TNF-stimulated MAP kinase activation mediated by a Rho family GTPase signaling pathway

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The biological response to tumor necrosis factor (TNF) involves activation of MAP kinases. Here we report a mechanism of MAP kinase activation by TNF that is mediated by the Rho GTPase family members Rac/Cdc42. This signaling pathway requires Src-dependent activation of the guanosine nucleotide exchange factor Vav, activation of Rac/Cdc42, and the engagement of the Rac/Cdc42 interaction site (CRIB motif) on mixed-lineage protein kinases (MLKs). We show that this pathway is essential for full MAP kinase activation during the response to TNF. Moreover, this MLK pathway contributes to inflammation in vivo.

[Keywords: MAP kinase; MLK; mixed-lineage protein kinase; TNF]

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The tumor necrosis factor [TNF] signaling pathway is established to be a target for the development of effective strategies for the treatment of human inflammatory diseases [Feldmann 2002]. Knowledge of the mechanism of TNF signaling is therefore important for the design of novel therapeutic approaches. Biological responses to TNF involve activation of signal transduction pathways, including MAP kinases and NF-κB [Karim 2005].

TNF recruits TRADD, TRAF2, and RIP1 to the cytoplasmic domain of TNF receptor 1 [Micheau and Tschopp 2003]. This complex initiates signal transduction mediated by NF-κB. Activation of the NF-κB pathway requires ubiquitin-mediated activation of the protein kinase TAK1 [Skaug et al. 2009]. Studies of Tak1−/− murine cells confirm that TAK1 is essential for TNF-induced activation of IκB kinase β [IKKβ] and the subsequent degradation of IκBα, a critical step in NF-κB signaling [Sato et al. 2005; Shim et al. 2005]. The TAK1 protein kinase therefore plays a central role in TNF-mediated activation of NF-κB.

TNF-stimulated MAP kinase activation is also mediated by the TRADD/TRAF2/RIP1 complex that is recruited to the cytoplasmic domain of TNF receptor 1 [Micheau and Tschopp 2003]. Several members of the MAP kinase kinase kinase (MAP3K) group [e.g., ASK1 [Ichijo et al. 1997; Nishitoh et al. 1998; Tobiume et al. 2001], MEKK1 [Xia et al. 2000], mixed-lineage protein kinase 3 [MLK3] [Sathyanarayana et al. 2002; Chadee and Kyriakis 2004; Brancho et al. 2005; Korchnak et al. 2009; Sondarva et al. 2009], TAK1 [Sato et al. 2005; Shim et al. 2005], and TPL2 [Das et al. 2005]] have been implicated in TNF-induced MAP kinase activation. The relative contribution of these MAP3Ks to TNF-stimulated MAP kinase activation is unclear. The roles of individual MAP3Ks may reflect differences between TNF-responsive cells and/or differences between separate MAP kinase pathways. These MAP kinase pathways include the c-Jun N-terminal kinase [JNK], p38 MAP kinase, and extracellular signal-regulated kinases [ERKs]. Each of these MAP kinases is activated by different MAP kinase kinase [MAP2K] isoforms. Thus, JNK activation requires MKK7 and cooperative signaling by MKK4 [Tournier et al. 2001], TNF-stimulated activation of p38 MAP kinase requires both MKK3 and MKK6 [Brancho et al. 2003], and ERK activation is mediated by MKK1 and MKK2 [Robinson and Cobb 1997]. These
pathways lead to ERK, JNK, and p38 MAP kinase activation by a dual phosphorylation (Thr and Tyr) mechanism.

It is established that TNF causes activation of Rho family GTPases—including Rac/Cdc42 [Wojciak-Stothard et al. 1998; Kim et al. 1999; Puls et al. 1999; Hanna et al. 2001]—that may contribute to actin cytoskeleton reorganization [Wojciak-Stothard et al. 1998] and the production of reactive oxygen species [Kim et al. 2007; Yazdanpanah et al. 2009]. The purpose of this study was to examine whether the TNF-stimulated Rac/Cdc42 pathway might contribute to MAP kinase activation [Coso et al. 1995; Minden et al. 1995]. We report that TNF can activate a PTPN1/Src/Vav pathway that causes MLK-dependent activation of MAP kinases.

Results

Requirement of the Rac/Cdc42 interaction site (CRIB motif) on MLK3 for TNF-stimulated MAP kinase activation

Treatment of primary murine fibroblasts [MEFs] [Fig. 1A] and bone marrow-derived macrophages [BMDMs] [Fig. 1B] with TNF causes rapid activation of Rac and Cdc42. We examined whether this TNF-stimulated Rac/Cdc42 pathway might contribute to MAP kinase activation [Coso et al. 1995; Minden et al. 1995] by binding to the Rac/Cdc42 interaction site [CRIB motif] on MLK3 [Teramoto et al. 1996]. To test this hypothesis, we investigated the effect of point mutations [Ile492 and Ser493 replaced with Ala] that disrupt the CRIB motif and prevent Rac/Cdc42-dependent activation of MLK3 [Bock et al. 2000]. Mice with germline point mutations in the MLK3 gene were established [MLK3CRI/CRI/CRI mice] and primary cultures of MEFs were prepared [Fig. 1C–F]. We found similar TNF-stimulated MAP kinase activation in control [MLK3CRI/CRI/CRI] and mutant [MLK3CRI/CRI/CRI] MEFs [data not shown]. This observation may reflect a redundant role of MLK3 in TNF-stimulated MAP kinase signal transduction.

Gene expression analysis demonstrated that MEFs primarily express MLK2 and MLK3 [Supplemental Fig. S1]. We therefore employed MLK2+/− mice [Supplemental Fig. S2], MLK3−/− mice [Brancho et al. 2005], and compound mutant MLK2−/− MLK3−/− mice [Supplemental Fig. S2] to prepare MEFs. Control studies demonstrated that MLK deficiency did not alter cell morphology or proliferation [Fig. 2]. Deficiency of MLK2 or MLK3 caused only minor changes in TNF-stimulated MAP kinase activation [Supplemental Fig. S3], but TNF-stimulated MAP kinase activation in MLK2−/− MLK3−/− MEFs was markedly reduced [Fig. 1G]. The reduced TNF-stimulated MAP kinase activation detected in MLK2−/− MLK3−/− MEFs was not associated with altered TNF-stimulated activation of IKKβ or degradation of IκBα [Fig. 1G]. Thus, the MLK pathway [mediated by redundant functions of MLK2 and MLK3] is required for maximal TNF-stimulated MAP kinase activation, but is not required for TNF-stimulated activation of the NFKB pathway. This selective requirement of MLK2/3 for MAP kinase activation was also observed in studies of MLK3−/− BMDMs treated with TNF or lipopolysaccharide [LPS] [Fig. 1H].

MLK2 and MLK3 have partially redundant functions [Fig. 1G,H]. We therefore re-examined the effect of the MLK3 CRIB mutation in a MLK2-deficient genetic background. This analysis demonstrated that TNF-stimulated MAP kinase activation in MLK2−/− MLK3CRI/CRI/CRI MEFs was markedly suppressed [Fig. 1I]. In contrast, no difference in TNF-stimulated IκBα degradation was detected between wild-type and MLK2−/− MLK3CRI/CRI/CRI MEFs [Fig. 1I]. These data confirm that the MLK pathway contributes to TNF-stimulated MAP kinase activation, but not TNF-stimulated NF-κB activation.

To test whether Rac-mediated activation of MAP kinase is mediated by the MLK pathway, we expressed constitutively activated Rac in wild-type MEFs, MLK2−/− MLK3−/− MEFs, and MLK2−/− MLK3CRI/CRI/CRI MEFs [Supplemental Fig. S4]. Activated Rac caused JNK activation in wild-type MEFs, but did not cause JNK activation in MEFs with MLK pathway defects. These data demonstrate that the MLK pathway is an essential mediator of Rac signaling.

The low-level TNF-stimulated MAP kinase activation detected in MLK2−/− MLK3−/− MEFs and MLK2−/− MLK3CRI/CRI/CRI MEFs [Fig. 1G–I] may be mediated by TAK1. Indeed, TNF can cause partial MAP kinase activation in Tak1−/− MEFs [Fig. 3A], and RNAi-mediated knockdown of TAK1 in MLK2−/− MLK3−/− MEFs strongly reduced TNF-stimulated MAP kinase activation [Fig. 3B–D]. Together, these data indicate that TNF-stimulated MAP kinase activation is mediated by the coordinated activation of at least two signaling pathways (MLK2/3 and TAK1).

Vav guanine nucleotide exchange factors mediate TNF signaling

The suppression of TNF-stimulated MAP kinase activation caused by mutation of the MLK3 CRIB motif [Fig. 1] indicates that Rac/Cdc42 may mediate TNF-induced MAP kinase activation. However, the mechanism that accounts for TNF-stimulated Rac/Cdc42 activation is unclear. To identify TNF-regulated guanine nucleotide exchange factors [RhoGEFs], we isolated proteins that interact with a nucleotide-free form of Rac [Rac1 Gly15Ala, a mimic of the guanine nucleotide transition state] from control and TNF-treated cells using affinity chromatography [Garcia-Mata et al. 2006]. Vav was identified as a TNF-activated RhoGEF [Fig. 4A]. In contrast, the RhoGEF isoforms GEF-T and TIA1 were not activated by TNF [Fig. 4A]. To test whether Vav contributes to TNF-stimulated Rac activation, we examined Rac activation in wild-type and Vav1/2/3-deficient primary BMDMs [Fig. 4B]. This analysis demonstrated that Vav contributes to TNF-stimulated Rac activation [Fig. 4B].

TNF causes tyrosine phosphorylation and activation of Vav

It is established that tyrosine phosphorylation represents a major mechanism of Vav regulation [Swat and Fujikawa 2005]. Indeed, TNF caused increased Vav tyrosine phosphorylation [Fig. 4C]. Candidate tyrosine kinases that might mediate this tyrosine phosphorylation include...
members of the Src family (e.g., Src, Fyn, and Yes). We found that TNF did not cause Vav tyrosine phosphorylation in
Src−/− Fyn−/− Yes−/− fibroblasts, but complementation analysis demonstrated that re-expression of Src was
sufficient to restore TNF-stimulated Vav tyrosine phosphorylation (Fig. 4D). Both Vav-deficient and Src/Fyn/Yes-
deficient cells exhibited defects in TNF-stimulated activation of MAP kinases (Fig. 4E,F). Together, these data

Figure 1. TNF causes activation of a Rac/Cdc42–MLK signal transduction pathway. (A,B) MEFs (A) or BMDMs (B) were treated
without or with 10 ng/mL TNFα. Activated (GTP-loaded) Rac/Cdc42 was isolated and quantitated by immunoblot analysis. The
amount of Rac/Cdc42 in cell lysates was measured by immunoblot analysis. (C) The structure of the Mlk3 genomic locus and the
targeting vector are illustrated. Homologous recombination causes the replacement of Mlk3 exon VII with a mutated form of exon VII
together with the insertion of a floxed Neo cassette. The floxed Neo cassette was excised using Cre recombinase. (D) The point
mutations in exon VII created by the targeting vector are illustrated. The nucleotide changes cause the elimination of an MslII
restriction site and the introduction of two amino acid substitutions [Ile492Ala and Ser493Ala] that disrupt the MLK3 CRIB domain.
(E) Genomic DNA from wild-type, Mlk3+/ΔCRIB, and Mlk3+/ΔCRIB/ΔCRIB mice was examined by PCR analysis to detect the wild-type and
mutant Mlk3 alleles. (F) Extracts prepared from wild-type (WT), Mlk3−/−, and Mlk3+/ΔCRIB/ΔCRIB MEFs were examined by immunoblot
analysis with antibodies to MLK3 and α-Tubulin. (G–I) Wild-type and Mlk2+/− Mlk3+/− MEFs (G), wild-type and Mlk2+/− Mlk3+/−
BMDMs (H), or wild-type and Mlk2+/− Mlk3+/− MEFs (I) were treated without or with 10 ng/mL TNF or 100 ng/mL LPS. MAP
kinase and IκKβ activation and the degradation of IκBβ were examined by immunoblot analysis.
The results of this study demonstrate that full activation of MAP kinase activation. The MLK and TAK1 pathways mediate different TNF-stimulated MAP kinase activation. Tyrosine phosphatases contribute to the regulation of MAP kinase activation (Fig. 5D). These data demonstrate that tyrosine phosphatases contribute to the regulation of MAP kinase activation and that PTPN2 inhibition augmented TNF-stimulated NF-κB signaling. We found that inhibition of PTPN1 and PTPN2 can cause opposite actions on Src family kinase activity by selectively dephosphorylating the inhibitory C-terminal site [PTPN1] or the activating T-loop site [PTPN2] of tyrosine phosphorylation (van Vliet et al. 2005). The related tyrosine phosphatases PTPN1 and PTPN2 can cause opposite actions on Src family kinase activity by selectively dephosphorylating the inhibitory C-terminal site [PTPN1] or the activating T-loop site [PTPN2] of tyrosine phosphorylation (van Vliet et al. 2005). The related tyrosine phosphatases PTPN1 and PTPN2 can cause opposite actions on Src family kinase activity by selectively dephosphorylating the inhibitory C-terminal site [PTPN1] or the activating T-loop site [PTPN2] of tyrosine phosphorylation (van Vliet et al. 2005).

Requirement of PTPN1 for TNF-stimulated Rac activation

Ssrc family protein kinases have been previously implicated in TNF-stimulated MAP kinase activation mediated by TRAF2-associated tyrosine phosphatases (van Vliet et al. 2005). This pathway mediates TNF-stimulated MAP kinase activation, but not TNF-stimulated NF-κB activation (van Vliet et al. 2005). The related tyrosine phosphatases PTPN1 and PTPN2 can cause opposite actions on Src family kinase activity by selectively dephosphorylating the inhibitory C-terminal site [PTPN1] or the activating T-loop site [PTPN2] of tyrosine phosphorylation (van Vliet et al. 2005). Increased PTPN1 and/or decreased PTPN2 function may therefore contribute to TNF-stimulated MAP kinase activation. We found that TNF caused decreased tyrosine phosphorylation of the C-terminal site phosphorylating the inhibitory C-terminal site (PTPN2) or the activating T-loop site (PTPN1) or the activating T-loop site (PTPN2) of tyrosine phosphorylation (van Vliet et al. 2005). Increased PTPN1 and/or decreased PTPN2 function may therefore contribute to TNF-stimulated MAP kinase activation. We found that TNF caused decreased tyrosine phosphorylation of the C-terminal site phosphorylating the inhibitory C-terminal site (PTPN2) or the activating T-loop site (PTPN1). A common strategy to modulate cellular responses is to either inhibit or activate specific enzymes. In this study, we examined the effect of selective small molecule inhibitors of PTPN1 and PTPN2. We found that inhibition of PTPN1 suppressed TNF-stimulated MAP kinase activation and that PTPN2 inhibition augmented TNF-stimulated MAP kinase activation (Fig. 5D). These data demonstrate that tyrosine phosphatases contribute to the regulation of TNF-stimulated MAP kinase activation.

The MLK and TAK1 pathways mediate different TNF biological responses

The results of this study demonstrate that full activation of MAP kinases caused by TNF requires a Rac-Cdc42 signaling pathway that is mediated by Src-induced Vav activation and engagement of MLK protein kinases. To examine the contribution of this pathway to TNF signaling, we compared the response of control and MLK-deficient MEFs to treatment with TNF, including the expression of inflammatory cytokines and cell death. We found that TNF-treated Mlk2−/− Mlk3−/− MEFs secrete markedly less interleukin 6 (IL6) than wild-type cells (Fig. 6A), consistent with reduced MAP kinase activation in MLK-deficient cells (Fig. 1G,H). Previous studies have established that the ERK, JNK, and p38 MAP kinase pathways can contribute to inflammation in vivo. Requirement of PTPN1 for TNF-stimulated Rac activation

We found that inhibition of PTPN1 suppressed TNF-stimulated MAP kinase activation and that PTPN2 inhibition augmented TNF-stimulated MAP kinase activation (Fig. 5D). These data demonstrate that tyrosine phosphatases contribute to the regulation of TNF-stimulated MAP kinase activation.

The MLK pathway contributes to inflammation in vivo

To test whether the MLK pathway can mediate inflammation, we examined the effect of MLK deficiency on the response of mice to endotoxin exposure. Treatment of wild-type mice with LPS caused increased expression of inflammatory cytokines [e.g., TNFα and chemokines (e.g., CCL3 and CCL5) in blood (Fig. 7A). These effects of LPS were suppressed in MLK-deficient mice (Mlk2−/− Mlk3−/−) and mice with MLK CRIB motif mutation (Mlk2−/− Mlk3+CRIB/ΔCRIB) (Fig. 7A). Control studies using in vitro cultures of BMDMs confirmed that the MLK pathway is required for LPS-stimulated cytokine production.
Studies of the MLK pathway in primary cells isolated from Mlk2 or Mlk3 knockout mice also caused markedly reduced TNF-stimulated NF-κB pathway (Hehner et al. 2000). We report that the functions of MLK3 are partially redundant with the related protein kinase MLK2 in MEFs (Fig. 1G) and macrophages (Fig. 1H). Compound gene disruption studies demonstrate that Mlk2−/− Mlk3−/− MEFs and macrophages exhibit a severe defect in TNF-stimulated MAP kinase activation (Fig. 1G,H). Moreover, the disrupted MLK CRIB motif in primary cells isolated from Mlk2−/− Mlk3ΔCRIB/ΔCRIB mice also caused markedly reduced TNF-stimulated MAP kinase activation (Fig. 1I). These data indicate that MLK protein kinases mediate the effects of TNF-stimulated Rac/Cdc42 on MAP kinase activation.

The MLK protein kinases have been implicated in the activation of the NF-κB pathway (Hehner et al. 2000). However, we found no defects in TNF-stimulated IKKβ activation or IkBα degradation in Mlk2−/− Mlk3−/− MEFs (Fig. 1G). These data indicate that MLK protein kinases are not involved in the TNF-stimulated NF-κB pathway. Studies of Tak1−/− MEFs demonstrated that Tak1 deficiency completely ablated the TNF-stimulated NF-κB pathway, but caused only partial loss of TNF-stimulated MAP kinase activation (Fig. 3A). Together, these data indicate that Tak1 plays a key role in TNF-stimulated NF-κB signaling.
activation and that both TAK1 and MLK protein kinases contribute to TNF-stimulated MAP kinase activation.

The TAK1 and MLK pathways represent different signaling mechanisms employed by TNF receptor 1. Both of these pathways provide an opportunity for therapeutic intervention that may be useful for the treatment of human inflammatory diseases. However, the effects of inhibition of these pathways are different because only...
TAK1 inhibition causes decreased NF-κB-mediated survival signaling [Fig. 6B,C]. The reduced TNF-mediated cytotoxicity caused by loss of MLK function, compared with loss of TAK1 function, may be a beneficial property of drugs that target MLK to inhibit TNF-stimulated inflammatory cytokine expression during disease progression in humans.

Materials and methods

Mice

C57BL/6J strain mice were obtained from The Jackson Laboratories. Mice with Mlk3 [Brancho et al. 2005], Pipt1 [Klanam et al. 2000], Tak1 [Shim et al. 2005], or Vav1, Vav2, and Vav3 [Fujikawa et al. 2003] gene disruptions have been described previously.

Mice with germline mutations in exon VII of the Mlk3 gene (Mlk3<sup>−/−</sup>) were constructed using homologous recombination in LCL1 embryonic stem (ES) cells [albino C57BL/6J genetic background]. The targeting vector was constructed using a mouse strain C57BL/6J genomic BAC clone containing the Mlk3 gene, a floxed Neo<sup>+</sup> cassette, and a thymidine kinase cassette [Fig. 1C]. The ES cells were electroporated and selected with 200 μg/mL G418 and 2 μM gancyclovir. Correctly targeted ES cell clones were injected into C57BL/6J blastocysts to create chimeric mice that transmitted the mutated Mlk3 allele through the germline. The floxed Neo<sup>+</sup> cassette was excised using Cre recombinase.

Mlk2<sup>−/−</sup> gene disruption by homologous recombination using 129/SvJ strain ES cells was used to create a deletion [exon I to exon VI] within the Mlk2 gene [Supplemental Fig. S2]. Correctly targeted ES cell clones were employed to create chimeric mice that transmitted the mutated Mlk2 allele through the germline [D.S. Dorow, Peter MacCallum Cancer Institute]. The Mlk2<sup>−/−</sup> mice were backcrossed to the C57BL/6J strain [10 generations]. The mice were housed in a facility accredited by the American Association for Laboratory Animal Care. All animal studies were approved by the Institutional Animal Care and Use Committee of the University of Massachusetts Medical School.

Genotype analysis

Wild-type [500-base-pair [bp]] and disrupted [600-bp] alleles of Mlk2 were detected by PCR using the amplifiers 5'-CCTGG TTCTCATTGGGACAACAG-3', 5'-GTCACATCCACTTTCC TGGGC-3', and 5'-CGGCTTCTATGCCTTCTTGAC-3'. Wild-type and disrupted alleles of Mlk3 [Brancho et al. 2005], Pipt1 [Klanam et al. 2000], Tak1 [Shim et al. 2005], or Vav1/2/3 [Fujikawa et al. 2003] were detected by PCR analysis using genomic DNA as the template. The Mlk3<sup>−/−</sup> allele [160 bp] was detected by PCR amplification of genomic DNA using the amplifiers 5'-CCCAAACCTTCCCCCTTTCC TTGAG-3', and 5'-CGGAGAACGCGCAGCC-3'. Wild-type and disrupted alleles of Mlk2 were detected using the amplifiers 5'-CCTGG TTCTCATTGGGACAACAG-3', and 5'-GTCACATCCACTTTCC TGGGC-3', and 5'-CGGCTTCTATGCCTTCTTGAC-3'. Wild-type and disrupted alleles of Mlk3 [Brancho et al. 2005], Pipt1 [Klanam et al. 2000], Tak1 [Shim et al. 2005], or Vav1/2/3 [Fujikawa et al. 2003] were detected by PCR analysis using genomic DNA as the template. The Mlk3<sup>−/−</sup> allele [160 bp] was detected by PCR amplification of genomic DNA using the amplifiers 5'-CCCAAACCTTCCCCCTTTCC TTGAG-3', and 5'-CGGAGAACGCGCAGCC-3'. Wild-type and disrupted alleles of Mlk2 were detected using the amplifiers 5'-CCTGG TTCTCATTGGGACAACAG-3', and 5'-GTCACATCCACTTTCC TGGGC-3', and 5'-CGGCTTCTATGCCTTCTTGAC-3'.
RNA analysis

The expression of mRNA was examined by quantitative PCR analysis using a 7500 Fast Real-Time PCR machine [Applied Biosystems]. TaqMan assays were used to quantitate Mlk1 [Mm00616834_m1], Mlk2 [Mm01175535_m1], Mlk3 [Mm01233534_m1], Mlk4 [Mm00524049_m1], Tak1 [Mm00554514_m1], Tnfr1 [Mm01182929_m1], Tnfr2 [Mm00441889_m1], and Gapdh [4352339E-0904201] mRNA [Applied Biosystems]. Standard curves were constructed using the threshold cycle (Ct) values for each template dilution plotted as a function of the logarithm of the amount of input template. The number of mRNA copies for each gene sample combination was calculated using the slope of the standard curve. To obtain a normalized abundance, copy numbers were corrected for the number of Gapdh mRNA in each sample.

Immunoblot analysis

Cell extracts were prepared using Triton lysis buffer [20 mM Tris at pH 7.4, 1% Triton X-100, 10% glycerol, 137 mM NaCl, 2 mM EDTA, 25 mM β-glycerophosphate, 1 mM sodium orthovanadate, 1 mM phenylmethylsulfonyl fluoride, 10 μg/mL aprotinin and leupeptin]. The lysates [50 μg of protein] were examined by protein immunoblot analysis. Immune complexes were detected by enhanced chemiluminescence [NEL]. Primary antibodies were obtained from Cell Signaling [Cdc42, phospho-IKKβ, IKKβ, MLK3, phospho-ERK1/2, phospho-JNK1/2, p38α, phospho-p38, Src, pyY527-Src, Vav1/2/3, Rac1/2/3, and IκBα, BD Pharmingen [JNK1/2], Millipore [Rac1, Vav, and phosphotyrosine], Santa Cruz Biotechnologies [ERK2, TAK1, and TIAM1], Sigma [α-Tubulin], and Proteintech Group [GEFT]. The polyclonal antibody to MLK2 was purified from serum obtained from rabbits immunized with a peptide that corresponds to MLK2 amino acids 898–911 [CSIPPRPDTPESPG-amide] conjugated to keyhole limpet hemocyanin [Yenzyem].

Immunoprecipitation

Cell extracts were prepared using lysis buffer [150 mM NaCl, 50 mM Tris at pH 8.0, 5 mM EDTA, 1% NP-40, 1 mM PMSF] and incubated [5 h at 4°C] with 10 μg of control nonimmune rabbit IgG [Santa Cruz Biotechnologies] or 10 μg of rabbit antibodies to Vav [Millipore] and Vav1/2/3 [Cell Signaling]. Immunocomplexes isolated using Protein G Sepharose were washed (five times) with lysis buffer.

Cytokine and chemokine analysis

Cytokines in cell culture medium were measured by multiplexed ELISA using a LumineX 200 machine [Millipore] and a serum mouse cytokine kit [Millipore].

Rac/Cdc42 activation

Assays were performed with the Rac/Cdc42 Activation Assay kit using the manufacturer’s recommendations [Millipore]. Cdc42 was detected by immunoblot analysis [Cell Signaling]. Rac was detected by immunoblot analysis using an antibody to Rac1 [Millipore] for studies of MEFs and an antibody to Rac1/2/3 [Cell Signaling] for BMDM studies.

Analysis of RhoGEF proteins

TNF-activated RhoGEFs were identified by affinity chromatography using a nucleotide-free transition state mimic of Rac1 [Garcia-Mata et al. 2006]. Cell extracts prepared using lysis buffer [150 mM NaCl, 50 mM Tris at pH 8.0, 5 mM EDTA, 1% NP-40, 1 mM PMSF] were incubated with GST-Rac1G12A immobilized on agarose beads and washed. The beads were mixed with GST-Rac1G12A immobilized on agarose beads and washed.
GSH-Sepharose for 1 h at 4°C. The GSH-Sepharose was washed, and bound proteins were examined by immunoblot analysis.

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