Persistent Activation of Mitogen-Activated Protein Kinases p42 and p44 and ets-2 Phosphorylation in Response to Colony-Stimulating Factor 1/c-fms Signaling

LINDSAY F. FOWLES,¹ MICHELE L. MARTIN,² LORI NELEN,² KATRYN J. STACEY,¹ DOUGLAS REDD,² YING MEI CLARK,² YOSHIKUNE NAGAMINE,³ MARTIN McMACHON,⁴ DAVID A. HUME,¹ AND MICHAEL C. OSTROWSKI²*

Departments of Microbiology and Biochemistry and the Centre for Molecular and Cellular Biology, University of Queensland, Queensland Q4072, Australia¹; Department of Molecular Genetics, Ohio State University, Columbus, Ohio 43210²; Friedrich-Miescher-Institute, Basel, Switzerland³; and DNAX Research Institute, Palo Alto, California 94304⁴

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An antibody that specifically recognized phospho-tyrosine 72 in ets-2 was used to determine the phosphorylation status of endogenous ets-2 in response to colony-stimulating factor 1 (CSF-1)/c-fms signaling. Phosphorylation of ets-2 was detected in primary macrophages, cells that normally express c-fms, and in fibroblasts engineered to express human c-fms. In the former cells, ets-2 was a CSF-1 immediate-early response gene, and phosphorylated ets-2 was detected after 2 to 4 h, coincident with expression of ets-2 protein. In fibroblasts, ets-2 was constitutively expressed and rapidly became phosphorylated in response to CSF-1. In both cell systems, ets-2 phosphorylation was persistent, with maximal phosphorylation detected 8 to 24 h after CSF-1 stimulation, and was correlated with activation of the CSF-1 target urokinase plasminogen activator (uPA) gene. Kinase assays that used recombinant ets-2 protein as a substrate demonstrated that mitogen-activated protein (MAP) kinases p42 and p44 were constitutively activated in both cell types in response to CSF-1. Immune depletion experiments and the use of the MAP kinase kinase inhibitor PD98059 indicate that these two MAP kinases are the major ets-2 kinases activated in response to CSF-1/c-fms signaling. In the macrophage cell line RAW264, conditional expression of raf kinase induced ets-2 expression and phosphorylation, as well as uPA mRNA expression. Transient assays mapped ets/AP-1 response elements as critical for basal and CSF-1-stimulated uPA reporter gene activity. These results indicate that persistent activation of the raf/MAP kinase pathway by CSF-1 is necessary for both ets-2 expression and posttranslational activation in macrophages.

Macrophage colony-stimulating factor 1 (CSF-1) controls the proliferation and differentiation of cells of the mononuclear phagocyte cell lineage. The actions of CSF-1 are mediated through an integral membrane receptor tyrosine kinase, the product of the c-fms proto-oncogene (22). As with other tyrosine kinase receptors, ligand binding leads to c-fms auto-phosphorylation, assembly of phosphotyrosine-dependent signaling complexes, and the subsequent activation of signal transduction pathways (25). Pathways controlled by CSF-1/c-fms include phosphatidylinositol 3-kinase (23), JAK-STATs (19), c-src-related kinases (6), and the ras pathway (3, 7). The latter two pathways have been demonstrated to be critical for the mitogenic action of CSF-1 (3, 6, 15).

CSF-1 stimulation results in the stable, persistent expression of specific genes, for example, the urokinase plasminogen activator (uPA) gene, in mature macrophages or in fibroblasts engineered to express c-fms (3, 14, 27). The uPA gene encodes an extracellular protease involved in cellular migration in many cell types, including metastatic tumor cells (2) and macrophages (5, 27).

The uPA promoter contains regions conserved across species up to 8.2 kb 5′ to the transcription start site (1, 5, 9). Within these regions of homology, two compound ets/AP-1 growth factor- and oncogene-responsive elements have been identified at −2.4 and −6.9 kb upstream of the transcription initiation site (1, 9, 27). In transient transfections, oncprotein ras collaborates with either ets-1 or ets-2 to superactivate the uPA promoter via the compound ets/AP-1 enhancer located at −2.6 kb relative to the transcription initiation site (34). Collaboration between ras and exogenously expressed ets factors depends on ras-dependent phosphorylation at threonine residues Thr 38 and Thr 72 in ets-1 and ets-2, respectively (34). The Thr 38 residue of ets-1 has been shown to be phosphorylated in a CSF-1-dependent manner in NIH 3T3 cells that exogenously express both ets-1 and c-fms (21). The phosphorylation sites are contained in a 100-amino-acid domain that is conserved between ets-1 and ets-2 and also in the Drosophila melanogaster protein pointed P2 (4, 20). The conserved N-terminal domain of the ets factor pointed P2 has been shown to be a nuclear target for ras signaling pathways critical for differentiation of the R7 photoreceptor cell in Drosophila, and thus defines a target for ras signaling pathways that is conserved through evolution from flies to humans (4, 20).

One well-characterized effector pathway activated by the ras-GTP complex is the raf/MEK-1/mitogen-activated protein (MAP) kinase pathway (16, 31). However, the exact identity of the ras effector pathways that CSF-1/c-fms engage to persistently activate the uPA promoter have not been defined. The ras/MAP kinase pathway has been shown to activate TCF/elk-1 ets family transcription factors, but these events occur early after growth factor stimulation and result in regulation of immediate-early genes such as c-fos (reviewed in reference 31). In PC-12 cells, activation of trkA has been shown to sustain ac-
tivation of ras and MAP kinases p42 and p44 over several hours, leading to the proposition that the duration and strength of the ras signal are the critical variables that distinguish how cells interpret ras/MAP kinase signals generated by different environmental stimuli (reviewed in reference 16).

In the present study, we present evidence for a signaling cascade initiated by CSF-1/c-fms in either macrophages or heterologous cells that ectopically express c-fms. This pathway involves stimulation of the ras pathway, resulting in continuous activation of MAP kinases p42 and p44 and stable phosphorylation of ets-2 at threonine 72, events that are correlated with the induction of uPA transcription by CSF-1.

MATERIALS AND METHODS

Cell culture and RNA analysis. NIH 3T3 cells containing genes expressing c-fms protein were grown in Dulbecco’s modified Eagle’s medium (DMEM) with 10% fetal calf serum (FCS). Prior to stimulation with CSF-1 (1 U/cell), 105 cells per ml (27). RAW264 cells were maintained in RPMI media containing heat-inactivated 5% FCS. RAW264 cells expressing the c-fms protein were grown in Dulbecco’s modified Eagle’s medium (DMEM) with 10% fetal calf serum (FCS). Prior to stimulation with CSF-1 (1 U/cell), 105 cells per ml (27). RAW264 cells were maintained in RPMI media containing heat-inactivated 5% FCS. RAW264 cells expressing the c-fms protein were grown in Dulbecco’s modified Eagle’s medium (DMEM) with 10% fetal calf serum (FCS).

RESULTS

Recombinant ets-2 protein is a specific substrate for purified MAP kinases p42 and p44 in vitro. In work that depended on transient transfection systems, we demonstrated that threonine 72 of ets-2 was phosphorylated in a ras-dependent fashion (34). In an attempt to define kinases that catalyze phosphorylation of this site in ets-2 in vitro, an N-terminal region of ets-2 corresponding to the region conserved in the Drosophila pointed P2 protein (amino acids 60 to 167) was overexpressed as a six-histidine-tagged fusion protein in bacteria. The fusion protein was subsequently purified and used as a substrate for in vitro kinase reactions. Purified recombinant MAP kinase p44 could utilize this portion of ets-2 as a substrate (Fig. 1A, lane 1). A recombinant ets-2 protein containing the Ala 72 substitution was not used as a substrate by MAP kinase p44 (Fig. 1A, lane 2). Furthermore, phosphoamino acid analysis of the [32P]-labeled threonine 72 ets-2(60–167) protein revealed exclusive phosphorylation at threonine (data not shown). Identical results were obtained with purified MAP kinase p42 (data not shown).

In contrast, the MAP kinase family member p55-JNK2 (13) did not utilize the ets-2 recombinant protein (Fig. 1B lane 3) as a substrate under conditions where the N-terminal region of c-jun (residues 1 to 79) could be phosphorylated in vitro (Fig. 1B, lanes 1 and 2). In these experiments, the ets-2 protein was a poorer substrate than even the c-jun substrate that lacked the major phosphorylation sites at positions 563 and 573 (Fig. 1B, lane 2), which was still detectably phosphorylated at minor sites by JNK2 and MKK4 (Fig. 2). ets-2 protein was incubated with the Ala 72 substitution was not used as a substrate by MAP kinase p44 (Fig. 1A, lane 2). Furthermore, phosphoamino acid analysis of the [32P]-labeled threonine 72 ets-2(60–167) protein revealed exclusive phosphorylation at threonine (data not shown). Identical results were obtained with purified MAP kinase p42 (data not shown).

Production and characterization of antisemur specific for ets-2 phosphothreonine 72. In order to directly measure the phosphorylation of endogenous ets-2 at amino acid position threonine 72, an antibody that was specific for the phosphorylated threonine 72 was developed. For this purpose, the peptide PPL-pT-PCS (corresponding to amino acids 69 to 77 of ets-2) was synthesized and used to produce polyclonal rabbit serum. Following affinity purification (see Materials and Methods), the specificity of the antibody for detecting phosphothreonine 72 ets-2 in Western blotting experiments was confirmed (Fig. 1C). These experiments showed that only wild-type threonine 72 protein which had been incubated with the MAP kinase preparation was recognized by the antibody (lane two...
versus lane 1 in Fig. 1C). Proteins containing the A72 substitution were not recognized by the antibody whether MAP kinase was present or absent (lanes 3 and 4). A second non-discriminating (i.e., phosphorylation independent) antiserum directed against the ets-2 N-terminal region (amino acids 60 to 167) was also produced. When the blot shown in Fig. 1C was stripped and reprobed with the second antibody, equal loading of the recombinant proteins could be demonstrated (Fig. 1D). The phosphopeptide-specific anti-peptide antibody did not react with blots that contained 10 μg of recombinant unphosphorylated threonine 72 protein per lane, nor did it react with other phosphoproteins, for example, the N-terminal region of c-jun (data not shown).

**Persistent phosphorylation of ets-2 in response to CSF-1/c-fms signaling in NIH 3T3 cells and in primary macrophages.** The anti-phosphopeptide T72 ets-2 antibody was used to determine the phosphorylation status of endogenous ets-2 in NIH 3T3 cells that express the human c-fms receptor tyrosine kinase (23, 24). Activation of c-fms tyrosine kinase activity by CSF-1 results in the activation of ras signaling pathways and the persistent activation of ras-responsive genes (3, 14, 27). For example, the activation of uPA mRNA expression in these cells following CSF-1 stimulation was demonstrated in Fig. 2A. In this experiment, Northern analysis reveals that uPA expression was stimulated within 30 min following growth factor treatment and that the expression of this mRNA persisted after 24 h of stimulation. In contrast, stimulation of the same NIH 3T3 cell line with PDGF resulted in only transient stimulation of uPA mRNA, with maximal stimulation after 30 min of PDGF treatment (Fig. 2A). We have previously reported this difference in the ability of CSF-1 and PDGF to stimulate the expression of ras-responsive genes in NIH 3T3 cells (3). Thus, if ets-2 is involved in growth factor-induced activation of uPA expression, it should be rapidly phosphorylated in response to
CSF-1 or PDGF stimulation, but in addition it should remain phosphorylated for extended periods following CSF-1 treatment.

Nuclear extracts were prepared from the NIH 3T3 cells expressing c-fms following CSF-1 treatment for increasing periods of time. These samples were analyzed by Western blotting with the anti-phosphopeptide T72 affinity-purified antibody (Fig. 2B). Specific binding of the antibody was not seen in the extracts prepared from serum-starved cells. However, the antibody detected a major band of 54 kDa, the predicted size for ets-2, within 30 min of CSF-1 treatment (Fig. 2B, upper panel, upper arrow). This band was observed throughout the CSF-1 time course up to 24 h after CSF-1 treatment. If antibody incubations were performed in the presence of the phosphopeptide used for immunization, the 54-kDa band was not detected (data not shown). The nuclear samples were analyzed with a nonphosphopeptide-selective ets-2 antibody raised against a recombinant ets-2 protein comprising amino acids 60 to 167 (Fig. 2B, lower panel). This antibody detected the same 54-kDa major species in all samples, including the serum-starved samples (Fig. 2B, lower panel, upper arrow). The 54-kDa band was not detected in cytoplasmic extracts (data not shown).

In contrast to the results obtained with CSF-1, treatment of the same NIH 3T3 cell line with PDGF resulted in a transient stimulation of ets-2 phosphorylation (Fig. 2D). The phosphorylation of ets-2 was maximal within 30 min following PDGF treatment and was undetectable after 8 to 12 h of treatment. The steady-state levels of ets-2 protein, determined by using the nondiscriminating antibody, were not affected by PDGF treatment (data not shown). Thus, ets-2 was phosphorylated at position threonine 72 in a manner consistent with the kinetics of activation of uPA mRNA by either CSF-1 or PDGF.

A mutation at an autophosphorylation site at tyrosine residue 809 in the human c-fms (809Y→809F) protein selectively abrogates the ability of ligand-activated receptor to stimulate mitogenic growth of NIH 3T3 cells and to stimulate expression of ras-responsive genes like that coding for uPA (14, 27). The F809 receptor also failed to stimulate the conversion of ras to the GTP complex, a conversion the wild-type Y809 receptor efficiently carries out (20a). This receptor failed to activate phosphorylation of ets-2 (Fig. 2D), providing an additional correlation between ets-2 phosphorylation and receptor-dependent activation of persistent gene expression.

In addition to the major band migrating at the predicted size for ets-2, a smaller, 45-kDa band was detected by both antibodies used (lower arrow in Fig. 2B and D). This band was especially prominent after 12 to 24 h of CSF-1 stimulation of cells. The identity of this cross-reacting species is under investigation, but preliminary data indicate that it may be derived by proteolysis of the 54-kDa protein species (data not shown).

The c-fms gene is usually predominantly expressed in monocytes and macrophages in adult mammals (22), and we have previously implicated ets-2 in uPA activation in this cell type (27). In BMMs deprived of CSF-1, the kinetics of uPA induction were delayed following restimulation with CSF-1 with respect to the situation observed in the artificial NIH 3T3 system. In BMMs, uPA expression was induced within 8 h following stimulation (Fig. 3A). When nuclear extracts from BMMs stimulated with CSF-1 were analyzed, the kinetics of ets-2 phosphorylation were also found to be delayed relative to those in the NIH 3T3 system, with little of the phosphothreonine 72 form of ets-2 seen until 4 to 8 h of CSF-1 treatment (Fig. 3B, upper panel, upper arrow). The phosphothreonine 72 form of ets-2 was observed following 12 to 24 h of growth factor stimulation and in cells continuously grown in the presence of CSF-1 (data not shown). When these samples were analyzed with nondiscriminating antibody [anti-ets-2(60–167) antibody], it was observed that in contrast to NIH 3T3 cells, ets-2 was not expressed in CSF-1-deprived BMMs, but was detectable after 4 h of CSF-1 treatment (Fig. 3B, lower panel, upper arrow).

As in the NIH 3T3 cells, the faster-migrating 45-kDa cross-reactive protein was again detected (Fig. 3B, lower arrows). In addition, the anti-phosphopeptide T72 antibody specifically cross-reacted with a protein with an apparent molecular mass of 100 kDa (Fig. 3B, arrowhead). This 100-kDa species was induced within 1 h following CSF-1 stimulation of BMMs and was detectable at 8 h after stimulation as well. However, the 100-kDa protein was not recognized by the non-phosphopeptide ets-2 antibody (Fig. 3B, lower panel). The nature of the 100-kDa species is currently under investigation.

The expression and phosphorylation of ets-2 in the macrophage cell line RAW264 were also analyzed. CSF-1 does not stimulate uPA transcription in these cells (27), and ets-2 expression was not detected with either phosphopeptide ets-2 or nondiscriminating ets-2 antibodies, regardless of whether CSF-1 was added to the cell culture medium (Fig. 3B, lanes R). The anti-phosphopeptide Thr 72 cross-reacting 100-kDa band was also absent in RAW264 cells.
MAP kinase p42 and p44 activity correlates with ets-2 phosphorylation in BMMs and in NIH 3T3 cells. Previous work has indicated that CSF-1 stimulation of MAP kinase p42 and p44 activity in macrophages is transient, with a peak of activity within 10 to 15 min following growth factor stimulation (12), suggesting that these kinases may not be the ets-2 kinase present in these cells. In order to identify kinases capable of phosphorylating ets-2 in primary macrophages, in-gel kinase assays were performed with the ets-2(60–167) threonine 72 or alanine 72 recombinant protein as a substrate (Fig. 4A, left panel, lanes 1 to 6). In extracts derived from BMMs, the two major specific protein species detected by this assay migrated with mobilities of 42 and 44 kDa. Within 1 min of addition of CSF-1, the activity of these two kinases was induced. In addition, the 42-kDa kinase remained active following 4 hours of CSF-1 stimulation, indicating that activation of this kinase was persistent in BMMs. In RAW264 cells treated with CSF-1, there was five- to sevenfold induction of this ets-2 kinase activity (Fig. 4A, lanes 7 to 12). When the Ala 72 form of the ets-2 protein domain (Fig. 4A, right panel) and probably represent autophosphorylation of resident kinases.

In order to confirm that the specific protein species detected in the in-gel kinase assay were MAP kinases p42 and p44, immune kinase assays were performed with BMM cell lysates with antibody that specifically recognizes these two MAP kinase species. Once again, the ets-2 recombinant protein was utilized as a substrate. These data were consistent with those of the in-gel kinase assays, demonstrating that MAP kinase was detected within 30 min of CSF-1 stimulation and that activity persisted up to 24 h following stimulation (Fig. 4B, upper panel). Analysis of these samples by Western blotting with an anti-MAPK kinase antibody revealed that the level of MAP kinase did not change during the CSF-1 time course (Fig. 4B, lower panel). Consistent with the in-gel kinase results, significant MAP kinase activity was not seen when such an assay was performed with CSF-1-treated RAW264 cells (data not shown).

The immune kinase assays as described above were repeated with lysates prepared from NIH 3T3 cells that express c-fms (Fig. 5A). Little MAP kinase activity was detected in CSF-1-starved cells, but persistent activation of MAP kinase activity was seen from 30 min up to 24 h following CSF-1 treatment (Fig. 5A, left panel). MAP kinase expression remains constant over this time course, as revealed by Western analysis with the same MAP kinase-specific antibody as that used above (Fig. 5A, right panel). Stimulation of F809-c-fms/NIH 3T3 cells with CSF-1 does not lead to increased MAP kinase activity (Fig. 5B), although Western analysis indicated that MAP kinase levels in these cells were comparable to those seen in the Y809-c-fms/NIH 3T3 cells (data not shown).

MAP kinases p42 and p44 are the major ets kinases detected in c-fms/NIH 3T3 cells. To determine if kinases other than MAP kinases p42 and p44 could be detected following CSF-1 stimulation, MAP kinase p42 and p44 activity was depleted by five successive rounds of immune precipitation from lysates prepared from CSF-1-stimulated c-fms/NIH 3T3 cell lysates (Fig. 6A). This analysis revealed that after four rounds of antibody treatment, >95% of MAP kinase activity was re-
moved from the cell lysates (lanes 3 to 7). At the same time, while ets kinase activity could be detected in the supernatant recovered after the second round of immunoprecipitation, no activity could be detected in the supernatant that was recovered after the fourth round (lane 1 versus lane 2).

To further confirm that the raf/MEK-1/MAP kinase p42 and p44 pathway was the major CSF-1-induced ets-2 kinase pathway, phosphorylation of ets-2 in the presence of the specific MEK-1 inhibitor PD98059 (10) was determined with the anti-phosphopeptide T72 ets-2 antibody (Fig. 6B). Figure 6A demonstrated that in fibroblasts expressing c-fms, PD98059 blocked ets-2 phosphorylation at both early (Fig. 6B, lane 2 versus lane 3) and late (Fig. 6B, lane 4 versus lane 5) times following growth factor stimulation and also blocked CSF-1 stimulation of uPA mRNA expression (data not shown). At the same time, ets-2 expression, as detected with the non-phosphopeptide-specific antibodies, was not affected by drug treatment (Fig. 6C). The same experiments were attempted with primary mouse BMMS, but ets-2 expression could not be detected following treatment of cells with both CSF-1 and PD98059 (data not shown). Within hours of exposure to the drug PD98059, BMMS lose viability, as determined by trypan blue dye exclusion, making it difficult to determine if the lack of ets-2 expression was a specific or general effect of the drug.

Conditional expression of activated raf kinase in RAW264 cells induces ets-2 expression and phosphorylation and uPA mRNA. CSF-1 is not able to stimulate ets-2 expression or phosphorylation in RAW264 cells. In order to determine where the defect in CSF-1 signaling occurs, RAW264 cells that express an estrogen-inducible form of raf kinase were used to activate MAP kinases in a CSF-1-independent fashion (11). We reasoned that such an analysis would reveal whether the signaling defect lies downstream or upstream of raf kinase.

Following estrogen treatment, analysis of uPA mRNA levels indicated that this gene was induced within 2 h and maximally stimulated 8 to 16 h after addition of estrogen (Fig. 7A, upper panel), after correction for RNA sample loading (lower panel, α-actin rehybridization control). Northern analysis also demonstrated that ets-2 mRNA was induced in these cells following stimulation of ets activity (data not shown).

The expression and phosphorylation status of ets-2 protein were studied by Western blotting (Fig. 7B and C). Use of the anti-phosphopeptide T72 ets-2 antibody again demonstrated that both ets-2 bands were detected (see above). Use of the nondiscriminating ets-2 antibody again demonstrated that both ets-2 bands were detected. The kinetics of ets-2 expression and phosphorylation paralleled expression of uPA mRNA.

In control experiments, β-estradiol had no effect on ets-2 or uPA expression in either normal RAW264 cells or cells that contained the estrogen receptor vector lacking the raf kinase coding sequences (reference 11 and data not shown).

**cis element requirements for CSF-1 induction of the uPA in RAW264 cells.** Given the results presented above, a possible explanation for the failure of CSF-1 signaling to induce uPA transcription in RAW264 cells is that the steady-state level of receptor is insufficient to provide the signal required for sustained activation of MAP kinases and subsequent phosphory-
tion, cells were treated with or without 10^4 U of CSF-1 per ml for 24 h, and the plasmid was included with the various uPA reporters in the transient transfec-

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transfected with pGL2-uPA-6.6 with either the c-fms expression plasmid or the reporter gene activity in RAW264 cells. (A) RAW264 cells were transiently enhancer mutations as represented in the first column. The

RAW264 cells were transiently transfected with a series of uPA promoter and

expression plasmid lacking the c-fms cDNA and a uPA reporter

promoter activity, RAW264 cells were cotransfected with a

heterologous promoter would rescue CSF-1 induction of uPA

transcription site had maximal basal activity and was activated eight-

fold by CSF-1 in cells cotransfected with c-fms. The deletion

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the level of c-fms mRNA are lower in RAW264 cells than in

BMMs (35) and that the relative transcription of c-fms in run-on transcription assays is lower (27).

To determine if transient overexpression of c-fms from a heterologous promoter would rescue CSF-1 induction of uPA promoter activity, RAW264 cells were cotransfected with a c-fms expression plasmid and a uPA reporter plasmid (Fig. 8A). Both CSF-1 and phorbol ester were able to stimulate the uPA reporter, and the effects of the two agents were approximately additive (Fig. 8A). Cells transfected with control expression plasmid lacking the c-fms cDNA and a uPA reporter responded only to phorbol ester, and there was no interaction between CSF-1 and phorbol ester (Fig. 8A).

The response of a series of uPA reporter plasmids to CSF-1/c-fms activation was studied in order to determine the cis requirements for cytokine activation (Fig. 8B). A construct containing 8.2 kb of information upstream of the mRNA initiation site had maximal basal activity and was activated eightfold by CSF-1 in cells cotransfected with c-fms. The deletion from −8.2 to −6.6 kb, which eliminates the distal ets/AP-1 site at −6.9 kb (9), reduced both basal and CSF-1/c-fms-induced promoter activities approximately twofold. Further deletions to −4.2 and −2.6 had no significant effect on either basal or CSF-1-induced activity of the uPA promoter. However, a deletion to −2.3, which eliminates a second ets/AP-1 element located at −2.4 kb (27), resulted in a further eightfold reduction in both basal and CSF-1-induced promoter activity. Deletion of the uPA upstream region to −114 bp had no additional effect on either basal activity or the CSF-1/c-fms response. However, site-directed deletion of the conserved ets/AP-1 enhancer region located at −2.4 kb also reduced both basal and CSF-1-stimulated activity seven- to eightfold (Fig. 8B). Thus, the ets/AP-1 site located at −2.4 kb distal to the uPA transcription initiation site is necessary, although not sufficient, for maximal CSF-1 induction of uPA promoter activity.

**DISCUSSION**

The data presented support a model in which CSF-1/c-fms receptor ligation leads to prolonged activation of MAP kinases p42 and p44, to sustained phosphorylation of ets-2 on residue threonine 72, and to stable induction of uPA transcription. These results emphasize a basic difference between macrophages and the fibroblast model for c-fms signaling and reinforce the importance of studying c-fms action in the biologically relevant monocyte/macrophage background (15). In macrophages, the expression of ets-2 is part of the CSF-1 immediate-early response, and both expression of this gene and activation of the factor by phosphorylation are mediated by the ras/MAPK kinase signaling pathway. Future studies will be directed toward understanding the regulation of the ets-2 gene in macrophages. Activation of immediate-early MAP kinase targets such as elk-1 (31, 32) or inactivation of repressors such as the ets factor erf-1 (26) may be involved in the induction of the ets-2 promoter.

The transient transfection studies with RAW264 cells support the hypothesis that ets-2 is necessary for CSF-1 induction of the uPA promoter. The ets/AP-1 element at −2.4 kb relative to the transcription initiation site has been shown previously to mediate the response to phorbol esters and oncprotein ras in these cells (27, 34). Mutation of this site, along with the deletion of the region containing a fibroblast growth factor-responsive ets/AP-1 site located at −6.9 kb (9), resulted in a 90 to 95% decrease in both basal and CSF-1-induced uPA promoter activity. Transcription of another CSF-1-responsive gene in macrophages, the scavenger receptor, has also been shown to be dependent on redundant promoter and enhancer elements that include ets/AP-1-type elements (18, 33), indicating that common mechanisms control the expression of CSF-1 target genes.

The dependence of the basal activity upon the ets/AP-1 elements was unexpected given that the ets-2 protein is not detected in RAW264 cells. A potential explanation of the data lies in the observation that RAW264 cells and primary macrophages are able to respond to unmethylated CpG residues contained in the plasmid DNA used for the transfections (28). The unmethylated DNA response is similar to the response stimulated by bacterial lipopolysaccharide (LPS) (28, 29), and both LPS and CpG DNA can mimic the ability of CSF-1 to induce ets-2 expression and phosphorylation (29). Hence, the basal activity of the uPA promoter in transfected RAW264 cells may be interpreted as a response to plasmid DNA, which likely acts through the same ets/AP-1 elements.

The persistent activation of MAP kinases by CSF-1 in BMMs contrasts with previous work where kinase activity was
reported to decline rapidly after an initial peak at 5 to 15 min following CSF-1 treatment (12). The ets-2 substrate employed in the present studies may be a more efficient monitor of specific MAP kinase activity than other substrates commonly used. The use of the ets-2 pointed P2 domain as a substrate has the additional advantage that it distinguishes activation of p42 and p44 from the activation of other proline-directed kinases, which were not able to phosphorylate this substrate. This is in contrast to the ets factor elk-1 and related proteins which are phosphorylated by multiple MAP kinase family members, including MAP kinase p42/p44, JNK, and p38 (31, 32).

How is the persistent signal in response to CSF-1 maintained? The results obtained with RAW264 cells suggest an answer to this question. In RAW264 cells, c-fms expression is likely below a threshold that allows persistent engagement of the ras/MAP kinase pathway and activation of the uPA promoter, and transient overexpression of c-fms rescues the signaling defect. In primary macrophages, CSF-1 and its receptor are rapidly internalized and degraded following CSF-1 binding so that there is a cycle of receptor-mediated ligand degradation (reviewed in reference 22). Thus, the steady-state level of c-fms could determine whether a transient or persistent signal is engaged in response to CSF-1. Similarly, the failure of PDGF to stimulate persistent phosphorylation of ets-2 in NIH 3T3 cells may reflect rapid turnover of the PDGF receptor with respect to c-fms following growth factor treatment. Such arguments are consistent with results obtained in other systems, for example, increasing steady-state levels of the epidermal growth factor or insulin receptors in PC-12 cells results in prolonged activation of the ras/MAP kinase pathway and neuronal differentiation of this cell type (8, 30).

In conclusion, the present studies indicate that CSF-1 action involves the continual activation of MAP kinase activity, leading to transcription factor phosphorylation and selective activation of gene transcription. Studies of CSF-1 signaling provide one paradigm for understanding how tyrosine kinase receptors trigger persistent signaling pathways as well as the biological consequences of such prolonged signaling events.

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