophages. Its function is not yet fully characterized, but its importance is indicated by the speed of its induction (2 h) and high copy number (3000 copies per fibroblast, which is comparable to TNF- $\alpha$  and IL-1 transcript copy number in macrophages) (ROLLINS et al. 1988; KAWAHARA and DEUEL 1989; PRPIC et al. 1989; HALL et al. 1989). The transcript for JE accumulates for longer time periods in macrophages than in fibroblasts (see Fig. 2). JE is a chemoattractant for macrophages (YOSHIMURA and LEONARD 1990).

## 2.3 Transforming Growth Factor- $\beta$

The TGF- $\beta$  family of growth factors, which affect macrophage function at many levels and whose function is controlled by macrophages at many levels, is pleiotropic (Table 7). TGF- $\beta$ 1 is one of the first major growth factors delivered to wounds by platelets. Most of the published data refer to TGF- $\beta$ 1, but other TGF- $\beta$ s have similar effects (ROBERTS and SPORN 1990). TGF- $\beta$  is highly chemo-attractive for macrophages; its ED<sub>50</sub> is 40–400 fM for macrophage chemotaxis in vitro. It is autoinductive for macrophages so that motile macrophages may synthesize TGF- $\beta$  transcript as they enter the inflammatory locus. TGF- $\beta$  also induces other growth factor transcripts in macrophages: PDGF-B, IL-1, TGF- $\alpha$ ,

Table 7.	TGF-β family							
Growth	Synthesis by	Induction	Specific	mRNA		Protein		Reference
tactor	macropnage	70	properties	Size (kb)	AUUUA instability sequence	Precursor amino acid number	Mature peptide (kDa)	
TGF- <i>β</i> 1	+	LPS	Heparin binding, proteolytic activation	2.5	+	390/112 × 2 <sup>a</sup>	25	Dervnck et al. 1985, 1986, 1987
TGF-β2	+		5	6.5/5.1/4.2		412/112×2		DE MARTIN et al. 1987; MaDISEN et al. 1988; MILLER et al. 1989
TGF-β3				0.0	+	412/112×2		TEN DUCE et al. 1988; DERYNCK et al. 1988; MILLER et al. 1989
				1 7		304/114 ~ 0		1008 - 1088
				30		382/112 × 2		KONDAIAH AT AI 1990
Va-1-07				2.8	÷	$387/114 \times 2$		REBAGLIATI et al. 1985
Var-1				3.5	- 1	132		Lyons et al. 1989
BMP-2A						396(110, 80)	30	Wozney et al. 1988
BMP-2B						408	30	Wozney et al. 1988
BMP-3				2.0		472	30	Wozney et al. 1988
MIS				2.0	+	575	72	CATE et al. 1986
Inhibin ø				1.8(4.5, 7.0)		$368/134 \times 2$	32	FORAGE et al. 1986;
								Mason et al. 1986
Activin B	+		Heparin binding	2.8		$407/115 \times 2$	32	Mason et al. 1986;
-				(6.0, 4.0, 1.7)				YING 1988;
								TAKAHASHI et al.
								1990
0p-1				2.4		431	30	ÖZKAYNAK et al. 1990
Activin <i>b</i>	Ð			~ 1.8		$407/115 \times 2$	22	Mason et al. 1989
<sup>a</sup> Dimeric BMP, bo	c molecules ne morphogenetic factor	; MIS, müllerian	inhibiting substance					

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TNF-a, and FGF (WAHL et al. 1987; CHANTRY et al. 1989; ROBERTS and SPORN 1990). It has been argued that IL-1 is induced by TGF- $\beta$  only at the transcriptional level and that a second signal may be required for translation (ROBERTS and SPORN 1990). Once TGF- $\beta$  is secreted, it must be activated by cleavage of the N-terminal fragment to liberate an active C-terminal fragment. TGF- $\beta$  can be activated by one of two macrophage-mediated steps: activation of plasminogen by macrophage-derived plasminogen activator or acidification of the local environment by lysosomal leakage (MASSAGUE 1987; FAVA et al. 1989; ROBERTS and SPORN 1990). Macrophages may also control the effects of TGF- $\beta$  by releasing  $\alpha_2$ -macroglobulin, which inactivates it (Hovi et al. 1977; ROBERTS and SPORN 1990). The effects of TGF- $\beta$  are important during the resolution of the wound. TGF- $\beta$  decreases both T cell-mediated cellular immunity and the production of hydrogen peroxide by macrophages (TSUNAWAKI et al. 1988; ROBERTS and SPORN 1990). The injection of TGF- $\beta$  into dermis causes formation of granulation tissue and neovascularization (ROBERTS et al. 1986; PIERCE et al. 1989). Although these effects may be secondary to the chemoattraction for macrophages, TGF- $\beta$  also has chemoattractive and synthetic effects on periwound fibroblasts. It causes fibrosis by up-regulating transcription and accumulation of the extracelluar matrix components collagen (types I, III, IV, V) and fibronectin (MASSAGUE 1987; KHALIL et al. 1989; ROBERTS and SPORN 1990). It also down-regulates transcription of extracellular matrixdegrading proteinases and up-regulates the transcription of their inhibitors, such as tissue inhibitor of metalloproteinases (TIMP) (EDWARDS et al. 1987). TGF- $\beta$  also increases the expression of integrins, specifically the  $\alpha$  and  $\beta$  units of fibronection receptor (ROBERTS and SPORN 1990). This may increase the adhesive characteristics of cells for basal lamina, where TGF- $\beta$  itself is found sequestered in basal lamina at times corresponding to peak TGF- $\beta$  expression by macrophages in lung disease (KHALIL et al. 1989). Finally, TGF-eta causes the immunoglobulin class switch of B cells preferentially to IgA while suppressing IgG (COFFMAN et al. 1989).

Another member of the TGF- $\beta$  superfamily, activin/erythrocyte differentiation factor, has been found to be synthesized by macrophages and may be important in the regulation of erythropoiesis by macrophages (ERÄMAA et al. 1990).

### 2.4 Platelet-Derived Growth Factor

Platelet-derived growth factor is found in serum at a concentration of 20 ng/ml but is not found in plasma (< 1 ng/ml). It stimulates a variety of cells through receptors with a  $K_d$  of 1–100 × 10<sup>-10</sup>. There are two isoforms of PDGF, A and B (isoform B is c-*sis*)(Table 8), which are composed of dimers of the related A and/or B chains of PDGF, and two receptors for these isoforms with overlapping biologic effects in wound healing and inflammation (DEUEL 1987). Macrophages produce both isoforms but with different kinetics (MARTINET et al. 1986; RAPPOLEE

Table 8. PDGF fai	mily							
Growth	Synthesis by	Induction	Specific	mRNA		Protein		Reference
	macrophiages			Size (kb)	AUUUA instability sequence	Precursor amino acid number	Mature peptide (kDa)	
PDGF-A	+	LPS	Heparin, collagen binding	1.3/1.9/2.1	+	211	31	BETSHOLTZ et al. 1986
PDGF-B/c-sis	+	LPS	Heparin, collagen binding	3.6, <sup>a</sup> 4.2	+	209	24	Josephs et al. 1984
PDGF-r	+		)				36	Pencev and GROTENDORST 1988
Vascular permeability factor	+			3.8		189/215	25/40	Keck et al. 1989; Leung et al. 1989
<sup>a</sup> Macrophage-sp∈	ecific size (Shimoka	po et al. 1985)						

and WERB 1989). The receptors number from 200 000 in fibroblasts to 50 000 in smooth muscle cells.

The PDGF isoforms have varied effects, causing immediate degranulation of fibroblasts, chemoattraction of neutrophils and monocytes (at 1 ng/ml and 20 ng/ml, respectively), membrane ruffling, actin reorganization, and mitosis. Early in hemostasis, PDGF delivered by platelets may act as a powerful vasoconstrictor and also attracts and activates leukocytes for microbicidal action (ROSS and VOGEL 1978; STILES 1983; BERK et al. 1986; DEUEL 1987). It also rapidly induces a transient increase in several immediate-response genes, including JE (induced to 3000 copies per cell), KC (induced to 700 copies per cell), and IL-6. A second immediate and transient response is that of nuclear *trans*-activating factors, c-fos (induced within 15 min by a cycloheximide-insensitive mechanism or superinduced by cycloheximide) and c-myc (induced to five to ten copies per cell) (DERYNCK 1988; ROLLINS et al. 1988; KAWAHARA and DEUEL 1989; OQUENDO et al. 1989). In the immediate phase of inflammation, PDGF liberates fibroblast enzymes and increases the potential of local cells to mount a second program of growth factor and cytokine expression whose inflammatory effects are poorly understood. Since PDGF also induces expression of prostaglandin  $E_2(PGE_2)$ , it may also limit its own production (via prostaglandins) and action on target cells (through the action of IL-6) (DANIEL et al. 1987). Macrophage-derived  $\alpha_2$ -macroglobulin is also known to sequester and inactivate PDGF (HovI et al. 1977; Ross et al. 1986).

Platelet-derived growth factor may also have pleiotropic actions in the later stages of wound healing and inflammation. It induces expression of both proteinases, such as collagenase, and extracellular matrix proteins, such as types I, III, IV, and V collagen (CHUA et al. 1985; BAUER et al. 1985; Ross et al. 1986). The actions of these induced molecules may mediate movement of cells, diapedesis, remodeling, or mitosis. In various molecular phases of wound healing, PDGF can act much later than TGF- $\beta$  when injected into dermis (PIERCE et al. 1989). However, PDGF also induces TGF- $\beta$ , and some of its effects may be mediated by this growth factor. Since both PDGF and TGF- $\beta$  bind to various matrix components, their effects may be residual to the expression of their corresponding mRNA and protein by local cells.

### 2.5 Transforming Growth Factor-α

Transforming growth factor- $\alpha$  is in the EGF family of growth factors (Table 9). It is transcribed by macrophages in response to lipopolysaccharides, lipids, and, under certain conditions, adhesion (RAPPOLEE et al. 1988; MADTES et al. 1988). TGF- $\alpha$  and EGF share a receptor (the proto-oncogene form of the *erb-B* gene) and bind with an identical K<sub>d</sub> of 10<sup>-9</sup> M. Macrophages derived from wound cylinders transcribe and translate TGF- $\alpha$ . Both macrophages and megakaryocytes (which generate platelets) transcribe TGF- $\alpha$  and liberate a protein that binds the EGF receptor (RAPPOLEE et al. 1988; MADTES et al. 1988).
Table 9. EGF famil	١							
Growth factor	Synthesis by macrophages	Induction	Specific	mRNA		Protein		Reference
				Size (kb)	AUUUA instability sequence	Precursor amino acid number	Mature peptide (kDa)	1
EGF	I		Transmembrane precursor	4.8	-	1218	9	Scorт et al. 1983; GRAY et al. 1983;
TGF-α	+	LPS	Transmembrane	4.5	+	160	9	BELL et al. 1986b DERYNCK et al. 1984;
Amphiregulin				1.4		162	6	LEE et al. 1990 Shoyab et al. 1989
DIVIT-1 NTERA/EGF				2.8/4.0 2.0		700+ 188	50	Wozney et al. 1988 CiccopicoLa et al.
Schwannoma- derived growth factor				1.7/3.0/4.5		243	31–35	1989 Кім∪яА et al. 1990
BMP, bone morphc	ogenetic factor; N	TERA. neurona	al teratoma					

morphogenetic factor; NIEHA, neuronal teratoma , pulle F

Neither macrophages (RAPPOLEE et al. 1988) nor megakaryocytes (RAPPOLEE, unpublished data) transcribe EGF mRNA. This suggests that TGF- $\alpha$ , which was originally thought to be an EGF isoform peculiar to transformed cells, may act in pathophysiologic events (DERYNCK et al. 1984). The amount of TGF- $\alpha$  polypeptide secreted by macrophages is low compared with that secreted by eosinophils and epithelial cells, but when acting in a local environment its concentration may be near the K<sub>d</sub> of its receptor (RAPPOLEE et al. 1988; DERYNCK 1990). It is also synthesized as a 159 amino acid residue transmembrane precursor of the mature secreted 50 amino acid polypeptide. The transmembrane molecule has been shown to mediate biologic effects on target cells bearing the EGF receptor (BRACHMANN et al. 1989). This indicates that macrophage-derived TGF- $\alpha$  may act as a secreted molecule or as a transmembrane "precursor." The relative activities of the various membrane-bound and secreted molecules are not understood.

Macrophages do not bind TGF- $\alpha$  (RAPPOLEE, unpublished data). This suggests that, unlike TGF- $\beta$ , PDGF, IL-1, M-CSF, TNF- $\alpha$ , and MIP-1, TGF- $\alpha$  must work "downstream" on other cell types in a paracrine manner and does not act in an autocrine manner or recruit or influence new monocytes. According to current information, TGF- $\alpha$  is the only macrophage-derived growth factor that mediates all three parts of dermal wound healing: reepithelialization, formation of granulation tissue, and induction of neovascularization (SCHREIBER et al. 1986; ROBERTS et al. 1986; SCHULTZ et al. 1987). It also induces interferon- $\gamma$  in lymphocytes (ABDULLAH et al. 1989). Like PDGF and FGF, TGF- $\alpha$  induces collagenases and stromelysin and the synthesis of collagens in fibroblasts (MATRISIAN et al. 1985; EDWARDS et al. 1987). It also induces interferons in fibroblasts (LEE and WEINSTEIN 1978).

#### 2.6 Fibroblast Growth Factors

The FGF family currently consists of seven sequenced members (Table 10), only one of which has been identified in macrophages (BAIRD et al. 1985). Basic FGF (bFGF) has no signal sequence and is "secreted" by stimulated P388D1 macrophages in vitro but not by stimulated primary macrophages in vitro (although these cells have bFGF in the cytosol). It has been hypothesized that bFGF may be liberated on cell death, and it is possible that P388D1 macrophages have a higher cell turnover rate in vitro (RAPPOLEE et al. 1988). At least two other members of the FGF family have signal sequences, but it is not known whether they are synthesized by macrophages. There are three receptors in the FGF receptor family, but they have not been well characterized. Two of them are related to the only FGF receptor that has been cloned by biochemical means (BURGESS and MACIAG 1989). All of the receptors have intrinsic tyrosine kinase activity and are more closely related to the M-CSF/PDGF receptor than to the insulin/EGF group. Biochemically, it is known that there are two FGF receptors on many cell types: a high-affinity receptor with low copy number

Table 10. FGF	family								
Growth factor	Synthesis by macrophages	Induction	Gene	Specific	mRNA		Protein		Reference
	0 1 1		(intron/ exon)		Size (kb)	AUUUA instability sequence	Precursor amino acid number	Mature peptide (kDa)	
FGF-1/ acidic FGF			3/2	Heparin binding; no signal	4.8	+	155	17	Jave et al. 1986
FGF-2/ basic FGF	+	LPS, thioglycollate	3/2	Heparin binding; no signal peptide	2.2/4.6/6.0	+	146–155	16	ABRAHAM et al. 1986a,b; SHIMASAKI et al. 1988
FGF-3/ . int-2			3/2	Heparin binding; partial signal	1.4/1.7/2.6/2.9	+	245	27	Moore et al. 1986
FGF-4/ kFGF			3/2	Heparin binding; full signal	1.2/3.5	+	245		DELLI-Bovi et al. 1987; Впоокеѕ et al. 1989; Невеят et al. 1990
FGF-5			3/2	Heparin binding; no signal	1.6/4.0		267		Zнам et al. 1988; Невект et al. 1990
FGF-6 FGF-7/ keratinocyte growth factor			3/2 3/2		2.8/3.9/4.7 2.4		267 206	22.5	Marics et al. 1989 Finch et al. 1989

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Table 11. Hem	atopoietic growth	factors <sup>a</sup>							
Growth	Synthesis by	Induction	Gene	Specific	mRNA		Protein		Reference
			(intron/ exon)		Size (kb)	AUUUA instability sequence	Precursor amino acid number	Mature peptide (kDa)	
IL-1 <i>a/</i> hemopoietin	+	LPS		Membrane form	2.0	+	271	27	Lomepico et al. 1984; MARCH et al. 1985; KURT-JONES
IL-6/IFN-β2/ B-cell stim. factor II	+	Adherence	5/4		1.3 2	+	211	22–29	Norban and Potter 1986; Hirano et al. 1986; Ziuberstein et al. 1986; Van Snick et al. 1980
G-CSF	+	LPS	5/4		1.4/1.6	+	204/208	25(20 human)	Tsuchiya et al. 1986
GM-CSF	+	Adherence	4/3	Binds GAGs	0.8/1.2	+	141	18–25	MIYATAKE et al. 1985; CANTRELL et al. 1985; GORDON et al. 1987
M-CSF/CSF-1	+	Adherence		Transmem- brane form	1.4/2.3/3.8/4.5	+	118 × 2 (dimer)	20	Каwasakı et al. 1985; RaJavasнısтн et al. 1987
Erythropoietin	+	LPS	5/4		1.0	+	193	18.4	Lin et al. 1985; SHOEMAKER and Mitsock 1986
IL-3	ł	Antigen	5/4		1.9	+	166	15–30	Fung et al. 1984; Yang et al. 1986
<sup>a</sup> Note that thes are not included GAG, glycosami	e factors represer d inoglycan	nt a partial list of t	he best-char	acterized mole	ecules. Activin, PF	<sup>-</sup> -4, ΜΙΡ-1α, <i>ε</i>	ind others that	have less w	ell characterized effects

 $(K_d = 50-500 \text{ pM}, 5-50 \times 10^3/\text{cell})$  and a low-affinity receptor with heparin-like qualities with high copy number ( $K_d = 10 \text{ nM}, 5-20 \times 10^5/\text{cell}$ ). Heparin binds and potentiates FGF when both are in solution, and it has been speculated that the cell surface heparin-like receptor may focus the FGF on the high-affinity receptor (BURGESS and MACIAG 1989).

Fibroblast growth factor may function late in inflammation in wound healing and remodeling. It is highly angiogenic, a chemoattractant and mitogen for endothelial cells, and a mitogen for smooth cells. It also has numerous immediate effects on fibroblasts as a secretagogue and chemoattractant and is a mitogen for 3T3 fibroblasts. It may have some of the same effects on fibroblasts in regulating proliferation fibrosis as do TGF- $\beta$ , TGF- $\alpha$ , and PDGF (GROSS et al. 1983; ABRAHAM et al. 1986a; EDWARDS et al. 1987).

## 2.7 Colony-Stimulating Factors

Of the major colony-stimulating factors (CSFs) currently characterized, macrophages synthesize M-CSF, G-CSF, GM-CSF, IL-1, and IL-6 (Table 11) but do not synthesize multi-CSF (IL-3) or IL-5 (NICOLA 1989). CSFs mediate survival, proliferation, functional modulation (chemotaxis, degranulation, activation, adhesion, cytotoxicity, mRNA phenotype changes), and differentiation on various populations of precursor and mature blood cells (GRABSTEIN et al. 1986; HORIGUCHI et al. 1987; BECKER et al. 1987; DONAHUE et al. 1988; RAPPOLEE and WERB 1989; ALVARO-GRACIA et al. 1989; BUSSOLINO et al. 1989; HOANG et al. 1989). A number of rules have emerged in classifying the activities of CSFs:

- 1. The  $ED_{50}$  for activating mature cells or causing mitosis in precursors is higher than that for maintaining survival (although the K<sub>d</sub> of all the CSFs for their cognate ligands is low—between 10 pM and 1000 pM). Bone marrow precursors in vitro do not survive longer than 24 h unless a specific CSF is present.
- 2. At low, limiting concentrations, CSFs are specific for a restricted lineage (M-CSF for macrophages and G-CSF for granulocytes; IL-3 and GM-CSF have their highest effects on macrophages).
- 3. CSFs often act synergistically; IL-3 synergizes with GM-CSF or IL-6 in maintaining proliferation of committed stem cells.

**Fig. 3. a** The three tiers of development of hematopoietic stem cells. **b** The effect of four macrophage-derived growth factors that affect the balance of hematopoietic proliferation and differentiation. The eight mature cell types produced from a common totipotent stem cell are red blood cells (*RBC*), polymorphonuclear leukocytes (*PMN*), macrophages (*MAC*), eosinophils (*EOS*), megakaryocytes (*MEGA*), mast cells (*MAST*), B lymphocytes (*B CELL*), and T lymphocytes (*T CELL*). *Heavy lines* indicate a mitogenic effect at low concentrations of growth factor; *light lines* indicate no effect. *Dots* indicate a modulation of function in the mature cell. (Modified from METCALF et al. 1985; NICOLA 1989)



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- 4. In the lineage of cells in blood cell formation, growth factors act in the following order during maturation: unknown CSFs for the earliest stem cells  $\rightarrow$  IL-1 $\alpha$ /hemopoietin  $\rightarrow$  IL-3  $\rightarrow$  IL-6/GM-CSF  $\rightarrow$  G-CSF  $\rightarrow$  M-CSF.
- 5. Synergism of CSFs operates at many levels, including induction of receptor and ligand expression, expansion of precursor populations, and modulation of receptors.
- 6. The history of a cell determines how it responds to a given CSF (METCALF 1985; NICOLA 1989). For example, granulocyte-macrophage precursor cell lines respond to G-CSF to become granulocytes or macrophages or mixed granulocytes and macrophages, depending on which factor these precursors have previously been exposed to (NICOLA 1989).

The concentrations of M-CSF and IL-6 in the blood rise after injection of LPS or in response to bacterial infection, but GM-CSF and IL-3 concentrations do not rise in response to the same stimulants. However, injection of recombinant CSFs has resulted in localized activation of macrophages and PMNs and some proliferation of progenitors, but little rise in numbers of blood cells because of endocrine activation or proliferation of stem cells in the bone marrow. The local production of CSFs at sites of inflammation is clearly important in regulating the functions of endothelial cells, fibroblasts, and invading blood cells through a large number of molecular mechanisms (see Sects. 4 and 8). CSFs are mitogenic for endothelial cells (BUSSOLINO et al. 1989) and white blood cells (METCALF 1985; DONAHUE et al. 1988) and modulate the molecular phenotype of white blood cells (HORIGUCHI et al. 1987; RALPH and NAKOINZ 1987; WEISBART et al. 1988; NATHAN 1989; ZUCKERMAN and SUPRENANT 1989). The endocrine, paracrine, and autocrine activities of macrophagederived CSFs are not defined (METCALF 1985; NICOLA 1989), although macrophage products can modulate granulocytopoiesis and monocytopoiesis in vitro (CHERVENICK and LOBUGLIO 1972; BROXMEYER et al. 1989). In vitro heparan sulfate-bound GM-CSF (and IL-3) activate hematopoiesis, suggesting a localization of these factors in a paracrine manner by bone marrow fibroblasts and macrophages (ROBERTS et al. 1988; Fig. 3). Macrophages are unique among blood-derived cells in their capacity to undergo a further mitotic division at sites of activity of the most differentiated cells. This may result in an increased number of local macrophages. The level of plasma M-CSF is regulated by the population size of macrophages because macrophages quickly remove M-CSF injected into the bloodstream (BARTOCCI et al. 1987).

## 2.8 Insulin-Like Growth Factors

Macrophages are induced by phorbol 12-myristate 13-acetate to transcribe insulin-like growth factor (IGF)-I (Table 12). In addition, macrophages have a preformed pool of IGF-I that is secreted on stimulation (NAGAOKA et al. 1990b). Since wound-derived macrophages express IGF-I mRNA, it is inferred that IGF-I is translated by macrophages and has a function in the wound (RAPPOLEE et al.

Table 12. Insulin	-like growth factor	family						
Growth	Synthesis by	Induction	Gene	mRNA		Protein		Reference
			siruciure (intron/ exon)	Size (kb)	AUUUA instability sequence	Precursor amino acid number	Mature peptide (kDa)	
IGF-I	+	LPS	5/4	0.9/5.3/7.7		130(70)	10	RINDERKNECHT and HUMBEL 1978; BELL
IGF-II Insulin (2 members)	I		8/7 3/2	2.0/4.9/6.0 0.6/0.7/2.4	I	180(67) 110(51)	10 7	et al. 1986a Stemplen et al. 1986 Muglia and Locker 1983: Wentworth
Relaxin (2 members)				1.2/1.6/2.5/3.3		182(54)	6.3	et al. 1986 На∟ЕҮ et al. 1987

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1988). IGF-I has insulin-like effects on glycogen synthesis and activation of anabolic processes in target cells. Macrophages do not synthesize either IGF-II or insulin (RAPPOLEE, unpublished results). The importance of IGF-I in macrophage function remains to be determined.

# **3 Negative Modulation of Macrophage-Derived** Growth Factors

It has become obvious that most, if not all, macrophage-derived growth factors are either positively cross-induced or autoinductive. These inductions theoretically allow for functionally different growth factors to reach peak concentrations quickly and in a set temporal order. The control of growth factor production and function must also be down-regulated. Much exciting research has recently been reported, and there is now an understanding of the complexity of the down-regulation of growth factors.

Many macrophage-derived growth factor transcripts are unstable. IL-1 $\alpha$  and IL-1 $\beta$ , PDGF-B, TNF- $\alpha$ , and GM-CSF share an AUUUA motif repeated in the 3' flanking sequence that is thought to target the transcript for destruction in the cytosol (SHAW and KAMEN 1986; BRAWERMAN 1989) and have a half-life of about 1 h. Similarly, growth factor polypeptides, such as insulin, are targeted for destruction by specific peptidases in the extracellular environment (DUCKWORTH 1988). A constitutive destructive process ensures that the powerful effects of growth factors do not linger when the inductive stimuli have abated.

A second mechanism for negatively modulating the function of growth factors is to buffer or inhibit the polypeptides. IGF-I has a binding protein with a binding affinity 100 times that of the IGF-I receptor (SARA and HALL 1990). Many macrophage-derived growth factors, such as TNF-a, IL-4, IL-2, and GM-CSF, have a soluble form of the cellular receptor that may have the same affinity as the cellular form (TREIGER et al. 1986; ENGELMANN et al. 1989; NOVICK et al. 1989). These proteins bind growth factors and prevent binding to receptors. In addition, a competitive inhibitor of IL-1 has recently been cloned (CARTER et al. 1990; HANNUM et al. 1990; EISENBERG et al. 1990). This inhibitor has sequence homology with IL-1 and binds to IL-1 receptors (in the brain, T cells, and fibroblasts) with the same affinity as IL-1, but does not activate the receptor. The IL-1 inhibitor can dampen or attenuate the effects of IL-1 in some tissues (LIAO et al. 1985; AREND et al. 1990; CARTER et al. 1990). It is produced by macrophages upon stimulation that also triggers IL-1, but the inhibitor is made more slowly and lasts longer. The inhibitor transcript has no AUUUA motif and may therefore attenuate the IL-1 ligand after the initial response in the absence of the inhibitor. Macrophages also produce  $\alpha_2$ -macroglobulin, which binds and activates PDGF and TGF- $\beta$ , both macrophage-derived growth factors (Ross et al. 1986; Graves and Antoniades 1988; McCaffrey et al. 1989; Danielpour and SPORN 1990; ROBERTS and SPORN 1990). In addition, TGF- $\beta$  can stimulate production of  $\alpha_2$ -macroglobulin in some cells (SHI et al. 1990). Binding proteins and inhibitors may attenuate ongoing responses or limit the responses spatially.

A third class of negative modulation of growth factors is negative feedback from either the target or producer cell on production. PDGF and IL-1 induce PGE<sub>2</sub> in target cells, and PGE<sub>2</sub> suppresses the synthesis of these growth factors (KUNKEL et al. 1986; DANIEL et al. 1987; DINARELLO 1989). Growth factors also induce polypeptides that down-regulate the production of the growth factor. For example, TNF- $\alpha$  induces IL-1, which then inhibits the autoinduction of TNF- $\alpha$ and attenuates TNF- $\alpha$  production (EPSTEIN et al. 1990). Growth factors such as TNF- $\alpha$  and M-CSF also induce factors such as interferon- $\beta$ , which act negatively on the target cell. When blocking antibody to interferon is added in vitro, cells responding to TNF- $\alpha$  and M-CSF increase their response time and effects (RESNITZKY et al. 1986; KOHASE et al. 1986). These forms of negative feedback limit the duration and magnitude of the growth factor response by inhibiting the production or effect of the factor.

Finally, more extended forms of feedback reside in the equilibrium of production of producer cells, which is governed by the growth factors they synthesize. Macrophages synthesize M-CSF, GM-CSF, interferon- $\alpha$ , interferon- $\beta$ , and IL-1, which positively regulate macrophage production, and PGE<sub>2</sub> and MIP-1 $\alpha$ , which negatively regulate macrophage production (KURLAND et al. 1978; MOORE 1984a, b; METCALF 1985; NICOLA 1989; GRAHAM et al. 1990). Mature macrophages quickly remove M-CSF from the blood and regulate M-CSF concentration in inverse proportion to the number of mature macrophages (BARTOCCI et al. 1987).

It is clear that macrophages and macrophage-derived growth factors stimulate self-limiting effects on the duration, magnitude, and location of action. Since each growth factor has unique effects, this may ensure a temporal series of specified effects. The mechanisms and significance of these self-limitations are beginning to be understood.

## **4** Inflammation

The role of macrophages in the early phases of acute inflammation is not clearly defined. Although resident tissue macrophages are present and able to respond to limited stimuli, their functions are unknown. Platelets and neurogenic spasms provide early hemostasis in the first seconds and minutes. Neutrophils form the mass of white cells in the first 12 h of inflammation. They are attracted by simple inflammatory stimuli. The activated macrophage is the primary cytotoxic cell in the inflammatory lesion at 24 h after stimulation (COHN 1978; NORTH 1978; RAPPOLEE and WERB 1989).

In the later phases of acute inflammation (the end of the first day after wounding), macrophages are the major leukocyte in the inflammatory locus. Migration and adhesion of macrophages are controlled by secreted factors,

including growth factors. Macrophages are attracted by TGF- $\beta$ , PDGF, IL-1, TNF- $\alpha$ , IL-2, and a large range of inflammatory debris such as N-formyl methionyl-capped bacterial proteins, complement split products, and fibrinopeptides (MING et al. 1987; DINARELLO 1989; RAPPOLEE and WERB 1989). Since many of the growth factors that attract macrophages are produced by macrophages, the stimulated macrophages arriving at the wound recruit other macrophages and white cells to the wound. For example, many macrophage products, such as TGF- $\beta$ , IL-1 $\alpha$ , TNF- $\alpha$ , platelet-activating factor, leukotriene  $B_4$ , IL-1 $\beta$ , and MIP-1, attract neutrophils (RAPPOLEE and WERB 1988, 1989). Adhesion or margination before diapedesis of macrophages is under the influence of growth factors. TNF- $\alpha$  down-regulates the constitutive expression of GMP-140-related adhesive molecules such as MEL-14 (by shedding), but up-regulates the expression of GMP-140 by immediate degranulation of endothelial cells and platelets. MEL-14 is shed from the cell surface of lymphocytes and monocytes within minutes of addition of growth factor in vitro. Both TNF- $\alpha$  and IL-1 induce slower changes in ELAM-1 and ICAM expression, which makes them more adhesive to macrophages and neutrophils as well as to lymphocytes. These changes in the adhesiveness of endothelial cells peak at 2–4 h and return to baseline at 24 h, even in the continued presence of TNF- $\alpha$ in vitro (GAMBLE et al. 1985; DOHERTY et al. 1987; BEUTLER and CERAMI 1988; KISHIMOTO et al. 1989; BEVILACQUA et al. 1989). IL-1 induces production of stromelysin in fibroblasts and macrophages, modulating the ability of these cells to move through the vascular basement membrane and interstitial extracellular matrix (FRISCH and RULEY 1987; RAPPOLEE and WERB 1989). It is interesting to note that TNF- $\alpha$  causes edema, which may be commensurate with increased transmigration of the macrophage vessel wall, but IL-1 causes only changes in adhesion without increasing vascular permeability (BEVILACQUA et al. 1989; BRETT et al. 1989). In addition, M-CSF and IL-4 increase the expression of two types of plasminogen activator synthesized by macrophages (WERB 1987; HART et al. 1989a, b). Other macrophage factors such as GM-CSF and G-CSF can induce endothelial cells to produce CSFs and alter their procoagulant ratios to become more adhesive to leukocytes and lymphocytes and to further wall off wounds (BUSSOLINO et al. 1989).

Macrophage growth factors such as PDGF have the capability of causing vascular spasm through their action on smooth muscle cells, although most of this activity may occur early in inflammation and be a function of platelet delivery (BERK et al. 1986). Vascular spasm can be neurogenically caused, as can macrophage influx as monocytes respond to neuropeptide substance P chemotactically and by producing IL-1, TNF- $\alpha$ , and IL-6 (RUFF et al. 1985; LOTZ et al. 1988). Production of macrophage TNF- $\alpha$  and IL-1 peaks later after LPS stimulation (at about 6 and 12 h, respectively, in vitro), suggesting that these growth factors regulate later maintenance of clot formation and inflammation. TNF- $\alpha$  and IL-1 may also contribute to pathologic conditions such as hemorrhagic necrosis, thrombosis, and intravascular coagulation (DURUM et al. 1985; OLD 1985; BEUTLER and CERAMI 1988). Macrophages predominate and

function well in the wound after 12h for several reasons. They produce an acid environment by releasing up to 25% of their acidic lysosomes, and they survive this acid and hypoxic environment better than neutrophils. They also have a more highly functional protein production apparatus than do neutrophils and are able to respond to changes in the resolving wound. In addition, they are much more phagocytic than neutrophils (RAPPOLEE et al. 1989). Inflammatory macrophages are probably the major source of IL-1 and TNF- $\alpha$ , as these two growth factors can approach 1%-5% of total macrophage protein production. These growth factors have pleiotropic actions. They have endocrine effects in regulating the hypothalamic temperature set point (and therefore are pyrogenic) and the production by liver of acute-phase proteins. A recent finding suggests that IL-1 also regulates the production of glucocorticoids in the adrenal gland, a pathway that may mediate potential negative feedback on IL-1 production (BESEDOVSKY et al. 1986). In addition IL-1 autoinduces its own production as well as inducing TNF- $\alpha$  itself. The kinetics of these inductions are slightly different, and it has been suggested that IL-1 also down-regulates the TNF-α autoinduction (EPSTEIN et al. 1990). IL-1 also induces the production by macrophages of lactoferrin, a molecule that attracts macrophages, neutrophils, and B and T lymphocytes. Both IL-1 and TNF-α are induced by the LPS produced by bacteria.

There is a dense network of autocrine and paracrine inductions of growth factors in the cells of the wound. In the wound-derived macrophage, C5a complement split product and TGF- $\beta$  induce IL-1. LPS-stimulated macrophages produce more TGF- $\beta$ . IL-1 produces further IL-1 mRNA and protein in macrophages, and this induces TNF-a mRNA and protein but inhibits the later autoinduction of TNF- $\alpha$ . Since TNF- $\alpha$  induces IL-1, this leads to a self-limitation of TNF- $\alpha$  production through a two-growth-factor circuit (EPSTEIN et al. 1990). In addition, it ensures that TNF- $\alpha$  is produced early but subsides as IL-1 production increases. Macrophage TNF- $\alpha$  also induces the production of IL-1 by endothelial cells and fibroblasts (DINARELLO 1989). Furthermore, macrophage TNF- $\alpha$  and IL-1 induce the production in endothelial cells of GM-CSF, G-CSF, and M-CSF (SEELENTAG et al. 1987). The first two of these CSFs have broad functions in the wound, as their receptors are expressed on many cell types. They modulate the procoagulant activity of endothelial cells (RYAN and GECZY 1986; ZUCKERMAN and SUPRENANT 1989) and modulate other functions such as angiogenesis in these cells (FRÄTER-SCHRÖDER et al. 1987; LEIBOVICH et al. 1987). The receptor for M-CSF (also known as the *c-fms* proto-oncogene) is expressed only on macrophages (METCALF 1985; NICOLA 1989) and, therefore, the M-CSF growth factor has a much narrower cellular function. M-CSF causes the macrophage to become highly secretory (beyond and in synergism with any other macrophage stimulator) (TAKEMURA and WERB 1984a, b; WARREN and RALPH 1986; NATHAN 1987; BECKER et al. 1987). The CSFs also increase the cytotoxicity of macrophages and neutrophils by inducing the respiratory burst and production of reactive oxygen intermediates (NATHAN 1987; NICOLA 1989). M-CSF may cooperate with the interferon- $\gamma$  or IL-2 produced by immune T cells to enhance

the cytotoxicity of macrophages (Li et al. 1989). Antiviral effects may be mediated by IL-6/interferon- $\beta$ 2, which is induced by LPS and TNF- $\alpha$ . The endocrine effects of IL-6 on the acute-phase response of liver mimic those induced by TNF- $\alpha$ and IL-1 (BEUTLER et al. 1986; DARLINGTON et al. 1986; DINARELLO 1989). However, IL-6 induces fibronectin production by the liver, an effect not produced by the other two growth factors (LANSER and BROWN 1989).

The extent of the endocrine effects of CSFs produced by macrophages is not known. The production of many other cells, such as fibroblasts, leads to the increased concentrations of M-CSF in serum characteristic of some infections. This increase may play a part in inducing further bone marrow production of macrophages and neutrophils. The M-CSF concentrations in the blood are negatively regulated by macrophages themselves (BARTOCCI et al. 1987).

The importance of growth factors in the early participation of macrophages in hemostasis and the early inflammatory response is great in magnitude, but not well defined. Certainly, macrophage-derived IL-1, TNF- $\alpha$ , PDGF, TGF- $\beta$ , IL-6/interferon- $\beta$ 2, GM-CSF, M-CSF, and G-CSF play potentially large roles. Newly discovered macrophage growth factors such as TGF- $\alpha$ , IGF-I, and the immediate-response growth factors KC/JE/MIP-1/MIP-2/IL-8 also may play a part. These macrophage-derived growth factors stimulate secretion and migration and reprogram the function of inflammatory cells. They also lead to increased vascular spasm and procoagulation and adhesive interaction between endothelial cells and blood cells. They lead to enhanced microbial and phagocytic capability in neutrophils and macrophages. The importance of growth factor autoinduction, cross-induction, and negative feedback is not well understood.

## **5 Wound Healing**

The resolving inflammatory loci provide a stage for the macrophage as central actor. In killing, debridement, and wound healing, macrophages are absolutely required (LEIBOVICH and ROSS 1975; RAPPOLEE and WERB 1989). When macrophages are eliminated by antileukocyte serum injected locally, and monocyte production is prevented by injection of glucocorticoids, wound healing proceeds very slowly.

Macrophage production of complement and lysosomal hydrolases is synergized by M-CSF and IL-1 (BENTLEY et al. 1981; TAKEMURA and WERB 1984a; PERLMUTTER et al. 1986; NICOLA 1989). M-CSF is produced by stimulated fibroblasts, endothelial cells, and macrophages in the wound. TNF- $\alpha$  and IL-1 induction has been discussed above. Reactive oxygen intermediates are synthesized by interferon- $\gamma$ -stimulated macrophages, but GM-CSF, IL-2, prolactin, somatotropin, M-CSF, IL-1, and TNF- $\alpha$  synergize in this induction (ADAMS and HAMILTON

1984, 1989; METCALF 1985; NATHAN et al. 1985; GRABSTEIN et al. 1986; WARREN and RALPH 1986; MALKOVSKY et al. 1987; RALPH and NAKOINZ 1987; EDWARDS et al. 1988; BERNTON et al. 1988; FRAKER et al. 1989). Interferon-y production by immune T cells is enhanced by macrophages (BENACERRAF and UNANUE 1979; LUCAS and EPSTEIN 1985). In addition, several macrophage-derived growth factors-IL-1, TNF-a, MIP-1, MIP-2, and IL-8-induce neutrophil chemotaxis and/or respiratory burst (ADAMS and HAMILTON 1984; DAHINDEN et al. 1989; DAVATELIS et al. 1989; DINARELLO 1989; LARSEN et al. 1989; WALZ et al. 1989; WOLPE et al. 1989). TNF- $\alpha$  kills a broader spectrum of tumor cells than does IL-1. TNF- $\alpha$ induces the fragmentation of DNA within tumor cells that contain the receptor for this ligand (ONOZAKI et al. 1985; URBAN et al. 1986; BEUTLER and CERAMI 1988; DINARELLO 1989). It is not clear how the macrophages control the cytotoxic molecules they secrete. Clearly, the macrophage is rather resistant to oxygen radicals. It produces catalase and superoxide dismutase, which inactivate reactive oxygen intermediates (ADAMS and HAMILTON 1984; TAKEMURA and WERB 1984b; NATHAN 1987). Macrophages also secrete several complement inhibitors, including  $\alpha_2$ -macroglobulin,  $\alpha_1$ -proteinase inhibitor, and C3-inhibitor, which may attenuate complement proteinases as well as restrict complement activation to its locus (TAKEMURA AND WERB 1984a, b; RAPPOLEE and WERB 1989). Production of reactive oxygen intermediates by macrophages is down-regulated by TGF- $\beta$ (TSUNAWAKI et al. 1988).

Wound debridement is mediated by lysosomal hydrolases and later by neutral proteinases, which break down debris in the extracellular milieu, and by phagocytosis by macrophages and neutrophils. M-CSF synergizes with other stimulators to induce lysosomal hydrolases. Neutral proteinases, such as the serine proteinase urokinase plasminogen activator, are induced by M-CSF and TGF- $\alpha$ , and metalloproteinases, such as collagenase, are induced in fibroblasts, endothelial cells, and synovial cells by IL-1 and PDGF (LEE and WEINSTEIN 1978; LIN and GORDON 1979; POSTLETHWAITE et al. 1983; BAUER et al. 1985; CHUA et al. 1985; MATRISIAN et al. 1985; EDWARDS et al. 1987; SCHNYDER et al. 1987; DERYNCK 1988; DINARELLO 1989). Tissue plasminogen activator is also produced by macrophages (HART et al. 1989a, b). Uptake of the matrix debris, such as collagen fragments, induces macrophages to produce IL-1 and PGE<sub>2</sub>, PGE<sub>2</sub>, in turn, induces macrophages themselves to produce collagenase (FRISCH and RULEY 1987; Table 3). Collagenase and stromelysin are induced in synovial cells by IL-1 and TNF- $\alpha$ , and IL-1 induces collagenase in dermal fibroblasts (FRISCH and RULEY 1987; see also Table 3). Collagenase expression can also be induced in fibroblasts by several macrophage-derived growth factors, including PDGF, bFGF, and TGF-α/EGF (POSTLETHWAITE et al. 1983; CHUA et al. 1985; DAYER et al. 1985; EDWARDS et al. 1987). PDGF and TGF-α are produced by wound-derived macrophages (RAPPOLEE et al. 1988; RAPPOLEE and WERB 1990). The metalloproteinases stromelysin and collagenase are down-regulated transcriptionally by TGF- $\beta$  (EDWARDS et al. 1987; ROBERTS and SPORN 1990). In addition, TGF- $\beta$ , PDGF, and IL-1 induce synthesis of TIMP (EDWARDS et al. 1987; DINARELLO 1989; ROBERTS and SPORN 1990). These effects may limit the effects of the proteinases in the wound and down-regulate the production of the proteinases as the wound clears. Phagocytosis by macrophages and neutrophils is enhanced by M-CSF, GM-CSF (which induces IgA receptor expression in neutrophils), and IL-1 (WEISBART et al. 1988).

As the wound resolves, 3–7 days after trauma, dead endothelial cells (vascular beds), fibroblasts, and epidermal cells must be regenerated and extracellular matrix must be replaced. By the end of the first week after wounding, fibroblasts and endothelial cells have filled in the wound with loose connective tissue and a dense capillary network, respectively. The mass of capillaries and fibroblasts is called "granulation tissue." By the end of the second week the capillary network has thinned and fibrosis of collagen has increased (STOSSEL 1988; RAPPOLEE and WERB 1989). Ablation experiments indicate that macrophages, but not neutrophils, are required for this wound healing and angiogenesis (LEIBOVICH and ROSS 1975). Others have found that activated macrophages and wound fluid induce wound healing (POLVERINI et al. 1977; GREENBURG and HUNT 1978; BANDA et al. 1982; KOCH et al. 1986).

Macrophages secrete a number of growth factors that are known to mediate angiogenesis and an overlapping group of growth factors that induce formation of granulation tissue and reepithelialization. bFGF is synthesized by stimulated macrophages and induces fibroplasia, DNA synthesis in endothelial cells, and angiogenesis. IL-1 has limited mitogenic capacity for fibroblasts but no angiogenic property. Fibroblast mitogenesis is mediated by the ability of IL-1 to induce fibroblast PDGF-A, and a blocking antibody to PDGF-A prevents IL-1-induced mitogenesis of fibroblasts (RAINES et al. 1989). Other macrophagederived growth factors that induce fibroblast proliferation of fibrosis in vivo or in vitro are PDGF, TGF- $\beta$ , TGF- $\alpha$ , IGF-I, and bombesin. Angiogenesis consists of endothelial sprouting, which can account for up to 1 mm of capillary growth, and endothelial cell mitosis, which is required for further capillary lengthening (FOLKMAN 1986; RAPPOLEE and WERB 1989). TGF- $\beta$  is known to cause endothelial cell chemotaxis in vitro (and sprouting in vivo) but actually inhibits endothelial cell mitosis (ROBERTS et al. 1986; HEIMARK et al. 1986; MASSAGUE 1987). TNF- $\alpha$ has been claimed by two investigative groups to be angiogenic. One group claims that TNF- $\alpha$  is directly angiogenic for endothelial cells, but because it is not mitogenic for these cells the angiogenesis is limited to capillary sprouting (LEIBOVICH et al. 1987). The second group concludes that the angiogenic effect is secondary to the chemoattractant activity of TNF- $\alpha$  for monocytes, which produce other angiogenic factors (FRÄTER-SCHRÖDER et al. 1987). Endothelial cells that are motile (e.g., those at sprouting capillaries) are more sensitive to TNF- $\alpha$  than are confluent endothelial cells in mature blood vessels (GERLACH et al. 1989). Other factors that have been shown to be mitogenic for endothelial cells in vitro or angiogenic in vivo are bFGF, TGF-a, G-CSF, and GM-CSF (THOMAS et al. 1985; SCHREIBER et al. 1986; BURGESS and MACIAG 1989; BUSSOLINO et al. 1989). It is interesting to note that hypoxia, a condition common to nonvascularized wound foci, induces macrophages to secrete a nonmitogenic angiogenic factor in vitro (KNIGHTON et al. 1983). PF-4 is an immediate-response growth factor produced by macrophages that is antiangiogenic (MAIONE et al. 1990; RAPPOLEE et al., unpublished data). It is likely that this factor is TNF- $\alpha$ . As well as being an inducer of granulation tissue and neovascularization, TGF- $\alpha$  also accelerates reepithelialization when applied in vivo (SCHULTZ et al. 1987).

It is clear that several macrophage-derived growth factors mediate the killing functions of leukocytes, the debridement functions of leukocytes, and the wound-healing functions of fibroblasts, endothelial cells, and epidermal cells.

# 6 Nerve Regeneration

Macrophages are prominent in peripheral nerve regeneration. Upon crushing or cutting of peripheral nerve, there is an immediate "wallerian" degeneration of the distal stump, which consists of the fragmentation of Schwann cell cytoplasm and breakdown of the distal axon. Within a few days of the trauma, monocyte-derived macrophages enter the nerve and begin to debride it (PERRY et al. 1987). During the next 2-3 weeks, the nerve is debrided and the axon regrows, and the Schwann cells undergo mitosis to populate the regenerating nerve to about 10 times their original number. If the nerve is cut and explanted to the peritoneum inside a millipore cylinder that prevents the entrance of macrophages, no fragmented axon and Schwann cell debridement and no Schwann cell mitosis occur (SCHEIDT et al. 1986). If the cylinder allows ingression of macrophages, then both debridement and Schwann cell gliosis occur (SCHEIDT et al. 1986). This suggests that both degeneration and regeneration (debridement and Schwann cell mitosis) are under the control of macrophages (HEUMANN et al. 1987; MAHLEY 1988; BAUER et al. 1989; BOYLES et al. 1989). The regenerating nerve undergoes waves of NGF and apolipoprotein E expression at times that correspond to the influx of macrophages. Macrophages synthesize apolipoprotein E after stimulation by products of injured peripheral nerves (BASU et al. 1981; BROWN and GOLDSTEIN 1983; WERB and CHIN 1983), and this synthesis is regenerative (IGNATIUS et al. 1987). If the peripheral nerve is explanted into culture, NGF is not expressed. However, IL-1 and TNF- $\alpha$  can replace the monocyte-derived macrophages (which do not enter the explanted nerve) and induce the transcription of NGF in cells in nerve (LINDHOLM et al. 1987, 1988; UNDERWOOD et al. 1990). Since macrophages do not synthesize NGF, macrophage-derived TNF- $\alpha$  and IL-1 are probably inducing NGF mRNA in the major cell of the nerve, the Schwann cell. In addition, TGF- $\beta$  induces the synthesis of TIMP in the nerve, and TGF- $\beta$  mRNA itself increases by more than tenfold in the crushed peripheral nerve (UNDERWOOD et al. 1990). It is tempting to speculate that TIMP protects the basal lamina in the nerve to guide the regrowing axons back to the correct target tissue.

### 7 The Immune Response

Macrophages are important in the afferent or generative arm of the immune response (MACKANESS 1964). Macrophages endocytose and digest antigens and then present them to T helper cells in a complex with the la antigens on the macrophage surface (BENACERRAF and UNANUE 1979; UNANUE and ALLEN 1987). This occurs in the immune tissues in lymph nodes, spleen, skin, and brain (UNANUE and ALLEN 1987; HICKEY and KIMURA 1988). GM-CSF enhances, but M-CSF suppresses, la expression in macrophages (WILLMAN et al. 1989). This presentation is required for the generation of immune responses to many T-dependent antigens and makes the T cells "competent" by inducing expression of IL-2 receptors. IL-1 can act as a cofactor to antigen/la antigen complex and stimulates T cells to produce IL-2, which stimulates progression into S phase by its receptors (RAPPOLEE and WERB 1989). IL-6 also can act as a thymocyte comitogen.

Interleukin-1 enhances the humoral immune response by several mechanisms. First, it stimulates B cell differentiation by inducing a pre-B-cell line with only cytoplasmic  $\mu$  chains to express  $\kappa$  light chains and subsequent surface immunoglobulin, IL-1 also enhances proliferation and the secretion of immunoglobulin in mature B cells (DURUM et al. 1985; PIKE and NOSSAL 1985; KURT-JONES et al. 1987; DINARELLO 1989). Stimulated macrophages additionally produce B cell stimulatory factor-2, also known as IL-6, and hybridoma growth factor (GAULDIE et al. 1987; VAN DAMME et al. 1987; TOSATO et al. 1988). IL-6 and IL-1 are major products of stimulated macrophages. Like IL-1, IL-6 induces B cell proliferation and immunoglobulin expression (BEAGLEY et al. 1989). TGF- $\beta$  also modulates immunoglobulin expression (COFFMAN et al. 1989; SONODA et al. 1989). It is difficult to distinguish the relative contributions of IL-1 and IL-6 to B cell and T cell activation because T cells can synthesize IL-1 and B cells can synthesize IL-6, and each factor induces the expression of the other (DINARELLO 1989). Another effect of IL-1 on immune cells is the induction of natural killer activity. There is more than one IL-1 gene, transcript, and protein in all species surveyed. The current hypothesis is that all IL-1 species have similar immune effects and act through a single immune cell receptor (DINARELLO 1989). The development of the humoral immune response requires the secretion of IL-1 and IL-6 by macrophages, as well as expression of class II MHC molecules and processed antigen on the macrophage surface.

The development of a cellular immune response requires an interaction between macrophages and T cells and is represented by delayed-type hypersensitivity. This reaction occurs in previously sensitized individuals and requires 48 h to develop, whereas the immediate hypersensitivity of the humoral immune response subsides by 48 h. Delayed-type hypersensitivity is characterized by class II MHC-restricted interaction between the T cells and macrophages that have migrated into the interstitial site of bacterial infection. The macrophages outnumber the T cells in these lesions by more than 10 to 1, but activated T cells are required to trigger macrophage microbicidal activity (BENACERRAF and UNANUE 1979). A complex of soluble factors may mediate communication between macrophages and T cells during delayed-type hypersensitivity. Activated T cells secrete factors IL-2, GM-CSF, and interferon- $\gamma$ , which attract macrophages, activate them, induce la expression by macrophages, and prevent their departure. In response, activated macrophages produce IL-1, TNF- $\alpha$ , M-CSF, and MIP-1, which further attract and activate T cells and macrophages (UNANUE and ALLEN 1987). In summary, macrophages and macrophage-derived growth factors are essential in the generation of the humoral and cellular immune responses. As previously mentioned, the cytocidal response of macrophages induced by activated T cells is an important part of the efferent immune response.

#### 8 Hematopoiesis

Since most blood cells are short-lived, they must be replaced constantly, and production must be increased under conditions of stress such as inflammation. The increase in production occurs in the bone marrow, but in times of stress the spleen can become the primary organ of hematopoiesis.

The eight major types of blood cells arise from a common precursor stem cell in a series of three tiers of differentiation and proliferation (Fig. 3). The first tier is composed of 5-hydroxyurea-resistant nonmitotic stem cells that respond to unknown growth factors and become hemopoietin (IL-1 $\alpha$ )-responsive and then IL-3-responsive stem cells en route to the second tier. The second tier consists of highly mitotic committed progenitor cells that respond to a broad array of CSFs in vitro by proliferating and differentiating. GM-CSF, G-CSF, M-CSF, and other factors (Fig. 3) stimulate these second-tier cells to become morphologically distinct but functionally immature end cells. At this stage the specific lineage cells may respond to primarily lineage-specific factors, such as IL-5 (eosinophils), G-CSF (meutrophils), erythropoietin (erythrocytes and megakaryocytes), and M-CSF (macrophages) (METCALF 1985).

Each growth factor has a hierarchical effect on hematopoiesis in regard to lineage specificity: M-CSF is macrophage lineage specific; GM-CSF most readily stimulates macrophages and secondarily stimulates neutrophils; IL-6 affects macrophages primarily and neutrophils secondarily; and G-CSF affects neutrophils primarily and macrophages secondarily (METCALF 1985). In any given circumstance in vivo, local cell types, interregulation of expression of CSF receptor, and factor concentration may have effects not predicted by in vitro dose-response experiments. In vitro CSFs maintain cell survival and mitosis but can also drive differentiation events. Cell lines dependent on one factor can be driven into terminal differentiation by other CSFs. This may mean that mitotically active cells can be driven to differentiate if a second factor is present (NICOLA 1989). In addition, recombinant CSFs are synergistic in vitro and in vivo. Taken together, these results suggest that expansion and differentiation can be uncoupled in such a way that the kinetics and magnitude of production of various growth factors will determine the outcome of the type and number of cells released from the bone marrow or spleen into the blood during various pathophysiologic responses. The type and number of cells released from the bone marrow will be determined by a combination of growth factors originating from blood, stromal cells, and the hematopoietic cells themselves.

Although recombinant CSFs can have hematopoietic effects when introduced in vivo or in vitro, there are small or subthreshold concentrations in the blood both normally and in times of inflammatory stimulation. Little is understood about the endocrine influences of CSFs on hematopoiesis in bone marrow. M-CSF is unique in that it can stimulate a limited proliferation of macrophages in nonhematopoietic tissues. The recent work of CROCKER and co-workers suggests that macrophages in bone marrow and spleen may be important in some form of trophic interaction during hematopoiesis (CROCKER and GORDON 1989). The production of erythrocyte differentiation factor (activin) by macrophages may be important in this interaction (ERÄMAA et al. 1990). Macrophages are the major producers of IL-1, IL-6, and G-CSF and produce large amounts of GM-CSF and M-CSF. The relative importance of macrophages or macrophagederived growth factors is poorly understood in relation to normal or pathophysiologic homeostasis of blood cell levels.

## **9 Conclusions and Future Directions**

Macrophages must grow, differentiate, and mediate homeostasis by conversing with other cells in their milieu. An important part of this cell communication is mediated by macrophage-derived growth factors. As the list of growth factors increases it will be important to expand the phenotype of macrophage-derived growth factors. About half of the currently known growth factors are uncharacterized with respect to macrophages. Other factors, such as soluble immune response suppressor and parathyroid hormone, may be processed but not synthesized by macrophages (AUNE and PIERCE 1981; DIMENT et al. 1989). More growth factors may be cloned directly with macrophages as a source; other extracellular matrix molecules (such as laminin) with functional growth factor domains (Table 13) will also be characterized in macrophages. Next, the transcriptional and translational controls of macrophage-derived growth factors will be defined in more detail. These can be defined in vitro by biochemical and molecular biologic methods and by examining genomic 5' flanking sequences for possible control by trans-acting factors (ECONOMOU et al. 1989). Regulation of growth factor transcription in macrophages by second messengers is also being studied (ADEREM et al. 1988; PRPIC et al. 1989). These phenotypes and controls will be correlated with functions of the various distinct subpopulations of macrophages in vitro and with macrophage ontogeny. Much of the functional capability of growth factors will be defined

by testing recombinant growth factors in vivo and in vitro with a knowledge of the expression of cognate receptors on the responding cells used to interpret responses. It will be important to determine the spatial expression of macrophagederived growth factors by macrophages and other cell types by in situ analysis, reverse transcription-polymerase chain reaction, or immunocytochemistry (BAYNE et al. 1986; RAPPOLEE et al. 1988; REMICK et al. 1988). There are few good genetic models for macrophage function. The osteopetrotic mouse (op/op), which lacks a functional M-CSF gene (WIKTOR-JEDRZEJCZAK et al. 1990), shows promise. The construction of transgenic animals that express macrophagederived growth factors is beginning to shed light on macrophage function, and tumor cells or macrophages that express macrophage-derived growth factors and can be injected into syngeneic mice are proving useful (LANG et al. 1987; JOHNSON et al. 1989; YOSHIDA et al. 1990). In mice, macrophage-derived growth factors can also be ablated by homologous recombination, although this is a more difficult technology (DE CHIARA et al. 1990). It may be possible to ablate macrophages or macrophage-derived growth factors by inserting heterologous promoters or macrophage-specific enhancer combinations into suicide genes or antisense growth factor constructs. In addition, understanding of macrophage-derived growth factors may allow better clinical applications through use of recombinant macrophage-derived growth factors, or expression of transformed endogenous macrophages expressing combinations of macrophage-derived growth factors.

The complex negative regulation of macrophage-derived growth factor expression is now partially understood. A large group of macrophage-derived growth factors are negatively regulated by the prostaglandins that also mediate some of their positive effects (OLD 1985; ROSS et al. 1986; DINARELLO 1989). However, one recently characterized macrophage-derived growth factor (MIP-1) does not act through prostaglandin, and its pyrogenic effects are not inhibited by indomethacin (DAVATELIS et al. 1989). Negative feedback of IL-1 is mediated by IL-1 induction of glucocorticoids (BESEDOVSKY et al. 1986). MIP-1 $\alpha$  was recently shown to inhibit bone marrow colony formation in vitro by GM-CSF or M-CSF (GRAHAM et al. 1990). A competitive inhibitor of IL-1 with sequence homology to IL-1 was also recently cloned (EISENBERG et al. 1990). As neuroimmunologic interactions are further characterized, they may define further negative regulatory loops between the nervous system and macrophages, although only inductive effects are currently known (EDWARDS et al. 1988; LOTZ et al. 1988). Finally, the kinetics of macrophage-derived growth factor induction and attenuation may be defined, as has been partially done for TNF- $\alpha$  and IL-1 in macrophages.

The macrophage is an excellent model system for understanding the production and function of growth factors. Not only will it provide a satisfactory understanding of mechanisms of communication of metazoan cells, but this understanding will lead to a clinically relevant understanding of macrophage function in pathophysiology and pathology.

Table 13. Miscella	aneous growth fac	stors					
Growth factor	Synthesis by macronhages	Specific	mRNA		Protein		Reference
			Size	AUUUA	Precursor	Mature	
			(KD)	Instability	amino acid	peptide	
				seducine	IIUIIUU	(RUA)	
OTP-1/IFN-α <sub>11</sub>			1.1	+	172		Iмакаwa et al. 1987
IFN-γ	1		0.8		155	40-80	GRAY and GOEDDEL 1983;
NGF-₿	I		1.3	+	118 × 2	27	ULLRICH et al. 1983; SCOTT
					(dimer)		et al. 1983
Neurotrophin-3		Related to NGF	1.4	+	120		MaisonPierre et al. 1990;
BDNF		Related to NGF	1.5	I	252	13.5	LIN et al. 1989; LEIBROCK
							et al.1989
CNTF			4.3		200	22.7	STÖCKLI et al. 1989
int-1			2.4	+	370		van Ooyen and Nusse 1984
(12 members)							
IL-3	I		1.0	+	166	15–30	Fung et al. 1984; Yang et al. 1986
IL-4	1		0.7		153	15/50	Arai et al. 1989
IL-5	I	Related to IL-4	1.7	+	132	32–62	Tanabe et al. 1987
Proliferin		Related to prolactin	1.0		224	25	Linzer and Nathans
Epithelin		-				6.0	SHOYAB et al. 1990
(2 members)							
IL-7	I		1.8/2.4	1	154	15	Goodwin et al. 1989
IL-10	Ι		1.0/1.5		178	17.4	Moore et al. 1990
PD ECGF			1.8	+	482	45	Ishikawa et al. 1989
HGF			6.0	I	728	82	Nakamura et al. 1989
Neuroleukin	I		2.0	I	558	56	GURNEY et al. 1986
Endothelin			2.3	+	200	2.5	Yanagisawa et al. 1988;
(3 members)					(21)		INOUE et al. 1989a, b; BLOCH
							et al. 1989

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Thymopoletin/				49	5.0	Аирнуа et al. 1987
spienin (2 members) Fibronectin	+	Heparin binding	24 forms 1.2–8.5	2500 (approx)	550 (dimer)	Schwarzbauer et al. 1983; BLATTI et al. 1988; BARONE et al. 1989
Bombesin/GRP	+		0.8/3.8/7.8	147(27)	3.0	Wiedermann et al. 1986; Sausvirle et al. 1986;
						LEBACQ-VERHEYDEN et al. 1988
	-		10/10	130/115(11)	1.2	KRAUSE et al. 1987
Substance P	+ -			109/111	43	GOODALL et al. 1986;
Thymosin	+	INO SIGUAI	0.0/ 1.2/ 1.4			Eschenfeldt and Berger
(2 members)		sequence				1986; Gonbo et al. 1987
					400	PANAYOTOU et al. 1989
Laminin A			0	1786	200	SASAKI et al. 1987
B1		domains	∼0.0 5.5/7.6	1599	200	Pikkarainen et al. 1988
B2			0.1/0.0			
OTP, ovine troph derived endothel	noblast protein; NC ial cell growth fac	aF, nerve growth f tor; HGF, hepatoc	actor; BDNF, brain-derived neurotro yte growth factor; GRP, gastrin-rele	ophic factor; CNTF, asing peptide	ciliary neuron tr	ophic factor; PU ECGF, platelet-

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# The Biology of CSF-1 and Its Receptor

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## 1 Introduction

The constant renewal of blood cells in vertebrate species depends on the proliferation and differentiation of hematopoietic stem cells in the bone marrow (HARRISON et al. 1988). These cells in turn give rise to progenitor cells which are committed to more restricted pathways of differentiation. The survival, proliferation, and differentiation of these progenitor cells are regulated by the colony stimulating factors (CSFs), so named because of their ability to promote the in vitro proliferation and differentiation of single progenitor cells into macroscopic colonies with discernible differentiated cell types (PLUZNIK and SACHS 1965; BRADLEY and METCALF 1966; ICHIKAWA et al. 1966). This group of hematopoietic growth factors includes interleukin-3 (IL-3), granulocyte-

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macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), interleukin-5 (IL-5), and colony stimulating factor-1 (CSF-1) (reviewed in STANLEY and JUBINSKY 1984; METCALF 1986).

Colony stimulating factor 1 is a lineage specific growth factor with the ability to control the survival, proliferation, and differentiation of the mononuclear phagocyte (reviewed in STANLEY et al. 1983). However, as will be discussed later in this chapter, it probably also plays an essential role in the regulation of the placenta during pregnancy (BARTOCCI et al. 1986; POLLARD et al. 1987; ARCECI et al. 1989; REGENSTREIF and ROSSANT 1989). The current review focuses initially on the biochemical, molecular, and cellular aspects of this growth factor and its receptor in order to provide a framework for a subsequent discussion of the in vitro and in vivo biologic activities of CSF-1.

# 2 CSF-1

### 2.1 Cellular Sources

Many methods, including radioimmunoassay, in situ hybridization, and Northern analysis, have been used to identify the numerous cell types that synthesize CSF-1 (reviewed in SHERR and STANLEY 1990). Fibroblasts, especially the conditioned medium from established cell lines of this type, e.g., mouse L cells, are a prominent source of this growth factor (STANLEY and HEARD 1977; YAN et al. 1990), as are bone marrow stromal cells, which compose the hematopoietic microenvironment (LANOTTE et al. 1982; FIBBE et al. 1988; YAN et al. 1990). While CSF-1 production is detectable in many tissues, including the uterus, there is a dramatic increase in this latter organ during pregnancy with production localized to the columnar epithelial cells of the glandular endometrium (POLLARD et al. 1987). Besides these uterine cells, there are additional reports of several other cell types which may exert local regulatory functions through the elaboration of this growth factor. These include thymic epithelium (LE et al. 1988), brain astrocytes (THERY et al. 1990), osteoblasts (ELFORD et al. 1987), and keratinocytes (CHODAKEWITZ et al. 1990). In addition, a variety of cells release CSF-1 following in vitro activation. These include endothelial cells (SEELENTAG et al. 1987), T lymphocytes (CERDAN et al. 1990), and B lymphocytes (REISBACH et al. 1989), as well as monocytes themselves (HORIGUCHI et al. 1986; RAMBALDI et al. 1987; GAFFNEY et al. 1988; HASKILL et al. 1988; LU et al. 1988; OSTER et al. 1989). The potential for CSF-1-responsive monocytes to produce CSF-1 raises the possibility of the involvement of autocrine or paracrine mechanisms in their activation. As is the case for activated normal human monocytes, a number of human tumors have been identified which coexpress CSF-1 and its receptor, including acute myeloblastic leukemia blasts (RAMBALDI et al. 1988; WANG et al. 1988) and adenocarcinoma cells of the breast, ovary, and endometrium (HORIGUCHI et al. 1988; KACINSKI et al. 1989a). Other tumors which have been

shown to express CSF-1 both in vivo and in vitro include cells derived from patients with lymphoblastic leukemia (TAKAHASHI et al. 1988), diffuse large cell lymphoma (JANOWSKA-WIECZOREK et al. 1991), myeloma (NAKAMURA et al. 1989), Hodgkin's disease (PAIETTA et al. 1990), adenocarcinoma of the lung (HORIGUCHI et al. 1988), and pancreatic carcinoma (RALPH et al. 1986b).

## 2.2 Biochemistry

Colony stimulating factor-1, which has been extensively characterized in both man and the mouse, was originally purified from mouse L cell conditioned medium (STANLEY and HEARD 1977) and human urine (DAS et al. 1981), respectively. It is a disulfide-linked homodimeric molecule with a molecular weight of 45-90 kDa but also exists in higher molecular weight forms. Although the number of amino acids in the mature monomeric subunit varies due to alternative splicing of RNA transcripts (Kawasaki et al. 1985; Wong et al. 1987; CERRETTI et al. 1988) and Cterminal proteolytic cleavage (RETTENMIER and ROUSSEL 1988) (Fig. 1), the Nterminal 158 amino acids are sufficient for biologic activity (Kawasaki et al. 1985; HEARD et al. 1987a; WONG et al. 1987). The polypeptide is also modified by glycosylation (MANOS 1988; RETTENMIER and ROUSSEL 1988; PRICE and STANLEY, manuscript in preparation). The ultimate disposition of the molecule as either a rapidly secreted growth factor or as a biologically active membrane-bound (STEIN et al. 1990) growth factor, depends in large part on the presence or absence of an exon 6-encoded proteolytic cleavage site (HEARD et al. 1987a; RETTENMIER et al. 1987; MANOS 1988; RETTENMIER and ROUSSEL 1988) (see Sect. 2.3) (Fig. 1). The presence of these two distinct forms of CSF-1 may have important implications for its ability to function both as a circulating growth factor and as a local mediator of cell-cell interactions.

## 2.3 Molecular Biology

The organization of the CSF-1 gene is highly conserved between man and the mouse in those aspects that have been thus far investigated. The human gene is 21 kb in length and consists of ten exons and nine introns, with exons 1–8 coding for the CSF-1 polypeptide itself and exons 9 and 10 coding for alternative 3'-untranslated regions (LADNER et al. 1987; reviewed in KAWASAKI and LADNER 1990) (Fig. 1). Genetic analysis has revealed that the human gene is localized to the long arm of chromosome 5 at position 5q33.1 (PETTENATI et al. 1987), closely linked to the genes for GM-CSF (HUEBNER et al. 1985; LE BEAU et al. 1986; YANG et al. 1988; VAN LEEUWEN et al. 1989), IL-3 (YANG et al. 1988), IL-4 (LE BEAU et al. 1989; VAN LEEUWEN et al. 1989), IL-5 (SUTHERLAND et al. 1988; LE BEAU et al. 1989; VAN LEEUWEN et al. 1989), acidic fibroblast growth factor (JAYE et al. 1986), and the CSF-1 receptor (LE BEAU et al. 1986). However, the mouse CSF-1 gene maps



**Fig. 1.** Human CSF-1 genomic organization, transcripts, and expression. In the *upper part of the figure*, the intron–exon relationships of the human CSF-1 gene are shown, together with schematic representations of the four cDNA clones that have been sequenced. Exons (1–10), 5' and 3'untranslated regions (*filled*), and coding region (*open*), including signal peptide (*hatched*) and transmembrane domain (*cross-hatched*), are indicated together with the N-linked (*arrowheads*) and O-linked (*open circles*) glycosylation sites and the intracellular proteolytic cleavage site (*dotted line*). The *lower part of the figure* depicts the later stages in the expression of homodimeric CSF-1. The short homodimers are derived from the 1.6-kb clone, the longer homodimers from the other clones. *Hatched regions*, mature CSF-1; *filled regions*, transmembrane domain

to chromosome 3 (GISSELBRECHT et al. 1989) on a different chromosome from the genes encoding its receptor (chromosome 18) (HOGGAN et al. 1988) and GM-CSF and IL-3 (chromosome 11) (BARLOW et al. 1987).

While several mRNA species (1.6–4.0 kb) have been observed in human cells and cDNAs corresponding to the 4.0-, 2.5-, 2.2-, and 1.6-kb species have been sequenced (Kawasaki et al. 1985; LADNER et al. 1987; WONG et al. 1987; CERRETTI et al. 1988), two species of 4.0 and 2.3 kb, respectively, predominate in the mouse (LADNER et al. 1988). Although these mouse species differ from each other only in their alternatively spliced 3'- untranslated regions (LADNER et al. 1988), this seems to be the case only for the 4.0- and 2.5-kb human transcripts (LADNER et al. 1987; WONG et al. 1987). The other human mRNAs result from alternative splicing within exon 6 and are translated into different forms of CSF-1 (LADNER et al. 1987; CERRETTI et al. 1988) (Fig. 1). Lower molecular weight mRNAs have also been isolated from mouse cells (RAJAVASHISTH et al. 1987). In both the human and the mouse, the 3'-untranslated region of the "long" (4.0-kb) species is rich in AU sequences which may confer short half-lives on their respective mRNA transcripts (KAWASAKI and LADNER 1990) and may be important in regulation. Aside from these sequence characteristics, a number of additional transcriptional regulatory motifs have been identified within 400 base pairs of the mRNA initiation site in exon 1 of the CSF-1 gene (reviewed in KAWASAKI and LADNER 1990). Among these are (a) two TATA boxes with the sequences TTAAA and CATAAA at positions -26 to -22 and -54 to -49, respectively (KAWASAKI and LADNER 1990), (b) a series of alternating T and G residues at positions -126to -80, which may favor the Z-DNA confirmation and affect transcription (Rich et al. 1984), (c) two GGCGGG sequences at positions -159 and -177, which may be involved in binding transcription factors (DYNAN et al. 1986), and (d) the sequences AGGAAAG and GGGAAAG at positions -317 and -377. respectively, which are both very similar to the consensus enhancer core sequence TGGAAAG that plays a role in the transcriptional level of genes with which it is associated (LAIMINS et al. 1983). While these various sequences offer the potential for regulation of CSF-1 expression at multiple levels, their definitive roles remain to be demonstrated.

# 3 CSF-1 Receptor

#### 3.1 Occurrence

The receptor for CSF-1 (CSF-1R) is distributed in many tissues but is primarily expressed on cells of the mononuclear phagocytic lineage (GUILBERT and STANLEY 1980, 1986; BYRNE et al. 1981). With maturation, the surface expression of this receptor increases to maximal levels of approximately  $5 \times 10^4$  molecules/up-regulated tissue macrophage (GUILBERT and STANLEY 1986). In contrast, multipotent hematopoietic cells, which give rise to committed mononuclear

phagocyte progenitors, express receptors at substantially lower densities of approximately  $2 \times 10^3$  molecules/up-regulated cell (BARTELMEZ and STANLEY 1985). Additional cell types related to the mononuclear phagocyte that have also been shown to bear CSF-1R include subsets of acute myeloid leukemia cells (DUBREUIL et al. 1988; ASHMUN et al. 1989) and microglia of the central nervous system (SAWADA et al. 1990).

Although originally thought to be restricted to mononuclear phagocytes, the CSF-1R has more recently been demonstrated on maternal decidual cells and fetal trophoblastic cells during placental development (ARCECI et al. 1989; REGENSTREIF and ROSSANT 1989) and on human choriocarcinoma cell lines (RETTENMIER et al. 1986). The role of CSF-1 and its receptor in this biologic setting will be discussed further below (Sect. 4.4). Finally, one group has reported the presence of CSF-1R on both normal and neoplastic myoblasts (LEIBOVITCH et al. 1989).

### 3.2 Biochemistry

The CSF-1R, which is encoded by the c-fms proto-oncogene (SHERR et al. 1985), is a member of a family of growth factor receptors with intrinsic tyrosine kinase activity. In fact, the receptor is most closely related to the A- and B-type receptors for platelet-derived growth factor (PDGF) (YARDEN et al. 1986) and the c-kit proto-oncogene product (BESMER et al. 1986; YARDEN et al. 1987), whose ligand in the mouse has recently been shown to be the stem cell growth factor product of the Steel locus (HUANG et al. 1990; WILLIAMS et al. 1990; ZSEBO et al. 1990). The CSF-1R, like other members of this group of tyrosine kinase receptors, has a alvcosylated extracellular ligand-binding domain, a hydrophobic membranespanning domain, and an intracellular tyrosine kinase domain (HAMPE et al. 1984; COUSSENS et al. 1986; ROTHWELL and ROHRSCHNEIDER 1987). Unlike other tyrosine kinase receptors, members of this family of receptors possess extracellular domains characteristic of members of the immunoglobulin gene superfamily and have unique hydrophilic spacer sequences of variable length within the tyrosine kinase domain that may play a role in substrate recognition (YARDEN et al. 1987). In the case of CSF-1R, the C-terminal tail also subserves a negative regulatory function as demonstrated by the increased transforming activity of both human and feline molecules mutated in this region (ROUSSEL et al. 1987) and the viral oncogene counterpart, v-fms, which lacks this sequence (BROWNING et al. 1986).

Studies of mononuclear phagocytes have demonstrated that these cells bear a single class of high affinity receptors for CSF-1 (GUILBERT and STANLEY 1980; STANLEY and GUILBERT 1981). Using a kinetic approach, this receptor has been shown to have dissociation constants of  $4 \times 10^{-10}$  M at 37 °C and of  $\leq 10^{-13}$  M at 4 °C, respectively (GUILBERT and STANLEY 1986). While the molecular weight of the purified mouse CSF-1R (165 kDa, YEUNG et al. 1987) agrees well with its molecular weight determined by chemical cross-linking experiments

in intact cells (165 kDa, MORGAN and STANLEY 1984), the human CSF-1R has a slightly lower apparent molecular weight (150 kDa, ROUSSEL et al. 1987). Although the density of receptors that can be expressed on individual cells varies between 2000 and 120 000 depending on cell type (BYRNE et al. 1981; STANLEY et al. 1983; BARTELMEZ and STANLEY 1985; Fig. 3), several other factors have been shown to regulate cell surface CSF-1R expression. The presence of CSF-1 results in receptor binding followed by internalization and degradation of receptorligand complexes, while removal of growth factor leads to increased cell surface receptor expression (STANLEY and GUILBERT 1981; GUILBERT and STANLEY 1986). Experiments involving other agents have shown that several bacterial products, including lipopolysaccharide (GUILBERT and STANLEY 1984), muramyl tripeptidephosphatidylethanolamine, lipopeptide CGP 31362, and pertussis toxin (HUME and DENKINS 1989), result in decreased CSF-1R density. In addition, phorbol esters, presumably through activation of protein kinase C, down-regulate receptor expression through mechanisms distinct from those involved in ligand-induced changes (CHEN et al. 1983; GUILBERT et al. 1983; DOWNING et al. 1989). Finally, many cytokines such as IL-3 and GM-CSF, through a presumed "hierarchical down-modulation" (WALKER et al. 1985), as well as others such as IL-4, interferon- $\gamma$ , and tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), through as yet undefined mechanisms (HUME and DENKINS 1989; SHIEH et al. 1989), also result in decreased cell surface CSF-1R expression. Thus, many factors may influence the proliferation, differentiation, and activity of mononuclear phagocytic cells via their effects on CSF-1R expression.

#### 3.3 Molecular Biology

As indicated above, the CSF-1R gene has been mapped to human chromosome 5 (5q33.3), in close proximity to the CSF-1 gene (GROFFEN et al. 1983; ROUSSEL et al. 1983; LEBEAU et al. 1986). In addition, this gene is the 3' neighbor of the gene for the B-type PDGF receptor (YARDEN et al. 1986; ROBERTS et al. 1988). Both genes, which have a similar intron–exon organization, are juxtaposed in head-to-tail fashion with the CSF-1R promoter located within 0.5 kb of the B-type PDGF-R polyadenylation signal, raising the possibility that transcription of the former is affected by transcription of the latter (ROBERTS et al. 1988).

The CSF-1R gene (Fig. 2) which is 58 kb in length, consists of 21 introns and 22 exons (reviewed in SHERR 1990). Exon 1, which encodes nontranslated sequences, is 26 kb upstream of exon 2, which encodes the signal peptide. The transcription of the gene proceeds in a tissue-specific manner from two distinct promoters. While the precise locations of these promoters are unknown, it has been established that transcription is initiated upstream of exon 1 in placental trophoblasts, while it is initiated immediately upstream of exon 2 in mononuclear phagocytes (VISVADER and VERMA 1989). Increases in the steady state levels of CSF-1R mRNA observed with the maturation of precursors to more differentiated cells of the mononuclear phagocyte lineage (SARIBAN et al. 1985) appear to be



**Fig. 2.** CSF-1 receptor genomic organization and transcripts. The intron-exon (*arabic numerals*) relationships of the CSF-1 receptor gene are shown, together with a schematic representation of the mRNAs expressed in placental trophoblasts and macrophages. The untranslated regions (*filled*), signal sequence (*hatched*), transmembrane domain (*cross-hatched*), and interrupted tyrosine kinase catalytic domain (*striped*) are shown together with the potential N-linked glycosylation sites (*arrowheads*), positions of the extracellular cysteine residues (*asterisks*), and tyrosine phosphorylation sites (*P*). (Based on HAMPE et al. 1989)

induced by factors that increase receptor expression through alterations in mRNA half-lives (WEBER et al. 1989). Furthermore, hierarchical down-modulation of the CSF-1R (WALKER et al. 1985) also appears to be regulated via post-transcriptional mechanisms (GLINIAK and ROHRSCHNEIDER 1990).

#### 4 Biologic Effects of CSF-1

#### 4.1 Early Events in Response to CSF-1

Colony stimulating factor-1 has been shown to exert pleiotropic effects on cells of the mononuclear phagocyte series (reviewed in STANLEY et al. 1983.) In order to induce monocytic cells to divide, CSF-1 must be present during the entire  $G_1$  phase to facilitate entry of cells into S phase and their subsequent progression through  $G_2$  and M (TUSHINSKI and STANLEY 1985). While numerous cellular responses have been observed following ligand activation, it is difficult to determine how they contribute to the processes of survival, proliferation, and differentiation induced by the growth factor.

Among the earliest effects observed following CSF-1 binding are changes in the cell membrane itself, including ruffling and the formation of filopodia, vesicles, and vacuoles (TUSHINSKI et al. 1982; BOOCOCK et al. 1989). Soon after, several metabolic changes are observed, including increases in glucose uptake (HAMILTON et al. 1988) and protein synthesis with a concomitant decrease in protein degradation (TUSHINSKI and STANLEY 1985). In addition, there is an early influx of sodium by an amiloride-sensitive mechanism, presumably the Na<sup>+</sup>/H<sup>+</sup> antiport, as well as an increase in Na<sup>+</sup>/K<sup>+</sup>-ATPase activity (IMAMURA and KUFE 1988; VAIRO and HAMILTON 1988). These latter changes are inhibited by pertussis toxin and are consequently believed to be mediated by G proteins (IMAMURA and KUFE 1988). The role of additional enzymatic systems in the cellular events leading to CSF-1- induced cell proliferation has been suggested by the increase in cyclooxygenase activity which results in increased prostaglandin E2 and thromboxane A<sub>2</sub> production (KURLAND et al. 1979; ORLANDI et al. 1989), as well as by the association of the "activated" CSF-1R with phosphatidyl inositol-3 kinase activity, which results in the production of novel phosphoinositides, which may contribute to mitogenesis (VARTICOVSKI et al. 1989; SHURTLEFF et al. 1990). Other early changes noted have been at the transcriptional level with increased levels of expression of the c-myc and c-fos proto-oncogene products (BRAVO et al. 1987; ORLOFSKY and STANLEY 1987), which have generally been associated with subsequent increases in DNA synthesis (HAMILTON et al. 1989).

The very earliest cellular events following CSF-1 binding to the CSF-1R are the phosphorylation of the receptor and other cellular proteins on tyrosine residues (DOWNING et al. 1988; SENGUPTA et al. 1988). CSF-1-induced protein tyrosine phosphorylation is maximal within 30s of CSF-1 addition to cells at 37 °C (SENGUPTA et al. 1988). A particular sequence of events has been discerned by studying these reactions at 4 °C (SENGUPTA et al. 1988; LI and STANLEY 1991; M. BACCARINI, W. LI, P. DELLO SBARBA, E.R. STANLEY, submitted for publication), a temperature at which neither CSF-1 nor the CSF-1R is internalized but at which transmembrane-stimulated protein tyrosine phosphorylation occurs. It appears that CSF-1 binding stimulates or stabilizes the formation of noncovalent CSF-1R homodimers. This dimerization apparently leads to activation of the receptor kinase and receptor autophosphorylation on tyrosine, a process that can occur via intermolecular phosphorylation of adjacent kinase domains (OHTSUKA et al. 1990). These events are followed by the tyrosine phosphorylation of several, mostly cytoplasmic, proteins prior to the formation of disulfide bonds between monomeric units of the CSF-1R dimer, a modification of one of the monomeric units that increases its molecular weight from 165 kDa to approximately 250 kDa (LI and STANLEY 1991), and an increase in receptor tyrosine and serine phosphorylation (M. BACCARINI, W. LI, P. DELLO SBARBA, E.R. STANLEY, submitted for publication). These results and other data (LI and STANLEY 1991) suggest that the noncovalent homodimeric receptor-ligand complex is the active signaling species, whereas the covalent heterodimeric receptor-ligand species is inactive and selectively internalized. The identities of the proteins that are rapidly phosphorylated in tyrosine have not been established. It has been recently claimed that the proto-oncogene product RAF-1, a 72-kDa cytoplasmic serine/threonine kinase, is a substrate of the PDGF-R and therefore potentially involved in transducing the signal from membrane to nucleus (MORRISON et al. 1988, 1989). However, recent studies with the CSF-1R, PDGF-R (BACCARINI et al. 1990), and EGF-R (BACCARINI et al. 1991) indicate that while RFA-1 is serine

phosphorylated and the RAF-1-associated kinase is activated following growth factor stimulation, it is not phosphorylated in tyrosine and therefore not a physiologic substrate of these receptor tyrosine kinases. Attempts to isolate cDNA clones encoding the genes for proteins rapidly phosphorylated in tyrosine in response to CSF-1 are currently underway. One of these proteins (57 kDa) is of particular interest as it is the only one that is phosphorylated in tyrosine in several cell types in response to different growth factors (LI et al. 1991). It should be noted that as a tyr-809 to phe-809 CSF-1R mutant which is unable to stimulate mitogenesis is able to stimulate protein tyrosine phosphorylation as effectively as the wild-type receptor (ROUSSEL et al. 1990), it is likely that only one or a few of the tyrosine phosphorylated proteins are involved in the signal transduction pathway for proliferation.

## 4.2 Monocytopoiesis

Colony stimulating factor-1 is capable of exerting its biologic effects on the mononuclear phagocyte lineage beginning with the committed progenitor cell, which proliferates and differentiates to give rise in sequence to the following cells: monoblast  $\rightarrow$  promonocyte  $\rightarrow$  monocyte  $\rightarrow$  macrophage (Fig. 3) (reviewed in STANLEY 1990). These responses have been demonstrated in vitro using human CSF-1, which is capable of stimulating the formation of macrophage colonies from both mouse and human precursor cells (DAS and STANLEY 1982; MOTOYOSHI et al. 1982; WAHEED and SHADDUCK 1982), as well as mouse CSF-1, which is species specific, stimulating macrophage production from mouse precursors only (DAS and STANLEY 1982). Interestingly, mouse cells show a greater proliferative response to human CSF-1 than do human precursor cells. However, it is not clear whether this phenomenon is due to poor definition of the culture conditions required for human cell proliferation (DAS and STANLEY 1982) or the requirement of additional growth factors (RALPH et al. 1986a; CHEN et al. 1988).

The primary role of CSF-1 in regulating mononuclear phagocyte production in vivo has been demonstrated in mice (HUME et al. 1989) and nonhuman primates (MUNN et al. 1990), in which administration of exogenous CSF-1 resulted in substantial increases in blood monocytes and tissue macrophages. Furthermore, work on the osteopetrotic *op/op* mouse has shown that its deficiency in cells of the mononuclear phagocyte lineage, including boneresorbing osteoclasts, results from a total deficiency of circulating and tissue CSF-1 (WIKTOR-JEDRZEJCZAK et al. 1990). While data in humans are less extensive, we have shown that the elevated peripheral blood monocyte counts in newborns are associated with serum CSF-1 concentrations that are three times adult values at birth and go on to double over the first week of life (ROTH 1990).

The steady state concentration of circulating growth factor in vivo is regulated by CSF-1R-mediated endocytosis and intracellular degradation by tissue macrophages, primarily in the liver (i.e., Kupffer cells) and spleen



Fig. 3. Schematic representation of the role of circulating CSF-1 in the regulation of mononuclear phagocyte production. CSF-1R expression is represented by *small semi circles*. (STANLEY 1990)

(BARTOCCI et al. 1987). This mechanism provides a negative feedback loop regulating the production of mononuclear phagocytes. Rapid increases in circulating CSF-1 are brought about by the increased synthesis and release of the growth factor from the endothelial cells of several organs (P. ROTH, A. BARTOCCI, E.R. STANELY, unpublished).

Although CSF-1 alone is capable of regulating mononuclear phagocyte proliferation and differentiation, these events are probably regulated in vivo by more complex interactions involving several growth factors. In fact, CSF-1 has been shown to synergise with IL-3 (CHEN and CLARK 1986), GM-CSF (CARACCIOLO et al. 1987; CHEN et al. 1988), and TNF- $\alpha$  (BRANCH et al. 1989), as well as the neuropeptides substance P (MOORE et al. 1988) and neurotensin (MOORE et al. 1989), in its in vitro actions on monocytic cells. Aside from its effect on committed precursor cells, CSF-1 is also capable of acting in concert with other factors to

direct primitive multipotent cells along the mononuclear phagocyte pathway of differentiation (BARTELMEZ and STANLEY 1985). This "channeling" of multipotent cells has been observed when CSF-1 is used in combination with IL-1 alone (MOCHIZUKI et al. 1987; WARREN and MOORE 1987; WILLIAMS et al. 1987), IL-1 + IL-3 (BARTELMEZ et al. 1989), GM-CSF (WILLIAMS et al. 1987; MCNIECE et al. 1988), and IL-6 (BOT et al. 1989) and results in an increase in the number of mononuclear phagocytes capable of being regulated by CSF-1 alone.

#### 4.3 Mononuclear Phagocyte Differentiation

Colony stimulating factor-1 induces mature monocytes and macrophages to perform various differentiated cell functions, such as the production of other cytokines (reviewed in RALPH and WARREN 1989), including interferon, IL-1, TNF- $\alpha$  (RALPH et al. 1986a; WARREN and RALPH 1986), and G-CSF (MOTOYOSHI et al. 1982). In addition, other important cell products involved in monocyte/macrophage immune function that are produced following CSF-1 exposure are thromboplastin (LYBERT et al. 1987), plasminogen activator (HAMILTON et al. 1980), prostaglandins (ORLANDI et al. 1989), acidic isoferritin (BROXMEYER et al. 1987), and oxygen radicals (BECKER et al. 1987; KANADA et al. 1987).

Aside from its effects on the production of soluble factors, CSF-1 also induces changes in the expression of mononuclear phagocyte membrane glycoproteins, including la antigens (WILLMAN et al. 1989), MAC1, asialo-GM1 (AKAGAWA et al. 1988), type III Fc receptor, LFA-3 (MUNN et al. 1990), and MY-4 (GEISSLER et al. 1989), all of which are presumed to be involved in cell-cell interactions in the immune response. The impact of these and other as yet undescribed molecular changes has been manifested by the several functional changes seen in CSF-1-stimulated mononuclear phagocytes (reviewed in RALPH and WARREN 1989) (see Sect. 4.5).

Aside from these effects on macrophage differentiation, which affect immune function, CSF-1 appears to play an important role in bone resorption. However, the results are somewhat confusing in that CSF-1, which is produced by osteoblasts (ELFORD et al. 1987), is a potent inhibitor of bone resorption by osteoclasts, which are themselves part of the mononuclear phagocyte series (HATTERSLEY et al. 1988). On the other hand, production of this cell type is dependent on CSF-1, as evidenced by its absence in the CSF-1-deficient osteopetrotic *op/op* mouse (WIKTOR-JEDRZEJCZAK et al. 1990). Another novel effect of CSF-1 is its ability in vivo to lower plasma cholesterol, predominantly the low density lipoprotein fraction, presumably through augmented macrophage phagocytosis (reviewed in GARNICK and STOUDEMIRE 1990; ISHIBASHI et al. 1990).

#### 4.4 Placental Regulation

While the major target for CSF-1 is the mononuclear phagocyte, the placenta is another putative site for its actions (reviewed in STANLEY 1990). More than 15



**Fig. 4.** Expression of CSF-1 and CSF-1R mRNA during placental development in the mouse. CSF-1 (*filled*) and CSF-1R (*stippled*, density of stippling proportional to intensity) mRNA expression is represented for days 4.5, 7, and 15 of pregnancy. Implantation takes place at day 5. *myo*, myometrium; *ut. ep.*, uterine epithelium; *bl*, blastocyst; *ut. lu.*, uterine lumen; *emb*, embryo; *tr. ec.*, trophoectoderm; *dec*, decidua; *gcl*, trophoblast giant cell layer; *sp. tr.*, spongiotrophoblast cells; *lab*, labyrinthine trophoblast cells; *ys*, yolk sac; *amn*, amnion. (STANLEY 1990)

years ago, it was shown that the pregnant uterus as well as the fetal and placental membranes were rich in colony stimulating activity (BRADLEY et al. 1971; ROSENDAAL 1975). Since then, CSF-1 has been identified as the growth factor responsible for this activity, with concentrations in the day 20 pregnant mouse uterus 1000 times higher than in the same nonpregnant organ (BARTOCCI et al. 1986). Further investigation using in situ hybridization has shown that expression of CSF-1 is confined to the luminal and glandular secretory epithelium (POLLARD et al. 1987) and is regulated by chorionic gonadotropin via synergistic action of the hormones, progesterone, and estrogen (BARTOCCI et al. 1986). Coincident with the increased expression of CSF-1, there is also substantial expression of CSF-1R mRNA in the murine placenta (MULLER et al. 1983; ARCECI et al. 1989) and human trophoblastic cells (HOSHINA et al. 1985). Studies employing in situ hybridization techniques have provided localization and temporal expression data that are compatible with CSF-1-regulated placental development (Fig. 4) (ARCECI et al. 1989; REGENSTREIF and ROSSANT 1989). CSF-1 mRNA expression in the uterine epithelium is increased above

baseline by the third day of gestation, achieves substantially elevated levels by days 8.5–9.5, and peaks at day 15. CSF-1R mRNA, on the other hand, first appears in the maternal decidua on the sixth day of gestation and continues to be expressed at low levels in the decidua basalis. On the fetal side, there is limited expression in trophoectodermal cells by day 7.5 and in diploid trophoblasts during placentation. Once the placenta is mature by day 9.5 of gestation, CSF-1R mRNA expression is most prominent in fetally derived giant trophoblastic cells followed by moderate expression in the spongiotrophoblastic layer and lower expression in the labyrinthine layers (ARCECI et al. 1989; REGENSTREIF and ROSSANT 1989). Placental CSF-1R mRNA expression peaks at day 17 of gestation (ARCECI et al. 1989).

The expression of CSF-1 in the uterine epithelium of the pregnant mouse is very local. In contrast to the large increase in uterine CSF-1 concentration, the concentration of CSF-1 in other tissues and the serum of the pregnant mouse increases only twofold. The ability of CSF-1 to stimulate trophoblastic cell proliferation (ATHANASSAKIS et al. 1987) and the in vitro proliferation and differentiation of ectoplacental cones (REGENSTREIF and ROSSANT 1989) together with the close apposition of CSF-1 and CSF-1R producing cells in the placenta make it likely that this growth factor plays an important role in placental regulation. In fact, maximal expression of uterine CSF-1 and placental CSF-1R coincides with the period of maximal placental growth, which occurs on days 9-15 of gestation (ARCECI et al. 1989). The existence of a local placental function for CSF-1 in the regulation of nonmononuclear phagocytic cells as distinct from its humoral function in regulating mononuclear phagocytes is entirely compatible with data which demonstrate that different promoters regulate the expression of CSF-1R mRNA in trophoblastic cells and mononuclear phagocytes, respectively (VISVADER and VERMA 1989). Further evidence for a distinct role for CSF-1 in placental regulation is the observation that the predominant mRNA species for this growth factor in the gravid mouse uterus is 2.3 kb and not the 4.0-kb species seen in most other tissues (POLLARD et al. 1987). These transcripts differ only in their 3'-untranslated sequences, with the larger molecule containing three repeats of the AUUUA sequence, which in the right context has been shown to decrease mRNA stability (SHAW and KAMEN 1986). It is therefore possible that the larger species, which appears following immunologic stimuli, is rapidly eliminated once the demand for macrophages ceases, whereas the shorter molecule, which is required over a sustained period of time during gestation, is a more stable, long-lived species (POLLARD et al. 1987).

### 4.5 Macrophage Activation in Inflammation, Infection, and Cytotoxicity

Colony stimulating factor-1 is an important mediator of the inflammatory response, as evidenced by its increased presence in inflammatory exudates (STANLEY et al. 1976). In addition, as noted above (Sect. 4.3), it induces monocytic

cells to release several cytokines, including IL-1, TNF- $\alpha$ , G-CSF, and interferon as well as proteolytic enzymes such as plasminogen activator. Furthermore, its ability to provide chemotactic signals for monocytic cells (WANG et al. 1988) makes it ideally suited for regulating the influx of cells to the site of an inflammatory stimulus.

The potential role for CSF-1 in host defenses against infection has been demonstrated in numerous systems. In a model system for the inflammatory response, we have shown that mice treated with lipopolysaccharide in vivo demonstrate rapid increases in serum and tissue CSF-1 concentrations, which are the result of increased growth factor synthesis rather than a decrease in the clearance of circulating growth factor (ROTH et al. 1990). Other investigators have focused on specific pathogens and have shown that CSF-1 enhances resistance to viral infection (LEE and WARREN 1987) as well as killing of the fungal species Candida albicans (KARBASSI et al. 1987; CHONG and LANGLOIS 1989; WANG et al. 1989; CENCI et al. 1991) and the intracellular pathogens Mycobacterium avium-intracellulare (BERMUDEZ and YOUNG 1990) and Listeria monocytogenes (CHEERS et al. 1989). Additional studies have shown that CSF-1 may play an important role in the response to parasitic infections, including leishmaniasis (Ho et al. 1989) and schistosomiasis (CLARK et al. 1988). In contrast, CSF-1 facilitates replication of the human immunodeficiency virus (GENDLEMAN et al. 1988) and causes monocytic cells to suppress both antigen- and mitogen stimulated T cell proliferation (WING et al. 1986).

Colony stimulating factor-1-stimulated mononuclear phagocytes exert modest increases in cytotoxic activity against tumors in an antibodyindependent (WARREN and RALPH 1986; RALPH and NAKOINZ 1987; SAMPSON-JOHANNES and GARLINO 1988) and antibody-dependent fashion (NAKOINZ and RALPH 1988; MUFSON et al. 1989; MUNN et al. 1990). However, in virtually all of these studies, cells are preincubated with CSF-1 for prolonged periods of time before assaying for cytotoxicity. Consequently, the effects observed may be the result of improved mononuclear phagocyte survival in vitro rather than a direct effect on tumor cytotoxicity.

### 4.6 Neoplasia

The v-fms oncogene derived from the Susan McDonough strain of the feline sarcoma virus is closely related to the c-fms-encoded CSF-IR (reviewed in SHERR 1990; SHERR and STANLEY 1990; STANLEY 1990). Despite its ability to bind ligand, v-fms is capable of stimulating cell growth and producing a transformed phenotype in the absence of CSF-1 (WHEELER et al. 1986). A number of differences between the amino acid sequences of v-fms and c-fms have been demonstrated and are thought to be responsible for differences in their respective abilities to transform cells which express them. First, there is a 3'-deletion in the v-fms gene resulting in replacement of the C-terminal 50 amino acids of c-fms with 11 unrelated residues encoded by the 3'-untranslated region

of the feline c-*fms* (COUSSENS et al. 1986). This deletion is necessary for (WOOLFORD et al. 1988) or at least greatly enhances (ROUSSEL et al. 1988) the transforming ability of this oncogene, possibly by eliminating a peptide that serves to negatively regulate the tyrosine kinase activity of the native receptor (ROUSSEL et al. 1987). Further comparison of v-*fms* and c-*fms* has revealed nine additional amino acid substitutions, of which two at residues 301 and 374 are required for transformation (WOOLFORD et al. 1988). Substitution at leucine-301 is thought to alter the conformation of the extracellular domain in a manner that mimics ligand binding and results in constitutive phosphorylation of the v-*fms* molecule (WOOLFORD et al. 1988).

While the v-fms molecule is capable of transforming cells and inducing the formation of tumors derived from mononuclear phagocytes and other hematopoietic lineages (HEARD et al. 1987b), the c-fms gene results in transformation in situations where it and/or its ligand, CSF-1, are inappropriately expressed (reviewed in STANLEY 1990). BAUMBACH et al. (1987) have shown that mice injected with spleen cells infected with a c-myc-containing retrovirus developed monocytic tumors due to a rearrangement in the CSF-1 gene. This provided a "secondary event," which resulted in increased growth factor secretion and autocrine stimulation of receptor-bearing cells. A similar hypothesis has been invoked for the development of endometrial and ovarian tumors in humans, where CSF-1 and CSF-1R are frequently coexpressed in tumor cells (KACINSKI et al. 1989a, b). Similar coexpression of ligand and receptor has also been demonstrated in a subpopulation of patients with acute myeloblastic leukemia (WAKAMIYA et al. 1987; RAMBALDI et al. 1988). In another situation, it has been shown that many murine myeloblastic leukemias induced by the Friend murine leukemia virus, both in vivo and in vitro, actually result from proviral integration at a site that results in greatey enhanced c-fms expression, leading to the possibility of inappropriately increased responsiveness of primitive hematopoietic cells to CSF-1 (GISSELBRECHT et al. 1987).

### 4.7 Clinical Applications

On the basis of data derived from in vitro studies, in vivo experiments in animal models, and some preliminary observations in humans, it is clear that CSF-1 has tremendous potential for a wide array of clinical applications. The ability of CSF-1 to augment host responses to a variety of pathogens (see Sect. 4.5) makes it a prime candidate as an adjunct in the treatment of infection. While this growth factor has been shown to exert a protective effect in mice exposed to *E. coli* (CHONG and LANLOIS 1988), there are limited data as yet for its effects on human infection.

In the area of neoplastic diseases, CSF-1 and its receptor may be useful in several areas. First, the c-*fms*-encoded CSF-1R and serum CSF-1 concentrations may be useful as tumor markers to classify as well as to follow the progress of

particular malignancies. In fact, several investigators have shown that a substantial proportion of patients with acute myeloblastic leukemia display the CSF-1R on their tumor cells, which in these instances generally show evidence of monocytic differentiation (DUBREUIL et al. 1988; ASHMUN et al. 1989). However, unlike the case of Friend virus-induced murine myeloblastic leukemias (GISSELBRECHT et al. 1987), there is no evidence of rearrangements in the region of the c-*fms* gene in these human leukemias (DUBREUIL et al. 1988; ASHMUN et al. 1989). Furthermore, recent studies have indicated that circulating CSF-1 concentrations are elevated in patients with myeloproliferative disease, especially those with peripheral bone marrow extension (GILBERT et al. 1989), and in a high proportion of patients with preleukemia, leukemia, and lymphoid malignancies (JANOWSKA-WIECZOREK et al. 1991).

Apart from lymphohemopoietic malignancies, this growth factor and its receptor may be important markers in the case of ovarian and endometrial cancers. Aside from their coexpression of growth factor and receptor in many cases, concentrations of circulating CSF-1 have been shown to reflect disease activity and can point to the presence of recurrent disease (KACINSKI et al. 1989a, b).

A second possible role for CSF-1 is as an adjunctive therapy in the treatment of malignancies. The ability of CSF-1 to induce terminal differentiation in vitro of blast cells from some patients with acute myeloblastic leukemia (MIYAUCHI et al. 1988) provided the basis for examining the role of this cytokine in vivo in several animal tumor models. CSF-1 has been shown to inhibit primary tumor growth in syngeneic mice (RALPH and WARREN 1989) as well as the development of metastases in a murine melanoma model (HUME et al. 1989). At the present time, data in humans are lacking.

A third role for CSF-1 in neoplastic disorders arises from its myelorestorative capabilities. In patients who have undergone ablative therapies followed by bone marrow transplantation for a variety of leukemias and neuroblastoma, CSF-1 accelerates the recovery of total leukocytes and granulocytes (MASAOKA et al. 1988). Similar results have also been seen in individuals undergoing intensive chemotherapy for other malignancies (MATSUMOTO et al. 1987). This therapeutic approach has also been employed in patients with primary deficiencies of granulocytes, e.g., chronic neutropenia of childhood, where CSF-1 treatment has resulted in increased neutrophil counts, which in some cases have been sustained (KOMIYAMA et al. 1988).

Aside from its hemopoietic activities, the role of CSF-1 in regulating the inflammatory response may be critical to clinical pathology. In both humans and experimental mice with systemic lupus erythematosus, there are increased concentrations of circulating CSF-1 and numbers of mononuclear phagocytes, which may contribute to the autoimmune injury seen in these individuals (A. BARTOCCI, V. PRALORAN, P. DELLO SBORBA, E.R. STANLEY, unpublished). Similarly, since circulating CSF-1 regulates osteoclast production (WIKTOR-JEDRZEJCZAK et al. 1990), it is conceivable that an increase in growth factor levels with age could in some way contribute to osteoporosis of the elderly. Thus, treatments for

these disease entities may involve the use of antagonists capable of attenuating the CSF-1-mediated inflammatory response (reviewed in SHERR and STANLEY 1990). In contrast, the absence of CSF-1 in the *op/op* osteopetrotic mouse (WIKTOR-JEDRZEJCZAK et al. 1990) makes it conceivable that administration of exogenous CSF-1 may be therapeutic in at least some forms of the human disease. In fact, administration of this growth factor has been shown to correct many of the defects of the *op/op* mouse (WIKTOR-JEDRZEJCZAK et al. 1990; FELIX et al. 1990; W. WIKTOR-JEDRZEJCZAK, E. URBANOWSKA, S.L. AUKERMAN, J.W. POLLARD, E.R. STANLEY, P. RALPH, A.A. ANSARI, K.W. SELL, M. SZPERL, unpublished).

## **5** Conclusions

Through the use of the techniques of cell biology, biochemistry, and molecular biology, a great deal has been learned regarding the biology of CSF-1 and its receptor. While at the molecular and cellular level a great deal regarding the signal transduction pathways regulated by CSF-1 remains to be elucidated, methods have been developed to allow isolation and characterization of the various intermediates as well as the kinases and phosphatases that act upon them. From a biologic point of view, considerable information regarding the role of CSF-1 in development may come from analysis of, and attempts to reconstitute, the CSF-1-deficient *op/op* mouse. While providing insights into the physiology of growth factors and their receptors in general, these findings should also provide specific data regarding CSF-1 that will serve as a basis for the development of novel approaches for the management of inflammatory and neoplastic disorders.

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# Lipopolysaccharide Receptors and Signal Transduction Pathways in Mononuclear Phagocytes

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# 1 Introduction

It is generally accepted that bacterial products are among the most potent stimuli leading to the activation of monocytes and macrophages. Of all the bacterial products which have been investigated during the past 50 years, the endotoxic lipopolysaccharides (LPS), derived from gram-negative microorganisms, have become recognized as the microbial activator of choice for many studies. This has, in part, been due to the fact that relatively low concentrations of LPS are required to effect macrophage stimulation. In addition, however, LPS may be obtained in highly purified form and active principle of LPS responsible for biologic activity has been identified and chemically characterized.

There is good experimental evidence from both in vivo and in vitro studies that LPS will elicit in macrophages most of the cellular responses usually attributable to these multifunctional inflammatory cells. In recent years, particular attention has focused upon the capacity of LPS to stimulate macrophages to synthesize and secrete immunologically important cytokines, including interferon- $\alpha/\beta$  (IFN- $\alpha/\beta$ ) (HAVELL and SPITALNY 1983), interleukin-1 (IL-1) (GERY et al. 1972), and cachectin/tumor necrosis factor- $\alpha$  (OLD 1985; AGGARWAL et al. 1985). Evidence has also accumulated which indicates that LPS-stimulated macrophages will release metabolic end products of both the cyclooxygenase and lipoxygenase pathways of arachidonic acid (SCHADE et al. 1987). In addition, LPS is now recognized to modulate the surface expression of macrophage receptors and other markers (HOTER et al. 1987; DING et al. 1989).

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Finally, LPS, either alone or in conjunction with IFN-γ, will stimulate macrophages to a fully activated state in which these cells achieve the capacity to kill tumor cells (ALEXANDER and EVANS 1971; PACE and RUSSELL 1981).

Investigations into the structural components of LPS which contribute to their capacity to stimulate macrophages have, for the most part, centered upon the structurally conserved lipid A region. That isolated, highly purified lipid A can, under the appropriate circumstances, activate macrophages has been well documented (DOE et al. 1978). Further, it has been shown by many investigators that agents such as polymyxin B, which bind the lipid A region of LPS, will inhibit virtually all of the LPS-dependent macrophage responses including synthesis and secretion of cytokines (CHIA et al. 1989), generation of procoagulant activity (NIEMETZ and MORRISON 1977), and macrophage-dependent tumor cell cytotoxicity (DOE et al. 1978). Final proof that lipid A alone can serve as a stimulus for macrophages has come from studies using synthetic lipid A and related structures (KOTANI et al. 1985; LOPPNOW et al. 1989). These latter studies have provided important new clues about structure–function relationship of lipid A-dependent macrophage activation.

The importance of lipid A to LPS-dependent activation of macrophages and monocytes is, therefore, undisputed. What is perhaps less clear is whether mechanisms involved in lipid A activation of these cells using isolated highly purified lipid A can always be extrapolated to results obtained with more intact polysaccharide-containing LPS, and several recently published studies in variety of experimental systems would indicate that this issue is far from resolved. For example, LUDERITZ et al. (1989) have reported major differences in relative amounts of lipoxygenase vs. cyclooxygenase products of arachidonate metabolism following stimulation of murine macrophages with various chemotypes of LPS and/or lipid A. One of the more significant findings of these studies was that stimulation of macrophages with a mixture of purified lipid A and biologically inactive deacylated Re-LPS reproduced results obtained with intact LPS. These studies suggest the provocative concept that, although lipid A may be necessary for LPS stimulation of macrophages, oligosaccharide components of LPS, and more specifically 2-keto-2-deoxyoctulosonic acid (KDO) determinants, may facilitate either the initial interaction or some biochemical signal transductive mechanism. These interesting results might, therefore, suggest the existence of carbohydrate-specific receptors for LPS in addition to lipid A-specific receptors.

Although space limitations preclude a more extensive discussion of this issue, several relevant studies merit comment. OHNO and MORRISON have reported that lysozyme, which binds with high affinity to the lipid A region of LPS (OHNO and MORRISON 1989a), will abrogate the capacity of Re-LPS and lipid A to stimulate murine macrophages to secrete IL-1 (OHNO and MORRISON 1989b); however, no inhibition of Ra-LPS, Rc-LPS was detectable. Similarly, FLEBBE et al. (1990) have demonstrated significant activation of endotoxin-hyporesponsive C3H/HeJ macrophages by R-chemotype LPS even though such cells remain refractory to stimulation with S-LPS or purified lipid A. Curiously, as will be

discussed below, significant differences have also been reported between LPS and lipid A in their capacity to bind to proteins suggested to function as potential receptors for lipid A. Therefore, while the use of purified lipid A as a tool by which to investigate LPS stimulation of macrophages and monocytes has certain advantages, including the investigation of lipid A-specific receptors, it should be recognized that the information obtained may not always be used to extrapolate to LPS-dependent mechanisms of macrophage activation.

In this respect, there is persistent experimental evidence in the scientific literature suggesting that totally lipid A-independent mechanisms also contribute to LPS activation of macrophages. The majority of such studies have documented polysaccharide-dependent activation of macrophages, and different investigators have reported a possible specific role for O antigen-specific carbohydrates as well as more compelling evidence for chemically conserved core oligosaccharide determinants (reviewed in HAEFNER-CAVAILLON 1985a). More recent studies by WRIGHT and colleagues (1989) have, in addition, defined a novel acute phase protein-dependent pathway for LPS activation of macrophages (to be discussed below). Thus, it would appear that multiple mechanisms exist by which LPS may stimulate macrophages, a concept consistent with the complex and diverse chemical structure of these unique microbial products. The initial interactions between LPS and putative macrophage membrane receptors which trigger the activation signal (s), as well as the biochemical nature of the signal (s), may therefore be diverse, and depend on the source of the LPS. We shall, in the following discussion, focus upon the more general lipid A-dependent mechanisms of macrophage activation, while recognizing that there are some important, and as yet not fully understood, differences between the activities manifested by lipid A and LPS, as well as between different LPS preparations. It should be appreciated, therefore, that multiple structural components of LPS, as well as physical-chemical factors which contribute to the formation of different aggregate structures, all may contribute via specific interactions with different membrane receptor components. We shall consequently also briefly discuss the evidence for potential carbohydrate-binding receptors and physical-chemical properties of LPS which may regulate nonspecific membrane interactions.

## 2 Lipopolysaccharide Receptors on Monocytes and Macrophages

It is clear that macrophages are only one of a variety of mammalian cells which can bind and/or be stimulated by LPS and lipid A. There are, as a consequence, a number of published studies which describe evidence for specific LPS receptors on B and T lymphocytes, hepatocytes, polymorphonuclear leukocytes, and even erythrocytes. While it may be compelling, from a conceptual point of view, to postulate a biochemical conservation of LPS receptor molecules expressed on different mammalian cells, and there is at least some experimental evidence to support this concept, this fact has not been established unequivocally. As a consequence, we shall limit our discussion to the current evidence for LPS receptors on macrophages and monocytes. For a discussion of LPS receptors expressed on other mammalian cell types, the reader is referred to several recent review articles (HAEFFNER-CAVAILLON et al. 1985a; MORRISON and RUDBACH 1981; MORRISON 1989; LEI et al. 1990).

Studies of LPS binding to macrophages/monocytes in addition are complicated by the fact that these cells may have the capacity to take up LPS from the surrounding medium by both phagocytosis and pinocytosis, and such contributions to the total LPS-macrophage interactions may complicate efforts to define specific LPS binding. Further, although specific, presumably lipid Adependent binding of LPS to human monocytes has been reported using radiolabeled preparations of LPS, many investigators have reported that binding of LPS to many cell types is nonsaturable (reviewed in MORRISON 1985). In the light of these high levels of nonspecific binding—presumably to the membrane phospholipid bilayer—studies to identify specific LPS receptors have been technically more difficult to perform.

While highly specific and structurally unique receptors for LPS/lipid A may well exist on the macrophage membrane, it is, in addition, clear that several already well-defined macrophage receptors may also function as LPS receptors. For example, both the D-mannose-specific receptor characterized by STEPHENSON and SHEPHERD (1987) and EZEKOWITZ et al. (1988) and the D-galactose-specific receptor defined by Roos et al. (1985) may function to bind LPS preparations in which D-mannose or D-galactose represents a major component of the O antigen-specific carbohydrate. Specific interactions of D-mannose-containing LPS with murine macrophages have, in fact, been demonstrated. Since many LPS preparations do not contain either galactose or mannose as a terminal residue in either the O antigen or core oligosaccharide (LIANG-TAKASAKI et al. 1982), it is unlikely that such carbohydrate-specific binding proteins are the major functional class of LPS receptors responsible for LPS activation of macrophages.

Perhaps the best experimental evidence to support the existence of carbohydrate-specific LPS receptors on macrophages is the work of HAEFFNER-CAVAILLON and his collaborators (HAEFFNER-CAVAILLON et al. 1985b, 1989; LEBBAR et al. 1986). These investigators have explored the binding of *Bordetella pertussis* LPS to rabbit macrophages, and about 8 years ago reported saturable and specific binding to peritoneal macrophages (HAEFFNER-CAVAILLON et al. 1982). It is of interest that similar studies with alveolar macrophages did not yield any detectable specific binding. Of particular importance was the authors' demonstration that binding could be inhibited by a lipid A-free polysaccharide fraction of *B. pertussis* LPS. Binding was not inhibited by *B. pertussis* lipid A, although possible degradation of critical lipid A structures during the chemical isolation procedures precludes definitive conclusions regarding such studies. Additional studies by HAEFFNER-CAVAILLON et al. (1985b) using *B. pertussis* LPS

showed apparently specific binding of this LPS to murine peritoneal macrophages and human monocytes. Again, binding specificity was suggested to reside in the polysaccharide component of the LPS. Of some interest was the fact that LPS binding could be enhanced by serum complement but not by immunoglobulin, albumin, or fibronectin. These results are consistent with the facts that LPS is well recognized as an activator of serum complement (MORRISON and KLINE 1977), and that macrophages and monocytes express a variety of complement receptors (FEARON and WONG 1983).

In more recent studies, the potential polysaccharide-dependent interaction of LPS with human monocytes has been examined. The collective results of these studies have implicated the KDO residues, common carbohydrate components of virtually all gram-negative bacterial LPS, as a potentially relevant structural feature for stimulation of monocytes for IL-1 production (LEBBAR et al. 1986). Chemical dissection of the KDO molecule has revealed that the aldehyde group in the 2-position of the KDO may be an important residue involved in monocyte activation (HAEFFNER-CAVAILLON et al. 1989). These latter studies suggest the potential existence of inner core oligosaccharide, KDO-specific binding sites on the monocyte and are consistent with earlier studies showing enhanced phagocytosis of latex particles covalently conjugated with Re-chemotype LPS relative to untreated particles or particles conjugated with S-LPS (LUBINSKY et al. 1983). There is, however, as yet no direct evidence to support the existence of specific KDO (or other inner core oligosaccharide) receptors on mononuclear phagocytes. Recent studies have suggested that the contribution of KDOdependent interactions relative to those of lipid A/LPS-dependent mononuclear phagocyte activation is not impressive (LOPPNOW et al. 1989); however, the multivalency of structures in LPS aggregates and potential conformational accessibility of various determinants in LPS macromolecular aggregates versus partial structures complicate the interpretation of these results.

Several of the findings of HAEFFNER-CAVAILLON and his co-workers have been confirmed independently by other investigators using different experimental systems. In this respect, perhaps one of the more noteworthy findings of HAEFFNER-CAVAILLON discussed above was the striking differences between rabbit peritoneal macrophages and alveolar macrophages as determined by specific binding of LPS. Examination of equivalent subpopulations of murine macrophages by AKAGAWA and TOKUNAGA (1985) indicated that alveolar macrophages were unresponsive to stimulation by LPS, as assessed by induction of tumor cell cytotoxicity. In contrast, peritoneal macrophages were readily activated by LPS to become tumoricidal. Importantly, when these cells were probed with fluoresceinated LPS to assess LPS binding, more than 90% of either resident or elicited peritoneal macrophages were positive for LPS binding, in comparison to less than 5% of alveolar macrophages. The addition of polymyxin B to cultures, an agent known to bind to the lipid A region of LPS (MORRISON and JACOBS 1976), inhibited LPS binding, suggesting, but not proving, a lipid A dependence of the interaction. This finding contrasts with the earlier studies of HAEFFNER-CAVAILLON et al. (1982). Nevertheless, the fact that

significant differences exist in LPS binding between different subpopulations of macrophages and/or macrophages from different species is of potential importance and should be considered in comparisons of LPS receptor studies. Of potential significance are the observations of AKAGAWA and TOKUNAGA that after treatment of alveolar macrophages with recombinant IFN- $\gamma$  for 20 h, up to 60% of these cells would bind fluoresceinated LPS by a polymyxin B-inhibitable mechanism. These results may suggest that IFN- $\gamma$  can up-regulate the expression of LPS receptors. However, in view of the well-recognized capacity of LPS to interact nonspecifically with cells, it is possible that IFN- $\gamma$  treatment simply alters macrophage membrane fluidity such that nonspecific binding of the LPS probe is markedly increased.

In more recent studies AkaGawa and her colleagues reported that macrophage colonies generated by alveolar macrophages in response to colony stimulating factor 1 also contained more than 90% FITC-LPS binding cells (AkaGawa et al. 1988). Using a somewhat similar approach, ERROI and his colleagues showed that certain tumor-associated macrophages (TAMs), isolated from a murine tumor which was poorly immunogenic in vivo, were unresponsive to LPS as assessed by activation for the production of procoagulant activity. The authors also demonstrated that these TAMs contained only 6% LPS positive cells as determined by fluorescence, whereas more than 80% of resident peritoneal macrophages were positive for the FITC-LPS (ERROI et al. 1988). Although these experimental results provide some evidence for specific binding of LPS to macrophages/monocytes, the membrane surface macromolecule(s) responsible for LPS binding, which would presumably be an LPS receptor(s), has not yet been established.

A second point which arises from the studies of HAEFFNER-CAVAILLON et al. relates to the interrelationship between complement and LPS in the activation of mononuclear phagocytes. Since LPS is well recognized as an activator of serum complement (MORRISON and KLINE 1977) and since these cells both secrete complement components (NATHAN 1987) and express complement receptors (FEARON and WONG 1983), an activation pathway which depends upon these factors was proposed many years ago by DIERICH et al. (1973). Indeed, there is good experimental evidence that LPS will initiate the enhanced secretion of complement components, particularly C3, from both human monocytes (STRUNK et al. 1985) and murine macrophages (GOODRUM 1987). However, an obligate role for complement components in LPS-dependent activation has not yet been established.

Studies by WRIGHT and his colleagues have, on the other hand, provided rather convincing evidence for a role for complement receptors as potential targets in LPS stimulation of human monocytes. Using LPS bound to erythrocytes, these authors showed that a monoclonal antibody with specificity for the CD11/18 surface complement receptor antigen (CR3) on human monocytes inhibited binding of LPS-coated erythrocytes (WRIGHT and JONG 1986). Further, depletion of surface expression of CD11/18 by monoclonal antibody-dependent capping abrogated LPS-erythrocyte binding, whereas

depletion of a variety of other surface antigens defined by a panel of monoclonal antibodies had no detectable effect. Additional studies to explore the specificity of this interaction suggested that the LPS binding site on CD11/18 was distinct from the C3bi binding site characterized by the Arg-Gly-Asp peptide (WRIGHT and LEVIN 1989).

While these studies clearly establish a solid relationship between the expression of CD11/18 surface receptors and binding of LPS-coated particles, more recent studies by WRIGHT and his colleagues have cast strong doubts on the obligate expression of these receptors for LPS-dependent human monocyte activation (WRIGHT et al. 1990). In these more recent studies, mononuclear cells from a number of patients genetically deficient in CD11/18 were shown to manifest in vitro cellular responses to isolated LPS indistinguishable from those of monocytes obtained from normal human volunteers; however, responses of these cells to LPS-erythrocytes was not investigated. Thus, whereas CD11/18 may contribute to the mononuclear phagocyte response to particulate LPS, it would appear not to be essential in order to achieve stimulation. It would be of interest to compare the relative efficacy of erythrocyte-bound LPS versus soluble LPS in initiating LPS-dependent monocyte responses, since the possibility of different LPS molecular forms mediating distinct responses via interactions with different surface structures remains an interesting possibility. Moreover, the question of whether monoclonal antibody to CD11/18 would either block or mimic LPS activation of these cells by either soluble or particulate preparations of LPS would be an interesting question to pursue.

Recent experiments published by TOBIAS et al. (1986) have shown that LPS will complex with a specific LPS-binding acute phase protein. Further studies by these authors have established that the induction of inflammatory responses in vivo results in the rapid synthesis of this acute phase protein, which binds with high affinity to all chemotypes of LPS (TOBIAS et al. 1989) Interestingly, this acute phase protein, termed LPS-binding protein (LBP), shares remarkable sequence homology (TOBIAS et al. 1988) with a neutrophil granule protein characterized previously by WEISS, ELSBACH, and their colleagues (1978) for its capacity to increase bacterial permeability (BPI) via interactions with LPS on the microbial surface. Of particular importance with respect to LPS-macrophage interactions, WRIGHT et al. have shown that complexes of LPS and LBP, but not LPS and BPI, will interact with human monocytes via specific binding to the CD14 molecule. These authors have further shown that CD14 binding requires the LPS-LBP complex and that high affinity binding of either component alone could not be demonstrated. This novel interaction of LPS with LBP and CD14 may be of considerable importance in the overall host response to endotoxin; however, the question as to whether CD14 serves an obligate receptor function for LPSdependent monocyte activation remains to be established. In this respect, it is clear that LPS can activate mononuclear phagocytes in the absence of LBP and thus, it can be concluded that the CD14-dependent pathway may not be essential for LPS interaction with and stimulation of macrophages and monocytes. It is possible, in this respect, that LBP, by complexing with LPS. passively focuses these complexes on the monocyte surface via interactions with CD14, where it then interacts with specific LPS/lipid A receptors. Again, the question of whether antibody to CD14 will either mimic or inhibit the effects of LPS on monocytes would appear relevant.

Probably the dominant issue within the framework of LPS interactions with mononuclear phagocytes as it relates to fundamental mechanisms of LPSinitiated host responses, is the identity of LPS/lipid A-specific receptors expressed on these cells. Although this has proven a difficult experimental problem, recent evidence from several laboratories has suggested that lipid Aspecific binding proteins can, in fact, be identified on mononuclear phagocytes and lymphocytes and that at least one of these may serve as a true receptor in the activation of these cells. While from a historical perspective, the earliest studies to define LPS receptors focused upon the latter cells, we will, as indicated earlier, restrict our comments to a review of macrophage receptors for LPS/lipid A. It is, of course, conceivable that more than one specific receptor may exist for LPS/lipid A and there is at least one suggestion in the scientific literature that lymphocyte receptors for LPS may be different than those on macrophages (JAKWAY and DEFRANCO 1985). Finally, the potential contribution of hydrophobic interactions of LPS with the membrane lipid bilayer as a necessary prerequisite to effective lipid A-receptor interactions remains as a potentially significant factor in LPS activation of macrophages and will be briefly discussed.

Early experiments yielding evidence that specific LPS binding sites might exist on human peripheral blood monocytes were carried out by LARSEN and SULLIVAN (1984a). These investigators used tritiated LPS to show that the binding of LPS to human monocytes was specific and saturable. The binding of radiolabeled LPS to human monocytes firstly involved a rapid, reversible, temperature-independent surface adsorption. Then there was a slower, irreversible, temperature-dependent uptake of radiolabeled LPS by the monocytes. Interestingly, the LPS-binding sites appeared to be decreased when monocytes were pretreated with an appropriate concentration of unlabeled LPS, suggesting competitive binding. In an accompanying report (LARSEN and SULLIVAN 1984b), the authors tested the binding of the same radiolabeled LPS to Percoll density gradient-isolated monocyte membranes. They reported that the binding of LPS to isolated membranes was considerably lower than binding to viable monocytes. The authors concluded that, besides the presence of specific surface receptor(s), "precise spatial arrangements and structural interrelationships of phospholipids and proteins as well as the surface charge distribution, the surface area, and the resting membrane potential of the cell are factors which may dictate membrane interactions with these macromolecules by directly affecting hydrophobic and ionic associations between endotoxin molecules and the cell membrane which are necessary for effective binding." This interesting hypothesis, although yet to be established unequivocally, receives at least indirect support through the well-established capacity of LPS to interact with membrane bilayers (reviewed in MORRISON 1985).
A different experimental approach taken by HAMPTON and his colleagues to investigate the existence of specific receptors for LPS was predicated upon fact that a lipid A precursor (lipid IVa) can be obtained in radiolabeled form with high specific radioactivity and can be used to probe solubilized extracts of a macrophage cell line, RAW264.7. HAMPTON et al. (1988) fractionated solubilized cell extracts by gel electrophoresis and transferred the fractionated extracts to nitrocellulose by electroblotting. When blots were subsequently probed with <sup>32</sup>plipid IVa, two major lipid IVa-binding proteins of approximately 95 kDa and 31 kDa were identified by autoradiography. A weaker lipid IVa-binding protein of approximately 80 kDa was also apparent in the published autoradiographs of these experiments but was not commented on by the authors. HAMPTON et al. stated that the binding of <sup>32</sup>p-lipid IVa to these proteins could be inhibited both by intact lipid A and by Re-chemotype LPS, suggesting that the binding specificity was for the lipid A. However, the binding of lipid IVa could not be inhibited by intact polysaccharide-containing LPS, although a number of factors, including the potential role for membrane phospholipids suggested above, could contribute to this observation. The authors suggested that the 30-kDa LPSbinding protein is most likely a nuclear histone, but that the 96-kDa protein may serve as a candidate LPS receptor. Experimental evidence that this 96-kDa protein may function as an LPS receptor has derived from studies showing saturable binding of lipid IVa to the macrophage cell line which is inhibited by Re-LPS and lipid A but not by unrelated phospholipids (RAETZ et al. 1988).

An alternative experimental approach, taken by MORRISON and co-workers, was to synthesize photoactivatable, radioiodinated LPS derivatives with which to probe LPS-binding sites on target cells. WOLLENWEBER and MORRISON (1985) established that the derivatized LPS behaved indistinguishably from native LPS in respect of a number of LPS biologic activities in vitro. Using this methodology, fractionation of LPS-photocrosslinked, reduced and solubilized mouse macrophage extracts on two-dimensional polyacrylamide gels allowed LEI and MORRISON (1988a) to identify an LPS-binding protein with an approximate pl of 6.5 and a molecular mass of approximately 80 kDa.

It appeared that the LPS-binding protein fractionated from mouse macrophages was indistinguishable from that fractionated from mouse lymphocytes as defined by mobility of this protein on two-dimensional polyacrylamide gels. The extension of these experimental protocols to peripheral blood mononuclear cells of a variety of mammalian species established that, as assessed by electrophoretic mobility on two-dimensional polyacrylamide gels, the 80-kDa LPS-binding protein was relatively highly conserved (ROEDER et al. 1989). Evidence in support of this 80-kDa protein serving as a potential receptor for LPS was provided by the facts that the protein was membrane localized and that binding of LPS was saturable and inhibited by underivatized homologous and heterologous LPS and by lipid A (LEI and MORRISON 1988b). Binding was not inhibited by a variety of peptidoglycans even at 100-fold excess by weight (unpublished observations). Binding was dependent upon both the time and the temperature of incubation, with maximal binding observed after 15 min at 37  $^{\circ}\text{C}.$ 

More recently, CHEN et al. (1989) have described a purification strategy to obtain the 80-kDa LPS-binding protein in partially purified form from C3Heb/FeJ splenocytes using photoaffinity labeling, butanol extraction, preparative SDS polyacrylamide gel electrophoresis, and electroelution. Using this partially purified 80-kDa protein as antigen, BRIGHT and his colleagues (1990) developed a panel of Armenian hamster monoclonal antibodies which react with the partially purified 80-kDa protein. Extensive characterization of one such monoclonal antibody (MoAb5D3) showed binding specificity for highly purified 80-kDa protein, as assessed by ELISA. Competitive binding assays have established that LPS and MoAb5D3 will reciprocally compete for binding to 80-kDa protein on intact cells, although MoAb5D3 more readily inhibits LPS binding than vice versa.

An evaluation of the functional properties of MoAb5D3 has recently provided evidence that this 80-kDa protein may function as an LPS receptor on the mouse macrophage surface. Using MoAb5D3 as the ligand, CHEN and his colleagues (1990) demonstrated that the addition of ion exchange columnpurified MoAb5D3 to cultures of bone marrow-derived C3H/HeN macrophages led to activation of these cells for tumor cell killing. In contrast, this antibody failed to activate macrophages from the C3H/HeJ mouse even though quantitative ELISA established equivalent binding of MoAb to these two cell populations. The fact that the activity of MoAb5D3 was heat labile and was not inhibited by polymyxin B suggested that the observed agonist activity was not the result of endotoxin contamination. In addition, significantly lower concentrations of MoAb5D3 were required to effect equivalent macrophage activation in the presence of IFN-y. This is consistent with the previously defined role of IFN-y as a "priming" signal and LPS as a "triggering" signal (PACE and RUSSELL 1981). These experimental results suggest that the 80-kDa membrane protein recognized by MoAb5D3 may be at least one of the entities through which activation for tumor cell killing is regulated by LPS. These studies also suggest that the LPS-like effect on macrophage activation may occur in the absence of potential secondary nonspecific hydrophobic interactions with the membrane bilayer. Although nonspecific interactions of this particular monoclonal antibody with the macrophage membrane cannot be formally excluded, this possibility is unlikely.

A very recent report by HARA-KUGE and collaborators (1990) has described an interesting and potentially important experimental approach for the identification of LPS receptors. These investigators have identified and characterized a mutant cell line from the murine J774 macrophage parental cell line which is phenotypically unresponsive to LPS stimulation. Examination of LPS-binding proteins by photoaffinity LPS crosslinking probes similar to those used by LEI and MORRISON (1988a) identified two proteins with molecular masses of approximately 65 kDa and 55 kDa on the parent cell line which were not detectable on the LPS-unresponsive mutant. These data provide provocative evidence for a role for one or both of these proteins in LPS responses. It is possible that the 65-kDa protein identified by HARA-KUGE and colleagues and the 80-kDa protein characterized by LEI and MORRISON are identical, given that the LPS and photocrosslinking probe used in the two studies were identical; the differences in apparent molecular weight might have been due to differences in gel electrophoresis conditions. Experiments to determine whether this is the case are currently underway between the two laboratories. Very preliminary results (unpublished) suggest that MoAb5D3 will inhibit binding of photolabeled LPS to both the 65-kDa and the 55-kDa macrophage LPS-binding proteins.

Collectively, these results indicate that one or more specific glycoproteins may be present on the membrane surface of mononuclear phagocytes which can function as specific binding sites and/or receptors for LPS or lipid A. There is also evidence to suggest that specific membrane-localized gangliosides may also function either directly as target binding sites for LPS or as accessory targets in modulating LPS responsiveness. As reported by MORRISON et al. (1985), LPS will form molecular complexes with a variety of purified gangliosides via interactions primarily with the lipid A region. Several investigators have reported that specific gangliosides will modulate LPS responsiveness in cultures of mouse macrophages, and recent studies by Ryan and co-workers have reported that only selected gangliosides on the macrophage membrane will bind LPS (J. RYAN, personal communication, 1990). It is also noteworthy that marked changes in macrophage ganglioside profiles are obtained upon stimulation with LPS (BERENSON et al. 1989). The precise relationship between ganglioside-LPS interactions and macrophage activation, and the potential role of these membrane-localized gangliosides as receptors, remain to be defined.

## **3** Biochemical Mechanisms of Macrophage Signal Transduction by LPS

Despite recent intensive studies by a number of laboratories, the LPS-triggered biochemical sequence of events leading to tumoricidal activation of macrophages remains to be fully defined. The problem arises mainly from the ambiguity as to whether any or all of the LPS-induced events studied in the macrophage actually serve as the primary inducer of macrophage activation or represent secondary processes. We will therefore briefly review and discuss the recent progress in studies of LPS-induced signal transduction pathways, which suggest probable involvement of guanine nucleotide-binding (G) protein, myristoyl transferase, phospholipase C (PLC), and protein kinase C (PKC) in macrophage activation.

The probable involvement of pertussis toxin-sensitive Gi protein, which inhibits adenylate cyclase, in mediating the effects of LPS on a mouse macrophage cell line was first demonstrated by JAKWAY and DEFRANCO (1986). Several lines of experimental evidence supporting this conclusion include: (a)

inhibition of macrophage membrane adenylate cyclase by LPS; (b) abrogation of this inhibition by prior treatment of the cells with pertussis toxin, which inactivates Gi function by ADP-ribosylation of the Gia subunit; (c) inhibition of ADP-ribosylation of Gi $\alpha$  by prior treatment of macrophage cell membranes with LPS; and (d) inhibition of LPS-induced membrane-associated IL-1 production. Collectively, these data suggest that the ability of LPS to activate Gi protein may be crucial for its ability to regulate these cells. More recently, DANIEL-ISSAKANI et al. (1989) suggested that the LPS response of phorbol myristate acetate (PMA)pretreated U937 cells is linked to a specific pertussis toxin-sensitive G protein which was tentatively identified as Gi<sub>2</sub>. However, it is recognized that pertussis toxin will inhibit not only adenylate cyclase-coupled Gi protein, but also other members of the G protein family which may be involved in the regulation of ion channels of neural cells (PFAFFINGER et al. 1985), histamine release by mast cells (NAKAMURA and UI 1985), and migration and lysosomal enzyme release from neutrophils (SMITH et al. 1985) and macrophages (BACKLUND et al. 1985). Since mast cells, neutrophils, and macrophages have been shown to respond to these stimuli by activation of PLC rather than adenylate cyclase, pertussis toxin could have modulated the function of a PLC-coupled G protein (BERRIDGE 1987).

In addition to these potential concerns, if adenylate cyclase-coupled Gi protein were to be the initial target of LPS action, then it would be predicted that LPS should regulate intracellular cAMP levels. However, there is no unequivocal evidence that the critical action of LPS involves regulation of cAMP levels. Furthermore, the specific mechanism by which LPS might modulate the function of G proteins is also unclear. In this regard, the suggestion by DANIEL-ISSAKANI et al. (1989) that LPS may activate a macrophage protein kinase which, in turn, might then phosphorylate  $Gi_2$ , is interesting, particularly in the light of several recent reports suggesting activation of macrophage PKC in response to LPS (described below). An interesting possibility that one of the LPS receptors discussed in the preceding paragraphs may be directly coupled to a  $Gi_2$  protein warrants further investigation. Such studies would clarify the interpretation of the observed inhibitory action of pertussis toxin, since it is possible that phosphorylation of  $Gi_2$  may result in the dissociation of  $Gi_2$  from the putative LPS receptor and thus render the latter sensitive to pertussis toxin.

Another early biochemical event that follows LPS stimulation of macrophages is probable activation of myristoyl transferase, which catalyzes myristoylation of proteins of 68 and 36–42-kDa (ADEREM 1988). This myristoylation appears to play an important role in subsequent arachidonate metabolic cascade triggered by other stimuli. The LPS-stimulated 68-kDa protein translocates from cytosol to membrane, where it may be phosphorylated by PKC (ADEREM et al. 1988). However, the exact role of this 68-kDa protein in signal transduction is unknown at present.

Several studies have recently suggested that LPS-triggered activation of phosphoinositide (PI)-specific PLC may be an early, critical biochemical event during LPS-triggered macrophage activation. Evidence that the treatment of

mouse peritoneal macrophages with LPS or lipid A promptly leads to activation of PI-specific PLC, which is accompanied by Ca<sup>2+</sup> fluxes and activation of PKC, has been presented by PRPIC et al. (1987). In these studies, the activation of PLC, as measured by the formation of inositol triphosphate (IP<sub>3</sub>), was rapid but rather modest in magnitude. The IP<sub>3</sub> formed in response to LPS was found to plateau within 1 min of stimulation, with a maximal change of about 130% from the time zero value. Significant PLC activation was shown to require relatively large doses (>1µg/ml) of LPS or lipid A.

Using two macrophage cell lines, J774 and P388D<sub>1</sub>, CHANG et al. (1990) partly confirmed the findings of PRPIC et al. (1987) by showing LPS-induced formation of IP<sub>3</sub> in both cell lines. The time required for maximal response of J774 cells was about 5 min, whereas that for P388D<sub>1</sub> cells was about 20 min. The degree of the maximal response was again modest (maximal response being about 130% of the control) and the dose of LPS required for significant PLC activation was more than 1 $\mu$ g/ml. It is of interest that only the J774 cell line responded to LPS by becoming activated for tumor cell killing; however as discussed below, the relevance of this information to the above-cited differences in the kinetics of IP<sub>3</sub> formation is unclear.

Thus, the data from several laboratories have shown that LPS treatment of macrophages can result in modest activation of PI-specific PLC within 1–20 min. However, a critical question remains as to whether or not LPS-triggered activation of PLC is a primary inducer for tumoricidal activation of macrophages. Addressing this question, CHANG et al. (1990) reported that the treatment of macrophages with neomycin (SCHNACHT 1976) inhibited LPS-triggered PLC activity of LPS-activated J774 cells, but failed to block LPS-induced tumoricidal activation of the cells. In addition, GRABAREK et al. (1988) recently showed that lipid A may activate PKC in platelets, without concomitant activation of PLC. These results suggest that LPS-triggered activation of PLC may not be an obligatory cellular event in response to LPS or lipid A.

Lipopolysaccharide-stimulated activation of PLC should result in production of two different second messengers, namely 1,2-diacylglycerol (DAG) and IP<sub>3</sub> (PRPIC et al. 1987; CHANG et al. 1990). DAG and Ca<sup>2+</sup> released from intracellular stores by the action of IP<sub>3</sub> would activate PKC. WEIEL et al. (1986) earlier suggested probable activation of PKC following stimulation of mouse macrophages by LPS, based upon the similarity of the LPS-induced phosphorylation pattern of cellular proteins to that induced by the well-characterized PKC activator, PMA. PKC-catalyzed phosphorylation of cellular proteins could lead to the modulation of gene expression of macrophages, which is probably essential for LPS-induced development of tumoricidal activity. In this regard, it is interesting to note that some investigators have reported that tumoricidal activation of macrophages induced by either IFN- $\gamma$  or IFN- $\beta$  could be blocked by inhibitors of PKC, such as H-7 (CELADA and SCHREIBER 1986; RADIOCH and VARESIO 19; HAMILTON et al. 1985) (although it should also be noted that there were some discrepancies in the reported results). However, the basic question of the mechanism by which LPS interaction with the macrophage leads to activation of

PKC remains unanswered. In considering this question, we will first briefly review the known properties of PKC and calpain.

Protein Kinase C has been shown to be involved in a wide variety of cellular functions, such as secretion and exocytosis, modulation of ion conductance, regulation of receptor interaction with components of the signal transduction apparatus, smooth muscle contraction, gene expression, and cell proliferation (NISHIZUKA 1986). The PKC enzymes in various tissues are recognized to be polymorphic, and at least seven isoenzymes, denoted as  $\alpha$ ,  $\beta$  and  $\beta$ III,  $\gamma$ ,  $\delta$ ,  $\varepsilon$ , and  $\xi$  have so far been identified (PARKER et al. 1986; NISHIZUKA 1988). The genes encoding these isoenzymes manifest a great degree of sequence homology, not only among themselves, but also with many other protein kinases. The Nterminal half of the single chain 80-kDa PKC is considered to be the regulatory domain. It contains two highly conserved regions, termed C1 and C2, and two highly variable regions,  $v_1$  and  $v_2$ . The C<sub>1</sub> region contains a tandem repeat of a cysteine-rich sequencem, C-X<sub>2</sub>-C-X<sub>13</sub>-C-X<sub>2</sub>-C, which is reminiscent of the cysteine-zinc-DNA-binding finger found in many metalloproteins and DNAbinding proteins related to transcriptional regulation, although there is no evidence that PKC binds DNA. The sites involved in binding of PKC regulatory molecules, such as Ca<sup>2+</sup>, 1,2-DAG, and phosphatidylserine, are thought to be contained in C<sub>1</sub> and C<sub>2</sub>, but have not yet been identified with certainty. The Cterminal half of the enzyme contains two conserved regions, C<sub>3</sub> and C<sub>4</sub>, and is considered to contain the catalytic domain. The conserved region C<sub>3</sub> has an ATP-binding sequence, Gly-X-Gly-X<sub>2</sub>-Gly, which marks the beginning of the kinase domain. A second ATP-binding site may be present in the conserved regions  $C_4$  with the consensus sequence. The site which is susceptible to the Ca<sup>2+</sup>-dependent neutral protease, calpain (SUZUKI et al. 1987; KISHIMOTO et al. 1989), has been shown to be within the  $V_3$  region which separates the regulatory and the catalytic domains.

The properties of PKC present in mouse macrophages have not yet been fully characterized. The LPS-mediated activation of PLC discussed above, which results in the generation of DAG and IP<sub>3</sub>, should lead to the activation of PKC. Since the pretreatment of J774 cells with either H-7 or PMA clearly blocked LPSinduced cytotoxicity in a dose- dependent manner (NOVOTNEY et al. 1990), LPSinduced activation of PKC may well be a critical step in tumoricidal activation, as already suggested for IFN- $\gamma$ - or - $\beta$ -induced macrophage activation (CELADA and SCHREIBER 1986; RADIOCH and VARIESO 1988). The critical questions are whether LPS activates macrophage PKC only through the generation of DAG and IP<sub>3</sub>, or also by some alternative pathway which involves the calpain/calpastatin system. NOVOTNEY et al. (1991) have recently presented evidence that certain types of PKC in LPS-activatable J774 cells undergo proteolytic cleavage which results in production of a 40-kDa regulatory domain fragment. This fragment could be recognized in Western blots of two-dimensional gels by specific rabbit anti-PKC regulatory domain serum (JAKWAY and DE FRANCO 1986). No proteolytic cleavage in response to LPS was observed in  $P388D_1$  cells (see above). The cytosol of J774 cells was found clearly to contain two types of protein kinase (one basic and the

other acidic) which were readily separable by HPLC. In contrast, the cytosol of P388D, cells was found to contain only one protein kinase, corresponding to the basic fraction of J774 cells. The acidic protein kinase, which is present in only J774 cells, may represent the catalytic domain fragment, because it bound the radiolabeled PKC-specific inhibitor [<sup>3</sup>H]staurosporine, and because its activity did not appear to be augmented by phosphatidyserine, diolein, and Ca<sup>2+</sup>. These data thus suggested that LPS treatment of macrophages may activate PKC by two distinct pathways: (a) via a classic DAG- IP<sub>3</sub>-mediated pathway which occurs in both LPS-activatable and LPS-nonactivatable cell lines; and (b) via the activation of Ca<sup>2+</sup>-dependent neutral protease (calpain) in LPS-activatable cells, which cleaves PKC to generate a catalytic domain fragment (denoted as PKM), the activity of which does not require regulatory molecules such as DAG, Ca<sup>2+</sup>, and phospholipid. The lack of generation of a 40-kDa protein recognizable by antiregulatory domain antibody in LPS-nonactivatable P388D<sub>1</sub> cells might be due to structural alteration of the V<sub>3</sub> region of PKC, which renders PKC resistant to the action of calpain. Although there is no direct evidence at present to indicate that LPS activates calpain, it is interesting to consider this as a possible pathway.

Calpain consists of two subunits, an 80-kDa and a 30-kDa protein (EMORI et al. 1986a, b). Upon autolysis, the 80-kDa calpain subunit is converted to the protease-active 76- to 78-kDa protein. In addition, calpain has been shown to be able to associate with plasma membranes through an N-terminal, glycine-rich hydrophobic domain of the 30-kDa subunit, which has been shown to interact with phospholipids and biologic membranes (IMAJOH et al. 1986) as well as galactosyl residue-containing polysaccharide (ZIMMERMAN and SCHLAEPFER 1988). LPS is expected to interact with membranes through its hydrophobic lipid A moiety and there is now good evidence for LPS binding to at least one membrane-localized 80-kDa receptor protein perhaps either related to, or identical with, the 80-kDa subunit of calpain. This interaction may facilitate the binding of LPS, through its polysaccharide component, with the N-terminal regulatory domain of the 30-kDa subunit, which, together with the 80-kDa subunit, is associated with the inner side of the plasma membrane. The interaction between the 30-kDa calpain subunit and LPS may then promote autolysis of the 80-kDa subunit to produce the proteolytically active 76- to 78kDa calpain fragment. This type of calpain activation was observed by ZIMMERMAN and SCHLAEPFER (1988) during the binding of calpain to agarose matrix.

Evidence that calpain may regulate the activity of PKC has been presented by many laboratories (TAPLEY and MURRAY 1985; MURRAY et al. 1987). Incubation of platelets or neutrophils with PMA was shown to result in the formation of a 50kDa protein kinase (PKM), active in the absence of added Ca<sup>2+</sup> and phospholipid, which eluted from DE52 cellulose at a higher salt concentration than PKC. Formation of this kinase was blocked by preincubation of permeabilized platelets with leupeptin, a calpain inhibitor (CELADA and SCHREIBER 1986). In addition, the patterns of phosphorylation of myosin light chain catalyzed by either PKC or PKM were basically identical. As described above, purified PKC could be cleaved at its V<sub>3</sub> region by the purified calpain (NISHIZUKA 1988; SUZUKI et al. 1987). The cleavage of PKC to PKM by calpain frees it from its regulatory constraint and releases active kinase (PKM) into the cytosol. Thus, PKM should have access to a different range of substrates than membranebound PKC. However, the questions remain as to whether or not: (a) LPS actually activates calpain by interacting with either type of calpain subunit and leads to the generation of PKM; and (b) the photoaffinity-labeled 80-kDa LPS-binding protein represents the 80-kDa calpain subunit.

## **4 Summary and Conclusions**

There is little question but that bacterial lipopolysaccharides (LPS) remain one of the most potent stimuli which can affect macrophage activation. Although the precise biochemical mechanisms responsible for this remain to be fully defined, there is now evidence accumulating from a number of laboratories that functional receptors for these bacterial products do exist and may contribute to the initial triggering event. Unfortunately, there is currently no consensus as to which of the candidate receptors identified to date serves as the primary binding target for LPS, and it is possible that the difference in macrophage cell types, LPS probes, and detection systems will all influence the nature of the binding. At the present time, therefore, macromolecules of 96-kDa, 95-kDa (adhesion  $\beta$  chain), 80-kDa, 65-kDa, and 55-kDa may be considered as possible LPS targets. With the exception of the 96-kDa protein identified by HAMPTON and his co-workers, there exists some experimental evidence for a functional role for each of the molecules so far identified. It is apparent that the molecular cloning and sequencing and subsequent biochemical characterization of these LPS receptors will be required to determine unequivocally their role in LPS-mediated triggering events. Such information will be invaluable in sorting out the relevant biochemical second signals involved in macrophage activation. Although much new information has recently been accumulated on potential signaling pathways for LPS, the definitive events remain far from unequivocally established. In view of the obvious importance of LPS-macrophage interactions in the overall capacity of the mammalian host to respond appropriately to the potentially hostile prokaryotic environment, a precise delineation of LPS-mediated macrophage activation is critical to our understanding of this important inflammatory mediator cell.

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# The Role of Myristoylated Protein Kinase C Substrates in Intracellular Signaling Pathways in Macrophages

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## **1 Introduction**

The protein kinases C (PKC) are a family of diacylglycerol-activated, calciumdependent protein kinases that regulate diverse cellular pathways in macrophages, including those leading to phagocytosis and the secretion of arachidonic acid metabolites and reactive oxygen intermediates (KIKKAWA et al. 1989; ADEREM 1988; CLARK 1990). Very little is known about the molecular mechanism by which PKC mediates such diverse responses. It is known,

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however, that PKC-mediated events in macrophages are profoundly influenced by inflammatory mediators such as bacterial lipopolysaccharide (LPS) and by cytokines such as gamma-interferon (IFN- $\gamma$ ) and tumor necrosis factor (TNF- $\alpha$ ) (HAMILTON and ADAMS 1987). Thus, while LPS alone is incapable of activating PKC, it can prime macrophages for vastly increased PKC-dependent responses such as the release of eicosanoids and prostanoids (ADEREM et al. 1986a, ADEREM and COHN 1988). Concomitant with priming, LPS also induces the transcription, translation, and myristoylation of three macrophage proteins with apparent molecular masses of 40, 42, and 68 kDa (ADEREM et al. 1986b, 1988a). All three proteins are substrates for PKC and are therefore excellent candidate effectors of PKC-induced responses. In addition, we have characterized a 48-kDa myristoylated PKC substrate which is induced in macrophages by IFN- $\gamma$  and which appears likely to mediate some of the responses of this macrophage-activating cytokine (ADEREM et al. 1988b).

This chapter will focus primarily on the properties of the 68-kDa and 48-kDa myristoylated PKC substrates, which are likely to act as effectors of PKC-dependent responses in macrophages. I will also include recent information on protein myristoylation which will situate the discussion in a broader context.

# **2** Protein N-Myristoylation

In all cases described, N-myristoylation of proteins occurs via an amide linkage to the  $\alpha$ -amino group of an N-terminal glycine (SCHMIDT 1989; SCHULTZ et al. 1988; TOWLER et al. 1988). N-myristoylation occurs cotranslationally or very soon after the completion of polypeptide synthesis, as demonstrated by the incorporation of myristic acid into nascent peptides, and blockage of this process by protein synthesis inhibitors (WILCOX et al. 1987; OLSON and SPIZZ 1986). The precise function of protein-bound myristic acid is not fully understood. In some cases it is required to target proteins to the plasma membrane, but myristoylated proteins are also found in the cytosol, endoplasmic reticulum, and nucleus (SCHULTZ et al. 1985; BUSS and SEFTON 1985; TOWLER et al. 1988; SCHMIDT 1989). The diversity of proteins known to be myristoylated suggests a number of possibilities regarding the functional role of this modification. The list of myristoylated proteins includes several known to be involved in intracellular signaling pathways, such as the tyrosine kinases p60<sup>src</sup> (SCHULTZ et al. 1985; BUSS and SEFTON 1985) and p56<sup>lck</sup> (MARCHILDON et al. 1984), the catalytic subunit of cAMP-dependent protein kinase (CARR et al. 1982), the regulatory subunit of protein phosphatase 2B (AITKEN et al. 1982), a prominent protein kinase C substrate (ADEREM et al. 1988a) (which will be the major focus of this review), and the G-proteins (BUSS et al. 1987; SCHULTZ et al. 1987). A number of viral proteins are also myristoylated and in most cases, this modification is required for membrane attachment and for an intact replication cycle (TowLER et al. 1988; SCHULTZ et al. 1988; SCHMIDT 1989).

#### 2.1 Enzymology

The acylation reaction is catalyzed by a myristoyl CoA: protein *N*-myristoyl transferase (NMT) which utilizes myristoyl CoA exclusively (TOWLER et al. 1988). An NMT has been purified and cloned from *Saccharomyces cerevisiae* (TOWLER et al. 1987; DURONIO et al. 1989). It exhibits a high degree of selectivity for the sequence of its substrate peptide, and a loose consensus sequence required for effective myristoylation has been elucidated (TOWLER et al. 1988).

#### 2.2 Regulation

There are a number of potential points of regulation of N-myristoylation. First, since acylation occurs cotranslationally or very soon after the completion of polypeptide synthesis (WILCOX et al. 1987), and since all cells examined contain active NMT, the transcription and translation of the candidate protein may directly regulate its N-myristoylation. Second, since the initiator methionine must first be removed by an *N*-methionine aminopeptidase to expose the acceptor glycine, this peptidase could potentially regulate N-myristoylation. Third, the activity or subcellular location of the NMT might be regulated. Thus, certain proteins bearing a myristoylation consensus sequence might be translated on ribosomes that are not in the proximity of the NMT. In this context it is interesting to note that a subset of G-proteins contains the N-terminal glycine but is not myristoylated (MUMBY et al. 1990; JONES et al. 1990). Finally, although all known N-myristoylated proteins that have been sequenced bear a glycine after the initiator methionine, it is possible that proteins could be acylated at a cryptic site exposed by proteolytic cleavage.

Lipopolysaccharide and IFN- $\gamma$  treatment of macrophages does not greatly influence NMT activity, and the increased levels of myristoylated PKC substrates observed in response to LPS and IFN- $\gamma$  are due to the cotranslational myristoylation of LPS- and IFN- $\gamma$ -induced gene products (J. SEYKORA and A. ADEREM, unpublished observations).

# 3 The Myristoylated, Alanine-Rich C Kinase Substrate (MARCKS)

The 68-kDa protein whose synthesis and myristoylation is induced by LPS proved to be an acidic PKC substrate which is the murine macrophage homologue of the 80- to 87-kDa PKC substrate. The protein was first described as an 87-kDa protein in rat brain synaptosomes, where it was found to be phosphorylated in response to phorbol esters and potassium depolarization (WU et al. 1982; ALBERT et al. 1987; PATEL and KLIGMAN 1987). In fibroblasts, where

it is called the 80-kDa protein, it is the major protein phosphorylated when the cells are treated with growth factors or with phorbol esters (ROZENGURT et al. 1983; BLACKSHEAR et al. 1986). Indeed, the 68- to 87-kDa protein is so ubiquitously distributed that its phosphorylation is synonymous with PKC activation, and its phosphorylation has been used as an assay for the intracellular activation of the kinase. The protein was first shown to be myristoylated in macrophages (ADEREM et al. 1988a) and this observation has been confirmed in a variety of cell types (JAMES and OLSON 1989; THELEN et al. 1990). This modification, together with its high proportion of alanine, led to the acronym MARCKS (for *m*yristoylated, *a*lanine- *r*ich *C k*inase *s*ubstrate) (STUMPO et al. 1989).

## 3.1 Primary Structure of MARCKS

The murine macrophage MARCKS gene encodes a 309 amino acid protein with a calculated molecular mass of 29.6 kDa and a theoretical pl of 4.1 (SEYKORA et al. 1991). The calculated pl is identical to that of the purified murine brain protein and to that of MARCKS immunoprecipitated from murine macrophages (ROSEN et al. 1989). On the other hand, the calculated molecular mass of 29.6 kDa is at variance with the apparent molecular mass of 68 kDa obtained from SDS-PAGE analyis (ADEREM et al. 1988a) Transfection of the complete coding region into TK-L cells produces a protein which migrates with an apparent molecular mass of 68 kDa on SDS-PAGE (SEYKORA et al. 1991). The anomalous migration of MARCKS in SDS-PAGE, which results in the discrepancy between the actual and apparent molecular mass of the protein, is attributable to its large Stoke's radius and to its rod-shaped dimensions (ALBERT et al. 1987; J. HARTWIG et al. 1992). The cDNAs for bovine brain and chicken brain MARCKS encode proteins of 31.9 and 28.7 kDa, respectively, which migrate on SDS-PAGE with apparent molecular masses of 87 and 67 kDa (STUMPO et al. 1989; GRAFF et al. 1989b). The coding region of the murine MARCKS gene exhibits a highly repetitive structure that is manifested in the protein as short amino acid motifs which are repeated numerous times throughout the length of the molecule. For example, the element Pro-Ala-Ala-(Ala) is repeated seven times in the molecule and the element (Ala)-Ala-Ala-Pro is repeated three times. These repetitive motifs are reminiscent of highly structured linear molecules such as collagen (PROCKOP 1990) and analysis of the protein's secondary structure by the method of Garnier suggests that it is approximately 76% helical, consistent with our rotary shadowing data, which define MARCKS as a rod-shaped molecule with the dimension of 33 nm x 2.5 nm (J. HARTWIG et al. 1992). The amino acid composition of murine MARCKS is unusual: alanine accounts for 28.8% of the residues while glutamate and proline constititute 16.5% and 11.0% of the residues. Ten amino acids (Ala, Glu, Pro, Gly, Ser, Lys, Gln, Thr, Asp, and Phe) represent more than 95% of the residues.

#### 3.2 Domain Structure of MARCKS

Comparison of the primary sequences of the murine, bovine, and chicken MARCKS reveals that the N-terminal and the phosphorylation domains are highly conserved, whereas the remainder of the protein is divergent (STUMPO et al. 1989; GRAFF et al. 1989b; SEYKORA et al. 1991). It would be reasonable to predict that these two conserved domains are important for the basic function of the MARCKS molecule. This appears to be the case. The N-terminal domain contains a myristoylation consensus sequence consisting of Gly-Ala-Gln-Phe-Ser-Lys-Thr-Ala which is necessary, but not sufficient, for membrane attachment of the protein (GRAFF et al. 1989; M. THELEN et al. 1991) (Fig. 1). The conserved domain spanning amino acids 128–180 of murine MARCKS contains all the known, phosphorylation sites of the protein (serines 152, 156, 163), as well as the calmodulin- (GRAFF et al. 1989c) and actin-binding sites (see below) (Fig. 1). The predicted secondary structure of the non-conserved regions of MARCKS is primarily helical, and this structure is further



**Fig. 1.** The domain structure of MARCKS. MARCKS has two highly conserved domains. The myristolated N-terminal membrane-targeting domain is indicated by *diagonal lines*, and the highly charged phosphorylation domain, which also bears the calmodulin- and actin-binding sites, is denoted by *vertical lines*. The phosphorylation domain is predicted to be  $\alpha$ -helical and a helical wheel representation of amino acids 146–163 of the murine protein is depicted (SEYKORA et al. 1991). The five lysine residues (indicated with @ positioned on one side of the helix form the calmodulin- and actin-binding sites. The phosphorylatable serines (indicated with \*) are positioned at the opposite side of the helix. The depicted peptide binds calmodulin and actin in vitro and this binding is regulated by PKC-dependent phosphorylation

reinforced by rod-shaped dimensions of the protein. All the data point to a functional domain organization of MARCKS consisting of a membrane-binding, N-terminal, region which is separated by a helical region from the calmodulinand actin-binding, phosphorylation domain (Fig. 1). Mutational analysis is currently underway, which will define precisely these structure-function relationships.

#### 3.3 The MARCKS Gene

Southern analysis of murine genomic DNA reveals that the MARCKS gene is most likely present at a single copy per haploid genome and has a simple gene structure (STUMPO et al. 1989; GRAFF et al. 1989b; SEYKORA et al. 1991). The appearance of weakly hybridizing bands on Southern blot analysis shows that some genes bear a moderate degree of homology to the MARCKS gene and suggest the possibility of a family of related proteins.

### 3.4 Regulation of MARCKS Gene

Highest levels of MARCKS mRNA are found in brain and spleen, intermediate levels are found in kidney and heart, and very low levels are expressed in the liver. All mouse tissues examined express multiple MARCKS transcripts, which are due to differential polyadenylation and incomplete processing (SEYKORA et al. 1991).

The steady state levels of MARCKS mRNA in murine macrophages are increased 20- to 50-fold by prior exposure of the cells to LPS (SEYKORA et al. 1991). This is consistent with our previous demonstration that the MARCKS protein is strongly induced by LPS in murine macrophages and in human neutrophils (ADEREM et al. 1988a; THELEN et al. 1990). In addition, MARCKS is also induced by TNF- $\alpha$  in human neutrophils, where it constitutes approximately 90% of all protein synthesized in response to this cytokine (THELEN et al. 1990). The fact that MARCKS constitutes the majority of all protein synthesized in response to TNF-a suggests that it has a role to play in TNF-a-dependent signal transduction. This is supported by the observation that chemotactic peptidedependent activation of PKC results in much higher levels of phosphorylated MARCKS in TNF-a-primed neutrophils, compared with unprimed cells (THELEN et al. 1990). Interestingly, while TNF- $\alpha$  stimulates the transcription and translation of MARCKS, it does not promote its phosphorylation in the absence of a second stimulus (THELEN et al. 1990). Since the phosphorylation of MARCKS is synonymous with the activation of PKC, it follows that TNF- $\alpha$  does not directly activate PKC, but rather, that it modifies PKC-dependent pathways by inducing the synthesis of an effector substrate of the kinase.

#### 3.5 LPS Regulates the Phosphorylation of MARCKS

Lipopolysaccharide promotes the synthesis and myristoylation of MARCKS and concomitantly alters its profile of phosphorylation (ADEREM et al. 1988a). Activators of PKC induce the much more rapid phosphorylation of MARCKS in LPS-treated macrophages than in control cells. In addition, thermolytic mapping of the phosphorylated protein reveals that treatment of macrophages with LPS induces the phosphorylation of the protein on a novel site (ROSEN et al. 1989). The three serine residues known to be phosphorylated have been identified and are indicated by asterisks in Fig. 1.

#### 3.6 Cycles of Phosphorylation and Dephosphorylation Govern the Reversible Association of MARCKS with the Plasma Membrane

The subcellular distribution of MARCKS is unusual in that the vast majority of the myristic acid-labeled protein is associated with the plasma membrane in quiescent cells, while most of the phosphorylated protein is found in the cytosol of activated cells (ADEREM et al. 1988a). These data suggested a model in which myristic acid targets MARCKS to the membrane where it comes in close apposition with PKC. Upon activation, PKC phosphorylates MARCKS, resulting in the release of the protein from the membrane (ADEREM 1988). This hypothesis has been confirmed experimentally. First, mutational analysis showed that the myristic acid moeity is required for the stable attachment of MARCKS with the membrane (GRAFF et al. 1989a). Second, activation of PKC in either macrophages or neutrophils results in the displacement of the myristoylated protein from the membrane, and this occurs without the deacylation of the protein (M. THELEN et al. 1991). This also occurs in an in vitro reconstituted system where phosphorylation of MARCKS by purified PKC promotes its release from isolated membranes (M. THELEN et al. 1991).

Since cytosolic MARCKS which has been released from the membrane by phosphorylation still contains its myristic acid, membrane-targeting, moeity, we investigated whether dephosphorylation is accompanied by the reassociation of the protein with the plasma membrane. Since phorbol myristate acetate (PMA) activates PKC irreversibly, studies on the reversibility of membrane binding of MARCKS were undertaken using a chemotactic peptide which stimulates transient PKC-dependent responses in human neutrophils via a receptor, G-protein coupled pathway (DEWALD et al. 1988). Treatment of neutrophils with f-Met-Leu-Phe results in the rapid, but transient, phosphorylation of MARCKS which is accompanied by its release from the plasma membrane and its accumulation in the cytosol. After 40 stimulation with f-Met-Leu-Phe the

equilibrium between kinase and phosphatase shifts to favor the dephosphorylation of MARCKS. As dephosphorylation proceeds there is a concomitant reassociation of the protein with the membrane, such that most of the protein is membrane-bound when phosphorylation has returned to basal levels (M. THELEN et al. 1991). This cycle of membrane release and attachment is not influenced by cycloheximide, indicating that de novo synthesis of MARCKS does not account for the increase in the membrane-bound form of the protein observed upon dephosphorylation.

Agents which shift the equilibrium of the steady state level of phosphorylated MARCKS also shift the equilibrium of membrane binding of the protein. Okadaic acid, a specific phosphatase inhibitor (BIALOJAN and TAKAI 1988; HAYSTEAD et al. 1989), blocks both the dephosphorylation of MARCKS and its reassociation with the plasma membrane. When dephosphorylation is accelerated by addition of the receptor antagonist, boc-met-leu-phe, the shift in the equilibrium towards the dephosphorylated species is accompanied by increased membrane binding (M. THELEN et al. 1991). The cycle of membrane attachment and detachment of MARCKS is illustrated in Fig. 2.



**Fig. 2.** A model indicating a possible role for MARCKS in macrophages. LPS and TNF- $\alpha$  induce the transcription and translation of MARCKS, following which it is myristoylated by the *N*-myristoyl transferase (*NMT*). MARCKS binds to the cytoplasmic face of the substrate-adherent plasma membrane, where it colocalizes with vinculin (*Vin*), talin (*Tal*), and PKC. MARCKS must be myristoylated for effective membrane binding and it may physically associate with a "myristoyl-protein" receptor (*R*?). MARCKS binds both actin and calmodulin/calcium (*Cal*). Upon activation of PKC, MARCKS is phosphorylated and this results in its translocation from the membrane to the cytoplasm, where it remains associated with F-actin. When MARCKS is dephosphorylated, it reassociates with the plasma membrane, and it may therefore provide a regulated cross-bridge between F-actin and the substrate-adherent plasma membrane

#### 3.7 A Myristoyl-MARCKS Receptor at the Plasma Membrane?

The capacity of MARCKS to shuttle to and from the plasma membrane, together with the observation that MARCKS is located in discrete punctate structures at the substrate-adherent surface of macrophage filopodia (ROSEN et al. 1990) (see below), suggests that the protein associates with a receptor at the cytoplasmic surface of the plasma membrane, rather than through the nonspecific insertion of a hydrophobic moiety in the lipid bilayer. Some insight into the mechanism of membrane attachment of MARCKS might be gleaned by comparing it to the proto-oncogenic tyrosine kinase, p60<sup>src</sup>, which also requires covalent modification with myristic acid for effective targeting to focal adhesions at the plasma membrane (PELLMAN et al. 1985; SHRIVER and ROHRSCHNEIDER 1981; ROHRSCHNEIDER and ROSOK 1983). While myristic acid is necessary for membrane attachment of p60<sup>src</sup>, it is not sufficient, since a transformation-defective mutant of p60<sup>src</sup> has been described which does not associate with the membrane despite its myristoylation. Direct evidence for a "myristoyl-src" receptor was obtained recently in experiments which demonstrated specific and saturable binding of p60<sup>v-src</sup> to plasma membranes in vitro (RESH 1989; GODDARD et al. 1989). Binding was dependent on myristoylation and was inhibited competitively by a myristoylated peptide corresponding to the first 11 amino acids of p60<sup>v-src</sup> but not by the nonmyristoylated peptide or by myristoylated peptides derived from the sequences of other myristoylated proteins. The myristoylated src peptide can be crosslinked to a 32-kDa membrane protein which may well prove to be a "myristoyl-src" receptor (RESH and LING 1990). Further evidence for a "myristoylated protein receptor" comes from another member of the src family of proto-oncogenes, p56<sup>/ck</sup>, which has been shown to associate with the CD4 and CD8 T-lymphocyte surface glycoproteins (BARBER et al. 1989; VEILLETTE et al. 1988). The myristic acid-moiety is necessary (but not sufficient) for its attachment to CD4, and in this sense. CD4 represents the first myristoyl-protein receptor to be defined.

The cycle of membrane attachment and detachment described above for MARCKS may also extend to other myristoylated PKC substrates such as p60<sup>src</sup> and p56<sup>lck</sup>, and it will be interesting to determine whether their association with the membrane is regulated in a similar way. The recent observation that phosphorylated p56<sup>lck</sup> has a lower affinity for CD4 than its nonphosphorylated counterpart is consistent with this proposal (HURLEY et al. 1989).

#### 3.8 MARCKS Localizes to Points of Focal Adhesion in Macrophage Filopodia

We have investigated the subcellular location of MARCKS in macrophages by immunofluorescence microscopy. The protein has a punctate distribution at the substrate-adherent surface of macrophage pseudopodia and filopodia (ROSEN

et al. 1990). When the cells are mechanically dislodged from the substratum, MARCKS continues to stain with a punctate pattern in residual patches of substrate-adherent membrane (ROSEN et al. 1990). Further evidence that the punctate staining pattern of MARCKS correlates with cellular adherence derives from an examination of murine resident peritoneal macrophages which are morphologically heterogeneous. MARCKS stains diffusely in rounded cells, while in elongated cells, punctate staining in membrane extensions is prominent (ROSEN et al. 1990). Since the punctate staining is due to association of MARCKS with areas of the macrophage membrane that are tightly associated with the substratum, we examined whether MARCKS colocalized with any components of focal adhesions. Many of the structures containing MARCKS also stain for vinculin and talin (ROSEN et al. 1990). A punctate distribution for vinculin and talin is in contrast to their typical plaque-like distribution in adherent fibroblasts (BURRIDGE et al. 1987), and has previously been observed in macrophages (MARCHISIO et al. 1987) and at the active cell edge of fibroblasts during the early stages of fibroblast attachment (BERSHADSKY et al. 1985). Punctate adhesions also predominate in fibroblasts transformed by Rous sarcoma virus (RSV), where adhesion to the substratum is less well developed (BERSHADSKY et al. 1985). It seems likely, therefore, that MARCKS is located in the initial, more transient adhesion complex that is formed at the leading edge of the motile macrophage.

Immunoelectron microscopy has further increased the resolution of our light microscopic observations. MARCKS is found in clusters near the plasma membrane in Lowicryl-embedded sections of fixed macrophages. To determine whether the immunogold particles that are bound near the membrane in cell sections are also associated with cytoskeletal fibers, we localized MARCKS in mechanically unroofed cells (A. ROSEN et al., submitted for publication). This technique preserves both membrane and its associated cytoskeletal elements, thereby allowing connections between filaments and the cytoplasmic side of the plasma membrane to be visualized (HARTWIG et al. 1989). Anti-MARCKS gold label is found in small, widely spaced clusters at points where actin filaments interact with the cytoplasmic surface of the plasma membrane.

## 3.9 LPS Increases Filopodia Formation and Induces MARCKS Synthesis and Clustering

Lipopolysaccharide induces the net synthesis of MARCKS (ADEREM et al. 1988a) and greatly increases the adherence of the cultured mouse macrophages to surfaces. This is accompanied by a striking increase in the number and prominence of lamellipodia, filopodia, and membrane veils (A. ROSEN et al., submitted for publication). Stimulation of macrophages with LPS also results in a dramatic increase in the number of punctate structures containing MARCKS, which are seen over the entire substrate-adherent surface of lamellipodia as well as along filopodia and veils of membrane. Electron microscopy confirms the

immunofluorescence data, showing that the total amount of membraneassociated MARCKS, as well as the concentration of MARCKS in the clusters, increases. The close correlation between synthesis and acylation of MARCKS and its enrichment in pseudopodia and filopodia suggest that MARCKS might serve a function in these plastic structures.

The pronounced staining of MARCKS in filopodia, and the presence in filopodia of a conspicuous, central actin bundle (MITCHISON and KIRSCHNER 1988), prompted us to examine the distribution of MARCKS and actin in the same cell. Double staining and electron microscopy experiments show MARCKS spotted alongside filopodial actin bundles in LPS-treated macrophages (A. ROSEN et al., submitted for publication). Furthermore, clusters of MARCKS are intimately associated with the cytoplasmic surface of the plasma membrane in unroofed cells at points where multiple filaments contact the cytoplasmic surface of the plasma membrane.

#### 3.10 The Effect of PKC Activation on the Distribution of MARCKS

Immunofluorescence studies have indicated that PKC is also a component of the substrate-adherent punctate structures which contain MARCKS, vinculin, and talin (ROSEN et al. 1990). This is not surprising, since it is known that PKC is a component of focal adhesions in fibroblasts (JAKEN et al. 1986), and that PKC very rapidly phosphorylates MARCKS when the cell encounters an activating stimulus (ROSEN et al. 1989). Activation of PKC with phorbol esters causes marked cell spreading and rounding and the almost complete disappearance of filopodia. This is accompanied by disappearance of punctate staining of MARCKS, and by a modest increase in the level of diffuse staining observed. The kinetics of the morphologic changes and the disappearance of punctate staining of MARCKS (ROSEN et al. 1990) mirror the kinetics of phosphorylation of MARCKS by PKC in intact macrophages (ROSEN et al. 1989), and the translocation of MARCKS from the membrane to the cytosol (ROSEN et al. 1990) (see above). In contrast, the effect of PMA on the distribution of vinculin and talin is quite distinct. After PKC treatment, vinculin and talin still stain prominently with a patchy, punctate organization and are particularly obvious at the phase-dense cell edge (ROSEN et al. 1990).

Immunoelectron microscopy confirms that the amount of plasma membrane-associated MARCKS markedly diminishes upon activation of PKC while cytoplasmic levels of the protein increase proportionally. Unexpectedly, experiments in mechanically unroofed macrophages show that MARCKS remains associated with the sides of actin filaments in PMA-treated cells, but that the filaments to which the gold label is attached are now spatially displaced from the membrane surface. MARCKS thus appears to be a component of the membrane-associated cytoskeleton, and is closely associated with actin filaments in this structure. Phosphorylation of MARCKS results in its translocation from the plasma membrane into the cytosol, where it appears still to be closely

associated with actin filaments. This phosphorylation-regulated translocation from the plasma membrane is accompanied by the marked reorganization of the actin cytoskeleton that occurs upon activation of PKC (PHAIRE-WASHINGTON et al. 1980; SCHLIWA et al. 1984). The phosphorylation-dependent regulation of membrane binding of MARCKS might therefore serve to modify the attachment of actin filaments to the membrane, thereby influencing cytoskeletal organization and morphology in response to signals that activate PKC.

### 3.11 MARCKS Is an Actin-Binding Protein

The data described above suggested a role for MARCKS in actin-based motility. It was therefore important to determine whether MARCKS binds actin in vitro and whether this binding is influenced by phosphorylation. Both dephosphorylated MARCKS, and MARCKS phosphorylated in vitro with PKC, bind to F-actin in a cosedimentation assay (J. HARTWIG et al. 1992). Scatchard analysis indicates that the binding affinity of both phospho- and dephospho-MARCKS for actin is in the micromolar range. The MARCKS protein also appears to interact with actin in situ since actin copurifies with MARCKS through numerous chromatography and centrifugation steps and the two proteins can only be separated by reverse-phase chromatography.

#### 3.12 Dephosphorylated MARCKS Is an Actin Filament Crosslinking Protein While Phosphorylated MARCKS Is Not

The interaction of MARCKS with actin filaments was studied in the electron microscope after negative staining. When actin is incubated at a ratio of 1 molecule of dephospho-MARCKS to 10 actin subunits, filaments become aggregated and are decorated with rod-shaped MARCKS molecules which attach along the actin fibers near the midpoints of the rods. At molar excess of MARCKS to actin subunits, the actin filaments become highly entangled and are now periodically decorated every – 20 nm with dephospho-MARCKS molecules. Actin filaments in the absence of MARCKS or incubated in the presence of phospho-MARCKS appear bare and unaggregated. Thus, while phosphorylation does not diminish the binding of MARCKS to the actin filament, it does change the manner in which the MARCKS molecule binds to the actin filament (J. HARTWIG et al. 1992).

The effect of MARCKS binding on the function of F-actin, and alterations mediated by phosphorylation, were further evaluated by morphologic, optical, and hydrodynamic methods. As discussed above, dephosphorylated MARCKS crosslinked actin filaments into loose aggregates which were easily discernible

by electron microscopy. The addition of molar ratios of  $\leq$  1 MARCKS to 20 actin filament subunits also increases the viscosity of actin, consistent with filament crosslinking. Higher ratios of dephosphorylated MARCKS to actin, however, decrease the viscosity of actin solutions relative to actin alone. These results suggest that low ratios of MARCKS link actin into a network and that higher concentrations aggregate filaments into bundles. Dynamic light scattering confirms that MARCKS causes the lateral alignment of actin filaments into larger structures. In contrast, phosphorylated MARCKS has minimal effects on the viscosity or light scatter intensity of F-actin solutions. These studies demonstrate that MARCKS binds to the sides of actin filaments and crosslinks them. High concentrations of the phospho- or dephosphoprotein do not affect the extent of linear actin assembly, making it unlikely that the MARCKS interacts with the ends of actin polymers. The stoichiometry of binding also indicates that the interaction of MARCKS with actin is not limited to the ends of polymers (J. HARTWIG et al. 1992).

#### 3.13 Calmodulin Inhibits the Actin Crosslinking Activity of MARCKS

Nonphosphorylated MARCKS binds calmodulin in the presence of calcium while the phosphorylated protein does not (GRAFF et al. 1989d). In addition, calmodulin prevents PKC-dependent phosphorylation of MARCKS (ALBERT et al. 1984). Taken together, these data suggest that the calmodulin-binding site and the phosphorylation sites of MARCKS are closely linked. Since the phosphorylation of MARCKS inhibits its actin-crosslinking activity, it was of interest to determine whether calmodulin prevented the actin-crosslinking activity of nonphosphorylated MARCKS. This proves to be the case: stoichiometric amounts of calmodulin completely inhibit the actin-crosslinking activity of nonphosphorylated MARCKS (J. HARTWIG et al. 1992).

#### 3.14 The Synthetic Phosphorylation Domain of MARCKS Crosslinks Actin in a PKC- and Calmodulin-Regulated Manner

As discussed above, the MARCKS protein contains two highly conserved domains: an N-terminal membrane-binding domain which is myristoylated, and a highly charged phosphorylation domain which also contains the calmodulinbinding site (GRAFF et al. 1989d) (See Fig. 1). A synthetic peptide which contains all the serine residues known to be phosphorylated, and corresponds to residues 146–163 of murine MARCKS (see Fig. 1) (SEYKORA et al. 1991), increases both the light scatter intensity of the F-actin in solution and aggregates actin filaments into tight bundles which are observable in the electron microscope. Phosphorylation of the serine residues in this peptide, however, prevents the peptide from crosslinking actin filaments, as determined by light scattering and viscosity measurements and by electron microscopy (J. HARTWIG et al. 1992). Phosphorylation, therefore, modulates the ability of this peptide to crosslink actin. Since calmodulin inhibits the actin-crosslinking activity of nonphosphorylated MARCKS, and since the synthetic peptide contains the calmodulin-binding site (GRAFF et al. 1989d), the effect of calmodulin on the actin-bundling activity of the peptide was determined. Calmodulin, at a molar ratio to the peptide of 1:1, completely inhibits the actin-bundling activity of the nonphosphorylated peptide.

The synthetic peptide containing the phosphorylation sites, the calmodulinbinding site, and the actin-binding site is predicted to form an  $\alpha$ -helix in aqueous solution. A helical wheel representation of this domain of the murine protein is depicted in Fig. 1. The lysine residues (indicated with @ positioned on one side of the helix form a consensus calmodulin-binding site (O'NEIL and DEGRADO 1990) and are similarly positioned to the lysine residues found in known actinbinding domains (VANDEKERCKHOVE 1989). The phosphorylatable serines (indicated with \*) are positioned on the opposite side of the helix. It is likely that the lysine residues comprise both the actin- and calmodulin-binding sites of MARCKS and this hypothesis is supported by the observation that calmodulin binding prevents actin-crosslinking activity. The crosslinking of actin filaments would require monomeric molecules to express a second actin-binding site or to dimerize. It is not yet clear whether the synthetic peptide has a second actinbinding site or whether it forms multimers.

The interaction of MARCKS with actin filaments is altered by phosphorylation or by calmodulin/calcium; although binding is not eliminated, filament crosslinking is. Phosphorylation or calmodulin/calcium, therefore, appears to inactivate one of the actin-binding site(s) contained between residues 146 and 163 of the murine protein.

During neurosecretion, leukocyte activation, and growth factor-dependent mitogenesis, cells undergo cytoskeletal rearrangements while MARCKS is both rapidly phosphorylated and redistributed to the cytoplasm from the cytoplasmic surface of the plasma membrane (ADEREM et al. 1988a; ROSEN et al. 1990; WANG et al. 1989). Upon dephosphorylation of MARCKS, it reassociates with the plasma membrane, demonstrating it to reversibly cycle to and from the plasma membrane (M. THELEN et al. 1991). Stimulation of leukocytes with chemotactic peptide results in the activation of PKC (THELEN et al. 1990) and an increase in cytosolic calcium levels. This generates two signals which can modify the interaction of MARCKS with actin and the attachment of MARCKS to the plasma membrane. Since MARCKS binds to points of plasma membrane substrate adherence, it may be important in physically coupling membrane stimulation to cell movement.

# 4 The 48-kDa Myristoylated PKC Substrate; a Candidate Effector of IFN-γ-Induced Responses in Macrophages

During cell-mediated immunity, macrophages acquire an increased capacity to secrete reactive oxygen intermediates and to kill microbes and tumor cells. Treatment of macrophages with IFN-y, and with other cytokines such as interleukin-4 and granulocyte-macrophage colony stimulating factor, induces properties that are similar to those of macrophages activated in situ (NATHAN et al. 1983; SCHREIBER et al. 1983). However, the intracellular events leading to the activation of macrophages by antigen-specific T cells are largely unknown, although it is clear that PKC has a role in these events [reviewed in (ADAMS and HAMILTON 1987)]. We have shown that physiologic concentrations of IFN- $\gamma$ greatly enhance the induction of a 48-kDa myristoylated PKC substrate (ADEREM et al. 1988b). The protein contains the fatty acid in an amide linkage to an N-terminal glycine and myristoylation appears to occur cotranslationally since it is rapidly blocked by inhibitors of protein synthesis. Myristoylation of the 48-kDa PKC substrate is observed within 1 h and reaches a maximum by 3-4 h (ADEREM et al. 1988b). These kinetics are relatively rapid when compared with the majority of IFN-y-induced responses in macrophages, which are generally observed 8–48 h after exposure to the cytokine (ADAMS and HAMILTON 1987). The kinetics are similar to those observed for IFN-y-dependent potentiation of PKC activity in macrophages (HAMILTON et al. 1985), and it is possible that the 48-kDa protein may be an effector of the PKC- dependent signaling pathway leading to macrophage activation.

Interferon- $\alpha$ , - $\beta$ , and - $\gamma$  share a number of properties, including the induction of antiviral and antiproliferative states in a number of cell types, but IFN- $\gamma$  is far more effective than IFN- $\alpha$  or - $\beta$  for activation of macrophage oxidative metabolism and antiprotozoal activity (NATHAN et al. 1984). The induction of the 48-kDa PKC substrate is quite specific for IFN- $\gamma$ , suggesting that this protein is related to the macrophage-activating capacity of the lymphokine and not to its antiviral or antiproliferative activity.

Consistent with it having a role in macrophage activation, the 48-kDa protein is constitutively induced in macrophages activated in vivo by intraperitoneal injection of formalin-killed *Corynebacterium parvum*. Indeed, we have been able to use the induction of the 48-kDa protein as an index of macrophage activation; an increase in the apparent "basal" level of this protein always correlates with increased numbers of activated macrophages in the peritoneal cavity, as evidenced by an increase in the number of cells expressing surface la molecules and by a decrease in the capacity of the macrophages to secrete leukotriene  $C_4$  (ADEREM et al. 1988c).

The LPS-primed macrophage has proved an excellent model system in which to study the convergence of three distinct signal transduction systems mediated by protein myristoylation, PKC-mediated phosphorylation, and calcium/calmodulin. The biologic readouts are clear and distinct, and since the cells are terminally differentiated, the signals are not obscured by those involved in the regulation of the cell cycle. A number of myristoylated PKC substrates that are likely to have a role in LPS-, TNF- $\alpha$ -, and IFN- $\gamma$ -induced signal transduction pathways have been identified. They include the MARCKS protein, which appears to regulate the reversible attachment of actin filaments to the substrate-adherent plasma membrane, the 48-kDa protein, which appears to have a role in immune activation of macrophages, and the macrophage-specific 42-, 40-kDa proteins which are induced by LPS. Future studies will concentrate on the identity and function of these proteins.

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# **Ribosomal RNA Metabolism in Macrophages**

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# 1 Introduction

Macrophages are ubiquitous cells critical for host defense (WILTROUT and VARESIO 1987; VARESIO 1985b). Metchnikoff's original report in the late nineteenth century first suggested that phagocytes are the body's prime detectors of foreign invaders; the functions of macrophages have since been delineated, initially at a cellular level and more recently at a molecular level.

Macrophages are active effector cells capable of tumoricidal and bactericidal activities and are integral regulatory components of the immune system, on which they exert stimulatory and inhibitory activities (VARESIO 1983, 1985b). The list of macrophage secretory products is impressive (NATHAN 1987) and clearly indicates that these cells learned to interact and communicate with the

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specialized and sophisticated structures that evolved around the ancestral ameba (VARESIO et al. 1980). In fact, there are no other cells as developmentally complex as macrophages that can adapt to so many different environments, including the secluded central nervous system, the variable lung, and the complex liver. As a result of the adaptation to different environments, of the contact with surrounding cells, and of the various stages of differentiation in which these cells may exist in the tissues, monocytic cells are a heterogeneous population with respect to morphologic and functional characteristics (LEUNG et al. 1985; GORDON et al. 1988; CROCKER et al. 1987).

One important feature of macrophage biology is that proliferation is not required and is not part of the activation program of the cell. Unlike activation of B or T lymphocytes, macrophage activation is not dependent upon clonal expansion or mitotic activity. The dissociation between macrophage activation and proliferation has been further documented by the demonstration that proliferating macrophage cell lines, immortalized by expression of various oncogenes, retain the biologic activities and characteristics of peritoneal macrophages (BLASI et al. 1985, 1987-1989; GANDINO and VARESIO 1990; COX et al. 1989). Under physiologic conditions, the expression of the activated phenotype is a transient event that is followed by a return of macrophages to a resting state (TAFFET et al. 1981). The magnitude of the macrophage-mediated response is determined mainly by number of responding cells and/or the accumulation of the macrophages into the inflammatory region, and it is modulated by the cellular feedback mechanisms and by the extent and nature of the environmental stimulation (ROSEN and GORDON 1990 a, b; CROCKER et al. 1988; PERRY and GORDON 1988). Proliferation is important to maintain an adequate supply of circulating monocytes ready to extravasate into the tissues in response to chemoattractants released during the inflammatory response. Monocytes can undergo limited proliferation in the circulation and in the tissues. However, the majority of circulating monocytes originate in the bone marrow from the proliferation of stem cells and their differentiation along the monocytic lineage. The proliferative ability of the cells decreases progressively during the differentiation (METCALF 1986). Thus, the majority of the mitotic activity is restricted to the bone marrow, and the balance of peripheral cells is dictated by cell death and replenishment from the bone marrow.

The recognition that proliferation is not part of the genetic program of a macrophage poses interesting questions of cell biology. Macrophages express receptors for a variety of growth factors specific for monocytic cells, such as the colony stimulating factor-1 (CSF-1) receptor (GUSELLA et al. 1990; BLASI et al. 1987), or typical of other lineages, such as the interleukin-2 (IL-2) receptor (Cox et al. 1990; ESPINOZA-DELGADO et al. 1990a). However, macrophages respond to stimulation by growth factors with functional changes. For example, CSF-1 receptor is present in bone marrow monocyte precursors, circulating monocytes, and tissue macrophages. In bone marrow monocyte precursors, CSF-1 induces proliferation, while in monocytes and macrophages it induces secretory activity (MOORE et al. 1984; WARREN and RALPH 1986), resistance to viral infection and

sustains cell viability and cytotoxic response (RALPH and NAKOINZ 1987; ESPINOZA-DELGADO et al. 1990b; LEE and WARREN 1987; SHERR 1990). Interestingly, in monocytes but not in macrophages, the CSF-1 receptor can be induced by IL-2 (ESPINOZA-DELGADO et al. 1990b), whereas in both cell types it is down-regulated by the ligand, phorbol esters, and endotoxins (GUSELLA et al. 1990; DOWNING et al. 1989). Thus, it appears that the differentiation from monocyte to macrophage is associated with a differential regulation of CSF-1 receptor expression. These considerations raise many questions on the nature of the molecular events initiated by CSF-1 in monocytic cells at different stages of differentiation. The signal transducing mechanisms of CSF-1 receptor may be different in the various monocytic populations. Alternatively, the same transducing signal initiated by the CSF-1 receptor could be filtered by a different genetic makeup typical of cells at different stages of differentiation and may initiate distinct programs of gene expression. Thus, the understanding of the molecular basis of growth factors and cytokine actions on macrophages involves answers to the following questions:

- 1. How is the proliferative potential of a cell gradually reduced?
- 2. What happens to the complex cellular machinery devoted to cell growth?

These problems are of major interest not only in understanding macrophage biology and cell differentiation, but also in developing and applying strategies to control neoplastic cell proliferation. Identification of the genes and mechanisms that induce the proliferative potential of a cell may lead to strategies to reduce the proliferative potential of tumor cells. An interesting aspect of this problem relates to the ribosomal genes, whose expression is readily activated during the proliferative response of a cell but is minimal in resting cells. The close association between proliferation and ribosomal RNA (rRNA) gene expression is a general phenomenon in nature occurring in normal and neoplastic cells, as well as in eukaryotic and prokaryotic cells. There are indications that ribosome biosynthesis can be induced in nonmitotic secretory cells (SCHMIT et al. 1985). Is the expression of ribosomal genes totally uncoupled to the response of macrophages to a growth factor or to an activating signal because the cells are not programmed to divide? If so, how do macrophages deal with the major changes in total protein synthesis occurring during the activation process? The finding of major changes in the metabolism of rRNA during macrophage activation suggested new and unexpected conclusions on the function of this molecule, and this will be one of the topics discussed in the present chapter.

The expression of a biologic function by macrophages is the net result of many events that include synthesis and secretion of biologically active mediators, expression of receptors, antigens, and ectoenzymes on the membrane, and activation of enzymatic pathways (ADAMS and HAMILTON 1987; VARESIO 1985b). The goal of the study of macrophage activation is to understand the sequence of molecular events initiated by the stimulus that result in the expression of the activated phenotype. We will focus our discussion on the pathways of macrophage activation that lead to the expression of tumoricidal

activity by murine macrophages; hence, unless otherwise specified, the term "activated macrophages" will indicate a macrophage population endowed with cytotoxic activity against tumor target cells.

In many instances it has been possible to define a precise combination of stimuli that induces the expression of tumoricidal activity, and extensive information exists on the biochemical and molecular events induced by macrophage activators, such as interferon (IFN) and endotoxins (CHEN et al. 1990; ADAMS and HAMILTON 1987; VARESIO 1985b). The progressive characterization of the responses elicited by different signals has shown that the biochemical pathways triggered by various activators are different with regard to the utilization of signal transducing mechanisms and modalities of gene expression. The existence of multiple pathways of activation of cytotoxic macrophages has been further documented by differential sensitivity to metabolic inhibitors of macrophage activation initiated by different agents (RADZIOCH and VARESIO 1988; BLASI and VARESIO 1984; KOVACS et al. 1988; RADZIOCH et al. 1987b). It is still difficult to distinguish the sequence of events responsible for the activation of tumoricidal macrophages from those events leading to other functional activities. If different activating agents, although utilizing different biochemical pathways, generate a similar functional response, e.g., cytotoxicity, there should be common events elicited by every activator. Indeed, events correlated with the manifestation of cytotoxic activity have been identified, and some of them will be extensively discussed here. The task still to be performed is to tie together and organize into a mechanistic model the growing information on both the broad cascade of events initiated by various activating agents (stimulus-specific responses) and the more limited and selective molecular manifestation responsible exclusively for the tumoricidal activity (function-specific response). In this chapter, we will focus on the changes in RNA metabolism that are associated with the expression of tumoricidal activity by murine macrophages, elicited by different macrophage activators.

# 2 Control of RNA Metabolism

Analysis of the response of macrophages to specific stimuli has revealed changes in the levels of mRNA coding for structural and secretory proteins (HAMILTON et al. 1989). Run-off experiments and evaluation of the half-life of mRNA have revealed that transcriptional and post-transcriptional mechanisms control macrophage gene expression. For example, lipopolysaccharide (LPS) induces the expression of TNF and JE mRNA in peritoneal macrophages, and dibutyryl cAMP inhibits the inducibility of both mRNAs. However, the modulation of TNF is associated with transcriptional changes, whereas the modulation of JE mRNA seems to involve mainly a post-transcriptional control (KOERNER et al. 1987). Moreover, LPS induces transcriptional activation of TNF (TANNENBAUM and HAMILTON 1989) and inhibits the transcription of c-fms (GUSELLA et al. 1990).

These results indicate that distinct mechanisms may modulate the expression of different genes in response to the same macrophage stimulus. Finally, transcriptional and post-transcriptional mechanisms contribute to control the levels of mRNA expression, as shown for IL-1 (LEE et al. 1988), TNF (SARIBAN et al. 1988), CSF-1 (HORIGUCHI et al. 1988). Information on the levels at which mRNA expression is controlled derives mainly from run-off experiments assessing RNA synthesis/elongation in isolated nuclei, or from RNA stability experiments in which the decay of mRNA is evaluated following block of RNA synthesis by specific inhibitors. Both approaches are indicative but not conclusive since they are often affected by artifacts, and the results may be difficult to interpret. A clear understanding of the control of RNA metabolism will require precise information on the molecular events responsible for the transcriptional activation of a gene and definition of the parameters determining the stability of mRNA. It is beyond the scope of this chapter to review the changes in various RNA levels associated with the response of macrophages to stimulatory signals, or the growing literature on the molecular biology of gene expression. We will briefly mention the general concepts in RNA metabolism as background to a detailed discussion of the changes in ribosomal RNA expression and the relationship with the process of activation of cytotoxic macrophages.

Transcriptional activation plays a fundamental role in the control of gene expression in every cell type (CLEVELAND and YEN 1989). The mechanisms controlling gene transcription are very complex, and a large body of literature points toward the fundamental role played by the interactions among nuclear trans-activating factors that, by binding to the promoter region of the gene, modulate its expression in a positive or a negative way. However, it is difficult to predict the transcriptional regulatory properties of promoter elements from the binding activity of *trans*-activating factors. In fact, the transcription of many genes is cell type specific or cell activation dependent, and it may involve multiple promoter regions and different DNA binding proteins. An interesting example is the expression of the tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) (GOLDFELD et al. 1990) or of the IFN- $\beta$  gene (MANIATIS 1918; TANIGUCHI 1988). It was found that the promoter sequences required for virus-induced TNF- $\alpha$  expression were different in L929 fibroblasts and in the P388D1 macrophage cell line, indicating the presence of cell type-specific sequences. These differences are likely to reflect lineagespecific differences in the types or amounts of transcription factors that interact with TNF- $\alpha$  or IFN- $\beta$  promoters. However, these conclusions are based on the expression of reporter genes driven by cytokine promoters in transfected cell lines. The availability and relative proportion of *trans*-activating factors may be different in tissue macrophages. Ideally, the promoter activity should be tested in fresh macrophages. Unfortunately, many attempts at establishing a transient expression system of transfected constructs in fresh macrophages have so far been unsuccessful. Presently, there is no information on the changes in nuclear trans-activating factors associated with the activation of macrophages.

Post-transcriptional events, including processing, transport, and stability of RNA, also play an important role in determining the final levels of gene
expression at the mRNA levels, as demonstrated by the wide range of half-life values of mRNAs (BRAWERMAN 1987; COSMAN 1987; RAGOW 1987). In mammalian cells, the mRNA for transiently expressed genes, such as c-fos and c-myc, has half-life values as low as 15 min, while  $\beta$ -globin mRNA, for example, appears to be fully stable (BRAWERMAN 1987). The stability of mRNA can be controlled by specific nucleotide sequences and/or by the secondary conformation of the molecule. Evidence indicating that distinct regions of the mRNA molecule are important for its stability is provided by the demonstration that deletions of part of the gene alter the stability of the truncated transcript. For example, deletion of the 3' end of c-fos untranslated region (MEULINK et al. 1985) or loss of the first noncoding exon of c-myc (RABBITTS et al. 1985) increases mRNA stability. A sequence stabilizing the mRNA molecule is the polyA tail. Degradation of mRNA is associated with shortening of the polyA tail, and removal of the poly A sequence results in rapid degradation of the RNA (BERGMANN and BRAWERMAN 1977). PolyA binding proteins have been implicated in the protection of mRNA from attack by ribonucleases (BERGMANN and BRAWERMAN 1977). AU-rich motifs at the 3' end of many untranslated regions of mRNAs appear to be a destabilizing sequence for many mRNA species including some coding for oncogenes and cytokines (SHAW and KAMEN 1986; JONES and COLE 1987; KABNICK and HOUSMAN 1988; WILSON and TREISMAN 1988; WRESHNER and RECHAVI 1988). The relationship between these regions and mRNA instability has been suggested by experiments in which insertion or deletion of such regions caused a decrease or an increase in the half-life of the mRNA (PEPPEL et al. 1991).

The mechanism by which specific sequences control mRNA stability is unclear. One possibility is that RNA-binding proteins recognize such regions and modulate the susceptibility of RNA to ribonucleases (MALTER 1989). Like transcription factors, stability factors would differentially regulate mRNAs based on the presence of target RNA sequences. In addition to specific sequences, the secondary conformation of the RNA molecule may be involved in the control of RNA stability. Single-stranded RNA is capable of forming secondary structures, and the protein-RNA interaction may be conformational rather than, or in addition to, sequence specific (KLAUSNER and HARFORD 1989; LEVINE et al. 1986; MEIJLINK et al. 1985; BELASCO and HIGGINS 1988). It has been shown that RNAbinding proteins can bind to stem loops caused by folding of the RNA molecule, and that the configuration as well as the sequences within the loop is important in determining specific protein-RNA interaction (LAZINSKI et al. 1989). Proteins capable of interacting with RNA stem loop have been demonstrated (LAZINSKI et al. 1989). Moreover, the HIV-tat protein, which shares an arginine-rich motif with other RNA loop binding proteins, can interact with stem loops in the RNA of the HIV virus (CHANG and SHARP 1989; DINGWALL et al. 1989; GATIGNOL et al. 1989; OLSEN et al. 1990; ZAPP and GREEN 1989).

We are still far from being able to predict the stability of a given mRNA on the basis of the primary sequence or the potential secondary structure. The complexity of the mechanisms regulating RNA stability is evidenced by the fact that multiple factors are involved, even within the same cell, in controlling the

stability of a given mRNA. Therefore, the relevance of specific sequences in determining the stability may vary substantially. This fact is exemplified by the observation of a differential post-transcriptional stabilization in the same cell of genes containing similar AU-rich regions at the 3' end. For example, post-transcriptional stabilization of GM-CSF mRNA in a monocytic tumor was not associated with a similar stabilization of c-*myc* or c-*fos* mRNA, despite the fact these mRNAs share AU-rich motifs at the 3' end (SHULER and COLE 1988).

In conclusion, the emerging information about the multiple mechanisms that may control the cellular content of RNA indicates that a major role is played by the interaction between nucleic acids and binding proteins. The evidence of differences among cell types in the control of mRNA expression indicates the need to extend the study of protein–nucleic acid interaction to the macrophage system in order to fully understand the mechanism of activation of these cells. In the following discussion, we will analyze the changes in ribosomal RNA (rRNA) occurring in macrophages and the potential role of the secondary structures of rRNA in the activation process.

#### **3 Ribosomal RNA**

Although a eukaryotic cell produces more than 10000 different RNA species, about half of its transcriptional capacity is devoted to the synthesis of one kind of RNA, namely rRNA. In virtually all eukaryotes, the 18S, 5.8S, and 28S mature rRNAs are initially transcribed as a large precursor encoded by genes in tandem arrays in the genome (rDNA) (SOLLNER-WEBB and TOWER 1986). In the mouse, the rDNA repeat unit is about 45 kb, and the largest detected rRNA precursor is approximately 47S or 14 kb (TIOLLAIS et al. 1971; GURNEY 1985). It extends from the initiation site (MILLER and SOLLNER-WEBB 1981) to a position 570 nucleotides downstream of the 28S coding region (GRUMMT et al. 1985b; GURNEY 1985). The presumptive primary transcript is rapidly processed, first at the 5' end at residue +650 (MILLER and SOLLNER-WEBB 1981; GURNEY 1985) and then in the vicinity of the 3' end of the 28S coding region (KOMIAMI et al. 1982; GRUMMT et al. 1985a), to yield the most prevalent precursor, the 45S rRNA. Subsequent processing gives rise to mature 18S, 5.8S, and 28S rRNAs (BOWMAN et al. 1983; CROUCH 1984). In general, more than 90% of the total cellular RNA is mature rRNA, and its half-life has been calculated as approximately 45 h (WEBER 1972). Because of its high synthetic rate and stability, rRNA is the predominant RNA species labeled by pulsing cells with radioactive uridine. The transcription of rDNA, the sole function of RNA polymerase I, is not only very efficient but also highly regulated, in large part reflecting the cellular need to produce more than a million new ribosomes per generation which, in turn, will be required to support protein synthesis in the daughter cells. Indeed, the biogenesis of ribosome particles is clearly coupled to the rate of cell proliferation. Quiescent cells accumulate ribosomes at a lower

rate than do rapidly dividing cells (PERRY 1972; HOSICK and STROHMAN 1971). Terminal differentiation of myoblasts to myotubes represents an example of rapidly proliferating cells being converted into a nondividing fused population. resulting in an approximately 80% decline in the rate of ribosome accumulation (KRAUTER et al. 1979). Nevertheless, even in resting cells rRNA represents the major RNA species that continues to be actively synthesized. It has been reported that in lymphocytes, rRNA is synthesized at a rate higher than is needed for ribosome formation, resulting in a "wastage" of rRNA that is degraded before forming a ribosome (COOPER 1970). Modulation of rRNA synthesis has been associated mainly with alterations in cell growth. A close association between these two events is clearly evident in prokaryotic cells and has been observed in the eukaryotic system as well (NIERHOUS 1982; HADJIOLOV and NIKOLAEV 1976). However, if the proliferative stage were the only modulator of rRNA metabolism, one would have expected rRNA not to change in terminally differentiated cells not committed to proliferation, such as tissue macrophages or granulocytes. Therefore, it was intriguing to observe that the process of activation of resting peritoneal macrophages was associated with major changes in rRNA metabolism. The nature of the changes, their association with the stages of macrophage activation, and their possible biologic roles will be discussed.

## 4 rRNA Metabolism in Activated Murine Macrophages

The first evidence of changes in rRNA during macrophage activation was provided by studies of <sup>3</sup>H-uridine incorporation into acid-precipitable material (VARESIO et al. 1983, 1984b), a method that mainly detects changes in rRNA synthesis. It was found that murine macrophages activated to express tumoricidal activity exhibited a marked decrease in RNA synthesis. This decrease in RNA synthesis was evident in cytotoxic peritoneal murine macrophages activated in vitro by lymphokines, endotoxins, or synthetic compounds, as well as in vivo by injection into the mice of killed bacteria or endotoxins (VARESIO 1986). Normal levels of rRNA synthesis were found in macrophages stimulated, for example, to express immunosuppressive but not cytotoxic functions (VARESIO 1984). It was also established that the decrease in <sup>3</sup>H-uridine incorporation was a late event in the process of macrophage activation, being detectable in vitro after 8–10 h of exposure of macrophages to the activating agent (VARESIO et al. 1983, 1984b). These observations suggested that the down-regulation of RNA synthesis was a functional marker of macrophage activation that could be of relevance in the physiology of the activation process.

Direct evidence that rRNA metabolism was altered during the process of macrophage activation was obtained by the analysis of metabolically-labeled rRNA and by Northern blotting utilizing rRNA-specific probes. Size fractionation on denaturing agarose gels of RNA metabolically labeled by a short pulse with <sup>3</sup>H-uridine allows the detection of changes in rRNA synthesized de novo during

the pulse with the radioactive tracer. Comparison of the radioactivity profile in resting and activated macrophages revealed an imbalanced accumulation of mature rRNA in activated cells (VARESIO et al. 1987; VARESIO 1985a). In cytotoxic macrophages, a major decrease in the accumulation of 28S rRNA relative to 18S rRNA was detected. 28S and 18S are the most prominent species of mature rRNA which are derived from a common high molecular weight 45S precursor. Pulse chase experiments, designed to follow the maturation of the 45S precursor, confirmed the existence of a selective block in the processing of the 28S rRNA in activated macrophages and provided clear evidence of a post-transcriptional level of regulation affecting the maturation of rRNA in cytotoxic macrophages (VARESIO 1985a). Since 18S and 28S rRNA derive from the same 45S precursor, these results indicated that the 28S rRNA was selectively degraded in activated macrophages. Alternatively, the maturation of the 45S precursor to 18S was normal, but the formation of the 28S rRNA was blocked (VARESIO et al. 1987). If this was the case, one would expect that rRNA precursors containing the 28S moiety would accumulate in activated macrophages.

Indeed, experiments in which total macrophage RNA was studied by Northern blotting followed by hybridization with probes specific for rRNA precursors showed that cytotoxic macrophages expressed significantly higher levels of 45S, 41S, and 36S rRNA precursors relative to resting peritoneal macrophages (RADZIOCH et al. 1987a). Northern blotting measures the steady state level of cellular RNA; therefore, these results demonstrated that 45S, 41S, and 36S rRNA precursors accumulate in cytotoxic macrophages.

The primary transcript of rRNA includes sequences for 18S and 28S mature rRNA. Formation of the final products occurs through a series of processing events which follow a general temporal sequence varying slightly from organism to organism and sometimes within a given organism (PERRY 1976). Generally, cleavage of the 41S by endonuclease separates the 18S and the 28S sequences in distinct precursor molecules (21S and 36S respectively). The 21S is coverted to 18S in a simple step; the 36S is sequentially cleaved to 32S and 28S species. In cytotoxic macrophages the levels of the 36S, but not of the 32S, are elevated. These results suggest that the process of activation inhibits the conversion of the 36S into 32S, thereby causing accumulation of the upstream precursors 36S, 41S, and 45S.

The steady state levels of mature 28S and 18S rRNA, however, do not change during the activation process, as shown by Northern blotting analysis (RADZIOCH et al. 1987a). There is no contradiction between these results and the reported decrease of the accumulation of de novo synthesized 28S rRNA detected in the analysis of metabolically labeled rRNA. The half-life of mature 28S rRNA is about 45 h (WEBER 1972a), and the changes in accumulation of 28S rRNA occurred during the last 6–8 h of the 18 h of activation. A decreased rate of 28S rRNA accumulation over 6–8 h is not sufficient to decrease the steady state level of 28S rRNA to such an extent as to be detected by Northern blotting.

In conclusion, the major changes in rRNA metabolism in cytotoxic macrophages can be summarized as being a decrease in rRNA synthesis and a

selective decrease in the accumulation of de novo synthesized 28S but not of 18S rRNA. The major impact of these metabolic changes on the cellular rRNA content is represented by an accumulation of rRNA precursors (45S, 41S, and 36S) in cytotoxic macrophages. The precise relationship among these changes in rRNA is speculative. Changes in the methylation of rRNA precursors may be involved in the alteration of rRNA metabolism since it has been shown that IFN- $\gamma$  augments the intracellular content of S-adenosylmethionine in macrophages, probably by inhibiting the transmethylation reactions (BONVINI et al. 1986). Little is known about the mechanisms of rRNA processing, the requisite protein species, or the nucleic acid sequences involved, and in vitro systems which produce fully processed rRNA have not yet been devised. It has been proposed that the key event is the block of the conversion of 36S to 32S pre-RNA. This event would affect the formation of the 28S but not the 18S rRNA, accounting for the imbalanced accumulation of de novo synthesized rRNA. Accumulation of the rRNA precursor would then feedback and inhibit the ribosomal DNA transcription. Evidence that rRNA can feedback and repress rDNA gene expression has been reported (GOURSE et al. 1985).

# **5 Modulation of rRNA in Different Cell Types**

An imbalance between 28S and 18S rRNA accumulation is not a unique event occurring in macrophages; rather it has been observed in various cell systems (BIZZOZZERO et al. 1985; TONIOLO and BASILICO 1975; BOWMAN and EMERSON 1977; JOHNSON et al. 1976; MAUCH and GREEN 1973; TONIOLO et al. 1973; ABELSON et al. 1974; EMERSON 1971; WEBER 1972b; COOPER 1973). Imbalanced accumulation of mature rRNA species can be induced by inhibiting the growth of fibroblasts by serum starvation (BIZZOZZERO et al. 1985) or by contact inhibition (EMERSON 1971), by shifting temperature-sensitive cell lines to temperatures non-permissive for cell growth (OUELLETTE et al. 1976; TONIOLO and BASILICO 1975), or by inducing myoblast differentiation (BOWMAN and EMERSON 1977). These studies demonstrated that imbalanced accumulation of rRNA occurs during the transition of proliferating cell lines from a growing to a resting state. Moreover, it was reported that picolinic acid, a metabolite of tryptophan, can induce selective downregulation of 28S rRNA, but not of 18S rRNA, in AKR normal rat kidney cells (COSTANTINI and JOHNSON 1981). These changes in rRNA metabolism have been attributed to the decrease in ribosome requirement associated with the decrease in proliferative activity. However, the mechanisms responsible for the occurrence of disproportionate accumulation of mature rRNA, RNA wastage, and alterations in rRNA metabolism characteristic of resting and rested cells have never been defined. The results obtained with macrophages indicate that rRNA metabolism can be modulated in the absence of changes in cell proliferation, since peritoneal macrophages are resting cells and the process of activation does not require or involve cell proliferation. Moreover, the dissociation between changes in rRNA metabolism and the cellular content of mature 28S and 18S rRNA indicates that the altered rRNA metabolism in macrophages is not directly related to the ribosome content. It is possible, instead, that the changes in rRNA metabolism detected in macrophages may reflect and be associated with the functional activity of the cells expressed in their lytic activity against tumor target cells. However, the occurrence of imbalanced accumulation of rRNA in other cell types suggests that such events may represent a more general mechanism of control of cellular functions.

#### 6 Association Between Altered rRNA Metabolism and Cytotoxic Activity

Murine macrophages can be activated in vivo and in vitro to express tumoricidal activity. The effector mechanisms of macrophage-mediated killing are still undefined, and probably more than one mediator may contribute to the expression of tumoricidal activity. Therefore, different protocols to measure the tumoricidal activity of macrophages may generate somewhat different results that can be reconciled only by a careful side by side comparison (RUSSELL et al. 1986; PACE et al. 1985b). In any case, a reproducible tumoricidal assay in vitro is a good marker of a given stage of macrophage activation, and the changes in rRNA metabolism correlate very well with the expression of tumoricidal activity measured in an 18-h <sup>51</sup>Cr or <sup>111</sup>In release assay (RUSSELL et al. 1986).

The strongest correlation between changes in rRNA metabolism was found in studies of murine macrophages activated in vivo by injection of *C. parvum* (VARESIO 1984). Depending upon the time of the harvest of macrophages, it is possible to recover peritoneal macrophages expressing (a) immune suppressive activity but not tumoricidal activity or (b) both functions. However, only the macrophages expressing tumoricidal activity have altered rRNA metabolism (VARESIO 1984).

Activation of macrophages in vitro requires multiple signals, for example IFN- $\gamma$  and traces of LPS (PACE et al. 1983). However, it was found that C57BL/6 macrophages can be activated by IFN- $\gamma$  alone without the need for LPS as a second signal (RUSSELL et al. 1986; VARESIO et al. 1984a). Moreover, IFN- $\gamma$ , IFN- $\alpha/\beta$ , endotoxins, or synthetic dsRNA (poly I:C) can activate macrophages in vitro alone or in the presence of a second signal (TARAMELLI and VARESIO 1981; BLASI et al. 1984; PACE et al. 1985a). The changes in rRNA followed exactly the pattern of expression of cytotoxic activity, since they were elicited by IFN- $\gamma$  alone in C57BL/6 mice (RADZIOCH et al. 1987a) but required IFN- $\gamma$  and traces of LPS in macrophages from C3H/HeN mice (VARESIO et al. 1983), high levels of endotoxins (VARESIO 1986), and IFN- $\alpha/\beta$  (RADZIOCH et al. 1987a) under conditions in which

these stimuli induced cytotoxic macrophages. Further evidence of an association between changes in rRNA metabolism and macrophage activation was provided by studies with macrophages from C3H/HeJ mice that can be activated in vitro by IFN- $\gamma$  plus a strong second signal, such as *Listeria monocytogenes*, but not by IFN- $\gamma$  alone or supplemented with traces of LPS (HOGAN and VOGEL 1988). As for the cytotoxic activity, only the combination of IFN- $\gamma$  plus *Listeria monocytogenes* was able to modify the rRNA metabolism in C3H/HeJ macrophages (VERESIO et al. 1990).

In conclusion, a strong association exists between altered rRNA metabolism and expression of tumoricidal activity. It is important to note that the changes in rRNA metabolism are not stimulus specific since they can be elicited by different activating agents. Moreover, the changes in rRNA metabolism are not a constant response to an activating agent. For example, macrophages from many strains of mouse, including C57BL/6, C3H/HeN, and C3H/HeJ, respond to IFN- $\gamma$  alone with induction of la antigens, of 2–5A synthetase, etc. However, IFN- $\gamma$  alone triggers changes in rRNA only in C57BL/6 macrophages, in which it also induces tumoricidal activity.

Changes in rRNA metabolism are not induced by costimulatory signals alone such as traces of LPS for macrophages from C3H/HeN or *Listeria monocytogenes* for macrophages from C3H/HeJ mice (VARESIO et al. 1990). Rather, only the combined action of two signals in conjunction with tumoricidal activity was able to induce changes in rRNA metabolism (VARESIO et al. 1990). Thus, the changes in rRNA are not a direct response to the first or the second signal but occur under conditions in which the stimulation is sufficient to induce tumoricidal activity.

Although results outlined above demonstrated the existence of a strong correlation between expression of tumoricidal activity and changes in rRNA metabolism, it was difficult to accept a causal relationship between these two distant phenomena since there is no obvious biochemical pathway that could theoretically connect these apparently unrelated events. Recent studies on the effects of picolinic acid on macrophages lend support to the existence of a causal connection between altered rRNA metabolism and cytotoxicity, and have led to the suggestion that there is a biochemical pathway going from rRNA to cytotoxic activity via tryptophan metabolism.

### 7 Picolinic Acid and the Tryptophan Connection

Picolinic acid is one end product of tryptophan catabolism, synthesized from the 2-amino-3-carboxymuconic semialdehyde by the enzyme picolinic decarboxylase. It has been shown that picolinic acid can inhibit the in vitro growth of various cell lines and that transformed cells are more sensitive to picolinic acid (FERNANDEZ-POL et al. 1977; FERNANDEZ-POL and JOHNSON 1977). The mechanism of action of picolinic acid is not known although it has been reported that

picolinic acid interferes with iron uptake (FERNANDEZ-POL 1977) and ribosomal RNA metabolism (COSTANTINI and JOHNSON 1981; COLLINS et al. 1979). In macrophages, picolinic acid affects rRNA metabolism by inhibiting the accumulation of de novo synthesized 28S but not 18S rRNA and by inducing accumulation of rRNA precursors (VARESIO et al. 1990). These changes in rRNA metabolism are remarkably similar to those occurring in activated murine macrophages. Thus, the analysis of the macrophage-activating properties of picolinic acid could provide the tool for determining whether the changes in rRNA metabolism are causally related to the tumoricidal stage. Experiments in which macrophages were exposed to IFN- $\gamma$  plus picolinic acid demonstrated that picolinic acid is a potent costimulator of macrophage activation. Specifically, picolinic acid acted synergistically with IFN- $\gamma$  in activating macrophages from C57BL/6 mice (VARESIO et al. 1990). Moreover, it was found that macrophages from C3H/HeJ and C3H/HeN mice, which do not become cytotoxic in response to IFN- $\gamma$  alone, could be fully activated by picolinic acid plus IFN- $\gamma$ (VARESIO et al. 1990). Therefore, picolinic acid functions as a second signal in macrophage activation. Since altered rRNA metabolism, whether induced by picolinic acid or by another appropriate stimulus, was necessary for the expression of cytotoxic activity, a causal connection between these two events is supported by these results. Picolinic acid alone altered the rRNA metabolism but did not elicit the cytotoxic response even in C57BL/6 macrophages, which can be activated by IFN- $\gamma$  alone (VARESIO et al. 1990), indicating that the accumulation of pre-RNA was a necessary but not sufficient event to trigger tumoricidal activity.

One difference between classical second signals and picolinic acid is that picolinic acid alone augments pre-rRNA, whereas low amounts of LPS or Listeria monocytogenes require the costimulatory activity of IFN- $\gamma$  to affect rRNA metabolism (VARESIO et al. 1990). This difference in the mechanism of action can be reconciled by the consideration that picolinic acid is a metabolite of tryptophan and in itself may be a macrophage product, acting in an autocrine manner. In this context, only the combined action of IFN- $\gamma$  plus a second signal may induce sufficient picolinic acid, or may deliver it to the correct intracellular compartment, to modify the rRNA metabolism. The possibility that picolinic acid is produced by activated macrophages is supported by several pieces of evidence. IFN- $\gamma$  can induce, in vivo and in vitro, indoleamine 2,3-dioxygenase (IDO), the first enzyme in a major pathway for degradation of tryptophan (WERNER-FELMAYER et al. 1989; CARLIN et al. 1989a, b, d; WERNER et al. 1987a, b, 1988; BYRNE et al. 1986a; BIANCHI et al. 1988; YASUI et al. 1986), and some biologic effects of IFN-y involve tryptophan degradation. (OZAKI et al. 1987, 1988; MAZA and PETERSON 1988; PFEFFERKORN 1984, 1986; PFEFFERKORN et al. 1986; AUNE and POGUE 1989; CARLIN et al. 1989c. MURRAY et al. 1989; BYRNE et al. 1986b). In the catabolism of tryptophan there is a branch point that leads to either picolinic or quinolinic acid. Picolinic acid is an end product whereas quinolinic acid is further metabolized to nicotinate mononucleotide, an important enzymatic cofactor. Thus IFN-y initiates a pathway of tryptophan metabolism in which picolinic acid may be one of the by-products. The ability of the body to catabolize

tryptophan to picolinic acid is shown by the identification of picolinic acid in human milk (Evans and JOHNSON 1980). Moreover, there is evidence that picolinic acid is active in vivo in animals and humans (RUFFMANN et al. 1984; LEUTHAUSER et al. 1982; KRIEGER and STATTER 1987; KRIEGER 1980; SEAL and HEATON 1985; EVANS and JOHNSON 1980; MENARD and COUSINS 1983; HURLEY and LONNERDAL 1982) and that it may be involved in vivo in the process of macrophage activation. In fact, intraperitoneal injection of picolinic acid into C57BL/6 mice induced antitumor activity in macrophages without affecting the levels of natural killer cell (NK) activity (RUFFMANN et al. 1984, 1987). These results suggest that this compound may enhance the sensitivity of macrophages to activation by low levels of cytokines present in the peritoneal cavity and may account for the observed antitumor effect of picolinic acid in tumor-bearing mice (LEUTHAUSER et al. 1982). In conclusion, the demonstration that picolinic acid is a macrophage costimulator in vitro, taken together with the evidence that picolinic acid is produced and active in vivo (RUFFMANN et al. 1984; LEUTHAUSER et al. 1982; KRIEGER and STATTER 1987; KRIEGER 1980), supports the hypothesis that picolinic acid can function as an autocrine signal for the activation of macrophages to a cytotoxic stage.

The process of macrophage activation could be depicted as follows (Table 1). IFN-y induces IDO, initiates the catabolism of tryptophan, and generates tryptophan degradation products. This process occurs in many cell types but does not necessarily lead to production of picolinic acid. In macrophages, however, the second signal activates the pathway generating picolinic acid and causes the build up of sufficient and/or available picolinic acid to alter the rRNA metabolism. The accumulation of the rRNA precursor, together with other IFN-yinduced proteins, will lead to the expression of tumoricidal activity (VARESIO 1986; VARESIO et al. 1990). As previously discussed, the second signal alone will not induce rRNA changes, because picolinic acid cannot be formed in the absence of tryptophan degradation induced by IFN-y. The reason why IFN-y alone causes changes in RNA metabolism and activation to a tumoricidal stage of C57BL/6 macrophages may be that IFN-y stimulates macrophages of this strain of mice to produce enough endogenous picolinic acid that an autocrine costimulatory signal is generated. This model is supported by indirect evidence, and the crucial piece of information is the identification of the source(s) of picolinic acid in the

Table 1. rRNA pathway in macrophage activation: a model

- 2. Induction of dsRNA-dependent enzymes
- 3. Induction of tryptophan catabolism with formation of picolinic acid
- 4. Alteration of rRNA metabolism by picolinic acid:
  - a) inhibition of 28S rRNA accumulation leading to
  - b) inhibition of rRNA synthesis and accumulation of rRNA precursors
- 5. Activation of dsRNA-dependent enzymes by the dsRNA structures present in the rRNA precursors and in their degradation products
- 6. Progression of macrophages in the activation process through phosphorylation of relevant substrates by the dsRNA-dependent kinase modulation of RNA levels by the 2–5A synthetase

<sup>1.</sup> Stimulation of macrophages by one signal or a combination of signals sufficient to trigger tumoricidal activity

body and the evaluation of contributing macrophages and macrophage activation.

#### 8 rRNA and Cytotoxic Activity: the Double-Stranded RNA Pathway

Although the correlation between changes in rRNA metabolism and expression of cytotoxic activity and the identification of picolinic acid as a second signal in macrophage activation provide compelling evidence for a causal association between rRNA and cytotoxic activity, it is difficult to transpose such a relationship to a biochemical/molecular level. As discussed previously, the alteration in the rRNA metabolism does not have a detectable impact on the content of mature rRNA during the time required to activate macrophages to a cytotoxic stage. Therefore, it seems unlikely that the altered rRNA metabolism will affect macrophage protein synthesis via a compromised ribosomal function. In contrast, the most prominent quantitative change affecting the cellular content of rRNA is the increase in rRNA precursors associated with the expression of cytotoxic activity. Is there a way by which rRNA precursors can affect cell biology independently of ribosome formation?

Ribosomal RNA precursors are very rich in cytidine and guanosine and the potential secondary structures, on the basis of computer modeling, predict the formation of very stable double-stranded structures (CROUCH 1984; WOESE et al. 1990; MICHOT et al. 1983). Thus, accumulation of rRNA precursors could be interpreted as a possible source of increase in the cellular content of double-stranded RNA (dsRNA). Changes in intracellular dsRNA are potentially relevant due to the existence of enzymes that require dsRNA as a cofactor to be active (SAMUEL 1987; FALTYNEK and KUNG 1988; LENGYEL 1982). We will briefly discuss the possibility that the rRNA precursors can function as an intracellular source of dsRNA to activate dsRNA-dependent enzymes and that such activation is needed for the expression of cytotoxic activity.

Two dsRNA-dependent enzymes have been described that are present in virtually every cell type and are induced by IFN (SAMUEL 1987; FALTYNEK and KUNG 1988; LENGYEL 1982). One of these is 2–5 A synthetase, which, when activated by dsRNA, synthesizes small 2'–5' linked oligomers of adenosine with the general formula pppA (2'p5'A)n, where n is 2 or more. For convenience this mixture of oligonucleotides is referred to as 2–5 A. The function of 2–5 A is to bind and activate a latent endoribonuclease that degrades RNA. The other well-described enzyme is the dsRNA-dependent protein kinase, which, when activated by dsRNA, phosphorylates the alpha subunit of protein synthesis initiation factor 2 (eIF2) and inhibits its recycling. The dsRNA protein kinase has been purified and characterized (MEURs et al. 1990). Activation of the kinase with dsRNA is accompanied by autophosphorylation of a 65-kDa protein

(p65) in mouse and in rabbit cells or of a 68-kDa protein (p68) in human cells. The p65 and p68 kinases are phosphorylated on several serine and threonine residues (HOVANESSIAN 1989; KURST et al. 1984), giving phosphate-saturated molecules that are more acidic and show higher molecular weights than those that are partially phosphorylated or unphosphorylated (KURST et al. 1984). p68 human kinase activity is independent of cAMP or cGMP, is markedly stimulated by manganese, and has two distinct activities: autophosphorylation and phosphorylation of exogenous substrates. The former is dependent on dsRNA, divalent cations, and ATP. The latter is not dependent on dsRNA and occurs as long as the p68 remains phosphorylated (GALBRU and HOVANESSIAN 1985). Dephosphorylation can be catalyzed by a manganese iondependent class I phosphatase (SzyszkA et al. 1989).

Three main forms of 2–5 A synthetase have been described, corresponding to proteins of 40-46, 69, and 100 kDa (HOVANESSIAN et al. 1988). The small forms of 2-5A synthetase are derived from the same gene by differential splicing between the fifth and an additional sixth exon of this gene (BENECH et al. 1985; SAUNDERS et al. 1985), and they thus differ in their C-terminus. The large forms of 2-5 A synthetase are probably encoded by another gene or genes. The small and large forms of 2-5A synthetase differ substantially in their kinetics of expression and response to inducers. p100 seems to be a monomer found in a diffuse state in the cytoplasm whereas p69 is partially myristilated, seems to exist in a dimeric form, and is partly concentrated around the nucleus and partly distributed in the cytoplasm in a somewhat specific pattern (MARIE et al. 1990). p69 has the capacity to synthesize longer oligomers, whereas p100 has a tendency to mainly synthesize the dimeric form of 2-5A (HOVANESSIAN et al. 1988). As the dimeric form has no known function and does not activate the latent ribonuclease, p100 may be involved in catalyzing other reactions. It is, therefore, possible that the different forms of 2–5 A synthetase may be activated under different physiologic conditions and in different cell types, and that they may have different functions. dsRNA-dependent enzymes were originally implicated in the antiviral effects of interferons since the kinase, by inactivating the eIF2, could block the translation of the viral proteins, and the 2-5A synthetase could cause degradation of the viral mRNA through activation of the RNase activity. The viral RNA would provide the dsRNA needed for the activation.

dsRNA-dependent enzymes are induced during the process of macrophage activation since most of the activators are either IFNs or IFN-inducers (ADAMS and HAMILTON 1984, 1987). IFN- $\gamma$  is among the most effective activators of macrophages. IFN- $\alpha/\beta$  can also induce cytotoxic macrophages, although the mechanisms of activation are different (BLASI et al. 1984; PACE et al. 1983). Poly I:C, LPS, and pyran copolymer among the many macrophage activators that are inducers of IFN, and the endogenous production of interferon could contribute to the activation process. Therefore, under conditions in which macrophages are activated and rRNA precursor accumulates, dsRNA-dependent enzymes are also induced in macrophages (GUSELLA et al., manuscript in preparation). Any biologic role of these dsRNA-dependent enzymes in macrophages requires that



**Fig. 1.** Ribosomal RNA precursors were generated by in vitro transcription of the 3.7-kb *E*coRI-*Bam*HI fragment of the mouse rDNA containing the 3' terminal domain of the 18S rRNA, internal transcribe spacers, 5.8 rRNA, and the 5' terminal domain of the 28S rRNA (MICHOT et al. 1983) cloned in the pGEM expression vector. Following in vitro transcription with the T7 polymerase, the rRNA transcript was purified and assayed for its ability to induced phosphorylation of histones by activating the dsRNA-dependent kinase. S100 pellets of IFN-*β*-treated fibroblasts were used as the source of dsRNA-dependent kinase, and the assay was performed as previously described (MINKs et al. 1979). The "*control*" *lane* depicts the background phosphorylation in the absence of rRNA; the *lane*  $T^+$  *ANase* A depicts the phosphorylation induced by 0.1 µg/ml of rRNA pretreated with RNase A for 30 min at 37 °C to digest single-stranded RNA; the *lane*  $T^+ + RNase$  V1 depicts the phosphorylation induced by 0.1 µg/ml of rRNA pretreated RNA; the double-stranded RNA

cellular RNA can function as a source of dsRNA structures. It is postulated that the rRNA precursors or their byproducts generated during the rRNA precursor maturation contain double-stranded structures capable of activating dsRNA enzymes. Indeed, it has been observed that pre-rRNA generated by in vitro transcription of cloned murine rRNA genes could serve as a source of dsRNA in the activation of 2-5A synthetase and kinase (BOTTAZZI et al., manuscript in preparation; VARESIO 1986). Activation of murine dsRNA-dependent kinase by rRNA precursors is shown in Fig. 1. Experiments in which the rRNA transcripts were digested with RNAse A (degrading single- stranded RNA) or RNAse VI (degrading double-stranded RNA) demonstrated that RNAse VI, not RNAse A, could abrogate the ability of the rRNA transcripts to activate dsRNA-dependent protein kinase (Fig. 1). These experiments indicated that the double-stranded secondary structure of the rRNA transcripts was responsible for the activation of dsRNA-dependent enzymes. It is difficult, however, to know the secondary conformation of rRNA precursors in the intact cell, where the RNA is rapidly processed and is coupled to protein. Therefore, these results indicate that in vitro rRNA precursor folds into secondary structures capable of activating dsRNA, but the extent to which these double- stranded regions exist and are available for the dsRNA-dependent enzymes in vivo remains to be established. On the other hand, if we think that dsRNA is biologically relevant in nonvirally infected cells, we must accept the notion that cellular RNA can fold into double-stranded structures available for the activation of dsRNA-dependent enzymes, and rRNA is a good candidate.

A potential problem of such model is that rRNA precursors are mainly present in the nucleolus and dsRNA-dependent enzymes have so far been described in the cytoplasm and the perinuclear region. It cannot be excluded, however, that dsRNA-dependent enzymes exist in the nucleus since the

components of this class of enzymes is growing, and a thorough analysis of the intracellular compartmentation has not been possible for lack of specific reagents. Moreover, it must be considered that degradation products of rRNA precursors generated during its maturation could reach the cytoplasm and activate dsRNA-dependent enzymes, particularly if folded in double-stranded structures. In fact, enzymes degrading dsRNA have not been described in eukaryotic cells and the double-stranded regions of rRNA precursors could be quite stable. Reports of small cytoplasmic RNA with various degrees of affinity for rRNA support this possibility (KING and GOULD 1970; BUSCH et al. 1982, MCLURE and PERRAULT 1986; PERKINS et al. 1986). However, a thorough investigation of the fate of the rRNA spacers, as well as of the introns of mRNA, has never been performed. We have evidence that discrete regions of the rRNA precursor spacers can activate dsRNA-dependent enzymes (BOTTAZZI et al., submitted for publication). In conclusion, the proposed model of activation of dsRNAdependent enzymes by rRNA precursors or their degradation products needs further experimental support but it contains a provocative working hypothesis on one activation pathway of macrophages.

# 9 Double-Stranded RNA-Dependent Enzymes in Cell Biology

dsRNA-dependent enzymes may have important biologic functions in non-virally infected cells in mediating the cellular response to IFN. Evidence that dsRNAdependent enzymes are also important in the biology of nonvirally infected cells is provided by studies on the effects of the kinase inhibitor 2-aminopurine (2AP). The two kinases that are known to be inhibited by 2AP in cell-free systems are the heme-regulated and the dsRNA-dependent eukaryotic initiation factor (eIF)-2a kinases (DE BENEDETTI and BAGLIONI 1983; FARRELL et al. 1977). Although the specificity of the inhibitory effects of 2AP has not been systematically studied in vivo, 2AP does not significantly alter the overall pattern of protein phosphorylation in HeLa cells. Thus, 2AP does not appear to be a general inhibitor of cellular kinases, although, like any other metabolic inhibitor, it may have unknown side-effects. It has been reported that 2AP specifically inhibits the induction of IFN- $\beta$ , c-fos, and c-myc at the level of transcription in human osteosarcoma cells stimulated with poly I:C or virus, suggesting that dsRNAdependent kinase could be involved in controlling gene expression (ZINN et al. 1988). Similar conclusions were reached in studies of the effects of 2AP on gene induction by interferons and double-stranded RNA in HeLa cells (TIWARY et al. 1988). Finally, 2AP has been shown to inhibit the activation of murine macrophages by high doses of LPS, providing preliminary evidence of the involvement of dsRNA-dependent kinase in the process of activation of macrophages to a tumoricidal stage (GUSELLA et al., manuscript in preparation). Macrophage activation is associated with expression of new proteins (MACKAY et al. 1989) and phosphorylation by dsRNA-dependent kinase could modulate their activity.

The potential role played by 2–5 A synthetase in the regulation of cell growth is supported by the demonstration of correlations between changes in enzymatic activities and the degree of confluence of the culture (STARK et al. 1979), the state of differentiation (SOKAWA et al. 1981), and the phase of the cell cycle (KRISHNAN and BAGLIONI 1981; WELLS and MALLUCCI 1985). In addition, agents such as hormones (STARK et al. 1979) and inducers of differentiation (BOURGEADE and BESANCON 1984; FERBUS et al. 1985) also influence the levels of 2–5 A synthetase. In general, growth-inhibited cells have higher levels of 2-5A synthetase than rapidly proliferating cells. Thus, 2-5A synthetase may serve as an important mediator of the antiproliferative actions of IFN- $\gamma$ . Moreover, studies on the antiproliferative affects of IFN- $\gamma$  revealed varying kinetics of expression of 2–5 A synthetase isoenzymes in the A431 human tumor cell line: the 100-kDa and 40kDa isoforms were induced early with a subsequent decline whereas the 67-kDa was induced late and remained high up to 9 days after IFN-y treatment (KUMAR and MENDELSON 1989). It is unclear, however, which is the source of the dsRNA activating the enzymes. It is possible that in these situations the rRNA precursors may also play a role as donors of dsRNA, because it has been shown that the transition of cell lines from a growing to a resting state is associated with altered accumulation of rRNA (OUELLETTE et al. 1976; BIZZOZZERO et al. 1985; TONIOLO and BASILICO 1975; BOWMAN and EMERSON 1977; EMERSON 1971) and that the eIF-4F and eIF-2 activities are inhibited by serum deprivation (DUNCAN and HERSHEY 1985). One can speculate that the accumulation of rRNA precursors is involved in the activation of the dsRNA-dependent kinase responsible for the phosphorylation and inactivation of the initiation factors for protein synthesis. Also, in nonmacrophagic cell types the imbalanced accumulation of rRNA appears to be linked with a functional state rather than a response to IFN. In fact, growth-arrested fibroblasts do not alter rRNA metabolism in response to IFN-y (RADZIOCH et al. 1987a). Degradation of rRNA but not of viral mRNA has been observed in IFN-treated L cells infected with DNA-containing viruses (Goswam and SHARMA 1984). Since the degradation pattern of rRNA is consistent with the action of the latent ribonuclease induced by 2-5A, it can be speculated that activation of 2-5A synthetase by dsRNA structures of rRNA results in rRNA degradation via a feedback type of mechanism.

Every RNA molecule, including mRNA, can fold into a secondary structure containing a certain degree of double-stranded structure. If these double-stranded secondary structures are sufficiently stable and accessible, they can activate the dsRNA-dependent enzymes in a localized and compartmentalized fashion. Indeed, there are indications that double-stranded loops of mRNA can control its expression via activation of dsRNA-dependent enzymes. For example, the activation of dsRNA-dependent kinase is a mechanism that may control the translation of HIV-1 mRNA (EDERY et al. 1989), although this possibility is still controversial (GUNNERY et al. 1990). It was found that the TAR region of the 5' end of the HIV-1mRNA, which responds to the *tat-trans*-activating protein, assumes a

stable secondary structure responsible for the ability of TAR to inhibit *in trans* the translation of other mRNAs in a cell-free system. This mechanism of translation inhibition involves the activation of dsRNA-dependent kinase and phosphorylation of the protein synthesis initiation factor 2 (eIF-2). Mutations in the TAR region that diminish the stability of the secondary structure cause a significant inhibition of the *trans*-activation (Roy et al. 1991).

Indications of a potential role of dsRNA-dependent kinase in the control of mRNA expression derive from experiments with 2AP. If local activation of dsRNAdependent kinase is an inhibitory signal for mRNA expression, one would expect 2AP to augment selectively the expression of mRNAs endowed with a stable double-stranded structure. Indeed, it has been shown that 2AP increases the translation efficiency of mRNA molecules from plasmid DNA transfected into COS-1 cells, presumably via alteration of the functional levels of eIF-2 (KAUFMAN and MURTHA 1987; KALVAKOLANU et al. 1991). These results confirm the pioneering work by DE BENEDETTI and BAGLIONI (1984), who demonstrated the specific inability to initiate translation of vesicular stomatitis virus mRNA containing a poly(U) tail hybridized to the poly(A) tail. Thus, the activation of the kinase would be bound specifically to the mRNA containing double-stranded features, resulting in specific, localized inhibition of protein synthesis. In conclusion, there is evidence that the dsRNA-dependent enzyme system may be involved in important cellular functions including macrophage activation. In order to delineate the role of dsRNA-dependent enzymes in cell biology it is crucial to define the endogenous dsRNA structures needed to activate these enzymes and the regulation of expression of these dsRNA species. The rRNAs are potential donor of double-stranded RNA capable of activating dsRNA-dependent enzymes, and rRNA is synthesized at a high enough rate to allow diversion of some of it to function as an enzyme activator rather than as a building block for the formation of ribosomes.

### **10 Conclusions**

The goal of this article has been to review the changes in RNA metabolism that occur in macrophages and their connection with the process of activation. Evidence was presented that imbalanced accumulation of rRNA and accumulation of rRNA precursors in macrophages are directly associated with the activation of these cells to a cytotoxic stage. A metabolite of tryptophan, picolinic acid, induces similar changes in rRNA metabolism and functions as a second signal for macrophage activation, suggesting that picolinic acid produced by macrophages or by surrounding tissues may be the mediator of the changes in rRNA. Stable double-stranded regions of the rRNA precursors that accumulate in cytotoxic macrophages activate, in a cell-free system, dsRNA-dependent enzymes and could be a physiologic source of dsRNA structures in vivo. It is likely that dsRNA-dependent enzymes activated by rRNA precursors (and/or their

degradation products) play a major role in the induction/expression of the activated phenotype.

Three players support the action in this scenario: rRNA, tryptophan metabolism, and dsRNA-dependent enzymes. The evidence implicating each of them in the process of macrophage activation is quite strong and the connection among the three of them is supported, although not yet unequivocally proven, by the results of ongoing research.

There is a consensus that the secondary structure of RNA is important for its stability and interactions with proteins. Although mRNA is being more actively studied at the present time, rRNA remains the most abundant and transcribed cellular RNA and the mechanisms controlling rRNA maturation are still largely obscure. A cyclical trend in the interest in rRNA and ribosome has indeed been noted (MOORE 1988). We feel that the macrophage activation system and the associated changes in rRNA metabolism provide an interesting and perhaps unique model for exploring the molecular basis of rRNA control since it has been established that transcriptional and post-transcriptional events modulate the expression of ribosomal genes in a nonproliferative system. Thereby, it may be possible to explore other functions of rRNA that might have been hidden by the ribosome formation task in proliferating cellular systems.

The study of dsRNA-dependent enzymes in the process of macrophage activation is important since IFNs are powerful activators of macrophages. Although the existence of these enzymes has long been known, only recently have some members of this family been cloned and only now can a critical evaluation of their functions be performed. Perhaps some hesitation in pursuing studies on these enzymes was due to questions concerning the origin and nature of the dsRNA needed for their activation. Growing evidence indicates that the secondary structure of rRNA and mRNA can activate dsRNA-dependent enzymes, supporting the notion that these enzymes may be of major biologic relevance even in the absence of viral infection.

Studies on tryptophan metabolism fell away decades ago. Picolinic acid was known to exist but questions regarding its function elicited merely sporadic interest. The discovery that IFN augments tryptophan metabolism and that picolinic acid affects rRNA maturation and macrophage activation gave rise to renewed interest in roles that this amino acid may have in the biology of macrophages and of the entire organism.

Since we have had to discuss so many varied topics in this chapter, and due to space limitations, we have not been able to cite all the important relevant papers; our apologies are offered to the authors of such papers.

J.H. Huxley made reference to "the great tragedy of science: the slaying of a beautiful hypothesis by an ugly fact." Ugly facts may modify our current view of macrophage activation. However, the questions addressed by our hypothesis are of basic relevance for macrophage and cell biology. Should an ugly fact disprove our hypothesis but also provide a definitive explanation for the interplay among rRNA, tryptophan, and the cytotoxic activity of macrophages, a major achievement would still have been accomplished and our hypothesis would

have had the merit of having set the stage for the exposure of such a fundamental uply fact.

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# Mononuclear Phagocytes as Targets, Tissue Reservoirs, and Immunoregulatory Cells in Human Immunodeficiency Virus Disease

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## 1 Mononuclear Phagocytes as a Tissue Reservoir for Virus in the HIV-Infected Patient

Infection by the human immunodeficiency virus (HIV) initiates a slowly progressive degenerative disease of the immune system termed the acquired immunodeficiency syndrome (AIDS). The primary immunologic defect in AIDS is an inexorable depletion of CD4<sup>+</sup> T cells, a depletion invariably associated with opportunistic infection, degenerative neurologic disease, a variety of neoplastic changes, and ultimately death (LIFSON et al. 1988). The fequency of infected cells in blood of asymptomatic HIV-seropositive subjects, as detected by polymerase chain reaction gene amplification of DNA from leukocyte lysates or by direct isolation of HIV from limiting dilutions of blood leukocytes, is about 1 in 40000 (0.0025%). This frequency increases about 1000-fold in patients with symptomatic disease: AIDS-related complex (ARC) and AIDS (SCHNITTMAN et al. 1989; PSALLIDOPOULOS et al. 1989; Ho et al. 1989a). Studies further show that virtually all infected blood leukocytes throughout HIV disease are CD4<sup>+</sup> T cells (SCHNITTMAN et al. 1989; PSALLIDOPOULOS et al. 1989). Indeed, in late-stage disease about 1 in 40 CD4<sup>+</sup> T cells harbor virus. Attempts to detect viral protein or mRNA in blood leukocytes of seropositive patients, however, reveal a frequency of productively infected cells in early or late disease of no more than 0.001%

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(HARPER et al. 1986). Thus, >99% of infected T cells are latently infected. But T cells are not the only target cell for HIV. In certain bodily tissues, such as those of the central nervous system, lymph nodes, or lung, the frequency of cells productively infected with HIV may be 10000-fold higher than that in blood. In each of these tissues, the predominant cell type infected with HIV and producing virus is not the CD4<sup>+</sup> T cell, but rather the macrophage (for reviews see GENDELMAN et al. 1989; MELTZER et al. 1990).

Neurologic disease is strongly associated with HIV infection: more than 60% of patients with AIDS show symptomatic CNS disease; 80%-90% have neuropathologic abnormalities at autopsy (Ho et al. 1989b). Such abnormalities are characterized by typical pathologic changes in brain and spinal cord. HIV-induced changes in the brain are most evident within the white matter and include atrophic changes without inflammation but associated with microglial nodules (clusters of microglia and reactive fibrous astrocytes) and multinucleated giant cells. Virus isolation from cerebrospinal fluid or homogenates of brain tissue is successful in most patients with AIDS-associated encephalopathy by (LEVY et al. 1985). Indeed, virus isolation from cerebrospinal fluid of patients with acute aseptic meningoencephalitis during HIV infection can occur before seroconversion (Ho et al. 1985b). The predominant infected cell (and in most studies, the only infected cell) is the macrophage (STOLER et al. 1986; KOENIG et al. 1986). In situ hybridization for HIV RNA in brain tissue of infected individuals shows a frequency of productively infected macrophages at 1%-10%. Brain macrophages (subarachnoid, perivascular, and parenchymal cells), microglia, and macrophage-derived, multinucleated giant cells possess 500-1500 copies of HIV RNA per cell. This amount of virus RNA per infected cell is at least ten fold higher than that found in blood leukocytes. Interestingly, almost all of the HIV-infected brain macrophages are negative for CD4 by immunocytochemistry (VAZEUX et al. 1987).

Pathologic changes induced in the spinal cord by HIV are different from those in the brain. Vacuolar myelopathy with macrophage infiltrates is found at autopsy in about 25% of patients with AIDS (EILBOTT et al. 1989). The high frequency of HIV-infected macrophages with myelin in phagocytic vacuoles suggests a proximate role for these cells in the pathogenesis of AIDS-associated myelopathy syndrome.

Transmission electron microscopic analysis of lymph nodes from HIVinfected individuals showed typical virions in virtually all specimens examined (26 of 30 lymph nodes), even in those patients with early asymptomatic infection (ARMSTRONG and HORNE 1984; LE TOURNEAU et al. 1986). Viral particles are found only in follicular dendritic cells with an approximate frequency of 10% (GYORKEY et al. 1985). Similarly, HIV can be isolated from cells in bronchoalveolar lavage fluids (>90% macrophages) (ZIZA et al. 1985). HIV proteins or nucleic acids are detected in 10%–50% of the macrophages in such fluids (CHAYT et al. 1986; PLATA et al. 1987). Epidermal Langerhans cells, the dendritic, CD4<sup>+</sup> antigen-presenting cell of skin, are also targets for HIV infection. In skin biopsies of 40 seropositive patients, HIV-infected Langerhans cells were identified in about 20%. However, such HIV-infected Langerhans cells were present at a frequency of infection much lower than that for macrophages of brain, lymph node, or lung (TSCHACHLER et al. 1987). Indeed, other investigators found immunocytochemical evidence for HIV infection in cells of the oral mucosa in only 2 of 26 seropositive patients (BECKER et al. 1988) or in 0 of 44 skin biopsies (KANITAKIS et al. 1989). These studies suggest that while Langerhans cells are susceptible targets for HIV infection (RAPPERSBERGER et al. 1988), the frequency of this event during HIV disease is much lower than that of other tissue macrophages.

The relatively high frequency of productively infected macrophages found in brain, lymph nodes, and lung (10%–50%) is not observed in all bodily tissues. For example, in the steady state about 60% of blood monocytes settle in the liver as Kupffer cells, yet Kupffer cell infection in HIV disease has not been described. Capacity to infect a tissue macrophages may be dependent upon cellular factors that change with differentiation. In visna-maedi disease of sheep, certain tissue macrophages are highly permissive for virus replication (macrophages of brain, lung, lymph nodes, and bone marrow), while other macrophages are resistant (connective tissue histiocytes, liver Kupffer cells) (GENDELMAN et al. 1985). Permissiveness of tissue macrophages to HIV and other lentivirus infection is dependent upon cell differentiation. Unlike many other cell types, however, changes in macrophage differentiation do not occur with cell cycle changes (tissue macrophages replicate at very low levels, if at all), but rather after exposure to any of a multitude of exogenous and endogenous stimuli. It is these stimuli that control the replication of HIV in mononuclear phagocytes.

#### 2 Changes in Mononuclear Phagocyte Number, Phenotype, or Function During HIV Infection

Numerical, phenotypic, or functional changes that occur in macrophage subpopulations during HIV infection are not well defined. Observations made by different investigators using similar experimental techniques are often contradictory. Moreover, virtually all studies to date suffer two major interpretive problems. First, patient selection has been limited to individuals with late-stage, symptomatic HIV infection. The average time interval from seroconversion for HIV antibody to onset of AIDS may be > 10 years (LIFSON et al. 1988). Analysis of macrophage numbers, morphology, phenotype, or function in this asymptomatic time interval is almost non-existent. Second, the macrophage subpopulation most frequently analyzed has been the blood monocyte. This precursor cell to all tissue macrophages has a relatively short circulating half-life in blood of about 30 h. Migration of blood monocytes into tissue is unidirectional: unlike T cell traffic patterns, there is no evidence for tissue macrophage reentry into the blood. As previously stated, the reservoir for HIV in blood is the CD4<sup>+</sup> T

cell. Thus, virtually no blood monocytes examined for any change during HIV disease are infected.

Most studies (but not all) document normal numbers of blood monocytes in HIV-infected patients even during late-stage disease where CD4<sup>+</sup> T cells may be undetectable (POLI et al. 1985; SIEGAL et al. 1986; ENK et al. 1986). Similarly, most studies document normal phenotypic expression of plasma membrane antigens by flow cytometric analysis with monoclonal antibodies. Expression of the class II major histocompatibility complex determinants (HLA-DP, HLA-DQ, HLA-DR) by monocytes from HIV seropositive individuals is indistinguishable from that of cells from seronegative donors (HAAS et al. 1987). Changes in class II major histocompatibility complex determinants induced in monocytes after treatment in vitro with interferon- $\gamma$  (IFN- $\gamma$ ) or bacterial endotoxic lipopolysaccharides (LPS) were similar to those induced in control cells (HEAGY et al. 1984). Expression of several other plasma membrane determinants (CD4, CD11, CD14, CR3, transferrin receptor, Fc receptor I and II, or Mo3e) by monocytes from HIV-infected patients was also normal (DAVIDSON et al. 1988). Other studies performed with similar methodologies document significant changes in the expression of these monocyte membrane antigens (SEI et al. 1986; RIEBER and RIETHMULLER 1986; ROY et al. 1987; KOETHE et al. 1989). While it is difficult to reconcile such disparate observations, recent reports that the envelope glycoproteins of HIV, gp41 and gp120, both act directly on monocytes to induce phenotypic or functional change provide a potential mechanism to explain such variability (WAHL et al. 1989; WAHL LM et al. 1989; NAKAJIMA et al. 1989; TAS et al. 1988; MERRILL et al. 1989). Indeed, that expression of HLA-DR on monocytes was decreased only in those patients with detectable levels of p24 capsid protein in their blood supports this hypothesis (BRAUN et al. 1988).

Analysis of macrophage function during HIV infection has been approached both in vivo and in vitro. Several studies by BENDER and colleagues showed impaired clearance from circulation of particles that express Fc (spleen macrophage-mediated clearance) or C3 (hepatic Kupffer cell-mediated clearance) determinants in most patients with late-stage HIV infection (BENDER et al. 1988). In vitro assays that assess monocyte function suffer the identical interpretive problems previously mentioned for phenotypic changes. Monocyte chemotactic responses to any of several different chemoattractants were each depressed below normal levels (POLI et al. 1985; SMITH et al. 1984). This phenomenon can be duplicated with monocytes from seronegative donors after exposure of cells of purified gp41 or gp120 proteins (WAHL SM et al. 1989; TAS et al. 1988). Monocyte mircrobicidal activity against any of several unrelated pathogens (Candida albicans, C. guelliermondi, C. neoformans, Aspergillus fumigatus, Thermoascus crustaceus, Toxoplasma gondii, Chlamydia psittaci) was normal both in steady state and after further in vitro exposure to IFN- $\gamma$ (MURRAY et al. 1984, 1987, 1988; NIELSEN et al. 1986; EALES et al. 1987; ESTEVEZ et al. 1986). Phagocytosis of latex beads or infectious microbes such as Candida or Toxoplasma was normal (POLI et al. 1985; MURRAY et al. 1984; ESTEVEZ et al. 1986). Release of toxic monocyte secretory products that serve as effector molecules in antimicrobial reactions such as  $H_2O_2$ , interleukin-1 (IL-1), or tumor necrosis factor (TNF- $\alpha$ ) was normal with cells from HIV-infected donors and appropriately increased after further in vitro treatment with IFN- $\gamma$  or LPS (HAAs et al. 1987; MURRAY et al. 1984, 1987; NIELSEN et al. 1986). Moreover, monocytes from HIV-infected patients treated with recombinant IFN- $\gamma$  in vivo also showed increased secretion of  $H_2O_2$  and microbicidal activity against *T. gondii* (MURRAY et al. 1987).

Analysis of tissue macrophages in HIV-infected patients suggests a very different picture from that of the relatively normal blood monocyte population. In skin, Langerhans cells undergo extensive morphologic change even in early disease. Up to 30% of epidermal Langerhans cells show condensation of cytoplasmic and nuclear chromatin, vacuole formation, and cytolysis in the absence of obvious HIV infection (TSCHACHLER et al. 1987). Detection of HIV virions by transmission electron microscopy or of HIV proteins by immunocyto-chemistry was rare. Other studies show profound phenotypic changes in epidermal Langerhans cells in otherwise unaffected, clinically normal skin: the numbers of cells that express HLA-DR or CD1 or show ATPase activity decrease to at least 50% of control levels with late-stage HIV disease (BELSITO et al. 1984; OXHOLM et al. 1986; DRENO et al. 1988).

Follicular dendritic cells in lymph nodes also show major degenerative changes early in HIV infection that increase in extent with disease progression (ARMSTRONG and HORNE 1984; LE TOURNEAU et al. 1986; GYORKEY et al. 1985). Indeed, in late-stage disease there can be complete loss of the follicular dendritic network so important for antigen presentation in lymph nodes (CAMERON et al. 1987). Unlike observations with the epidermal Langerhans cell, viral particles are easily detected in follicular dendritic cells (LE TOURNEAU et al. 1986; CAMERON et al. 1987). Interestingly, Langerhans cells of lymph nodes also do not show HIV virions even in close proximity to obviously infected follicular dendritic cells. It is possible that the degenerative changes observed in epidermal Langerhans cell and lymph node follicular dendritic cell populations represent a special event not apparent with macrophages of other tissues. Unlike other tissue macrophages, the Langerhans cell and the follicular dendritic cell have exceedingly high levels of expression of cell membrane CD4. Mechanisms (largely unknown) that induce depletion of CD4<sup>+</sup> T cells with time after HIV infection may also affect the Langerhans and follicular dendritic cells. Blood monocytes and tissue macrophages have low to undetectable levels of CD4 and may therefore not be susceptible to these degenerative or lytic events.

### **3 Mononuclear Phagocytes as Susceptible Target Cells** for HIV In Vitro

Initial attempts to infect blood monocytes or alveolar macrophages with HIV were suggestive for productive infection but the results were inconclusive. Monocytes cultured with HTLV-IIIB, a strain of HIV passaged continuously in T cells or T cell

lines, bound virus to the cell membrane and ingested viral particles into phagocytic vacuoles within 10 min. HIV was detected in such vacuoles by transmission electron microscopy through 3 days of culture, but no virions were observed budding from the plasma membrane. Assays for reverse transcriptase (RT) activity, p24 antigen (Ag), or other viral proteins by direct immunofluorescence were uniformly negative (NICHOLSON et al. 1986). Addition of mitogeninduced lymphoblasts from seronegative donors to such HIV-infected monocyte cultures 2–3 weeks after the initial virus exposure initiated a productive infection in the T cell targets. Thus, at the very least, monocytes were able to sequester viable HIV and to transmit these infectious particles to T cells (SALAHUDDIN et al. 1986). Other studies with HTLV-IIIB and cultured monocytes showed low levels of RT activity (twice background) 2 weeks after virus inoculation, but no cytopathic effects were induced in the cell monolayer and no cell-associated virions were observed by transmission electron microscopy. The frequency of HIV-infected cells in these cultures as quantified by direct immunofluorescence for HIV proteins was 1%-5% (Ho et al. 1986).

The first evidence for productive HIV infection of monocytes in vitro developed from studies using primary cultures of brain tissue from patients with AIDS-associated encephalopathy (GARTNER et al. 1986). Primary brain explants, enriched for macrophages by repeated trypsin digestion of adherent cell monolayers, released RT activity through 6 weeks of culture. Virus budding from plasma membranes of cultured cells was evident by transmission electron microscopy in a small fraction of cells. This relatively low number of infected cells after 6 weeks of culture was confirmed by in situ hybridization for HIV RNA. Passage of progeny virus on blood monocytes from seronegative donors initiated a productive infection sustained in the monocyte target cells through 2 months. Such monocytes infected with HIV showed a frequency of infected cells in culture of 5%-20% by immuno-fluorescence with monoclonal anti-p17 capsid protein and developed profound HIV-associated cytopathic effects of multinucleated giant cells not present in the uninfected control cultures. Serial dilutions of virus inoculum derived from brain explant cultures were 10- to 100fold more efficient for infection of other monocyte target cells than for T cells. Conversely, HTLV-IIIB was 10 000-fold more efficient in infection of T cell targets than monocytes.

Such distinct differences in target cell tropism for different HIV isolates were confirmed in a subsequent study (KOYANAGI et al. 1987). HIV isolated from cerebrospinal fluid of a patient with AIDS-associated encephalopathy replicated in phytohemagglutinin (PHA)-induced lymphoblasts from seronegative donors, but not in blood monocyte cultures. In contrast, virus isolated from brain tissue infected both lymphoblasts and monocyte target cells. Restriction endonuclease cleavage maps of these two HIV strains were different at only 4 of 26 restriction enzyme sites (15%), a difference much less than that found between two isolates from different patients (15 of 33 sites or 45%). Thus, biologically different but closely related strains of HIV with distinct target cell tropism coexist in various tissues within the same infected patient.

Detailed analysis of HIV-monocyte interaction was impeded by the inability to culture blood monocytes for extended intervals. Conventional culture of monocytes as an adherent monolayer in medium with fetal calf serum results in death of most of the initial cell population (80% loss of viable cells in 1 week). In contrast, monocytes cultured in medium with human serum and recombinant human macrophage colony stimulating factor (MCSF) survived for weeks with little or no loss of cell viability (BECKER et al. 1987; GENDELMAN et al. 1988a). MCSF is made by many cells of the body, including the macrophage itself (but not by T cells). Indeed, in the steady state, normal human blood has about 300-800 U/ml MCSF (HANAMURA et al. 1988). The MCSF receptor, a tyrosine kinase identical to the c-fms proto-oncogene product, is found only on mononuclear phagocytes; the number of receptors per cell increases with cell differentiation. In murine systems, MCSF is a potent growth factor. Bone marrow myeloid precursors and tissue macrophages respond to MCSF with a strong proliferative response and colony formation in growth medium: a single progenitor cell can yield  $> 1 \times 10^9$ progeny (about 1 gram of macrophages). For human macrophages, MCSF is a survival and differentiation factor, not a growth factor (CLARK and KAMEN 1987). Low levels of <sup>3</sup>H-thymidine incorporation are observed in treated cultures, but the numbers of proliferating cells as quantified by counting cells with mitotic figures or nuclear grains on <sup>3</sup>H-thymidine autoradiography were < 3% of the total cell population. Phenotypic analysis of this monocyte population (blood leukocytes obtained through leukapheresis, and the monocytes purified by ficoll-diatrizoate

Antibody	Antigen cluster	% positive cells	
		Blood monocytes	MCSF-treated monocytes (10 days)
leukocyte			
HLe-1	CD45	99	99
transferrin receptor	CD71	2	82
myeloid M01 Leu-15 M02 Leu-M3 HLA-DR <i>B cell</i> B4	CD11b CD11b CD14 CD14 — CD19	90 87 85 88 64	96 94 96 97 73
<i>Т сеll</i> T11 ОКТ3 ОКТ4 Leu-3a ОКТ8	CD2 CD3 CD4 CD4 CD8	3 2 4 5 6	5 3 5 3 8

 Table 1. Phenotypic characterization of fresh and cultured monocytes by monoclonal antibodies and flow cytometry

density gradient centrifugation and counter-current centrifugal elutriation) at 2 weeks in culture documented a cell population > 98% pure (Table 1). The CD4 determinant, the HIV receptor for T cells, was undetected in this cell population by any of several different monoclonal antibodies. Although CD4 is present at low concentrations in blood monocytes, the number of cells that display this plasma membrane determinant has been reported to range from <5% to 90% (HAAS et al. 1987; GARTNER et al. 1986; GENDELMAN et al. 1988a; CROWE et al. 1987; FALTYNEK et al. 1989; MCELRATH et al. 1989). Studies with radiolabeled recombinant gp120 are consistent with the lower estimates. The MOLT/4 T cell line has about 7000 specific gp120 binding sites/cell, and the U937 myeloid cell line about 4000 specific binding sites/cell. In both instances, specific binding is inhibited by monoclonal anti-CD4 and soluble recombinant CD4 (sCD4). In contrast, blood monocytes tested at the time of isolation or after 7 days in culture have < 200specific sites/cell. Almost all binding of radiolabeled gp120 to monocytes is nonspecific and not inhibited by cold gp120, by monoclonal anti-CD4, or by sCD4 (D.S. FINBLOOM, D.L. HOOVER and M.S. MELTZER, unpublished).

Repeated attempts to infect MCSF-treated monocytes with HTLV-IIIB were uniformly negative even at viral inoculum 100000-fold higher than that necessary to infect T cells. In contrast, virus isolation onto MCSF- treated monocytes from blood leukocytes of HIV-infected patients was much more successful. Peripheral blood mononuclear cells (PBMCs) from 33 individuals seropositive for HIV or at risk for HIV infection were cocultivated with MCSFtreated monocytes from seronegative donors (GENDELMAN et al. 1990b). Culture fluids were assayed at 2- to 3-day intervals for p24 Ag by ELISA. Significant levels of p24 Ag were detected in 31 of 33 cultures, an overall viral isolation frequency of 93%. HIV was detected in cultures of MCSF-treated monocyte target cells with PBMCs from patients independent of the subject's age, sex, numbers of CD4<sup>+</sup> T cells, or clinical stage (POPOVIC and GARTNER 1987; WEISS et al. 1988). This relatively high frequency of virus isolation was also unaffected by coincident 3'azido-3'-deoxythymidine therapy. The average time interval to first detect p24 Ag in culture fluids was  $20 \pm 2$  days (mean  $\pm$  SEM for 25 patients), with a median time of 18 days (range of 7-45 days). The time interval necessary to first detect p24 Ag in cultures with PBMCs of patients with normal numbers of CD4<sup>+</sup> T cells  $(830 + 160 \text{ cells/mm}^3)$  and early disease was significantly longer than that required in cultures with PBMCs of patients with decreased numbers of CD4<sup>+</sup> T cells  $(160 + 20 \text{ cells/mm}^3)$  and later stages of disease:  $29 \pm 5$  days for seven early-stage patients vs  $17 \pm 2$  days for 17 later-stage patients (GENDELMAN et al. 1990b)

Human immunodeficiency virus isolates from patient PBMCs in MCSF-treated monocytes were serially passaged in MCSF-treated monocyte cultures. Passage was successful with 17 of 20 isolates, an efficiency of 84%. The average time interval necessary to first detect p24 Ag in these cultures was  $7 \pm 1$  days (mean  $\pm$  SEM for 16 isolates), with a median time of 7 days (range of 2–19 days). HIV-associated cytopathic changes in monocyte monolayers (multinucleated giant cells, cell syncytia, and lysis in about 20%–40% of the cell population) were



**Fig. 1.** HTV-1 induced cytopathic effects in MCSF-treated monocytes. PBMC from HIV-seronegative donors purified to >98% monocytes and cultured as abherent monolayers in medium with human serum and MCSF were exposed to ADA, a monocyte HIV isolate, at a multiplicity of infection of 0.01 infectious virus/cell. Cultures were refed with fresh medium every 2 to 3 days. Photomicrographs of adherent cells 15 days after infection are at 200 X original magnification: (*left*) uninfected MCSF-treated monocytes; (*right*) HIV-1 infected monocytes (GENDELMAN et al. 1988)

apparent at 2 weeks in all cultures (Fig. 1). There was no correlation between these cytopathic effects and the clinical stage at which the virus was isolated.

Human immunodeficiency virus isolates serially passaged three times in MCSF-treated macrophages were added to PHA/IL-2 treated lymphoblasts: levels of p24 Ag released into culture fluids were indistinguishable from those of HTLV-IIIB infected lymphoblasts through 2 weeks of infection. Analysis of such HIV-infected lymphoblasts by levels of RT activity, by in situ hybridization for HIV-specific RNA (5%–20% frequency of cells expressing HIV-specific mRNA), by formation of cell syncytia during infection (3%–10% of total cells), by down-modulation of T cell plasma membrane CD4 (60% CD4<sup>+</sup> PHA/IL-2 treated lymphoblasts prior to infection vs 10% CD4<sup>+</sup> cells 1 week after infection), and by transmission electron microscopy (progeny virions budding at the plasma membrane only, with no intracytoplasmic accumulation of viral particles) showed no qualitative or quantitative differences between HTLV-IIIB and the MCSF-treated monocyte-derived HIV isolates. These experiments document little

or no target cell restriction in virus replication for HIV isolated from patient PBMCs into MCSF-treated macrophages; viral isolates grew equally well in macrophages or PHA/IL-2 treated lymphoblasts.

The preceding observations contrast previous reports of target cell restriction in the propagation of HIV isolates (GARTNER et al. 1986; KOYANAGI et al. 1987; GENDELMAN et al. 1988a). It is possible that target cell permissiveness to HIV infection may vary with different viral isolates. To clarify this point, we examined the serial passage of five clinical isolates of HIV in both MCSF-treated monocytes and PHA/IL-2 treated lymphoblasts: a representative isolate is shown in Fig. 2. PBMCs from five different patients seropositive for HIV were cocultivated with both MCSF-treated monocytes and PHA/IL-2 treated lymphoblasts from seronegative donors. In each of the five patients, an HIV primary isolate was recovered in both monocyte and lymphoblast culture systems. For each of the five patients, HIV isolated in PHA/IL-2 treated lymphoblasts or MCSF-treated monocytes were serially passaged into cultures of the homologous cell type. Furthermore, HIV isolated in MCSF-treated monocytes also infected PHA/IL-2 treated lymphoblasts. In marked contrast, five of five viral isolates recovered from PHA/IL-2 treated lymphoblasts showed no growth in the heterologous MCSFtreated monocytes by the criteria of p24 Ag release, RT levels, or infectious titer. Moreover, viral isolates initially recovered in MCSF-treated monocytes and then passaged in PHA/IL-2 treated lymphoblasts showed little or no evidence of virus growth when placed back into MCSF-treated monocytes. The preceding experiments document the existence of two distinct species of HIV: viruses isolated in MCSF-treated monocytes show dual tropism and infect monocytes and T cells equally; viruses isolated in PHA/IL-2 treated lymphoblasts replicate only in T cells.



**Fig. 2.** Serial passage of HIV isolated from patient blood leukocytes in MCSF-treated monocyte and PHA/IL-2 treated lymphoblast cultures. PBMC from patient 359 were added to 7 day MCSF-treated monocytes or 3 day PHA/IL-2 treated lymphoblasts. Dilutions of culture fluids from the primary isolation and each successive passage were added to other monocyte or T lymphoblast cultures. All cultures were incubated for a 2 hour viral adsorption interval, then washed, and refed with fresh medium every 2 to 3 days through 2 months. HIV infection in monocyte cultures at 2 to 3 weeks and lymphoblast cultures at 1 to 2 weeks were estimated through 2 serial passages by infectious titer and p24 antigen (ng/ml) in pooled culture fluids shown in parenthesis (GENDELMAN et al. 1990b)

The phenomenon of distinct HIV variants with different target cell tropism is found both in vitro and in vivo. Whatever the mechanism for cell tropism, several lines of evidence suggest that the major determinant for this biologic feature of HIV resides in the envelope. HIV released from infected monocytes are very different from those of infected T cells. Radioimmunoprecipitation analysis of HIV proteins in infected monocytes and in the virions released from infected monocytes underscores this profound difference (Fig. 3). The predominant viral proteins synthesized by HIV-infected T cells are *env* gene products. Envelope glycoproteins and their breakdown products exceed those capsid proteins (gag gene products) and their breakdown products. This ratio (env > qag gene products) is maintained for both T cell synthesis of viral proteins and the proteins assembled into viral particles. In the virions released from HIV-infected T cells, > 35% of total viral proteins (gp160 + gp120)/(gp160 + gp120 + p55 + p24) are env gene products. In contrast, the dominant viral proteins synthesized in the HIV-infected monocyte and assembled into viral particles are causid proteins: envelope glycoproteins in the virions released from HIV-infected monocytes represent < 10% of total virus protein. At equivalent levels of RT activity and infectious titer, HIV particles released from infected T cells have at least five times

HTLVIIIB/H9 ADA/MONOCYTES



**Fig. 3.** Radioimmunoprecipitation analysis of HIV proteins in infected monocyte and T cell targets. HIV-specific proteins shown after gel electrophoresis and autoradio-graphy were isolated by radioimmuno-precipitation with pooled HIV-seropositive sera of <sup>35</sup>S-methionine labeled cell lysates and ultracentrifuged culture fluids (virions) from MCSF treated monocyte infected with ADA, a monocyte tropic HIV isolate, or the H9 T cell line infected with HTLVIIIB. Infected cells were to the radiolabel for 30 minutes, then washed with medium and cultured for an additional 1, 2 or 4 h

more envelope glycoproteins than the virions released from infected monocytes. Transmission electron microscopic analysis of progeny virus from infected monocytes and T cells confirms the radioimmunoprecipitation analysis. Characteristic surface projections or envelope "spikes," the morphologic representation of gp120, are evident in the HIV released from infected T cells. Progeny virus released from HIV-infected monocytes show little or no "spikes" and are relatively bald. Perhaps the strongest evidence for the envelope as prime determinant of cell tropism derives from studies with hybrid virions. Proviral clones derived from T cell trophic HIV will not replicate in monocytes. Hybrid constructs of T cell tropic clones with the *env* gene of the monocyte tropic HIV infect both T cells and monocytes (W.A. O'BRIAN and I.S.Y. CHEN, unpublished observations).

Functional consequences of the changes that produce envelope-deficient virions from HIV-infected monocytes are illustrated in experiments with sCD4 (GOMATOS et al. 1990). Soluble recombinant CD4 binds with high affinity to gp120, the envelope glycoprotein of HIV, and at relatively low concentration (0.1- $1 \mu g/ml$  completely inhibits infection of many HIV strains in T cells or T cell lines (SMITH et al. 1987; FISHER et al. 1988; HUSSEY et al. 1988; DEEN et al. 1988; CLAPHAM et al. 1989). HTLV-IIIB infection of the H9 T cell line is completely inhibited by prior treatment of virus with 10  $\mu g/ml$  sCD4 (50% inhibitory dose at 1  $\times$  10<sup>5</sup> TCID  $_{50}$ HTLV-IIIB: <2 µg/ml sCD4). No p24 Ag or HIV-induced syncytia are detected in cultures of H9 cells exposed to  $1 \times 10^5$  TCID<sub>50</sub> HTLV-IIIB in the presence of sCD4. Under identical conditions and at a 100-fold lower viral inoculum, 10µg/ml sCD4 has little or no effect on infection of monocytes by any of six different monocyte tropic HIV isolates as assessed by three different criteria: levels of p24 Ag and RT activity, virus-induced cytopathic effects, and the frequency of infected cells that express HIV specific mRNA (GOMATOS et al. 1990). At 10- to 100-fold higher concentrations of sCD4, however, infection is completely inhibited. Monoclonal anti-CD4 (Leu-3a or OKT4a) also prevents infection of these same viral isolates in monocytes. The relative inefficiency of sCD4 for inhibition of HIV infection in monocytes (about 10 000-fold) is a property of the virion and not the target cell: HIV isolates that infect both monocytes and T cells require similarly high levels of sCD4 for inhibition of infection (50% inhibitory dose at 1  $\times$  10<sup>3</sup> TCID<sub>50</sub> ADA: 100- $200\,\mu\text{g/ml}$  sCD4). These data suggest that the gp120 of HIV derived from macrophages interacts with sCD4 differently than that of virions derived from T cells. For both variants of HIV, however, the predominant mechanism of virus entry for infection is CD4 dependent.

All of the preceding data are consistent with the hypothesis that HIV interaction with CD4 is an obligate reaction for infection of both T cells and monocytes. None of these observations, however, preclude another, CD4-independent route of infection. HIV may enter macrophages through phagocytosis, FcR-mediated endocytosis (NICHOLSON et al. 1986; ROBINSON et al. 1988, 1989; HOMSY et al. 1988; TAKEDA et al. 1988), or interaction with receptors for mannosylated proteins (EZEKOWITZ et al. 1989). Infection of T cells or monocytes
with HIV is markedly enhanced (five to ten fold increase in RT activity in culture fluids) by sera from certain HIV-infected patients. Such antibody-mediated enhancement is not inhibited by monoclonal anti-CD4 (HOMSY et al. 1989). Most impressively, HIV isolates that do not replicate in monocytes (T cell tropic HIV) will infect these cells after treatment with enhancing antibodies (HOMSY et al. 1989). In monocytes, antibody-mediated enhancement of HIV infection is inhibited by monoclonal anti-FcRIII (the predominant Fc receptor in tissue macrophages and monocytes in culture, but absent on circulating blood monocytes) but not monoclonal antibodies directed against FcRI or FcRII. Antibody-mediated enhancement of HIV infection in the myeloid cell line U937, which lacks FcRIII but does express FcRI and FcRII, is blocked by heat-aggregated IgG (TAKEDA et al. 1988). In these studies, the infection pattern of U937 stimulates more closely that of T cells rather than that of monocytes or macrophages. Interestingly, U937 is also a susceptible target cell for several T cell tropic HIV, but not monocyte tropic viruses (KOYANAGI et al. 1987; COLLMAN et al. 1989).

The numbers of monocytes infected with HIV in vitro as quantitated by in situ hybridization for HIV RNA is at least three-fold greater than in lymphoblast cultures. But the number of virions released into culture fluids of HIV-infected monocytes as quantified by infectious titer or RT activity is 10- to 100-fold less than that of infected lymphoblasts. The basis for this apparent dissociation



**Fig. 4.** Virion budding and release in HIV-infected MCSF-treated monocytes and PHA/IL-2 treated lymphoblasts. Transmission electron microscopy of an HIV infected MCSF-treated monocyte (*left*) (viral particles sequestered within intracytoplasmic vacuoles; few or no virions at the plasma membrane) and PHA/IL-2 treated lymphoblasts (*right*) (numerous viral particles budding at the plasma membrane; no intracellular virions), X 9400 (GENDELMAN et al. 1988; ORENSTEIN et al. 1988). (The authors thank DR. Jan M. Orenstein, Dept. of Pathology, George Washington University Medical Center, Washington, DC, for electron microscopy)

between high numbers of infected cells and low levels of infectious virus released into the culture is shown by transmission electron microscopic analysis (Fig. 4). HIV-infected T cells show hundreds of viral particles associated with the plasma membrane: HIV assembles and buds only from the plasma membrane of infected T cells; there is no intracellular accumulation of mature or even immature virions. HIV interaction with macrophages is quite different from that of T cells. Ultrastructural analysis of HIV-infected macrophages 2-6 weeks after infection (time intervals at which 60%-90% of cells express both HIV-specific mRNA and proteins) shows little or no virions at the plasma membrane. Yet these infected cells contain large numbers of viral particles. Virus is localized almost exclusively to intracellular vacuoles. Infected macrophages display numerous vacuolar structures not associated with the plasma membrane, each of which contains scores of mature and immature virions. Indeed, HIV not only accumulates within these intracellular vacuoles but also assembles and buds from the vacuolar membranes. Morphologic evidence strongly suggests that these vacuoles are not endosomes, but rather are derived from the Golgi complex (ORENSTEIN et al. 1988). The macrophage handles HIV much like any other secretory glycoprotein: HIV is assembled in the Golgi complex and transported in Golgi complex-derived vacuoles towards the plasma membrane. Significantly, the final step of secretion, exocytosis into the extracellular milieu, appears suppressed: the amount of virus released from HIV-infected macrophages, quantitated by RT activity or p24 Ag in culture fluids, is ten fold less than that released by an equal number of infected T cells. Thus, the HIV-infected macrophage represents a veritable virus factory, but a factory whose entire output remains hidden from the host. Experiments confirm that the intracellular virions of HIV-infected macrophages are infectious: release of these viral particles by freeze-thaw cycles increases the infectious titer of the culture fluids at least ten fold (GENDELMAN et al. 1988a). Most importantly, these in vitro observations have been confirmed in the AIDS patient. Macrophages in the brain of a seropositive individual also showed intracellular localization of virus particles within vacuoles; little or no virus was detected at the plasma membrane (ORENSTEIN et al. 1988). Such virus, sequestered from host immunity within cytoplasmic vacuoles, represents a true reservoir for continued infection. Release of infectious virus from this macrophage reservoir and dissemination of HIV into other macrophages or T cells could be initiated by any agent that perturbs macrophage function: factors released during inflammation, normal tissue remodeling, or host response to intercurrent infection.

# 4 Mononuclear Phagocytes as Regulatory Cells in the Pathophysiology of HIV Infection

The preceding observations clearly document major roles for macrophages as both target cell and tissue reservoir for infectious virus during HIV disease. HIVinfected macrophages are found in brain, lung, lymph node, skin, bone marrow, and blood of seropositive patients. It is probable that these infected cells directly participate in the pathogenesis of HIV-induced immunosuppression and CNS dysfunction. However, the means and mediators for this participation are not yet understood. A major role for macrophages in the steady state and during disease is regulation of tissue function. This regulatory role is mediated by the literally hundreds of secretory molecules released by the macrophage under a variety of pathophysiologic conditions (NATHAN 1987). Changes in the secretion or release of certain mediators occur during HIV infection and underlie the symptomatology of AIDS.

The paucity of virus-infected lymphocytes in AIDS and the absence of cytolytic infections of neurons or neuroglia suggest an indirect mechanism for immune and rervous system dysfunction in HIV infection (Ho et al. 1989b). For example, macrophages release many secretory products that have direct effects on nerve growth, function, or repair of injury. Inappropriate secretion of these monokines (IL-1, IL-6, TNF- $\alpha$ , platelet-derived growth factor, apolipoprotein e) by HIV-infected macrophages in brain may induce both neurologic symptoms and tissue injury. Moreover, macrophages have receptors for and respond to several neuropeptides (ACTH,  $\beta$ -endorphins, somatotropin, neurotensin, substance P, and vasoactive intestinal peptide) to secrete toxic oxygen metabolites and other injurious monokines. Indeed, recent reports document induction of prostaglandins, IL-1, IL-6, and TNF- $\alpha$  by gp120, the HIV envelope glycoprotein (WAHL SM et al. 1989; WAHL LM et al. 1989; NAKAJIMA et al. 1989; MERRILL et al. 1989). These individual observations provide the basis for a regulatory network in which HIV-infected macrophages affect nerve cells through any of several monokine or virus-derived secretory factors; the injured neural tissue reciprocally affects the HIV-infected macrophage to release even more toxic secretory products (GENDELMAN et al. 1988b).

Similar cytokine networks regulate virus production and latency in HIVinfected macrophages and T cells. But such cytokine networks are very complicated. The sequela of any single cytokine treatment is often unpredictable. For example, HIV replication in monocytes pretreated with granulocytemacrophage colony ctimulating factor (GMCSF) is markedly reduced, yet GMCSF added to monocytes after HIV infection increases virus production (Fig. 5) (HAMMER et al. 1986; MELTZER and GENDELMAN 1988; KOYANAGI et al. 1988; PERNO et al. 1989). Moreover, cytokines almost never operate alone. Most monokines are autocrine factors that induce other monokines (IL-1, IL-6, IL-8, TNF- $\alpha$ , MCSF) which in turn induce cytokines in lymphocytes, endothelial cells, and fibroblasts of adjacent tissue. Effects of cytokines on the replication of HIV are dependent upon the mixture of cytokines that the cell is exposed to, the time of exposure, and the state of differentiation of the responsive cell.

The long interval of clinical latency during HIV infection (50% of infected individuals develop AIDS 10 years after infection) (LIFSON et al. 1988), may be associated with true viral latency (perhaps intermittent) with no expression of HIV in infected cells. In the latent state, HIV exists in T cells as a provirus integrated within host genomic DNA without transcriptional activity. HIV becomes transcrip-



Fig. 5. Effect of GMSCF on replication of HIV in monocytes at various times of virus infection. PBMC from HIV-seronegative donors purified to > 98% monocytes, and cultured 7 days as adherent monolayers in medium with human serum and MSCF were exposed to ADA, a monocyte tropic HIV isolate, at a multiplicity of infection of 0.01 infectious virus/cell. In certain cultures, monocytes were treated with 200 U/ml GMCSF 24 h before viral inoculation, washed free of cytokine, and exposed to HIV. In other cultures, 200 U/ml GMCSF was added 2 h after virus inoculation and maintained at this concentration through 3 weeks. RT activity (cpm/ml 10<sup>-6</sup>), was determined in culture fluids

tionally active and reenters the replicative cycle after exposure of the T cell to any of a variety of apparently unrelated stimuli that include cytokines, mitogens, phorbol esters, infection with herpesvirus, adenovirus, and exposure to sunlight. Control of HIV replication in such infected cells in mediated in large part by cellular rather than viral factors. An animal model that simulates latent HIV infection in man was produced to further identify factors that affect induction of viral gene synthesis in latently infected target cells. Transgenic mice that contain integrated copies of the HIV long terminal repeat (LTR) linked to the bacterial gene for chloramphenicol acetyltransferase (CAT) were constructed (LEONARD et al. 1989). Thus HIV LTR-directed expression of the CAT gene in cells of transgenic animals would be analogous to HIV gene expression for progeny virus production in infected patients whose cells harbor latent integrated proviruses. Under steady state conditions in blood and in tissue, neither macrophages nor lymphocytes express detectable levels of CAT activity. CAT activity in macrophage populations is increased by in vitro treatment with any of several recombinant murine cytokines (IL-1, IL-2, IL-4, MCSF, and GMCSF). A similar phenomenon was observed in vivo. Resident peritoneal macrophages or cells elicited by a sterile, chronic irritant (thioglycollate) showed no CAT activity. However, macrophages recovered from an intraperitoneal immune reaction to Mycobacterium bovis, strain BCG or Proprionibacterium acnes (Corynebacterium parvum) were strongly positive. Purified splenic T cells also showed no constitutive CAT activity. Significantly, cultivation of these T cells in murine IL-2 increased CAT expression 20-fold. Infection of both macrophages and T cells with certain DNA viruses (herpes simplex 1, adenovirus, murine cytomegalovirus) increased CAT activity by as much as 50-fold. Thus, HIV activation in this mouse model system is clearly regulated by endogenous cytokines released from both T cells and macrophages.

Human immunodeficiency virus subverts cellular transcriptional factors and other cellular gene products to direct virus gene expression. For example, the HIV LTR contains a number of *cis*- acting sequences that are targets for transactivators including the cellular DNA-binding proteins NF-kB and Sp1 (NABEL and BALTIMORE 1987; JONES et al. 1986). Activation of the HIV LTR in proliferating T cells after treatment with mitogens or phorbol esters is associated with synthesis of the endogenous DNA-binding protein, NF-kB. Monocytes exposed to LPS release IL-1 and INF-a, monokines that also induce NF-kB binding activity and thereby increase HIV expression in T cells (CLOUSE et al. 1989; GRIFFIN et al. 1989; OSBORN et al. (1989). HIV gene expression in the myeloid cell line U937 is similarly regulated by NF- $\kappa$ B: treatments that induce NF- $\kappa$ B binding activity in U937 (phorbol esters, TNF- $\alpha$ ) markedly increase HIV replication. But the HIV LTR can also be activated by endogenous signals independent of NF- $\kappa$ B: GMCSF, which does not induce NF-  $\kappa$ B binding activity, also activates HIV expression in U937. In contrast to observations with the U937 myeloid cell line, NF-  $\kappa$ B binding activity is present constitutively in blood monocytes (GRIFFIN et al. 1989). The precise regulatory role for this DNA binding protein for HIV replication in monocytes is therefore less clear. MCSF increases HIV expression in monocytes at concentrations equivalent to that normally found in human blood (300-800 U/ml MCSF). Interestingly, levels of MCSF in the blood of patients with infectious disease (sepsis, pneumonia) can increase three to eight fold. Thus, as with the macrophage-neural tissue interactions, complex cytokine networks are formed in the steady state and during immune reactions that regulate HIV expression in macrophages and T cells.

A major player in these regulatory networks in interferon (IFN). Indeed, there is a well-established precedent for IFN as a dominant regulatory molecule in the pathogenesis of several retroviral diseases: murine and avian leukemia, and a number of lentiviral diseases (FRIEDMAN and PITHA 1984). In visna-maedi infection of sheep, virus replication in macrophages is reduced  $\ge$  1000-fold by IFN released from T cells (NARAYAN et al. 1985; KENNEDY et al. 1985). Levels of IFN released by ovine lung leukocytes directly correlate with lentivirus infection of alveolar macrophages (LAIRMORE et al. 1988). In man, IFN activity is found in sera of patients with late-stage HIV disease and is an index of poor prognosis (PREBLE et al. 1985; VADHAN et al. 1986). In a survey of 15 different HIV isolates in both monocytes and lymphoblasts, we found no IFN activity in culture fluids through 3 weeks of infection (GENDELMAN et al. 1990a). But antiviral activity is reported with addition of IFN- $\alpha$ , IFN- $\beta$ , and IFN- $\gamma$  to HIV-infected T cells and macrophages (Ho et al. 1985; PUTNEY et al. 1986; YAMAMOTO et al. 1986; DOLEI et al. 1986; HARTSHORN et al. 1986, 1987; KOYANAGI et al. 1988; MACE et al. 1988; WONG et al. 1988; YAMADA et al. 1988; KORNBLUTH et al. 1989; MICHAELIS and LEVY 1989; CRESPI 1989; CROWE et al. 1989). Any effects of IFN on HIV replication in human traget cells must therefore depend upon exogenous sources for this cytokine. Possible sources for such INF include direct induction of IFN by coincident infection with another microorganism, IFN production as a consequence of immune reactions to foreign antigens, or administration through immunotherapeutic intervention.

Monocytes treated with recombinant human IFN- $\alpha$  at the time of virus challenge show no evidence of HIV infection 3 weeks later: no viral protein, no viral mRNA, and no proviral DNA (Fig. 6). IFN interrupts one or more early event in the virus replication cycle *before* the formation of proviral DNA: binding, uptake, uncoating, or reverse transcription. The exact mechanisms for this antiviral activity are conjectural and include: (a) changes in virus receptor number or distribution (IFN-treated monocytes show marked changes in CD4, FcR, CD11a, and mannosylated protein receptors, each of which is implicated in the uptake of HIV into monocytes); (b) changes in the monocyte plasma membrane that interrupt fusion or uptake of the virion into the cell (IFN-treated cells show alterations in membrane fluidity, microfilament organization, and membrane proteases that could damage bound virus); and (c) changes in subcellular compartments or cytosolic milieu that preclude reverse transcription [IFN- treated cells synthesize 2'-5'(A)oligonucleotides that induce RNases and directly inhibit reverse transcription].

The effect of IFN on monocytes infected with HIV prior to treatment is equally dramatic. Monocyte cultures infected with HIV 7 days before IFN treatment show a gradual decrease in levels of p24 Ag and reverse transcriptase activity to baseline by 3 weeks. HIV-induced cytopathic changes (multinucleated giant cells and cell lysis) are markedly reduced, and the frequency of productively infected cells as quantified by in situ hybridization for HIV mRNA is  $\leq 1\%$  of total cells. In the interim, viral particles released from the IFN-treated, HIV-infected cells are 1000- to 100-fold less infectious than equal numbers of control virions. But,



**Fig. 6.** Effect on IFN on replication of HIV in monocytes at various times after infection, PBMC from HIV-seronegative donors purified to > 98% monocytes, and cultured 7 days as adherent monolayers in medium with human serum and MCSF were exposed to ADA, a monocyte tropic HIV isolate, at a multiplicity of infection of 0.01 infectious virus/cell. At the time of infection (0 h) and 7 days infection, 500 IU/ml rIFN $\alpha$  was added and maintained at this concentration throughout the culture interval. Levels of p24 antigen in culture fluids were determined by ELISA (GENDELMAN et al. 1990a)

unlike the outcome of IFN pretreatment, monocytes treated with IFN 7 days after HIV infection are not free of the retroviral pathogen: levels of proviral DNA in the IFN-treated and control HIV-infected cells were indistinguishable. The presence of large quantities of proviral DNA in cells with little or no evidence for active transcription suggests true microbiologic latency—and this in a nonreplicating cell with no direct evidence for integrated virus. Such transcriptional restriction of virus replication in the IFN-treated, HIV-infected monocytes has no precedent in previously described retroviral systems.

# 5 Summary

We have presented evidence in this review for the following:

- 1. Macrophages are likely the first cell infected by HIV. Studies document recovery of HIV into macrophages in the early stages of infection in which virus isolation in T cells is unsuccessful and detectable levels of antibodies against HIV are absent.
- 2. Macrophages are major tissue reservoirs for HIV during all stages of infection. Unlike the lytic infection of T cells, many HIV-infected macrophages show little or no virus-induced cytopathic effects. HIV-infected macrophages persist in tissue for extended periods of time (months) with large numbers of infectious particles contained within intracytoplasmic vacuoles.
- 3. Macrophages are a vector for the spread of infection to different tissues within the patient and between individuals. Several studies suggest a "Trojan horse" role for HIV-infected macrophages in dissemination of infectious particles. The predominant cell in most bodily fluids (alveolar fluid, colostrum, semen, vaginal secretions) is the macrophage. In semen, for example, the numbers of macrophages exceed those of lymphocytes by more than 20-fold (WOLF and ANDERSON 1988).
- 4. Macrophages are major regulatory cells that control the pace and intensity of disease progression in HIV infection. Macrophage secretory products are implicated in the pathogenesis of CNS disease and in control of viral latency in HIV-infected T cells.

This litany of events in which macrophages participate in HIV infection in man parallels similar observations in such animal lentivirus infections as visnamaedi or caprine arthritis-encephalitis viruses. HIV interacts with monocytes differently than with T cells. Understanding this interaction may more clearly define both the pathogenesis of HIV disease and strategies for therapeutic intervention.

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# **1** Introduction

Legionella pneumophila, the first member of the family Legionellaceae, is aerobic, motile, gram-negative bacterium that causes Legionnaires' disease and Pontiac fever (FRASER et al. 1977; MCDADE et al. 1977; GLICK et al. 1978). Although the family Legionellaceae now contains more than 40 species, *L. pneumophila* causes over 90% of human infections. *L. micdadei*, the second most frequently isolated species in human infection, evidently has lower virulence for humans than *L. pneumophila* as it appears to infect only immunocompromised hosts (MYEROWITZ et al. 1971). *L. pneumophila* normally inhabits aquatic environments,

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and thus humans are accidental, albeit frequent hosts. The bacterium is spread to humans by the airborne route in aerosols arising out of contaminated sources; possibly, the organism is also spread to humans by the waterborne route (MUDER et al. 1986).

L. pneumophila is a facultative intracellular parasite that parasitizes human mononuclear phagocytes (HORWITZ and SILVERSTEIN 1980). The bacterium has been shown to multiply in vitro in cultures of human monocytes and alveolar macrophages (HORWITZ and SILVERSTEIN 1980; NASH et al. 1984), monkey alveolar macrophages (KISHIMOTO et al. 1979; JACOBS et al. 1984), guinea pig alveolar macrophages (ELLIOTT and WINN 1986), guinea pig peritoneal macrophages (KISHIMOTO et al. 1981; YOSHIDA and MIZUGUCHI 1986; YAMAMOTO et al. 1987), hamster peritoneal macrophages (YOSHIDA and MIZUGUCHI 1986), rat alveolar macrophages (ELLIOTT and WINN 1986), rat peritoneal macrophages (YOSHIDA and MIZUGUCHI 1986), and thioglycolate-elicited but not resident peritoneal macrophages from A/J mice (YAMAMOTO et al. 1988). However, thioglycolateelicited and resident peritoneal macrophages of BDF-1 mice and thioglycolateelicited peritoneal macrophages of DBA2, C3H/HeN, C57BL/6, and Balb/c mice do not support growth of *L. pneumophila* (YAMAMOTO et al. 1987, 1988). L. pneumophila has also been shown to multiply in various cell lines, including differentiated HL-60 (MARRA et al. 1990) and U-937 (CIANCIOTTO et al. 1989a) human macrophage-like cell lines, MRC-5 human embryonic lung fibroblasts (WONG et al. 1980; DAISY et al. 1981; OLDHAM and RODGERS 1985), Hep2 human epithelial laryngeal carcinoma cells (DAISY et al. 1981; OLDHAM and RODGERS 1985), HeLa human cervical carcinoma cells (DAISY et al. 1981), Vero African green monkey cells (OLDHAM and RODGERS 1985), and McCoy mouse synovial cells (DAISY et al. 1981). Although it can be cultured on artificial media, L. pneumophila multiplies exclusively intracellularly under tissue culture conditions (HORWITZ and SILVERSTEIN 1980) and, presumably, this is also the case in vivo. In the environment, L. pneumophila evidently multiplies in protozoa. The bacterium has been demonstrated to multiply in vitro in association with Acanthamoeba palestinensis (ANAND et al. 1983), Acanthamoeba royreba (TYNDALL and DOMINGUE 1982), Acanthamoeba castellanii Neff (HOLDEN et al. 1984), Naegleria Iovaniensis (TYNDALL and DOMINGUE 1982), Naegleria fowleri (NEWSOME et al. 1985), Tetrahymena pyriformis' (FIELDS et al. 1984), Cylidium sp. (BARBAREE et al. 1986), and Hartmannella sp. (WADOWSKY et al. 1988).

Initial studies of *L. pneumophila*-mononuclear phagocyte interaction that followed recognition of the bacterium as an important pathogen in 1977 revealed its capacity to multiply intracellularly in human mononuclear phagocytes, described its unusual form of entry into phagocytes, defined its intracellular pathway in mononuclear phagocytes (including its capacity to inhibit phagosome-lysosome fusion and phagosome acidification), and delineated the roles of humoral and cell-mediated immunity in host defense against *L. pneumophila*. More recent studies have begun to elucidate the molecular basis for *L. pneumophila*-mononuclear phagocyte interaction. This review will summarize major advances in our understanding of these interactions.

### 2 Phagocytosis

#### 2.1 Morphology of Entry

Legionella pneumophila enters phagocytes, including monocytes, alveolar macrophages, polymorphonuclear leukocytes, and differentiated HL-60 cells, by an unusual process termed "coiling phagocytosis," in which long phagocyte pseudopods coil around the organism as it is internalized (HORWITZ 1984; MARRA et al. 1990) (Fig. 1). Treatment of L. pneumophila with high-titer anti-L. pneumophila antiserum neutralizes the coiling phenomenon. Such antibody-coated organisms are ingested by "conventional phagocytosis" in which phagocyte pseudopods move circumferentially and more or less symmetrically about the organism until they meet and fuse at the distal side (HORWITZ 1984). Whether anti-L. pneumophila antibody masks surface determinants that mediate coiling phagocytosis or provides ligands that allow Fc receptormediated conventional phagocytosis to dominate internalization of L. pneumophila is unknown. In any case, the end result of both phagocytic processes is the same: the organism comes to reside in a membrane- bound phagosome in which it subsequently multiplies.

Viability is not a determinant of the phagocytic process. Both live and killed *L. pneumophila* enter by coiling phagocytosis (HORWITZ 1984).

Coiling phagocytosis may not be unique to *L. pneumophila. Leishmania donovani* (CHANG 1979) and *Chlamydia psittaci* (WYRICK and BROWNRIDGE 1978) may also enter by coiling phagocytosis. However, other intracellular pathogens including *Mycobacterium leprae* (SCHLESINGER and HORWITZ 1990), *Mycobacterium tuberculosis* (PAYNE et al. 1987; SCHLESINGER et al. 1990), *Trypanosoma cruzi* (NOGUEIRA and COHN 1976; TANOWITZ et al. 1975), and *Toxoplasma gondii* (JONES and HIRSCH 1972) enter by conventional phagocytosis. Thus, the significance of the coiling phenomenon to intracellular pathogenesis, if any, is not clear.

#### 2.2 Receptors Mediating Entry

Complement receptors CR1 and CR3 on human monocytes, which primarily recognize complement fragments C3b and C3bi, respectively, mediate phagocytosis of *L. pneumophila* (PAYNE and HORWITZ 1987). Monoclonal antibodies against these receptors block uptake of *L. pneumophila* into monocytes, and consequently, intracellular multiplication of *L. pneumophila* in these phagocytes (PAYNE and HORWITZ 1987).

As monocytes differentiate to so-called monocyte-derived macrophages in culture, they become increasingly permissive to *L. pneumophila* infection (HORWITZ and SILVERSTEIN 1981a). This may in part reflect the enhanced CR1 and CR3 expression (ESPARZA et al. 1986; FIRESTEIN and ZVAIFLER 1987) and function (NEWMAN et al. 1980) that accompany in vitro maturation.

Δ в С

**Fig. 1A–C** Coiling phagocytosis. **A** Long monocyte pseudopods are coiled around the bacterium, which contains a large lucent fat vacuole. x 33 000. The monocyte pseudopod coils have broken down, presumably as a result of fusing together, so that the bacterium is enclosed in an intermediate-stage intracellular vacuole. Incomplete fusion of monocyte plasma membrane has resulted in the temporary formation of an intracellular sinus cavity. x 50 000. **C** The bacterium residues in a membrane-bound intracellular vacuole. x 52 000. (**A** and **B**: HORWITZ 1984; **C**: HORWITZ 1983a)

Complement receptors appear to provide a general pathway for entry of intracellular pathogens into mononuclear phagocytes (PAYNE and HORWITZ 1987). These receptors have been shown to play a role in the uptake of Leishmania donovani (BLACKWELL et al. 1985), Leishmania major (MOSSER and EDELSON 1985), Mycobacterium tuberculosis (PAYNE et al. 1987; SCHLESINGER et al. 1990), Mycobacterium leprae (SCHLESINGER and HORWITZ 1990), and Histoplasma capsulatum (BULLOCK and WRIGHT 1987). Complement receptors may provide such pathogens safe passage into mononuclear phagocytes because ligation of these receptors by particles coated with fragments of complement component C3 does not trigger an oxidative burst and the release of toxic oxygen metabolites (WRIGHT and SILVERSTEIN 1983; YAMAMOTO and JOHNSTON 1984). Consistent with this hypothesis, L. pneumophila (JACOBS et al. 1984) and several other intracellular pathogens, including M. leprae (HOLZER et al. 1986), T. gondii (WILSON et al. 1980), and H. capsulatum (EISSENBERG and GOLDMAN 1986), have been reported to elicit little or no oxidative burst upon entry into mononuclear phagocytes.

Legionella pneumophila's capacity to avoid toxic oxygen molecules may be important to its intracellular survival, because the bacterium is susceptible to relatively low concentrations of hydrogen peroxide (LOCKSLEY et al. 1982; HORWITZ 1985). This may reflect its low stores of scavengers that might protect it from the toxic effects of hydrogen peroxide, including catalase, glutathiose peroxidase, glutathione reductase, and glutathione (LOCKSLEY et al. 1982). As is typical of microorganisms, *L. pneumophila* is susceptible to lower concentrations of hydrogen peroxide in the presence of a peroxidase, including myeloperoxidase (LOCKSLEY et al. 1982), LOCHNER et al. 1983), eosinophil peroxidase (LOCKSLEY et al. 1982), and lactoperoxidase (HORWITZ 1985), and a halide. In addition to hydrogen peroxide, *L. pneumophila* is sensitive to hydroxyl radical (LOCKSLEY et al. 1982), a more distal product of the oxidative burst. However, the bacterium is relatively resistent to superoxide, perhaps reflecting its relatively abundant stores of superoxide dismutase (LOCKSLEY et al. 1982).

Aside from avoiding it, *L. pneumophila* may possess other mechanisms for protecting itself from the toxic consequences of the oxidative burst. *L. pneumophila* has been reported to elaborate a toxin that inhibits polymorphonuclear leukocyte oxygen consumption, hexose monophosphate shunt activity, bacterial iodination, and bacterial killing (FRIEDMAN et al. 1980, 1982). Along these lines, *L. pneumophila* has also been reported to contain a factor that blocks myeloperoxidase-mediated protein iodination (PERRY et al. 1987). The identifies of molecules possessing these inhibitory capacities have not been determined.

#### 2.3 Ligands Mediating Entry

Fragments of complement component C3 covalently bound to the bacterial surface mediate ingestion of *L. pneumophila* by complement receptors (PAYNE

and HORWITZ 1987; BELLINGER-KAWAHARA and HORWITZ 1987a). Consequently, *L. pneumophila* uptake is markedly reduced in heat- inactivated serum or in the absence of serum (PAYNE and HORWITZ 1987). C3 fixes to *L. pneumophila* by the alternative pathway of complement activation (BELLINGER-KAWAHARA and HORWITZ 1987a).

Consistent with a general role for C3 fragments in phagocytosis of intracellular pathogens, serum has been shown to promote uptake of other intracellular pathogens including *Leishmania donovani* (BLACKWELL et al. 1985; WILSON and PEARSON 1987); *Leishmania major* (MOSSER and EDELSON 1984), *Mycobacterium tuberculosis* (PAYNE et al. 1987; SCHLESINGER et al. 1990), and *Mycobacterium leprae* (SCHLESINGER and HORWITZ 1990), and C3 has been shown to fix to these pathogens, generally by the alternative pathway of complement activation (BLACKWELL et al. 1985; MOSSER and EDELSON 1984; PUENTES et al. 1988; PAYNE et al. 1987; SCHLESINGER et al. 1990; SCHLESINGER and HORWITZ 1990).

As macrophages secrete the complement components of the alternative and classic complement pathways, complement may be generally available in tissues to mediate phagocytosis by complement receptors. Consistent with this idea, macrophages have been shown to deposit C3 on *Leishmania donovani* in the absence of serum (WOZENCRAFT et al. 1986). Along these lines, monoclonal antibodies against complement receptors have been found to block monocyte phagocytosis of *L. pneumophila* (PAYNE and HORWITZ, unpublished data) and *M. tuberculosis* (SCHLESINGER et al. 1990) in the absence of serum. Whether this effect of antibody is due to inhibition of complement receptor binding to C3 fragments deposited on the organisms by the monocytes or to other ligands on the organisms is unknown.

#### 2.4 Acceptor Molecules for C3 on the L. pneumophila Surface

C3 fixes selectively to the *L. pneumophila* surface. The major outer membrane protein (MOMP), a 29-kDa cation selective porin (GABAY et al. 1985), is an acceptor molecule for C3 (BELLINGER-KAWAHARA and HORWITZ 1987b). MOMP fixes C3 on Western blots of whole *L. pneumophila*, *L. pneumophila* membranes, or purified MOMP, and it is the only molecule of *L. pneumophila* that does so. The lipopolysaccharide (LPS) of *L. pneumophila* does not fix C3 on Western blots (BELLINGER-KAWAHARA and HORWITZ 1987b).

The major outer membrane protein also fixes C3 when incorporated into liposomes. As measured by an ELISA for C3, liposome–MOMP complexes fix approximately 20 times more C3 than liposomes alone, which fix just over background levels of C3 (BELLINGER-KAWAHARA and HORWITZ, unpublished data).

When opsonized in serum, liposomes with MOMP incorporated into their membranes are ingested by monocytes. Phagocytosis of such liposomes is dose dependent upon serum. The liposome-MOMP-C3 complexes are ingested

by conventional phagocytosis and come to reside in membrane-bound phagosomes (BELLINGER-KAWAHARA and HORWITZ, unpublished data).

Complement receptors CR1 and CR3, C3 fragments, and MOMP thus appear to constitute a complete receptor–ligand–acceptor molecule system mediating monocyte recognition and ingestion of *L. pneumophila*.

#### **3 Intracellular Pathway**

After phagocytosis, the *L. pneumophila* phagosome interacts sequentially with monocyte smooth vesicles, mitochondria, and ribosomes until a novel ribosomelined replicative vacuole is formed (HORWITZ 1983a) (Figs. 2, 3). *L. pneumophila* then multiples within this phagosome with a doubling time at mid-log phase of about 2 h until the host cell becomes packed full with bacteria and ruptures (HORWITZ and SILVERSTEIN 1980).

The *L. pneumophila* phagosome does not fuse with monocyte lysosomes, as revealed by electron microscopic studies employing electron-opaque lysosomal markers and acid phosphatase cytochemistry (HORWITZ 1983b). The *L. pneumophila* phagosome also does not become acidified to the low pH levels characteristic of phagolysosomes (HORWITZ and MAXFIELD 1984). Quantitative fluorescence microscopy of individual *L. pneumophila* phagosomes has revealed that phagosomes containing live *L. pneumophila* have a mean pH of 6.1, which is 0.8 pH units higher than phagosomes containing formalin-killed *L. pneumophila*. The "defect" in acidification is localized to the *L. pneumophila* phagosome, as phagolysosomes containing lgG-coated erythrocytes in the same monocytes have a pH of <5 (HORWITZ and MAXFIELD 1984).

In contrast to live *L. pneumophila*, formalin-killed *L. pneumophila* do not enter phagosomes that interact with monocyte smooth vesicles, mitochondria, and ribosomes (HORWITZ 1983a). Instead, they enter phagosomes that fuse with lysosomes, and they are rapidly digested in the phagolysosome (HORWITZ 1983b).

Intracellular pathogens follow at least three distinct pathways through the mononuclear phagocyte: intraphagosomal, intraphagolysosomal, and extraphagosomal pathways. As noted, *L. pneumophila* takes the intraphagosomal pathway. *L. pneumophila* shares this pathway with *T. gondii* and *Chlamydia psittaci*, and to some extent with *M. tuberculosis*. All of these pathogens inhibit phagosome–lysosome fusion (HORWITZ 1983b; JONES and HIRSCH 1972; FRISS 1972; TODD and STORZ 1975; WYRICK and BROWNRIDGE 1978; EISSENBERG et al. 1983; ARMSTRONG and D'ARCY HART 1971). Like *L. pneumophila*, *T. gondii* (JONES and HIRSCH 1972) and *C. psittaci* (FRISS 1972) reside in phagosomes that interact with mitochondria, and *T. gondii* inhibits phagosome acidification (SIBLEY et al. 1985). The factors that determine the common selection of the intraphagosomal pathway by these phylogenetically disparate pathogens are unknown.

Intracellular pathogens are exquisitely adapted to their intracellular milieu. Presumably for this reason, a mutant *L. pneumophila* that enters monocytes like



**Fig. 2 A, B.** Intracellular multiplication of *L. pneumophila* in human alveolar macrophages. Human alveolar macrophages were obtained by bronchoalveolar lavage, cultured as a monolayer, and infected with *L. peneumophila*. The macrophages were incubated for 24 h and processed for electron microscopy. **A** The alveolar macrophage is heavily infected with *L. pneumophila* (arrows). x 57 000. **B** At a higher magnification of a portion of the macrophage shown in **A**, *L. pneumophila* bacteria are observed in ribosome-lined phagosomes (arrowheads). The ribosomes are separated from the phagosome membrane by a gap of approximately 100Å. x 21 000. (NASH et al. 1984)



**Fig. 3.** Comparative intracellular biology of wild-type and mutant *L. pneumophila*. Wild-type and mutant *L. pneumophila* enter monocytes similarly—by coiling phagocytosis—but thereafter they follow different intracellular pathways. Wild-type *L. pneumophila* resides in a distinctive ribosome-lined phagosome formed after interaction of the phagosomal membrane with monocyte smooth vesicles, mitochondria, and ribosomes. The wild-type phagosome does not fuse with monocyte lysosomes. The wird-type bacterium multiplies within the ribosome-lined phagosome until the monocyte becomes packed full with bacteria and ruptures. In contrast, the mutant *L. pneumophila* does not interact with monocyte lysosomes. The mutant *L. pneumophila* phagosome fuses with monocyte lysosomes. The mutant bacterium survives but does not multiply in a phagolysosome. (HORWITZ 1989)

the wild type, by coiling phagocytosis, but then resides in a phagosome that fails to inhibit phagosome–lysosome fusion, is avirulent (Fig. 3). The mutant survives but fails to multiply in the phagolysosome (HORWITZ 1987).

Although its precise role in pathogenesis has not been defined, the *mip* protein, the 24-kDa product of the *mip* gene, potentiates *L. pneumophila* infection of macrophages. An isogenic mutant lacking this protein exhibits diminished virulence for U937 cells and human alveolar macrophages in vitro (CIANCIOTTO et al. 1989a) and guinea pigs in vivo (CIANCIOTTO et al. 1989b).

#### 4 Immunity

#### 4.1 Humoral Immunity

#### 4.1.1 Role in Host Defense

Patients respond to *L. pneumophila* infection with the production of antibody against the organism. In vitro studies indicate that humoral immunity does not play a primary role in host defense against *L. pneumophila* (HORWITZ and

SILVERSTEIN 1981a, b). First, anti-*L. pneumophila* antibody does not promote complement-mediated killing of *L. pneumophila* (HORWITZ and SILVERSTEIN 1981b); indeed, as discussed above *L. pneumophila* utilizes the complement system to gain entry into monocytes. Second, while anti-*L. pneumophila* antibody promotes uptake of *L. pneumophila* by monocytes, alveolar macrophages, and polymorphonuclear leukocytes, this antibody does not promote substantial killing of the bacteria (HORWITZ and SILVERSTEIN 1981 a–c; NASH et al. 1984). The net result is that more bacteria gain access to the intracellular milieu in which they multiply. Finally, anti-*L. pneumophila* antibody does not inhibit intracellular multiplication of *L. pneumophila*; antibody-coated bacteria multiply intracellularly at the same rate as bacteria phagocytized in the absence of antibody (HORWITZ and SILVERSTEIN 1981c).

#### 4.1.2 Antigens Stimulating Humoral Immunity

The LPS of *L. pneumophila* is the dominant antigen recognized by anti-*L. pneumophila* antibody; greater than 98% of the antibody produced by patients with Legionnaires' disease recognizes this antigen (GABAY and HORWITZ 1985). It is serogroup specific (CIESIELSKI et al. 1986).

The major cytoplasmic membrane protein (MCMP), a 60- to 65-kDa protein, is the major protein antigen recognized by anti-*L. pneumophila* antibody (GABAY and HORWITZ 1985; SAMPSON et al. 1986). This protein is a genus common antigen and heat shock protein (LEMA et al. 1988) cross-reactive with *M. tuberculosis* 65-kDa and *E. coli* Gro EL heat shock proteins (SHINNICK et al. 1988). Interestingly, relatively little antibody is made to MOMP, the most abundant protein of the bacterium (GABAY and HORWITZ 1985).

# 4.2 Cell-Mediated Immunity

#### 4.2.1 Role in Host Defense

Patients also respond to *L. pneumophila* infection by expanding the pool of lymphocytes that recognize the pathogen (HORWITZ 1983c). In vitro studies indicate that, in contrast to humoral immunity, cell-mediated immunity plays a primary role in host defense against *L. pneumophila*. Human monocytes or alveolar macrophages treated with *L. pneumophila* antigen- or mitogenstimulated lymphocyte supernatant fluids become activated and inhibit the intracellular multiplication of *L. pneumophila* (HORWITZ and SILVERSTEIN 1981a; HORWITZ 1983c; NASH et al. 1984). Similarly, interferon- $\gamma$ -activated human monocytes or alveolar macrophages inhibit the intracellular multiplication of *L. pneumophila* (BHARDWAJ et al. 1986; NASH et al. 1988; JENSEN et al. 1987).

Activated monocytes or alveolar macrophages inhibit *L. pneumophila* multiplication but do not kill the intracellular bacteria (HORWITZ and SILVERSTEIN 1981a; NASH et al. 1984), even at very high concentrations of interferon- $\gamma$  (BHARDWAJ et al. 1986; NASH et al. 1988). Moreover, in the presence of anti-*L*.

pneumophila antibody, activated monocytes exhibit no more capacity to kill *L.* pneumophila than nonactivated monocytes (HORWITZ and SILVERSTEIN 1981a; BHARDWAJ et al. 1986). Indeed, interferon- $\gamma$ -activated monocytes do not kill *L.* pneumophila even in the presence of high concentrations of antibiotic inhibitors of bacterial protein or RNA synthesis (BHARDWAJ and HORWITZ 1988), which by themselves are able only to inhibit but not kill intracellular bacteria (HORWITZ and SILVERSTEIN 1983).

Activated monocytes inhibit *L. pneumophila* intracellular multiplication in two general ways. First, activated monocytes phagocytize fewer organisms, thereby limiting access of the bacteria to the intracellular milieu in which they multiply (HORWITZ and SILVERSTEIN 1981a). Activated monocytes may accomplish this by down-regulating the function of complement receptors (WRIGHT et al. 1986; FIRESTEIN and ZVAIFLER 1987; ESPARZA et al. 1986), which mediate phagocytosis of *L. pneumophila*, as discussed above. Second, activated monocytes inhibit the multiplication of bacteria that are internalized (HORWITZ and SILVERSTEIN 1981a). They accomplish this by limiting the availability of iron to intracellular *L. pneumophila*, as will be discussed below.

#### 4.2.2 Antigens Stimulating Cell-Mediated Immunity

The major secretory protein (MSP) of *L. pneumophila*, a 39-kDa metalloprotease (DREYFUS and IGLEWSKI 1986), is a potent stimulator of cell-mediated immunity to *L. pneumophila* in the guinea pig model of Legionnaires' disease (BREIMAN and HORWITZ 1987; BLANDER and HORWITZ 1989). Guinea pigs infected sublethally with *L. pneumophila* by aerosol exhibit strong splenic lymphocyte proliferation and cutaneous delayed-type hypersensitivity to MSP (BREIMAN and HORWITZ 1989). Guinea pigs immunized with MSP subcutaneously also develop a strong cell-mediated immune response to the molecule, as manifested by splenic lymphocyte proliferation and cutaneous delayed-type hypersensitivity 1989). As will be discussed below, such animals also develop protective immunity.

Legionella pneumophila antigenic preparations lacking MSP, such as *L. pneumophila* membranes, also induce cell-mediated immune responses (BLANDER and HORWITZ 1990a). Therefore, other *L. pneumophila* molecules capable of inducing cell-mediated immune responses remain to be identified. Interestingly, the two major components of the outer membrane, LPS and MOMP, do not induce strong cell-mediated immune responses (BREIMAN and HORWITZ 1987).

#### 4.3 Protective Immunity

#### 4.3.1 The Guinea Pig Model

The guinea pig provides a superb animal model of Legionnaires' disease. When exposed to aerosols of *L. pneumophila*, guinea pigs develop a pneumonic illness that clinically and pathologically mimics Legionnaires' disease in humans.

Sublethally infected guinea pigs develop humoral and cell-mediated immune responses to *L. pneumophila* antigens and strong protective immunity to lethal aerosol challenge with *L. pneumophila*. Such animals limit the multiplication of *L. pneumophila* in their lungs (BREIMAN and HORWITZ 1986).

#### 4.3.2 Antigens Stimulating Protective Immunity

Several antigenic preparations, in addition to live *L. pneumophila* in sublethal concentrations, induce protective immunity in guinea pigs to lethal aerosol challenge with *L. pneumophila*. First, the avirulent mutant *L. pneumophila* described above, which fails to inhibit phagosome–lysosome fusion and which survives but does not multiply in human monocytes, induces strong protective immunity in guinea pigs immunized with it by the aerosol route (BLANDER et al. 1989). Protection with the avirulent mutant is comparable to that provided by sublethal aerosol infection with the wild type (BLANDER et al. 1989).

Second, as noted above, the MSP of *L. pneumophila* induces strong protective immunity in guinea pigs immunized with it by subcutaneous inoculation (BLANDER and HORWITZ 1989). MSP can also induce cross-protective immunity between different serogroups of *L. pneumophila* (BLANDER and HORWITZ 1990b). Interestingly, this immunoprotective molecule is not a virulence determinant in the guinea pig model of Legionnaires' disease (BLANDER et al. 1990). Studies comparing a cloned isogenic mutant *L. pneumophila* that does not produce MSP with its progenitor MSP-producing strain have revealed that the two strains have comparable virulence in the guinea pig model. The two strains have equivalent  $LD_{50}$ s and  $LD_{100}$ s for guinea pigs, multiply in the lungs of challenged guinea pigs at the same rates, and produce indistinguishable pathologic lesions in guinea pig lungs (BLANDER et al. 1990).

Third, *L. pneumophila* membranes induce strong protective immunity in guinea pigs when administered either by aerosol or subcutaneously. Interestingly, in contrast, formalin-killed *L. pneumophila* does not induce strong cellmediated immune responses or protective immunity (BLANDER and HORWITZ 1990a).

#### 4.4 Processing and Presentation of L. pneumophila Antigens

Very little is known about the processing and presentation of parasite antigens by infected mononuclear phagocytes. It seems likely that immunodominant T cell antigens such as the MSP are processed intracellularly in mononuclear phagocytes to immunogenic epitopes that are displayed on the surface of these antigen-presenting cells. In support of this hypothesis, immunocytochemistry employing affinity-purified monospecific anti-MSP antibody has demonstrated that *L. pneumophila* produces MSP intracellularly and that this molecule colocalizes with *L. pneumophila* phagosomes (CLEMENS and HORWITZ 1990). Erythromycin, which inhibits *L. pneumophila* protein synthesis, abolishes MSP immunoreactivity. Furthermore, immunoelectron microscopic studies have revealed that MSP localizes to the *L. pneumophila* phagosome and cytoplasmic clusters of infected monocytes (CLEMENS and HORWITZ 1990).

# **5** Role of Iron in Monocyte Activation

Legionella pneumophila intracellular multiplication is iron-dependent. Multiplication is inhibited by deferoxamine, an iron chelator, and this inhibition is reversed by iron-saturated transferrin (BYRD and HORWITZ 1989).

Interferon- $\gamma$ -activated monocytes inhibit *L. pneumophila* intracellular multiplication by limiting the availability of iron to the bacterium. The capacity of interferon- $\gamma$ -activated monocytes to inhibit *L. pneumophila* intracellular multiplication is reversed by iron transferrin (BYRD and HORWITZ 1990a). The capacity of such activated monocytes to inhibit *L. pneumophila* multiplication is also reversed by iron lactoferrin and by nonphysiologic iron compounds (BYRD and HORWITZ 1990a). The reversing effect of iron lactoferrin raises the interesting possibility that release of lactoferrin by polymorphonuclear leukocytes at sites of inflammation in the *L. pneumophila*-infected lung may be counterproductive to host defense.

Interferon- $\gamma$ -activated monocytes may limit intracellular iron availability to *L. pneumophila* in at least two ways. First, such monocytes markedly down-regulate transferrin receptors, which mediate internalization of iron transferrin by these cells (BYRD and HORWITZ 1989). Second, such monocytes markedly down-regulate the concentration of intracellular ferritin, the major iron storage protein in these cells (BYRD and HORWITZ 1990b).

The potential importance of transferrin receptors to *L. pneumophila* iron acquisition is underscored by the study of an individual whose monocytes have low numbers of transferrin receptors. This person's monocytes are uniquely nonpermissive to *L. pneumophila* intracellular multiplication. However, the addition of ferric ammonium citrate, which may enter monocytes independent of the transferrin receptor endocytic pathway, completely reverses the non-permissive state of these monocytes and allows *L. pneumophila* to multiply in them at the same rate as in normal monocytes (BYRD and HORWITZ 1990c).

### 6 Conclusion

Over the past decade, the *Legionella pneumophila* model of intracellular parasitism has come of age. There is now a basic understanding of the bacterium's interactions with mononuclear phagocytes and the host immune

system. Key bacterial and host molecules governing these interactions are being identified, and the development of genetic systems for studying *L. pneumophila* should spur this process. With these elements in place, the next decade should see the study of this model providing important new insights into intracellular pathogenesis and the molecular basis of intracellular parasitism.

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# Chronic Granulomatous Disease: An Update and a Paradigm for the Use of Interferon- $\gamma$ as Adjunct Immunotheraphy in Infectious Diseases

R. A. B. EZEKOWITZ

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# **1 Introduction**

Chronic granulomatous disease (CGD) is a rare inherited disorder in which the phagocyte NADPH oxidase is disabled. The failure of the enzyme to generate superoxide and related oxygen intermediates renders the patients with this disease susceptible to recurrent bacterial and fungal infections. The clinical syndrome (reviewed FORREST et al. 1988) usually presents within the first years of life with a history of recurrent infections, mostly pneumonias, abscesses of the liver or lungs, or subcutaneous bacterial infections. Despite the use of high dose antibiotics, the phagocytes' failure to kill ingested organisms serves as a stimulus for the chronic inflammatory state and granuloma formation. The granulomas are attempts to wall off infectious foci and if they occur in vital organs, like the gastrointestinal tract, kidney, liver, and brain, they contribute to the mortality and morbidity of this disorder.

Early attempts at the characterization of the phagocyte oxidase were hindered by its complexity (reviewed in SMITH and CURNUTTE 1991). Despite disparate findings on the molecular weights and relative importance of individual components, a consensus held that most, although not all, X-linked CGD kindred lacked a spectrally detectable cytochrome  $b_{559}$  (SEGA 1988). Although 60% of CGD patients follow the X-linked dominant pattern of

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inheritance, 40% have an autosomal recessive pattern of inheritance. Recently, genetic approaches, imporved biochemical purification procedures, and the development of cell-free systems which enabled segregation of subcellular fractions required to reconstitute the oxidase system in vitro have led to the characterization and elucidation of most of the components of the NADPH oxidase (reviewed by EZEKOWITZ and NEWBURGER 1988).

# 2 The NADPH Oxidase

It has long been recognized that the NADPH oxidase is a multicomponent system (CURNUTTE and BABIOR 1987). Recent evidence has elucidated at least four different components for which genetic defects have been described and result in the CGD phenotype. A phagocyte-specific cytochrome b heterodimer believed to be the terminal electron donor in the oxidase complex is absent in two different genetic forms of CGD (SEGAL 1988). Most commonly, X-linked recessive disease (xb-CGD, accounting for 60% of cases) is due to mutations in the gene encoding a 91-kDa membrane glycoprotein (referred to as gp91-phox) that is the larger subunit of cytochrome b (ORKIN 1989). The molecular cloning of gp91-phox gene was performed without knowledge of the gene product, based on the correct chromosomal assignment to Xp21.1 (ORKIN 1989; ROYER-POKORA et al. 1986). By reverse genetics, a cDNA with a translation product of 571 amino acids was identified and found to correspond to a phagocyte-specific 91-kDa protein that was absent in X-CGD. Formal proof that this was indeed the heavy chian of the b cytochrome rested on the N-terminal sequence from the purified protein, (SEGAL 1987; PARKOS et al. 1987). In addition to classic X-CGD, the phagocyte b cytochrome is also lacking in this subgroup of CGD due to mutations in the gene for the 22-kDa subunit (p22-phox) of cytochrome b (PARKOS et al. 1988).

The majority of patients with autosomal recessive CGD have normal levels of b cytochrome, but are lacking cytosolic factors required for activation of the NADPH oxidase (VOLPP et al. 1988; NUNOL et al. 1988; CURNUTTE et al. 1989; BOLSCHER et al. 1989). In a recent study of 25 autosomal recessive CGD patients, 22 lacked a 47-kDa phosphoprotein p47-*phox* and the remainder lacked a 67-kDa protein p67-*phox* (CLARK et al. 1989). cDNA for both proteins have been isolated and recombinant and purified proteins reconstitute the corresponding cytosol deficiencies in cell-free oxidase assays (VOLPP et al. 1989; LOMAX et al. 1989).

Figure 1 is a current model [as proposed by SMITH and CURNUTTE (1991) of the NADPH oxidase and its components. The model predicts assembly of cytosolic and membrane-bound components to constitute an electron transfer chain allowing molecular oxygen to be converted into superoxide and other oxygen intermediates like hydrogen peroxide. The precise interactions of each component are not known for certain, but studies in progress are aimed at mutating various sites of each specific component to address this problem in



Fig. 1. A current model of the phagocyte NADPH oxidase based on a model proposed by SMITH and CURNUTTE (1991)

reconstituted in vitro systems. Such analyses have indicated the necessity for components other than those characterized, which are indicated in the diagram as other components.

#### **3 Molecular Basis of Chronic Granulomatous Disease**

Recent progress in elucidating the molecular genetic basis of all CGD has included the isolation of cDNAs for a group of essential oxidase proteins. It is now recognized that CGD phenotype can arise from genetic defects in at least four different components of the NADPH oxidase, as described in Table 1. Defects in the gene encoding for gp91-phox most commonly lead to the absence of the gene product without any obvious abnormality in the gene structure as determined by Southern blot and restriction fragment length polymorphism studies (DINAUER and ORKIN 1988). This suggests that point mutations rather than aene deletions result in a defective gp91-phox protein. In fact, a point mutation in the gp91-phox gene resulting in a Pro > His at position 415 (DINAUER et al. 1989) has been found in an Xb<sup>+</sup> CGD patient. (Xb<sup>+</sup> refers to the presence of spectrally normal cytochrome although functionally disabled with respect to its electron transfer capacity). In another study (BOLSCHER et al. 1991), point mutations in the gp91-phox gene were found in Xb<sup>-</sup> and Xb<sup>+</sup> CGD patients. In one patient, the point mutation resulted in a premature termination signal at codon 73, providing an unequivocal explanation for the CGD phenotype. In the other five patients, distinct mutations resulted in a signal amino acid substitution. Although the reason why these changes should result in a dysfunctional gene product is not clear, in two patients with Xb<sup>-</sup> CGD, who are RNA<sup>+</sup>, a histidine was replaced by either a tyrosine or an arginine. It is possible that the histidine may be critical in heme binding and that loss of this residue could account for the CGD phenotype. The other substitutions are scattered throughout the protein and may alter its structure and hence its stability or interactions with other oxidase components, particularly p22-phox, the cytochrome light chain.

Inheritance	Cyt b	Affected gene	Chromosomal location	Protein product	References
X-linked recessive	Neg. (rarely pos.)	СҮВВ	Xp21.1	gp 91- <i>phox</i> (91-kDa subunit cyt b)	Royer-Pokora et al. 1986; Dinauer et al. 1989; Teahan et al. 1987; Francke 1984; Francke et al. 1985; Baehner et al. 1986
Autosomal recessive	Neg.	СҮВА	16q24	p22- <i>phox</i> (22-kDa subunit	Dinauer et al. 1990; Nathan et al. 1986; Weening et al. 1985
Autosomal recessive	Pos.	NCF1	7q11.23	cyt b) p47- <i>phox</i>	Volpp et al. 1989; Lomaxet al. 1989; Francke et al. 1990
Autosomal	Pos.	NCF2	1q25	p67-phox	Francke et al. 1990; Leto et al. 1990

Table 1. CGD: genetic defects in phagocyte NADPH-oxidase proteins (DINAUER and EZEKOWITZ 1991)

Most autosomal recessive forms of CGD have normal cytochrome b levels and lack either the p47-*phox* or the p67-*phox*, two soluble proteins required for oxidase function. It appears that in some patients the identical mutation on both alleles of the p47-*phox* gene occurs at a splice junction, accounting for the CGD phenotype (CASMEYER et al. 1991). It is likely that mutations other than this might also occur, but have yet to be reported. A rare subgroup of autosomal recessive CGD resembles the X-linked form in that both chains of the cytochrome b are absent, so-called A-CGD. Specific genetic mutations in the gene of the 22-kDa light chain of the cytochrome, p22-*phox*, have been identified (DINAUER et al. 1990). In one patient there is a 10-kb homozygous deletion which accounts for the lack of the gene product. In yet another patient there is a frame shift mutation in one allele and a missense mutation in the other allele. In a third patient, a homozygous missence mutation appears to account for the genetic defect.

# 4 Interferon-γ: The Rationale for Its Use in Chronic Granulomatous Disease

The convergence of three independent but related events led to the idea that recombinant interferon- $\gamma$  may be of use in the treatment of a rare group of inherited disorders of phagocytes that result in the phenotype of CGD. Firstly there was the presentation of a patient with an atypical presentation of the disease. Secondly there was the characterization of the molecular defect underlying the X-linked form of CGD which accounts for two-thirds of the patients (ROYER-POKORA et al.1986). The triad was completed by the realization

that intradermal administration of interferon- $\gamma$  was able to affect the oxidative capacity of circulating phagocytes as shown in patients with lepromatous leprosy (NATHAN et al. 1986). In the rest of this review, I will elaborate on each of these aspects and point out how they relate to one another. The end result is that interferon- $\gamma$  is highly effective in reducing the time to serious infection in all genetic types of CGD and that its effects are due to more than its ability to upregulate the respiratory burst in phagocytes and hence may have more general applications in adjunct thereapy for infectious disease.

# 4.1 The Patient

Chronic granulomatous disease is characterized by recurrent severe bacterial and fungal infections usually within the first few years of life (FORREST et al. 1988). Although phagocytes from patients with CGD ingest microorganisms normally, killing is deficient due to the failure of a membrane-associated NADPH oxidase to produce superoxide and related toxic derivatives (TAUBER et al. 1983). The index patient presented with a life-threatening pneumonia due to Aspergillus fumigatus as the first manifestatioin of CGD at age 14 (autumn of 1984). The patient had been otherwise well except for severe pustular acne. The patient was exposed to an unusually high inoculum of Aspergillus fumigatus from wood shavings and this infectious event first drew attention to his underlying immunodeficiency. The diagnosis of CGD was suspected given the unusual nature of the organisms and was confirmed by a negative nitroblue tetrazolium (NBT) test. The question therefore was why did this patient survive 14 years before his first serious infection? The hypothesis generated was that the patient's phagocytes were able to generate reduced amounts of reactive oxygen intermediates which under many circumstances were sufficient. However, on this occasion the inoculum of Aspergillus was so great that it overwhelmed his crippled oxidase. This raised questions as to the nature of the phagocyte oxidase and the molecules that regulate its function.

# 4.2 Interferon-γ

Interferon- $\gamma$ , a glycoprotein secreted by activated T cellls and NK cells, has a powerful role as an immunomodulatory cytokine (PESTKA et al. 1987). The biologic action of this lymphokine is mediated via a specific 90-kDa receptor present on a wide variety of cell type (AUGET et al. 1988). Interferon- $\gamma$  induces many pleiotypic effects on target cells but its predominant role is as a macrophage-activating factor (NATHAN and TSUNAWAKI 1986). The administration of this cytokine in vivo and in vitro enhances phagocyte killing of bacterial and protozoan pathogens (MURRAY 1988). The enhanced killing correlates with increased production of reactive oxygen intermediates by phagocytes, which accounts for most but not all of the cytocidal function. The
recent advances in the characterization of the molecular components of the NADPH oxidase provided us with the opportunity to examine the molecular mechanisms underlying the augmentation of phagocyte superoxide production by interferon- $\gamma$ . Initial studies revealed that in vitro treatment of human monocyte-derived macrophages and neutrophils with interferon- $\gamma$  increased gp91-*phox* RNA transcripts although levels of p22-*phox* RNA were unaffected (NEWBURGER et al. 1988). Preliminary work indicates that p47-*phox* gene expression is also augmented by interferon- $\gamma$  (ABRAHAMSON et al. 1990). It is noteworthy that interferon- $\gamma$  up-regulation of transcripts of NADPH oxidase components alone does not account for the activation phenotype. However, the interferon responsiveness of these oxidase genes provides an experimental basis for attempts to correct the functional deficiency in phagocytes in CGD patients.

## 4.3 The Patient, the Oxidase, and Interferon- $\boldsymbol{\gamma}$

How did the index patient survive for 14 years before his first serious infection? Our hypothesis was that under normal circumstances of low bacterial load, he was able to transiently up-regulate his NADPH oxidase to produce sufficient reactive oxygen intermediates. However, exposure to a large inoculum of *Aspergillus* overwhelmed his already crippled oxidase (NEwBURGER et al. 1986). The question therefore was, would interferon- $\gamma$ , the physiologic up-regulator of the phagocyte NADPH oxidase, and specifically gp91-*phox*, in this instance the aberrant gene, affect this patient's phagocyte function? If this proved to be the case, would this apply to other CGD patients? Initial in vitro studies showed that addition of interferon- $\gamma$  to granulocytes and monocytes from this patient and his affected brother resulted in a partial correction of both the defect in superoxide production and very low levels of gp91-*phox* transcripts (EZEKOWITZ et al. 1987), while two other X-CGD patients' cells failed to respond.

The availability of recombinant interferon- $\gamma$  and its extensive use in cancer trials provided safety information and the expectation that in vivo administration of interferon- $\gamma$  may be a rational approach. The immunomodulatory dose and route of administration became obvious after it was shown that intradermal injection into lesions in lepromatous leprosy resulted in a systemic effect on circulating monocytes (NATHAN et al. 1986). It was observed in this study that the depressed oxidative capacity of phagocytes was enhanced after treatment (NATHAN et al. 1986). This led us to administer 0.1 mg/m<sup>2</sup> of interferon- $\gamma$  subcutaneously to our index patients. Treatment resulted in a near-normal level of superoxide production in granulocytes and monocytes. Granulocyte bactericidal capacity was indistinguishable from normal control treatment and there was a small but detectable increase in gp-91-*phox* protein, which was not detectable before treatment (EZEKOWITZ et al. 1988). Surprisingly, the improvement in phagocyte function peaked at 2 weeks and was sustained for 4 weeks after one subcutaneous administration of interferon- $\gamma$ , despite an estimated 4- to

6-h circulating time of neutrophils. Of note is that at the dose of subcutaneous interferon- $\gamma$  administered, serum levels were undetectable.

These observations suggested that the in vivo effect of interferon- $\gamma$  cannot be explained by its action on mature phagocytes alone and implies an effect on immature cells. We set out to test the idea that the lymphokine affects progenitor cells which later give rise to mature progeny that express the corrected phenotype. These experiments are possible as in this CGD kindred the phagocyte responses to interferon-y fall within a range that is easily detectable by in situ NBT dye reduction. Progenitor-derived colonies from peripheral blood examined before treatment were unable to generate superoxide as visualized by lack of NBT reduction compared with normal controls. By contrast, colonies derived 7 days after a single interferon- $\gamma$  injection were able to generate superoxide, as shown by increased NBT reduction. Colonies harvested 21 days after treatment contained only rare cells capable of NBT reduction (EZEKOWITZ et al. 1990). When one relates the kinetics observed in these progenitor-derived colonies to the kinetics of the circulating phagocytes, it is clear that interferon- $\gamma$ must act on progenitor cells and their mature progeny. The effect on circulating cells was not immediate and was first observed 36 h after treatment. Moreover, it was maximal at 14 days. Our favored explanation is that interferon- $\gamma$  acts on progenitor cells and their differentiated products that begin to repopulate the circulating pool. This effect is first observed on mature cells in the bone marrow, which egress within 24–36 h and are found in the circulation. There appears to be a lag period of 5–7 days before a corrected progenitor can be assayed in the peripheral blood. It would appear, therefore, that these studies more broadly represent basic determinants of maturation from myeloid progenitors and provide a unique estimate of the kinetics of myeloid differentiation. Interferon- $\gamma$ has been shown to influence myeloid differentiation and commitment and probably exerts its action in vivo in conjuction with other growth factors like GM-CSF and tumor necrosis factor (CASSATELLA et al. 1989). These factors have been shown to act synergistically with interferon- $\gamma$  in augmenting cytochrome b heavey chain expression in vitro (CASSATELLA et al. 1989). The molecular mechanisms by which interferon- $\gamma$  is able to reprogram the phenotype of early progenitor cells are unknown but must represent a fundamental step in determination of differentiated phenotype.

## **5 Other CGD Patients**

In our original in vitro studies, we also included a few selected CGD patients who represented the spectrum of the clinical coruse, with the kindred described above at the upper end and classic X-CGD at the lower end. We were able to show that these patients had an intermediate to low in vitro and in vivo response (EZEKOWITZ et al. 1987, 1988). This work was extended by SECHLER et al. (1988), who examined the effects of the lymphokine on 30 patients, including some with

autosomal recessive inheritance. These workers observed enhancement of bacterial killing in responders as well as nonresponders, suggesting that interferon- $\gamma$  therapy may benefit CGD patients even in the absence of demonstrable extracellular production. These studies formed the basis for a phase III study to evaluate the efficacy and potential toxicity of interferon- $\gamma$ in CGD. An international, multicenter, randomized, double-blind placebocontrolled study was undertaken in which 128 eligible patients were enrolled, including patients with different patterns of inheritance and requiring, in most cases, prophylactic antibiotic therapy. Patients received interferon-y or placebo 3 times weekly for up to 1 year. Time to serious infection as defined as an event requiring hospitalization and intravenous antibiotics was the primary end point. Seventy-nine percent of interferon- $\gamma$ -treated patients were free of serious infection at 1 year, as compared with 30% of those receiving placebo. The latter group required three times as many in-patient hospital days and had more multiple infections (International Chronic Granulomatous Disease Cooperative Study Group 1991). Of particular note was the fact that there appeared to be no statistically significant correlation between improved in vitro function and clinical course. This probably reflects the genetic heterogeneity underlying the CGD phenotype and raises questions as to the precise molecular mechanisms underlying the dramatic clinical benefit. Clearly, a subset of patients did show enhanced oxidative capacity; however, the majority appear to utilize other interferon-y-triggered responses, suggesting that interferon-y may have more general applications as an adjunct to conventional antimicrobicidal therapies in the treatment of infectious diseases. The effective use of this lymphokine in leprosy and leishmaniasis (BADARO et al. 1990) opens the way for investigating its efficacy in other infectious disease settings like septic neonates. In this way, the study of an unusual patient with an esoteric genetic disease may lead to a more general understanding of the clinical usefulness of interferon- $\gamma$  in clinical practice.

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