

Rac-1 dependent stimulation of the JNK/SAPK signaling pathway by Vav

Piero Crespo¹, Xose R Bustelo^{1,2}, David S Aaronson¹, Ornar A Coso¹, Monica Lopez-Barahona¹, Mariano Barbacid¹ and J Silvio Gutkind¹

The protein product of the human *vav* oncogene, Vav, exhibits a number of structural motifs suggestive of a role in signal transduction pathways, including a leucine-rich region, a plekstrin homology (PH) domain, a cysteine-rich domain, two SH3 regions, an SH2 domain, and a central Dbl homology (DH) domain. However, the transforming pathway(s) activated by Vav has not yet been elucidated. Interestingly, OH domains are frequently found in guanine nucleotide-exchange factors for small GTP-binding proteins; of the Ras and Rho families, and it has been recently shown that, whereas Ras controls the activation of mitogen activated kinases (MAPKs), two members of the Rho family of small GTPases, Rae 1 and Cdc42, regulate activity of stress activated protein kinases (SAPKs), also termed c-Jun N-terminal kinases (JNKs). The structural similarity between Vav and other guanine nucleotide exchange factors for small GTP-binding proteins, together with the recent identification of biochemical routes specific for members of the Ras and Rho family of GTPases, prompted us to explore whether MAPK or JNK are downstream components of the Vav signaling pathways. Using the COS-7 cell transient expression system, we have found that neither Vav nor the product of the *vav* proto-oncogene, proto-Vav, can enhance the enzymatic activity of a coexpressed, epitope tagged MAPK. On the other hand, we have observed that, whereas proto-Vav can slightly elevate JNK/SAPK activity, oncogenic Vav potently activates JNK/SAPK to an extent comparable to that elicited by two guanine-nucleotide exchange factors for Rho family members, Dbl and Ost. We also show that point mutations in conserved residues within the cysteine rich and OH domains of Vav both prevent its ability to activate JNK/SAPK and render Vav oncogenically inactive. In addition, we found that coexpression of the Rac-1 N17 dominant inhibitory mutant dramatically diminishes JNK/SAPK stimulation by Vav, as well as reduces the focus-forming ability of Vav in NIH3T3 murine fibroblasts. Taken together, these findings provide the first evidence that Rac-1 and JNK are integral components of the Vav signaling pathway.

Keywords: Vav; signal transduction; JNK; MAP kinases; GTP-binding proteins

Introduction

The human *vav* gene was first identified by virtue of its oncogenic activation during the course of gene transfer assays when using tumor-derived DNA (Katzav *et al.*, 1989). The normal *vav* allele, the *vav* proto-oncogene, encodes a protein of 95 kDa, designated proto-Vav, which is preferentially expressed in cells of the hematopoietic lineage (Katzav *et al.*, 1991; Bustelo *et al.*, 1993). Recently, it has been shown that proto-Vav is rapidly phosphorylated on tyrosine residues upon activation of a variety of growth factor (Bustelo *et al.*, 1992; Bustelo and Barbacid, 1992; Margolis *et al.*, 1992; Alai *et al.*, 1992; Dosil *et al.*, 1993; Evans *et al.*, 1993; Plataniotis and Sweet, 1994) and hematopoietic cell-specific receptors (Margolis *et al.*, 1992; Bustelo and Barbacid, 1992). However, the normal function of Vav is still unknown, although analysis of its primary sequence reveals a number of structural motifs suggestive of a role in signal transduction pathways. These motifs include a leucine-rich N-terminal region (Coppola *et al.*, 1991), a plekstrin homology (PH) domain (Mussachio *et al.*, 1993), a cysteine-rich domain (Coppola *et al.*, 1991), two SH3 regions flanking a single SH2 domain within its carboxyl-terminus (Bustelo *et al.*, 1992; Margolis *et al.*, 1992), and a central DH domain (Boguski and McCormick, 1993) which bears strong homology to Dbl (Eva *et al.*, 1988), a guanine nucleotide-exchange factor (GEF) for Rho related small GTP-binding proteins.

DH domains are a common motif in most GEFs for small GTP-binding proteins. As such, these domains are present in both Ras GEFs, Ras-GRF and SOS (Boguski and McCormick, 1993). However, these DH domains appear not to be directly involved in nucleotide exchange activity towards Ras (Shou *et al.*, 1992). DH domains are also present in the Rho/Cdc42 GEF Ost (Horii *et al.*, 1994), in the yeast Cdc42-specific GEF, Cdc24 (Ron *et al.*, 1991), in the *ecr2* oncogene product which associates with RhoA, RhoC and Rae1 (Miki *et al.*, 1993), as well as in Abr (Heisterkamp *et al.*, 1993) and Bcr (Ron *et al.*, 1991), both GTPase activating proteins (GAPs) for the Rho GTP-binding protein family. Taken together, these data suggest that DH domains are characteristic of regulatory molecules for small GTPases, thus raising the possibility that Vav might affect the function of GTP-binding proteins. In this regard, it has been suggested that Vav could act as a Ras-specific GEF (Gulbins *et al.*, 1993), although these data are in conflict with recently available reports (Bustelo *et al.*, 1994; Khosravi-Far *et al.*, 1994).

Work from a number of laboratories has demonstrated that certain small GTP-binding proteins control

the enzymatic activity of a family of closely related serine-threonine kinases, known as mitogen activated protein kinases (MAPKs) (Cano and Mahadevan, 1995). The function of MAPKs is to convert extra-cellular stimuli to intracellular signals which, in turn, control the expression of genes that are essential for many cellular processes, including cell growth and differentiation (Marshall, 1995). MAPKs have been classified in three subfamilies: extracellular signal regulated kinases (ERKs), including ERK1 and ERK2) also known as p44mapk and p42mapk respectively (referred to herein as MAPKs); stress activated protein kinases (SAPKs), also termed c-jun N-terminal kinases (JNKs); and p38 kinase (Cano and Mahadevan, 1995). Whereas Ras controls the activation of MAPK (Marshall, 1995), we and others have recently observed that two members of the Rho family of small GTP-binding proteins, Rac1 and Cdc42, regulate the activity of JNKs (Coso *et al.*, 1995; Minden *et al.*, 1995). Thus, the similarity between Vav and the large family of DH-containing GEFs for small GTPases, and the identification of biochemical routes specific for Ras and Rho related GTP-binding proteins, prompted us to explore whether MAPK or JNK are downstream components of the Vav signaling pathways. Here, we report that expression of Vav in COS-7 cells fails to elevate the enzymatic activity of MAPK. However, we show that oncogenic forms of Vav can potentially activate JNK, acting on a Rac-1 dependent signaling pathway.

Results

Vav activates JNK but not MAPK

The transforming pathway(s) activated by Vav has not been yet elucidated, but recent reports have suggested that Vav might act as a Ras-specific GEF (Gulbins *et al.*, 1993). On the other hand, a wide array of studies have positioned Ras upstream of MAPK and shown that Ras is capable of potentially elevating the activity of this serine-threonine kinase (Marshall, 1995). Thus, we hypothesized that if Vav were a Ras GEF, it would be expected to induce signals leading to the activation of MAPK. To test that, we took advantage of a simple *in vivo* model, consisting of the transient expression of Vav and an epitope-tagged MAPK in COS-7 cells, as previously reported (Crespo *et al.*, 1994; Coso *et al.*, 1995). Cells were cotransfected with the expression vectors for p95 proto-Vav or its oncogenically activated form, p85 Vav, together with a hemagglutinin-tagged p42 MAPK (HA-MAPK). Expression of the HA-MAPK was assessed by Western blot analysis of total cell lysates with the anti-epitope murine monoclonal antibody, and found to be similar for each transfected cell (Figure 1a). Under these experimental conditions, we found that, whereas coexpression of activated Ras, v-Ras, or EGF treatment potentially elevates the MBP phosphorylating activity of the HA-MAPK, neither proto-Vav nor Vav had any demonstrable effect on MAPK. These data strongly suggest that in COS-7 cells Vav does not activate that MAPK signaling pathway.

Recent work from our laboratory has demonstrated that small GTP binding proteins of the Rho family, Rac1 and Cdc42, can control the activity of a proline-directed

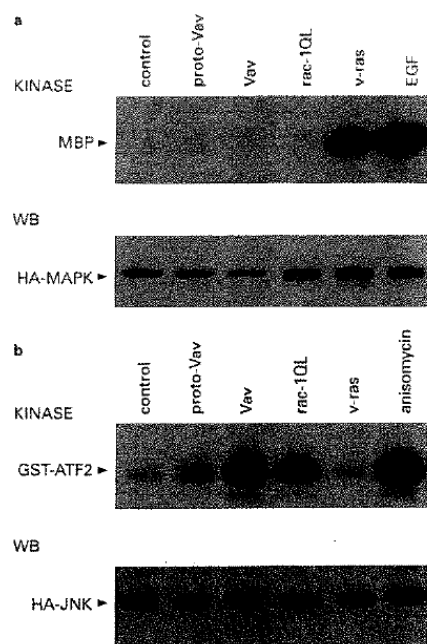


Figure 1 Effect of Vav on MAPK and JNK activity. COS-7 cells were transfected with pcDNA3-HA-JNK1 (1 μ g/plate) or pcDNA3-HA-MAPK (1 μ g/plate) for (a) MAPK and (b) JNK assays, respectively, together with pcDNA3 vector (control) or expression vectors carrying cDNAs for proto-Vav, Vav, v-ras, or a constitutively active form of Rac-1 (Rac-1 QL) (2 μ g per plate in each case), as indicated. Treatment of cells with 10 μ g/ml of anisomycin for 20 min or 100 ng/ml EGF was used as a control. Kinase reactions were performed in anti-HA immunoprecipitates from the corresponding cellular lysates as described in Materials and methods. 3 P labeled products are indicated. Equal levels of expression of HA-MAPK or HA-JNK were ascertained by Western Blotting as described in Materials and methods. Similar results were obtained in four independent experiments.

kinase related to but distinct from MAPK, known as JNK or SAPK (Coso *et al.*, 1995). The finding that Vav fails to activate MAPK, and the presence of a domain bearing homology to GEFs for Rho-like GTPases, DH domain (Ron *et al.*, 1991), prompted us to explore whether Vav could activate JNK. As an experimental approach, we coexpressed the Vav proteins with HA-JNK in COS-7 cells. Our results expressed that, while proto-Vav could induce JNK activity poorly, Vav causes a dramatic increase in JNK activity (sixfold), to an extent comparable to that exerted by a constitutively active Rac-1 mutant (Rac-1QL) (Figure 1b). Increased JNK activity cannot be attributed to differences in expression of HA-JNK, as equal levels of HA-JNK were detected in lysates from each transfected cell culture.

It has been recently shown that other DH-containing proteins such as Ost and DbL can potentially activate JNK (Coso *et al.*, 1995). Thus, we next set out to investigate how does JNK activation by Vav compare with that induced by Ost and DbL. As shown in Figure 2, we found that when equal amounts of expression

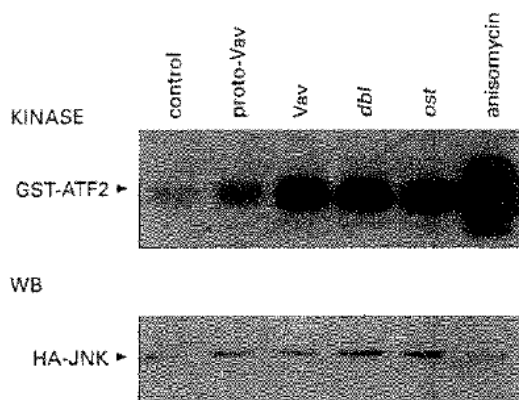


Figure 2 Activation of JNK by expression of Vav and guanine nucleotide exchange factors for the Rho-family of small GTP-binding proteins. COS-7 cells were transfected with the indicated expression plasmids for Vav, *dbf* and *ost* (2 μ g per plate in each case), together with plasmids carrying HA-JNK. Cells cotransfected with the pcDNA3 vector (control) untreated or stimulated with anisomycin (10 μ g/ml, 20 min) served as controls. Similar results were obtained in four independent experiments. Expression of each exchange factor was confirmed by Western blotting with the corresponding antibodies (data not shown). Equal levels of expression of HA-JNK were assayed by Western Blotting as described in Materials and methods

plasmids for each of these three proteins were transfected into COS-7 cells together with the HA-JNK DNA construct, the activation of JNK caused by Vav was nearly as potent as that elicited by Ost or Dbf

JNK elevation by Vav is inhibited by inactivating mutations within the DH and the cysteine-rich domains

Mutation of the first cysteine residue of the cysteine-rich domain of Vav, Vav C464S, inhibits Vav biological activity (Coppola *et al.*, 1991). Similarly, it has been recently found that substitution in Vav of leucine 213 to glutamine, Vav L213Q, completely abolishes the focus-forming ability of Vav (Bustelo *et al.* manuscript in preparation). Interestingly, sequence alignment analysis revealed that this leucine residue is conserved in all DH-containing proteins so far described (unpublished observation). Thus, we assessed whether these inactivating mutations in the DH or cysteine-rich domain affect signaling to the JNK pathway. As shown in Figure 3a, all Vav constructs were similarly expressed when transfected into COS-7 cells. However, JNK activation by Vav L213Q and Vav C464S was markedly decreased as compared with JNK induction elicited by Vav, although they still exhibited a higher activity than that of proto-Vav (Figure 3b). Thus, these data demonstrate that intact cysteine-rich and DH domains of Vav are necessary to fully activate JNK and also suggest that JNK activation correlates with the biological activity of Vav proteins.

Activation of JNK by Vav is blocked by a Ras-1 dominant inhibitory mutant

Several studies have shown that Dbf and other DH-domain bearing proteins such as Ost, act as exchange factors of the Rac/Rho family of small GTP binding proteins (Hart *et al.*, 1991; Horii *et al.*, 1994).

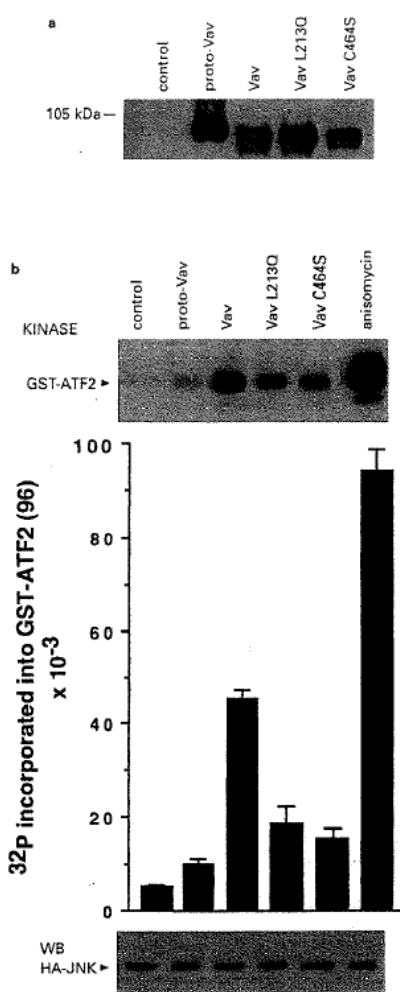


Figure 3 Activation of JNK by Vav mutants. COS-7 cells were transfected with pcDNA3-HA-JNK (1 μ g per plate) together with pcDNA3 vector (control), or with the same expression vector carrying cDNAs for the wild type (proto-Vav) or activated forms of Vav, or Vav L213Q and Vav C464S mutants (2 μ g per plate in each case). (a) lysates containing 40 μ g of protein from transfected COS-7 cells were subjected to Western blot analysis with antibodies against Vav (Santa Cruz). Bands were visualized by the enhanced chemiluminescence technique using anti rabbit HRP-conjugated goat antiserum. (b) cells cotransfected with the pcDNA3 vector (control) untreated or stimulated with anisomycin (10 μ g/ml, 20 min) served as controls for JNK assays. In the upper panel, a representative autoradiogram of phosphorylated substrate is indicated. In the middle panel, data represent the mean \pm SEM of five independent experiments, expressed as radioactive counts of 32 P incorporated into GST-ATF2(96) when used as a substrate. Parallel lysates from transfected cells containing 40 μ g of total cellular protein were subjected to Western blot analysis with anti-Ha antibody 12CA5 (bottom panel)

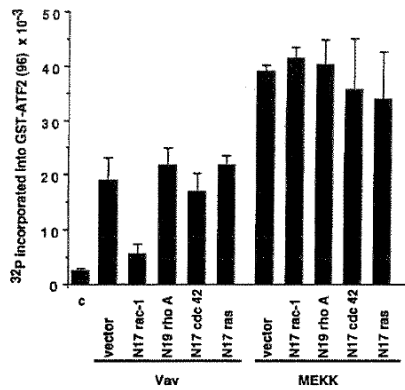


Figure 4 Effect of Ras and Rho family-inhibitory molecules on JNK activation by Vav. COS-7 cells were transfected with expression plasmids for Vav or MEKK (2 μ g per plate in each case) and plasmids expressing the dominant inhibitory mutants Rac-1 N17, Cdc42 N17, Rho N19 and Ras N17, together with pcDNA3-HA-JNK., as indicated. Data represent the mean \pm SEM of five independent experiments, expressed as radioactive counts of 32 P incorporated into GST-ATF2(96)

Moreover, results from our laboratory support a role for Rac-1 and Cdc42 regulating JNK activity (Coso *et al.*, 1995). Thus, it is conceivable that JNK activation by Vav is mediated by one of these GTPases. To test this hypothesis, we cotransfected Vav together with dominant inhibitory mutants of Rho A (Rho A N19), Rac-1 (Rac-1 N17), Cdc42 (Cdc42 N17) and Ras (Ras N17). These mutants are thought to act by competitively inhibiting the interaction of small GTPases with their respective GEFs (Feig and Cooper, 1988). When transfected into COS-7 cells, these mutants were found to be expressed at detectable levels (data not shown; Coso *et al.*, 1995). As shown in Figure 4, none of these mutants affected JNK activation by MEKK, a kinase acting downstream of the small GTP binding proteins (Lange-Carter *et al.*, 1993), when utilized as a control. In contrast, JNK activation by Vav was markedly decreased upon cotransfection by Rac-1 N17, whereas it was not significantly affected by Cdc42 N17, Rho N19 or Ras N17. Taken together, these findings suggest that Rac-1 function is required for JNK activation by the *vav* oncogene product. Whether Vav directly affects Rac-1, or acts upstream of a yet to be characterized Rac-1 guanine-nucleotide exchange factor is still unknown and it is currently being investigated.

Transformation by Vav is diminished by a Rac-1 dominant inhibitory mutant

vav behaves as a very potent oncogene when transfected into NIH3T3 cells (Katzav *et al.*, 1991; Coppola *et al.*, 1991). To study whether Rac-1 participates in the signaling pathway mediating the transforming function of *vav*, we scored *vav*-induced foci-formation in NIH3T3 fibroblasts upon cotransfec-

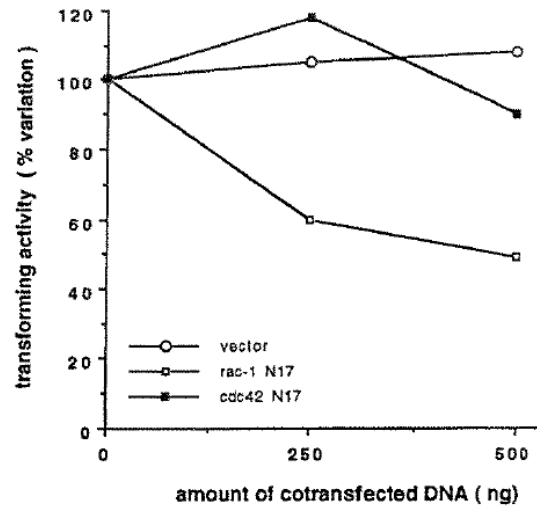


Figure 5 Effects of Rac-1 and Cdc42 dominant inhibitory mutants on *vav*-induced focus-formation. The indicated amounts of plasmid DNA expressing Rac-1 N17, Cdc42 N17 or the expression vector pMEX were transfected with 50 ng of expression plasmid for Vav into NIH3T3 fibroblast as described in Materials and methods. Foci of transformation were scored 2-3 weeks after transfection. Results represent the average of three independent experiments

tion with expression plasmids for the dominant inhibitory mutants of Rac-1 and the closely related GTPase, Cdc42. NIH3T3 cells were transfected with 50 ng of *vav* plasmid together with the expression vector (pMEX) alone or with increasing concentrations (250 and 500 ng) of plasmids for Rac-1 N17 or Cdc42 N17. As shown in the Figure 5, cotransfection with Rac-1 N17 results in a significant reduction of *vav*-transformed foci. On the other hand, cotransfection with Cdc42 N17 cDNA did not significantly alter the number of foci induced by *vav*, thereby suggesting that Rac-1, but not Cdc42, is necessary for *vav*-induced transformation.

Discussion

Accumulating evidence suggests that small GTP binding proteins control divergent kinase cascades leading to the activation of each member of the MAPK superfamily. As such, MAPK is regulated by Ras (Marshall, 1995), and Rac-1 and Cdc42 control the activation of JNK (Coso *et al.*, 1995; Minden *et al.*, 1995). In addition, Rho regulates the pathway leading to the activation of a putative kinase that affects SRF function (Hill *et al.*, 1995). In this context, GEFs for the Rac/Rho/Cdc42 family such as Dbp and Ost can activate JNK, whereas GEFs for Ras such as SOS (Aronheim *et al.*, 1994) and Ras-GRF (Famsworth *et al.*, 1995) can activate MAPKs. Although the function of the protein encoded by the human *vav* oncogene, p85^v, is still unknown, it exhibits structural features common to GEFs for GTPases of the Rho and Ras families. Thus, in this study we set out to investigate the Vav signaling pathway by exploring the ability of

Vav to activate MAPK or JNK, using the transient expression in COS-7 cells as a model system,

Our results indicate that neither proto-Vav nor Vav is capable of activating MAPK to any significant extent. Several studies have shown otherwise (Khosravi-Far *et al.*, 1994; Gulbins *et al.*, 1994), however, in these cases MAPK activation was determined in stable Vav-transformed cell lines. Thus, it cannot be ruled out that the enhanced MAPK activity reported represents an event secondary to the transformed state of the cells, rather than being a direct effect caused by Vav. Moreover, in those earlier reports (Khosravi-Far *et al.*, 1994; Gulbins *et al.*, 1994), MAPK activation was scored by change in its electrophoretic mobility in SDS-PAGE gels, a less specific assay than the direct determination of the MBP phosphorylating activity of MAPK. We conclude that Vav is incapable of directly activating MAPK, thus suggesting that Vav does not act as a Ras GEF, in agreement with recent studies (Bustelo *et al.*, 1994).

In contrast, our results indicate that Vav potently activates JNK, and to an extent comparable to that induced by Dbl and Ost, both GEFs for Rho related proteins (Coso *et al.*, 1995). These three proteins share a common structural domain known as the Dbl-homology (DH) domain (Ron *et al.*, 1988; Eva *et al.*, 1988; Boguski and McCormick, 1993). Mutations within this domain impair Dbl activity, abolishing Dbl-induced focus formation upon expression in NIH3T3 cells, as well as its ability to stimulate GDP dissociation on Rho when studied by *in vitro* assays (Hart *et al.*, 1994). Here we show that point mutations within the DH domain, Vav L213Q, or the cysteine-rich domain, Vav C464S, of Vav dramatically diminish JNK stimulation. Interestingly, both Vav L213Q and Vav C464S are biologically inactive mutants, incapable of transforming NIH3T3 fibroblasts (Coppola *et al.*, 1991; Bustelo *et al.*, manuscript in preparation). Taken together, these findings suggest that the cysteine rich and DH domains of Vav participate in a biologically relevant pathway, and that JNK activation may contribute to the transforming potential of *vav*.

The structural similarities (Adams *et al.*, 1992) and the fact that the disruption of their respective DH domains impairs Vav and Dbl transforming potential suggests that these two proteins could be acting on the same signaling pathway. Accordingly, Vav and Dbl-transformed fibroblasts have been shown to exhibit similar morphology and nearly identical pattern of distribution of stress fibers (Khosravi-Far *et al.*, 1994), resembling that found in cells transformed by the Rho family of small GTP-binding proteins (Ridley and Hall, 1992; Ridley *et al.*, 1992). In addition, JNK activation by Dbl has been shown to be Rae-1 dependent (Minden *et al.*, 1995, our unpublished results). Likewise, our results indicate that JNK activation by Vav is mediated by Rac-1, as we have observed that the Rae-1 N17 dominant inhibitory mutant markedly diminishes JNK activation by Vav. Moreover, we have observed that cotransfection with Rac-1 N17 reduces the focus-forming ability of Vav. Taken together, these data strongly suggest that Rae-1 is an integral component of the transforming pathway activated by the *vav* oncogene. However, further work will be required to elucidate fully the role of Rae-1 and JNK in *vav*-mediated transformation.

Stimulation of JNK by external stimuli such as IL-1, EGF and TNF- α has also been found to be dependent on Cdc42 (Coso *et al.*, 1995). This seems not to be the case in Vav signaling, as neither activation of JNK mediated by Vav nor Vav-induced transfection was affected by the Cdc42 N17 dominant inhibitory mutant. Thus, Vav appears to have a greater effector specificity when signaling to the JNK cascade, favoring the Rac-1-mediated pathway. However, is Vav an exchange factor for Rae-1? So far, we and others (Gulbins *et al.*, 1993) have been unsuccessful in providing a conclusive answer. Although it is possible that Vav may not be able to induce guanine-nucleotide exchange on Rac-1 in the *in vitro* assays utilized, we cannot rule out that other factors are essential for Vav exchange activity, including the possibility that Vav may act upstream or in conjunction with additional GEFs to induce Rae-1 guanine nucleotide exchange. These issues are under current investigation. Finally, our results may also have implications with respect to the normal function of proto-Vav, raising the possibility that proto-Vav acts as a mediator in the signaling pathways leading to JNK activation in hematopoietic cells, including T and B-lymphocytes. As neither the role of proto-Vav nor the biological consequences of JNK activation in these cells is yet understood, our present study linking these two proteins opens new avenues that warrant further investigation.

Materials and methods

Expression plasmids

An NruI-NotI DNA fragment from pKLS45 (Coppola *et al.*, 1991), containing the *vav* cDNA, lacking sequences for the aminoterminal 65 aminoacids of proto-Vav, was subcloned into the EcoRV-NotI sites of the pcDNA3 (Invitrogen) mammalian expression vector. pcDNA3 *vav* L213Q was obtained by replacing the *vav* BglII 1956 bp fragment with the corresponding sequences from pLC4, an expression plasmid carrying a *vav* cDNA mutated in codon 213 (Bustelo *et al.*, manuscript in preparation). pcDNA3 *vav* C464S was generated by replacing the *vav* BglII fragment with the corresponding sequence from pJCI 7 (Coppola *et al.*, 1991). DNA plasmids expressing epitope-tagged MAPK and JNK, Ras V12, Rac-1 QL, Rac-1 N17, RhoA N19, Cdc42 N17, Ras N17, Ost, Dbl and MEKK have been described elsewhere (Coso *et al.*, 1995).

Kinase assays

Jun-kinase assay Subconfluent COS-7 cells were transfected with pcDNA3-HA-JNK and additional DNAs by the DEAE-dextran technique as previously described (Coso *et al.*, 1995). Total amount of plasmid DNA was adjusted to 5-10 μ g/plate with vector DNA (pcDNA3, Invitrogen) when necessary. Two days later, transfected COS-7 cells were cultured 2 h in serum-free medium. Cells were then washed with cold PBS, and lysed at 4°C in a buffer containing 25 mM HEPES, pH 7.5, 0.3 M NaCl, 1.5 mM MgCl₂, 0.2 mM EDTA, 0.5 mM DTT, 1% Triton X-100, 20 mM β -glycerophosphate, 1 mM sodium vanadate, 1 mM phenylmethylsulfonyl fluoride, 20 μ g/ml aprotinin, and 20 μ g/ml leupeptin. The epitope-tagged JNK was immunoprecipitated from the cleared lysates by incubation with the HA-specific antibody 12CA5 (BABC0) for 1 h at 4°C. Immunocomplexes were recovered with the aid of Gamma-

bind sepharose beads (Pharmacia) and washed three times with PBS containing 1% NP-40 and 2 mM sodium vanadate, once with 100 mM TRIS, pH 7.5, 0.5 M LiCl, and once in kinase reaction buffer (12.5 mM MOPS, pH 7.5, 12.5 mM β -glycerophosphate, 7.5 mM MgCl₂, 0.5 M EGTA, 0.5 mM sodium fluoride, 0.5 mM sodium vanadate). The JNK activity present in the immunoprecipitates was determined by resuspension in 30 μ l of kinase reaction buffer containing 1 μ Ci [γ -³²P]ATP per reaction and 20 μ M of unlabeled ATP, using 1 μ g of GST-ATF2 fusion protein as a substrate, as previously described (Coso *et al.*, 1995). After 20 min at 30°C, reactions were terminated by addition of 10 μ l 5x Laemmli buffer. Samples were heated at 95°C for 5 min and analysed by SDS-gel electrophoresis on 12% acrylamide gels. Autoradiography was performed with the aid of an intensifying screen.

MAPK kinase assay MAPK kinase activity in COS-7 transfected with an epitope-tagged MAPK (HA-ERK2, referred here as HA-MAPK) was determined as previously described (Crespo *et al.*, 1994), using myelin basic protein (MBP) as a substrate.

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Western blots

Lysates containing approximately 40 μ g of total cellular protein were analysed by Western-blotting after SDS/polyacrylamide gel electrophoresis, transferred to nitrocellulose and immunoblotted with the corresponding rabbit antisera or mouse monoclonal antibody. Immunocomplexes were visualized by enhanced chemiluminescence detection (Amersham) using goat anti-rabbit or anti-mouse coupled to HRP as a secondary antibody (Cappel). Anti HA-epitope mouse monoclonal antibody (12CA5) was purchased from BABCO, rabbit polyclonal antibodies against Vav, Rac-1, RhoA and Cdc42, and anti-Ras monoclonal Y13-259 were purchased from Santa Cruz Laboratories.

Focus-forming assays in NIH3T3 cells

Plasmid DNA transfection of NIH3T3 fibroblasts was performed by the calcium phosphate precipitation technique (Wigler *et al.*, 1977). Transformed foci were scored after 2-3 weeks as previously described (Gutkind *et al.*, 1991).