

REVIEW ARTICLE**Colony-Stimulating Factor-1 Receptor**

By Charles J. Sherr

COLONY-STIMULATING factor-1 (CSF-1), also called macrophage colony-stimulating factor (M-CSF), is a lineage-specific hematopoietin that stimulates proliferation and supports differentiation and survival of cells of the mononuclear phagocyte series.^{1,2} Its activity was originally detected in biological fluids, including serum³ and urine,⁴ in various tissues,⁵ and in the medium conditioned by certain established cell lines.⁶⁻⁸ The purified growth factor is a 70- to 90-Kd homodimeric glycoprotein synthesized primarily by fibroblasts,^{9,10} but its synthesis can be induced in endothelial cells¹¹ and in monocytes and macrophages¹²⁻¹⁵ in response to other cytokines. CSF-1 induces formation of pure macrophage colonies from individual bone marrow (BM) precursors plated in semisolid medium and can stimulate proliferation of macrophages isolated from peritoneal and pleural exudates, alveoli, lymph nodes, and spleen.¹⁶ It also potentiates the ability of mature mononuclear phagocytes to perform their differentiated functions by enhancing their ability to kill infectious microorganisms^{17,18} and tumor cells^{19,20} and by regulating release of macrophage cytokines, such as interferon, tumor necrosis factor (TNF), interleukin-1 (IL-1), and granulocyte-CSF (G-CSF),²¹⁻²⁵ as well as inflammatory modulators, such as prostaglandins, biocidal oxygen metabolites, thromboplastin, and plasminogen activator.²⁶⁻³¹ Biologically active, secreted, and membrane-bound forms of CSF-1³²⁻³⁵ are encoded by alternatively spliced messenger RNAs (mRNAs) transcribed from a single gene^{36,37} that maps to the long arm of human chromosome 5 at band q33.1.³⁸ CSF-1 differs in its physicochemical properties and spectrum of action from other known hematopoietins, including granulocyte-macrophage CSF (GM-CSF) and IL-3, each of which stimulates proliferation of immature myeloid cells, including the progenitors of macrophages.^{39,40}

Although originally defined through its activities on blood cells, CSF-1 may have important functions outside the context of hematopoiesis. The growth factor is produced by uterine epithelium during pregnancy,⁴¹⁻⁴³ and the levels of uterine CSF-1 production increase more than a thousand-fold during gestation and are highest at parturition.⁴¹ Detection of CSF-1 receptors on placental trophoblasts and on choriocarcinoma cell lines⁴³⁻⁴⁵ suggests that CSF-1 may be an important modulator of placental development. The possibility that other cell types might also respond to CSF-1 has not been well-studied.

In the hematopoietic system of adult animals, CSF-1 exerts its pleiotropic effects by binding to a single class of high-affinity receptors^{46,47} expressed predominantly on monocytes, macrophages, and their committed BM precursors.⁴⁸ The CSF-1 receptor (CSF-1R) is encoded by the *c-fms* protooncogene⁴⁹ and is a member of a family of growth factor receptors that exhibit ligand-induced tyrosine-specific protein kinase activity.^{50,51} Activation of the receptor kinase triggers a cascade of biochemical events, some of which convey signals from the plasma membrane to the cell nucleus that affect the transcription of CSF-1-responsive genes and lead to cell division. Critical mutations in the *c-fms* gene, such as those observed in the transduced feline retroviral *v-fms* oncogene, can unleash their latent oncogenic potential by altering CSF-1R so as to upregulate its kinase activity in a ligand-independent manner.⁵²⁻⁵⁴ Expression of "activated" *fms* oncogene products in susceptible cells provides sustained signals for cell growth in the absence of appropriate environmental cues, leading to cell transformation and tumorigenesis.

**STRUCTURE AND TRANSCRIPTION OF THE CSF-1R GENE
(C-FMS)**

The *c-fms* protooncogene maps near the CSF-1 locus on human chromosome 5 at band 5q33.3⁵⁵⁻⁵⁷ in relative proximity to other growth factor and receptor genes that play

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important roles in hematopoiesis. These include the GM-CSF, IL-3, IL-4, and IL-5 genes,⁵⁷⁻⁶³ as well as the gene encoding the B isoform of the platelet-derived growth factor receptor (PDGF-R_B), previously mapped to 5q31-32.⁶⁴ Molecular cloning of a PDGF-R_B cDNA established that it shared a relatively high degree of amino-acid sequence homology to CSF-1R, particularly in its kinase domain.⁶⁴

Although cytogenetic assignments had suggested that the CSF-1R and PDGF-R_B genes were at least one megabase apart, we found that the two genes were juxtaposed in a tandem head-to-tail array.⁶⁵ By aligning the CSF-1R and PDGF-R_B cDNA sequences and knowing the positions of splice junctions within the *c-fms* gene,⁶⁶ it was possible to predict correctly the organization of PDGF-R_B exons.⁶⁵ Together, these results imply that CSF-1R and PDGF-R_B were derived from an ancestral gene that underwent duplication and subsequent evolutionary divergence. Recently, the A isoform of PDGF-R was cloned and assigned to human chromosome 4.^{67,68} The same region of chromosome 4 harbors the *c-kit* protooncogene,⁶⁹ which encodes a structurally related receptor for an as-yet-uncharacterized ligand, raising the possibility that the *c-kit* and PDGF-R_A genes might also be organized in a tandem array.

A schematic diagram of the CSF-1R and PDGF-R_B loci is shown in Fig 1. Transcription of CSF-1R RNA appears to be initiated at two independent promoters that function in a tissue-specific manner.⁷¹ In placental trophoblasts, transcripts include 5' sequences originating from *c-fms* exon 1,^{65,70,71} which specifies only nontranslated sequences of *c-fms* mRNA and is separated by a 26-kilobase (kb) intron from the remaining 21 exons encoding the receptor itself. The location of *c-fms* exon 1 is less than 0.5 kb from the polyadenylation signal of the PDGF-R_B gene, suggesting that transcription of PDGF-R_B might influence the activity of a putative *c-fms* promoter mapping between the two genes. Thus, the tandem organization of PDGF-R_B and CSF-1R might underlie a mechanism for their mutually exclusive expression in different cells of the developing placenta. In monocytes, however, *c-fms* transcripts are initiated from an independent promoter⁷¹ located directly upstream of exon 2, which specifies the amino-terminal signal peptide of CSF-1R.⁶⁶ The exact locations of the two

c-fms promoters are presently unknown, as are the positions of putative tissue-specific enhancer elements that regulate expression of alternative CSF-1R mRNAs in placenta and mononuclear phagocytes.

The size of the *c-fms* gene makes it unlikely that its mRNA levels can be rapidly regulated by transcriptional mechanisms. The minimal length of genomic CSF-1R coding sequences is 32 kb, so that the formation of its unspliced mRNA precursors should require more than 30 minutes, based on the estimated rate of transcription by RNA polymerase II and barring attenuation of RNA synthesis within the gene.⁶⁶ This means that receptor synthesis is more likely to be governed by posttranscriptional mechanisms involving RNA stabilization or translation. Although the steady-state levels of *c-fms* mRNA gradually increase as precursors of mononuclear phagocytes differentiate and mature,⁷² the gene is continuously transcribed during cell maturation and the half-life of its mRNA in mature monocytes is regulated by inducers of CSF-1R expression.⁷³

STRUCTURE AND BIOSYNTHESIS OF CSF-1R

Human CSF-1R is an integral transmembrane glycoprotein 972 amino acids long.⁷⁰ Including the signal peptide, it consists of a 512 amino-acid *N*-terminal extracellular segment containing the ligand-binding domain, a hydrophobic 25 amino-acid membrane-spanning region, and a 435 amino-acid intracellular domain that includes all the sequences necessary for tyrosine kinase activity (Fig 2). Similar structures are predicted for the mouse⁷⁴ and feline⁵² CSF-1 receptors. These show 75% and 84% overall homology to human CSF-1R, with the greatest degree of sequence conservation occurring between their intracellular kinase domains. Based on a consideration of conserved structural motifs as well as its genomic organization, CSF-1R is most closely related to the A and B isoforms of PDGF-R,⁶⁴⁻⁶⁸ the *c-kit* protooncogene product,⁶⁹ and the recently cloned receptor for basic fibroblast growth factor (FGF-R).⁷⁵ In contrast, CSF-1R shows much less overall homology to other receptors of the protein tyrosine kinase (PTK) gene family, such as the epidermal growth factor (EGF-R), insulin (I-R), and insulin-like growth factor-1 (IGF-1R) receptors.^{50,51}

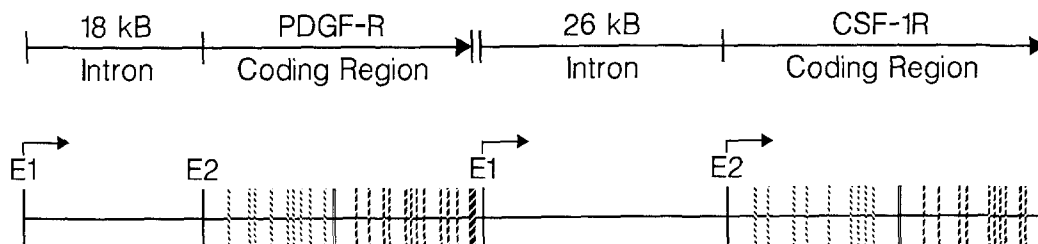


Fig 1. Genomic organization of the human CSF-1R and PDGF-R_B genes. The CSF-1 and PDGF-R_B genes are aligned in a head-to-tail array on the long arm of human chromosome 5. Both are shown in 5' to 3' orientation (coding strand); their orientation with respect to the centromere is unknown. Each gene is approximately 60 kb long and contains coding sequences organized into small exons (vertical bars) separated by longer introns (horizontal lines). The positions of two *c-fms* promoters are indicated by arrows positioned just upstream of exons 1 and 2 (E1 and E2). The unstippled exon indicated by a double vertical bar in the middle of each gene encodes the transmembrane segment of the receptor. Exons 5' and 3' to these segments encode the ligand-binding and kinase domains of the receptors, respectively. Data regarding organization of CSF-1R were derived from a previously reported genomic nucleotide sequence⁶⁶; data concerning PDGF-R were derived from our unpublished observations and from reference 65.

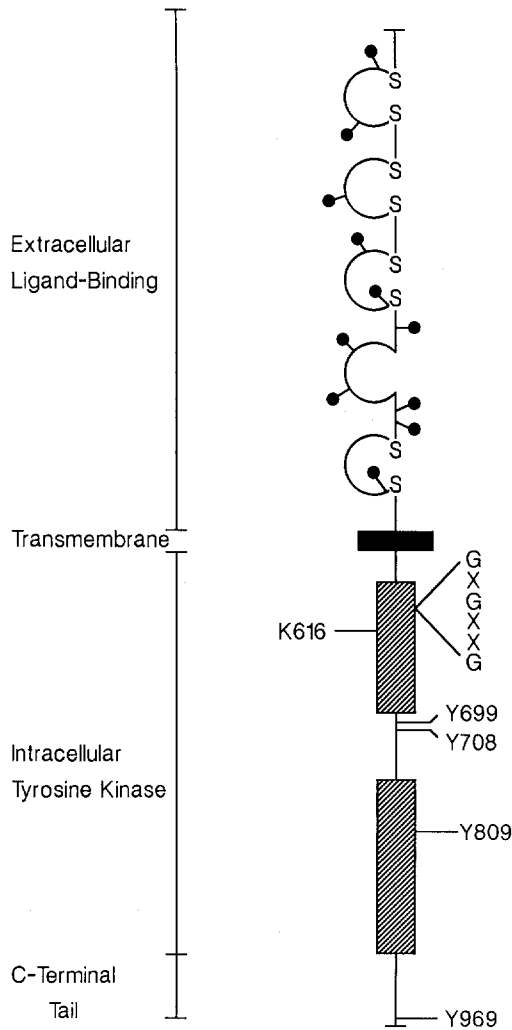


Fig 2. Predicted structure of human CSF-1R. The extracellular ligand-binding portion is organized into five immunoglobulin-like domains, four of which are stabilized by disulfide bonds (S-S). All such domains are homologous to sequences of the C2-SET.⁷⁶ Positions of asparagine-linked oligosaccharide chains are indicated (●). The intracellular kinase domain (stippled bars) is interrupted by spacer sequences containing two predicted sites of receptor phosphorylation at tyrosines (Y) 699 and 708. A third phosphorylation site (Y809) occurs in the distal core consensus sequences. The membrane-proximal kinase segment includes a glycine-rich signature sequence (G-X-G-X-X-G) characteristic of kinases in general. This is followed by the ATP binding site at lysine (K) 616. The C-terminal tail contains a single tyrosine residue (Y969) whose removal upregulates receptor kinase activity.¹³¹ The data are taken from a previously reported human *c-fms* cDNA sequence.⁷⁰ Unpublished information regarding sites of phosphorylation within the murine receptor was provided by Drs P. Tapley, A. Kazlauskas, and L. R. Rohrschneider and was aligned with the human amino-acid sequence.

The extracellular segment of CSF-1R is predicted to include a series of disulfide-bonded loops, each representing motifs characteristic of members of the immunoglobulin gene superfamily (Fig 2).⁷⁶ Analogous immunoglobulin-like domains have been predicted for the two PDGF receptors and FGF-R, but not for EGF-R, I-R, or IGF-1R, which instead contain interspaced blocks of cysteine-rich sequences

also found in the EGF precursor and low-density lipoprotein receptor.⁵¹ The extracellular domain of CSF-1R is heavily glycosylated and contains 11 sites of addition of asparagine-linked (but not *O*-linked) oligosaccharide chains. The presence of these carbohydrate side chains contributes approximately 45 Kd to the molecular mass of the mature 150-Kd human glycoprotein.^{45,77}

The intracellular portion of CSF-1R contains a characteristic sequence consisting of a gly-X-gly-X-X-gly motif at amino acids 589 to 594, followed by a lysine residue at position 616, which was predicted to be the site of ATP binding.⁷⁸ Indeed, mutation of lysine 616 to a methionine residue abolishes receptor tyrosine kinase activity and renders CSF-1R incapable of transducing mitogenic signals.⁷⁹ Sequences flanking the ATP binding site show a high degree of amino acid similarity to other members of the PTK gene family, as does a second, more extended cluster of amino acid residues closer to the receptor C-terminus (Fig 2).⁵⁰ As compared with other prototypic tyrosine kinases, such as EGF-R, I-R, IGF-1R, and members of the *src* protooncogene family, the intracellular kinase domain of CSF-1R contains an additional 72 amino-acid "spacer" or "kinase insert" sequence that separates sequences surrounding the ATP binding site from the remainder of the PTK consensus sequences. These spacer sequences are conserved among the human, mouse, and feline CSF-1 receptors, but are unrelated to analogous spacer elements of different lengths found in PDGF-Rs, FGF-R, and the *c-kit* product, suggesting that they may function in specific substrate recognition.⁶⁹

CSF-1R is synthesized as an integral transmembrane glycoprotein, oriented with its *N*-terminal domain in the cisternae of the rough endoplasmic reticulum (ER) and its kinase domain in the cell cytoplasm.⁵⁴ The 105-Kd polypeptide is cotranslationally glycosylated, acquiring *N*-linked oligosaccharides of the high-mannose type, so that the immature intracellular glycoprotein has an apparent molecular mass of 130 Kd. During intracellular transport of the glycoprotein to the plasma membrane, the *N*-linked carbohydrates undergo modification in the Golgi complex, resulting in an increase in the apparent molecular mass of human CSF-1R to 150 Kd. Variations in molecular masses of mature receptors in different species result in part from differences in processing of the carbohydrate side chains. Transport of the receptor from the ER to the plasma membrane occurs efficiently, so that newly synthesized molecules can be detected at the cell surface within 30 minutes of synthesis. Several lines of evidence suggest that expression of the receptor at the cell surface is necessary for biologic activity,⁸⁰⁻⁸² implying that physiologic substrates for the receptor kinase may also be preferentially disposed at the inner surface of the plasma membrane.

DOWNREGULATION AND TRANSMODULATION OF CSF-1R

In the absence of ligand, the mature cell-surface form of CSF-1R is relatively stable, with a half-life of 3 to 4 hours.³³ The receptors can move into clathrin-coated pits,⁸³ and the possibility that a proportion are continuously being internalized into peripheral endosomes and reshuttled back to the cell surface has not been well studied. On CSF-1 binding,

however, ligand-receptor complexes are rapidly internalized, targeted to lysosomes, and degraded,^{33,47,84} a process known as downregulation. Complete receptor degradation occurs within 15 minutes of stimulation with saturating concentrations of CSF-1, so that cells become completely refractory to restimulation by ligand until they resynthesize and reaccumulate new receptors at the cell surface. Although this process can attenuate the duration of ligand-induced PTK activity, it is unlikely that complete receptor downregulation occurs *in vivo*, because mononuclear phagocytes do not normally encounter saturating concentrations of CSF-1, nor do they require them for biologic responses to ensue. Kinase-inactive CSF-1R mutants do not undergo accelerated ligand-induced turnover, indicating that PTK activity is required for directing ligand-receptor complexes to the degradative pathway.⁷⁹ The extent of receptor downregulation and the relative "strength" of PTK signals can also be influenced by other cell-surface proteins (eg, by stabilizing CSF-1R at the cell surface, the bovine papillomavirus E5 protein can potentiate the CSF-1-induced mitogenic response, leading to cell transformation).⁸⁵

A loss of CSF-1 binding sites,^{86,87} resulting from accelerated turnover of mature CSF-1R molecules,^{79,84} also occurs after treatment of macrophages with phorbol esters, such as 12-*O*-tetradecanoylphorbol-13-acetate (TPA), or with other physiologic inducers of protein kinase C (PKC) such as bacterial lipopolysaccharide (LPS).⁸⁸ Several lines of evidence suggest that the mechanisms of ligand- and TPA-induced receptor turnover are different. First, kinase-inactive receptor mutants remain sensitive to TPA-induced, but not ligand-induced, degradation. Conversely, if cells are chronically treated with phorbol esters so that PKC is itself downregulated, CSF-1R molecules reexpressed at the cell surface are sensitive to ligand- but not phorbol ester-induced, degradation.⁷⁹ Thus, PKC activity is not required for ligand-induced receptor degradation. Third, the turnover of the feline *v-fms*-coded glycoprotein is not accelerated by TPA treatment,⁸⁴ indicating that mutational differences which distinguish the *v-fms*- and *c-fms*-coded molecules (described below) must affect their sensitivity to PKC-induced degradation. Chimeric receptors containing half of the extracellular domain of human CSF-1R fused to the remaining portion of the feline *v-fms* gene product are rapidly downregulated in response to human CSF-1, but not by phorbol esters, further demonstrating that these two properties can be genetically segregated from one another.⁸⁹

Activation of PKC by phorbol esters induces proteolytic cleavage of CSF-1R in its extracellular domain at a site(s) near the membrane-spanning sequence.⁷⁹ This results in release of the glycosylated 100-Kd ligand-binding domain from the cell and the simultaneous appearance of a cell-associated 50-Kd fragment representing the CSF-1R tyrosine kinase domain, which then undergoes rapid intracellular degradation. Because receptor cleavage can occur in response to a variety of physiologic inducers of PKC and does not appear to involve receptor internalization through the endocytic pathway, this process has been termed "transmodulation." CSF-1R is phosphorylated only on serine residues in the absence of ligand stimulation, and its transmodulation by

PKC is not accompanied by a detectable increase in receptor serine or threonine phosphate or by phosphorylation at new sites. Thus, PKC does not directly modify and "target" the receptor for cleavage, but rather activates a protease that recognizes CSF-1R as a substrate. The 50-Kd tyrosine kinase fragment produced by this reaction lacks phosphotyrosine, the hallmark of an activated enzyme (described below), and therefore is unlikely to be functional. The receptor ligand-binding domain released from the cells retains the ability to bind CSF-1 (S. Morris, J.R. Downing, C.J. Sherr, unpublished observations), enabling it to compete with cell-surface receptors for ligand.

The significance of CSF-1R transmodulation may be to regulate the inflammatory response. Physiologic inducers of PKC, such as the macrophage activator LPS, would be expected to inhibit CSF-1-dependent cell proliferation and survival by this mechanism. Moreover, unlike its inductive effects in HL-60 cells, TPA treatment of mature monocytes does not increase *c-fms* transcription but instead destabilizes *c-fms* mRNA,⁷³ thereby inhibiting new receptor synthesis. Because macrophage activation and proliferation are likely to represent antagonistic processes, transmodulation of CSF-1R might not only enhance macrophage differentiated functions but would also limit subsequent survival of activated phagocytes at sites of inflammation. PKC induces transcription of many genes, one of which is the CSF-1 gene itself.^{12,15} Although activated macrophages should release CSF-1, transmodulation of CSF-1R and concomitant diminution in levels of CSF-1R mRNA would make such cells refractory to autocrine stimulation. Perpetuation of the inflammatory response might therefore necessitate recruitment of naive macrophages in response to local CSF-1 production.

RECEPTOR SIGNAL TRANSDUCTION

CSF-1 binding alters the receptor's conformation in such a way as to upregulate PTK activity. The nature of these conformational changes is poorly understood, but work in other systems suggests that the receptors form dimers or higher order aggregates in response to ligand, thereby activating the receptor kinase through an intermolecular mechanism.⁹⁰⁻⁹³ Induction of PTK activity leads to phosphorylation of the receptor itself on tyrosine, possibly owing to transphosphorylation by aggregated CSF-1R subunits. Three major sites of tyrosine phosphorylation within the CSF-1R kinase domain have been identified. One of these appears to be tyrosine 809 (Fig 2), whose position and context are analogous to those of the major sites of tyrosine phosphorylation in the *src* gene product and insulin receptor. Two other sites have been mapped within the kinase insert region of murine CSF-1R (P. Tapley, A. Kazlauskas, L.R. Rohrschneider, personal communication). In contrast to the ligand-induced phosphorylation of EGF-R which occurs at multiple sites clustered within the receptor C-terminal tail, the CSF-1R C-terminus contains only a single tyrosine residue at position 969 (Fig 2), which is not detectably phosphorylated either in the absence or presence of ligand (J.R. Downing and C.J. Sherr, unpublished observations). It is not known whether "autophosphorylation" of CSF-1R on

tyrosine plays any direct role in regulating its PTK activity, determining its specificity for heterologous protein substrates or governing its rate of ligand-induced internalization and degradation. Recent studies with PDGF-R_B suggest that phosphorylation within its kinase insert sequences can affect its interaction with certain substrates.⁹⁴

Activation of CSF-1R PTK activity leads to rapid phosphorylation of heterologous protein substrates within seconds of CSF-1 stimulation.⁹⁵⁻⁹⁷ With use of antibodies to phosphotyrosine for immunoblotting analysis, several tyrosine-phosphorylated polypeptides can be detected in stimulated macrophages after CSF-1 treatment, but none of these proteins has yet been purified or characterized in detail. That CSF-1 can elicit a pleiotropic response that includes both rapid and delayed biochemical events strongly suggests that multiple physiologic substrates for the receptor kinase will be identified. CSF-1 induces rapid effects on membrane ruffling and vacuolization,⁹⁸ immediate cytoplasmic alkalization through Na⁺/H⁺ exchange,⁹⁹ increased hexose transport,¹⁰⁰ and induction of a family of "immediate early response" genes, including the protooncogene *c-fos*,^{101,102} within minutes of stimulation. These rapid events appear insufficient for mitogenesis, because CSF-1 is required throughout the entire G1 phase of the cell cycle to ensure a proliferative response.¹⁰³ Thus, an evolution of different substrates for the receptor kinase may occur as the cells progress toward S phase. Moreover, submitogenic doses of the growth factor can support the viability of nonproliferating cells that become growth arrested in early G1,¹⁰³ indicating that the family of CSF-1-responsive genes must include those that support cell metabolism as well as those that regulate cell growth.¹⁰²

A major challenge, then, is to pinpoint tyrosine phosphorylated substrates that lie along the "mitogenic pathway" and act to relay signals from the receptor to the cell nucleus. Excitement was generated by recent observations that ligand-stimulated EGF-R and PDGF-R_B could bind and phosphorylate phospholipase C- γ (PLC- γ),¹⁰⁴⁻¹⁰⁸ an enzyme that cleaves phosphatidylinositol 4,5-bisphosphate (PIP2) to yield soluble inositol 1,4,5-trisphosphate (IP3) and 1,2-diacylglycerol (DAG). Both IP3 and DAG act as "second messengers" in signal transduction, the former in mobilizing calcium from intracellular stores and the latter in activating PKC.¹⁰⁹ Thus, phosphorylation of PLC- γ by EGF-R and PDGF-R_B could affect the activity or topology of PLC- γ so as to increase second messenger production. However, in parallel studies we were not able to demonstrate that PLC- γ is a direct substrate of the CSF-1R kinase,¹¹⁰ consistent with a lack of evidence for rapid mobilization of soluble phosphoinositides in macrophages responding to CSF-1 stimulation.¹¹¹ Although our studies have not ruled out the possibility that CSF-1R can bind and phosphorylate other PLC isoforms, the simplest interpretation is that CSF-1R uses alternative second-messenger pathways.

Other protooncogene products that function "downstream" of CSF-1R along the mitogenic pathway may also represent, or communicate with, candidate substrates; eg, stimulation of fibroblasts by PDGF or their transformation by the *v-fms* oncogene induces phosphorylation of the *c-raf* protooncogene product,^{112,113} itself a serine/threonine protein kinase.¹¹⁴ The

kinase activity of the *c-raf* protein is encoded in its C-terminal moiety, implying that the N-terminal half of the polypeptide plays a modulatory role. Because N-terminally truncated versions of the *c-raf* gene product can transform cells, this domain appears to regulate *raf*-coded kinase activity negatively. Receptor-mediated tyrosine phosphorylation of its N-terminal domain might provide one mechanism by which the *c-raf*-coded enzyme is physiologically regulated.

Microinjection of monoclonal antibodies (MoAbs) to the Harvey *c-ras* gene product (p21*ras*) inhibits growth of fibroblasts transformed by the retroviral *v-fms* oncogene, but not by *v-raf*, suggesting that the activity of a *ras*-coded protein might be independently coupled to CSF-1R.¹¹⁵ The mechanism by which antibodies to p21*ras* suppress *v-fms* action and, by extension, normal CSF-1R function, is not understood. By analogy to prototypic guanine nucleotide-binding (G) proteins that function in signal transduction,¹¹⁶ *ras* gene products require bound GTP for activity. Hydrolysis of bound GTP to GDP is mediated by the intrinsic GTPase activity of p21*ras* itself, thereby attenuating its signal. Conversely, oncogenic p21*ras* mutants which fail to hydrolyze GTP provide sustained signals for cell proliferation and induce cell transformation and tumorigenesis.¹¹⁷ In eukaryotes, a GTPase-accelerating protein (GAP) that binds to p21*ras*-GTP complexes is required for maximal levels of GTP hydrolysis,¹¹⁸ implying that inhibition of GAP activity might also modulate p21*ras*-induced mitogenic signals. Candidate regulators of *ras* proteins and/or GAP activity include certain phospholipids.¹¹⁹ If substrates of the CSF-1R kinase that upregulate p21*ras* or inhibit GAP activity could be identified, inhibition of *v-fms* transformation by anti-*ras* MoAbs might be explained.

The physical association of a novel phosphatidylinositol (PI)-3' kinase with both the PDGF-R_B receptor and the *v-fms* gene product, and the possibility that this form of PI kinase is activated by tyrosine kinases,¹²⁰⁻¹²² indicate an alternative mechanism by which synthesis of phospholipids might be regulated by growth factor receptors. Mutant PDGF-R_B molecules lacking their kinase insert sequences are impaired in triggering fibroblast mitogenesis, although they retain PTK activity.^{121,123} Such mutants fail to regulate either the *c-raf* product or with PI kinase,¹¹³ reinforcing the view that each of these putative substrates may play a critical role in signal transduction. Analogous kinase insert deletion mutants of murine CSF-1R retain both their PTK activity and mitogenic potential when expressed in fibroblasts,¹²⁴ but their signal-transducing capability in macrophages has not yet been examined.

Prostaglandins of the E series (PGE₁ and PGE₂) can negatively regulate mononuclear phagocyte proliferation,^{26,29,125,126} suggesting that elevated levels of cAMP, induced through the action of the PGE₂ receptor, might attenuate CSF-1 responsiveness. In the SV40-immortalized, CSF-1-dependent mouse macrophage cell line, BAC1.2F5,¹²⁷ PGE₂ inhibited CSF-1-induced DNA synthesis and cell division; its effects were mimicked by dibutyryl-cAMP and potentiated by 1-methyl-3-isobutyl xanthine, an inhibitor of cAMP phosphodiesterase (S. Jackowski, C.W. Rettenmier,

C.O. Rock, personal communication). CSF-1 activates a pertussis toxin-sensitive GTP-binding protein in monocyte membranes,¹²⁸ suggesting that it might limit cAMP levels through an effect on a G protein coupled to adenylyl cyclase. In BACL.2F5 cells, however, CSF-1 does not attenuate the rise in cAMP levels induced by PGE₂. Instead, BACL.2F5 cells produced PGE₂ when starved for CSF-1 but terminated release on stimulation with the growth factor. In the presence of both CSF-1 and PGE₂, nondividing BACL.2F5 macrophages remained viable, whereas those starved for CSF-1 did not (S. Jackowski, C.W. Rettenmier, C.O. Rock, personal communication). That PGE₂ did not abrogate functions of CSF-1 necessary for cell survival indicates that CSF-1R signal transduction continues in the presence of elevated cAMP concentrations and that cAMP interdicts some but not all downstream signals.

How does second-messenger synthesis ultimately lead to alterations in the transcription of target genes? Posttranslational modification of preexisting transcriptional regulatory factors in the cytoplasm and their transduction to the nucleus represent basic requirements for activation of several early response genes.^{129,130} Efforts to identify and clone candidate transcriptional regulatory factors and to delineate modifications that regulate their functions represent topics of investigation for many laboratories and are likely to pinpoint critical connections along the mitogenic pathway.

TRANSDUCTION OF THE CSF-1R GENE

Expression of *c-fms* cDNA under the control of retroviral vectors has enabled receptor function to be evaluated in cells that normally do not express CSF-1R. When human CSF-1R was expressed in naive mouse NIH-3T3 fibroblasts, the cells were able to form colonies in semisolid medium in response to physiologic concentrations of human recombinant CSF-1. Cotransfection of the same cells with a second vector encoding human CSF-1 closed an autocrine loop and led to cell transformation and tumorigenicity.¹³¹ Thus, CSF-1R can interact functionally with elements of the mitogenic pathway, even in cells that normally do not respond to the growth factor. NIH-3T3 cells expressing CSF-1R, like the CSF-1R⁻ parental line, required PDGF and IGF-1 (or insulin) for growth in chemically defined medium, but in the presence of CSF-1 their requirements for exogenous PDGF and IGF-1 were abrogated.¹³² Although the doubling times of the cells in CSF-1 or in PDGF plus insulin were identical, cells grown in CSF-1 were no longer contact inhibited and appeared morphologically transformed. That their growth response was qualitatively altered in response to CSF-1 suggests that PDGF-R and CSF-1R might differentially interact with substrates that regulate contact-mediated growth arrest.

Insertion of human CSF-1R into Chinese hamster lung fibroblasts (CCL39) also enabled them to respond mitogenically to CSF-1.¹³³ In these cells, CSF-1 stimulated Na⁺/H⁺ exchange and DNA synthesis in the absence of PI breakdown, consistent with previous observations in macrophages.¹¹¹ Pertussis toxin weakly inhibited CSF-1-induced proliferation, again suggesting that the receptor can communicate with a signal-transducing G protein.¹²⁸ In the absence of

CSF-1, receptor-bearing CCL39 cells exhibited a higher basal level thymidine incorporation and decreased anchorage independence as compared with parental cells.¹³³ Both processes were inhibited by an MoAb that abrogates signal transduction by human CSF-1R.¹³⁴ The observation that "relaxation" of growth control depended on receptor expression suggested that basal levels of receptor kinase activity per se might provide certain cells with a proliferative advantage.

The mouse myeloid cell line FDC-P1 does not normally express CSF-1R and requires IL-3 for proliferation and survival.¹³⁵ Introduction of human CSF-1R under the control of an inducible metallothionein promoter enabled the cells to grow in CSF-1.¹³⁶ In the absence of CSF-1 or IL-3, a low percentage of receptor-bearing (but not parental) cells remained able to proliferate and their frequency was increased when receptor expression was further induced by heavy metal treatment. Again, an MoAb that inhibits signal transduction through human CSF-1R was able to arrest the growth of both CSF-1-dependent and factor-independent receptor-bearing cells. These results raise the possibility that unscheduled expression of CSF-1R in immature myeloid cells might not only alter their factor dependence but might also relax their growth factor requirements. Introduction of the murine *c-fms* gene into FDC-P1 cells induced monocytic characteristics in response to CSF-1, further suggesting that CSF-1R-mediated signals can directly trigger the expression of genes differentially expressed in mononuclear phagocytes.¹⁶³

TRANSFORMING POTENTIAL OF THE C-FMS GENE

The *v-fms* gene of the Susan McDonough strain of feline sarcoma virus (SM-FeSV) was derived by recombination between a feline leukemia virus and *c-fms* protooncogene sequences of the domestic cat.¹³⁷ The *v-fms* oncogene can transform cultured cat, mouse, rat, canine, and mink fibroblasts to anchorage-independent, tumorigenic derivatives⁵⁴ and can abrogate the growth factor requirements of both CSF-1-dependent and IL-3-dependent murine myeloid cells, rendering them tumorigenic in nude mice.^{84,138} When SM-FeSV-infected BM cells were used to reconstitute lethally irradiated mice, the transplanted recipients developed a variety of hematopoietic proliferative disorders, including clonal erythroleukemias and B-cell lymphomas.¹³⁹ Recently, *v-fms* was shown to recapitulate effects of the *v-abl* oncogene in transforming murine pre-B cells in long-term BM cultures.¹⁴⁰ Thus, although it was derived from a lineage-specific receptor, the *v-fms* gene product is promiscuous in its transforming activity and can contribute to tumorigenesis in a variety of settings.

Although analogous in structure to CSF-1R, the *v-fms*-coded glycoprotein can act as a ligand-independent tyrosine kinase. The oncogene product is itself constitutively phosphorylated on tyrosine^{77,141} and induces phosphorylation of a series of cellular proteins on tyrosine in the absence of CSF-1,¹⁴² thereby providing sustained signals for cell growth. The SM-FeSV *v-fms* and feline *c-fms* gene products differ by only nine scattered point mutations and by a C-terminal truncation in which 50 amino acids of the *c-fms*-coded C-terminal tail were replaced by 11 unrelated *v-fms*-coded residues.⁵² Truncations, mutations, or sequence substitutions

engineered within the C-terminus of human CSF-1R appear to disrupt a negative regulatory domain and upregulate its ligand-dependent receptor kinase activity.^{131,143} However, these genetic alterations in themselves are insufficient to activate *c-fms* as an oncogene.¹³¹ In contrast, specific amino acid substitutions in the receptor extracellular domain act as potent "activating mutations" that enable mutant CSF-1R to transform cells in the absence of CSF-1.^{52,53} When mutant feline receptors were assayed in rat-1 cells, point mutations at codons 301 and 374, as well as the C-terminal truncation, were required to generate a fully transforming phenotype.⁵² When programmed into human CSF-1R, the single substitution of serine for leucine at codon 301 enabled the receptor to convert NIH-3T3 cells to a tumorigenic phenotype⁵³; mutation of codon 374 had no independent or additive effect in this system (M.F. Roussel and C.J. Sherr, unpublished observations). However, human receptors bearing an activating mutation at codon 301 together with cooperating C-terminal modifications, such as substitution of tyrosine 969 by phenylalanine, were more active in transformation,⁵³ showing that in either system multiple genetic events occurring within *c-fms* can cooperate to augment its transforming efficiency incrementally.

Although the activating mutation at codon 301 is located in the receptor extracellular domain, it does not perturb the ligand-binding site⁵³; indeed, cells transformed by *v-fms* show a further enhancement in their growth rate in the presence of CSF-1.^{89,144} As expected, equilibrium binding studies performed with ¹²⁵I-labeled human recombinant CSF-1 and cell lines expressing either activated forms of human CSF-1R or the feline *v-fms* product showed that the *K_d* for binding was 1 to 4×10^{-10} mol/L, similar to that calculated for the wild-type receptor.^{53,144} In recent studies, we found that certain amino acid substitutions at codon 301 other than serine are effective in activating the transforming potential of human CSF-1R, whereas others had no effect.¹⁴⁵ The activating mutations must therefore induce a specific conformational change that mimics an effect of ligand binding on receptor kinase activity. The ability of an MoAb directed to an extracellular receptor epitope to inhibit the growth of cells transformed by human CSF-1R mutants^{132,134} is consistent with the possibility that the activating mutations alter the aggregation state of the receptor at the cell surface, thereby enhancing receptor dimer formation in the absence of ligand. Similar effects have recently been observed with the product of the *neu* (*erbB-2*, HER-2) oncogene,¹⁴⁶ which is activated by specific point mutations within its transmembrane domain.^{147,148}

POSSIBLE ROLES FOR C-FMS IN HUMAN NEOPLASIA

Activating mutations within the *c-fms* gene in myeloid cells might contribute to human hematopoietic malignancies involving receptor-positive cells of the mononuclear phagocyte series.^{149,150} Sophisticated methodologies and available reagents should permit rapid evaluation of these possibilities. It is now possible to screen human leukemic blasts quickly for activating mutations at *c-fms* codon 301 by polymerase chain reaction techniques. An initial survey of leukemic blasts from 20 cases of receptor-positive acute myeloid leukemia has not

shown the presence of such mutations (S. Kramer, M.F. Roussel, C.J. Sherr, unpublished observations). The experimental results to date do not preclude the possibility that point mutations elsewhere in the receptor might similarly activate its oncogenic potential, however. Apart from SM-FeSV, *c-fms* sequences were independently transduced in only one other acutely transforming mammalian retrovirus, the HZ-5 FeSV strain.¹⁵¹ Nucleotide sequencing of the HZ-5 *v-fms* gene showed no activating mutation at codon 301, but rather the presence of mutations elsewhere in the gene (M.F. Roussel, P. Besmer, C.J. Sherr, unpublished observations). Assuming that the latter mutation(s) can also be shown to convert human CSF-1R to a ligand-independent kinase, the search for *c-fms*-activating mutations in human leukemias would at least need to be extended to these codons as well.

Alterations in the developmental timing of *c-fms* expression could also contribute to disease development. In mice, integration of the Friend strain of murine leukemia virus (F-MuLV) 5' to exon 2 of the *c-fms* gene (Fig 1) results in greatly increased levels of *c-fms* transcription and CSF-1R expression in immature myeloid cells.¹⁵² Based on experiments with cultured myeloid cell lines programmed to express CSF-1R (already described), high levels of receptor expression might not only alter the growth factor dependence of such cells but might also provide them with an intrinsic proliferative advantage.¹³⁶ Indeed, after F-MuLV infection, cells bearing viral integrations within the *c-fms* locus proliferate as dominant clones in the spleen, even before they can be successfully explanted into culture or have the potential to induce transplantable leukemias in mice. Thus, although *c-fms* activation appears to act as an initiating carcinogenic event, progression to frank malignancy must involve secondary genetic perturbations. Theoretically, chromosomal rearrangements affecting *c-fms* promoter/enhancer sequences might contribute in an analogous fashion to human myeloid malignancies. With MoAbs as probes for CSF-1R expression, at least 30% of human acute myeloid leukemia cells expressed detectable levels of the receptor at their cell surface irrespective of their French-American-British (FAB) classification.¹⁴⁹ Results obtained with more sensitive assays for *c-fms* mRNA indicated that the incidence of cells transcribing the gene is even higher.¹⁵⁰ The apparent lack of concordance between CSF-1R expression and other characteristics of monocytic differentiation in leukemic cells could reflect aberrant gene regulation in certain instances. No rearrangements of the *c-fms* gene have yet been detected, however, in an initial survey of both pediatric and adult leukemic cells.¹⁴⁹ A more precise characterization of the *c-fms* promoters and the elements that determine their developmental and tissue-specific regulation is needed to define the mechanisms governing *c-fms* expression by human myeloid leukemic blasts.

Normal monocytes produce CSF-1 in response to certain physiologic inducers.¹²⁻¹⁵ Assays of *c-fms* and CSF-1 mRNA levels in human myeloid leukemic cells have indicated that both genes may be simultaneously and stably expressed in some cases,^{153,154} suggesting that the growth of such cells might be enhanced through an autocrine mechanism. Rearrangements of the CSF-1 gene, such as have been observed in

a case of murine *c-myc*-induced monocytic leukemia,¹⁵⁵ might therefore facilitate disease progression. Despite the attraction of autocrine models for cell transformation, however, GM-CSF expression in transgenic mice¹⁵⁶ or retrovirus vector-mediated IL-3 expression in BM progenitors in vivo¹⁵⁷⁻¹⁵⁹ induced profound hematologic proliferative disorders but failed to yield leukemias. Similarly, introduction of the human CSF-1 gene into a CSF-1-dependent, SV40-immortalized mouse macrophage cell line abrogated their dependence on exogenous CSF-1 but did not render them tumorigenic in nude mice.¹⁶⁰ In contrast, expression of *v-fms* in these same cells induced both factor independence and tumorigenicity.⁸⁴ Therefore, the *v-fms* and *c-fms* gene products may elicit qualitatively different growth-promoting responses owing to mutations in the *v-fms* product that affect kinase activity, substrate recognition, or receptor turnover.

FUTURE EXPECTATIONS

Despite progress arising from application of molecular biological techniques to studies of CSF-1 and its receptor, many fundamental questions remain. For example, human CSF-1 paradoxically stimulates formation of fewer macro-

phage colonies from human than from mouse BM precursors,^{10,22,134,161} perhaps suggesting that its actions need be potentiated by other cytokines or that its primary role is to regulate the survival and effector functions of mature mononuclear phagocytes in the inflammatory response. Alternatively, despite its discovery as a hematopoietin, the dominant physiological actions of CSF-1 might well be exerted on other cell types, such as placental trophoblasts. Emerging genetic techniques now provide novel avenues for testing the function of CSF-1 in different cell lineages. As one approach, homologous recombination in embryonic stem cells¹⁶² can now be used to create transgenic strains of mice bearing defective or mutant CSF-1 and CSF-1R genes. A better understanding of CSF-1 activity should also derive from animal experiments and from human clinical trials with the purified recombinant growth factor and, possibly, from in vivo studies with MoAbs that interfere with ligand-receptor interactions or with drugs that inhibit receptor tyrosine kinases. Although major challenges lie ahead, such information will not only contribute to the way in which we conceptualize disease processes but should also yield novel approaches for manipulating CSF-1-dependent responses.

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