Cyp26 enzymes generate the retinoic acid response pattern necessary for hindbrain development

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Retinoic acid (RA) is essential for normal vertebrate development, including the patterning of the central nervous system. During early embryogenesis, RA is produced in the trunk mesoderm through the metabolism of vitamin A derived from the maternal diet and behaves as a morphogen in the developing hindbrain where it specifies nested domains of Hox gene expression. The loss of endogenous sources of RA can be rescued by treatment with a uniform concentration of exogenous RA, indicating that domains of RA responsiveness can be shaped by mechanisms other than the simple diffusion of RA from a localized posterior source. Here, we show that the cytochrome P450 enzymes of the Cyp26 class, which metabolize RA into polar derivatives, function redundantly to shape RA-dependent gene-expression domains during hindbrain development. In zebrafish embryos depleted of the orthologs of the three mammalian CYP26 genes CYP26A1, CYP26B1 and CYP26C1, the entire hindbrain expresses RA-responsive genes that are normally restricted to nested domains in the posterior hindbrain. Furthermore, we show that Cyp26 enzymes are essential for exogenous RA to rescue hindbrain patterning in RA-depleted embryos. We present a ‘gradient-free’ model for hindbrain patterning in which differential RA responsiveness along the hindbrain anterior-posterior axis is shaped primarily by the dynamic expression of RA-degrading enzymes.

KEY WORDS: Retinoic acid, Hindbrain, Cyp26, Hox, Morphogen, Zebrafish

INTRODUCTION

Retinoic acid (RA) is a known teratogen with crucial roles in the patterning of the vertebrate nervous system. In the hindbrain, RA is essential for the establishment of the anterior-posterior pattern, as demonstrated by embryos in which RA is depleted either dietarily, pharmacologically or genetically (Begemann et al., 2004; Dupe and Lumsden, 2001; Maden et al., 1996; Niederreither et al., 1999). RA is produced in the anterior paraxial mesoderm by the activity of aldehyde dehydrogenase 1 family, member A2 (Aldh1a2), which oxidizes retinal to RA (Begemann et al., 2001; Gavalas, 2002; Niederreither et al., 1999). RA either diffuses or is transported from the paraxial mesoderm into the adjacent central nervous system. RA directly regulates gene expression through its nuclear hormone receptor (RAR) and co-receptor (RXR), which bind RA response elements (RAREs) in the enhancers of target genes (Bastien and Rochette-Egly, 2004). In the hindbrain, RA regulates the expression of 3′-Hox genes through direct (in the case of Hox-1 and Hox-4 genes) or indirect (in the case of Hox-3 genes) mechanisms (Gould et al., 1998; Hernandez et al., 2004; Marshall et al., 1994; Nolte et al., 2003; Studer et al., 1994; Zhang et al., 2000). Other anterior RA-responsive genes (Hox-1 family genes) are expressed earlier and at lower RA concentrations than the more-posterior RA-responsive genes (Hox-4 family genes) (Dupe and Lumsden, 2001; Maves and Kimmel, 2005; Simeone et al., 1990). Based on the effects of switching the RAREs of the Hox-1 and Hox-4 genes, Gould et al. proposed that Hox-1 genes are expressed at more anterior levels than Hox-4 genes because their RAREs are more sensitive to RA (Gould et al., 1998).

These data have lead to a model in which a continuous spatio-temporal gradient of RA through the hindbrain generates nested domains of RA-responsive gene expression. These domains are then resolved by secondary mechanisms into non-overlapping domains that correspond with the morphological segments of the hindbrain – the rhombomeres (r). However, a number of observations suggest that an RA gradient is neither detectable nor required for normal hindbrain development. First and foremost, embryos depleted of endogenous RA can be fully rescued by a uniform concentration of exogenous RA (Begemann et al., 2004; Begemann et al., 2001; Gale et al., 1999; Grandel et al., 2002; Mic et al., 2002; Niederreither et al., 2000). Second, this rescue can be accomplished by a range of RA concentrations and over a range of developmental stages (Dupe and Lumsden, 2001; Maves and Kimmel, 2005). Third, when RA responsiveness is measured by the expression of a RARE-LacZ reporter, no gradient of expression is detected in the hindbrain. Instead, distinct boundaries of reporter expression that shift over time are detected (Rossant et al., 1991; Sirbu et al., 2005). Finally, in contrast to earlier findings (Gould et al., 1998), recent evidence has suggested that, in the context of their intact enhancers, a Hox-1 RARE is equally responsive to RA as a Hox-4 RARE (Nolte et al., 2003).

These data suggest that cells in the presumptive hindbrain neuroepithelium can be patterned by RA in a manner that is independent both of concentration and of duration of exposure, necessitating a new model for RA-dependent hindbrain patterning. Here, we propose such a model based on the hindbrain patterning defects caused by the prevention of RA metabolism by the cytochrome P450 enzymes of the Cyp26 class. The Cyp26 enzymes (Cyp26a1, Cyp26b1 and Cyp26c1) have been proposed to function in the regulation of RA-dependent gene expression through their ability to metabolize RA into hydroxylated polar derivatives (Fujii et al., 1997; White et al., 1996). In the mouse tailbud and limbs, loss

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Accepted 18 October 2006
of Cyp26 function leads to increased RA-dependent gene expression, spina bifida and caudal agenesis similar to the teratogenic effects of high concentrations of exogenous RA (Abu-Abed et al., 2001; Sakai et al., 2001; Yashiro et al., 2004).

With regard to hindbrain patterning, cyp26a1 is expressed during gastrulation in the anterior neurectoderm (Dobbs-McAuliffe et al., 2004; Kudoh et al., 2002). Based on this expression domain, it was hypothesized that localized regions of RA synthesis in the anterior trunk mesoderm and degradation in the anterior neural plate provide a classical ‘source-and-sink’ mechanism for the spatial regulation of RA in the central nervous system (Kudoh et al., 2002; Swindell et al., 1999). However, cyp26a1 mutants in fish and mouse exhibit relatively subtle hindbrain-patterning defects inconsistent with a global role for cyp26a1 in hindbrain patterning (Abu-Abed et al., 2001; Emoto et al., 2005; Kudoh et al., 2002; Sakai et al., 2001). The recent identification of other cyp26 genes has suggested that these may participate in shaping RA responsiveness in the hindbrain (Abu-Abed et al., 2002; Gu et al., 2005; MacLean et al., 2001; Reijntjes et al., 2005; Reijntjes et al., 2004; Sirbu et al., 2005; Tahayato et al., 2003; Taimi et al., 2004; Zhao et al., 2005). Here, we demonstrate that the zebrafish orthologs of mammalian CYP26B1 and CYP26C1 function redundantly with cyp26a1 to pattern the hindbrain, because embryos depleted of all three proteins exhibit a profound posterior transformation of the hindbrain. Furthermore, we demonstrate that cyp26 genes are responsible for the ability of exogenous RA to rescue embryos depleted of endogenous sources of RA. In embryos depleted of Cyp26 activity, the low RA concentrations that normally rescue the RA-depleted hindbrain are highly teratogenic. Based on our results, we present a ‘gradient-free’ model for RA-dependent hindbrain patterning in which the spatially regulated inactivation of RA by Cyp26 enzymes is responsible for the establishment of RA-responsive gene-expression domains in the hindbrain.

MATERIALS AND METHODS

Cloning

Cyp26b1 was initially identified as an EST (Nelson, 1999), and we cloned the 5’ end of the coding sequence with the SMART RACE kit (Clontech). cyp26c1 was identified in a Blast search of the zebrafish genome sequence using the human CYP26C1 protein sequence and was then amplified from 12 hour post fertilization (hpf) whole-zebrafish-embryo cDNA.

Morpholinos, RNA in situ hybridizations and genotyping

Table 1 summarizes the sequences of the morpholinos (MOs) used in this study, the combinatorial depletion experiments performed and their outcomes. To determine the efficacy of cyp26b1 MO1, we made a cyp26b1-GFP fusion construct by cloning a fragment of the 5’ UTR and 5’ coding sequence including the MO target sequence into pCS2-GFP,TLXLT. The resulting plasmid was linearized with NotI and mRNA was prepared for injection with the SP6 mMessage mMachine kit (Ambion). Embryos were injected with 470 pg mRNA plus 5 ng MO. Embryo lysates were prepared as described (Waskiewicz et al., 2001), separated on 4-12% NuPAGE Bis-Tris gels and transferred to InvitroGen PVDF membranes (Invitrogen). For immunoblotting, we used anti-GFP (Torey Pines, 1:2000) and anti-Actin (SantaCruz, sc1616, 1:200), and proteins were detected with SuperSignal West Dura substrate (Pierce) according to the manufacturer’s directions. Quantitation of the GFP bands showed that cyp26b1 MO blocked 95-98% of the translation of the injected cyp26b1-GFP mRNA.

We used RT-PCR to determine the efficacy of cyp26c1 MO1, which is targeted to the exon-3–intron-3 splice junction of the pre-mRNA. RT-PCR analysis with multiple primer pairs revealed no detectable wild-type transcript. Three alternately spliced transcripts were detected and sequenced: two resulted in the introduction of a premature stop codon either by the inclusion of intron 3 or the exclusion of exon 3. A third transcript resulted in the deletion of the last 18 bases of exon 3, which leaves the transcript in frame but deletes six amino acids, several of which are conserved across Cyp26 family members.

All of the experiments described in this manuscript used cyp26b1 MO1 and cyp26c1 MO1; however, cyp26b1 MO2 and cyp26c1 MO2 gave the same phenotypes. Unlike cyp26c1 MO1, cyp26c1 MO2 was toxic at higher concentrations. Our control MO was targeted to the dead-end mRNA and eliminates primordial germ cells but does not affect other aspects of development (Weidinger et al., 2003). To assay for redundancy between the cyp26 genes, MOs were injected alone or in combination into embryos from a cyp26a1+/− intercross (Emoto et al., 2005). In order to control for non-specific effects due to MO injections, all embryos were injected with a total of 5 ng MO as determined by measuring the diameter of the injected bolus in mineral oil (see Table 1).

Two-color RNA in situ hybridizations were performed, essentially as described (Prince et al., 1998), except that Iodio-Nitrotetrazolium Violet (Sigma) was used as the red Alkaline Phosphatase substrate. Embryos were de-yolked and flat-mounted for photomicroscopy using a Zeiss Axioplan II microscope. After photographing, individual embryos were un-mounted and genotyped for the cyp26a1 mutation as described (Emoto et al., 2005).

Drug treatments

Dechorionated embryos from wild-type or cyp26a1+/− parents were incubated in the dark in pharmacological agonists and antagonists of the RA-metabolism pathway as follows: 4-(diethylamino)benzaldehyde [DEAB, an inhibitor of retinaldehyde dehydrogenases (Russo et al., 1988); Aldrich]: 10 μM, beginning at 50% epiboly [5.25 hpf (Kimmel et al., 1995)]; 4-(diethylamino)benzaldehyde [DEAB, an inhibitor of retinaldehyde dehydrogenases (Russo et al., 1988); Aldrich]: 10 μM, beginning at 50% epiboly [5.25 hpf (Kimmel et al., 1995)]; R115866, a specific inhibitor of Cyp26 enzymes (Janssen Pharmaceutica): 10 μM, beginning at dome stage (4.3 hpf); all-trans RA (Sigma): 0.1-100 nM, beginning at 50% epiboly.

Table 1. Summary of combinatorial cyp26 knock-down experiments and their outcomes

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Summary of phenotype</th>
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<tbody>
<tr>
<td>Control</td>
<td>Cyp26a1+</td>
</tr>
<tr>
<td>5 ng control MO</td>
<td>None</td>
</tr>
<tr>
<td>2.5 ng cyp25b1 MO1 + 2.5 ng control MO</td>
<td>None</td>
</tr>
<tr>
<td>2.5 ng cyp25c1 MO1 + 2.5 ng control MO</td>
<td>None</td>
</tr>
<tr>
<td>2.5 ng cyp25b1 MO1 + 2.5 ng cyp26c1 MO</td>
<td>None</td>
</tr>
<tr>
<td>5 nM RA</td>
<td>None</td>
</tr>
<tr>
<td>10 μM DEAB + 5 nM RA</td>
<td>None</td>
</tr>
</tbody>
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Morpholino sequences:

Cyp26b1 MO1 (ATG) 5’-CTCGAAGAGCATGCTGAAAGCTG-3’
Cyp26b1 MO2 (exon-2–intron-2 splice) 5’-ATTGAACCTTAATACCCCTCTTTTG-3’
Cyp26c1 MO1 (exon-3–intron-3 splice) 5’-AAAAACTGTTATCTCCACCTTGGC-3’
Cyp26c1 MO2 (intron-1–exon-2 splice) 5’-GGAAACCTGTCAACAACTAACAAGG-3’
Control (dead-end MO) 5’-GCTGGGCGATCCATGTCTTCCGACC-3’
**RESULTS**

**cyp26b1 and cyp26c1 are expressed dynamically during hindbrain development**

Mammalian genomes contain three CYP26 genes: CYP26A1, CYP26B1 and CYP26C1. Cloning of the zebrafish cyp26a1 ortholog has been described (White et al., 1996). We cloned zebrafish homologs of cyp26b1 and cyp26c1, and examined their expression during development. Cyp26c1 has been previously described as cyp26d1 (Gu et al., 2005) and cyp26b1-like (Kawakami et al., 2005) (ZDB gene 050714-2). Based on two lines of evidence, we argue that this gene is in fact the ortholog of mammalian CYP26C1. First, phylogenetic analysis of zebrafish cyp26 genes places it in the same clade as mouse and human CYP26C1 genes with moderate bootstrap support (see Fig. S1A in the supplementary material). Second, CYP26A1 and CYP26C1 are adjacent to one another on human chromosome 10q23-q24, and current zebrafish genomic sequence data and radiation-hybrid data places zebrafish cyp26a1 and cyp26c1, cyp26d1- and cyp26b1-like in regions of zebrafish linkage groups (LGs) 12 and 17, respectively, which show synteny to human chromosome 10 (see Fig. S1B in the supplementary material) (Woods et al., 2005). Because draft genomes for other tetrapod vertebrates also show CYP26A1 and CYP26C1 as adjacent genes, it is likely that they were adjacent genes in the ancestral vertebrate genome and that, following the proposed genome duplication early in teleost evolution, the duplicate of cyp26c1 was lost from LG 12 and the duplicate of cyp26a1 was lost from LG 17. Henceforth, we refer to the gene previously named cyp26d1 or cyp26b1-like as cyp26c1.

The expression patterns of zebrafish cyp26a1, cyp26b1 and cyp26c1 have been described (Dobbs-McAuliffe et al., 2004; Gu et al., 2005; Kudoh et al., 2002; Zhao et al., 2005). We focus here on their expression during hindbrain development. During gastrulation, cyp26a1 is expressed in the anterior neurectoderm (bracket in Fig. 1B) and in a narrow domain at the margin at 8.5 hpf (arrowhead in Fig. 1B). The posterior limit of cyp26a1 expression at 8.5 hpf abuts the anterior limit of hoxb1b expression at the r3-r4 boundary (Kudoh et al., 2002), but rapidly recedes anteriorly to lie at the r2-r3 boundary at 10 hpf and lies further anterior still at 11 hpf (Fig. 1F,G). As described previously, cyp26a1 is directly RA-inducible, even at sub-teratogenic concentrations of RA (5 nM), which cause the neurectodermal domain of expression to expand towards the margin (Fig. 1B). The posterior limit of cyp26a1 expression at 8.5 hpf abuts the anterior limit of hoxb1b expression at the r3-r4 boundary (Kudoh et al., 2002), but rapidly recedes anteriorly to lie at the r2-r3 boundary at 10 hpf and lies further anterior still at 11 hpf (Fig. 1F,G). As described previously, cyp26a1 is directly RA-inducible, even at sub-teratogenic concentrations of RA (5 nM), which cause the neurectodermal domain of expression to expand towards the margin (Fig. 1B).
in wild-type (left column) and at 18 hpf (right column) embryos injected with MOs as shown on the left. (A-H) pax2a (blue) marks the optic stalk (os), posterior midbrain and cerebellum (bracket), and the otic vesicles (ov); whereas hoxd4 (also blue) marks the r7-r8 territory and krox20 (red) marks r3 and r5. MO depletion of Cyp26b1 and/or Cyp26c1 does not affect this pattern in wild-type embryos (C,E,G), but progressively posteriorizes the hindbrain in cyp26-depleted embryos (D,F,H). Arrowhead marks the r6-r7 boundary, which is shifted to the anterior hindbrain in Cyp26-depleted embryos. (I,J) en3 (red) marks the posterior midbrain and cerebellum (bracket) and hoxb1a (blue) marks r4, which is shifted anteriorly in Cyp26-depleted embryos. (K,L) pax2a (blue) and krox20 (red) are expressed as described above. vhfn1 (also blue) is expressed in the posterior hindbrain up to the r5-r6 boundary (arrowheads) and is also shifted anteriorly in Cyp26-depleted embryos. (M,N) The isl1-GFP transgene (green) marks cranial motor neurons (nV; trigeminal motor neurons in r2 and r3; nVII; facial motor neurons in r4-6; nX: vagal motor neurons in r8) whereas the zn5 antibody (red) marks spinal motor neurons (arrows), pharyngeal arch endoderm (pe, arrowheads mark individual pharyngeal arches) and other structures. The large white arrowhead indicates the mid-hindbrain boundary. In Cyp26-depleted embryos, the motor neurons of the vagus nerve (nX) are expanded anteriorly, as are the spinal motor neurons. Scale bars: 100 μm. Scale bar in A is for A-H,K,L; scale bar in I is for I,J.

**cyp26b1 and cyp26c1 function redundantly with cyp26a1 to pattern the hindbrain.** Whole-mount RNA in situ hybridizations at 18 hpf (A-J) and 13 hpf (K,L) and immunostaining at 48 hpf (M,N) in wild-type (left column) and cyp26a1+/– (right column) embryos treated with 4-(diethylamino)benzaldehyde (DEAB), a specific inhibitor of retinaldehyde dehydrogenase (Fig. 1D) (Dobbs-McAuliffe et al., 2004; Sirbu et al., 2005). Throughout the hindbrain-patterning period, neurectodermal cyp26b1 expression lies significantly anterior to that of aldh1a2, which is restricted to the anterior mesoderm (Fig. 1E,H,I) (Dobbs-McAuliffe et al., 2004; Kudoh et al., 2002; Loudig et al., 2000; White et al., 1996). In spite of its strong RA-inducibility, cyp26b1 is expressed in DEAB-treated embryos (see Fig. S3C,F in the supplementary material). Briefly, in 100 nM RA, r4 is expanded anteriorly, and with increasing concentrations of DEAB, r4 is expanded further anteriorly, and r3 expression is downregulated in r4. Cyp26b1 expression is not detected in r4 in the absence of Cyp26a1 function both in the presence and in the absence of Cyp26a1 function (Table 1). The hindbrain phenotype of cyp26a1 mutants is
subtle: r4 [marked by hoxb1a and bounded by the r3 and r5 stripes of krox20 (also known as egr2b – Zebrafish Information Network)] is slightly expanded in length and the anterior hindbrain (r1-r3) is slightly reduced (Fig. 2A,B, Fig. 4A,B and see Fig. S4A,B in the supplementary material) (Emoto et al., 2005). Furthermore, the posterior-most hindbrain – marked by high levels of hoxd4 expression, and comprising r7 and the long unsegmented ‘vagal’ rhombomere, r8, which lies between the segmented hindbrain and the first somite (Lumsden, 1990) – is expanded in length as described previously (Emoto et al., 2005) (Fig. 2A,B and Fig. 4A,B).

Depleting embryos of either Cyp26b1 or Cyp26c1, or of both enzymes, caused no brain-patterning phenotype in wild-type embryos, aside from a subtle shortening of the hindbrain (Fig. 2 and see Fig. S4 in the supplementary material, left columns). However, depleting both enzymes strongly enhanced the cyp26a1 in the supplementary material, left columns). However, depleting both enzymes strongly enhanced the cyp26a1 phenotype (Fig. 2 and see Fig. S4 in the supplementary material, right columns). In cyp26b1 MO-injected cyp26a1+/– embryos, r4 is further expanded (Fig. 2D and see Fig. S4C,D in the supplementary material) and the r6-r7 boundary is shifted slightly towards r5 (arrowhead in Fig. 2C,D). Knocking-down cyp26c1 caused a stronger enhancement of the cyp26a1+/– phenotype, consistent with its earlier onset of expression in the presumptive hindbrain. In these embryos, r3 is strongly reduced or absent, whereas r4 is expanded anteriorly so that its anterior limit lies adjacent the posterior limit of en3 (also known as eng2b – Zebrafish Information Network) expression in the presumptive cerebellum (Fig. 2F and see Fig. 4F in the supplementary material). The r6-r7 boundary is again shifted anteriorly, but remains posterior to a narrow r5 (arrowhead in Fig. 2F).

Embryos depleted of all three Cyp26 proteins have a strongly posteriorized hindbrain (Fig. 2G-L and see Fig. S4G,H in the supplementary material). Both r3 and r5 are eliminated (Fig. 2G,H) and r4 abuts the cerebellum (Fig. 2J and see Fig. S4G,H in the supplementary material). The anterior limit of vhnf1 expression, which, by the 8-somite stage (13 hpf), marks the r5-r6 boundary, is also shifted to abut the cerebellum (arrowheads in Fig. 2K,L). The r6-r7 boundary of hoxd4 expression is similarly shifted, coming to lie within a few cell diameters of cerebellum (arrowhead in Fig. 2H).

Thus, three RA-responsive genes (hoxb1a, vhnf1 and hoxd4) that normally form nested expression domains in the hindbrain are all expanded into the anterior-most hindbrain in embryos depleted of all three Cyp26 proteins. In spite of this strong transformation of the hindbrain, the patterning of the mid- and fore-brain, marked by pax2a, otx2, dlx2a and eomes, appears unaffected, except for a decrease in length detectable in cyp26a1 single mutants (data not shown) (Emoto et al., 2005).

We examined the neuronal organization of Cyp26-depleted embryos. In cyp26a1–/– embryos injected with control MOs or with cyp26b1 and/or cyp26c1 MOs, we observed normal patterns of cranial and spinal motor-nerve differentiation (Fig. 2M). However, in cyp26a1–/– embryos injected with both cyp26b1 MO and cyp26c1 MO, the vagal neurons (nX in Fig. 2M,N) characteristic of r8 are expanded to the mid-hindbrain boundary (large arrowhead in Fig. 2M,N) and spinal motor roots (arrows in Fig. 2M,N) extend from hindbrain levels into a disorganized branchial region (small arrowheads in Fig. 2M,N). This occurs in spite of the fact that there are no somites to innervate at this level (data not shown). These neuronal phenotypes are consistent with our analysis of marker gene expression, in which the RA-inducible box gene characteristic of r7-8 (hoxd4) is expanded anteriorly throughout the hindbrain region.

A pharmacological inhibitor of Cyp26 activity phenocopies Cyp26 depletion

Pharmacological antagonists that inhibit RA metabolism have been developed as tools for the treatment of dermatological diseases and cancer (Njar, 2002; Njar et al., 2006). The compound R115866 is a highly selective antagonist of Cyp26a1 activity in vitro, and exerts retinoidal effects in adult rats (Stoppie et al., 2000). Its effects on Cyp26b1 and Cyp26c1 have not been examined. We observed that treating zebrafish embryos with 10 μM R115866 caused a phenotype identical to that of embryos depleted of all three Cyp26 enzymes (compare Fig. 2J,H with Fig. 3B,D). This suggests that R115866 inhibits Cyp26b1 and Cyp26c1 as effectively as does knocking-down their expression with MOs, and confirms our above observation that Cyp26 activity is essential for normal hindbrain patterning. The effects of R115866 treatment are completely reversed by the addition of DEAB, so that embryos treated with both drugs resemble embryos treated with DEAB alone (Fig. 3E,F). This demonstrates that, as for other phenotypes observed in cyp26a1–/– mutant fish and mice (Emoto et al., 2005; Niederreither et al., 2002), the posteriorized hindbrain phenotype caused by blocking all Cyp26 activity is due to the accumulation of excess RA and not to the absence of bioactive Cyp26-generated RA derivatives. Although such derivatives have been observed to have significant retinoidal effects in cells and in embryos, and have been postulated to have functions in vivo (Idres et al., 2002; Pijnappel et al., 1993), we see no evidence for their having a role in hindbrain patterning.

Cyp26a1 protects against RA teratogenicity.

The long-standing observation that depletion of endogenous RA can be rescued by treatment with a low concentration of exogenous RA demonstrates that a RA gradient is not strictly necessary for hindbrain patterning (Begemann et al., 2004; Begemann et al., 2001; Gale et al., 1999; Niederreither et al., 2000). However, the basis of this rescue phenomenon has not been determined, and has significant implications for the mechanism of hindbrain patterning. We hypothesized that Cyp26 enzymes enable this rescue by inactivating exogenous RA in a patterned manner. We tested the roles of the cyp26 genes by performing the RA-rescue experiment in Cyp26-depleted embryos.
The effects of blocking RA synthesis with DEAB in zebrafish have been described previously (Begemann et al., 2004; Maves and Kimmel, 2005). They include the loss of posterior hindbrain identities (r5-r8, Fig. 4C), expansion of anterior hindbrain identities (r2-r4), and a dramatic anterior shift of paraxial- and lateral-plate mesoderm-derived tissues (pronephros and somites; Fig. 4C). In wild-type (cyp26a1+/+ and cyp26a1+/−) DEAB-treated embryos, this phenotype is rescued by treatment with between 0.5 and 10 nM RA: concentrations that are non-teratogenic or weakly teratogenic in wild-type embryos (Fig. 4E,G,I,K and data not shown). In the experiments described below, we used 5 nM RA as our ‘rescuing’ concentration. Whereas in wild-type embryos 5 nM RA is non-teratogenic, it strongly posteriorizes cyp26a1−/− embryos, either in the presence or in the absence of DEAB, causing anterior expansion of r7-r8 identity (Fig. 4E,F and data not shown) and the loss of all brain regions anterior to r7: r3 and r5 (marked by krox20; Fig. 4E,F,I-L); r4 (marked by hoxb1a; Fig. 4G,H); the cerebellum and posterior tectum (marked by en3; Fig. 4G-J); the diencephalon and midbrain (marked by otx2; Fig. 4K,L); and the telencephalon and eyes (marked by dlx2 (Fig. 4I,J) and by eomes (data not shown)). Embryos posteriorized in this manner typically exhibited an accordion-like folding of the anterior neural tube. Exactly the same effects are observed in cyp26a1−/− embryos treated with 5 nM RA in the absence of DEAB (data not shown). This phenotype strongly resembles the effects of 40-fold-higher levels of RA on wild-type embryos (inset in Fig. 4I), demonstrating that it is the ability of cyp26a1 to inactivate RA that enables RA-deficient embryos to be rescued by exogenous RA. Furthermore, these results demonstrate that cyp26a1 is able to protect embryos from the potentially teratogenic effects of low concentrations of RA. We did not see a similar sensitivity to exogenous RA in cyp26b1 and/or cyp26c1 MO-injected embryos.

We asked why, under normal circumstances, cyp26b1 and cyp26c1 can compensate for a lack of cyp26a1 (Fig. 2), whereas, in the presence of 5 nM RA, they cannot (Fig. 4). A total of 5 nM RA is sufficient to induce expression of cyp26a1 far posterior to its normal limit in the hindbrain (Fig. 1C). In spite of this, the expressions of cyp26b1 and cyp26c1 are initiated at the correct anterior-posterior level, and subsequent hindbrain patterning is unaffected (Fig. 5C,G and data not shown). By stark contrast, in cyp26a1−/− embryos treated with 5 nM RA, cyp26b1 and cyp26c1 are not expressed, and the entire brain is strongly posteriorized (Fig. 4 and Fig. 5D,H).

cyp26a1 protects against potentially teratogenic RA precursors

Our findings demonstrate that cyp26a1 protects against the potentially teratogenic effects of RA. Maternally-derived RA is present at very low levels in zebrafish eggs and early embryos prior to the onset of embryonic RA synthesis, and is therefore unlikely to be a teratogenic risk (Costaridis et al., 1996). However, the levels of maternally loaded retinal – the immediate precursor of RA – are higher (9 pmol/egg) (Costaridis et al., 1996; Lampert et al., 2003). We asked whether Cyp26a1 protects against teratogenicity of RA precursors. We increased retinal levels in wild-type and cyp26a1−/− eggs by injecting retinal directly into the yolk of one-cell stage embryos. Although wild-type embryos tolerate over ten-times the normal amount of retinal in the yolk (data not shown), cyp26a1−/− embryos are strongly posteriorized by only a three-times the normal amount of retinal (27 pmol; Fig. 6). The teratogenic effects of a small increase in RA precursor in the absence of Cyp26a1 demonstrates that Cyp26a1 may normally play an important role in protecting the embryo against the potentially teratogenic effects of maternally derived RA precursors. They also suggest that the RA
nor the localization of its synthesis are crucial for this pattern; and (2) RA-dependent gene expression occurs in a spatio-temporal sequence, with anterior RA-responsive genes being expressed earlier than posterior ones; however, the duration of RA exposure is not crucial for this temporal sequence (Maves and Kimmel, 2005).

We have identified a crucial role for Cyp26 RA-metabolizing enzymes in establishing hindbrain pattern, because depleting them alone and in combination leads to a progressive posteriorization of the hindbrain. In fully Cyp26-depleted embryos, three RA-dependent genes that normally form nested expression domains with distinct anterior limits (hoxb1a, r3-r4; vhnf1, r4-r5; and hoxd4, r6-r7) are all expanded up to the anterior-most hindbrain (Fig. 7A). Based on the dynamic expression of the cyp26 genes in the hindbrain and on the effects of depleting embryos of Cyp26 activity, we propose a gradient-free model for RA-dependent events in hindbrain patterning, in which RA degradation by Cyp26 enzymes determines progressively more-posterior limits of RA-dependent gene expression in a step-wise manner (Fig. 7B). We note that cyp26 genes are expressed similarly, although not identically, in tetrapods, predicting a similar combinatorial role for Cyp26 enzymes in mammalian hindbrain development.

In step 1, complete by 9 hpf, the anterior limit of hoxb1b and hoxb1a – the functional homologs of mammalian HOXA1 and HOXB1 – are established by the posterior limit of cyp26a1 expression. This event establishes the r3-r4 boundary (Kudoh et al., 2002), the first morphological boundary in the hindbrain (Moens et al., 1998). This function can be compensated for by cyp26c1, because the anterior limit of r4 is strongly affected only in the absence of both cyp26a1 and cyp26c1. In step 2, complete by 11 hpf, the anterior limit of the next RA-responsive gene, vhnf1, is determined by the posterior limit of cyp26c1 expression at the r4-r5 boundary. This function can be partially compensated for by cyp26b1. In step 3, complete by 12 hpf, the anterior limit of the last RA-responsive gene, hoxd4, is determined by the posterior limit of cyp26c1 at the r6-r7 boundary, a function that can also be compensated for by the overlapping expression of cyp26b1. Some of the mechanistic underpinnings of this model and its broader implications are discussed further below.

A similar model was previously proposed based on the correspondence between cyp26a1 and cyp26c1 expression domains and boundaries of RA-dependent reporter-gene expression in the mouse (Sirbu et al., 2005). These authors predicted that cyp26a1 establishes the r2-r3 boundary and that cyp26c1 subsequently establishes the r4-r5 boundary. Our combinatorial functional analysis of cyp26 genes confirms this model in the general sense that Cyp26 activity determines sequential boundaries of RA-responsive gene expression in the hindbrain. However, our observations demonstrate a different and broader role for cyp26 genes in hindbrain patterning, involving all three cyp26 genes functioning to establish three sequential RA-responsiveness boundaries: r3-r4, r4-r5, and r6-r7. We do not observe a function for Cyp26 enzymes at the r2-r3 boundary: r1-r3 are entirely lost while r4 identity shifts anteriorly to abut the forming cerebellum.

**Fig. 5.** Exogenous RA disrupts cyp26b1 and cyp26c1 expression in cyp26a1–/– embryos but not in wild type. cyp26b1 (A-D) and cyp26c1 (E-H) expression (blue) is established normally in wild-type (A,E) and cyp26a1–/– (B,F) embryos at the 6-somite stage (12 hpf). cyp26b1 and cyp26c1 expression is also established normally in wild-type embryos treated with a sub-teratogenic concentration of RA (5 nM; C,G), but not in cyp26a1–/– embryos treated with 5 nM RA (D,H). krox20 expression is shown in red.

**Fig. 6.** cyp26a1 protects against teratogenic effects of the RA precursor retinal. Wild-type (A) and cyp26a1–/– (B) embryos injected with 20 pmol retinal at the one-cell stage. Wild-type embryos are only mildly affected by approximately triple the normal levels of retinal, whereas cyp26 mutants are strongly posteriorized, with hoxd4 expression extending throughout the brain. Scale bar: 100 μm.
We find that cyp26a1 and cyp26c1 are both required to establish the anterior limit of hoxb1a expression at the r3-r4 boundary, and that all three genes are required to establish the r4-r5 and r6-r7 boundaries. This degree of redundancy is unexpected given the lack of overlap between the expression domains of the Cyp26 genes in the hindbrain. The posterior limit of cyp26a1 expression lies in the anterior hindbrain (Dobbs-McAuliffe et al., 2004; Kudoh et al., 2002; Sirbu et al., 2005), whereas both cyp26b1 and cyp26c1 mark, sequentially, the r4-r5 and r6-r7 boundaries. However, it is important to notice that cyp26a1 is also expressed in the anterior trunk mesoderm near the RA source, where it probably functions to reduce global RA levels (Emoto et al., 2005; Niederreither et al., 2002). We propose that the severe posteriorization of Cyp26-depleted embryos results from the combined effects of deleting segment-restricted Cyp26 activity within the hindbrain and increasing global RA levels due to the loss of Cyp26a1 activity in the anterior trunk mesoderm (Fig. 7B).

Because hindbrain patterning is unaffected in cyp26b1; cyp26c1-depleted embryos when cyp26a1 is wild type, we hypothesize that redundant mechanisms can control boundaries of RA-dependent gene expression in the hindbrain, but that these mechanisms are overridden in cyp26a1 mutants in which global RA levels are elevated. One trivial possibility is that our MOs have not fully depleted Cyp26b1 and Cyp26c1 activity; however, our validation experiments with these MOs indicate that they deplete over 95% of the wild-type gene products. A second possibility is that non-homogeneous expression of RA receptors or RA modulators may modulate RA responsiveness. During the stages when RA is patterning the zebrafish hindbrain, two receptors – RARα and RARβ – are expressed throughout the hindbrain, but RARβ mRNA levels are higher in the presumptive r5 and r6 whereas RARα mRNA levels are higher posterior to the presumptive r6-r7 boundary (Hale et al., 2006). Furthermore, RXRγ, a RA co-receptor, is exclusively expressed posterior to the r6-r7 boundary (Tallas, 2006). By increasing the RA response, these non-homogeneously distributed RARs and RXRs may help to establish the r4-r5 and r6-r7 boundaries. A third possibility is that spatially restricted transcription factors repress RA-responsive gene expression even when ligand and receptor are present. Iro7 (also known as Irx7 – Zebrafish Information Network) is a TALE homeodomain protein expressed in the anterior hindbrain that represses vhnf1 expression anterior to the r4-r5 boundary (Lecluse et al., 2004). Other TALE homeodomain proteins have been shown to repress transcription from retinoic-acid-responsive elements by binding to RXR retinoid receptors and recruiting general corepressors to the complex (Bartholin et al., 2006). Thus, Iro7 may compensate for Cyp26b1 and Cyp26c1 by directly suppressing RA-responsive gene expression anterior to the r4-r5 boundary. Finally, a diffusion gradient of RA from its source in the anterior trunk mesoderm may compensate for the absence of hindbrain Cyp26 expression. RA can act as a classical morphogen, specifying distinct rhombomere identities at different threshold concentrations (Dudde and Lumsden, 2001; Maves and Kimmel, 2005), and an RA gradient may initiate nested domains of RA-responsive gene expression in the hindbrain when cyp26b1 and cyp26c1 are depleted. We note that any or all of the mechanisms we have proposed above (a diffusion gradient, receptor expression or other transcription factors that modulate RAR activity) may contribute to hindbrain patterning under normal circumstances. However, none of these mechanisms are sufficient to limit RA responsiveness in the hindbrain when all three Cyp26 enzymes are depleted.

**cyp26a1 is required to establish hindbrain pattern in the absence of a localized source of RA**

We have shown that, in the zebrafish, cyp26a1 is essential for the ability of exogenous RA to rescue embryos in which endogenous RA synthesis is inhibited. Although 5 nM RA can fully rescue the hindbrain and anterior trunk patterning defects of wild-type embryos in which RA synthesis is inhibited with DEAB, in cyp26a1−/− embryos it causes a strong posteriorization similar to that normally caused by 40 times more RA. From this, we conclude that Cyp26a1 is responsible for the normal pattern generated in the presence of otherwise teratogenic amounts of RA.

How does Cyp26a1 protect the embryos from exogenous RA? We observe that, in embryos treated with 5 nM RA, cyp26a1 expression expands throughout the epiblast. This expanded expression presumably eliminates the excess RA and allows the normal onset of expression of cyp26b1, cyp26c1 and other redundant factors described above that can modulate RA-responsive gene expression in the...
hindbrain, and the hindbrain develops normally under these conditions. In cyp26a1 mutants treated with 5 nM RA, the excess RA is not eliminated, cyp26b1 and cyp26c1 expression is not initiated, and the entire brain is transformed to posterior hindbrain and/or anterior spinal cord identity. Unlike in untreated cyp26a1 mutants, cyp26b1 and cyp26c1 cannot compensate for the lack of cyp26a1 because they are not expressed.

The phenotype of cyp26a1−/− embryos treated with 5 nM RA is significantly more severe than that of embryos depleted of all three Cyp26 enzymes in the absence of exogenous RA. In the former, the entire brain is transformed to an r7 and/or r8 identity whereas, in the latter, only the hindbrain territory is transformed. This difference may be because, in untreated embryos, RA simply does not diffuse as far as the midbrain, so Cyp26 enzymes are not required to inactivate it there. However, we have noted a surprisingly sharp anterior limit of RA-responsiveness in Cyp26-depleted embryos that corresponds with the posterior limit of the presumptive cerebellum. It is possible that other mechanisms prevent RA signaling anterior to this boundary. The development of the mid- and fore-brain has been shown to require active repression of gene expression by unliganded RARs (Koide et al., 2001), a mechanism that is expected to be easily destabilized by the presence of RA. It seems likely that multiple mechanisms exist that protect the mid- and fore-brain from the teratogenic effects of RA.

Regulation of cyp26 expression
A major outstanding question is how is cyp26 expression normally regulated in the hindbrain? Kudoh et al. (Kudoh et al., 2002) showed that the normal posterior limit of cyp26a1 in the hindbrain is established by signals (FGFs and Wnts) from the margin because, in embryos treated with antagonists of these pathways, the cyp26a1 boundary is shifted posteriorly. Although cyp26a1 is directly inducible by RA, its anterior neur ectodermal expression arises independently of RA (Dobbs-McAuliffe et al., 2004, Sirbu et al., 2005) (our work). The factors that positively regulate cyp26a1 in the anterior neur ectoderm remain to be identified.

We also do not know how cyp26b1 and cyp26c1 expression is initiated in r2–r4, or what regulates their subsequent expansion into r5 and r6. In general, the mechanisms controlling gene expression in the anterior rhombomeres are poorly understood in any vertebrate (Moenes and Prince, 2002). Similar to other anterior hindbrain genes, the initiation of cyp26b1 and cyp26c1 expression is independent of RA, because both genes are expressed in DEAB-treated embryos. cyp26b1 and cyp26c1 expression is also independent of the prior establishment of hindbrain boundaries by Cyp26a1, because both genes are expressed normally in cyp26a1 mutants and in embryos in which cyp26a1 expression is globally up-regulated by sub-teratogenic concentrations of RA. The early expression domain of cyp26b1 and cyp26c1 in r3 and r4 is similar to that of ino7, suggesting that they may be downstream of, or co-regulated with, ino7 (Lecaudey et al., 2004). Modern genetic and genomic resources available for the zebrafish will allow the important mystery of cyp26 regulation to be addressed in the future.

Implications for the regulation of retinoic acid during hindbrain patterning
The model we propose for hindbrain patterning through localized RA inactivation by Cyp26 enzymes (Fig. 7B) accounts for a number of previously unexplained aspects of hindbrain patterning. First among these is the observation that embryos depleted of endogenous RA can be rescued by exogenous RA. This rescue can be achieved over a 20-fold range of RA concentrations, indicating that RA-dependent gene expression is also not strictly concentration-dependent. By generating a stepwise pattern of RA degradation during hindbrain development, Cyp26 enzymes eliminate the need for a continuous RA gradient. Secondly, a major tenet of the RA morphogen model has been that more-posterior RA-responsive genes, such as the hox-4 genes, are less sensitive to RA than more-anterior ones, such as the hox-1 genes (Gould et al., 1998); however, this has recently been challenged by the observation that, in the context of the intact enhancer, the RARE of hoxd4 is no less sensitive to RA than the RARE of hoxa1 (Nolte et al., 2003). Furthermore, posterior RA-responsive genes do not require a longer exposure to RA than anterior ones, as has been proposed (Dupe and Lumsden, 2001; Sirbu et al., 2005), because identical concentrations of RA applied shortly before the normal initiation of expression are sufficient to rescue this expression in RA-depleted embryos, irrespective of the anterior limit of the RA-responsive gene in question (Maves and Kimmel, 2005). According to our model, the anterior limit of hoxa1, vhfn1 and hoxd4 are determined not by different RA concentrations or length of exposure of cells to RA, but simply by the posterior limit of Cyp26 activity at the time of their expression onset. In its most extreme version, each ‘step’ in the model is essentially a binary decision in which cells posterior to the Cyp26 domain experience RA and initiate RA-responsive gene expression appropriate for that developmental time, while cells within the Cyp26 domain do not. What determines which RA-responsive genes are available to be expressed at a given time is the subject of ongoing studies. Recent work has shown that, within a Hox cluster, the timing of hindbrain expression may be regulated by the progressive opening of chromatin rather than the local accumulation of active transacting factors (Chambeyron et al., 2005).

A RA-dependent patterning mechanism that does not require the formation of a stable gradient in either space or time is expected to be robust to environmental fluctuations. RA is a potent teratogen that is derived from dietary sources of vitamin A, so a robust mechanism for controlling its activity is particularly important. This control does not appear to be exerted at the level of RA biosynthesis, because we have observed that, in the absence of Cyp26a1, even low amounts of precursor are highly teratogenic. Our step-wise model for hindbrain patterning by RA is robust in that it tolerates a broad range of environmental conditions.

Although our model provides robustness to the hindbrain-patterning process and explains how patterning can be established in the presence of uniform RA, our data does not rule out the possibility that other mechanisms act redundantly with RA degradation to pattern the hindbrain under normal circumstances. Indeed, our observation that hindbrain Cyp26b1 and Cyp26c1 activity is dispensable when global RA levels are kept in check by Cyp26a1 suggests that such mechanisms are at work. It is possible that a RA-responsive pre-pattern is established by a transient RA-diffusion gradient, but that Cyp26 enzymes are required to ‘lock in’ this pattern. As with other developmental processes, it is likely that RA-dependent nervous system patterning events are controlled by overlapping, redundant mechanisms that modulate RA signaling at multiple levels. Our work demonstrates that Cyp26-dependent RA degradation is a crucial component of this complex regulation.

The cyp26a1-l-mutant strain was obtained from Yoshiyuki Imai under the support of the National Bioresource Project of Japan. The Cyp26 antagonist R115866 was provided by Janssen Pharmaceutica N.V. (Belgium). We thank Elizabeth Kwan for her helpful contribution to this work. We gratefully acknowledge Phil Soriano, Lisa Maves and the members of the Moens lab for their thoughtful comments during this work and on the manuscript. R.E.H. was supported by NIH...
Note added in proof

Institute.

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