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

Shashi Kant,1,2 Wojciech Swat,3 Sheng Zhang,4 Zhong-Yin Zhang,4 Benjamin G. Neel,5 Richard A. Flavell,6,7 and Roger J. Davis1,2,8

1Howard Hughes Medical Institute, University of Massachusetts Medical School, Worcester, Massachusetts 01605, USA; 2Program in Molecular Medicine, University of Massachusetts Medical School, Worcester, Massachusetts 01605, USA; 3Department of Pathology and Immunology, Washington University School of Medicine, St. Louis, Missouri 63110, USA; 4Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, Indiana 46202, USA; 5Ontario Cancer Institute, Toronto, Ontario M5G 1L7, Canada; 6Howard Hughes Medical Institute, Yale University School of Medicine, New Haven, Connecticut 06520, USA; 7Department of Immunobiology, Yale University School of Medicine, New Haven, Connecticut 06520, USA

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.

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

Supplemental material is available for this article.

Received June 13, 2011; revised version accepted August 26, 2011.

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 [Karlin 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 α (IKKα) and the subsequent degradation of IκBα, a critical step in NF-κB signaling [Sato et al. 2005; Shim et al. 2005].

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 (MAP3Ks) 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; Branco 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 cJun 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 [Branco 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 GTPase proteins—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 [MLK3^CRIB/ΔCRIB mice] and primary cultures of MEFs were prepared [Fig. 1C–F]. We found similar TNF-stimulated MAP kinase activation in control [MLK3^+/+] and mutant [MLK3^ΔCRIB/ΔCRIB] MEFs [data not shown]. This observation may reflect a redundant role of MLK3 in TNF-stimulated 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 NFκB pathway. This selective requirement of MLK2/3 for MAP kinase activation was also observed in studies of MLK2^+/−; 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^+/−; MLK3^ΔCRIB/ΔCRIB MEFs was markedly suppressed [Fig. 1I]. In contrast, no difference in TNF-stimulated IκBα degradation was detected between wild-type and MLK2^+/−; MLK3^ΔCRIB/ΔCRIB 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^−/−; MLK3^ΔCRIB/ΔCRIB 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^−/−; MLK3^ΔCRIB/ΔCRIB 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 GEFT and TIAM1 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−/−, and Yes−/− fibroblasts, but complementation analysis demonstrated that re-expression of Src was sufficient to restore TNF-stimulated Vav tyrosine phosphorylation (Fig. 4D). Both Src-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 TNF. 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 NeoR cassette. The floxed NeoR 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 MslI 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+/+CRIB, and Mlk3−/−CRIB 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−/−CRIB/−/− 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−/− MEFs (H) were treated without or with 10 ng/mL TNF or 100 ng/mL LPS. MAP kinase and IKKβ activation and the degradation of IκBα were examined by immunoblot analysis.
demonstrate that a Src/Vav pathway contributes to TNF-stimulated MAP kinase activation.

Requirement of PTPN1 for TNF-stimulated Rac activation

 Src 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 NFκB 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 of inhibitory tyrosine phosphorylation on Src [pY-527] in BMDMs isolated from control mice, but not from Ptpn1−/−mice (Fig. 5A). Moreover, TNF-stimulated Rac activation (Fig. 5B) and MAP kinase activation (Fig. 5C) was suppressed by PTPN1 deficiency. To confirm this observation, 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 MEts to treatment with TNF, including the expression of inflammatory cytokines and cell death. We found that TNF-treated Mlk2−/− Mlk3−/− MEts secrete markedly less interleukin 6 (IL6) than wild-type cells [Fig. 6A], consistent with reduced MAP kinase activation in MLK-deficient cells (Fig. 1G). Previous studies have established that the ERK, JNK, and p38 MAP kinase pathways can contribute to Il6 gene expression (Tuyt et al. 1999; Kim et al. 2004; Ventura et al. 2006), but increased IL6 expression caused by the Vav pathway is primarily mediated by JNK (Song et al. 1999). We found that Mlk2−/− Mlk3−/− MEts exhibit resistance to the cytotoxic effects of TNF [Fig. 6B,C]. In contrast, Tak1−/− cells were sensitive to TNF-mediated cytotoxicity [Fig. 6B,C] and failed to activate the NF-κB pathway [Fig. 3A]. Together, these data demonstrate that the MLK and TAK1 pathways mediate different TNF-dependent cellular responses.

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−/− Mlk3ΔCRIB/ΔCRIB] (Fig. 7A). Control studies using in vitro cultures of BMDMs confirmed that the MLK pathway is required for LPS-stimulated cytokine
and chemokine expression [Fig. 7B]. Together, these data establish that the MLK pathway contributes to inflammation.

Discussion

The biological response to TNF is mediated by the integrated actions of several signaling pathways. The NF-κB, MAP kinase, and caspase pathways are key mediators of the TNF response. TNF can also activate Rho family GTPases, including Rac/Cdc42 [Wojciak-Stothard et al. 1998; Kim et al. 1999; Puls et al. 1999; Hanna et al. 2001]. Previous studies have established that Rac/Cdc42 may contribute to the effects of TNF on actin cytoskeleton reorganization [Wojciak-Stothard et al. 1998] and the production of reactive oxygen species [Kim et al. 2007; Yazdanpanah et al. 2009]. Rac/Cdc42 therefore plays an important role in the cellular response to TNF. Our study demonstrates that TNF-stimulated Rac/Cdc42 activation also contributes to MAP kinase regulation [Fig. 1].

The mechanism of TNF-stimulated Rac/Cdc42 activation requires Vav [Fig. 4B], a guanine nucleotide exchange factor that is activated by tyrosine phosphorylation [Creso et al. 1997; Han et al. 1997] and can activate both Rac and Cdc42 [Abe et al. 2000; Liu and Burridge 2000]. TNF causes tyrosine phosphorylation and activation of Vav by Src family protein kinases [Fig. 4C,D] that are activated by dephosphorylation on the inhibitory C-terminal site of tyrosine phosphorylation [Fig. 5A]. Src activation requires the protein tyrosine phosphatase PTPN2 [Fig. 5A]. The related phosphatase PTPN2 can oppose the activation of Src and functions to suppress TNF-stimulated MAP kinase activation [van Vliet et al. 2005]. The balance of PTPN1 and PTPN2 can therefore determine the activation state of Src and, consequently, the extent of Vav-mediated Rac activation. PTPN2 interacts with TNF signaling complexes containing TRAF2 [van Vliet et al. 2005]. The mechanism of TNF signaling may therefore be mediated by sequestration of the inhibitory phosphatase PTPN2, by recruitment of the activating phosphatase PTPN1, or by coordinated regulation of both phosphatases [activity and/or substrate access]. Further studies are required to define this mechanism and to test whether Src activation might also require engagement of the Src SH3 domain. Indeed, it is possible that the Src-binding protein Sam68 [Fumagalli et al. 1994; Taylor and Shalloway 1994], which acts as an adapter in TNF receptor signaling complexes [Ramakrishnan and Baltimore 2011], links TNF signaling to the Src pathway. Nevertheless, the data reported here demonstrate that TNF can activate Rac by a PTPN1/Src/Vav pathway.

It is established that Rac/Cdc42 can cause MAP kinase activation [Coso et al. 1995; Minden et al. 1995]. The effects of Rac/Cdc42 may be mediated by binding to the CRIB motif on MLK3 [Teramoto et al. 1996]. 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 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 IκBα 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
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

Figure 4. TNF-stimulated Rac activation is mediated by Src and Vav. [A] Lysates prepared from BMDMs treated without or with 10 ng/mL TNF (15 min) were incubated with immobilized Rac1G15A. Bound proteins and the cell lysates were examined by immunoblot analysis using antibodies to GEFT, TIAM1, and VAV. [B] Wild-type (WT) and Vav1−/− Vav2−/− Vav3−/− BMDMs were treated without or with 10 ng/mL TNFa. Activated (GTP-loaded) Rac was isolated and quantitated by immunoblot analysis. The amount of Rac in cell lysates was measured by immunoblot analysis. [C] Lysates prepared from wild-type BMDMs treated without or with TNF were examined by immunoprecipitation with a control antibody (IgG) or with an antibody to Vav. The immunoprecipitates were examined by immunoblot analysis using antibodies to phosphotyrosine (pTyr) and Vav. The cell lysates were examined by probing with an antibody to α-Tubulin. [D] Src−/− Fyn−/− Yes−/− fibroblasts complemented with Src (Control) or without Src were treated without or with TNFa. Lysates were examined by immunoprecipitation with a control antibody (IgG) or with an antibody to Vav. The immunoprecipitates were examined by immunoblot analysis using antibodies to pTyr and Vav. The cell lysates were examined by probing with an antibody to α-Tubulin. [E,F] Wild-type and Vav1−/− Vav2−/− Vav3−/− BMDMs [E] or Control and Src−/− Fyn−/− Yes−/− fibroblasts [F] were treated without or with 10 ng/mL TNF. MAP kinase activation was examined by immunoblot analysis.

Figure 5. The protein tyrosine phosphatase PTPN1 contributes to TNF-stimulated MAP kinase activation. [A] Lysates prepared from wild-type (WT) and Ptpn1−/− BMDMs were treated without or with 10 ng/mL TNFa and examined by immunoblot analysis using antibodies to Src and pY527 Src. [B] Wild-type and Ptpn1−/− BMDMs were treated without or with 10 ng/mL TNF (15 min). Activated (GTP-loaded) Rac1 was isolated and quantitated by immunoblot analysis. The amount of Rac1 in cell lysates was measured by immunoblot analysis. [C] Wild-type and Ptpn1−/− BMDMs were treated without or with 10 ng/mL TNF. MAP kinase activation and the degradation of IκBα was examined by immunoblot analysis. [D] BMDMs were treated with solvent or with drugs that selectively inhibit PTPN1 and PTPN2 (30 min). The cells were then treated with or without 10 ng/mL TNFa (10 min). Cell lysates were examined by immunoblot analysis using antibodies to phospho-JNK, JNK, phospho-p38, p38α, phospho-ERK, and ERK2.
**Materials and methods**

**Mice**

C57BL/6j strain mice were obtained from The Jackson Laboratories. Mice with Mlk3 [Brancho et al. 2005], Ptpn1 [Klaman 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>cre</sup>/C0] were constructed using homologous recombination in LC1 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>B</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>B</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 TTCTCAGTGGAACACG-3', 5'-GTCATCACTTTCCTG-3', and 5'-CGCTCTTTATCGACTTTCGAC-3'. Wild-type and disrupted alleles of Mlk3 [Brancho et al. 2005], Ptpn1 [Klaman 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>cre</sup>/C0 allele [160 bp] was detected by PCR amplification of genomic DNA using the amplifiers 5'-CCCAACCCCAAAATAAGC-3' and 5'-CGGAGAAGCGCAGGAC-3'; the corresponding wild-type allele [180 bp] was detected using the amplifiers 5'-CCCACCTAAAATAAGC-3' and 5'-GGGAGAAGCGCGAGCAC-3'.

**Cell culture**

BMDMs were prepared [Das et al. 2009] and cultured in Dulbecco’s modified Eagle’s medium supplemented with 30% L929 supernatant [source of M-CSF], 20% fetal bovine serum, 100 U/mL penicillin, 100 μg/mL streptomycin, and 2 mM L-glutamine [Invirtogen].

Src<sup>−/−</sup>, Fyn<sup>−/−</sup>, Yes<sup>−/−</sup> fibroblasts complemented without and with Src [Klinghoffer et al. 1999] were obtained from the American Type Culture Collection [no. CRL2459 and no. CRL2498] and were cultured in Dulbecco’s modified Eagle’s medium supplemented with 10% fetal bovine serum, 100 U/mL penicillin, 100 μg/mL streptomycin, and 2 mM L-glutamine [Invirtogen].

Embryonic day 13.5 [E13.5] primary MEFs were cultured in Dulbecco’s modified Eagle’s medium supplemented with 10% fetal bovine serum, 100 U/mL penicillin, 100 μg/mL streptomycin, and 2 mM L-glutamine [Invirtogen]. Retroviral transduction assays [Lamb et al. 2003] were performed using the vectors pBABE-puro and pBABE-Rac1<sup>Q61L</sup>-puro. Transfection assays were performed.

Figure 6. The MLK pathway contributes to TNF-stimulated signal transduction. (A) Wild-type (WT) and Mlk<sup>2<sup>−/−</sup> Mlk<sup>3<sup>−/−</sup> MEFs were treated with 10 ng/mL TNFs. The amount of IL6 in the culture medium was measured by ELISA [mean ± SD; n = 6]. Statistically significant differences between wild-type and Mlk<sup>2<sup>−/−</sup> Mlk<sup>3<sup>−/−</sup> MEFs are indicated. [*] P < 0.05; [**] P < 0.01. (B, C) Wild-type, Mlk<sup>2<sup>−/−</sup> Mlk<sup>3<sup>−/−</sup> MEFs were treated with 10 ng/mL TNF [24 h]. Cell death was examined by measuring the presence of lactate dehydrogenase in the medium [B], and cell viability was measured by staining with crystal violet [C]. The data presented are the mean ± SD [n = 4]. Statistically significant differences between wild-type and Tak1<sup>−/−</sup> MEFs are indicated. [**] P < 0.01. No statistically significant differences between wild-type and Mlk<sup>2<sup>−/−</sup> Mlk<sup>3<sup>−/−</sup> MEFs were detected.

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.
RNA analysis

The expression of mRNA was examined by quantitative PCR analysis using a 7500 Fast Real-Time PCR machine (Applied Biosystems). The expression of mRNA was examined by quantitative PCR analysis using a 7500 Fast Real-Time PCR machine (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 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

Immunoblot analysis

Cell extracts were prepared using Triton lysis buffer (20 mM Tris at pH 7.4, 1% Triton X-100, 10% glycerol, 150 mM NaCl, 50 mM Tris at pH 8.0, 1% NP-40, 1 mM EDTA, 1% BME, and leupeptin). The lysates (50 μg of protein) were examined by protein immunoblot analysis. Immune-complexes were detected by enhanced chemiluminescence (ECL). Primary antibodies were obtained from Cell Signaling [Cdc42, phospho-IKKβ, IKKβ, MLK3, phospho-ERK1/2, phospho-JNK1/2, phospho-p38, Src, py^Y527^-Src, Vav1/2/3, Rac1/2/3, and lx/β], BD Pharmingen [JNK1/2], Millipore [Rac1, Vav, and phosphotyrosine], Santa Cruz Biotechnologies [ERK2, TAK1, and TIA1], Sigma (α-Tubulin), and Proteintech Group (GFP). The polyclonal antibody to MLK2 was purified from serum obtained from rabbits immunized with a peptide that corresponds to MLK2 amino acids 898–911 (CISPPSRPDTPESPG-amide) conjugated to keyhole limpet hemocyanin (Zymed).

Immunoprecipitation

Cell extracts were prepared using lysis buffer (150 mM NaCl, 50 mM Tris at pH 8.0, 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). Immune-complexes 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). The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01). The BMDMs were treated with and without 100 ng/mL LPS [24 h]. The amount of TNFα, CCL3/MIPα, and CCL5/RANTES in the culture medium was measured by ELISA (mean ± SD; n = 6). Statistically significant differences between wild-type and MLK-deficient BMDMs are indicated. (*P < 0.05; **P < 0.01).
GSH-Sepharose for 1 h at 4°C. The GSH-Sepharose was washed, and bound proteins were examined by immunoblot analysis.

Acknowledgments

We thank S. Ghosh and D.S. Dorow for providing mice; K. Burridge and I.S. Gutfkind for plasmids; R. Kaushik, N. Kennedy, C. Morel, G. Sabio, C. Staden, and A. Vertii for advice; V. Benoit, L. Lesco, J. Reilly, H.-F. Hung, and T. Barrett for technical assistance; and K. Gemme for administrative assistance. These studies were supported by grants from the National Institutes of Health (CA065861 to R.J.D., AI06107 to W.S., and CA126937 to Z.-Y.Z.). Core facilities at the University of Massachusetts used by this study were supported by the NIDDK Diabetes and Endocrinology Research Center (DK52530). W.S. is a Scholar of the Leukemia and Lymphoma Society. R.J.D. and R.A.F are Investigators of the Howard Hughes Medical Institute.

References


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

Shashi Kant, Wojciech Swat, Sheng Zhang, et al.

*Genes Dev.* 2011, 25:
Access the most recent version at doi:10.1101/gad.17224711

---

**Supplemental Material**
http://genesdev.cshlp.org/content/suppl/2011/10/06/25.19.2069.DC1

**References**
This article cites 52 articles, 24 of which can be accessed free at:
http://genesdev.cshlp.org/content/25/19/2069.full.html#ref-list-1

**License**
Freely available online through the Genes & Development Open Access option.

**Email Alerting Service**
Receive free email alerts when new articles cite this article - sign up in the box at the top right corner of the article or [click here.](http://genesdev.cshlp.org/content/25/19/2069.full.html#ref-list-1)