Mesodermal patterning defect in mice lacking the Ste20 NCK interacting kinase (NIK)

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SUMMARY

We have previously shown that the Drosophila Ste20 kinase encoded by misshapen (msn) is an essential gene in Drosophila development. msn function is required to activate the Drosophila c-Jun N-terminal kinase (JNK), basket (Bsk), to promote dorsal closure of the Drosophila embryo. Later in development, msn expression is required in photoreceptors in order for their axons to project normally. A mammalian homolog of msn, the NCK-interacting kinase (NIK) (recently renamed to mitogen-activated protein kinase kinase kinase kinase 4; Map4k4), has been shown to activate JNK and to bind the SH3 domains of the SH2/SH3 adapter NCK. To determine whether NIK also plays an essential role in mammalian development, we created mice deficient in NIK by homologous recombination at the Nik gene. Nik⁻/⁻ mice die postgastrulation between embryonic day (E) 9.5 and E10.5. The most striking phenotype in Nik⁻/⁻ embryos is the failure of mesodermal and endodermal cells that arise from the anterior end of the primitive streak (PS) to migrate to their correct location. As a result Nik⁻/⁻ embryos fail to develop somites or a hindgut and are truncated posteriorly. Interestingly, chimeric analysis demonstrated that NIK has a cell nonautonomous function in stimulating migration of presomitic mesodermal cells away from the PS and a second cell autonomous function in stimulating the differentiation of presomitic mesoderm into dermomyotome. These findings indicate that despite the large number of Ste20 kinases in mammalian cells, members of this family play essential nonredundant function in regulating specific signaling pathways. In addition, these studies provide evidence that the signaling pathways regulated by these kinases are diverse and not limited to the activation of JNK because mesodermal and somite development are not perturbed in JNK1-, and JNK2-deficient mice.

Key words: Ste20 kinase, NCK interacting kinase (NIK), misshapen, Gastrulation, knockout, N-terminal JUN kinase (JNK), Mouse

INTRODUCTION

Ste20 kinases constitute a large family of protein kinases that are best known for their roles in activating the JNK MAP kinase pathway and in the regulation of the actin cytoskeleton (Kyriakis, 1999). Based on sequence similarity to the kinase domain of the yeast Ste20 kinase protein, two broad families of Ste20 kinases have been identified in mammalian cells and lower organisms, the p21 activated protein kinase (PAK) and the germinal center kinase (GCK) families (Kyriakis, 1999; Manser and Lim, 1999). However, despite the distant homology between their kinase domains, these two kinase families exhibit many differences in both regulation and function. For example, PAKs, unlike GCK family kinases, possess a CRIB motif and therefore bind and are regulated by Rho family GTPases (Burbelo et al., 1995; Martin et al., 1995). In addition, unlike PAKs which have a C-terminal kinase and an N-terminal regulatory domain, GCK family members contain an N-terminal kinase and a C-terminal regulatory domain whose function is distinct from the regulatory domain of PAK (Kyriakis, 1999; Su et al., 1997). As a result, it has now been proposed to classify PAK and GCK family members into two distinct protein kinase families (Kyriakis, 1999).

At least 20 different GCK family members have been identified in mammalian cells so far. These GCK members can be further subdivided into 5 subgroups based on similarities in sequence, structure and function (Kyriakis, 1999). Although the specific function served by individual GCK members or by subgroups of GCK in mammalian cells is still poorly defined, most studies have focussed on the role of these kinases in activation of the JNK MAP kinase pathway. With respect to JNK activation, GCK family members can be subdivided into two broad groups, group 1 and group 2 (Kyriakis, 1999). Group 1 kinases activate JNK, and include GCK, GCK related (R), hematopoietic progenitor kinase 1 (HPK1) and NIK (Diener et al., 1997; Hu et al., 1996; Pombo et al., 1995; Su et al., 1997). All group 1 kinases share a conserved C-terminal regulatory domain that may function to couple these kinases to downstream MAP kinase kinase kinase (MAP3Ks) (Su et al., 1997). Less is known about the second group of GCK, which...
includes Ste20-like oxidant stress kinase 1 (SOK1), mammalian sterile20 like 1 and 2 (MST1 and 2) and lymphocyte oriented kinase (LOK) (Creasy and Chernoff, 1995a; Creasy and Chernoff, 1995b; Kuramochi et al., 1997; Pombo et al., 1997). Members of this group contain a C-terminal domain that is significantly different from those of group 1 members and as yet members of this group have not been linked to activation of a signaling pathway (Kryriakis, 1999).

Recent experiments in both Drosophila and C. elegans have confirmed an essential role for one member of the GCK family, NIK, in both JNK activation and development in a biologically relevant system (Su et al., 1998; E. Hedgecock and X. Zhu personal communication). We have placed the Ste20 kinase encoded by misshapen (msn), the Drosophila homolog of mammalian NIK, genetically upstream of the JNK MAP kinase pathway in Drosophila (Su et al., 1998). The failure to activate JNK in Drosophila leads to embryonic lethality due to defects in embryonic dorsal closure; in embryos mutant for components of the JNK pathway the lateral epithelial sheets fail to elongate and migrate dorsally (Noselli, 1998). A number of signaling molecules that are critical for stimulating dorsal closure and JNK activation in Drosophila can now be ordered on a signaling pathway. Msn likely functions as a MAP kinase kinase kinase (M4K) and activates the JNK pathway by activating a yet to be defined DM3K. A DM3K would likely phosphorylate and activate the JNK kinase encoded by activating a yet to be defined DM3K. A DM3K would likely phosphorylate and activate the JNK kinase encoded by hemipterosis (hep) (Glise, 1995), which in turn phosphorylates and activates Drosophila JNK, encoded by basket (bsk) (Riesgo-Escovar, 1996; Sluss et al., 1996). DJNK phosphorylates and activates DJun, which in turn cooperates with DFos to stimulate transcription of dpp, a member of the transforming growth factor-β family (Glise, 1997; Hou, 1997; Kockel, 1997; Riesgo-Escovar and Hafen, 1997a; Riesgo-Escovar and Hafen, 1997b). In addition to its role in dorsal closure, Msn also couples Fizzled (Fz) and Dishevelled (Dsh) to JNK activation in the planar polarity pathway; msn mutants show defects in epithelial planar polarity in both the eyes and wings due to defective JNK activation (Mlodzik, 1999; Paricio et al., 1999). In C. elegans, mig-15, the homolog of mammalian NIK and Drosophila msn, has also been found to be an essential gene in development. mig-15 mutants have a number of developmental defects including defects in Q neuroblast migration and muscle arm targeting, although it is not yet clear whether these defects are due to defective activation of JNK (E. Hedgecock and X. Zhu personal communication).

In addition to activating JNK, NIK contains PX motifs that mediate its interaction with the SH3 domains of Nck (Nck1; Su et al., 1997). Nck is a ubiquitously expressed protein composed of one SH2 and three SH3 domains (Lehman et al., 1990). Adapter molecules like Nck are proposed to regulate signaling pathways downstream of tyrosine kinases by coupling catalytic subunits, bound to their SH3 domains, to phosphotyrosine-containing proteins that interact with their SH2 domains (Pawson and Nash, 2000; Schlessinger, 1994). Recent experiments in Drosophila have shed light on some functions of Nck in mammalian cells and provide evidence that Ste20 kinases are downstream effectors of Nck. A Drosophila homolog of mammalian Nck encoded by dreadlock (dock) is required for correct targeting of photoreceptor axons (Garrity et al., 1996). Drosophila Pak has been shown to be one of the key targets for regulation by dock in this pathway and an interaction between Pak and the SH3 domains of Dock is required for Dock regulation of R cell axon guidance and targeting (Hing et al., 1999). We and others have found that Msn also binds the SH3 domains of Dock and that expression of Msn in photoreceptors is also required for the correct targeting of photoreceptor axons (Ruan et al., 1999; Su et al., 2000). In mammalian cells, NCK couples NIK to tyrosine phosphorylated p62 Dok in Eph-stimulated cells, and this interaction is important for the EphB1 and EphB2 receptors to activate NIK kinase activity as well as JNK and integrins (Becker et al., 2000).

Owing to the important roles of msn, dock and mig-15 in Drosophila and C. elegans development, we determined whether NIK also performs an essential role in mammalian development by creating mice with a targeted disruption of the NIK locus. Mice containing a homozygous loss-of-function of NIK die around E9.5. The most obvious defect in NIK−/− embryos is the failure of mesodermal cells derived from the anterior end of the primitive streak to migrate away from the streak. As a result, NIK−/− embryos are truncated posteriorly and somitogenesis is greatly affected. The most affected embryos have no somites, while less affected mutants have 1-2 pairs of somites, compared to the 10-15 somites found in control littermates. Interestingly, the failure of mesodermal cells to migrate away from the PS is not due to loss of NIK in these cells because chimeric analysis showed that presomitic mesoderm arising from NIK−/− ES cells migrated to the appropriate position in the chimeric embryos. Thus, NIK is most probably required in the PS to regulate the production of factors that are required for proper cell migration. In addition, NIK also acts in presomitic mesoderm to stimulate its differentiation into somites, because NIK−/− ES cells failed to differentiate into dermomyotome in the chimeric embryos. These findings provide the first evidence for an essential function of a Ste20 kinase in mammalian development.

MATERIALS AND METHODS

Gene targeting

A targeted mutation was introduced into the murine Nik gene by homologous recombination in embryonic stem cells as described previously (Joyner, 1993). The Nik genomic DNA was isolated by screening a 129 mouse genomic library (Stratagene) with the Nik cDNA. A 15 kb genomic Nik clone containing the 5′ start ATG of Nik was isolated, subcloned into Bluescript KS, and a restriction map was constructed. The 5′ homology arm of the targeting vector was the 4 kb KpnI-Apal murine genomic fragment, which was subcloned into targeting vector pPNT (Tubulewicz et al., 1991). The 3′ homology fragment was a 3.5 kb Smal-KpnI genomic fragment. In the final targeting vector an Apal fragment in the Nik genomic DNA is deleted and replaced with a PGK-neo cassette. This removes part of exons VI and all of exon VII of the kinase domain is removed. These exons encode subdomain VIII and IX in the kinase domain (at amino acid 165 of Nik) and therefore the targeted Nik allele lacks critical residues that are essential for a functional kinase (Fig. 1). Following electroporation, G418 and gancyclovir-resistant ES clones were selected and successful targeting of the Nik locus was determined by PCR (4/300). The primer pairs used for PCR genotyping the 5′ arm were: Nik exon primer (sense) 5′-GAGATCAGACGCCTCTGTTCCACA-3′ and an antisense primer to the untranslated region in pGK 5′-GAGATCABGACGCCTCTGTTCACA-3′; for the 3′ arm:
sense primer to pGK promoter 5’ GTCA CGGTG GATG GAG AAA-TGTG 3’ and an antisense primer to a Nik intron 5’ GCAA GCAG GA GTTAAGTTAGCCTGCAG 3’. Aggregation chimeras between the targeted ES cell and BALB/c morulas were generated and founders were bred to 129Svev mice or outbred to CD-1 mice. Transmission of the targeted ES clone was determined by coat color analysis and genotyping of offspring. The targeted mutation was propagated in a Swiss Webster genetic backgrounds. Mutant analysis and genotyping of offspring. The targeted mutation was propagated in a Swiss Webster genetic backgrounds. Mutant Nik-/+ homozygous embryos were obtained by crossing Nik+/- mice and Nik-/- mice were determined by their characteristic phenotype or by PCR analysis as described in Fig. 1.

In situ hybridization
Whole-mount embryo in situ hybridization was performed as described using riboprobes as indicated (Swiatek et al., 1994). To section whole-mount stained embryos, after postfixing in 4.0% formaldehyde overnight, embryos were incubated in 30% sucrose/PBS for 2 days. The embryos were embedded in paraffin wax and sectioned at between 10 and 20 μm. Sections were then mounted onto glass slides and after dewaxing were photographed. The probes used for whole-mount in situ staining were Shh (Echelard et al., 1993), Brachury (Herrmann, 1991), Mox1 (Candia et al., 1992), HNF3β (Ang et al., 1993), fgf4, Tbx6 (Chapman et al., 1996), Otx2 (Simeone et al., 1993), En1 (Davis and Joyner, 1988), Glx2 (Bouillet et al., 1995), and lim1 (Barnes et al., 1994). The Nik probe corresponds to nucleotides 1347-1845 in full length Nik. This region is located between the kinase domain and C-terminal domain and is the region least conserved between Nik and other Ste20 kinases.

Generation of Nik-/- ES cells
Nik-/- ES cells were generated from Nik K+/- ES cells by culturing in high concentration of G418 (1.4 mg/ml; Mortensen et al., 1992). G418 resistant ES cells were expanded and genotyped by Southern blot analysis. 2 Nik-/- ES cell lines were obtained out of 35 clones examined.

Generation of chimeric mice and β-galactosidase staining
Chimeric embryos were generated by injecting 8 or 14 Nik-/- ES cells into ROSA lacZ+/- blastocysts. Injected blastocysts were surgically transferred into the uteri of pseudopregnant CD-1 foster mothers and chimeric embryos were dissected at E9.5, fixed and stained for β-galactosidase as described above.

RESULTS
Targeted disruption of the Ste20 kinase Nik in ES cells by homologous recombination
To create mice with a targeted disruption of the Ste20 kinase Nik, we generated the targeting construct pNikneo in the vector pPNT (Tybulewicz et al., 1991). This construct contains 9 kb of Nik genomic sequence in which half of exon 6 and all of exon 7 of the kinase domain are replaced by a PGKneo cassette. These exons encode for subdomains VIII and IX of the Nik kinase domain (at amino acid 165 of the Nik protein) and therefore the targeted Nik allele lacks residues that are essential for a functional kinase domain. To prevent potential read through transcription from the PGK promoter and to introduce stop codons in all 3 reading frames, PGK-neo was cloned in an opposite orientation to that of NIK. This would be predicted to truncate the coding region after subdomain VI of the kinase domain at amino acid 164 of NIK and would disrupt all major isoforms of NIK that have been described (Fig. 1A). We confirmed that Nik-/+ mice are unlikely to express either a truncated or alternatively spliced NIK protein because northern analysis did not detect binding of a Nik cDNA probe to RNA derived from Nik-/- fibroblasts or ES cells, whereas NIK expression was easily detected in wild-type cells (figure 1D). Four ES clones containing a targeted Nik mutation were identified by screening for the 5´ and 3´ insertion sites by PCR and by Southern blot analysis (Fig. 1B and data not shown).

Morula aggregation was performed for three of the four clones with Balb/c mice. All of the clones generated high-degree chimerisms and when crossed with CD-1 mice generated agouti pups indicating germline transmission. Germline transmission was confirmed by both PCR and Southern blot analysis (Fig. 1C and data not shown). In analysis of the mice, identical results were obtained from all three lines and therefore for simplicity the results described are from pooled data from all 3 lines.

Nik-/- mice die embryonically between day 9.5 and day 10.5
All heterozygous progeny were viable and fertile and did not manifest any overt phenotypes. To determine whether Nik-/- mice were viable, Nik+/- mice were crossed and litters were genotyped 3 weeks after birth. No homozygous Nik mutant littermates were present (0/37) as determined by both PCR and Southern blot analysis (Fig. 1C and data not shown). Since no perinatal lethality was observed in these litters, these findings indicate that Nik is a recessive embryonically lethal allele.

To determine the point at which Nik-/- mice die, embryos from a cross between Nik heterozygous mice were dissected at different gestational stages. Analysis of E10.5 embryos revealed that about 1/4 of the decidua were much smaller, very necrotic and were partially resorbed whereas the remaining were phenotypically normal. To genotype the normal and abnormal embryos, embryos were dissected away from maternal tissues and genotyped by PCR (data not shown). This analysis demonstrated that all of the abnormal embryos were Nik-/-, while the remaining normal embryos were either Nik+/- or Nik+/+ at the expected ratio of 1:2. Thus, these findings, when coupled with the finding that E9.0 Nik-/- embryos have a beating heart, indicate that homozygous mutant Nik embryos die about 9.5 days after implantation.

To determine whether the expression pattern of Nik may give an insight into the lethality of Nik mutants, the expression pattern of Nik mRNA in both E7.5 and E8.5 embryos was determined. Whole-mount in situ hybridization revealed that Nik transcripts are widely expressed at both time points (figure 1E). The staining for Nik mRNA was specific because the same probe did not give a signal in similarly aged Nik-/- embryos and a similarly made sense probe did not give a signal in wild-type embryos (data not shown).

Nik mutant embryos are truncated posteriorly and lack somites and presomitic mesoderm
Morphological and histological analysis of E8.5-9.0 Nik-/- embryos demonstrated that Nik-/- embryos exhibited a distinct
phenotype. \( \text{Nik}^{+/+} \) embryos appeared developmentally retarded and were smaller than control embryos (compare Fig. 2A and B). The most obvious defect in the \( \text{Nik} \) mutants was the absence of somites in most E8.5-9.0 \( \text{Nik}^{-/-} \) embryos, while comparably staged wild-type and heterozygous \( \text{Nik} \) littermates developed between 10 and 15 somites (compare Fig. 2C and E with D and F). While occasional \( \text{Nik} \) mutants (<10%) formed 1-2 somites anteriorly, no posterior somites were seen in any of the \( \text{Nik} \) mutants. In addition, \( \text{Nik} \) mutants failed to elongate posteriorly and a large mass of cells protruded from the region of the posterior primitive streak (PS) in most E8.5 \( \text{Nik}^{-/-} \) embryos (Fig. 2A,C). This led to a truncated body axis that connected a relatively normal anterior neural fold-like structure to a relatively normal allantoid. These findings suggested that the major defect in \( \text{Nik} \) mutants is the failure to form normal mesodermal precursors that give rise to presomitic mesoderm as well as the mesoderm that contributes to the elongation of the body axis.

A defect in migration of mesodermal precursors away from the PS could account for both the failure to form presomitic mesoderm and the accumulation of cells in the \( \text{Nik} \) mutants (Fig. 2). Alternatively, a defect in ingress of epiblasts into the streak could account for the \( \text{Nik} \) mutant phenotype. In order to distinguish between these two possibilities and to determine the origin of the cells stuck in the region of the PS in \( \text{Nik}^{-/-} \) embryos, expression of two T-box transcription factors, \( \text{Tbx6} \) and \( \text{brachyury} \) (\( T \)), was examined. Mesodermal tissue arises during gastrulation when epiblast cells move through the primitive streak forming a new layer of mesodermal cells located between the epiblasts and the outer visceral endodermal cells, beginning at E6.5 (Beddington, 1998; Beddington and Robertson, 1999). Previous experiments have indicated that induction of the T-box gene family of DNA binding transcription factors plays a central role in specifying the transition of epiblast to presomitic mesoderm (Yamaguchi et al., 1999). More recent data has shown that \( T \) gene expression is induced in epiblasts entering the streak via a Wnt3A stimulated pathway and brachyury in turn induces...
either directly or indirectly the expression of Tbx6 (Yamaguchi et al., 1999). While Tbx6 was expressed in cells adjacent to the PS in both control and Nik−/− embryos, it was also expressed in the large mass of cells that accumulated adjacent to the PS in E8.5 Nik−/− embryos (figure 3). In contrast, T, which is normally expressed in the PS, notochord and head process, and whose expression is normally turned off after cells leave the streak, was not expressed in the extra cells that accumulate in Nik−/− embryos. These findings indicate that the extra cells that accumulate in Nik−/− embryos have ingressed through the PS and have acquired a mesodermal fate. Since these extra cells in Nik−/− embryos express Tbx6 but not T, they are most likely early presomitic mesoderm cells that fail to migrate to their appropriate paraxial position.

To confirm that Nik mutants have decreased presomitic mesoderm, E8.5 Nik mutants were stained for mox1 (meox1) a homeobox gene whose expression is restricted to presomitic mesoderm and developing somites (Candia et al., 1992). Whole-mount in situ hybridization revealed that the Mox1 transcript was markedly decreased in Nik mutants when compared to control embryos; Mox1 expression was limited to the anterior paraxial region of the Nik−/− embryos in a more restricted area when compared to control embryos (Fig. 3). The extra cells that accumulate in the PS in Nik mutants do not express Mox1 and therefore are likely arrested as presomitic mesodermal cells.

Previous studies have demonstrated that different signals are required for the generation of the first 7-9 somites up to the level of the proximal forelimb and for the remaining somites (Takada et al., 1994; Chapman and Papaioannou, 1998). For example, Wnt3a is required for the development of the more posterior somites, but is not required for the generation of the first 7-9 somites (Takada et al., 1994). Thus, our findings suggest that NIK is most important for generating presomitic mesoderm that develops into the more posterior somites. However, NIK likely plays other roles that are important for the organization of presomitic mesoderm into somites, because even when presomitic mesoderm is present, it is rarely found to organize into somites (Figs 2 and 3 and data not shown).

**Mesodermal precursors other than presomitic mesoderm are present in Nik−/− embryos**

Fate mapping studies have demonstrated that several different types of mesodermal cells arise from the PS and the specificity of these cells is determined by the position along the streak into which the epiblasts enter (Tam and Behringer, 1997). Epiblasts that migrate early through the posterior primitive streak are destined to become extraembryonic mesoderm, blood vessels, and cardiac mesoderm. Epiblast cells that migrate through the midstreak region are destined to become lateral and intermediate mesoderm, while epiblasts migrating through the anterior PS are destined to become presomatic mesoderm and hindgut endoderm. The most anterior region of the streak is the node or organizer and epiblasts that migrate through the node give rise to the notochord and the fore and midgut endoderm.

To determine whether defects in mesodermal development
were confined to the presomitic mesoderm or whether development of other mesodermal compartments and endoderm were affected in the \textit{Nik} mutants, \textit{Nik}\textsuperscript{-/-} embryos were analyzed morphologically and for a number of different markers expressed in mesodermal tissues of specific origin. We found that \textit{Nik}\textsuperscript{-/-} embryos formed extraembryonic mesodermal tissue such as the allantois, which eventually fuses with the chorion to form part of the placenta (see Fig. 2). In addition, \textit{Nik} mutant embryos formed blood vessels. We used \textit{Tie2-lacZ} expression as a marker to label endothelial cells (Schlaeger et al., 1997). Although the vasculature is disorganized in E9.5 \textit{Nik} mutants when compared to wild-type embryos, endothelial cells are clearly visible in the yolk sac, head process and in the midline in E9.5 \textit{Nik}\textsuperscript{-/-} embryos (Fig. 4). \textit{Nik}\textsuperscript{-/-} embryos also contain a heart (Fig. 4). Cardiac mesoderm is formed and organizes into a functional organ in the \textit{Nik}\textsuperscript{-/-} embryo as is evident by a beating heart in E9.0 \textit{Nik}\textsuperscript{-/-} embryos. Thus, these findings indicate that mesoderm that arises from the posterior and middle region of the PS is specified normally.

To determine whether structures derived from the anterior end of the streak, specifically the node and notochord are normal in \textit{Nik} mutants, we examined the expression of \textit{sonic hedgehog} (\textit{Shh}). \textit{Shh} has previously been shown to be expressed in the notochord, hindgut and the ventral midline of the brain (Echelard et al., 1993). In control embryos, \textit{Shh} expression was visible throughout the entire anteroposterior axis (Fig. 4). In contrast, \textit{Shh} expression was visible only in the notochord and head process in the NIK mutants (Fig. 4). Expression of \textit{Shh} was not visible posteriorly in the NIK mutants in the region corresponding to the hindgut in wild-type

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**Fig. 3.** Whole-mount in situ hybridization analysis of E8.5 \textit{Nik}\textsuperscript{-/-} embryos for markers of paraxial mesoderm. E8.5 control (cont) or \textit{Nik} homozygous mutant embryos (\textsuperscript{-/-}) stained for \textit{Mox1}, Brachury (\textit{T}) and \textit{Tbx6} as indicated. All panels are lateral views except D and H which are dorsal views. N, notochord; PS, primitive streak. \textit{mox1} staining cells are markedly decreased in the mutant and confined to the anterior domain of the embryo. The extra mass of cells that accumulate adjacent to the PS in the mutant embryos (marked with an arrowhead) do not stain for \textit{T} or \textit{mox1}, but do stain for \textit{Tbx6}.

**Fig. 4.** Analysis of E8.5 and E9.5 \textit{Nik}\textsuperscript{-/-} embryos for regional-specific markers of mesodermal differentiation. (A,B) Whole-mount staining for \textit{b}-galactosidase, of embryos that are transgenic for \textit{Tie2/lacZ} alone (A) or transgenic for \textit{Tie2/lacZ} and homozygous mutant for \textit{Nik} (B). Although the vasculature is disorganized in \textit{Nik}\textsuperscript{-/-} embryos, \textit{b}-galactosidase staining is clearly visible throughout the embryo. In addition, a heart is visible in \textit{Nik} mutants indicating that mesoderm that gives rise to cardiac mesoderm forms normally in \textit{Nik}\textsuperscript{-/-} embryos. Whole-mount staining of wild-type (C) or \textit{Nik}\textsuperscript{-/-} embryos (D) for \textit{sonic hedgehog} (\textit{Shh}). Lateral views are shown in C and D. While \textit{Nik}\textsuperscript{-/-} embryos have a notochord, they lack staining in the posterior part of embryos which corresponds to hindgut endoderm.
Mesodermal patterning in Nik mutant mice

Fig. 5. (A) Morphology, histologic analysis and gene expression of E7.5 Nik−/− embryos. In all panels anterior is to the left and posterior is to the right. (a,b) Whole-mount of normal and mutant E7.5 embryos. Nik−/− embryos (b) show extra cells projecting into the amniotic cavity (arrow) not present in wild type (a). Sagittal section of normal (c) and mutant (d) embryos. Thickening of the PS due to the accumulation of cells is visible in mutant embryos (d). (e,f) Whole-mount staining of normal and mutant embryos for T. (g,h) Sagittal section of embryos shown in e and f and a transverse section (i) of a mutant embryo stained for T. The extra cells that accumulate in the PS do not express T. ac, amniotic cavity; al, allantois; PS, primitive streak.

(B) Whole-mount staining of E8-8.5 control and mutant embryos for lim1, Hnf3β and Fgf4. Cells that accumulate in the PS in mutant embryos (−/−) stain positive for lim1 indicating that they have differentiated into mesoderm. The anterior end of PS in mutant embryos (−/−) stain positive for Hnf3β indicating the PS is regionalized normally in mutant embryos.
embryos. In addition, in some mutants there was discontinuous staining in the region between the notochord and head process. These findings, when coupled with the staining for T shown in Fig. 3, suggest that axial mesoderm is formed normally in Nik\(^{-/-}\) embryos. The failure of Shh to stain gut endoderm suggests that precursor cells destined to form these structures are either not specified or are specified but fail to migrate to their proper location. It is intriguing that cells destined to form hindgut, but not mid and foregut endoderm, derive from common epiblast precursors that also give rise to presomatic mesoderm (Dufort et al., 1998). Thus, a defect in migration of a common meso/endoderm precursor could account for the decrease in both presomitic mesoderm and hindgut endoderm in Nik\(^{-/-}\) embryos.

**Nik** mutant embryos have a thickened anterior primitive streak

If failure of presomitic mesoderm to migrate away from the PS accounts for the defect in presomitic mesoderm and hindgut endoderm, thickening of the PS should be visible early in development. To evaluate the PS, midstreak E7.5 embryos and control embryos were dissected and sectioned in their decidua. At this early time, Nik\(^{-/-}\) embryos could clearly be distinguished from wild-type embryos by thickening on their posterior side (compare Fig. 5, A and B). In comparison to Nik\(^{+/+}\) and Nik\(^{-/-}\) embryos, Nik\(^{-/-}\) embryos contained an extra mass of cells on their posterior side that formed an indentation into the proamniotic cavity which in transverse sections were revealed as a thickening of the mid to anterior region of the PS (compare Fig. 5A, A and C with B and D).

To further examine the PS in Nik mutants, expression of several markers were evaluated by in situ hybridization. At E7.5, the T gene normally marks cells of the PS and axial mesoderm (Fig. 5A, c; Wilkinson et al., 1990). In Nik\(^{-/-}\) embryos, T is expressed in the bulge of cells adjacent to amniotic cavity along the proximodistal axis as well as in cells anterior to the PS. T is not expressed in the more posteriorly localized cells that accumulate in the PS in the Nik\(^{-/-}\) embryos (Fig. 5A f, h and i).

We next determined whether the cells in Nik\(^{-/-}\) embryos that accumulate in the PS and fail to stain for T express lim1 (Lhx1). lim1 is expressed at high levels in mesodermal cells migrating away from the PS (Barnes et al., 1994). Therefore, if the T-negative cells that accumulate in Nik\(^{-/-}\) embryos have undergone a transition to mesoderm they would be expected to stain for lim1. Consistent with this idea, we found that these cells do express lim1 RNA (Fig. 5B). These findings, when taken with the results in Fig. 2, indicate that the extra cells that accumulate in Nik\(^{-/-}\) embryos have undergone an epiblast to mesoderm transition.

Nik mutants were also examined for Hnf3B (Foxa2) expression to determine whether the anterior half of the PS was correctly patterned, as patterning defects could account for the lack of presomitic mesoderm and hindgut endoderm in the Nik mutants; Hnf3B is normally expressed in cells at the anterior end of the PS (Ang et al., 1993). We found that Hnf3B is expressed in cells in the anterior half of the bulging PS in Nik mutant embryos indicating that defects in patterning of the PS do not account for the phenotype in Nik\(^{-/-}\) embryos (Fig. 5B).

**Patterning of the anterior neuroectoderm is normal in the NIK mutants**

To assess whether patterning of the anterior neuroectoderm is normal in Nik mutants, E8.5 control and Nik\(^{-/-}\) embryos were stained with engrailed 1 (En1), Krox20 (Egr2), Otx2 and Gbx2. En1, normally expressed at the midbrain hindbrain boundary (Davis and Joyner, 1988) and, Otx2, normally expressed in the prospective forebrain and midbrain (Simeone et al., 1993), are expressed at relatively normal levels and in the correct distribution in Nik\(^{-/-}\) embryos (Fig. 6). In addition, Gbx2, which is expressed in the anterior hindbrain as well as distally through the PS to the posterior end of the embryo, and Krox20 which is expressed in rhombomeres 3 and 5 are expressed in a normal distribution in the Nik\(^{-/-}\) embryos (Fig. 6). These findings indicate that patterning of the anterior neuroectoderm is not perturbed in Nik\(^{-/-}\) embryos.

**Chimera analysis with Nik\(^{-/-}\) ES cells**

The above data suggest that the major abnormality in Nik mutant embryos is the failure of committed mesodermal cells to migrate away from the PS. In an attempt to directly demonstrate a defect in migration of Nik\(^{-/-}\) cells, and to confirm that the defect in cell migration is cell autonomous, we generated Nik\(^{-/-}\) ES cells. Nik\(^{-/-}\) ES cells were then used to aggregate ROSA26 lacZ mice. The ROSA lacZ transgene is ubiquitously expressed throughout early to mid gestational development and has been shown to be a good marker for distinguishing mutant and wild-type cells in chimeric embryos (Friedrich and Soriano, 1991). In these experiments, Nik\(^{-/-}\) ES cells lack β-galactosidase and do not stain while wild-type cells express β-galactosidase and stain blue. We obtained embryos with variable degrees of chimerism with Nik\(^{-/-}\) ES cells (Fig. 7). High degree chimerisms resulted in an embryonic phenotype that was similar to the Nik knockout (Fig. 7A). However, analysis of embryos with lower amounts of chimerism (Fig. 7B) failed to demonstrate the accumulation of Nik\(^{-/-}\) ES cells in regions adjacent to the primitive streak (data not shown). Nik\(^{-/-}\) ES cells also contributed to hindgut (Fig. 7K,L). Thus, these findings indicate that migration of Nik\(^{-/-}\) ES cells away from the PS is normal in chimeric embryos.

We next evaluated the contribution of Nik\(^{-/-}\) ES cells to somites. Each somite begins as an epithelial sphere with a centrally arranged lumen of mesenchymal cells called a somitocoel (reviewed by Keynes and Stern, 1988; Tam and Trainor, 1994). In response to signals arising from surrounding structures the somitocoel eventually matures into three distinct compartments, which are, the sclerotome, myotome and dermatome. The sclerotome, which gives rise to the ribs and vertebrae, forms from the medial ventral half epithelium of the somitocoel that has reacquired a mesenchymal phenotype, as well as from the mesenchymal cells in the center of the somitocoel. The dorsolateral epithelium that remains forms a cap that is termed the dermomyotome. Cells of the dermomyotome ultimately give rise to the dermis of the dorsal skin and to myotome cells which form the hypaxial and epaxial muscles of the trunk and limbs.

We found that mesoderm arising from Nik\(^{-/-}\) ES cells migrated to the appropriate position in the chimeric embryos (Fig. 7). Nik\(^{-/-}\) ES cells contributed equally well as wild-type ES cell to presomitic mesoderm and hindgut endoderm (Fig. 7K,L and data not shown). However, in contrast to the wild-
type cells, that were incorporated into the dermomyotome. *Nik*−/− ES cells were excluded from the segmented dermomyotome in all embryos examined (7/7) (Fig. 7C-J). The inability of *Nik*−/− ES cells to contribute to the dermomyotome layer of the somite is likely specific because *Nik*−/− ES cells contributed to and competed equally well with wild-type cells in all other tissues examined including the neural tube and heart (Fig. 7L and data not shown).

To evaluate somites at different stages of differentiation in chimeric embryos, additional sections from control and chimeric embryos were stained for β-galactosidase. Somites develop over time in a rostral to caudal progression, and thereby the more rostrally localized somites have the opportunity to undergo further differentiation towards a mature somite compared to the newly formed somites that are located caudally. Examination of somites at the early somitocoel stage of somite development demonstrated that *Nik*−/− ES were virtually completely excluded from the surrounding epithelium (Fig. 7H). In contrast, the centrally located mesenchymal cells were composed almost entirely of *Nik*−/− ES cells (Fig. 7H). We hypothesize that the phenotype of the mature somite in which *Nik*−/− ES are excluded from the epithelial cap of the dermomyotome arises as the wild-type ventromedial epithelium reacquires a mesenchymal phenotype. At present, we do not know whether the centrally localized *Nik*−/− ES are trapped passively by the wild-type cells or are actively recruited to this compartment and are able to go on to form more mature structures that arise from the sclerotome. Nevertheless, these findings indicate that NIK plays two roles in generating somites: (1) NIK has a cell nonautonomous function to stimulate migration of presomitic mesoderm away from the PS; and (2) NIK is cell-autonomously required for differentiation of the dermomyotome of the somite.

Expression of FGF4 in E8.0 Nik mutants

The accumulation of mesodermal cells in the PS in *Nik* mutants resembles in some respects knockout studies of fibroblast growth factor (FGf) 8 and Fgr1 (fibroblast growth factor receptor 1; Deng et al., 1994; Sun et al., 1999; Yamaguchi et al., 1994). In Fg8−/− embryos, epiblast cells pass through the PS and undergo an epithelial to mesenchyme transition, but essentially no mesodermal precursors move away from the PS, leading to almost complete absence of mesodermally and endodermally derived embryonic tissue (Sun et al., 1999). The defect in migration of Fg8−/− ES cells from the PS is, like NIK, cell nonautonomous (Sun et al., 1999). Thus, these data are consistent with the possibility that NIK mediates some of FGF8’s functions in the PS to stimulate production of a secreted molecule(s) required for cell migration. FGF4 has been hypothesized to be one of the molecules that functions downstream of FGF8 and whose production in the PS is required for the normal migration of mesodermal cells away from the PS (Sun et al., 1999). Therefore, to determine whether NIK may impinge on a common pathway with FGF8, we determined the expression of Fgf4 in *Nik*−/− embryos by in situ hybridization. We found that expression of Fgf4 in the PS is normal in E8.5 *Nik*−/− embryos (Fig. 5B). These findings are consistent with either NIK and FGF8 functioning in independent pathways or NIK functioning downstream of FGF8 and FGF4.

DISCUSSION

Requirement for NIK in early embryonic development

Homologs of the mammalian Ste20 kinase NIK have previously been shown to be essential for development in both Drosophila and C. elegans. In view of the large number of Ste20 kinases in mammalian cells, it was possible that NIK would not be essential for mammalian development because of redundant function with other Ste20 kinases. However, despite the large number of Ste20 kinases in mammalian cells, we found that NIK is indeed essential for development in mammalian cells. *Nik*−/− mice die postgastrulation between E9.5 and E10.5. The most striking phenotype in mice containing a targeted disruption of NIK is the failure of mesodermal and endodermal cells that arise from the anterior end of the PS to migrate to their correct location. As a result *Nik*−/− embryos fail to develop somites or a hindgut and contain an extra mass of cells that accumulate in the region of the PS. These extra cells are most likely to be committed mesoderm cells that fail to migrate away from the PS, since they stain positively for the mesodermal markers lim1 and Tbx6. *Nik*−/− mice are also developmentally delayed and truncated posteriorly, suggesting that NIK also regulates the mesodermal migration that contributes to the elongation of the body axis. While we cannot exclude the possibility that decreased proliferation and/or survival of mesodermal precursors accounts for the growth retardation and posterior truncation of *Nik*−/− embryos, the finding that *Nik*−/− ES cells contribute equally to wild-type cells in chimeric embryos suggests that NIK does not regulate either cell proliferation or survival.

While paraxial mesoderm and hindgut endoderm are affected in *Nik*−/− embryos, defects were not found in several other mesodermal and endodermal lineages. Extraembryonic mesoderm including the allantois, yolk sac and blood vessels are present in *Nik*−/− embryos. In addition, *Nik*−/− embryos form a heart and axial mesoderm. Fate mapping studies have indicated that the specific fate of mesodermal cells correlates with the level along the proximodistal (PD) border in which epiblasts migrate through the PS (Tam and Behringer, 1997; Beddington, 1998; Beddington and Robertson, 1999). The finding that both presomitic mesoderm and hindgut endoderm arise from the region of the PS just posterior to the node suggests that NIK plays a critical and specific role in regulating the migration of cells that arise from this position of the PS. Evidence for regional variation in the signals required for migration of cells leaving the PS has recently been provided by a study of Fg8 knockout mice (Sun et al., 1999). Although migration of mesodermal precursors is more severely affected in Fg8 knockouts than in *Nik* knockouts, leading to an almost complete lack of development of embryonic tissues, migration of mesoderm arising from more proximal regions of the PS that gives rise to extraembryonic mesoderm and blood is not affected in such Fg8 knockouts.

Chimeric analysis of mice using *Nik*−/− ES cells demonstrated that the inability of *Nik*−/− cells to migrate away from the PS is not due to loss of NIK in these mesodermal precursors. We found that E9.5 chimeric embryos with less than 50% contribution of *Nik*−/− ES cells were phenotypically normal and accumulation of cells adjacent to the PS was not found. In addition, *Nik*−/− cells contribute to paraxial mesoderm in chimeric embryos and the contribution of *Nik*−/− cells to
paraxial mesoderm is proportional to their contribution to the rest of the embryo. These findings indicate that NIK functions cell nonautonomously to regulate the production of a factor that stimulates the migration of mesodermal precursors destined to from paraxial mesoderm away from the PS. The effector cell on which NIK is acting is currently not known; in situ analysis has demonstrated that NIK is ubiquitously expressed in most tissues including the primitive streak. In addition to NIK’s cell nonautonomous effect to stimulate migration of paraxial mesodermal precursors away from the PS, NIK also has a cell autonomous effect to stimulate epithelialization of somites. We found that in contrast to the wild-type cells, Nik−/− ES cells were excluded from the surrounding epithelium compartment of the somitocoel as well as the segmented dermomyotome.

**Phenotype in the Nik mutant embryos is not due to defective activation of JNK**

While Nik and its *Drosophila* homolog msn have been linked both genetically and biochemically to the activation of the JNK MAP kinase pathway, the phenotype in *Nik* nullizygous embryos is unlikely to be due to defective activation of JNK (Su et al., 1997; Su et al., 1998). The JNK family consists of at least 10 isoforms of alternatively spliced genes arising from alternative splicing of three JNK genes. While JNK1 (Mapk8) and JNK2 (Mapk9) are ubiquitously expressed, JNK3 (Mapk10) has been found to be mainly expressed in the CNS (Martin et al., 1996). While mice lacking individual members of JNK1, JNK2 and JNK3 all survive normally, mice deficient in both JNK1 and JNK2 die embryonically at day 11.5 (Kuan et al., 1999). The most obvious phenotype in JNK1, JNK2 double deficient embryos is hindbrain exencephaly as a result of reduced apoptosis in the lateral edges of the hindbrain (Kuan et al., 1999). However, the overall morphology of the JNK1, JNK2 double mutants is similar to wild-type embryos and somite formation in the JNK1, JNK2 double mutants is normal. Thus, these findings, coupled with the finding that the only other JNK gene, JNK3, is restricted to the CNS, would suggest that the defects observed in the Nik homozygous mutants are unrelated to JNK activation. We cannot, however, exclude the possibility that NIK also functions later in development to activate JNK because the Nik−/− mice die before the JNK1, JNK2 double knockouts.

The ability of NIK to activate JNK-independent pathways and to function during gastrulation is also consistent with genetic experiments in *Drosophila*. In evaluating msn mutant flies rescued with a kinase defective Msn, we observed that many msn mutants had ventral cuticular abnormalities, suggesting a defect in gastrulation (Su et al., 2000). The role of msn in this phenotype is likely independent of JNK activation because ventral defects are not observed in embryos lacking both maternal and zygotic *Drosophila* (D)JNK (bsk) or the *Drosophila* JNK kinase encoded by hep (Gli, 1995; Riesgo-Escovar, 1996). Given the conservation between NIK and Msn, it is intriguing to speculate that the defects in cell migration in Nik−/− mice, and the ventral defects in msn mutant flies, are due to the failure of both kinases to activate similar signaling pathways. The nature of the signaling pathways regulated by either NIK or Msn that regulate either of these processes are currently not known.

**Signaling pathways in which NIK functions in development**

In addition to determining NIK’s role in development, we also hoped to identify, in these genetic studies, the upstream signals that regulate NIK in mammalian cells. We initially identified NIK on the basis of its ability to bind the SH3 domains of Nck (Su et al., 1997). Thus, we hypothesized that NIK may function downstream of a tyrosine kinase during development; in response to activation of a tyrosine kinase, NIK bound to the SH3 domains of NCK may be recruited to phosphotyrosine-containing proteins via the SH2 domain of NCK. In this regard, NCK has been shown to be recruited to the FGFR signaling pathway in experiments in cells (Gupta and Mayer, 1998; Liu et al., 1999; Rockow et al., 1996), and mice containing a targeted disruption of Fgfl8 or Fgfl1 resemble the Nik mutant phenotype reported here in some aspects (Sun et al., 1999;
Yamaguchi et al., 1994). Mice nullizygous for Fgf8 or Fgfr1 are similar to Nik nullizygous mice in that they both have a thickened PS due to the failure of mesodermal cells to migrate away from the PS (Deng et al., 1994; Sun et al., 1999; Yamaguchi et al., 1994). With respect to Fgf8 and Fgfr1 knockouts, the mice nullizygous for Nik more closely resemble less severely affected mice nullizygous for Fgf8. The cells that accumulate in the PS in mice nullizygous for both Fgf8 and Nik have undergone an epithelial-to-mesenchymal (E-M) transition (Sun et al., 1999). In addition, chimeric analysis of Fgf8-/ES cells is similar to chimeric analysis of Nik-/ES cells in that the defect in migration of Fgf8-/ mesodermal cells away from the PS is cell nonautonomous; Fgf8-/ ES cells contributed to all tissues in chimeric embryos (Sun et al., 1999). However, while these findings are consistent with the possibility that the phenotype in Nik-/- embryos is due to inhibition of some aspects of Fgf signaling, differences exist between the Nik and the Fgf8 knockouts that suggest that the phenotype of the Nik-/- embryos is not due to loss of FGF signaling. Decreased expression of Fgf4 and Tbx6 in the PS in Fgf8 knockouts has been proposed to be responsible for the mesodermal defect in mice nullizygous for Fgf8 (Sun et al., 1999). The finding that Nik-/- embryos express both Fgf4 and Tbx6 in the PS indicates that NIK does not mediate the induction of either of these genes by Fgf8. The large number of Fgfs and their receptors, as well as the importance of FGFs in mediating numerous processes during development, may complicate the comparison between phenotypes of mice nullizygous for a single FGF ligand and/or receptor with mice nullizygous for a signaling molecule functioning downstream of these receptors. As a result, genetic analysis of Nik mutant mice and Fgf double mutants as well as analysis of Fgf responses in Nik-/- cell lines will be required to determine whether NIK ultimately regulates signals downstream of FGFs and their receptors.

The Nik knockout phenotype also resembles some aspects of phenotypes identified during knockout studies of components of the fibronectin (FN) signaling pathway. Analysis of embryos mutant for the extracellular matrix protein FN, integrin α5 which is a component of the fibronectin receptor, and Focal adhesion kinase (FAK), which

**Fig. 7.** Chimeric analysis of Nik-/- ES cells. (A,B) Whole-mount staining of E9.5 chimeric embryos for β-galactosidase. Chimeric embryos with a range of contribution of Nik-/- ES cells were obtained. Embryos with high contribution from Nik-/- ES cells (A) displayed a similar phenotype to Nik mutant embryos. Embryos with a lower contribution from Nik-/- ES cells (B as an example) were also sectioned sagitally (C,D) or transversely (E-J). E (100× magnification) and F (400× magnification) correspond to the lower transverse section shown in B while G-I correspond to the upper transverse section shown in B. Nik-/- ES cells which do not stain because they do not express β-galactosidase are excluded from the segmented dermomyotome (marked by an arrow) in mature somites (D-I). I is a higher magnification (400×) of the more mature anterior somite shown in G while H is a higher magnification (400×) of a posterior somites at an early somitocoel stage of development. Examination of somites at the early somitocoel stage of somite development demonstrated that Nik-/- ES were virtually completely excluded from the surrounding epithelium whereas the centrally located mesenchymal cells were composed almost entirely of Nik-/- ES cells (H). The ability of Nik-/- ES to contribute to hindgut endoderm is shown in J-L. K (200×) and L (400×) are higher magnifications of J showing that Nik-/- ES contribute to hindgut endoderm (HG) which is marked by 2 arrowheads. L shows that Nik-/- ES contribute to other tissues such as the neural tube (NT) which is marked by an arrowhead. f, forebrain; m, midbrain; op, oropharynx; h, heart; LB, limb bud; CC, coelomic cavity; AS, anterior somite; PS, posterior somite; and LB, limb bud.
is a cytosolic tyrosine kinase that mediates downstream signaling from the FN receptor, all have defects in mesoderm and lack somites (Furuta et al., 1995; Georges-Labouesse et al., 1996; Goh et al., 1997). However, the lack of somites in these mutants is primarily due to the failure of condensation of presomitic mesoderm into somites, rather than to the migration of mesodermal precursors cells away from the PS (Georges-Labouesse et al., 1996; Goh et al., 1997). Both FN and integrin α5 knockout express the presomitic markers notch1 and moxl in a normal pattern and do not have a thickened PS. It is tempting to speculate that the cell autonomous defect in differentiation of the dermomyotome of Nik−/− ES cell in chimeric embryos may reflect defects in signaling downstream of the FN receptor. In this regard, the SH2 region of NCK has been shown to bind tyrosine phosphorylated p130Cas, a substrate for FAK, in FN-stimulated cells (Schlaepfer et al., 1997). The importance of p130Cas as a downstream target of FAK is supported by the finding that the defect in FN-stimulated assembly of actin filaments into stress fibers and migration of FAK−/− fibroblasts is rescued by ectopic expression of wild-type FAK, but not by expression of a mutant FAK that is unable to bind p130Cas (Sieg et al., 1999). We found that Nik−/− fibroblasts also exhibit defects in FN-stimulated assembly of actin filaments into stress fibers that resembles FAK−/− fibroblasts (data not shown). Thus, these findings raise the possibility that recruitment of a NCK/Nik complex to tyrosine phosphorylated p130Cas mediates one of the signals that is required for segmentation of presomitic mesoderm into somites.

Genetic experiments in flies have also indicated that Msn functions downstream of the Frizzled (Fz) receptor. msn mutants show a defect in planar polarity in both the wing and eyes due to the failure of Dsh, a downstream target of Fz, to activate JNK (Mlodzik, 1999; Paricio et al., 1999). The Fz protein in Drosophila functions as a receptor for Wingless (Wg), the Drosophila homolog of mammalian Wnts (Cadigan and Nusse, 1997). Interestingly, mice nullizygous for Wnt3a also lack caudal somites and are truncated posteriorly (Takada et al., 1994). However, NIK is not required for the activity of this Wnt3a signaling pathway. In Wnt3a mutants, unlike Nik mutants, epiblasts fail to undergo an E-M transition and form ectopic neural tubes rather than somites (Yoshikawa et al., 1997). Wnt3a induces the E-M transition by stimulating T gene expression in epiblasts ingressing through the PS via the activation of a signaling pathway that requires a transcriptional complex composed of β-catenin and a member of the Tcf family (Galceran et al., 1999; Yamaguchi et al., 1999). Brachyury in turn induces, either directly or indirectly, the expression of Tbx6, a T-box gene, which plays a critical role in specifying presomitic mesoderm (Chapman and Papaioannou, 1998; Yamaguchi et al., 1999). Experiments in Drosophila and in tissue culture cells have indicated that Fz couples Fz receptors to two distinct signaling pathways which include the β-catenin/Tcf pathway and a second pathway that utilizes msn to activate the JNK MAP kinase pathway (Boutros et al., 1998; Li et al., 1999). While the biological relevance of the β-catenin/Tcf pathway in Wnt signaling and somite development in mammalian cells is now apparent, future studies will likely uncover critical roles for NIK and JNK in other mammalian Wnt signaling pathways.

**Conclusion**

Little is known about the specific roles played by members of the GCK Ste20 kinase family in mammals. The difficulty in studying these kinases has been augmented by the large number of kinases in this family coupled with the lack of information about the specific biological functions played by individual members of this group. Most studies to date have focused on the regulation of the JNK MAP kinase pathway by members of this family of kinases. However, studies in Drosophila as well as studies reported here demonstrate that the repertoire of signaling pathways regulated by GCK family of kinases needs to be expanded beyond activation of the JNK MAP kinase pathway. The difficulty in determining the function of Ste20 kinases in cell culture and the signaling pathways that they regulate reinforces the importance of identifying genetic systems in which to study individual members of this kinase family. In this regard, the study of msn in Drosophila and Mig-15 in C. elegans has been extremely fruitful in clarifying and expanding our knowledge of Ste20 kinases in mammalian cells. The finding that NIK is critical for normal development demonstrates that redundancy among the many Ste20 kinases in mammals may be limited, and therefore that knockout studies of other Ste20 kinases are likely to yield important insights into the function of this interesting but complex family of kinases.

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Mesodermal patterning in Nk mutant mice


