

Activation of the C-Fos Promoter by Increased Internal pH

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Abstract Changes in intracellular pH (pH_{in}) take part in the mitogenic response. Their importance has been stressed by the finding that mouse fibroblasts expressing a yeast proton pumping ATPase (*PMA1*) exhibit a transformed phenotype and are tumorigenic. These cells do maintain a higher pH_{in}, supporting the idea that elevated pH_{in} may act as a proliferative trigger. Here we show that cells constitutively expressing *PMA1* have higher levels of the AP-1 transcription factor. The use of stable transfectants and transient transfection assays show that *PMA1* activity induces transactivation of the *c-fos* promoter. The activation of the promoter is mediated throughout the serum response element (SRE). The use of protein kinase C inhibitors suggests that AP-1 activation is achieved through a pathway independent of protein kinase C. © 1995 Wiley-Liss, Inc.

Key words: internal pH, transformation, *c-fos*, AP-1

Serum stimulation of quiescent fibroblasts induces a highly regulated series of events that results in changes in gene expression and ultimately lead to cell division [Rozengurt and Mendoza, 1985]. One of the first events that occurs after a growth factor interacts with its receptor is a change in ion fluxes across the cytoplasmic membrane [Pouysségur, 1985]. An increase in sodium influx and an efflux of protons that produces a rise in pH_{in} of 0.15–0.3 pH units develops usually 15 seconds to 1 min after mitogen addition. This increase is maximal within 5 min and persists as long as the mitogen is maintained [Pouysségur, 1985]. The cytoplasmic alkalinization results from the activation of the Na⁺/H⁺ exchanger (NHE), because it is abolished in the presence or amiloride, in Na⁺-free medium, or in fibroblast mutants lacking NHE activity [L'Allemain et al., 1984; Pouysségur et al., 1984]. On the other hand, the microinjection of activated H-ras [Hagag et al., 1987] or the expression of v-mos [Doppler et al., 1987] and H-ras [Kaplan and Boron, 1994] are able to induce intracellular alkalinization through the

activation of the sodium proton exchanger. Inhibition of the activity of the NHE produced by microinjection of H-ras by using the inhibitor amiloride is able to block DNA synthesis [Hagag et al., 1987]. The activation of different G-protein coupled receptors such as α -thrombin, bradikinin, vasopresin, etc., also results in an increased amiloride-sensitive Na⁺/H⁺ antiport. Recently it has been described that G α 13 is able to stimulate the NHE [Voyno-Yesenetskaya et al., 1994]. This activation is agonist independent when a mutant with a constitutively active GTPase (α 13-Q226L) is used [Voyno-Yesenetskaya et al., 1994]. All together, this evidence suggests that increased pH_{in} may function as a second messenger. The activation of either tyrosine kinase or G-protein coupled receptors as well as the transformation induced by some activated oncogenes leads to the activation of multiple signal transduction pathways making it difficult to evaluate the contribution of the increase in pH_{in} to the mitogenic response. In order to investigate this point, we used a more direct approach, transfecting NIH3T3 fibroblasts with the gene of a yeast proton-pumping ATPase *PMA1* [Perona and Serrano, 1988]. These cells have pH_{in} 0.3 units higher than the parental ones even in the presence of bicarbonate [Gillies et al., 1990] and are tumorigenic in

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nude mice and able to grow in the absence of serum [Perona and Serrano, 1988]. By using site-directed mutants of the *PMA1* gene, it has been demonstrated that pHin and the degree of transformation and tumorigenicity of fibroblasts expressing the ATPase mutants correlate with the activity of the different enzymes [Perona et al., 1990]. The expression of the yeast ATPase results in higher intracellular alkalization than that provided by either the activation of the NHE by growth factors and oncogenes or the cooperation of the bicarbonate systems [Burns and Rozengurt, 1983; Perona et al., 1990]. This difference could explain why the large increase in proton transport and pHin produced by expressing the yeast ATPase is mitogenic, while the smaller increase produced by growth factors, oncogenes, and bicarbonate is only permissive for the growth response.

Fos is a nuclear protein whose expression is induced by a variety of growth factors and oncogenes and by external agents such as inducers of oxidative stress and phorbol esters [Müller et al., 1984; Rao et al., 1993]. Furthermore, Fos protein expression is required for growth of cells in response to serum. Expression of c-fos antisense RNA [Nishikura and Murray, 1987] or the microinjection of antibodies raised against Fos into quiescent fibroblasts [Riabowol et al., 1988] has been found to block serum-stimulated reentry into the cell cycle. Fos, together with Jun, composes the AP-1 transcription factor whose activity is to propagate the mitogenic signal by controlling the expression of downstream genes that are required for proliferation [Riabowol et al., 1988; Angel and Karin, 1991]. Several oncogenes have been shown to modulate AP-1 activity. Transient expression of v-src, v-mos, polyoma middle T, Ha-ras, neu, or v-raf leads to enhanced AP-1 activity [Riabowol et al., 1988; Franza et al., 1988]. Since the *PMA1* gene, when expressed in fibroblast, behaves as an activated oncogene [Perona and Serrano, 1988], we were interested in investigating if its expression involved changes in the levels of the transcription complex AP-1. We here present evidence showing that the expression of the yeast proton pump is able to induce transactivation of the c-fos promoter that results in an increase in the levels of transcriptionally active AP-1 complex. The pathway is independent of protein kinase C activity.

MATERIALS AND METHODS

Cell Lines and Transfections

RN1a and RNT3a cell lines are two independent clones of NIH3T3 cells constitutively expressing the *PMA1* gene [Perona and Serrano, 1988]. The N-213 cell line is a clone stably transfected with the plasmid pma1-213 [Perona et al., 1990]. NIH3T3 cells and derived cell lines were maintained at 37°C in growth media containing 90% DMEM and 10% CS (GIBCO) in a humidified atmosphere of 5% CO₂. For transfection, cells were seeded into 100 mm dishes and cotransfected 24 h later by the calcium phosphate method [Chen and Okayama, 1987]. After transfection, cells were rinsed twice with PBS and incubated for 32 h in DMEM with 0.5% FCS. The agents indicated in each experiment were added for the last 6 h of incubation before collection of the cells.

Plasmids

The basic expression plasmid (pSV_hAT₅) has already been described [Perona and Serrano, 1988]. It contains the coding region of wild type yeast ATPase under the control of SV40 promoter. The pma1-213 plasmid [Perona et al., 1990] has also been described. Briefly, it was constructed by replacing the 3.8 Kilobase ClaI fragment of the pSV_hAT₅ with the equivalent fragment containing the mutation Glu233-Gln [Perona et al., 1990]. The plasmid pFC4 was kindly provided by Inder Verma and contains 400 residues from the 5' flanking region of the human c-fos promoter linked to the CAT reporter gene [Deschamps et al., 1985]. p4XSRETK-CAT, p4XCRETk-CAT, and p4XTRETK-CAT [Schönthal et al., 1991] are plasmids derived from pBLCAT₂. The respective promoter elements were synthesized and inserted into the multiple cloning site in front of the thymidine kinase (TK) promoter of pBLCAT₂. The TRE sequence was taken from the human collagenase gene [Schönthal et al., 1991]. The CRE sequence is the one in the c-fos promoter at the position -60.

CAT and β-Galactosidase Assays

For CAT assay, cells were serum starved for 48 h and induced for 6 h with the indicated agents. Extracts were prepared as previously described [Gorman et al., 1982]. Protein content was determined by a commercial kit (Bio-Rad).

The lysates (50–100 µg of protein) were incubated in 0.2 ml of reaction mixture containing 50 mM (14C)chloramphenicol (0.5 µCi) and 2 mM acetyl-CoA in 250 mM Tris-HCl at pH 7.8 for 4 h at 37°C. CAT activity was detected and quantified by thin layer chromatography. Transfection efficiencies were standardized with the pCH110 plasmid containing the β-gal gene under the control of the simian virus 40 promoter (SV40). β-galactosidase activity was assayed in a buffer containing Na₃PO₄ (pH 7.5), 1 mM MgCl₂, and 200 mg of O-nitrophenyl-β-D-galactopyranoside. Samples were incubated at 37°C for 10 min and the reaction stopped by addition of Na₂CO₃. Activity was measured by absorbance at 420 nm. Mean CAT activities were calculated from at least three independent transfections and the level of induction determined by calculating the ratio of the stimulated to the control values.

Preparation of Nuclear Extracts

NIH3T3 and RN1a cells were serum-starved for 48 h and stimulated with mitogens when indicated, and nuclear extracts were prepared as described [Andrews and Faller, 1991]. Briefly, cells were scraped and centrifuged at 1,000 rpm for 5 min. The pellet was resuspended in Buffer A (10 mM Hepes-KOH (pH 7.4), 1.5 mM MgCl₂, 10 mM KCl, 5 mM DTT, 0.2 mM PMSF). Samples were incubated for 5 min at 4°C and vortexed for 10 seconds. Nuclei were sedimented at 12,000 rpm for 20 seconds and resuspended in buffer C (20 mM Hepes-KOH (pH 7.9), 25% glycerol, 420 mM NaCl, 1.5 mM MgCl₂, 0.2 mM EDTA, 0.5 mM DTT, 0.2 mM PMSF) and incubated for 20 min at 4°C. Samples were centrifuged at 6,000 rpm for 5 min, and the protein concentration was determined with a commercial BioRad kit.

Electrophoretic Mobility Shift Assays

A ³²P-labelled TRE oligo (5'-GATCCATCTGC-GTCAGCAGGTTT-3') corresponding to the c-fos AP-1 binding site was used as a probe. Labelled oligo (0.2 ng) and 10 µgr of nuclear extract were incubated in a final volume of 20 µl (in 40 mM Hepes-KOH (pH 7.9), 0.5 mM DTT, 0.2 mM EDTA, 50 mM KCl, 3 µg poly(dI-dC), and 5% (v/v) glycerol and separated in a 5% polyacrylamide (TBE) gel. Specificity for AP-1 binding was confirmed by competition with a 100-fold excess of nonlabelled TRE or SRE oligos (5'-AGGATGTCCATATTAGGACATCT-3') (indicated as TRE or SRE).

RESULTS

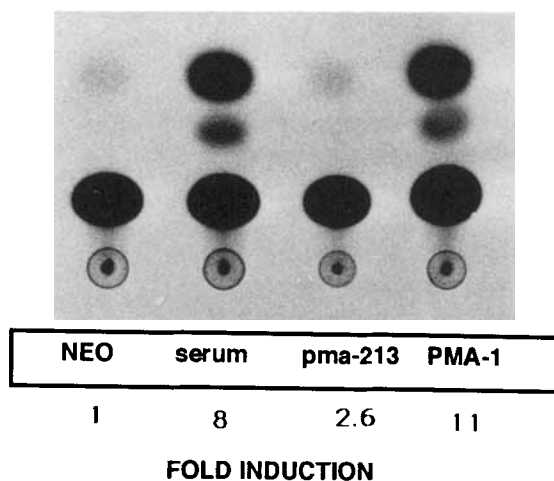
Transactivation of the C-Fos Promoter Is Induced by the PMA-1 Gene

We determine if the transient expression of the *PMA1* gene was able to trigger activation of the c-fos promoter in NIH3T3 cells. The pSV2 expression vector carrying the wild type yeast ATPase gene *PMA1* was transfected [Perona and Serrano, 1988] into NIH3T3 cells together with the pFC4 plasmid containing the c-fos promoter [Deschamps et al., 1985]. As a negative control, the pma1-213 mutant that encodes an ATPase gene with a Glu233-Gln point mutation that expresses an enzyme with 10% the wild type activity [Perona et al., 1990] was also cloned in pSV2 and cotransfected with pFC4. As shown in Figure 1A, the *PMA1* gene stimulates elevenfold c-fos promoter activity when cells are incubated in low serum as compared with the transactivation produced by the pSV₂neo plasmid. The pma1-213 gene induces 2.6-fold the c-fos promoter, indicating a good correlation between transactivation and enzymatic activity of the proton pump. The stimulation obtained with the *PMA1* gene was comparable to that detected when the promoter was stimulated with 20% serum (eightfold) in three different experiments. These results suggest that the activity of the proton pump is sufficient to induce c-fos transactivation.

Altered Response of the C-Fos Promoter in PMA1 Transfected NIH3T3 Cells

Different regulatory elements have been identified in the c-fos promoter that respond to specific mitogens. The SRE has been shown to mediate induction of the c-fos gene by serum, growth factors (such as platelet-derived growth factor or epidermal growth factor), insulin, TPA, and UV light [Sassone-Corsi et al., 1988]. In addition, the c-fos promoter contains several CREs that confer responsiveness of the gene to cAMP [Sheng et al., 1988]. We investigated if the cells transfected with the *PMA1* gene showed any alteration in the response to serum, TPA, and forskolin. Figure 1B shows the response of pFC4 activation to the inducers mentioned above. For this study we used RN1a and N-213 cells expressing, respectively, the *PMA1* and the pma1-213 allele. N-213 cells do not have a higher pH_{in} than the parental NIH3T3 cells and are not tumorigenic. Quiescent NIH3T3 and N-213 cells show a low level of transactivation of the

A



B

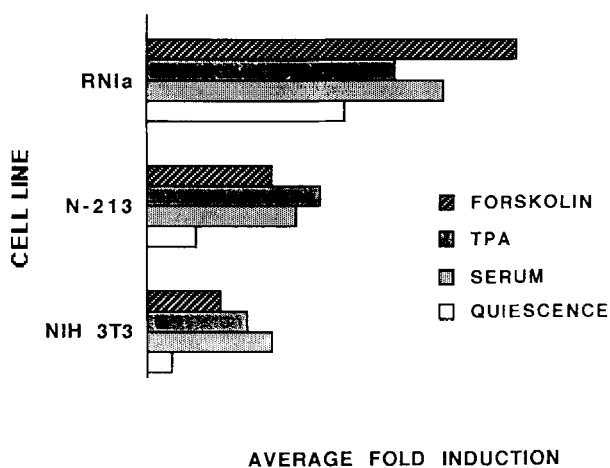


Fig. 1. Transactivation of pFC4 by the yeast H⁺-ATPase gene. **A:** The *PMA1* gene transiently expressed transactivates pFC4. NIH3T3 cells were cotransfected with the pFC4 plasmid and either the *PMA1*, the *pma1-213*, or the pSV2neo plasmid. *Serum* indicates cells transfected with the pSV2neo plasmid (NEO) and stimulated with 20% FCS. **B:** Transfection of pFC4 in stable cell lines expressing the wild type (RN1a) or the *pma1-*

213 (N-213) mutant ATPase genes in control NIH3T3 cells. Thirty-two hours after transfection the cells were either non-treated (quiescent) or induced for 6 h with the following agents: FCS (20%), TPA (200 nm), or forskolin (10 μM). The data shown were obtained in a representative experiment, but essentially the same results were obtained in three independent experiments with less than 10% variation between experiments.

c-fos promoter, while RN1a cells are able to constitutively activate the pFC4 sevenfold higher than the parental cells. These results are very similar to those obtained using transient assays on NIH3T3 cells (Fig. 1A). In relation with the inducibility of the *c-fos* promoter, while NIH3T3 and N-213 cells are responsive to serum and

TPA, (six- and fivefold induction, respectively), RN1a cells show a very low response to serum (1.2-fold) and TPA (1.3-fold). When forskolin was used, the three cell lines showed quite similar responses. The results presented above suggest that the transcription factors involved in the transactivation of the SRE are already in-

duced in the absence of serum in RN1a cells and can only be induced slightly by serum and phorbol esters. On the other hand the factors involved in CRE transactivation are not constitutively induced in the absence of stimulation.

Activity of the *PMA1* Gene Induces Transactivation of the SRE and TRE

The transfection of the *PMA1* gene is sufficient to activate the *c-fos* promoter (Fig. 1A). In order to study the signal transduction pathway activated by the *PMA1* gene, we analyzed defined cis-acting elements of the *c-fos* promoter and their responsiveness to expression of the yeast proton pump. To do these experiments we used reporter plasmids containing four tandem repeats of the SRE or CRE element fused to a herpes simplex thymidine kinase-CAT gene construct [Schönthal et al., 1991]. NIH3T3 cells were transiently cotransfected with the reporter plasmids and either the *PMA1* or *pma1-213* expression plasmids. As shown in Figure 2, the *PMA1* gene is able to induce activation of the SRE (fivefold), while serum was able to induce this element thirtyfold. This situation is similar to the one described for oncogenes such as *abl*, *src*, or *raf* [Angel and Karin, 1991; Hori et al., 1990; Kaibuchi et al., 1989]. On the contrary, the CRE is not transactivated by the *PMA1* gene, while forskolin was able to induce the activity of this promoter element. The responses to cotransfection with the *pma1-213* plasmid are similar to those obtained with pSV₂neo. A construct that contained four copies of the gene of the human collagenase TRE (4XTRE) was induced by the expression of the *PMA1* gene (Fig. 2). This indicates that activation of transcription of *c-fos* might result in active Fos/Jun (AP-1) complexes.

In order to compare if the activation of the *c-fos* promoter induced in NIH3T3 cells by the *PMA1* gene was similar to the one observed in stable transfectants, we performed experiments in RN1a and N-213 cells. The activity of the SRE was constitutively high only in the RN1a cells. The CRE was not activated in any cell line (Fig. 3). We also detected constitutive activation of the TRE in the RN1a cells, indicating the presence of transcriptionally active AP-1 complexes. These results are in complete agreement with those obtained in NIH3T3 cells cotransfected with the *PMA1* gene and the reporter plasmids. The results presented above indicate that the change in pH_{in} induced by the yeast proton pump was able to activate signal transduction

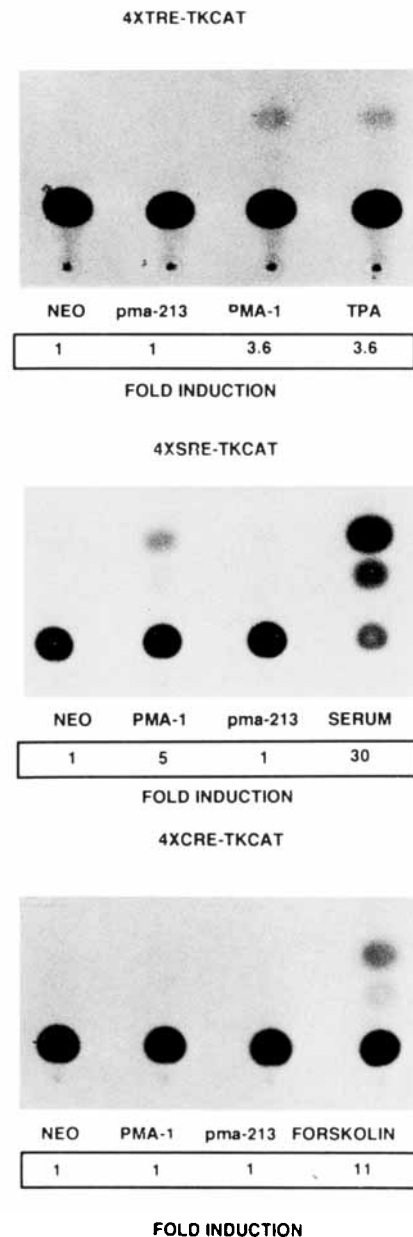


Fig. 2. Transactivation of single promoter elements by the *PMA1* gene. NIH3T3 cells were seeded and transfected with reporter plasmids containing four tandem repeats of the SRE, CRE, or TRE regulatory elements linked to the minimal thymidine kinase gene promoter and the CAT reporter gene and the *PMA1*, *pma-213*, or pSV₂neo expression vectors. Some of the cells transfected with pSV₂neo were induced with serum (4XSRE-TKCAT reporter), forskolin (4XCRE-TKCAT reporter), or TPA (4XTRE-TKCAT reporter) under the same conditions described in the legend of Fig. 1. The data shown were obtained in a representative experiment, but essentially the same results with less than 10% variation between each were obtained in three independent experiments.

pathways commonly activated by growth factors and oncogenes and that transactivation of *c-fos* promoter should be an intermediary step in the transformation induced by the *PMA1* gene.

Expression of *PMA1* induces AP-1 Activity

Transactivation of the TRE element has been shown to be mediated by AP-1 complexes [Franza et al., 1988]. To determine if the AP-1 transcription factor was involved in the transactivation of the TRE element in RN1a cells, we performed band shift assays on RN1a cells and NIH3T3 cells using an oligonucleotide containing the AP-1 site of the *c-fos* promoter. We observed low levels of complex formation on the TRE site when quiescent NIH3T3 cells were used (Fig. 4A). A stronger retarded band appeared after treatment of the cells with TPA. This band was efficiently competed with an excess of cold TRE oligo but not with an oligo containing the SRE. RN1a cells constitutively show similar levels of the retarded band as NIH3T3 cells induced with TPA. The levels of this band do not increase any further after treatment of the cells with TPA (data not shown).

The expression of the *PMA1* gene is sufficient to induce the formation of AP-1 complexes in quiescent NIH3T3 cells. We performed transient transfection followed by band shift assays using an oligonucleotide containing the AP-1

site of the *c-fos* promoter. The cells were transfected with increasing amounts of the *PMA1* expression vector pSV_hAT₅ and nuclear extracts prepared and tested for AP-1 activity by band shift assays. The plasmid pSV2neo was used as a negative control and to complete the amount of DNA used in each transfection up to 20 μ g. The formation of the complex was dependent on the amount of *PMA1* gene used to transfect the cells (Fig. 4B). A maximal amount of complex was obtained with 10 μ g of *PMA1*. A complex with similar movility was obtained when the cells were stimulated with serum (Fig. 4B) or TPA (not shown). The results shown above suggest that *PMA1* expression induces AP-1 transcription factor activity. Further support of this hypothesis was obtained by manipulating the expression of one of the AP-1 components, *c-fos*, in these cells. NIH3T3 or RN1a cells were transfected with either pSVfos (expressing *fos*) or pSVsof (expressing an antisense of *fos*) vectors [Guo and Cole, 1989] together with the TRE reporter construct. As previously described, TRE-mediated transcriptional activity increases sevenfold upon transfection of NIH3T3 cells with pSVfos (Fig. 5) [Schönthal et al., 1988]. This activity was abolished when the *fos* antisense vector was cotransfected together with pSVfos. In the case of RN1a cells, the constitutive TRE-mediated transcriptional activity was

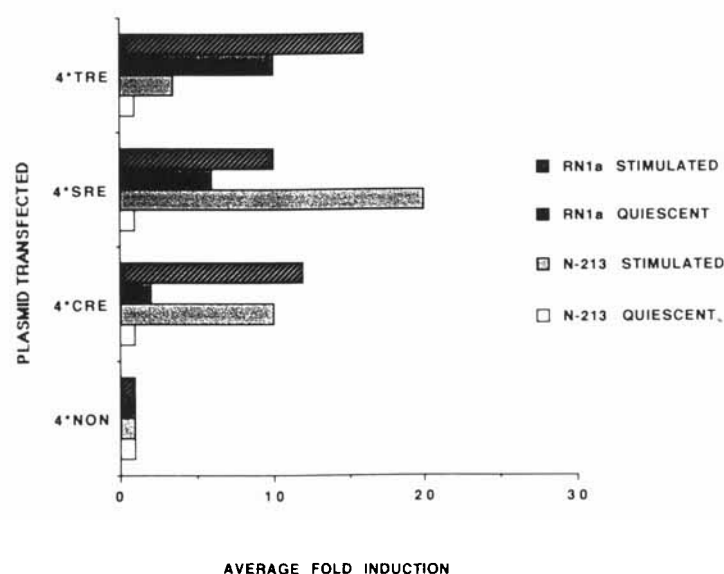


Fig. 3. Transfection of stable cell lines expressing the proton pump genes with single promoter elements. NIH3T3, RN1a, or N-213 cells were seeded and transfected with reporter plasmids 4XTRETK-CAT and 4XSRETK-CAT or 4XCRETK-CAT. Transfected cells were either noninduced (quiescent) or induced with TPA

(4XTRE transfected cells), serum (4XSRE transfected cells), or forskolin (4XCRE transfected cells) as described in the legend of Fig. 1. Essentially the same results were obtained in three independent experiments with less than 10% variation between each experiment.

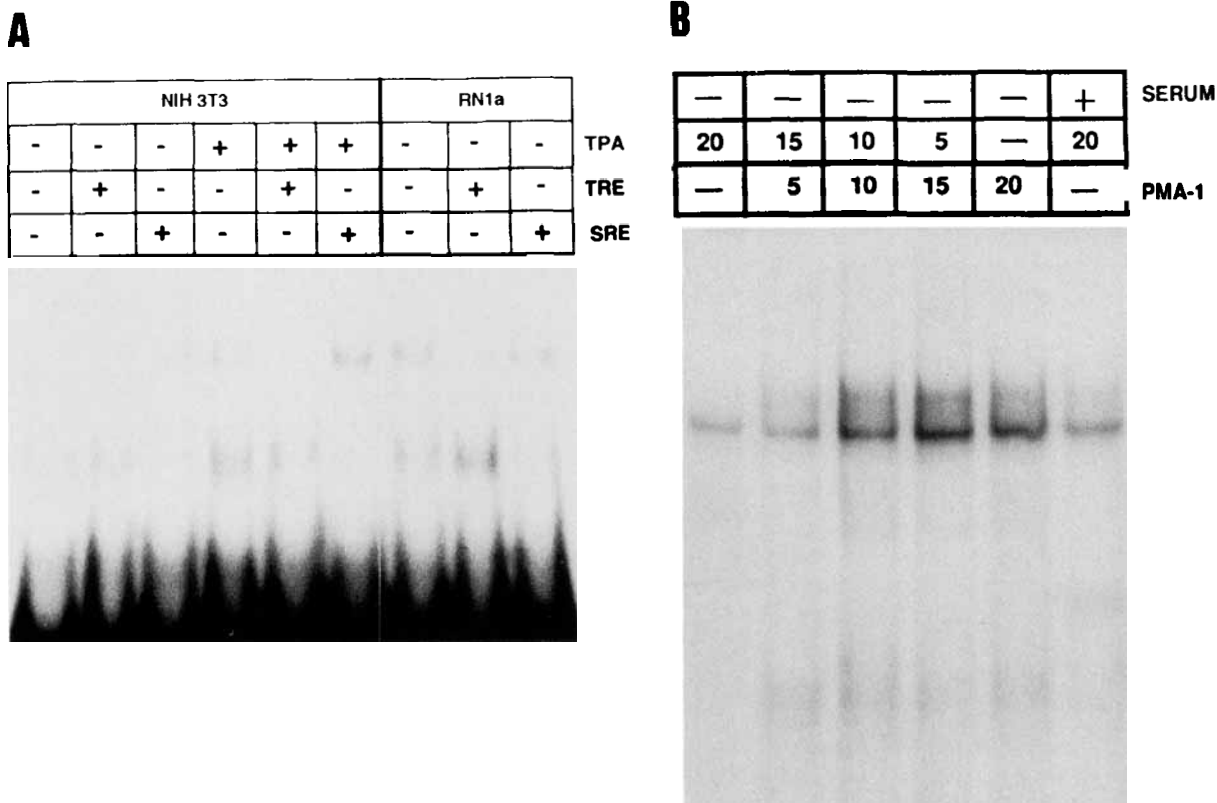


Fig. 4. Expression of the *PMA1* gene induces AP-1 complex formation. **A:** Band shift assay of extracts from cell lines expressing the *PMA1* gene with the AP-1 binding site. NIH3T3 and RN1a cells were serum-starved for 48 h. Half of the 3T3 plates were stimulated with 200 nM TPA, and nuclear extracts were prepared as described [Hori et al., 1990]. A ³²P-labelled TRE oligo corresponding to the c-fos AP-1 binding site was used as a probe. Competitors are nonlabelled TRE or SRE (100-fold ex-

cess) oligos indicated as TRE or SRE. **B:** Analysis of AP-1 complex formation in transient transfection assays. NIH3T3 cells were transfected with the indicated amounts of the *PMA1* expression (*PSV_hAT₅*) plasmid or the control plasmid *pSV₂neo* (NEO) and serum-starved for 48 h. Cells transfected with *pSV₂neo* alone were induced with 20% FCS for 1 h (SERUM). Essentially the same results were obtained in three independent experiments.

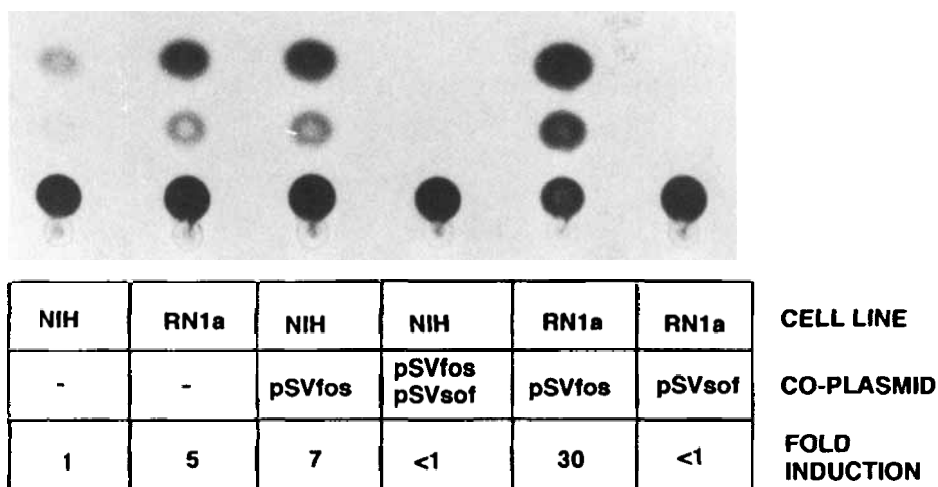


Fig. 5. Antisense fos RNA inhibits CAT expression from the 4XTRETK-CAT reporter construct. NIH3T3 and RN1a cells were transfected with 5 µg of the reporter construct 4XTRETK-CAT and 10 µg of either pSVfos and/or pSVsof plasmids (CO-PLASMID). After transfection, cells were serum-starved for 48

h, and protein extracts were prepared and tested for CAT activity as described above. Fold induction was calculated over the CAT activity of untreated NIH3T3 cells. Essentially the same results, with less than 10% variation, were obtained in three independent experiments.

fivefold higher than that of the control cells, as described above (Fig. 3). This activity increased dramatically upon transfection of the pSVfos plasmid, suggesting that the amount of fos is limiting in these cells and that other components of the AP-1 complex, probably one of the members of the Jun family [Angel and Karin, 1991], might also be overexpressed. The constitutive transcriptional activity of RN1a cells is abolished upon pSVsof transfection, indicating that the fos protein is one of the components of the complex whose basal activity is high in RN1a cells. These results were confirmed using band shift assays. NIH3T3 cells transiently transfected with the *PMA1* gene (Fig. 6) show high levels of the AP-1 complex that decrease when cells are cotransfected with the pSVsof plasmid. We are not able to compete totally AP-1 binding, maybe because c-fos expression is not totally abolished by the pSVsof plasmid in the conditions used in the experiment (data not shown). These results strongly support the hypothesis that Fos protein is one of the members of AP-1 complexes induced by the *PMA1* gene.

Increase in AP-1 Activity Is Independent of Protein Kinase C (PKC) and A (PKA)

It has been shown that the TRE can be stimulated by PKC-dependent and PKC-independent pathways [Hori et al., 1990; Kaibuchi et al., 1989]. Depletion of PKC activity in RN1a cells by TPA pretreatment [Kaibuchi et al., 1990] causes only a small decrease in the constitutive transactivation of the TRE element (Fig. 7A). On the other hand, staurosporine, an inhibitor of PKC, does not have any effect on the basal transactivation observed on the SRE in RN1a cells (data not shown). Even more, no change was observed in the constitutive levels of AP-1 complex in RN1a cells after pretreatment of the cells with TPA (not shown) or with the inhibitor H-7 (Fig. 7B), an inhibitor of PKA and PKC [Hidaka et al., 1991]. On the contrary, when NIH3T3 cells were stimulated either with forskolin or TPA, a decrease in the level of AP-1 complex was observed in the presence of the inhibitor. These results strongly suggest that the *PMA1* gene activates AP-1 through a PKC- and PKA-independent signal transduction pathway.

DISCUSSION

The role of internal pH in proliferation and transformation has been elusive for a long time.

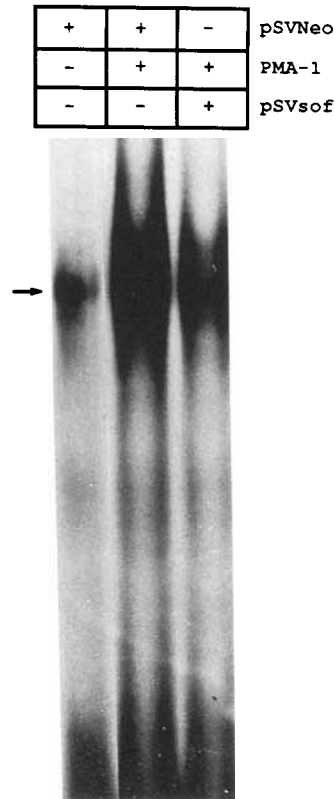


Fig. 6. Inhibition of AP-1 complex formation induced by the *PMA1* gene by fos antisense RNA. NIH3T3 cells were transiently transfected with 20 μ g of pSV2neo, 10 μ g of *PMA1* and 10 μ g pSV2neo, or 10 μ g of *PMA1* plus 10 μ g of pSVsof. Cells were serum-starved and nuclear extracts prepared and incubated with an oligonucleotide containing the AP-1 binding site. The arrow shows the position of the AP-1 complex. Essentially the same results were obtained in three independent experiments.

We have demonstrated that NIH3T3 cells expressing a yeast proton pump have constitutively higher pHin than control cells [Perona and Serrano, 1988]. Increased pHin correlates in these cells with tumorigenicity and serum independence [Perona et al., 1990]. Experiments described in this paper show that transfection of NIH3T3 cells with the *PMA1* gene produces changes in gene expression. In particular, we have studied the c-fos promoter.

Since c-fos plays an important role in the cells' proliferative responses and is one of the earliest genes induced after cell activation by growth factors, we have tried to examine the mechanisms underlying its transcriptional activation in *PMA1*-transfected cells. The expression of the *PMA1* gene is able to induce the c-fos promoter. The magnitude of the transactivation produced is similar to the one produced by serum. Furthermore, the proton pump activity of the yeast enzyme is necessary for the physiological alter-

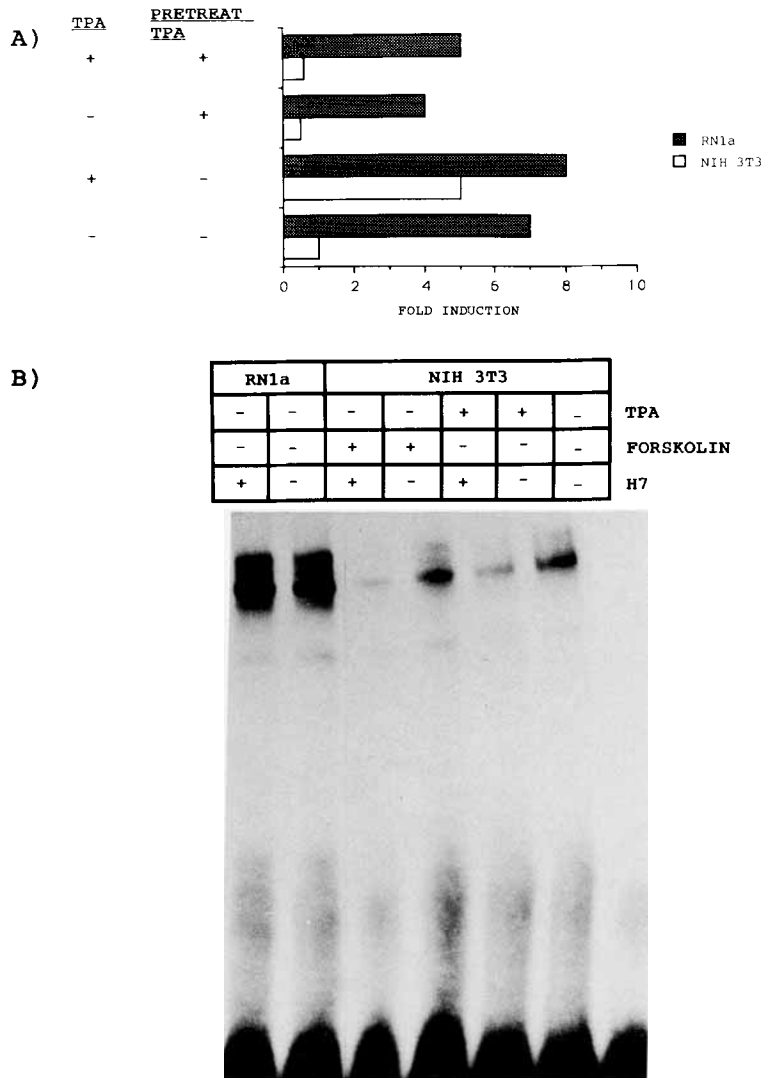


Fig. 7. Transactivation of *c-fos* by *PMA1* is independent of PKC and PKA activities. **A:** NIH3T3 and RN1a cells were transfected with the 4XTRETK-CAT reporter plasmid. Cells were incubated in the presence of 0.5% FCS. Downregulation of PKC was achieved by treatment with TPA (200 nM) for 48 h. When indicated, the cells were incubated with 100 nM TPA for 6 h after 48 h in the presence of TPA or 0.5% FCS. The CAT activity

of the extracts was determined and the fold induction over NIH3T3 untreated cells calculated. **B:** NIH3T3 and RN1a cells were serum-depleted for 48 h and treated as follows: TPA: 100 nM TPA for 1 h; forskolin: 10 μ M for 1 h; and H-7: 10 μ M for the last 2 h. Nuclear extracts were prepared and incubated with a 32 P-labelled oligo corresponding to the *c-fos* AP-1 binding site for the band shift assay.

ations of the cell lines [Perona et al., 1990] and transactivating activity, because a site-directed mutant *pma1-213*, whose proton pumping activity is decreased to 10%, shows very weak activity transactivating the *c-fos* promoter. As a consequence of the increased expression of *c-fos*, the *PMA1* gene induces the formation of transcriptionally active AP-1 complexes that could be involved in the transformation of the transfected cells.

The transactivation of the *c-fos* promoter induced by the *PMA1* gene seems to be mediated

by the SRE. The SRE can be activated by growth factors in a manner dependent and independent of protein kinase C. Our results suggest that the expression of the *PMA1* gene activates a signal transduction pathway that induces transactivation of the *c-fos* promoter through the SRE independently of protein kinase C activity. The induction of the SRE can be mediated by binding of the phosphorylated *p62^{tef}* to a *p67^{SRF}* bound to the SRE [Ryan et al., 1989]. MAP-2 kinases have been shown to phosphorylate the *p62^{tef}* [Gille et al., 1992]. The role of MAP-2

kinases in the *PMA1* signal transduction pathway is currently being investigated.

We think that these results show for the first time that there is a link between the elevation of intracellular pH, a common signal transduction event observed in normal cell proliferation [Burns and Rozengurt, 1993] and transformation [Doppler et al., 1987; Hagag et al., 1987], and the activation of gene transcription. In agreement with our results, Prpic et al. [1989] have demonstrated that physiological doses of IFN- γ induce a rapid Na⁺/H⁺ exchange in murine macrophages and that these amiloride-sensitive fluxes are important for mediating some subsequent genomic responses to IFN- γ . There are several enzymes that can serve as targets for activation by an increase in pHin because their activity is regulated by pH changes within the physiological range. Examples are Phospholipase C [Murase et al., 1988], Phospholipase A2 [Balsinde et al., 1988], and tyrosine kinases [Wanping et al., 1991]. Evidence has been presented in the literature of activation of tyrosine kinases by elevation of pHin during sea urchin fertilization [Wanping et al., 1991]. Physiologic changes in pH regulate IP3 binding to its receptor with a sharp increase in binding throughout the physiologic range, tripling between pH 7.5 and 8.5 [Worley et al., 1987]. Increases in pHin augment IP3's ability to release Ca⁺⁺ [Joseph et al., 1989] which presumably reflects the influence of pH in IP3 binding to its receptor. In the case of RN1a cells, we still do not know the mechanism that transduces the signal of elevation of pHin to the nucleus, but we are checking the possibilities mentioned above. Another way in which pH changes can be transduced into changes in gene expression is by affecting the chromatin aggregation state. In relation with this, it has been reported that, at least in vitro, changes of pH within the physiological range are important in regulating the chromatin aggregation [Guo et al., 1989]. As the pH is increased less and less, chromatin is aggregated, and also histone dissociation from the chromatin is pH dependent. Interestingly, His-Pro-rich (HX)_n repeats have been found to be protein sequences sensitive to pH changes in the physiological range [Janknecht et al., 1991]. These sequences, first observed in PRD domain of the *Drosophila* paired protein, have been found in other proteins such as bicoid [Frigerio et al., 1986], deformed [Sasaki et al., 1990], old skipped [Angiolillo et al., 1985], Chrox 1.4 [Frigerio et al.,

1986], and the rabbit T-cell receptor β -chain precursor [Coulter et al., 1990]. It has been suggested that (HX) repeats mediate in pH-dependent fashion protein-protein interactions, which are known to be necessary for the function of transcription factors. Independently of the way in which the transactivation of c-fos by the *PMA1* gene is triggered, the observation that a protein involved in the cellular responses to several proliferative stimuli, such as Fos, is also implicated in cell transformation by *PMA1* could be important and opens a way to the study of these regulatory pathways.

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