The Vg1-related protein Gdf3 acts in a Nodal signaling pathway in the pre-gastrulation mouse embryo

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The formation of the anterior visceral endoderm (AVE) in the pre-gastrulation mouse embryo represents a crucial event in patterning of the anterior-posterior axis. Here, we show that the transforming growth factor β (Tgfβ) family member Gdf3 (growth-differentiation factor 3), a close relative of Xenopus Vg1, resembles the Tgfβ ligand Nodal in both its signaling activity and its role in AVE formation in vivo. Thus, in cell culture, Gdf3 signaling requires the EGF-CFC co-receptor Cripto and can be inhibited by Lefty antagonists. In Xenopus embryos, Gdf3 misexpression results in secondary axis formation, and induces morphogenetic elongation and mesendoderm formation in animal caps. In mouse embryos, Gdf3 is expressed in the inner cell mass and epiblast, and null mutants frequently exhibit abnormal formation or positioning of the AVE. This phenotype correlates with defects in mesoderm and definitive endoderm formation, as well as abnormal Nodal expression levels. Our findings indicate that Gdf3 acts in a Nodal-like signaling pathway in pre-gastrulation development, and provide evidence for the functional conservation of Vg1 activity in mice.

KEY WORDS: Tgfβ signaling, EGF-CFC proteins, Anterior visceral endoderm, Mesendoderm formation

INTRODUCTION

A key event in formation of the anteroposterior axis of the mouse embryo is the induction of the anterior visceral endoderm (AVE), a specialized population of cells within the extra-embryonic visceral endoderm that overlies and patterns the adjacent epiblast (reviewed by Lu et al., 2001; Rossant and Tam, 2004). The AVE is formed in the most distal region of the post-implantation egg cylinder at 5.5 days post coitum (dpc), but then translocates to the prospective anterior side by 6.0 dpc (Rivera-Perez et al., 2003; Srinivas et al., 2004; Thomas et al., 1998), prior to the onset of gastrulation. Both formation as well as movement of the AVE require activity of the Nodal signaling pathway, whereas the AVE itself produces Nodal antagonists that are essential for patterning of the anterior epiblast (Brennan et al., 2001; Ding et al., 1998; Perea-Gomez et al., 2002; Yamamoto et al., 2004). As a consequence, anti-Nodal signals from the distal visceral endoderm become opposed to Nodal signals from the proximal epiblast, and together pattern the anteroposterior (AP) axis following movement of the AVE. The molecular regulation of AVE induction and Nodal signaling activities is therefore of central importance for AP axis patterning in the mammalian embryo.

However, despite many recent advances in understanding early embryo patterning, the function of one of the first Tgfβ superfamily members to be implicated in vertebrate development has remained poorly understood. The Xenopus Vg1 gene was originally identified in a screen for vegetally localized maternal transcripts in the blastula stage embryo, and was proposed to act as an axial mesoderm inducer (Kessler and Melton, 1995; Melton, 1987; Thomsen and Melton, 1993; Weeks and Melton, 1987). Although subsequent analyses have identified Vg1 orthologs in zebrafish (Dohrmann et al., 1996; Helde and Grunwald, 1993) and chick (Seleiro et al., 1996; Shah et al., 1997), no clear ortholog has been identified in mammalian genomes. An initial screen for Vg1-related genes in mice had isolated growth-differentiation factor 3 (Gdf3), which shares 79% amino acid similarity with Vg1 (Jones et al., 1992). Early phylogenetic comparisons had suggested that Gdf3 was most closely related to Xenopus Vg1 and mammalian Gdf1 (Burt and Law, 1994), but more recent analyses have grouped Gdf3 with members of the Bmp subfamily (e.g. Chang et al., 2002; Newfeld et al., 1999).

Several lines of evidence have suggested that Vg1 can signal through a pathway similar to that for Nodal, which plays crucial roles in AP patterning, formation of mesoderm, definitive endoderm and axial mesendoderm, and specification of the left-right axis (reviewed by Schier, 2003; Schier and Shen, 2000; Whitman, 2001). In particular, signaling by processed Vg1, like that of activin and Nodal, results in activation of Smad2, and can be antagonized by dominant-negative Smad2 mutants (Graff et al., 1996; Hoodless et al., 1999). In addition, the effects of Vg1 overexpression in Xenopus can be blocked by a dominant-negative form of Foxh1/FAST, a winged-helix transcription factor that mediates many key aspects of Nodal signaling (Watanabe and Whitman, 1999). Notably, recent work has shown that the effects of Vg1 and Gdf1 overexpression in zebrafish require the EGF-CFC protein Oep, and that mature Vg1 and Gdf1 proteins can interact with Oep as well as the mouse EGF-CFC protein Cripto (Tdgf1) (Cheng et al., 2003). This requirement for EGF-CFC proteins, which act as putative co-receptors for Nodal ligand (Gritsman et al., 1999; Reissmann et al., 2001; Yan et al., 2002; Yeo and Whitman, 2001), indicates that Vg1 and Gdf1 signal through a Nodal-like pathway.
Owing to the similar activities of Vg1 and Nodal, it has remained unclear whether there is a conservation of Vg1-related activities during mammalian development, or indeed whether endogenous Vg1 has essential functions. To address these issues, we have investigated the potential conservation of Vg1 function through analyses of mouse Gdf3. We find that Gdf3 has activity in a cell culture assay for Nodal signaling, can form a complex with activin receptors and the EGF-CFC protein Cripto, and has activities similar to that of Nodal in Xenopus embryos and animal caps. We show that Gdf3 is expressed in pre-implantation and early post-implantation mouse embryos, and that ~35% of null mutants display pre-gastrulation and gastrulation defects consistent with the absence or mispositioning of the AVE, with the remainder surviving to adulthood. Our results suggest that Gdf3 has a crucial Nodal-like activity and is likely to represent a functional homolog for Vg1 in early mouse development.

**MATERIALS AND METHODS**

**Cell culture assay for Gdf3 activity**

The mouse pcDNA3-bf-Gdf3 and pcDNA3-by-Gdf3 expression constructs were generated by PCR from a mouse Gdf3 cDNA template (McPherron and Lee, 1993), and contain a heterologous Xenopus Bmp2 prodomain and a FLAG or V5 epitope-tag inserted immediately after the proprotein convertase cleavage site (Fig. 1A). Luciferase assays for Gdf3 and Nodal activities were performed as described (Yan et al., 2002). Co-transfection of an expression construct for β-galactosidase was used to normalize for transfection efficiency, and addition of pcDNA3 vector was used to maintain constant amounts of transfected DNA. Protein expression was detected by western blotting using a goat anti-mouse Gdf3 monoclonal antibody or a monoclonal anti-FLAG M2 antibody (Chen and Shen, 2004), or a monoclonal anti-FLAG M2 antibody (Sigma).

**Protein cross-linking and co-immunoprecipitation analysis**

Reversible chemical crosslinking with 0.5 mM DTSSP [3,3′-dithiobis(sulfosuccinimidyl propionate)] (Pierce) and co-immunoprecipitation were carried out as described previously (Chen and Shen, 2004). To detect the association of Gdf3 and Lefty1 in conditioned media, 293T cells were transfected with pcDNA3-bf-Gdf3 and pcDNA3-Lefty1; culture supernatants were collected 48 hours post-transfection and directly subjected to immunoprecipitation with anti-FLAG M2 antibody (Sigma). For all other experiments, crosslinking with DTSSP was carried out prior to co-immunoprecipitation, using whole-cell lysates prepared with RIPA114 buffer (Yan et al., 2002). The kinase-inactive receptor mutants ActRIIB(K217R)-Myc and ActRIB(K234R)-HA have been described previously (Yeow and Whitman, 2001). Western blotting was performed using the antibodies described above, as well as monoclonal anti-HA antibody (Covance) and anti-Myc antibody (Santa Cruz).

**Xenopus microinjection and animal cap assays**

Ovalution, in vitro fertilization, and embryo and explant cultures were carried out as described (Habas et al., 2001; Kato et al., 2002). Sequences corresponding to mouse Gdf3, bf-Gdf3 and Nodal were cloned into the pCS2+ vector for in vitro transcription using a mMachine SP6 system (Ambion). Capped mRNA was injected into the two ventral marginal zones of the four-cell embryo for phenotypic assays or into the animal hemisphere of Xenopus embryos at the two-cell stage. Animal caps were explanted at blastula stages 8.5-9 and cultured to early gastrula stage 11 for total RNA extraction and RT-PCR analysis. For phenotypic assays, embryos were raised to stage 30 in 0.1×MMR.

**Gene targeting and phenotypic analysis**

Gene targeting was performed as described (Bradley, 1987; Matzuk et al., 1992), using a 129S6 Sv-Ev-derived ES cell line derived from AB2.1. Sixty-two percent of clones resistant to both HAT and FIAU (n=52) were correctly targeted, as determined by Southern blot analysis using both 5′ and 3′ probes. Four independent clones were injected into mouse blastocysts, giving rise to germline male chimeras that sired mutant mice with identical phenotypes.

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**Fig. 1. Comparison of Gdf3 and Nodal signaling activities.**

(A) Schematic depiction of mouse Gdf3 and modified Gdf3 proteins; the sites of prodomain cleavage is indicated (arrows). (B) Gdf3 activity is Cripto and Foxh1 dependent. The indicated plasmids were co-transfected into 293T cells together with the A3-luc reporter. (Insets) Western blot detection of mature Gdf3 (~17 kDa) proteins in cell lysates using a goat anti-mouse Gdf3 polyclonal antiserum (R&D Systems), polyclonal antiserum (Sigma). Protein expression was detected by western blotting using a goat anti-mouse Gdf3 monoclonal antibody or a monoclonal anti-FLAG M2 antibody (Sigma).

(B) Relative luciferase activity (fold).

(C) Relative luciferase activity (fold).

(D) Relative luciferase activity (fold).
Whole-mount in situ hybridization was carried out as described (Ding et al., 1998; Wilkinson, 1992), using probes labeled by the DIG RNA Labeling Kit (Boehringer Mannheim). Most of the marker analysis was performed using a C57BL/6j congenic strain, although similar data were obtained using a C57BL/6j-129S6/SvEv mixed genetic background. Histological analysis was performed on formalin-fixed paraffin sections of whole decidua stained using a C57BL/6J congenic strain, although similar data were obtained using Kit (Boehringer Mannheim). Most of the marker analysis was performed using a Mx4000 quantitative PCR instrument with SYBR Green QPCR Master Mix (Stratagene). The primer pairs used were: for Nodal, 5′ CCA TGC CTA CAT CCA GAG GCT GC 3′ and 5′ TGG TGT GTC AGG AGG ACC CTG GC 3′; for Gdf1, 5′ TTC TGC CAG GGC AGC TGC G 3′ and 5′ GGA GCA GCT GCG TGC ATG AG 3′; and for Gapdh, 5′ TGC GAC TTC AAC AGC AAC TC 3′ and 5′ GCC TCT CTT GCT CAG TGT CC 3′. Three independent reverse-transcription reactions were performed on each total RNA, followed by real-time PCR amplification in triplicate and normalization against Gapdh levels.

**RESULTS**

Gdf3 activity in a Nodal-like signaling pathway

To investigate the properties of Gdf3, we examined whether Gdf3 protein can be expressed and signal in a Nodal-like pathway in mammalian cell culture. When we transfected a native Gdf3 expression construct into 293T human embryonic kidney cells, we observed that this native construct was processed poorly, with very low levels of mature ligand detected in conditioned media (Fig. 1A; see Fig. S1A in the supplementary material). To circumvent the inefficient processing of native Gdf3, we replaced the Gdf3 prodomain with that of *Xenopus* Bmp2, which is processed efficiently in 293T cells (Chen and Shen, 2004), and added a FLAG or V5 epitope tag at the N terminus of the mature ligand for ease of protein detection (Fig. 1A). The result of bf-Gdf3 (Bmp2 prodomain-FLAG-mature Gdf3) fusion protein is expressed and processed efficiently in conditioned media of transfected 293T cells (see Fig. S1A in the supplementary material). We noted that there were several Gdf3 proprotein and mature species detected by western blotting; consensus glycosylation sequences located in the mature Gdf3 sequence and in the Gdf3 and Bmp2 prodomains suggest that these species differ in their levels of N-glycosylation.

Given the body of evidence that Vg1 signals in a pathway similar to that of Nodal, we examined the activity of these Gdf3 protein products using a luciferase reporter assay that we developed for Nodal activity in transfected 293T cells (Yan et al., 2002). This assay relies upon reconstitution of the essential signaling components Cripto and Foxh1, which are not expressed in 293T cells [nor are Nodal, Gdf1, Gdf3, Lefty 1 or Lefty 2 (Chen and Shen, 2004; Yan et al., 2002) (C.C. and M.M.S., unpublished)]; moreover, Bmp4 does not display activity in this assay (Yan et al., 2002). When Nodal is co-transfected with Cripto and Foxh1 into 293T cells, signaling activity can be detected using the activin/Nodal-responsive luciferase reporter A3-luc (Fig. 1B). When co-expressed with Cripto and Foxh1, native Gdf3 gives a low but detectable level of activity, consistent with the low levels of mature ligand detected in conditioned media, whereas the modified bf-Gdf3 results in significant signaling activity (Fig. 1B; see Fig. S1 in the supplementary material).

As Gdf3 and Nodal displayed similar activities in this cell culture assay, we examined whether these ligands would behave identically if parameters of this assay were altered. As is the case for Nodal (Yan et al., 2002), we found that Gdf3 activity was absolutely dependent upon expression of EGF-CFC proteins and Foxh1 (Fig. 1B). We further explored the EGF-CFC dependence of Gdf3 by examining whether other EGF-CFC proteins could mediate Gdf3 signaling, and observed that Gdf3 displayed less activity in combination with mouse Cryptic (Cfci) or fish Oep than with mouse Cripto (Fig. 1C). Finally, we found that co-expression of Lefty1 or Lefty2 could inhibit Gdf3 signaling activity (Fig. 1D; data not shown), analogous to Nodal (Chen and Shen, 2004).Taken together, these results indicate that Gdf3 can use a signaling pathway highly similar to that for Nodal.

Interaction of Gdf3 and Cripto in a receptor complex

To address whether Gdf3 signaling is mediated by activin receptors, and examine the formation of a Gdf3 receptor complex, we used reversible protein crosslinking/co-immunoprecipitation. We co-expressed epitope-tagged type I (ActRIB/ALK4) and type II (ActRIIB) receptors together with bf-Gdf3 and FLAG-tagged Cripto (f-Cripto) in 293T cells, and examined the proteins immunoprecipitated together with ActRIIB following crosslinking with the membrane-impermeable agent DTSSP (Chen and Shen, 2004).

Interestingly, we found that bf-Gdf3 proprotein interacted equally well with activin receptors in the absence or presence of Cripto, similar to our previous observations with Nodal (Fig. 2A) (Chen and Shen, 2004). However, the interaction of mature Gdf3 ligand with activin receptors was greatly enhanced in the presence of Cripto, similar to previous observations of EGF-CFC dependent receptor complex formation with mature Nodal in frog animal caps (Fig. 2A, compare lanes 4 and 6) (Cheng et al., 2003; Yeo and Whitman, 2001). We also obtained similar results with native Gdf3 in this assay, although the levels of mature ligand present in activin receptor complexes were low (data not shown), indicating that our findings are not a consequence of the use of a heterologous Bmp2 prodomain. Furthermore, in crosslinking/co-immunoprecipitation experiments in the absence of co-transfected activin receptors, we found that Cripto interacted equally well with the bv-Gdf3 proprotein (Bmp2 prodomain-V5-mature Gdf3) as with the mature ligand (Fig. 2B). In combination, these findings indicate that Cripto specifically enhances and/or stabilizes receptor complex formation by mature Gdf3 ligand with activin receptors.

Finally, we investigated the basis by which Lefty1 can inhibit Gdf3 signaling activity (Fig. 2C). We and others have shown that Lefty proteins can inhibit Nodal signaling through an interaction with EGF-CFC proteins (Chen and Shen, 2004; Cheng et al., 2004), as well as with mature Nodal ligand in conditioned media (Chen and Shen, 2004). Consequently, we examined whether Lefty1 could interact with Gdf3 in conditioned media in the absence of crosslinking. We found that Gdf3 could specifically immunoprecipitate the mature Lefty1 protein, but not the Lefty1 proprotein (Fig. 2C), similar to our previous findings with Nodal (Chen and Shen, 2004).

Similar effects of Gdf3 and Nodal misexpression in *Xenopus* embryos

To examine whether Gdf3 signals in a Nodal-like pathway in vivo, we performed gain-of-function assays in *Xenopus laevis* embryos to compare the effects of Gdf3 and Nodal misexpression. Previous studies have shown that misexpression of mouse Nodal in the ventral marginal zone can dorsaointerize *Xenopus* embryos, and induce dose-dependent expression of dorsal mesoderm markers in animal caps (Jones et al., 1995; Joseph and Melton, 1997; Takahashi et al., 2000). Following microinjection of mRNAs into the two ventral
marginal zones of four-cell stage embryos, we observed the formation of partial secondary axes in response to low levels of Nodal (10 pg) and higher levels of Gdf3 or bf-Gdf3 (100 pg and 50 pg, respectively) (Fig. 3A-D; Table 1). Similarly, expression of low doses of Nodal (50 pg) and higher levels of Gdf3 or bf-Gdf3 (100 pg and 50 pg, respectively) in animal caps induced morphogenetic elongation with high doses of native Gdf3 (500 pg), but not the dorsal marker Mixer (Fig. 3E-I). We also observed morphogenetic elongation with high doses of native Gdf3 (500 pg) in animal caps induced morphogenetic elongation (79%, n=33 for Nodal; 39%, n=31 for bf-Gdf3), and expression of markers of early pan-mesoderm [Xbra (brachyury)], dorsal mesoderm [Xwnt8, chordin, Gsc (goosecoid)] and endoderm (Mixer), but not the dorsal marker Xnr3 (Fig. 3E-I). We also observed unmodified Gdf3 is poorly processed in Xenopus embryos, but possesses similar activity to bf-Gdf3 (Fig. 3I).

Restricted expression of Gdf3 in inner cell mass and epiblast

To gain insight into potential roles for Gdf3 in vivo, we assessed its expression pattern in wild-type mouse embryos at pre-implantation and early post-implantation stages. We found that Gdf3 expression initiates in a population of inner cells at the morula stage (Fig. 4A), with no expression detected at earlier pre-implantation stages (data not shown). Subsequently, Gdf3 expression is limited to the inner cell mass at the blastocyst stage (Fig. 4B), consistent with its conserved expression in mouse and human ES cells (Sato et al., 2003). During post-implantation development, Gdf3 expression occurs uniformly throughout the epiblast at 5.5 and 6.0 dpc, but is not detectable in the extra-embryonic ectoderm or visceral endoderm (Fig. 4C-F). Notably, Gdf3 expression appears to cease by 6.5 dpc, prior to the onset of gastrulation, with no further expression detected by in situ hybridization during gastrulation or through 9.5 dpc, including in primordial germ cells. Thus, Gdf3 expression is highly restricted to the pluripotent cells of the inner cell mass and epiblast.

Early embryonic lethality in a subset of Gdf3 homozygous null mutants

To investigate the biological functions of Gdf3, we produced mice with a null mutation at the Gdf3 locus (see Fig. S2 in the supplementary material). Although we could readily recover fertile and healthy Gdf3+/− homozygous mice, we observed these were significantly under-represented among progeny from heterozygote intercrosses (data not shown). Consequently, we examined the phenotypes of Gdf3 mutants at embryonic stages, and found that ~35% (n=127) of Gdf3 homozygotes displayed abnormal phenotypes at 6.0 to 8.5 dpc (Table 2). The most severely affected embryos were either resorbing (5%), or corresponded to empty placenta (21%) (Fig. 5A). Less severely affected embryos exhibited characteristic morphological phenotypes, including prominent constriction at the embryonic/extra-embryonic junction, poorly differentiated anterior structures and abnormal mesoderm derivatives (21%) (Fig. 5B-G). Similar frequencies of embryonic lethality, as well as embryonic phenotypes were observed in Gdf3−/− 129SvEv inbred and C57BL/6J congenic mice that had been backcrossed for seven generations (Table 2; data not shown), suggesting that the phenotypic heterogeneity is not strongly

Fig. 2. Interactions of Gdf3 with activin receptors, Cripto and Lefty1. (A) Formation of a Gdf3 receptor complex. 293T cells were transfected with the indicated expression constructs, followed by crosslinking with the membrane-impermeable reagent DTSSP, immunoprecipitation of Myc-tagged ActRIIB from cell lysates and reversal of crosslinking; kinase-inactive activin receptor mutants were used in order to decrease receptor internalization. Western blots of immunoprecipitated and input proteins are shown, detected using the following antibodies: α-Gdf3 (bf-Gdf3 proprotein, ~49 kDa; mature bf-Gdf3, ~17 kDa); α-FLAG (f-Cripto, ~21 kDa); α-HA (ActRIB-HA, ~54 kDa); α-Myc (ActRIIB-6xMyc, ~75 kDa). (B) Cripto interacts with Gdf3. Expression constructs were co-transfected into 293T cells, followed by crosslinking with DTSSP, immunoprecipitation of FLAG-tagged Cripto (f-Cripto) from cell lysates and reversal of crosslinking. Western blots are shown using the following antibodies: α-FLAG (bf-Gdf3 proprotein, ~49 kDa; mature bf-Gdf3, ~17 kDa) and α-Lefty1 (Lefty1 proprotein, ~40 kDa; mature Lefty1, ~30 kDa). (C) Gdf3 interacts with Lefty1 in conditioned media in the absence of crosslinking. The mature form of Lefty1 is preferentially immunoprecipitated; the expected positions of the Lefty1 proprotein (arrow) and a mature Lefty1 variant generated by use of an alternative polyprotein cleavage site (asterisk) are indicated. Proteins were detected by western blotting using the following antibodies: α-FLAG (bf-Gdf3 proprotein, ~49 kDa; mature bf-Gdf3, ~17 kDa) and α-Lefty1 (Lefty1 proprotein, ~40 kDa; mature Lefty1, ~30 kDa).
influenced by strain background. Phenotypic analysis of embryos from homozygous by heterozygous crosses excluded the possibility of a Gdf3 maternal effect (C.C. and M.M.S., unpublished).

**Defects in AVE and primitive streak derivatives in Gdf3 mutants**

To analyze the phenotypic abnormalities observed in Gdf3 mutants, we performed whole-mount in situ hybridization using tissue-specific markers at gastrulation and pre-gastrulation stages. Initially, we examined the expression of early mesoderm markers, such as Foxa2 (Hnf3β), which is expressed in the anterior primitive streak and subsequently in the node and axial mesendoderm, but is greatly diminished or absent in 50% (n=6) of Gdf3 homozygotes at 6.75 dpc (Fig. 6A,B). We also found that expression of Lhx1 (Lim1) in lateral mesoderm emerging from the primitive streak was reduced or absent in 50% (n=4) of Gdf3 homozygotes at 6.75 dpc (Fig. 6C,D), and in 64% (n=11) of Gdf3 homozygotes at 7.5 dpc (data not shown).

Similar defects in nascent mesoderm formation were observed using the markers Wnt3 and Fgf8 (data not shown). By contrast, early neural specification and patterning appeared to be normal, as Otx2 expression in prospective forebrain and midbrain regions was unaffected in Gdf3 homozygotes (n=15) at 7.0-7.5 dpc (Fig. 6E,F). However, this early expression was often not maintained, as shown by the severely decreased or absent expression of Otx2 in 63% (n=8) of Gdf3 mutants at 8.5 dpc (data not shown).

Further analyses demonstrated severe defects in AVE formation and movement as well as loss of definitive endoderm in a subset of Gdf3 homozygotes. Using the marker Cerl (cerberus-like), we observed that definitive endoderm formation was greatly reduced or absent in 60% of (n=5) Gdf3 homozygotes at 7.0 dpc (Fig. 6G,H). Additional analyses showed that Gdf3 homozygotes had defects in expression of Hesx1 at 6.75 dpc (38%, n=8) and Hex at 6.5-7.0 dpc in the AVE (31%, n=13) (Fig. 6I-M); similar results were observed for Lhx1, which is also expressed in the AVE (Fig. 6C,D; data not shown). Notably, these analyses identified Gdf3 homozygotes with reduction or absence of the AVE (19%, n=26) (Fig. 6D,J,L), or mislocalization of the AVE in the distal visceral endoderm (8%, n=26) (Fig. 6M), suggesting a failure in AVE movement to the prospective anterior side.

Examination of less severely affected Gdf3 mutants failed to reveal additional defects in body patterning at later stages of development, including left-right axis specification (Fig. 6N,O; data not shown). In particular, morphologically normal Gdf3 homozygotes displayed correct left-sided Nodal expression in the lateral plate mesoderm at 8.0 dpc (67% four- to eight-somite stage embryos, n=9) (Fig. 6N); a few morphologically abnormal Gdf3 embryos lacked left-sided Nodal expression (Fig. 6O), but this was probably due to absence of the lateral plate mesoderm.

Surprisingly, our marker analyses also revealed an unusual subset of Gdf3 homozygotes that display a partial axis duplication. Although Gdf3 homozygotes frequently displayed reduced or absent expression of T (brachyury), which is normally found in the node and axial mesoderm at 8.0 dpc (Fig. 6P,Q), rare homozygous embryos (5%, n=57) showed twinned axial mesoderm staining, corresponding to duplicated notochords in sections (Fig. 6R,S) and indicating that secondary axis formation is an infrequent consequence of Gdf3 inactivation.

**Altered expression of Nodal in Gdf3 mutant embryos**

Overall, the phenotypic abnormalities observed in affected Gdf3 mutants strongly resemble those observed in mutants for several genes in the Nodal signaling pathway (see Discussion). To assess potential effects on this pathway, we examined expression of Nodal itself in Gdf3 homozygotes at 6.0-6.75 dpc. In wild-type embryos prior to gastrulation, Nodal displays graded expression in the epiblast, with highest levels in the posterior and proximal region (Fig. 6T,Z). Interestingly, we found that 2/15 (13%) Gdf3 homozygotes showed apparent downregulation of Nodal expression at 6.0 dpc, with limited staining in the proximoposterior epiblast (Fig. 6U), whereas 3/15 (20%) Gdf3 mutants showed strong

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**Fig. 3. Gdf3 induces secondary axis and mesendoderm formation in Xenopus embryos.** (A-D) Secondary axis formation following ventral marginal zone injection. Morphology of control uninjected embryo (A) and embryos injected with the indicated doses of Nodal (B), Gdf3 (C) or bf-Gdf3 (D) mRNAs; arrows indicate secondary axis formation. (E-H) Gdf3 induces morphogenetic elongation in animal cap explants. Unlike control uninjected caps (E), animal caps injected with the indicated doses of Nodal (F), Gdf3 (G) or bf-Gdf3 (H) mRNAs undergo morphogenetic elongation, as scored at stage 20. (I) Mesendoderm formation in animal cap assays. High doses of Gdf3 (500-1000 pg) result in weak induction of Xbra and Mixer, while low doses of Nodal (50 pg) and bf-Gdf3 (50-100 pg) result in strong induction of markers for mesoderm (Xbra, Gsc, chordin and Xwnt8) and endoderm (Mixer), but not the dorsal marker Xnr3. Ornithine decarboxylase (Odc) is used as an internal control. –RT, no reverse transcriptase added.
upregulation of Nodal expression throughout the epiblast (Fig. 6V,A'). Similarly, quantitative real-time RT-PCR analysis of individual embryos at 6.0 dpc revealed significant downregulation of Nodal expression in 5/26 Gdf3 homozygotes relative to wild-type controls, while 3/26 Gdf3 homozygotes displayed significant Nodal upregulation (see Fig. S3A in the supplementary material). Notably, the percentage of embryos showing altered levels of Nodal expression by real-time PCR (34%, n=73) (analysis of 26 embryos is shown in Fig. S3A in the supplementary material; data for an additional 47 are not shown), is similar to the percentage displaying AVE defects by marker analyses (27%, n=26), as well as to the percentage with morphological defects at 6.75 and 7.5 dpc (29% and 35%, respectively; Table 2). This correlation suggests that the Gdf3 homozygotes with AVE defects also display altered Nodal expression at 6.0 dpc and undergo abnormal development, while the remaining Gdf3 homozygotes are phenotypically wild type.

At later stages, we also observed considerable variation in the Nodal expression patterns and morphologies of Gdf3 homozygotes. In wild-type embryos at early and mid-streak stages, Nodal expression persists in the posterior epiblast and is downregulated in the primitive streak, but is slightly upregulated in the posterior visceral endoderm overlying the streak (Fig. 6W,B'). We found that a significant number of Gdf3 homozygotes (44%, n=9) showed abnormal morphology and Nodal expression at 6.75 dpc. We observed more intense posterior Nodal expression in one out of nine Gdf3 homozygotes, which showed a greatly expanded primitive streak in sections (Fig. 6X,C'); such embryos may give rise to the axis duplications observed at later stages (Fig. 6R,S). Furthermore, two out of nine (22%) homozygous mutants displayed a 'conical' morphology that was associated with a radially symmetric shape in cross-section (Fig. 6Y,D'). Strikingly, these embryos were filled with cells of mesodermal appearance and displayed circumferential upregulation of Nodal expression in the visceral endoderm, suggesting that most of the epiblast had undergone streak formation and become mesoderm.

Additional marker analyses were consistent with the interpretation that Gdf3 mutants have primary defects in AVE formation and movement, with consequent effects on expression of Nodal. Examination of Cripto expression at 6.75 dpc showed that most Gdf3 homozygotes showed normal expression in the posterior epiblast, with the exception of the unusual 'conical' mutants, which showed strong upregulation throughout the epiblast (Fig. 6E,F'; data not shown). The expression patterns of Lefty1 in the AVE at 6.0 dpc and Lefty2 in nascent mesoderm at 6.75 dpc were similar to that described above for other AVE and mesodermal markers, respectively (data not shown). Furthermore, expression of Bmp4 in the extra-embryonic ectoderm is dependent upon Nodal signaling in the adjacent proximal epiblast (Brennan et al., 2001), but no effects on Bmp4 expression were observed in Gdf3 mutants at 6.5 dpc (n=7) (Fig. 6G',H'), suggesting that Nodal activity in the proximal epiblast remains at least partially intact. Finally, as Gdf1 can also signal through a Nodal-like pathway, we examined the expression of Gdf1, which is expressed at low levels throughout the epiblast at 5.5 dpc and becomes upregulated at ~5.75 dpc (Wall et al., 2000) (this

### Table 1. Phenotypes resulting from ventral marginal zone injections in Xenopus embryos

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</tbody>
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*Embryos with posterior defects had abnormal blastopore closure, resulting in an open neural tube in the posterior; in addition, many embryos contained a small darkly pigmented protrusion in the posterior region that could not be classified as a partial axis.

### Table 2. Frequency of embryonic phenotypes in Gdf3−/− embryos

<table>
<thead>
<tr>
<th></th>
<th>6.0 dpc</th>
<th>6.75 dpc</th>
<th>7.5 dpc</th>
<th>8.5 dpc</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abnormal</td>
<td>20</td>
<td>31</td>
<td>40</td>
<td>27</td>
</tr>
<tr>
<td>Empty yolk sac/resorbed</td>
<td>0</td>
<td>3</td>
<td>11</td>
<td>20</td>
</tr>
<tr>
<td>Total</td>
<td>117</td>
<td>119</td>
<td>144</td>
<td>127</td>
</tr>
<tr>
<td>Ratio</td>
<td>17%</td>
<td>29%</td>
<td>35%</td>
<td>37%</td>
</tr>
</tbody>
</table>

Mice were in a C57BL/6J congenic background for the 6.0, 6.75 and 7.5 dpc analyses, and in a C57BL/6J-129SvEv mixed genetic background for the 8.5 dpc analysis.
work). We observed a similar expression pattern and temporal onset of *Gdf1* upregulation in *Gdf3* homozygotes (n=22) and wild-type controls (n=17) at 5.5-6.0 dpc (Fig. 6I’; data not shown). In addition, quantitative real-time PCR analysis confirmed similar levels of *Gdf1* expression in individual wild-type and *Gdf3* mutant embryos at 6.0 dpc (see Fig. S3B in the supplementary material).

**DISCUSSION**

Our combined biochemical and molecular genetic analyses of Gdf3 function have provided strong evidence for its Nodal-like activity. The characteristic features of the *Gdf3* null phenotype imply that Gdf3 represents an important component of Nodal pathway activity at pre-gastrulation stages. Moreover, our findings uncover conserved functions of *Vg1*-related genes in vertebrate development, and raise the possibility that Nodal pathway activity may play an earlier role in mouse embryogenesis than hitherto appreciated.

**Gdf3 functions in a Nodal-related pathway**

Our studies provide three principal lines of evidence that Gdf3 acts in a Nodal-related pathway. First, we have shown that Gdf3 signaling in cell culture displays the defining features of the Nodal pathway in its requirement for EGF-CFC proteins and ability to be inhibited by Lefty proteins. At the biochemical level, Gdf3 can form complexes with activin receptors, and interacts with both Cripto and Lefty proteins in a manner highly reminiscent of Nodal. In signaling in cell culture displays the defining features of the Nodal pathway in its requirement for EGF-CFC proteins and ability to be inhibited by Lefty proteins. At the biochemical level, Gdf3 can form complexes with activin receptors, and interacts with both Cripto and Lefty proteins in a manner highly reminiscent of Nodal. In signaling in cell culture displays the defining features of the Nodal pathway in its requirement for EGF-CFC proteins and ability to be inhibited by Lefty proteins. At the biochemical level, Gdf3 can form complexes with activin receptors, and interacts with both Cripto and Lefty proteins in a manner highly reminiscent of Nodal.

**Based on our findings, we propose that Gdf3 functions through a Nodal-like pathway to provide a crucial signal for AVE formation and movement in pre-gastrulation development (Fig. 7A). The variability of the *Gdf3*-null phenotype might thus be due to stochastic differences in the ability of *Nodal* to provide sufficient pathway activity to compensate for the absence of *Gdf3*. Gdf3 may also be required subsequently for mesoderm and definitive endoderm formation; however, as *Nodal* expression is perturbed in the absence of *Gdf3*, we are unable to distinguish whether the gastrulation phenotypes of *Gdf3* mutants represent primary or secondary consequences of *Gdf3* inactivation. A second, non-mutually exclusive possibility is that Gdf3 may act to upregulate *Nodal* expression itself, through its potential to activate the Nodal positive autoregulatory loop. This model is perhaps less plausible as deletion of the *Nodal* autoregulatory enhancer results in a relatively mild left-right patterning defect (Norris et al., 2002); however, the recent elucidation of a second Nodal-responsive enhancer raises the possibility that autoregulation may play an important role at earlier stages of development (Saijoh et al., 2005).

Unexpectedly, we have observed that *Nodal* expression can either be downregulated or upregulated in the absence of *Gdf3*. These apparently opposite outcomes can potentially be explained by the requirement of *Gdf3* for AVE induction and movement. In the absence of *Gdf3*, the AVE may be able to form, but be unable to move, leading to retention of *Nodal* expression in the proximal epiblast, resulting in reduction or absence of mesoderm and definitive endoderm formation (Fig. 7B). However, if the AVE fails to form, *Nodal* expression would remain at high levels throughout the epiblast (Fig. 7B), similar to the phenotype of...
Smad2-null mutants (Brennan et al., 2001; Waldrip et al., 1998). In addition, overexpression of Nodal might lead to expansion and splitting of the primitive streak at early gastrulation stages, as well as partial axis duplications, as expression of Nodal pathway inhibitors in the AVE is necessary to suppress formation of a secondary axis (Bertocchini and Stern, 2002; Perea-Gomez et al., 2002). Similar phenotypes have been observed in other cases of Nodal pathway upregulation, such as in mutants for the transcriptional repressor Drap1 (Iratni et al., 2002), or combined inactivation of the Nodal antagonists Lefty1 and Cerl (Perea-Gomez et al., 2002).

In the simplest case, Gdf3 may upregulate Nodal pathway activity by signaling in parallel to Nodal itself. However, we cannot exclude the possibility that Gdf3 might create a novel enhanced or diminished activity through heterodimerization with Nodal. The possibility of such heterodimerization with Nodal has been...
Fig. 7. Model for Gdf3 function. (A) In wild-type embryos, Nodal activity promotes AVE induction and movement as well as primitive streak formation, and maintains its expression through an autoregulatory feedback loop. Gdf3 is also required for AVE formation and movement, and may additionally be necessary for streak formation and maintenance of Nodal expression. (B) In wild-type embryos (top), expression of Nodal antagonists by the AVE provides essential signals for patterning of the anterior epiblast; the distribution of Nodal pathway activity (including Gdf3) in the epiblast is depicted in blue, while that of Nodal antagonists is shown in red. In the absence of Gdf3, the AVE may form but be unable to move (middle), thereby resulting in embryos with downregulated Nodal expression that is restricted to the proximal epiblast. Alternatively, if the AVE fails to form (bottom), the absence of Nodal antagonists will result in upregulation of Nodal expression throughout the epiblast, potentially leading to expansion of the primitive streak and axis duplication.

Potential overlapping activities of Nodal pathway ligands in early embryogenesis

Our functional analysis of Gdf3 suggests that the activities of Vg1-related genes at pre-gastrulation stages are conserved in vertebrate embryos. In particular, chick Vg1 is expressed at early pre-streak stages in the epiblast of the posterior marginal zone from stage X to XII (Shah et al., 1997), and has been proposed to cooperate with Wnt and FGF signals in primitive streak formation and initiation of Nodal expression (Bertocchini et al., 2004; Skromne and Stern, 2001). Similarly, Xenopus Vg1 transcripts are localized to vegetal cells at the blastula stage, and have been suggested to play a central role in dorsal mesoderm and endoderm formation (Joseph and Melton, 1998; Kessler and Melton, 1995; Thomsen and Melton, 1993; Weeks and Melton, 1987). These putative functions of Vg1-related genes are generally consistent with our findings that mouse Gdf3 mutants display defects in formation of the AVE, mesoderm and definitive endoderm.

Interestingly, the conserved functions of Xenopus Vg1 may have been divided between Gdf1 and Gdf3, its mammalian counterparts. The patterns of Gdf1 and Gdf3 expression in the epiblast are strikingly complementary, with Gdf3 being downregulated shortly after 6.0 dpc and Gdf1 being upregulated at ~5.75 dpc, when it can be detected throughout the epiblast (Wall et al., 2000) (this work). Null mutants for Gdf1 are defective for left-right axis specification (Rankin et al., 2000), consistent with the proposed role for Vg1 in coordinating left-right patterning in Xenopus (Hyatt et al., 1996; Hyatt and Yost, 1998; Kramer and Yost, 2002). Notably, the phenotype of Gdf1 mutants is indistinguishable from that of Cryptic mutants (Yan et al., 1999), suggesting that Gdf1 signaling may be facilitated by Cryptic in vivo.

The potential overlapping functions of Nodal, Gdf3 and Gdf1 suggest that the Nodal signaling pathway may play as yet poorly understood roles in pre-implantation and early post-implantation development. This possibility is supported by the expression patterns of Gdf3 and Nodal in pre-gastrulation embryos, as well as by the conserved expression of Nodal, Cripto, Lefty1 and Gdf3 in undifferentiated mouse and human ES cells (Besser, 2004; Bhattacharya et al., 2004; Ramalho-Santos et al., 2002; Sato et al., 2003). Moreover, recent studies have also suggested a role for Nodal signaling in maintaining the undifferentiated state of human ES cells (James et al., 2005; Vallier et al., 2004). These observations lead us to speculate that this pathway may play a broader role in mammalian embryogenesis than previously conceived.

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Supplementary material

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/133/2/319/DC1

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