Corrigendum

Combinatorial gene regulation by Bmp and Wnt in zebrafish posterior mesoderm formation

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The labelling in Fig. 6 of this article is incorrect. The label for A-F should read mut1-2.0-gfp/Xex-bfp and the label for G-L should read mut1,2-2.0-gfp/Xex-bfp. The authors apologise to the readers for this mistake.
Combinatorial gene regulation by Bmp and Wnt in zebrafish posterior mesoderm formation

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Summary

Combinatorial signaling is an important mechanism that allows the embryo to utilize overlapping signaling pathways to specify different territories. In zebrafish, the Wnt and Bmp pathways interact to regulate the formation of the posterior body. In order to understand how this works mechanistically, we have identified tbx6 as a posterior mesodermal gene activated by both of these signaling pathways. We isolated a genomic fragment from the tbx6 gene that recapitulates the endogenous tbx6 expression, and used this to ask how the Bmp and Wnt signaling pathways combine to regulate gene expression. We find that the tbx6 promoter utilizes distinct domains to integrate the signaling inputs from each pathway, including multiple Tcf/LEF sites and a novel Bmp-response element.

Surprisingly, we found that overexpression of either signaling pathway can activate the tbx6 promoter and the endogenous gene, whereas inputs from both pathways are required for the normal pattern of expression. These results demonstrate that both Bmp and Wnt are present at submaximal levels, which allows the pathways to function combinatorially. We present a model in which overlapping Wnt and Bmp signals in the ventrolateral region activate the expression of tbx6 and other posterior mesodermal genes, leading to the formation of posterior structures.

Supplemental data available online

Key words: Bmp, Wnt, Posterior mesoderm, T-box genes, Zebrafish

Introduction

The posterior body of the zebrafish embryo is formed by a network of intercellular signaling molecules that pattern the formation of the ventrolateral mesoderm, which ultimately gives rise to the posterior (trunk and tail) mesoderm. These signaling factors include Bone morphogenetic proteins (Bmps) (reviewed by Hammerschmidt, 2002), Wnt8 (Kelly et al., 1995; Lekven et al., 2001), Fibroblast growth factors (Fgfs) (Amaya et al., 1993; Griffin et al., 1995; Rodaway et al., 1999; Draper et al., 2003; Griffin and Kimelman, 2003), and the Nodal-related proteins (Schier and Shen, 2000; Schier and Talbot, 2001). Whereas the Nodals appear to be critical for mesoderm induction and the Fgfs are important for maintaining mesodermal gene expression (reviewed by Kimelman and Schier, 2002), the exact roles of Bmp and Wnt signaling in forming the ventral/posterior mesoderm have been uncertain.

Three bmps are expressed in the mesoderm of the gastrula-stage embryo and their expression continues at the most posterior end of the embryo throughout somitogenesis (Martinez-Barbera et al., 1997; Nikaido et al., 1997). As in Xenopus, a large body of evidence demonstrates that the Bmps are key regulators of the posterior mesoderm patterning in zebrafish (reviewed by Hammerschmidt, 2002). For example, bmp2b/swirl is expressed in a gradient along the dorsoventral axis (Barth et al., 1999; Wagner and Mullins, 2002) and zebrafish mutants lacking bmp2b/swirl do not form tails (Mullins et al., 1996; Kishimoto et al., 1997). Like the bmps, zebrafish wnt8 is also expressed in the ventrolateral mesoderm during gastrulation and at the posterior end of the embryo during somitogenesis (Kelly et al., 1995). In mutants lacking wnt8, the formation of the ventrolateral and posterior mesoderm is severely disrupted, demonstrating a requirement for Wnt signaling in the development of these mesodermal territories (Lekven et al., 2001).

Two studies have suggested that the Wnt and Bmp pathways cooperate to form the ventral and posterior mesoderm in Xenopus (Hoppler and Moon, 1998; Marom et al., 1999). The importance of such a cooperative interaction between these pathways has been further highlighted in a recent zebrafish study, demonstrating that combined overexpression of Wnt8 and Bmp is capable of inducing ectopic tail formation (Agathon et al., 2003). How these pathways integrate to regulate mesodermal gene expression is unknown.

In order to understand mechanistically how these two pathways interact, we sought a posterior mesodermal gene whose expression required input from both the Bmp and Wnt pathways. The T-box transcription factor tbx6 (Hug et al., 1997) was found to meet this criterion, and we therefore identified a minimal region of the tbx6 gene that reproduces the endogenous gene expression pattern. Analysis of the tbx6 promoter shows that Bmp and Wnt8 regulate tbx6 expression through different domains within the promoter, demonstrating that these pathways intersect by regulating transcription of specific target genes. Elimination of regions that respond to Bmp or Wnt signaling revealed that the promoter is able to respond to overexpression of a single pathway, whereas normally the promoter integrates responses to both pathways to provide normal tbx6 expression. Analysis of the expression
of the endogenous gene under conditions in which either Bmp or Wnt signaling is blocked together with analysis of the tbx6 promoter has allowed us to put forth a model in which submaximal levels of Bmp and Wnt signals cooperate to regulate the formation of the posterior mesoderm. 

Materials and methods

Embryos and morpholino oligonucleotides injections

Zebrafish embryos were obtained by natural spawning of adult AB strain zebrafish. Embryos were raised and maintained at 28.5°C in system water and staged as described (Westerfield, 1995). Wnt8-specific morpholino antisense oligonucleotides were a generous gift from Randy Moon. At the one-cell stage, each embryo was injected with approximately 1 nl volume of morpholino oligonucleotides (5 ng) using a Picospritzer II (Parker Hannifin). Embryos were collected at the appropriate stages and fixed in 4% paraformaldehyde, pH 7.0, in phosphate-buffered saline (PBS), overnight at 4°C. Fixed embryos were dechorionated, washed three times with PBS and stored in methanol at −20°C.

Plasmids and constructs

Various gfp reporter constructs were made by cloning the tbx6 promoter fragments into the BamHI restriction site of the gfp reporter plasmid vector. The dual fluorescence system was created by inserting the pXen-bfp DNA (gift of Stephen C. Ekker) into the existing gfp reporter constructs. The luciferase reporter constructs were made by cloning the tbx5 promoter fragments into the multiple cloning sites of the PGL3 promoter vector (Promega).

Site-directed mutagenesis

The two proximal Tcf site mutations in the tbx6 promoter were generated using the QuikChange procedure (Stratagene). Mut1-2.0 was constructed by using primers: 5′-ctaggcttctaccttcttccatca-3′ and 5′-ctacctccacatcagttgctacc-3′. Mut2-2.0 was constructed by using primers: 5′-ctacctccacatcagttgctacc-3′ and 5′-cttctgtcaaaacatcagtctcctcgttaacctgtcttttgtct-3′. Mut1,2-2.0 construct was generated by combining the two mutated Tcf sites.

DNA and RNA injections

DNA was isolated with a Qiagen midi kit and resuspended in RNase-free water. DNA at a concentration of 0.1 mg/ml was used for injection. RNAs were synthesized from Snail linearized SP64T-Xbmp4 (gift of Jim Smith), Asp718 linearized CS2-zwnt8 (gift of Randy Moon) and Norl linearized CS2-TVGR (gift of Paul Wilson) templates using the mMessage Machine Kit (Ambion) and dissolved in RNase-free sterile water. RNA (at concentrations indicated in the text) was injected in the presence or absence of 0.1 μg of reporter DNA into one-cell zebrafish embryos. The expression of the reporter gene was analyzed at the appropriate stages using bright field or fluorescence microscopy.

In situ hybridization

Whole-mount in situ hybridization was performed using digoxigenin-labeled antisense RNA probes and visualized using anti-digoxigenin Fab fragments conjugated with alkaline phosphatase (Roche Molecular Biochemicals) as described (Griffin et al., 1998). Riboprobes were made from DNA templates, which were linearized and transcribed with either SP6 or T7 RNA polymerases. Embryos were processed and hybridized as described (Griffin et al., 1998), except that 5 μg/ml of Proteinase K in PBS/0.1% Tween-20 was used for 5 to 10 minutes depending on the age of the collected embryos.

Xenopus and zebrafish transgenesis

PAC DNA was isolated with the Qiagen midi kit. To generate Xenopus transgenic embryos, we used 200 pg of PAC DNA for each injection as described (Amaya and Kroll, 1999) with the exception that no restriction enzyme was used. To generate stable transgenic zebrafish lines, reporter plasmid DNA was digested with BssHII to completion, and then separated on a 1% agarose preparative gel overnight. The gel slice containing the DNA insert was isolated and DNA was electrophoresed using a Schleicher and Schuell ELUTRAP. DNA was extracted once with equal volume of phenol and once with an equal volume of chloroform. After extraction, DNA was ethanol precipitated and then resuspended in distilled water. For injection, 80 mg/ml of purified DNA insert was used to inject one-cell stage zebrafish embryos. Injected embryos were examined at the 15- to 18-somite stage for the presence of GFP fluorescence. Embryos showing specific GFP fluorescence in the tail region were collected and raised to sexual maturity as founders. Different combinations of founder crosses were set up for the identification of F1 embryos showing mosaic GFP fluorescence in the tail region at the 15- to 18-somite stage.

Luciferase assays

Injected embryos were collected at the shield stage and then separated into three pools of 10 embryos each for assay in triplicate. Experiments were repeated at least three times. Excess zebrafish embryo medium was removed, embryos were homogenized in 100 μl of 1×Cell Culture Lysis Reagent (Promega), and cleared by 10 minutes’ microcentrifugation at room temperature. Fifty microliters of the resulting supernatant was used for luciferase activity assays that were performed according to the Promega protocol with a Berthold luminometer.

Results

Regulation of tbx6 expression by Wnt and Bmp signals

In our initial attempts to find a gene regulated by both the Wnt and Bmp pathways, we identified the T-box transcription factor tbx6 as a candidate. Tbx6, along with two other T-box genes, spadetail (spt) and no tail (ntl), is expressed in the posterior mesoderm from the gastrula stage through the end of somitogenesis (Schulte-Merker et al., 1994; Hug et al., 1997; Griffin et al., 1998). Wnt8 was previously shown to be required for the expression of tbx6 in the ventrolateral mesoderm (Lekven et al., 2001), which we confirmed using a pair of wnt8-specific morpholino oligonucleotides (MOs) (Fig. 1A,B) (n=55). Whereas the lateral expression was completely absent, some residual tbx6 expression was observed in the ventral region (Fig. 1B). In contrast, ntl expression was unaffected by the inhibition of Wnt8 function (Fig. 1E,F) and spt expression was only partially affected (Fig. 1C,D), indicating that tbx6 is the most dependent of the three mesodermal genes on Wnt function at the gastrula stage.

To determine if tbx6 is regulated by Bmp signaling, we examined tbx6 expression in swirl mutants, which have a defective bmp2b gene (Kishimoto et al., 1997; Nikaido et al., 1997). In approximately one quarter of the embryos collected from the crosses of swirl heterozygotes, we observed a strong reduction in the expression of tbx6 (Fig. 1G,H) (n=75), whereas the expression of spt and ntl was normal in all the embryos examined (Fig. 1I-L). Interestingly, unlike the result observed with the wnt8MOs (Fig. 1B), swirl embryos showed residual tbx6 expression in both the ventral and lateral regions (Fig. 1H). Similar results were obtained with embryos injected with RNA encoding the Bmp inhibitor Noggin (Fig. 2A,B).
(85%, n=65). These results demonstrate that normal tbx6 expression requires input from both the Wnt and Bmp pathways, which is consistent with the observation that both Bmp and Wnt signals are required for the formation of the posterior body in zebrafish (Lekven et al., 2001; Agathon et al., 2003).

To further examine the regulation of tbx6 by Bmp and Wnt signals, we overexpressed these factors in the early zebrafish embryo. We observed that overexpression of either signaling molecule caused ectopic tbx6 expression throughout the embryo (Fig. 2C,F) (80%, n=43). These results suggest that tbx6 can be separately activated by each of these signaling pathways alone, although it was possible that each of the overexpressed signals also activated the other signaling pathway. To eliminate the effect of the other pathway, we coinjected wnt8 with the Bmp inhibitor noggin, and coinjected Xenopus bmp4 (Xbmp4) RNA (Xbmp4 causes the same effects as the zebrafish Bmps) (Kishimoto et al., 1997) with the wnt8MOs. Whereas 50 pg of noggin alone caused a strong reduction in tbx6 expression, as was observed in swr mutant embryos (Fig. 2B, compare with Fig. 1H), noggin only caused a partial reduction in the ectopic tbx6 induced by overexpression of wnt8 (Fig. 2D) (70%, n=35). This result suggests that only a part of the wnt8-mediated activation of tbx6 depends on the ability of Wnt8 to upregulate endogenous bmp2b expression (Agathon et al., 2003). Conversely, whereas the wnt8MOs strongly downregulated tbx6 expression (Fig. 2G), the wnt8MOs did not inhibit marginal tbx6 expression in Xbmp4-injected embryos, although it reduced the animal pole expression of tbx6 (Fig. 2H) (87%, n=45). Because bmp overexpression does not alter zygotic wnt8 expression (Agathon et al., 2003), our results suggest that maternal wnt8 (Kelly et al., 1995) is required for the high-level ectopic animal pole expression of tbx6 in Xbmp4-injected embryos, but it is not required for Xbmp4 to activate tbx6 expression at the margin. In summary, our results show that both Wnt and Bmp can induce tbx6 expression when the other pathway is blocked, although the two factors alone can activate tbx6 in specific patterns.

Identification and characterization of the tbx6 promoter

In order to understand how these two pathways regulate tbx6 expression, we screened a zebrafish PAC genomic library and obtained three tbx6 positive clones. Using the frog transgenesis approach (Amaya and Kroll, 1999), we tested one of these tbx6 positive PAC clones (PAC-tbx6) for its ability to target zebrafish tbx6 by Wnt and Bmp. (A-H) Lateral views with the animal pole to the top. (A,B) Expression of endogenous tbx6 in an uninjected embryo (A) and in an embryo injected with 50 pg of noggin RNA (B). The injected embryo shows dramatic reduction of tbx6 expression. (C) An embryo injected with 75 pg of wnt8 RNA shows ectopic expression of tbx6. (D) An embryo co-injected with 75 pg of wnt8 RNA and 50 pg of noggin RNA showing ectopic expression of tbx6 in the animal pole. (E-H) Expression of endogenous tbx6 in an uninjected embryo (E) and in an embryo injected with 150 pg of Xbmp4 RNA (F). The injected embryo shows ectopic expression of tbx6. (G) An embryo injected with wnt8MOs shows decreased expression of tbx6. (H) A zebrafish embryo co-injected with wnt8MOs and 150 pg of Xbmp4 RNA showing strong marginal and ectopic dorsal domains of tbx6 expression.
at http://dev.biologists.org/supplemental). This expression pattern matches the endogenous Xenopus tbx6 (Uchiyama et al., 2001) as well as that of the ntl ortholog Xbra (Smith et al., 1991) (see Fig. S1D at http://dev.biologists.org/supplemental). These results demonstrate that PAC-tbx6 has all of the regulatory elements necessary for expression within the posterior mesoderm, and that these regulatory sites are conserved between fish and frogs.

Having determined that PAC-tbx6 targets expression to the posterior mesoderm in developing Xenopus embryos, we subcloned smaller fragments and characterized them in zebrafish. We initially focused on two constructs fused in frame to GFP, ptbx6-1.7-gfp and ptbx6-2.0-gfp, which contain 1.7 and 2.0 kb of DNA upstream from the start of translation, respectively, and the first intron (Fig. 3A). These constructs were injected into one-cell stage zebrafish embryos and then analyzed for GFP fluorescence at different stages of development. At 60-75% epiboly, we observed GFP fluorescence at the margin where endogenous tbx6 is normally expressed (Fig. 3B,C, Table 1). At the 15- to 18-somite stage, GFP fluorescence was detected in the tail mesoderm, again matching the endogenous pattern of expression (Fig. 3D,E, Table 1). Although both reporter constructs were expressed in the same pattern, we noticed that ptbx6-2.0-gfp produced consistently higher fluorescence levels than ptbx6-1.7-gfp, suggesting the presence of a general enhancer between –1.7 and –2.0 kb. The fluorescence results were confirmed by in situ hybridization with a gfp probe on zebrafish embryos injected with either of the two reporter constructs (see Fig. S2 at http://dev.biologists.org/supplemental).

Because expression from injected DNA is mosaic (non-uniform), we wanted to confirm that the tbx6 promoter constructs faithfully matched the endogenous gene expression by producing transgenic embryos. We therefore created stable transgenic zebrasih lines [Tg(tbx6:gfp)] expressing ptbx6-1.7-gfp. As shown in Fig. 3, the expression of transcripts from ptbx6-1.7-gfp was the same as the endogenous tbx6 gene expression pattern (Fig. 3H-O). The GFP fluorescence matched the transcript pattern, although it extended more anteriorly (Fig. 3F,G). This was expected because the posterior mesodermal cells originate at the most posterior end and are incorporated into somites as the posterior end extends (Kanki and Ho, 1997). Because GFP is a stable protein, it perdures for a while in more anterior regions as the posterior end extends caudally, producing a posterior to anterior gradient of fluorescence (Fig. 3G). We also tested ptbx6-1.7-gfp in transgenic Xenopus embryos and found that it produced the same pattern of expression as PAC-tbx6 (data not shown). These data demonstrate that ptbx6-1.7-gfp and ptbx6-2.0-gfp have all of the necessary regulatory elements to recapitulate
expression of the tbx6 gene in both transient expression assays and in transgenic embryos.

**Regulation of the tbx6 promoter by Wnt and Bmp**

During the development of the posterior mesoderm, the endogenous tbx6 promoter must be able to integrate inputs from both the Wnt and Bmp pathways, as shown above. We therefore tested the ability of ptbx6-1.7-gfp to respond to these signaling pathways by injecting the promoter with wnt8 RNA and compared the response of the endogenous gene with the same levels of exogenous Wnt and Bmp signaling inputs. Similar to the response of the endogenous tbx6 gene in the presence of Wnt8 overexpression, we observed ectopic GFP fluorescence in embryos coinjected with the presence of Wnt8 overexpression, we observed ectopic expression at the margin (Fig. 5C,D). At later stages, the BFP was ubiquitous but the GFP was restricted to the most posterior end of the embryo (Fig. 5F,G). We used this system in our subsequent studies such that we only scored the presence or absence of GFP fluorescence in embryos in which there was substantial BFP fluorescence in the ventral-lateral mesoderm during the gastrula stages or in the posterior mesoderm during somitogenesis. We found that this was a much more reliable method for analyzing gene expression from exogenous promoters in transient zebrafish assays.

**Mutational analysis of the tbx6 promoter**

To understand how the tbx6 promoter is regulated by Wnt and Bmp signals, we undertook a systematic analysis of the tbx6 promoter. The canonical Wnt signaling pathway typically works through regulation of the Tcf transcription factor (reviewed by van Noort and Clevers, 2002). Consistent with this, ectopic expression of a constitutively activated Tcf (TVGR) (Darken and Wilson, 2001) caused widespread activation of ptbx6-1.7-gfp (Fig. 4I), as did ectopic wnt8 expression (Fig. 4C,D). Examination of the tbx6 promoter constructs revealed three consensus Tcf binding sites within the 900 bp proximal region of the promoter (Fig. 3A). The presence of multiple Tcf sites in the tbx6 promoter suggested that the expression of tbx6 is directly regulated by Wnt8 signaling during posterior mesoderm formation.

Using our dual fluorescence system, we asked whether the activation of ptbx6-2.0-gfp in the posterior mesoderm required these Tcf DNA binding sites. To do this, we mutated the two proximal Tcf sites (Tcf-1 and Tcf-2) (Fig. 3A), generating mut1-2.0-gfp/Xex-bfp containing a mutation in the first Tcf site, mut2-2.0-gfp/Xex-bfp containing a mutation in the second Tcf site, and mut1,2-2.0-gfp/Xex-bfp containing both mutations. We found that either single mutation alone did not dramatically affect the expression of the tbx6 promoter in the developing posterior mesoderm as indicated by the presence of strong GFP fluorescence (Fig. 6A-F, Table 1). In contrast, zebrafish embryos injected with the double Tcf site mutation construct showed almost no detectable GFP fluorescence in the majority of the embryos and the remainder had only occasional BFP-positive mesodermal cell expressing GFP (Fig. 6G-L, Table 1). The double Tcf site mutant promoter was still functional, however, because overexpression of the constitutively active Tcf was able to activate transcription from this promoter, probably through the remaining Tcf site (Table 1). In addition, this promoter was activated when coinjected with Xbmp4, a reporter gene under the control of a ubiquitous Xenopus EF1α (pXex) promoter, which has been characterized and shown to produce ubiquitous BFP fluorescence in developing zebrafish embryos (Finley et al., 2001). Our dual fluorescence (blue and green) system allows simultaneous detection of the regions of the embryo that inherited the injected DNA by examining the location of GFP fluorescence, in addition to revealing the specific expression of GFP under the control of the tbx6 promoter. For example, a construct containing ptbx6-2.0-gfp and pXex-bfp (Fig. 5A) showed scattered BFP fluorescence throughout the embryo at 70% epiboly with specific GFP expression at the margin (Fig. 5C,D). At later stages, the BFP

### Table 1. Comparison of the targeting ability and promoter activity of different reporter constructs

<table>
<thead>
<tr>
<th>Reporter constructs (GFP and Luciferase)</th>
<th>GFP expression</th>
<th>Relative promoter activity</th>
<th>Responsiveness</th>
</tr>
</thead>
<tbody>
<tr>
<td>ptbx6-2.0</td>
<td>91% (n=90)</td>
<td>100%</td>
<td>Yes</td>
</tr>
<tr>
<td>ptbx6-1.7</td>
<td>88% (n=100)</td>
<td>34%</td>
<td>Yes</td>
</tr>
<tr>
<td>mut2-2.0</td>
<td>90% (n=50)</td>
<td>n/d</td>
<td>Yes</td>
</tr>
<tr>
<td>mut2-2.0†</td>
<td>85% (n=50)</td>
<td>n/d</td>
<td>Yes</td>
</tr>
<tr>
<td>mut1,2-2.0†</td>
<td>16% (n=50)†</td>
<td>11%</td>
<td>Yes</td>
</tr>
<tr>
<td>ptbx6-0.9†</td>
<td>0% (n=60)†</td>
<td>6%</td>
<td>No</td>
</tr>
</tbody>
</table>

n/d, not determined.

*Tested with overexpression of Xbmp4.
†Tested with overexpression of TVGR only.
‡Tested with overexpression of wnt8 and TVGR.
§Only a few cells showed marginal GFP fluorescence.
More importantly, we determined that the promoter activity of the promoter activity of ptbx6-1.7-luc, we found that stronger GFP fluorescence than luc reporter genes, constructs. These gene to quantify the promoter activity of our reporter luciferase gfp ptbx6-2.0 activity of. We replaced the and in an embryo injected with 150 pg of (E-H) Expression of endogenous tbx6 in an uninjected embryo (A) and in an embryo injected with 75 pg of wnt8 RNA (B). The injected embryo shows ectopic expression of tbx6. (C,D) Bright field (C) and fluorescence (D) pictures of a zebrafish embryo coinjected with ptbx6-1.7-gfp and 75 pg of wnt8 RNA showing ectopic GFP fluorescence in the animal pole. (E-H) Expression of endogenous tbx6 in an uninjected embryo (E) and in an embryo injected with 150 pg of Xbmp4 RNA (F). The injected embryo shows ectopic expression of tbx6. (G,H) Bright field (G) and fluorescence (H) pictures of a zebrafish embryo coinjected with ptbx6-1.7-gfp and 150 pg of Xbmp4 RNA at the shield stage showing ectopic GFP fluorescence in the animal pole. (I,J) Bright field (I) and fluorescence (J) pictures of a zebrafish embryo coinjected with ptbx6-1.7-gfp and 25 pg of TVGR RNA showing ectopic GFP fluorescence in the animal pole. TVGR is a constitutively active form of the Tcf transcription factor (Darken and Wilson, 2001). The in situ hybridizations are at shield stage whereas the bright field and fluorescence images are at 50% epiboly.

Consistent with our early finding that using a quantitative assay, we further confirmed the using a quantitative assay, we further confirmed the ability to respond to Bmp signaling. We observed ectopic GFP fluorescence in the embryos, showing that Tcf6-0.9 is functional and capable of responding to Tcf activation (Table 1). Thus the 900 bp proximal region of the promoter is capable of responding to Tcf activation, but it is not sufficient to drive the expression of gfp in the developing posterior mesoderm, possibly because it lacks the ability to respond to Bmp signaling.

Identification of a Bmp responsive domain within tbx6 promoter

To better define the Bmp-responsive element of the tbx6 promoter, we generated a series of deletion constructs of the together, these data show that the normal expression of tbx6 in the developing mesoderm is regulated directly by Wnt activation through the Tcf sites in the proximal region of the promoter.

A 900 bp tbx6 promoter fragment is insufficient for normal expression

Because all three Tcf DNA binding sites are located in the 900 bp proximal promoter region, we wanted to know if this region of the promoter is sufficient to correctly target expression to the developing posterior mesoderm. To answer that, we constructed the reporter gene, ptbx6-0.9-gfp/pXex-bfp, by placing the sequence of the 900 bp proximal region of the tbx6 promoter in front of the gfp gene, together with pXex-bfp. We observed no detectable GFP fluorescence in any of the embryos injected with ptbx6-0.9-gfp/pXex-bfp, even though these embryos had robust BFP expression (Table 1). In support of this, when the ptbx6-0.9 was fused to luciferase, we found that it was only 6% as active as ptbx6-2.0 (Table 1).

To determine if the Tcf sites were still functional in this construct, we examined the responsiveness of ptbx6-0.9-gfp to the constitutively active Tcf and to ectopic Wnt8. In both cases we observed ectopic GFP fluorescence in the embryos, showing that ptbx6-0.9 is functional and capable of responding to Tcf activation (Table 1). Thus the 900 bp proximal region of the promoter is capable of responding to Tcf activation, but it is not sufficient to drive the expression of gfp in the developing posterior mesoderm, possibly because it lacks the ability to respond to Bmp signaling.

Identification of a Bmp responsive domain within tbx6 promoter

To determine whether ptbx6-0.9-gfp can respond to Bmp, we coinjected either ptbx6-1.7-gfp or ptbx6-0.9-gfp with Xbmp4 RNA into one-cell stage embryos and examined GFP fluorescence. At 50% epiboly, we observed no GFP fluorescence in embryos coinjected with ptbx6-0.9-gfp and Xbmp4 RNA (Table 1). In contrast, we observed ectopic GFP fluorescence in embryos coinjected with ptbx6-1.7-gfp and Xbmp4 RNA (Fig. 4G,H, Table 1). These results show that ptbx6-0.9-gfp has a WNT response element but lacks a promoter element necessary for the Bmp response.

Two regions were deleted in ptbx6-1.7 to produce ptbx6-0.9, the distal 800 bp region (dr800) and the first intron. To ask whether either of these regions can mediate Bmp responsiveness, we placed them in front of the SV40 minimal promoter driving the luciferase gene, generating dr800-SV40-luc and intron-SV40-luc. These reporter constructs were coinjected with and without Xbmp4 RNA into one-cell stage zebrafish embryos and luciferase activity was assayed at the shield stage. Addition of dr800 to SV40-luc enhanced the promoter activity approximately 3-fold, probably because of the endogenous Bmp present in the embryo (Fig. 7A). Coinjection of Xbmp4 RNA and dr800-SV40-luc resulted in a further 3-fold increase in activity. In contrast, with intron-SV40-luc the promoter activity was the same with or without the addition of Xbmp4 RNA (Fig. 7A). These data demonstrate that the Bmp response element is located in the 800 bp distal region of the tbx6 promoter.

To better define the Bmp-responsive element of the tbx6 promoter, we generated a series of deletion constructs of the
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We initially found that the 3'-half of the dr800 region retains the ability to respond to Bmp activation, whereas the 5'-half did not (Fig. 7B). Further analysis of this 3'-half of the dr800 region revealed that a 65 bp domain is capable of conferring Bmp responsiveness, and that further reduction of this 65 bp region into smaller domains eliminated the Bmp response (Fig. 7C). These data demonstrate that the core Bmp response element must be located within the 65 bp distal region of the tbx6 promoter and suggest that multiple sites within this region are necessary to obtain the Bmp response. Collectively, our data show that the tbx6 promoter has two distinct regulatory regions that confer the ability to respond to Wnt and Bmp signals. Moreover, we find that both regulatory elements must function cooperatively to confer full promoter activity in the developing posterior mesoderm.

Discussion

We show here that tbx6 is regulated by combinatorial signaling from the Wnt and Bmp pathways. This fits well with a recent study demonstrating that the combination of Wnt and Bmp induces tail formation in zebrafish (Agathon et al., 2003), and suggests that tbx6 is one of a series of posterior mesodermal genes regulated by these two pathways. Indeed, eve1, which has a similar expression pattern to tbx6 (Joly et al., 1993), was also found to be jointly regulated by these two pathways (Agathon et al., 2003), although the mechanism of its regulation is at present unknown. Although the role of eve1 in posterior mesoderm formation is unclear, a recent study indicates that tbx6 functions as part of a network of T-box transcription factors to regulate domains within the posterior mesoderm (Goering et al., 2003).

Although the normal expression of tbx6 is dependent on Wnt and Bmp signaling, we find that inhibition of either one of these signaling pathways does not lead to a complete loss of tbx6 expression in the ventrolateral mesoderm. Interestingly, wnt8 morphants show a graded reduction of tbx6 expression with the strongest effect in the lateral domains of the ventrolateral mesoderm. In embryos injected with wnt8MOs, bmp expression becomes ventrally restricted even at the shield stage (see Fig. S3A-D at http://dev.biologists.org/supplemental), and tbx6 expression is restricted to this region. In contrast, loss of Bmp function causes a strong uniform reduction in tbx6 expression, but does not significantly alter the expression of wnt8 (see Fig. S3E-H at http://dev.biologists.org/supplemental). These findings show that the Wnt and Bmp signaling pathways have
distinct impacts on the overall expression of tbx6 in the posterior mesoderm.

Although the contribution of Bmp and Wnt8 signals has a qualitative and quantitative difference in their ability to activate tbx6 expression, their cooperation is essential to give the normal expression pattern during posterior mesoderm formation. This raises the question, why is combinatorial signaling used to regulate tbx6 and other mesodermal genes?

The expression patterns of the bmp genes and wnt8 are very dynamic during early embryogenesis, yet tbx6 expression is maintained in the ventrolateral mesoderm throughout somitogenesis. Combinatorial signaling not only restricts the domain in which tbx6 is expressed to regions where both signals are present, but it permits tbx6 to be expressed in regions where Bmp signaling is very low (the lateral regions) and where Wnt8 signaling is very low (the ventral regions from 90% epiboly onwards). Thus as the levels of the signals vary, tbx6 expression is maintained.

Interestingly, a family of three Drosophila genes, Dorsocross1-3, encode T-box genes most closely related to tbx6 (Reim et al., 2003). Although the expression patterns of these genes is complex, the expression of all three genes in the dorsal ectoderm and mesoderm requires both Wnt and Bmp signals (Reim et al., 2003). Whether this represents conservation of regulation or convergent evolution awaits further analysis, but it is an intriguing parallel.

Analysis of the tbx6 promoter during posterior mesoderm development

Two models can be used to account for the required input of both Wnt and Bmp signals for the normal tbx6 expression in the posterior mesoderm. One is that these pathways may signal independently of each other, but function together in a cooperative fashion to activate the expression of tbx6. Alternatively, these pathways may function in a linear pathway such that one signal is upstream of the other as was suggested from Xenopus studies (Hoppler and Moon, 1998; Marom et al., 1999) and a recent zebrafish study (Agathon et al., 2003).

To delineate the interplay between Wnt8 and Bmp signaling pathways in regulating the expression of tbx6 during posterior mesoderm development, we isolated and characterized the promoter of tbx6. We found that a genomic fragment including sequences from 1.7 kb upstream of the start of translation through the second exon recapitulated the normal tbx6 expression pattern in both zebrafish and Xenopus embryos, demonstrating that the regulatory elements are conserved between these species. The normal domain of tbx6 expression was observed when the intron was removed from the promoter; however, we also observed some ectopic expression outside of the mesodermal domain, indicating that the intron contains a repressor of non-mesodermal expression (D.P.S. and D.K., unpublished).

Analysis of the tbx6 promoter revealed independent
elements that respond cooperatively to Wnt and Bmp signals. In the proximal 900 bp, we discovered three Tcf sites and demonstrated that mutation of both of the two most proximal sites prevents normal tbx6 expression. Because Tcf is activated by Wnt signaling, these results demonstrate that tbx6 is a direct target of Wnt signaling. We located the Bmp response element to a distinct region of the tbx6 promoter, located between 1.7 kb and 0.9 kb (dr800) from the start of translation. In the presence of high levels of Bmp signal, this region alone can activate transcription when attached to a SV40 minimal promoter, but the activity is much weaker than that of the full 1.7 kb promoter. Within this dr800 region, we identified a 65 bp domain, which is capable of responding to Bmp activation. Smaller fragments did not respond to Bmp signaling, suggesting that the Bmp response element is composed of more than one transcription factor binding site. How this element is activated by Bmp signaling is not yet known. A transcription factor required for the function of Bmp-type Smads called OAZ was shown to be required for the activation of a key Bmp target gene in Xenopus (Hata et al., 2000), but no OAZ site was found in the tbx6 promoter. Moreover, during somitogenesis OAZ is expressed anteriorly (Hata et al., 2000), whereas tbx6 is expressed at the most posterior end of the embryo (Hug et al., 1997), suggesting that a novel transcription factor regulates the Bmp response of tbx6.

**Regulation of tbx6 by combinatorial Wnt and Bmp signaling**

Because the normal regulation of tbx6 requires input from both the Wnt and Bmp pathways, we were surprised to find that ectopic expression of either signal at the level used to produce tails (Agathon et al., 2003) resulted in strong activation of the endogenous tbx6 gene and of the tbx6 promoter. Using inhibitors of Bmp and Wnt8 signaling, we found that overexpression of each signaling pathway alone is able to activate tbx6 expression when the other pathway is blocked, demonstrating that Bmp and Wnt8 have the potential to activate tbx6 without the contribution of the other signaling pathway. Because the endogenous Bmp and Wnt8 can not activate tbx6 when the other pathway is inhibited, our results suggest that Bmp and Wnt signals are present in the embryo at relatively low levels such that they can combinatorially activate tbx6 only when both are present. This mechanism ensures that tbx6 is only expressed in the regions where these two factors overlap. How this works in regulating the promoter remains to be determined. At endogenous levels of signaling, it could be that the Wnt and Bmp response sites are only active transiently when a single signal is present, and only when both signals are present does a stable transcription complex form. At higher levels of signaling through one factor, the sites are occupied continuously and this promotes transcription of the tbx6 gene.

From all of this data we have put together a model to explain how tbx6 is regulated in the normal embryo and in mutants. In the normal embryo, wnt8 is expressed at the margin in the gastrula-stage embryo and bmps are expressed in a ventral to dorsal gradient (Fig. 8A). Together they combine to activate tbx6 at the margin, with both signals working at submaximal levels. In bmp mutants (and noggin-injected embryos), Wnt8 causes a low level of tbx6 expression in the lateral and ventral regions (Fig. 8B). In wnt8 mutants (or in embryos injected with wnt8MOs), Bmps activate tbx6 in the ventral region where they are most abundant (Fig. 8C).

**Tbx6: a platform for multiple levels of regulation**

Our study has focused only on the regulation of tbx6 by the Wnt and Bmp pathways. Earlier analyses have shown that tbx6 is also strongly regulated by spt (Griffin et al., 1998) and weakly by ntl (Hug et al., 1997; Griffin et al., 1998). Although Agathon et al. (Agathon et al., 2003) demonstrated that tails can be induced by overexpression of Wnt and Bmp at levels similar to those used here, they also found that co-expression of a member of the Nodal pathway lowered the amount of Wnt and Bmp necessary to form tails. Because Nodal signaling regulates spt (Griffin and Kimelman, 2003), one explanation for the synergism between the Nodals and the Wnt and Bmp pathways is that Spadetail contributes directly or indirectly to tbx6 expression. Thus tbx6 will continue to serve as a useful paradigm for understanding how multiple regulatory inputs lead to the formation of the posterior mesoderm.
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