Dorsoventral patterning of the *Xenopus* eye: a collaboration of Retinoid, Hedgehog and FGF receptor signaling

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Summary

In the developing spinal cord and telencephalon, ventral patterning involves the interplay of Hedgehog (Hh), Retinoic Acid (RA) and Fibroblast Growth Factor (FGF) signaling. In the eye, ventral specification involves Hh signaling, but the roles of RA and FGF signaling are less clear. By overexpression assays in *Xenopus* embryos, we found that both RA and FGF receptor (FGFR) signaling ventralize the eye, by expanding optic stalk and ventral retina, and repressing dorsal retina character. Co-overexpression experiments show that RA and FGFR can collaborate with Hh signaling and reinforce its ventralizing activity. In loss-of-function experiments, a strong eye dorsalization was observed after triple inhibition of Hh, RA and FGFR signaling, while weaker effects were obtained by inhibiting only one or two of these pathways. These results suggest that the ventral regionalization of the eye is specified by interactions of Hh, RA and FGFR signaling. We argue that similar mechanisms might control ventral neural patterning throughout the central nervous system.

Key words: Ventral retina, Dorsal retina, Optic stalk, Retinoic acid, Hedgehog, FGF receptor, *Xenopus*

Introduction

Dorsoventral (DV) patterning of the vertebrate eye underlies important properties of the visual system. First, it controls subdivision of the eye into optic stalk (OS) and retina, which form from the ventromedial and the dorsolateral parts of the optic vesicle, respectively (Chow and Lang, 2001). Second, the retina itself is patterned along the DV axis. A landmark of retina DV polarity is the choroid fissure at the ventral pole of the retina. Retinal neurogenesis is initiated in this region and then progresses to the DR (Peters, 2002; Russell, 2003). DV asymmetries also exist in the distribution of differentiated cell types within the retina (Peters, 2002). Finally, ganglion cells located in the dorsal retina (DR) and the ventral retina (VR) send their axons to the lateral and medial optic tectum, respectively, creating an inverted topographic map of retinotectal projections (McLaughlin et al., 2003).

Before these morphogenetic events of DV specification, asymmetrically expressed transcription factors regionalize the optic vesicle into three main DV compartments. From ventral to dorsal, these are: the OS, which expresses Pax2, Vax1 and Vax2, but not Pax6 and Tbx5; the VR, which expresses Vax2 and Pax6, but not Pax2, Vax1 or Tbx5; the DR, which expresses Pax6 and Tbx5, but not Pax2, Vax1 and Vax2 (Barbieri et al., 2002; Bertuzzi et al., 1999; Hallonet et al., 1999; Koshiba-Takeuchi et al., 2000; Liu et al., 2001; Mui et al., 2002; Schwarz et al., 2000; Torres et al., 1996).

How is this transcriptional code established? In the developing spinal cord, opposing ventralizing and dorsalizing activities of Hedgehog (Hh) and Bone Morphogenetic Protein (BMP) signaling pathways have key roles in the specification of DV polarity upstream of transcription factors (Ruiz i Altaba et al., 2003). Nonetheless, recent studies have indicated that ventral patterning cannot be ascribed to Hh signaling alone, and Retinoic Acid (RA) and Fibroblast Growth Factor (FGF) signaling are also crucial players in this process (Appel and Eisen, 2003; Diez del Corral and Storey, 2004; Harris, 2003). Recent work has also shown that RA and FGF are required, in addition to Hh signaling, to elicit full specification of the ventral telencephalon (Lupo et al., 2002; Marklund et al., 2004; Shinya et al., 2001).

By analogy to the neural tube, it has been suggested that eye DV polarity may also be established by Hh and BMP antagonistic activities (Russell, 2003; Wilson and Houart, 2004; Yang, 2004). BMP overexpression in the retina has a strong dorsalizing effect (Koshiba-Takeuchi et al., 2000; Sasagawa et al., 2002), while BMP inhibition ventralizes the eye (Murali et al., 2005; Sakuta et al., 2001; Sasagawa et al., 2002). As to Hh signaling, although its role in OS specification
is well known on the basis of both loss- and gain-of-function assays (Russell, 2003; Yang, 2004), its role in DV patterning of the retina is less clear (Perron et al., 2003; Zhang and Yang, 2001). RA and FGF signaling pathways may also play a role in the ventralization of the eye. The VR is richer in RA than the DR (Drager et al., 2001), suggesting that high RA levels may specify ventral character in the eye. RA treatments upregulate the OS marker Pax2 in zebrafish embryos (Hyatt et al., 1996). By contrast, reduction of embryonic RA signaling by means of vitamin A deficiency, knock out of RA receptors (RAR) or exposure to citral caused morphological deficits in the VR (Kastner et al., 1994; Marsh-Armstrong et al., 1994; Ross et al., 2000). However, a lack of appropriate molecular markers meant that it was not possible to determine whether the observed morphological defects were due to impaired DV specification rather than abnormal morphogenesis, growth or survival of the VR. As to FGF signaling, although it may be responsible for maintaining some ventral eye gene expression in the absence of all Nodal and Hh signaling in zebrafish (Takeuchi et al., 2003), in the studies reported so far, inhibition of FGF signals produced only weak effects on the expression of ventral eye genes (Shannugalingam et al., 2000; Walshe and FGFR1 (Pownall et al., 2003); and pT7TS-Xbhh (Ekker et al., 1995); RAL-3F 5′ AT(CT) TT(AG) AAI CCI CC(AG) AAI GG-3′ and RAL-3R 5′(CT) AT(ACT) AA(CT) AA(CT) GAI TGG-3′ corresponded to Xenopus Raldh1; 2 to Xenopus Raldh2, while five clones showed the highest homology to chick and mouse Raldh3 and corresponded to Xenopus Raldh3 (Xraldh3). Full-length Xraldh3 cDNA was obtained by RACE-PCR using a SMART RACE cDNA amplification kit (Clontech).

**Materials and methods**

**Cloning of full-length Raldh3 cDNA**

A 1.3 kb fragment was amplified by RT-PCR from stage 40 head cDNA using the following primers: RAL-3F 5′-AA(A)G AT(AC) TT(T)T AT(AC) AA(CT) GAI TGG-3′; RAL-3R 5′-GAC AT(CT) TT(T)T AT(AG) AA(C) AA GG-3′. After gel purification, the PCR product was cloned into pGEM-T vector (Promega). Plasmid DNA was recovered from 18 independent clones: 11 corresponded to Xenopus Raldh1; 2 to Xenopus Raldh2, while five clones showed the highest homology to chick and mouse Raldh3 and corresponded to Xenopus Raldh3 (Xraldh3). Full-length Xraldh3 cDNA was obtained by RACE-PCR using a SMART RACE cDNA amplification kit (Clontech).

**Xenopus embryos and in situ hybridization**

Embryos were obtained and staged as previously described (Nieuwkoop and Faber, 1967). Whole-mount in situ hybridization was performed as described by Harland (Harland, 1991). Whole-mount in situ hybridization on dissected retinas, double in situ hybridizations, and sectioning of whole-mount hybridized embryos were carried out as previously described (Liu et al., 2001).

**RNA methods and microinjections**

Capped mRNAs were synthesized from linearized plasmid templates using mMESSAGE mMACHINE kits (Ambion). Embryos were injected as previously described (Vignali et al., 2000). Injections were performed at the eight-cell stage in one or both dorsal-animal blastomeres. The following template plasmids were used: banded hedgehog, pT7TS-Xbhh (Ekker et al., 1995); iFGFR1, pCS2+-iFGFR1 (Pownall et al., 2003); and Raldh3, pCS2+-Xraldh3. iFGFR1 activity was induced by immersion of embryos in 0.1×MBS supplemented with 1.25 µM AP20187 (ARIAD Pharmaceuticals; http://www.ariad.com), from 1 mM stock in 100% ethanol. When β-galactosidase (β-gal) was used as a lineage tracer, embryos were co-injected with 100-500 pg of β-gal mRNA and stained as previously described (Andreazzoli et al., 1999).

**Treatments with retinoids and receptor antagonists**

For retinoid treatments, embryos were treated in the dark with all-trans-Retinoic Acid (Sigma) or all-trans-Retinal (Sigma), diluted in 0.1×MBS from 10-100 mM stocks in DMSO. Loss-of-function experiments were performed with the following compounds: AGN194310 (Allergan; http://www.allergan.com), dissolved in 25 mM stock in DMSO; cyclopaamine (a gift from W. Gaffield, and Toronto Research Chemicals), dissolved in 20 mM stock in 95% ethanol; SU5402 (Calbiochem), dissolved in 25 mM stock in DMSO. Embryos were exposed in the dark to appropriate concentrations of these inhibitors diluted in 0.1×MBS. Control embryos were treated with identical concentrations of DMSO and/or ethanol.

**Results**

**Overexpression of Hh, RA and FGFR signaling pathways causes ventralization of the eye with dose-dependent effects**

The Xenopus eye at stage 33 comprises three main regions (Fig. 1): the most ventral OS, which is Pax2, Vax1b, Raldh3 and Vax2 positive but Pax6 negative; the VR, which is Pax2 and Pax6 positive but negative for both OS markers and ET; and the DR, which is ET and Pax6 positive but negative for all the ventral eye markers. This DV organization was clearly affected in embryos unilaterally injected with high doses (250 pg) of bhh mRNA (Fig. 1B). On the injected sides, both Vax2 and the OS markers Pax2, Vax1b and Raldh3 were upregulated, while Pax6 and ET were downregulated, suggesting that high levels of Hh signaling transform the retina into OS. To address whether Hh overexpression could also modify the DV character of the retina, without transforming it into OS, we injected low doses (1 pg) of bhh mRNA. As shown in Fig.1A, these doses caused a partial expansion of OS markers and slightly reduced the DR marker Pax6 domain. However, expression of the VR marker Vax2 spread throughout the retina, while expression of the DR marker ET was reduced, suggesting that the DR has, at least in part, acquired VR, rather than OS, character. Similar results were obtained after overexpression of shh mRNA (data not shown).

RA treatments during gastrulation cause caudalization and loss of head structures (Durston et al., 1989). Therefore, we started exposure to RA at early neurula stages (stage 12.5/13), and performed dose-response experiments with concentrations of RA varying from 0.01 µM to 10 µM. As shown in Fig. 2B and see Fig. S1 in the supplementary material, treatments of Xenopus embryos with high doses of RA (10 µM) from stage 12.5/13 to stage 33 expanded Vax2 expression throughout the eye, while both DR markers (Vent2 and ET) and OS markers (Pax2, Vax1b and Raldh3) were repressed. In these embryos, Pax6 was normally expressed in the retina. Although doses of 10 µM repressed the OS, lower RA doses (0.1-0.2 µM) caused a different effect. In these cases, the expression of Vax2 and ET was only slightly affected, while the expression domains of the OS markers Pax2, Vax1b and Raldh3 were all significantly
Dorsoventral patterning of the *Xenopus* eye

To minimize the known effects of early FGF signaling on anteroposterior patterning along the body axis, we took advantage of an inducible form of FGF receptor 1 (iFGFR1) (Pownall et al., 2003). iFGFR1 mRNA was unilaterally injected into early *Xenopus* embryos, and receptor activity was induced from stage 12.5/13. As shown in Fig. 3B, injection of 4 pg iFGFR1 mRNA caused ventralization of the eye. In these eyes, the expression of the OS markers Pax2, Vax1b and Raldh3, as well as that of Vax2, was expanded dorsally, while expression of the DR marker ET was reduced. The Pax6 domain was also clearly reduced on the injected side, suggesting that these doses of iFGFR1 mRNA expand the OS at the expense of the retina (Fig. 3C). As this effect is similar to that induced by high Hh levels, we tested whether FGFR signaling could also produce similar dose-dependent effects on OS and VR specification by performing dose-response experiments with iFGFR-1. As shown in Fig. 3A, 2 pg iFGFR1 mRNA caused only a partial enlargement of Pax2, Vax1b and Raldh3 domains, while Pax6 expression was only slightly reduced in the ventralmost part of the eye. At this same dose, only weak effects were detected on the VR and DR markers Vax2 and ET, respectively. These results suggest that, unlike Hh, FGFR signaling cannot ventralize the

**Fig. 1.** Effects of Hh signaling overexpression on eye DV polarity. (A,B) The red or light-blue β-gal staining identifies the injected side. The broken yellow circles highlight the eye region. (A) Unilateral injection of low doses of bhh mRNA (1 pg) upregulates Vax2 in the DR and reduces ET in stage 33 *Xenopus* embryos. Pax2, Vax1b and Raldh3 are partially upregulated, but not in the DR, and the Pax6 domain is slightly reduced in these embryos. On the uninjected side, Vax2 is normally expressed in the OS and the VR; ET is expressed in the DR; Pax2, Vax1b and Raldh3 are expressed in the OS region and Pax6 is expressed in the retina region. (B) High doses of bhh mRNA (250 pg) upregulate Vax2, Pax2, Vax1b and Raldh3 throughout the eye, and repress ET and Pax6 expression. (C) Schematic representation of the results shown in A and B. Low Hh levels partially expand the OS and ventralize in part the DR. Purple indicates the overlap of ventral and dorsal character in the most dorsal retina. High Hh levels transform the entire retina into OS.

**Fig. 2.** Effects of RA signaling overexpression on eye DV polarity. (A) Low RA doses (0.1 µM) expand Pax2, Vax1b and Raldh3 expression domains, but do not significantly affect Vax2- and ET-positive regions in stage 33 *Xenopus* embryos. Pax2-hybridized embryos are also shown in frontal view (right column). (B) High RA doses (10 µM) upregulate Vax2 in the DR and repress Vent2, Pax2, Vax1b and Raldh3, but do not change Pax6 expression. (C) Schematic representation of the results shown in A and B. Low RA levels enlarge the OS. High RA levels ventralize the retina and repress OS formation.
DR at conditions where the OS is moderately expanded (Fig. 3).

In conclusion, Hh and RA signaling can affect DV specification in the eye with dose-dependent effects. In particular, high Hh and low RA levels preferentially induce OS character, high RA levels preferentially induce VR character, while low Hh levels locally induce OS character ventrally and VR character dorsally. FGFR signaling can induce OS character, but is not efficient at inducing VR character.

Localization of Hh, FGF and RA signaling components supports a role in patterning the Xenopus eye field

In all model systems examined so far, Shh is expressed in the anterior midline at gastrula and neurula stages, then in the ventral forebrain adjacent to the developing eye during later development (Wilson and Houart, 2004). By double in situ hybridization with the eye field marker Rx1 (Casarosa et al., 1997), we confirmed that the most anterior domain of Shh expression overlaps with the medial part of the eye field at neurula stages (Fig. 4D). FGF8 is expressed in the anterior neural ridge (ANR) adjacent to the eye field from neurula stages onwards. At later stages, FGF8 expression is maintained in ventral forebrain regions close to the ventral eye and in the OS (Wilson and Houart, 2004). Double in situ hybridization with Rx1 shows that, at early neurula stages, FGF8 expression

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**Fig. 3.** Effects of FGFR signaling overexpression on eye DV polarity. (A) Unilateral injection of 2 pg iFGFR1 mRNA, followed by induction with AP20187 at stage 12.5/13, partially expands the expression domains of Vax2, Pax2, Vax1b and Raldh3 in the ventral eye, and weakly represses ET and Pax6 in stage 33 Xenopus embryos. (B) Injection of 4 pg iFGFR1 mRNA upregulates Vax2, Pax2, Vax1b and Raldh3 in the dorsal eye and strongly repress ET and Pax6. (C) Schematic representation of the results shown in A and B. Increasing FGFR levels progressively expands the OS at the expense of the retina.

**Fig. 4.** Expression pattern of Raldh3 during Xenopus development. (A) Raldh3 expression as detected by whole-mount in situ hybridization of whole embryos (stage 10.25-31) or dissected neural retinas, without lens and pigmented epithelium (stage 59). (B) Raldh3 expression in transverse sections of stage 33 embryos after whole-mount in situ hybridization. From left to right, sections show expression at progressively posterior levels. op, olfactory placode; os, optic stalk. (C) Comparison of Pax2, Raldh3 and Vax2 expression in the optic cup in transversal sections of stage 33 embryos after whole-mount in situ hybridization. (D) Double in situ hybridizations of Rx1 with Raldh2, Shh or FGF8 on mid- to late neurula embryos shown from anterior view. The inset shows a double in situ hybridization of Rx1 with FGF8 on an early neurula embryo.
in the ANR is adjacent to the eye field. However, during mid-late neurula stages, this FGF8 domain becomes more medially restricted and overlaps with the medial part of the eye field (Fig. 4D). Hh and FGF receptors are also expressed in the prospective anterior neuroectoderm from early stages of Xenopus development (Hongo et al., 1999; Koebernick et al., 2001).

Less is known about RA signaling in the eye field region, although RAR receptors are widely distributed in early Xenopus embryos (Shiotsugu et al., 2004), RA synthesis has been detected in neurula stage Xenopus embryos (Ang and Duester, 1999b) and high levels of RA synthesis are present in the ventral retina at later stages of development (Drager et al., 2001). To investigate the regulation of RA synthesis during eye development, we screened for Raldh homologs, coding for retinaldehyde dehydrogenases, in Xenopus. Some of the isolated clones corresponded to Raldh1, which is not expressed during early eye development in Xenopus (Ang and Duester, 1999a), or Raldh2, which is expressed in the ANR adjacent to eye field during neurula stages, and subsequently in the ectoderm flanking the ventrolateral regions of the evaginating optic vesicle (Chen et al., 2001). Double in situ hybridization with Rx1 showed that Raldh2 expression in the ANR is stronger next to the anterolateral part of the eye field, and weaker next to the medial part of the eye field (Fig. 4D). Finally, a third group of clones showed the highest homology to chick, mouse and human Raldh3, thus corresponding to the Xenopus Raldh3 ortholog, Xraldh3 (Accession Number, AY692028). Isolation of full-length Xraldh3 cDNA indicated that Xraldh3 codes for a predicted protein of 512 amino acids, showing 79.9%, 78.7% and 79.9% homology with chick, mouse and human Raldh3, respectively (see Fig. S2 in the supplementary material).

Raldh3 is transcribed in the dorsal blastopore lip by early gastrula stages, and, later in gastrulation, in the involuting anterior mesendoderm underlying the anterior neural plate (Fig. 4A). This expression is quickly downregulated, but a new expression domain becomes evident by late neurula stages in the ventral part of the evaginating optic vesicle (data not shown). At early tailbud stages (stage 22/23), Raldh3 is expressed in the ventral optic vesicle, the midbrain-hindbrain boundary and the dorsal part of the otic vesicle; at later stages (stage 33) it is also expressed in the olfactory placode (Fig. 4A). Transverse sections of Raldh3-hybridized embryos at this stage confirmed these expression domains (Fig. 4B and data not shown). Comparative in situ hybridization analysis revealed that Pax2, Raldh3 and Vax2 show nested expression domains within the ventral optic cup (Fig. 4C). Raldh3 transcripts persist in the ventral part of the eye throughout development, including metamorphosis (stage 59/60), in a domain still contained within that of Vax2 (Fig. 4A; data not shown).

Raldh2 can mediate RA synthesis from all-trans Retinal (ATR) in Xenopus embryos (Chen et al., 2001). In order to determine whether Raldh3 could also efficiently promote RA synthesis in vivo, we performed overexpression experiments by bilateral microinjection of Raldh3 mRNA, and checked whether it could mimic the ventralizing activity of RA on the developing eye. No significant effects on DV specification in the eye were detected after injection of up to 5 ng Raldh3 mRNA (data not shown), possibly because of the complex regulation of substrate availability in vivo (Chen et al., 2001). To test this, we provided low doses of exogenous ATR. Injection of 1 ng Raldh3 mRNA in combination with 0.5 µM ATR treatment from stage 12.5/13 induced a similar expansion of Pax2 expression to that observed after treatments with low doses of RA (Fig. 5A; compare with Fig. 2A). By increasing the doses of ATR to 2.5 µM ATR and

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**Fig. 5.** Raldh3 overexpression in the presence of ATR reproduces the effects of RA treatments on eye DV polarity. (A) Embryos were bilaterally injected with a total of 1 ng Raldh3 mRNA and treated with 0.5 µM ATR from stage 12.5/13, followed by molecular marker analysis at stage 33. The combination of Raldh3 and ATR expands Pax2 expression, while ATR alone has only a weak effect. A comparable expansion of Pax2 is obtained by a dose of 2 µM ATR in the absence of exogenous Raldh3. (B) The combination of 4 ng Raldh3 mRNA and 2.5 µM ATR can upregulate Vax2 in the DR, while ATR alone has only a weak effect. Strong Vax2 upregulation is also caused by a dose of 10 µM ATR in the absence of exogenous Raldh3, as shown in both lateral (upper row) and anterior view (lower row).

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**Fig. 6.** RA, Hh and FGFR signaling pathways can partially ventralize the eye field at neurula stages. (A) In embryos treated with 10 µM RA from stage 12.5/13 (right column), the lateral region of Vax2 domain (indicated by the yellow brackets) is expanded at late neurula stages with respect to control embryos, while Vent2 domain is reduced. (B) Mid-late neurula embryos unilaterally injected either with 500 pg bhh mRNA or with 2.5 pg IFGFR1 mRNA, followed by induction with AP20187 from stage 12.5/13. Compared with the uninjected side, Vax2 expression is expanded, while ET is repressed. The broken yellow lines indicate the embryo midline.
Raldh3 mRNA to 4 ng, we could phenocopy the strong Vax2 upregulation produced by treatments with high RA doses (Fig. 5B; compare with Fig. 2B). At the same doses of ATR alone, Pax2 and Vax2 expression was only slightly increased. Thus, Raldh3 can efficiently convert ATR to RA in vivo. We also observed similar ventralizing effects after treatments with higher doses of ATR in the absence of injected Raldh3 mRNA (Fig. 5A,B), which were prevented by the RAR antagonist AGN194310 (Hammond et al., 2001) (see Fig. S3 in the supplementary material).

In conclusion, components of the Hh, FGFR and RA signaling pathways are already localized in the eye field at neurula stages, and they remain expressed in or close to the ventral eye at later stages (Figs 4, 9). To test whether these signaling systems play an early role in patterning of the eye field, we performed overexpression experiments in Xenopus embryos (as above), but examined the relative expression of eye field markers at neurula stages, and found expansion of ventral eye markers and repression of dorsal eye markers in the eye field (Fig. 6).

RA and FGFR signaling can collaborate with Hh signaling in ventral eye specification

We then performed co-overexpression experiments, in which we simultaneously activated two pathways at a time, at doses that were sub-optimal for each factor alone.

We first unilaterally injected doses of 1 pg bhh mRNA, which partially expanded the expression domain of OS markers (Fig. 1A), and exposed injected embryos to different doses of ATR. In these experiments, we scored activation of the OS marker Pax2 by classifying Pax2-hybridized embryos in three classes: (1) class I embryos, where Pax2 expression was approximately confined to the ventral half of the eye; (2) class II embryos, where Pax2-positive domain spread to the dorsal half of the eye, without covering it completely; (3) class III embryos, in which Pax2 expression covered all or nearly all the eye region. Examples of class I, II and III eyes are shown in Fig. 8A. Although doses of ATR in the range of 2 µM can expand the expression domain of OS markers in the ventral eye, they never upregulate OS markers in dorsal eye regions (Fig. 5A). However, as shown in Fig. 7A, ATR treatments clearly reinforced induction of the OS marker Pax2 by low...
doses of Hh signaling. At doses of 2-2.5 µM ATR, the majority of the embryos had upregulated Pax2 in the dorsal eye, while only a minority of mock-treated bhh-injected embryos showed upregulation of Pax2 in the dorsal eye (Fig. 7C). On the uninjected side of ATR-treated embryos, Pax2 was upregulated only within the ventral eye region (Fig. 7A). Therefore, RA and Hh signaling can collaborate in OS specification. As described before, low doses of bhh mRNA in the range used for these experiments can ventralize the DR as shown by the upregulation of the VR marker Vax2 in nearly the whole of the eye region, and the downregulation of the DR marker ET (Fig. 7A). We found that the percentages of embryos showing Vax2 upregulation throughout the eye region, and nearly complete ET repression in the DR, were increased by ATR treatments, suggesting that RA and Hh signaling can also collaborate in VR specification (Fig. 7C). In order to clarify this issue, we used lower doses of bhh mRNA, which do not significantly affect DV specification in the eye, in combination with ATR treatments. As shown in Fig. 7B, doses of 0.2 pg bhh mRNA caused only a slight upregulation of Pax2 and Vax2 in the eye, whereas doses of 5 µM ATR locally expanded Pax2 in the ventral part of the eye, and only slightly increased Vax2 expression in the VR. Both bhh and ATR partially reduced ET expression at these doses. When embryos unilaterally injected with 0.2 pg bhh mRNA were also treated with 5 µM ATR, no strong increase was detected in the expression of Pax2 on the injected side with respect to the uninjected side and few class II and no class III embryos were detected. By contrast, the expression of Vax2 was upregulated throughout the eye region and the expression of ET was almost completely repressed in the DR in substantial fractions of injected eyes (Fig. 7B,C), indicating ventralization of the DR. Similar results were obtained with the DR marker Tbx5 (data not shown). Therefore, RA and Hh signaling can also cooperate in ventralizing the DR, in conditions where OS specification is weakly affected.

To address whether Hh and FGFR signaling can also collaborate in ventral eye specification, we co-injected suboptimal doses of bhh and iFGFR1 mRNAs, followed by induction of iFGFR1 activity from stage 12.5/13 as before. As already reported (Fig. 1A, Fig. 7A), low doses of 1 pg bhh mRNA only partially upregulated the OS marker Pax2, and ventralized the DR as shown by Vax2 upregulation over nearly the whole of the eye region in a proportion of the embryos. Low doses of 0.5-1 pg iFGFR1 mRNA did not cause significant effects on the expression of Pax2 and Vax2. However, co-injection of 1 pg bhh and 0.5-1 pg iFGFR1 mRNAs caused
a clear increase in the percentage of class II and class III Pax2-hybridized eyes compared with single bhh overexpression (Fig. 8). Co-overexpression of bhh and iFGFR1 also slightly increased the proportion of embryos showing roughly complete upregulation of Vax2 in the eye region, compared with single bhh overexpression, and the percentage of these embryos was slightly higher than the percentage of class III Pax2-hybridized embryos (Fig. 8A,B). In addition, the percentage of eyes with nearly complete repression of the DR marker Tbx5 was increased in embryos co-injected with bhh and iFGFR1 compared with bhh alone (Fig. 8A,B). Expression of the DR marker ET was also decreased after co-injection of bhh and iFGFR1, compared with single bhh injection, although some ET expression in the dorsalmost eye was still retained in the majority of the embryos (data not shown). These data suggest that, when the eye does not completely acquire OS character, bhh and iFGFR1 may also ventralize, at least in part, the remaining retina tissue. Similar results were obtained after co-overexpression of 1 pg iFGFR1 mRNA with lower doses of 0.5 pg bhh mRNA (Fig. 8B). Therefore, FGFR1 and Hh signaling can collaborate in OS specification and they may also weakly interact in VR specification (Fig. 8C).

In conclusion, Hh, RA and FGFR signaling can collaborate in ventral eye specification. In particular, OS character is preferentially specified at higher Hh and FGFR signaling levels, and lower RA signaling levels, whereas VR character is preferentially specified at lower Hh and higher RA levels.

**RA, Hh and FGF signaling pathways can cross-regulate each other at the transcriptional level.**

Eye ventralization by RA, Hh and FGF signals may involve crossregulatory interactions among these three signaling pathways. We found that both bhh and iFGFR1 overexpression upregulate Raldh3 expression in the eye at stage 33 (Fig. 1B, Fig. 3B). Unilateral injection of 500 pg bhh mRNA did not have appreciable effects on Raldh2 expression in the ANR at neurula stages (Fig. 9B), but upregulated it in stage 33 eyes (Fig. 9B); it also caused the FGF8-positive domain in the ANR to expand laterally and upregulated FGF8 in the eye region at stage 33 (Fig. 9B).

We also found that RA treatments downregulated Shh expression in the anterior midline (Fig. 9A). Treatments with high RA doses (10 µM) from stage 12.5/13 repressed the most anterior domain of Shh transcription at neurula stages, which overlaps with the medial part of the eye field (Fig. 4D). This effect was also evident at stage 33. Low RA doses (0.1 µM) partially downregulated Shh expression in the anterior midline at neurula stages, while no clear effect was evident at stage 33. FGF8 expression was also affected in RA-treated embryos.
At neurula stages, \textit{FGF8} mRNA is transcribed in two anterior stripes, one in the ANR, and the other in the anteroventral ectoderm outside the neural plate. These two stripes were closer to each other in low dose RA-treated embryos, and appeared to be merged in one broader stripe of expression in high dose RA-treated embryos. At tadpole stages, a strong general repression of \textit{FGF8} transcription was caused by high RA doses.

As shown in Fig. 9C, 4 pg \textit{iFGFR1} mRNA injections did not affect \textit{Raldh2} expression in the ANR at neurula after induction at stage 12.5/13, while \textit{Shh} expression was expanded on the injected side at the level of the prospective hypothalamic region. Ectopic upregulation of \textit{Shh} in the eye region at stage 33 was also detectable in these conditions. At lower doses (2 pg), only weak effects on \textit{Shh} and \textit{Raldh2} expression were detected. Analysis of \textit{Pax2} and \textit{Vax2} expression showed that, in this experiment, 2 pg \textit{iFGFR1} mRNA induced eye ventralization similar to that reported in Fig. 3, while a 4 pg dose caused eye reductions (Fig. 9C and data not shown).

In conclusion, RA, Hh and FGF signals are able to crossregulate the expression of one another, although these effects are mainly mediated by doses of signal higher than those required to ventralize the eye. \textit{Shh} downregulation in the anterior midline of RA-treated embryos suggested that the loss of the OS seen with high RA may be a secondary consequence of this effect. To address this issue, we analyzed whether Hh signaling could rescue OS formation in RA-treated embryos. Indeed, we found that expression of OS markers was recovered in embryos injected with 25 pg \textit{bhh} mRNA followed by incubation in 10 \(\mu\)M RA from stage 12.5/13 (see Fig. S4 in the supplementary material). Therefore, RA treatments may repress OS formation indirectly by downregulating \textit{Shh} expression in the anterior midline, although a direct inhibitory effect on OS gene expression cannot be ruled out.

**Loss-of-function experiments suggest that ventral eye specification involves interactions among Hh, RA and FGFR signaling**

To address whether interactions between Hh, RA and FGFR signaling pathways play an important role in ventral eye specification, we inhibited them in all possible combinations. Hh signaling was blocked with cyclopamine (Incardona et al., 1998). RA signaling was inhibited with the pan-RAR

**Fig. 10.** Loss-of-function effects of RA, Hh and FGFR signaling pathways on eye DV polarity. Embryos were treated from stage 10.5 with 10 \(\mu\)M AGN194310 (AGN), 100 \(\mu\)M cyclopamine (CPM) and 25 \(\mu\)M SU5402 (SU) in different combinations, and analyzed for molecular marker expression at stage 30/31. (A) Effects of the single inhibition of any of the RA, Hh and FGFR signaling pathways, when compared with mock-treated embryos. (B) Effects of double and triple inhibition of RA, Hh and FGFR pathways. (C) Schematic representation of the results shown in A and B. Strong eye dorsalization is caused by triple inhibition of RA, Hh and FGFR signaling, while double inhibitions produce weaker effects.

**Fig. 11.** A proposed model for signaling events controlling DV patterning of the eye. Interaction of high levels of Hh and FGFR with low levels of RA signaling repress \textit{Pax6} and induce the expression of \textit{Vax1}, \textit{Pax2} and \textit{Vax2}, leading to OS specification. High levels of RA in collaboration with low levels of Hh and FGFR signaling repress ET and induce the expression of \textit{Vax2} in the absence of \textit{Vax1} and \textit{Pax2}, but in the presence of \textit{Pax6}, thus specifying VR identity. BMP signaling inhibits \textit{Vax2} and induces ET expression, causing DR specification. In addition, high levels of RA repress the expression of Hh and FGFR signals, while Hh and FGFR signaling crossactivate each other at the transcriptional level.
antagonist AGN194310, which specifically antagonizes activity of all RAR receptors, but not RXR receptors (Hammond et al., 2001). FGFR signaling was inhibited with SU5402 (Mohammadi et al., 1997). *Xenopus* embryos were treated with these antagonists from stage 10.5, at conditions in which each inhibitor effectively reduced the levels of its target signaling pathway, without significantly affecting the other two (see Figs S5, S6 in the supplementary material). As shown in Fig. 10, significant DV organization was retained after any of the single inhibitions of Hh, RA or FGFR signaling. Double inhibition of Hh, RA and FGFR signaling in different combinations increased reduction of ventral eye territories when compared with single inhibitions, especially after Hh and FGFR or RA and FGFR inhibitions. The strongest effects were obtained with the simultaneous inhibition of all three (Hh, RA and FGFR) signaling pathways, which caused a dorsalized eye phenotype, with strong repression of ventral eye markers and upregulation of the DR markers *ET* within the ventral eye. In conclusion, the results of loss-of-function experiments support a model where ventral eye specification involves interactions among Hh, RA and FGFR signaling pathways.

**Discussion**

**Roles of Hh, RA and FGFR signaling pathways in OS and VR specification**

Hh signaling has a crucial role in OS specification. In zebrafish, *Xenopus* and chick embryos, Hh overexpression can upregulate OS markers in the retina region, while repressing the expression of retinal markers. By contrast, downregulation of Hh signaling by *Shh* knock out in mouse, *smoothened* knock out in zebrafish or cyclopamine treatments in *Xenopus* all cause suppression of OS fate, thus indicating that Hh signaling is both necessary and sufficient for OS specification (Russell, 2003; Yang, 2004). Within the spinal cord, *Shh* released from the floor plate has been shown to work as a morphogen, inducing the expression of ventral genes at high doses, and more dorsal genes at lower doses (Ruiz i Altaba et al., 2003). By analogy to the neural tube, it has been suggested that Hh signals may also act in a graded manner in the eye, specifying OS, VR and DR fates at different threshold concentrations (Wilson and Houart, 2004). We show that, in the DR, low doses of Hh signaling can upregulate *Vax2*, but not OS markers, and decrease the expression of *ET*, but not *Pax6* (Fig. 1A), suggesting that low Hh levels can at least partially ventralize the DR without concomitant expansion of the OS.

RA has been suggested as an alternative signaling molecule that may control DV specification within the retina (Drager et al., 2001). RA treatments upregulated the OS marker *Pax2* in zebrafish (Hyatt et al., 1996), while reduced RA signaling caused abnormal development of the VR in different animal models (Marsh-Armstrong et al., 1994; Ross et al., 2000), at least at the morphological level. In this paper, we confirm in a different model system that increasing RA levels can induce OS character in the eye (Fig. 2A). More importantly, we provide evidence that RA can act as a ventralizing factor within the retina. This ventralizing effect requires higher levels of RA than those required to induce OS expansion, and it is accompanied by a strong repression of OS genes, probably owing to the downregulation of *Shh* in the anterior midline (Fig. 9A). Upregulation of *Vax2* in the presence of *Pax6*, but in the absence of OS markers, together with the strong downregulation of DR markers, indicates that high RA levels cause the DR to acquire VR character (Fig. 2B, see Fig. S1 in the supplementary material). These ventralizing activities of RA can be mimicked, albeit less efficiently, by the intermediate metabolic precursor ATR, suggesting that correct localization of endogenous RA-generating enzymes is important for DV patterning of the eye (Fig. 5). These effects are strongly inhibited by a RAR antagonist, indicating that they are specifically mediated by activation of RAR receptors (see Fig. S3 in the supplementary material).

Loss-of-function analyses of FGF signals in zebrafish have suggested that this pathway may play a role in OS specification, although decreased FGF signaling seems to have much more profound effects on the adjacent ventral forebrain (Take-uchi et al., 2003; Walshe and Mason, 2003). There are no reports that we are aware of suggesting that FGF signaling may have a role in DV patterning within the retina. We show that overexpression of FGFR signaling has a strong ventralizing effect on the developing *Xenopus* eye. At all doses analyzed, FGFR signaling expands the expression of *Vax2* and OS markers to a similar extent, while the expression domain of *Pax6* is proportionally reduced, suggesting that FGFR signaling on its own can enhance specification of OS character, but it cannot efficiently modify the DV character of the retina (Fig. 3). FGFR and Hh signaling can collaborate in the specification of OS character, and they may weakly interact in specifying VR character (Fig. 8). Finally, strong effects on VR specification were observed when FGFR signaling was inhibited together with RA and Hh signaling (Fig. 10). Although further work is needed to determine the precise role of FGFR signaling in DV patterning of the retina, our results suggest that it may be involved in controlling patterning throughout the eye DV axis; higher levels of FGFR activation may promote OS fates, while lower levels of FGFR activation may collaborate with other signals in the specification of VR fates.

**RA, Hh and FGFR signaling interact in Xenopus ventral eye specification**

The fact that RA, Hh and FGFR overexpression cause similar ventralizing effects in the eye, and the observation that these signaling components are expressed in adjacent or overlapping domains at early stages of eye development, suggested that these pathways may interact during DV patterning of the eye in *Xenopus*. Two lines of evidence in this work support this idea. First, in co-overexpression experiments, Hh, RA and FGFR signaling can collaborate in ventral eye specification (Figs 7, 8). Second, in loss-of-function experiments, stronger effects on eye DV patterning were observed by inhibiting more than one pathway compared with single inhibitions (Fig. 10).

We propose a model of ventral eye specification that involves interactions among RA, Hh and FGFR signaling pathways (Fig. 11). According to this model, high levels of Hh and FGFR signaling interact with low levels of RA signaling to specify the OS by repressing retina-determination genes such as *Pax6*, and promoting the expression of *Vax1* and *Pax2*. By contrast, high levels of RA act in concert with lower levels of Hh and FGFR signaling to specify the VR by repressing DR-specific genes such as *ET* and by inducing the expression of *Vax2* in the presence of *Pax6*, but not *Vax1* and *Pax2*. As
Developmental programs. Different signaling pathways interact to execute specific compositions, its finely graded topography and its experimental process, and the eye, because of its distinct regional composition. Clearly, DV patterning of the vertebrate CNS is a complex and the mechanism of action of these signaling systems. Questions remain to be addressed concerning the precise role of RA signaling play a crucial role in OS specification, although low levels of RA signaling may also be involved. Moreover, RA signaling play a crucial role in the specification of the LGE (Gunhaga et al., 2000; Marklund et al., 2004). In addition, FGF signaling is involved in the specification of V1 and V0 interneurons (Pierani et al., 1999). In addition, although FGF signaling appears to function as a general repressor of ventral neural patterning, RA and FGF in combination can efficiently induce motoneuron progenitors both in explants and in vivo (Novitch et al., 2003).

In the telencephalon, the medial ganglionic eminence (MGE) originates from the ventral part of the telencephalic vesicle, while the lateral ganglionic eminence (LGE) originates from a more intermediate region. Hh signaling is involved in the specification of the MGE, while RA signaling appears to play a crucial role in the specification of the LGE (Gunhaga et al., 2000; Marklund et al., 2004). In addition, FGF signaling is involved in the specification of ventral, but not intermediate, telencephalic fates (Marklund et al., 2004; Shinya et al., 2001). In the developing eye, cells located more ventrally in the anlage give rise to the OS, while the VR originates from a more intermediate region. As shown in Fig. 11, Hh and FGF signaling play a crucial role in OS specification, although low levels of RA signaling may also be involved. Moreover, RA signaling could control specification of the VR in collaboration with low levels of Hh and possibly FGF signaling.

In conclusion, similar mechanisms of ventral specification involving Hh, RA and FGF signaling pathways appear to be at least partially conserved in different CNS regions. Several questions remain to be addressed concerning the precise role and the mechanism of action of these signaling systems. Clearly, DV patterning of the vertebrate CNS is a complex process, and the eye, because of its distinct regional composition, its finely graded topography and its experimental accessibility, is an exciting model with which to study how different signaling pathways interact to execute specific developmental programs.

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Supplementary material
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