Smad5 determines murine amnion fate through the control of bone morphogenetic protein expression and signalling levels

Erika A. Bosman1,*, Kirstie A. Lawson2,†, Joke Debruyn1, Lisette Beek1, Annick Francis1, Luc Schoonjans3, Danny Huylebroeck3 and An Zwijsen1,‡

Smad5 is an intracellular mediator of bone morphogenetic protein (Bmp) signalling. It is essential for primordial germ cell (PGC) development, for the development of the allantois and for amnion closure, as demonstrated by loss of Bmp signalling. By contrast, the appearance of ectopic PGC-like cells and regionalized ectopic vasculogenesis and haematopoiesis in thickened Smad5 mutant amnion are amnion defects that have not been associated with loss of Bmp signalling components. We show that defects in amnion and allantois can already be detected at embryonic day (E) 7.5 in Smad5 mutant mice. However, ectopic Oct4-positive (Oct4+) and alkaline phosphatase-positive (AP+) cells appear suddenly in thickened amnion at E8.5, and at a remote distance from the allantois and posterior primitive streak, suggesting a change of fate in situ. These ectopic Oct4+, AP+ cells appear to be Stella negative and hence cannot be called bona fide PGCs. We demonstrate a robust upregulation of Bmp2 and Bmp4 expression, as well as of Erk and Smad activity, in the Smad5 mutant amnion. The ectopic expression of several Bmp target genes in different domains and the regionalized presence of cells of several Bmp-sensitive lineages in the mutant amnion suggest that different levels of Bmp signalling may determine cell fate. Injection of rBMP4 in the exocoelom of wild-type embryos can induce thickening of amnion, mimicking the early amnion phenotype in Smad5 mutants. These results support a model in which loss of Smad5 results paradoxically in gain of Bmp function defects in the amnion.

KEY WORDS: Allantois, Amnion, Bmp, Chimera, PGC, Smad5/Madh5, Stem cell, Tgf

INTRODUCTION

In mouse embryos, extra-embryonic mesoderm cells of the prospective visceral yolk sac, chorion, allantois and amnion are among the first mesoderm cells to emerge early at gastrulation. Cell labelling studies have shown that a population of posterior and posterolateral epiblast cells that enters the primitive streak proximally will give rise to this extra-embryonic mesoderm and also to primordial germ cells (PGCs) (Lawson and Hage, 1994; Parameswaran and Tam, 1995; Kinder et al., 1999). Genetic evidence and epiblast culture experiments have shown that germ cell competence and formation of the allantois are induced in the proximal epiblast before gastrulation, in response to bone morphogenetic proteins (Bmps) produced in the extra-embryonic ectoderm, but depend also on the presence of visceral endoderm (reviewed by Zhao, 2003; de Sousa Lopes et al., 2004).

Bmps are ligands of the transforming growth factor β (Tgfβ) family that use various receptor complexes to directly activate intracellular effector proteins (Smad1/5/8). Smads transmit the signal to the nucleus and participate in the regulation of target gene expression (Shi and Massagué, 2003). Analysis of conventional knockout mice showed that the repertoire of Bmp signalling proteins involved in PGC induction comprise Bmps (Bmp2, -4 and -8b), a type I Bmp receptor (Alk2; Acrv1 – Mouse Genome Informatics) and two Bmp-Smads (Smad1/5) (Lawson et al., 1999; Ying et al., 2000; Ying et al., 2001; Ying and Zhao, 2001; Chang and Matzuk, 2001; Tremblay et al., 2001; Hayashi et al., 2002; de Sousa Lopes et al., 2004; Okamura et al., 2005). Recently, it was shown that Blimp1 (Prdm1 – Mouse Genome Informatics), a transcriptional regulator thought to be induced by Bmp4, is a key regulator of germ cell specification (Vincent et al., 2005; Ohinata et al., 2005). Subsequent PGC localization and survival, as well as allantois differentiation, also depend on the presence of Bmp4 in the extra-embryonic mesoderm (Fujiiwara et al., 2001).

Several Bmps have been implicated in the specification and growth of extra-embryonic mesoderm. The induction of the allantois crucially depends on Bmp4 (Winnier et al., 1995; Fujiiwara et al., 2001), and on Alk2-mediated signalling in visceral endoderm (Mishina et al., 1999; Gu et al., 1999). Bmp5;Bmp7 double mutant mouse embryos display impaired allantois maturation (Solloway and Robertson, 1999). Bmp2 plays a unique role in amnion development, as the pro-amnietic canal does not close in Bmp2 mutant mice, which has been ascribed to reduced and thus insufficient production of extra-embryonic mesoderm (Zhang and Bradley, 1996).

Smad1 and Smad5 null embryos die at mid-gestation and have defects in PGC specification and allocation, and in the development of extra-embryonic tissues (Chang et al., 1999; Chang et al., 2000; Yang et al., 1999; Lechleider et al., 2001; Tremblay et al., 2001; Hayashi et al., 2002; Umans et al., 2003). The presence on the amnion of aggregates of cells that contain ectopic primitive red blood cells, and endothelial and PGC-like cells, is a unique feature of Smad5 mutants (Chang et al., 1999; Chang and Matzuk, 2001). However, the molecular mechanism underlying this unique phenotype remained unknown. Our present chimera study reveals
that Smad5 functions non-cell-autonomously in the amnion mesoderm. In addition, we observe ectopic Bmp expression and signalling in the affected amnion. We therefore propose a new model in which Smad5 deficiency paradoxically leads to gain of Bmp function defects. Additional support for this model comes from injection of rBMP4 protein in the exocoelom of wild-type embryos, which results in abnormal thickening of the amnion.

MATERIALS AND METHODS

Mouse strains and production of chimeric embryos

The Smad5m1 allele (Chang et al., 1999) was outcrossed in C57BL/6J and F2 crosses of F1 (C57BL/6J × CBA) background for at least five generations. Rosa-β-gal-exo mice, expressing *Escherichia coli lacZ* ubiquitously (Friedrich and Soriano, 1991), were maintained in the F2 background. Embryonic stem (ES) cells were established from blastocysts of Smad5m1/1 (C57BL/6J) intercrosses as described (Schoonjans et al., 2003), and genotyped by PCR and Southern blotting (Chang et al., 1999).

Chimeras between ES cell lines and diploid Rosa-β-gal-exo morulae were generated as described (Goumans et al., 1999). The majority of wild-type→WTm1, Smad5+/-m1→WTlacZ, and of Smad5m1/1→WTlacZ chimeric embryos had a high ES cell contribution (>90%), with only few acceptor-morula derived, β-galactosidase-positive cells present in hindgut endoderm. The minority of Smad5m1/1→WTlacZ embryos (four out of 18) with a high contribution from the wild-type acceptor morula in epiblast-derived tissues (20-80% ES cell-derived embryos) are here referred to as low-percentage chimeras.

Animal care and experiments were approved by the Institutional Ethical Committee of the Catholic University of Leuven.

Collection of post-implantation embryos, in situ hybridization and immunohistochemistry

Embryos from timed matings were dissected in ice-cold PBS at embryonic day (E) 7.0-9.5 and staged according to Downs and Davies (Downs and Davies, 1993), modified for C57BL/6 × CBA embryos (Edinburgh Mouse Atlas Project: http://genex.hgu.mrc.ac.uk/Databases/Anatomy/MAstaging.shtml), or on somite number. Radioactive in situ hybridization was performed as described (Dewulf et al., 1995). Non-radioactive in situ hybridization (*Stella* Dppa3 – Mouse Genome Informatics), fragi1 (Httm3 – Mouse Genome Informatics) on sections and immunohistochemistry for P-ERK (cat. no 9101, Cell Signalling Technologies) and P-Smad1/5/8 (cat. no 9511, Cell Signalling Technologies) were performed with the automated Ventana Discovery system and Ventana reagents according to the manufacturer’s instructions. NBT/BCIP and DAB were used as chromogens for automated non-radioactive in situ hybridization and immunohistochemistry, respectively. We used antisense RNA probes for Bmp2 (Lyons et al., 1989), Bmp4 (Jones et al., 1991), periostin/OP12 (Delot et al., 2003), Stella and fragi1 (Saitou et al., 2002), and Msx2 (MacKenzie et al., 1992).

Immunohistochemistry for Oct4 (Pou5f1 – Mouse Genome Informatics; sc5279, Santa Cruz Biotechnology) and SSEA-1 (Fut4 – Mouse Genome Informatics; MC480 DHSB) was performed as described (Van Eynede et al., 2004). AEC (Sigma) was used as a chromogen.

Detection and counting of PGCs

Dissection of embryos, followed by fixation, and detection of alkaline phosphatase (AP)-positive PGCs with α-naphthyl phosphate/Fast Red TR (Ginsburg et al., 1990) in whole-mount embryos or with ASMX/Fast Red TR in serial section, were as described (Lawson et al., 1999). PGCs were counted on the basis of the strong surface AP staining and intensely stained cytoplasmic spot (Ginsburg et al., 1990; Lawson and Hage, 1994). The anterior portion of the embryo was retained for genotyping (Chang et al., 1999).

Measurements

Allantois dimensions were measured on intact embryos after staining for AP. The axial length of the allantois was measured from the line of intersection with the yolk sac when viewed posteriorly and from the junctional line between amnion and yolk sac when viewed laterally. Width at the base was measured in posterior view along the intersection with the yolk sac.

The length of the anterior-posterior embryonic axis was estimated on images of intact embryos stained for AP and viewed laterally. Axis length was taken as the sum of the three longest cords along the curved axis – from the anterior embryo/amnion junction or the most proximal edge of the neural fold, from the intersection of amnion, allantois and primitive streak to the node, and a cord connecting these two.

Injection of rBMP4 and whole embryo culture

CD1 embryos between neural plate (NP) and headfold (HF) stages were isolated in 22 mmol/l Hepes and 10% heat-inactivated fetal calf serum (FCS; HyClone): Reichert’s membrane was removed, but yolk sac integrity with the ectoplacental cone was maintained. Whole embryo culture and manipulations were in Dulbecco’s modified essential medium (Gibco), 1 mmol/l glutamine, non-essential amino acids, 0.5 mmol/l Na-pyruvate, 50% heat-inactivated horse serum (Gibco) in a rolling culture system at 37°C and 5% CO2 for 15 to 24 hours (0.5 ml medium per embryo). Embryos were either control injected or injected with 1 μg human rBMP4/ml PBS (R&D Systems) with a mouth-controlled glass capillary in the exocoelom (1-2 nl; corresponding to about one-tenth of the luminal volume of the exocoelom). Control injected embryos developed normally, as judged by embryo viability, somite number, axial rotation, allantois elongation and fusion, and neural tube closure. Yolk sac vasculogenesis appeared normal, but the yolk sac was sometimes enlarged when compared to freshly isolated embryos. Only embryos in which the heart was beating were assessed for amnion development. Embryos were fixed and processed for paraffin embedding.

RESULTS

**Smad5m1/1 mouse embryos have extra-embryonic and embryonic defects**

The Smad5m1 allele was bred into C57BL/6J and F2 (C57BL/6J×CBA) backgrounds to reduce phenotype variation. In both backgrounds we observed the same defects in gross morphology as in Smad5m1/1 embryos in a mixed background (Chang et al., 1999), although relatively fewer mildly affected embryos were recovered and anterior defects were more pronounced (data not shown). The very first defects visible in Smad5 mutants were the delayed appearance of the allantois at late streak (LS) stages (P<0.01 with Wilcoxon’s summed ranks test) (Fig. 1A) and the relatively posterior closure of the amnion visible in late streak-early bud (LSEB) to HF stage embryos (Table 1, data not shown). The delayed appearance of the allantois was followed initially by normal extension

<table>
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<td>2 (25%)</td>
<td>1 (13%)</td>
<td>5 (62%)</td>
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<tr>
<td>13-28S</td>
<td>19</td>
<td>2 (11%)</td>
<td>2 (11%)</td>
<td>2 (11%)</td>
<td>13 (58%)</td>
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*These defects are often associated with posterior closure of the amnion (see Fig. 1D,E; Fig. 3B and Fig. 4 for examples).
DEVELOPMENT

until the late neural plate (LNP) stage. There was negligible extension between the LNP and 1-2 somite (S) stage, but cellular material accumulated into the base of the allantois, expanding its width (Fig. 1B) and producing irregularities. Normal extension was resumed after the 1/2S stage until fusion with the chorion at ~6S stage, which occurred in most mutants with an irregularly shaped and short allantois (Fig. 1A,B,D,E).

Initiation of the allantois was also delayed in the heterozygotes at LS stages (*P<0.01) (Fig. 1A); extension was then parallel to that of the wild type until chorion-allantoic fusion. This phenotype is very similar to that in Bmp4 heterozygotes (see Fig. S1A in the supplementary material). The delay in allantoic initiation and the later growth defect in the Smad5 mutant are not due to general growth retardation, as shown by relating allantois length to embryonic axis length (Fig. 1C, Fig. S1B): the differences remained.

Fig. 1. Impaired allantois and PGC development in Smad5m1/m1 embryos. (A-C) Allantois dimensions measured in embryos collected from Smad5m1/+ crosses in F2 (C57BL/6J × CBA) background. Results at different developmental stages were expressed as means ± s.e. The numbers under the histogram represent the number of embryos in each group. A numerator indicates the embryos with an allantoic bud. Zero values are not included in the mean. (A) Allantois length (µm). (B) Allantois width (µm) was measured at the base of the allantois (right-left axis). (C) The ratio of the allantois length over the embryonic axis length. (D) Wild-type (5S) embryo with a well-developed head, hindgut entrance (open arrowhead) and heart, and an elongated allantois. The amnion is thin and smooth. (E) Representative stage-matched Smad5m1/m1 (KO) littermate with abnormal body curvature, underdeveloped anterior structures and foregut, ventral heart, broad base of the allantois and an aggregate on the amnion (*). (F) Number of PGCs detected in embryos of the three Smad5 genotypes at late streak, neural plate and headfold stages. Wilcoxon's summed ranks test was used for statistical analysis (***, P<0.001; **, P<0.01; *, P<0.05), and medians are depicted by a bar. (G,H) Dorsal view of wild-type (28S) and Smad5m1/m1 (26S) mutant embryos dissected free from their yolk sac. The amnion is a thin, smooth membrane that envelops the embryo (G, arrowheads). A characteristic aggregate of cells is present on the mutant amnion (H, arrow). (I) Whole-mount staining for alkaline phosphatase (AP) activity in a mutant amnion (10-11S stage) with an aggregate of cells. A cluster of ectopic AP+ (brown; arrow) PGC-like cells projects from the amnion ectoderm side of the amnion. (J) AP staining of a section through the aggregate of cells on the mutant Smad5m1/m1 amnion shown in H, at the level of the hindbrain. Ectopic PGC-like cells (red) are localized in close association with the amnion ectoderm. Scale bars: 500 µm in G,H; 200 µm in K; 100 µm in C,D,J, AI, allantois; Am, amnion; AmEc, amnion ectoderm; AmMe, amnion mesoderm; EHF, early headfold; He, heart; Hf, headfold; Hg, hindgut; LNP, late neural plate; LS, late streak; NF, neural plate; Nt, neural tissue.
At the HF stage, the amnion is a thin membrane composed of two layers of squamous epithelium: the amnion ectoderm is continuous with the embryonic surface ectoderm and the amnion mesoderm is continuous with the yolk sac mesoderm and, posteriorly, with the allantois mesothelium. The two layers are derived from slightly different regions of the early-streak stage epiblast (Lawson et al., 1991) (K.A.L., unpublished). The amnion was markedly thickened in Smad5<sup>m1/m1</sup> embryos (Table 1). The amnion of somite-stage mutants typically contained aggregates of cells (Table 1) that were often localized very anteriorly at a remote distance from the allantois. From the 5S stage onwards, Smad5<sup>m1/m1</sup> embryos had an underdeveloped forebrain and heart when compared with stage-matched control littermates, and an aggregate of cells was visible on the amnion in more than half of the mutants (Fig. 1D,E). Failure of embryo turning, defects in heart looping and dilation of embryonic and yolk sac blood vessels were as previously described (Chang et al., 1999; Chang et al., 2000).

**Fig. 2. Epiblast/stem cell and PGC-markers in Smad5<sup>m1/m1</sup> embryos.** Transverse sister sections through hindgut region (A,E,I,M) and head region (B,F,J,N) of an E8.5 wild-type embryo, and of an E8.5 Smad5<sup>m1/m1</sup> litterate with multiple aggregates of cells on the amnion (C,D,G,H,K,L,O,P). The arrow points to the amnion. (A-D) Anti-Oct4 antibody staining demonstrates the presence of PGCs in the hindgut (A; open arrowheads). Oct4<sup>+</sup> cells are absent in control (B) and non-thickened mutant amnion (C,D). Ectopic Oct4<sup>+</sup> cells can be observed regionally in some aggregates in mutant amnion. Oct4<sup>+</sup> cells have an ectoderm oriented localization (C,D). (E-H) PGCs in the hindgut are marked by their fragilis expression (E; open arrowheads). Ectopic fragilis<sup>+</sup> cells can be observed within the aggregate of mutant amnion, but not in the non-thickened amnion (G,H). (I-L) Stella is expressed in PGCs in the hindgut (I; open arrowheads). Stella expression was never observed in wild-type (J) or mutant (K,L) amnion, also not in regions where Oct4<sup>+</sup>, SSEA-1<sup>+</sup> and fragilis<sup>+</sup> cells are residing (K,L). (M-P) Anti-SSEA-1 antibody staining demonstrates the presence of SSEA-1 in surface ectoderm, visceral endoderm and the neuroectoderm (N). At this stage of development PGCs in the hindgut are SSEA-1 negative (M). There is intense SSEA-1 staining in the mutant amnion ectoderm, and weaker staining can be observed in the aggregates. (Q) Schematic representation of the different regions that can be recognized within the mutant amnion. Scale bars: 100 µm.
De-novo appearance of AP-positive cells in the Smad5 mutant amnion
Chang and Matzuk (Chang and Matzuk, 2001) described a Smad5 gene dosage effect, reminiscent of, although less pronounced than, the Bmp4 null allele, on the size of the PGC founder population in a 129S1/EV/C57 mixed genetic background. We confirm these observations now in the C57BL/6J and F2 background (see Fig. S2 in the supplementary material), and have determined that the incidence and number of PGCs is already reduced in Smad5 mutants at the LS stages, with an intermediate effect in the heterozygotes (Fig. 1F). Chang and Matzuk (Chang and Matzuk, 2001) observed AP- and Oct4+ cells in the aggregate of cells in the amnion of early somite-stage embryos, and concluded that they are mislocated PGCs. We explored the timing of appearance of these PGC-like cells in the amnion. Although half of the NP up to the 4S stage embryos had defects in allantois development, amnion closure and amnion thickening, no AP+ PGC-like cells were seen in the Smad5m1/m1 amnion at these stages (Table 1), or elsewhere outside the normal PGC domain. Only after the 5S stage, did we find AP+ cells in some of the distinct aggregates of cells on the amnion (Fig. 1H,J; Table 1). These were located in the part of the aggregate projecting into the amniotic cavity and therefore associated with amnion ectoderm (Fig. 1J), unlike the ectopic haematopoietic and endothelial cells that bulged into the mesoderm side of the amnion facing the exocoelom. By contrast to previous data (Chang and Matzuk, 2001), we found that AP+ clumps were still prominent at E9.5 (11/14 embryos: 16-28S) (Fig. 1H,J; Table 1). The sudden appearance of PGC-like cells in appreciable numbers in the aggregates (33 to 119 PGC-like cells in 5S-12S embryos; 142 cells in the aggregate of the 26S mutant shown in Fig. 1H,J), and the anterior position of the aggregates containing them, make it unlikely that they are PGCs mislocated from the founder population, and supports the argument for a change in cell fate in situ in the mutant amnion.

The AP+ cells in the Smad5 mutant amnion are not bona fide PGCs
We used a panel of markers to address the possibility that the AP+ cells in the aggregates were de-novo induced PGCs. The epiblast expresses Oct4. During gastrulation the expression of Oct4 is downregulated and is thereafter only maintained in the germ cell lineage (Schöler, 1991) (Fig. 2A). Wild-type and non-affected Smad5m1/m1 amnion was always devoid of Oct4 protein (Fig. 2B-D), but the cell aggregates often contained Oct4+ cells (Fig. 2C,D). At E6.5, fragilis (Ilitm3/Mil1) is expressed in proximal epiblast (Saitou et al., 2002), the region in which PGC-competent cells reside (Lawson and Hage, 1994). During gastrulation, fragilis expression increases within a cluster of cells at the base of the allantoic bud. At E7.5 (early bud stage) cells with the highest expression of fragilis initiate at the germ cell-characteristic expression of Stella/PGC-7/Dppa3 (Saitou et al., 2002; Tanaka et al., 2004; Tanaka et al., 2005). Fragilis expression level in non-thickened amnion was comparable to wild-type amnion. In the aggregate, an ectopic fragilis expression domain was observed that contained Oct4+ cells, but exceeded this domain (Fig. 2G,H, compared with 2C,D). Although we observed Stella-expressing PGCs in the hindgut of wild-type and Smad5m1/m1 embryos (Fig. 2I, data not shown), we did not find any Stella-expressing cell in the cell aggregates in the Smad5m1/m1 amnion (Fig. 2K,L, data not shown).

Mouse SSEA-1 is expressed in epiblast, postgastrulation ectoderm and endoderm, and in migrating PGCs (Fox et al., 1981). We detected expression in visceral and gut endoderm, and in surface ectoderm (Fig. 2M,N), but at E8.5, PGCs in the hindgut were still SSEA-1 negative (Fig. 2M) (Donovan et al., 1986). Remarkably, Smad5m1/m1 embryos had a robust SSEA-1 staining throughout the entire ectoderm, and sporadically also in the mesoderm, of the bilayered amnion (Fig. 2N,O). In addition, we observed that SSEA-1+ regions largely overlapped with fragilis+ cells of the aggregate (Fig. 2N,O).
Based on this marker analysis we identified several distinct areas in Smad5<sup>m1/m1</sup> mutant amnion (Fig. 2Q): (1) SSEA-1<sup>+</sup> amnion with normal appearance resembling surface ectoderm; (2) SSEA-1<sup>+</sup> and fragilis<sup>+</sup> areas in the cell aggregates, and within these areas; (3) SSEA-1<sup>+</sup>, fragilis<sup>+</sup>, Oct4<sup>+</sup>, AP<sup>+</sup> cells that did not express Stella. Further co-localization and marker studies may rule out whether cells exist that are either SSEA-1<sup>+</sup> or fragilis<sup>+</sup>, and unravel the precise provenance and identity of the cells. The absence of Stella expression rules out the possibility that the AP<sup>+</sup> cells are fully specified PGCs; the expression pattern found is compatible with reversion by the mutant amnion to a pluripotent state. At the mesodermal side of the aggregate facing the exocoelom, cells could be detected that did not express any of the PGC/epiblast/ES cell markers.

**Smad5 is essential for both cell layers of the amnion to preserve homeostasis**

Chimeric embryos offer the possibility of analysing interactions between normal and mutant cells. Although the majority of the Smad5<sup>m1/m1</sup>→WT<sup>lacZ</sup> chimeras (14 out of 18) of Smad5<sup>m1/m1</sup> ES cells in wild-type lacZ transgenic (WT<sup>lacZ</sup>) host embryos were high chimeras with >90% mutant cells in the epiblast derived tissues, the low-percentage chimeras (estimated between 20 and 80% chimerism, depending on the embryo) were very instructive. They had the typical mutant phenotype in the extra-embryonic tissues, with large cell aggregates in the amnion (Fig. 3A,B). Smad5<sup>m1/m1</sup> cells made, just like descendants from wild-type ES cells (Fig. 3C), an unbiased contribution to the mesodermal and ectodermal components of the amnion (Fig. 3D,E). Intriguingly, the aggregates in low-percentage chimeras were not composed solely of disorganized mesodermal cells, which we anticipated from our earlier work (Chang et al., 1999), but the amnion ectoderm was also sometimes thickened, and was even entirely of wild-type origin in one chimera (Fig. 3E). This suggests that loss of Smad5 in the mesoderm affects not only the mesodermal but also the ectodermal component of the amnion, and attributes a non-cell-autonomous function to Smad5 in mesoderm. Based on this result, we re-evaluated the expression of Twist (amnion mesoderm) and AP-2 (amnion ectoderm) in Smad5<sup>m1/m1</sup> amnion. Aggregates of cells are predominantly of mesodermal origin but sometimes contain locally a thickened Twist negative and AP-2 positive ectodermal component (Fig. 3F,G).

**Loss of Smad5 leads to an increase in expression of Bmp genes and Bmp target genes in the amnion**

The expansion of the amnion may result from a change in either cell proliferation or cell shape from a columnar or cuboidal to an extreme squamous morphology. Bmp2 has been implicated in amniotic expansion, but the mechanisms remain elusive (Zhang and Bradley, 1994).
1996). We evaluated the expression of Bmp genes, and some of their target genes and modulators. Bmp2 transcript levels were extremely low in the wild-type amnion at E8.5, if at all above background (Fig. 4A,B), whereas Bmp4 expression was detectable in amnion (Fig. 4E). A dramatic increase of Bmp2 and Bmp4 transcripts was observed in the Smad5m1/m1 amnion. Bmp2 was upregulated in the cells of the aggregates and neighbouring unaffected amnion, but not in squamous amnion distant from the aggregate (Fig. 4C,D). Bmp4 was significantly upregulated, also in squamous amnion (Fig. 4F), but the expression of Bmp7 appeared unaffected (data not shown). During gastrulation, Bmp4 expression is dynamic. Expression persists within the extra-embryonic ectoderm, and Bmp4 transcripts become detectable in the extra-embryonic mesodermal components of the amniotic folds, and subsequently in the amnion, yolk sac and chorion that line the exocoelom, as well as within the allantoic bud/allantois (Lawson et al., 1999) (data not shown). At the NP stage, before detectable thickening of the mutant amnion, Bmp4 levels appeared already more robust in the amnion of mutants when compared with control littersmates (Fig. 4G-J). Bmp2 expression was low at this stage of amnion development, without clear differences between mutants and controls (Fig. 4K,L).

The observed upregulation of Bmp2/4 may cause increased Bmp signalling via Smad1/8 or non-Smad pathways, including ERK1/2 (Nakamura et al., 1999; Qi et al., 2004). The pattern of phosphorylated (P)-ERK1/2 staining at E7.5 and 8.5 in wild-type littersmates is very variable and reflects the dynamic nature of phosphorylation-dependent signalling cascades (data not shown). At E7.5 and 8.5 P-ERK1/2-positive cells are very rare in the wild-type amnion (Fig. 5A, data not shown). No dramatic increase in P-ERK1/2 staining was observed in non-thickened amnion (Fig. 5B,C, data not shown); however, manifest ERK signalling was observed within the aggregates. Likewise, the P-Smad1/5/8 staining pattern was very dynamic in E7.5 and 8.5 wild-type littersmates, and could be observed only sporadically in amnion (Fig. 5D). In the Smad5m1/m1 amnion enhanced P-Smad1/8 staining was most evident in the aggregate (Fig. 5E,F). These results illustrate enhanced Bmp signalling in the mutant amnion.

We then analysed the expression of acknowledged Bmp target genes in the Smad5m1/m1 amnion. Periostin/Osf2 is involved in cell adhesion and spreading (KruzynskFrejtag et al., 2001), and at E8.5 its only sites of expression are the amnion and the yolk sac (Fig. 5G). In the Smad5m1/m1 amnion, periostin expression was more pronounced, although excluded from the aggregate of cells (Fig. 5H). Msx2 is expressed in surface ectoderm (Monaghan, 1991) but barely in amnion (Fig. 5I). Msx2 is robustly expressed in the mutant amnion, predominantly in its ectodermal component (Fig. 5J). This shows that higher Bmp2/4 levels indeed result in increased expression of Bmp target genes in the Smad5m1/m1 amnion. Genes

Fig. 5. Ectopic Bmp signalling in Smad5m1/m1 amnion. (A-C) Anti-P-ERK1/2 antibody staining can barely be detected in the amnion (arrowhead) at E8.5 (A). It is increased in non-thickened Smad5 mutant amnion but especially elevated in the aggregate of cells (B,C). B and C represent two different Smad5 mutants. (D-F) Anti-phospho-Smad1/5/8 antibody staining can only be detected sporadically in an isolated cell of the amnion (arrowhead) at E8.5 (A). P-Smad1/5/8 is upregulated in non-thickened mutant amnion and within the aggregates of Smad5 mutant amnion. Sections in D-F are sister sections of A-C. (G,H) The Bmp target gene periostin is expressed in the amnion (arrowhead) at E8.5. It is strongly upregulated in the non-thickened Smad5 mutant amnion, although excluded from the aggregate of cells (H). (I,J) The Bmp target gene Msx2 is barely detectable in wild-type amnion (I) but highly expressed in mutant amnion at E8.5 (J). Msx2 expression is primarily confined to the ectodermal component of the amnion (arrowhead) and the aggregate of cells (arrow). The expression of Msx2 in the embryo proper is not altered significantly. AmMe, amnion mesoderm; He, heart; Nt, neural tube; Se, surface ectoderm; Ys, yolk sac. Scale bars: 100 μm.
encoding Bmp antagonists like noggin, chordin and Smad7 are expressed at low levels in the amnion and no significant changes in their expression domain were detected in Smad5<sup>m1/m1</sup> embryos (data not shown).

**Administration of BMP4 can mimic the early Smad5 deficiency amnion defect**

The ectopic expression of Bmp2 and Bmp4, and of several Bmp target genes, as well as the different Bmp-sensitive cell types that arise in a regionalized fashion in the Smad5 mutant amnion, favours a gain-of-Bmp-function model underlying the Smad5<sup>m1/m1</sup> amnion defect. To test this hypothesis, we injected recombinant mature BMP4 (rBMP4) in the exocoelom of NP- to HF-stage wild-type embryos, and cultured these whole embryos until early somite to 10-15S stages, when the amnion was then screened for the presence of cell aggregates. Small clumps of cells were observed sporadically in embryos injected with rBMP4 (2/10 NP, 6/25 EHF to HF stages), whereas control-injected embryos never developed a similar defect (0/10 NP, 0/15 EHF to HF) (Fig. 6A-F). The aggregates were sometimes only recognizable after histological analysis. These results show that even in a wild-type context, excess BMP4 can induce thickening of the amnion, confirming that BMP levels are crucial for preserving amnion homeostasis.

**DISCUSSION**

**Smad5 in extra-embryonic development**

Smad5 is essential for PGC development and for correct extra-embryonic development, including the development of the allantois and the amnion. We can now order the appearance of these defects in the Smad5-deficient proximal epiblast and its extra-embryonic descendants as follows: (1) delayed appearance of the allantois, presumably associated with the reduced PGC founder population in Smad5 mutants (both evident at the LSEP stage); (2) a relative posterior and delayed closure of the amnion visible in LSEP to HF stages, and abnormal morphogenesis of the allantois after the LNP stage; (3) anterior defects involving the delineation between anterior neural plate and ectoderm, including the amnion ectoderm (first identifiable at NP and EHF stages), and a thickened amnion at HF stages; and (4) distinct aggregates of cells on the amnion of early somite embryos, which become vascularized and haematopoietic, and often contain Oct4<sup>+</sup> and AP<sup>+</sup> cells from 5S stage onwards.

The delay in allantoic bud formation in Smad5 mutants, and the reduced incidence and number of PGCs at the LSEP stage, reflects a well documented loss of Bmp signalling effect initiated in the extra-embryonic ectoderm and visceral endoderm (reviewed by Zhao, 2003). The relatively short allantois in Smad5 heterozygotes, and in Bmp4 heterozygotes, is a consequence of the slight delay in allantois initiation, rather than an effect on cell recruitment to, and proliferation in, the bud. Absence of Smad5 results in abnormal morphogenesis of the allantois after delayed initiation and early normal extension. Failure to extend further during the rest of the cell recruitment and proliferation phases (Downs and Bertler, 2000), and the accumulation of material in the base of the allantois, suggest that cell redistribution may be more affected than the addition of cells. The resumption of extension after the 2S stage coincides with the normal end of recruitment and rapid proliferation and the onset of extension by cavitation and vascularization (Downs and Bertler, 2000). This process appears to be Smad5-independent or open to functional compensation, presumably by Smad1 or Smad8. These latter Bmp-Smads are also expressed in the amnion and allantois (Tremblay et al., 2001; Hayashi et al., 2002) and could implement its closure, the delay of which is probably caused by reduced Bmp2 signalling during an earlier phase of amnion development (Zhang and Bradley, 1996).

A more striking Smad5<sup>m1/m1</sup> defect is the ectopic vasculogenesis, haematopoiesis and development of Oct4<sup>+</sup> and AP<sup>+</sup> cells that can be observed in the aggregate of cells in the Smad5<sup>m1/m1</sup> amnion. Previously, we proposed an exclusive mesodermal origin for these aggregates of cells (Chang et al., 1999). New evidence from the low-percentage chimeras showed that the aggregates are not exclusively comprised of mesodermal cells but occasionally also contain thickened ectoderm. The mesodermal part of the aggregates in mutants can result from
Smad5 is required for amnion homeostasis

**Fig. 7. Model for the role of Smad5 signalling in amnion homeostasis.**

(A) The squamous, bilayered wild-type amnion at the early somite stage is composed of a mesoderm layer facing the exocoelom that expresses Twist, whereas an epithelial cell layer that expresses AP-2 lines the amniotic cavity. The chimera analysis demonstrates that Smad5 is essential in the mesoderm, where it functions in a non-cell-autonomous fashion, because mutant mesoderm cells can elicit thickening of wild-type amnion ectoderm. Reciprocally, however, we cannot conclude that Smad5 functions also non-cell-autonomously and/or cell autonomously in the ectoderm.

(B) At the early somite stage the Smad5-/- mutant amnion displays an altered cellular organization with a zone of primarily thickened mesoderm but also thickened ectoderm. The mutant amnion ectoderm is positive for SSEA-1. The anterior amnion ectoderm remains cuboidal (squares), and is in continuity with anterior surface ectoderm and anterior neural tissue. Robust ectopic expression of Bmp2 and Bmp4 in mutant amnion is associated with increased Smad1/5/8 and ERK1/2 signalling and expression of periostin, Tbx2, fragilis and Msi2. The differential but overlapping ectopic expression patterns of all these Bmp-target genes suggest that cells in the mutant amnion sense different levels of Bmp signalling. How these different levels of Bmp signalling are established in the mutant amnion remains to be explored.

(C) The transformation of the amnion to a complex tissue with different Bmp-sensitive cell types, such as e.g., Oct4*, AP*, SSEA-1* and fragilis* region reminiscent of PGc-competent epiblast, Flk1-expressing endothelial cells and ζ-globin-expressing cells (see Discussion). The ectopic and appreciable numbers of AP* cells arise suddenly from the 5S stage onwards, which arguments strongly for their in situ change in fate. The AP* cells are localized near the ectodermal component of the aggregate, whereas haematopoietic and endothelial cells are positioned at the exocoelomic side. Our data suggest that Smad5 is the predominant Bmp signal-mediator in the amnion, and controls Bmp expression levels and amnion homeostasis tightly. Upon Smad5 removal the control of Bmp expression is released, which results in an excess of Bmp, in take-over by non-Smad5 pathways and ultimately in gain of Bmp signalling defects.

**Smad5 deficiency results in gain-of-Bmp-function defects**

The Smad5-/- amnion defect is accompanied by a specific and robust upregulation of Bmp2 and Bmp4, whereas the expression of Bmp7 appears unaffected. This suggests that Smad5 is normally a predominant Bmp-Smad in the amnion that, directly or indirectly, negatively regulates Bmp2/4 expression. Ectopic Bmp4 expression is readily visible before local thickening of the amnion at the LSEB stage, and subsequently in the aggregate of cells, but also in the neighbouring, seemingly unaffected amnion.
The mutant amnion displays elevated Smad-dependent (Bmp-regulated phospho-Smad1/5/8) and Smad-independent (P-ERK1/2) signalling. Enhanced Bmp signalling is also demonstrated by alterations in the expression pattern of target genes of Bmp. A patent upregulation of periostin can be appreciated in seemingly unaffected mutant amniotic cells. Tbx2 (Chang et al., 1999), fragilis and Msx2 are, unlike periostin, highly upregulated in the aggregate of cells in the mutant amnion. Msx2 is predominantly expressed in the ectoderm component of the aggregate and non-thickened amnion. The increased or ectopic expression of these Bmp target genes in distinct but overlapping domains may indicate that expression of these target genes requires different dose windows of (combined) Bmp(s), which is reminiscent of the different doses of Bmp4 signalling that are required for dorsoventral patterning of mesoderm in Xenopus embryos (Dosch et al., 1997). A localized source of ligand(s) or antagonists/modulators, or several sources of ligands (e.g. Bmp2 and Bmp4) could establish graded signalling. Alternatively or additionally, differences in presence and (e.g. Bmp2 and Bmp4) could establish graded signalling. Enhanced Bmp signalling is also demonstrated by regulated phospho-Smad1/5/8 and Smad-independent (P-ERK1/2) signalling. The increased or ectopic expression of these Bmp target genes in the mutant amnion.

The Smad5m1/m1 amnion acquires features of different Bmp-sensitive lineages, such as allantois and blood island tissue but also PGC-competent epiblast (Lawson et al., 1999) (reviewed by Zhao, 2003; Fujisawa et al., 2001). In the mutant amnion, epiblast-like cells are localized near the ectodermal component, whereas ectopic endothelial and haematopoietic cells are positioned at the exocoelomic side of the aggregate. Concurrent with the differential ectopic expression patterns of several Bmp target genes, this regionalization of the aggregates makes it conceivable that cells indeed interpret different levels of Bmp signalling – whether quantitative and/or qualitative – that determine their subsequent fate (Fig. 7). Bmp4 is not only implicated in differentiation of different cell lineages, but it is also pivotal in maintaining self-renewal of ES cells (Ying et al., 2003; Qh et al., 2004).

Our gain-of-Bmp-function model is especially challenging, as no other mutant mouse model of a Bmp signalling component has been associated so far with ectopic vasculogenesis, haematopoiesis and development of (PGC-competent) epiblast-like cells in the amnion. Evidence that gain of Bmp function may indeed underlie the Smad5 mutant amnion phenotype comes from the induction of amnion thickening in wild-type amnion when rBMP4 is topically administered. Single injection of rBMP4 in the exocoelom compared to constitutive secretion of Bmp4 and Bmp2 in Smad5 mutants is just one out of many explanations why clumps could be significantly smaller in rBMP4-injected embryos than in mutants. The converse experiment, in which Smad5m1/m1 embryos would be rescued by injecting Bmp antagonists such as Noggin and/or Chordin, is appealing. However, it is far more complicated to accomplish, as systemic administration of excess amounts of antagonists would be required to neutralize endogenous Bmps.

Our study has revealed novel aspects of Smad5 signalling, i.e. a non-cell-autonomous function for Smad5 in amnion mesoderm and an in situ change in amnion cell fate upon Smad5 deficiency, and links these to an unexpected gain-of-Bmp-function model that is supported by the exogenous rBMP4 phenocopy experiment. Amnion cultures may be exploited in the future to dissect and to clarify the Bmp signalling pathway that determines change in cell fate of the amnion.

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**Supplementary material**

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/133/7/3399/DC1

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