The pro-apoptotic activity of a vertebrate Bar-like homeobox gene plays a key role in patterning the Xenopus neural plate by limiting the number of chordin- and shh-expressing cells

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Summary
Targeted disruption of effectors molecules of the apoptotic pathway have demonstrated the occurrence and magnitude of early programmed cell death (EPCD), a form of apoptosis that affects proliferating and newly differentiated cells in vertebrates, and most dramatically the cells of the central nervous system (CNS). Little is known about the molecular pathways controlling apoptosis at these early developmental stages, as the roles of EPCD during patterning of the developing nervous system. We describe a new function, in Xenopus neurodevelopment, for a highly conserved homeodomain protein Barhl2. Barhl2 promotes apoptosis in the Xenopus neuroectoderm and mesoderm, acting as a transcriptional repressor, through a mechanism that cannot be attributed to an unspecific cellular stress response. We show that the pro-apoptotic activity of Barhl2 is essential during normal neural plate formation as it limits the number of chordin- and Xshh-expressing cells in the prospective notochord and floorplate, which act as organizing centers. Our findings show that Barhl2 is part of a pathway regulating EPCD. They also provide evidence that apoptosis plays an important role in regulating the size of organizing centers.

Key words: Barhl, Apoptosis, Shh, Organizer, Diencephalon

Introduction
The neuroectoderm emerges from the dorsal ectoderm during gastrulation. Experiments performed mainly in amphibian embryos have established crucial roles for several secreted signaling proteins, including bone morphogenic proteins (BMPs), fibroblast growth factors (FGFs), Hedgehogs (HHs) and Wnt proteins, in neural induction and the establishment of the future dorsoventral (DV) and anteroposterior (AP) axes of the developing nervous system (reviewed by Gamse and Sive, 2000; Kiecker and Niehrs, 2001; Schier and Sive, 2001; Stern, 2002). Small groups of specialized cells serve as local sources of secreted factors and thereby act as ‘organizing centers’, patterning the neural tube by establishing the regional identity of adjacent domains.

Early in Xenopus development, the major source of secreted signaling proteins is the Spemann’s organizer that give rise to the notochord underlying the neural plate and tube (reviewed by Joubin and Stern, 2001; Niehrs, 2004). The Spemann’s organizer secretes the BMPs inhibitors Chordin, Noggin and Follistatin, which are involved in the decision of ectodermal cells to become epidermal or neural cells (Munoz-Sanjuan and Brivanlou, 2002; Stern, 2002; Wilson and Edlund, 2001), and Sonic Hedgehog (Shh), which is initially produced by the notochord and then later by the overlying neural floor plate. Both BMPs and Shh act as concentration-dependent morphogen, and specify the cell types produced in the neural tube (Barth et al., 1999; Dale and Jones, 1999; Lee et al., 2000). Shh also acts as a survival factor and as a mitogen, by driving the extensive expansion of the early brain (Brito et al., 2002; Dahmane et al., 2001; Lee et al., 2000; Thibert et al., 2003; Wallace, 1999). In these ways, BMPs and Shh help to regionalize the DV axis of the developing nervous system (Jacob et al., 2003; Ruiz i Altava et al., 2003).

The position, size and shape of an organizing center has a major influence on the position, size and shape of the compartment that it patterns (Agarwala et al., 2001). It is less clear, however, how the size of organizing centers themselves is determined. Apoptosis plays a major role in controlling cell number during development (Jacobson et al., 1997). In Xenopus embryos, apoptosis occurs in a reproducible pattern in the neuroectoderm and the mesoderm, starting at the onset of gastrulation (Hensey and Gautier, 1998; Yeo and Gautier, 2003). BMP and Shh, have both been reported to have apoptosis-inducing and apoptosis-inhibiting properties, raising the possibility that morphogens may regulate apoptosis to help control the size of the organizing centers (Charrier et al., 2001; Golden et al., 1999; Litingtung and Chiang, 2000; Mabie et al., 1999).

Among the important target genes regulated by morphogens are homeobox genes. These genes encode gene regulatory proteins and specify regional identity by regulating ‘effector’ genes, which influence cell proliferation, adhesion, shape, migration, differentiation and survival (Puelles and Rubenstein, 2003; Rubenstein et al., 1998). Two Drosophila
homeobox genes deformed (Dfd) and abdominal-B (Abd-B), contribute to the maintenance of intersegmental boundaries through the regional activation of apoptosis (Lohmann et al., 2002). However, it is not known if Hox proteins directly regulate apoptosis during vertebrate development.

This study describes a novel function for Barhl2 gene, a vertebrate homologue of Drosophila barH genes. In fly, the barH genes are expressed in the developing nervous system, act as pre-patterning genes and are involved in preventing ectopic retinal neurogenesis (Higashijima et al., 1992; Kojima et al., 2000; Lim and Choi, 2003; Sato et al., 1999). Vertebrate homologs of the barH genes have been isolated and their function examined during retina and ear development (Li et al., 2002; Mo et al., 2004; Poggi et al., 2004). In the vertebrate eye, Barhl2 function appears highly variable depending on the species. In the mouse retina it helps specify glycnergic amacrine cells from retinal progenitors (Mo et al., 2004); and in the Xenopus retina, it promotes ganglion cell fate, downstream of the retinal genes Xath3 and Xath5 (Poggi et al., 2004). We have isolated the Xenopus and mouse Barhl2 genes, and studied their functions in Xenopus neurodevelopment. Barhl2 loss-of-function and gain-of-function mutations produce defects in the establishment of the neural plate. Our data suggest that Barhl2 normally regulates a cell survival pathway in the neural plate and dorsal mesoderm. Barhl2 overexpression induces apoptosis in these tissues by a mechanism dependent on transcription, which differs from an unspecified cellular stress response. Specific inhibition of Barhl2 expression by morpholinos leads to a decrease in apoptosis and an increase in the number of chordin- and Xshh-expressing cells. Finally Barhl2-defective embryos and embryos overexpressing the anti-apoptotic human BCL2 gene have a similar phenotype. We propose that Barhl2-dependent apoptosis is necessary for correct formation of the axial organizing center of the Xenopus neural plate.

Materials and methods

Isolation of Barhl genes and construction of plasmids

A Xenopus stage 30 head and an E8.5 mouse embryo cDNA libraries were screened by PCR using degenerate primers (TAFSDHQ and KWKQR). Fragments containing the Bar-homebox encoding sequence were used to screen for cDNA clones. Mouse Barhl2 and Xbarhl2 coding sequences (from ATG to TGA) were subcloned in the pCS2 vector (Turner and Weintraub, 1994). A construct encoding the mouse protein, without the first 134 amino acids, was generated by PCR and subcloned into pCS2 to produce Barhl2ΔFIL. Barhl2ΔFIL was fused at its C-terminal end with amino acids 1 to 298 of the Drosophila Engrailed protein (Jaynes and O’Farrell, 1991), and subcloned into pCS2. Xbarhl2-coding sequences, without the stop codon, were amplified by PCR and subcloned in pCS2-Myc (Turner and Weintraub, 1994).

Embryos and injection

Xenopus embryos were obtained by in vitro fertilization, injected with synthetic RNA or morpholino and staged according to Nieuwkoop and Faber (Nieuwkoop and Faber, 1967). Capped RNAs were prepared from pCS2-derivatives (Ambion) and Bc12-β RNA from pRC/CMV (Invitrogen). Antisense oligonucleotides coupled to the fluorescein were made by Gene Tools (Fig. 2C) and diluted into RNase-free water. For Xbarhl2ASI, we used 10 ng for all experiments. For Xbarhl2ASI, 50 ng was generally used.

Reverse-transcription PCR

RNA from embryos was extracted using the Qiagen RNeasy Kit. RT-PCR analysis was carried out using the Superscript one-step Kit (Invitrogen). Sterile water was used as a control. Specific primers were used: Xbarhl2, 5′GCTCAACCCACGCGAGAGCCTTGA-CCG3′ and 5′TGTAGTGGGTTGGGCGCAGGGGAATC3′; XEF-1α, 5′CAAGATGGCTGGATGATGC-3′ and 5′ACTGCGTTGATACCTCTAG3′; Chordin, 5′GTGGAATATGCGTGATTGCTCTGC3′ and 5′AGCCGACATCATCAAGACTCAGATA-AGG3′. Ncam 5′GTGTTAGCTAACCAAGCAGGACCCTAGT3′ and 5′GCAGTGGAGAAACCAGCTCAGAACG3′.

Whole-mount in situ hybridization

In situ hybridization was performed using digoxigenin (DIG)-labeled probes, as described previously (Harland, 1991), with modifications (Turner and Weintraub, 1994). Antisense probes were generated for Xbarhl2, Xshh, Xsox3, XK81, Xvent2, chordin, gli1 and gli3 according to the manufacturer’s instructions (Roche). Specimens were sectioned and embedded in agarose or Tissu-Tek. Frozen sections (10 µm) were cut on a Leica 2800 Frigocut-E cryostat at −24°C, thicker sections (50 µm) were cut on a Leica VT1000E vibratome.

Immunostaining

Immunostaining was performed using either a mouse monoclonal anti-Myc Cy3-conjugated antibody (Sigma) or a rabbit anti-phospho-histone H3 antibodies (Euromedex), as described previously (Saka and Smith, 2001). The anti-phospho-histone H3 antibody was detected using anti-rabbit (Ig) antibodies conjugated to alkaline phosphatase (Roche), followed by a staining using BCIP (5-bromo-4-chloro-3-indoyl-phosphate) as a substrate.

Protein isolation and western analysis

Total protein from embryos was extracted by shearing through a 22G needle in lysis buffer (Triton X-100 1%, 5 mM EDTA, 5 mM EGTA, 50 mM Tris, pH 8.0, 0.3 M NaCl and proteases inhibitors from Roche). Samples (3 and 10 µg) were processed for western analysis, using antibodies against Myc (Roche, #1667149) or activated Caspase 3 (Cell Signalling Technology, #9661).

Hydroxyurea (HU) treatment

Embryos were allowed to develop to stage 9.5 and grown until fixation in a solution of 30 mM hydroxyurea (Sigma) in 0.1×MMR, as described previously (Harris and Hartenstein, 1991; Saka and Smith, 2001).

TUNEL staining

Whole-mount TUNEL staining was performed as previously described (Hensey and Gautier, 1998; Yeo and Gautier, 2003). Early apoptosis is independent of cell proliferation (Yeo and Gautier, 2003); however, blocking cell division by incubation in HU appears to increase the number of embryos exhibiting a specific spatiotemporal pattern of cell death (our data) (Yeo and Gautier, 2003). The TUNEL analysis shown in Fig. 4A was performed on wild-type and Xbarhl2ASI-injected embryos grown in HU from stage 9.5 onwards.

Cell death detection by ELISA

Cytoplasmic nucleosomal DNA was detected using a cell death detection ELISA kit (Roche). Five embryos were isolated for each time point and lysed in 50 µl incubation buffer. Lysates (10 µl) were incubated in 190 µl incubation buffer for 30 minutes on ice. The extracts were centrifuged for 10 minutes at 4°C. An aliquot (160 µl) of the supernatant was carefully removed, and ELISA was performed according to the manufacturer’s instructions.

Microdissection and transplantation

Neurula stage embryos were devitellinized and embedded in a clay-covered dish in 0.5×MMR. The tip of a 25G needle was used to cut
out different parts of the embryo at the indicated stage. The explant was peeled off, separated from the embryo and either RNA was extracted or the explant was inserted into a longitudinal incision made along the presumptive neural plate midline of the host embryo, down to the blastocoel and held in place for 30 minutes using a curved glass bridge.

X-gal staining
Embryos were fixed in MEMFA for 30 minutes, washed in phosphate buffer and transferred into X-gal staining solution (Coffman et al., 1990).

Results
Barh2 cDNAs are highly conserved between metazoan species and XBarhl2 is expressed from stage 10.5 onwards in Xenopus embryo
We isolated two complete cDNAs that contained a single open reading frame encoding proteins of, respectively, 327 (XBarhl2) and 384 amino acids (mouse Barhl2). Phylogenetic analysis shows that Barhl2 proteins are more closely related to Drosophila BarH, nematode CEH-30 and CEH-31, and vertebrate Barhl1 proteins than to mammalian Barx proteins (Fig. 1A).

We examined the expression pattern of Xbarhl2 during early Xenopus embryogenesis. By RT-PCR analysis we detected Xbarhl2 transcripts from stage 10.5 onwards in the dorsal part of the embryo (Fig. 1B, parts a,b). Whole-mount in situ analysis at stage 14 confirmed the described presence of Xbarhl2 transcripts in a region fated to become the dorsal diencephalon (Fig. 1C) (Patterson et al., 2000). It also suggested its presence along the midline (Fig. 1D), confirmed by RT-PCR analysis on the posterior neural plate and posterior dorsal mesoderm, as on the midline of stage 14 embryos (Fig. 1E, parts a,b). We focused our study on deciphering the role of Xbarhl2 in these tissues between stage 10.5 and stage 18.

Manipulation of the level of Xbarhl2 expression interferes with neural plate formation
The N-terminal region of the Barhl2 protein contains two conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998).

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The N-terminal region of the Barhl2 protein contains two conserved domains, FIL1 and FIL2, that are composed mainly of phenylalanine, isoleucine and leucine (Saito et al., 1998). A sequence comparison between the FIL domains and the Eh1 repression domain present in the Engrailed protein established that these domains are similar (Fig. 2A). Eh1 domains are present in Engrailed, Goosecoid, Nkx1 and Msh classes of homeoproteins, and have been shown to repress transcription in vivo and in vitro (Smith and Jaynes, 1996). We removed the eh1 domains from the mouse Barhl2 cDNA, generating Barhl2ΔFIL (Fig. 2B). We fused the repressor domain of the Drosophila Engrailed protein to Barhl2ΔFIL (Barhl2ΔFILenR, Fig. 2B). We used two different Xbarhl2 antisense morpholinos (Xbarhl2ASI and Xbarhl2ASII) to inhibit Xbarhl2 activity, together with a control morpholino (Xbarhl2ASIII). These oligonucleotides were designed in a region overlapping the translational initiation site, so that they do not bind to mouse Barhl2 or Barhl1 mRNA (Fig. 2C). We used Xsox3 as an early marker of neural induction (Penzel et al., 1997) and epidermal keratin 81 (XK81) (Jamrich et al., 1987) as an epidermal marker. For all constructs we injected the specified RNA together with GFP RNA used as a tracer.

We injected Xbarhl2 or mouse Barhl2 RNA or antisense morpholinos into one dorsal blastomere of four-cell embryos. Results were similar with mouse Barhl2 and Xbarhl2, and we
mostly used mouse Barhl2 for further experiments. At stage 14, we observed a dose-dependent decrease in the width of the Xsox3 expression domain on embryos injected with mouse Barhl2 (Fig. 2D, part b). Injection of over 50 pg of mouse Barhl2 caused the Xsox3 expression domain to partially disappear (Fig. 2D, part c). The effects on XK81 expression were complementary to those seen with Xsox3 (Fig. 2D, part d). Injection of Barhl2AFIL produced embryos similar to control siblings (Fig. 2D, part e), when injection of Barhl2AFIL-enR produced a phenotype similar to that produced by injections of mouse Barhl2 (Fig. 2D, part f), indicating that Barhl2 functions as a repressor at these stages. In contrast to the effect produced by mouse Barhl2, the neural plate of Xbarhl2ASI- or Xbarhl2ASII-treated embryos was
Development

28, (P > 10 pg) was reversed by co-injection of human Barhl2 (500 pg) reduced apoptosis (Fig. 3).

larger on the injected side than on the control side (Fig. 2D, parts g,h). This effect was observed along the entire AP axis at all stages analyzed. The expansion of the neural plate was dose dependent, as shown by injection of 20 ng (no effect, Fig. 2D, part i), 50 ng (a 30% increase in size, Fig. 2D, part j) and 100 ng (50%, Fig. 2D, part k) of Xbarhl2ASII. Conversely, the extent of the epidermal territory was decreased in Xbarhl2ASI or Xbarhl2ASII-treated embryos (Fig. 2D, part l). We did not detect any changes in expression pattern of either Xsox3 or XK81 upon injection of Xbarhl2ASIII (data not shown, n=60).

To establish the specificity of the morpholino effect, we tested the ability of Xbarhl2ASI to inhibit translation of the Xbarhl2 mRNA. Myc-tagged Xbarhl2 (Xbarhl2-myc, Fig. 2B) was co-injected with Xbarhl2ASI or Xbarhl2ASII as a control. Immunostaining of the embryos revealed that Xbarhl2ASI inhibited the translation of Xbarhl2-myc mRNA (Fig. 2E, part b), while Xbarhl2ASIII did not (Fig. 2E, part c). A specific dose-dependent inhibition of Xbarhl2-myc messenger translation by the Xbarhl2ASI in embryos was confirmed by western blot analysis on extracts from embryos injected with increasing doses of Xbarhl2ASII (Fig. 2F).

We tested Xbarhl2ASI as a specific inhibitor of endogenous XBarhl2 activity by co-injecting 10 pg mouse Barhl2 (Fig. 2G, part a) with 50 ng (Fig. 2G, part b) of Xbarhl2ASI. When Xsox3 was used to assess neural plate development, we observed that Xbarhl2ASI rescued the phenotype induced by mouse Barhl2 overexpression in 60% of the embryos (Fig. 2G, part c). These data provide strong evidence that the Xbarhl2ASI were acting by specifically inhibiting endogenous XBarhl2 activity in our injection experiments. As the effects of Xbarhl2ASI and Xbarhl2ASII were similar, we refer to it as Xbarhl2AS.

Thus, increasing Barhl2 activity reduces the neural plate territory, whereas reducing Barhl2 activity increases it. The effect of Barhl2 depends on its two Eh1 domains, and is likely to involve Barhl2-mediated transcriptional repression.

Barhl2 induces apoptosis in neuroectodermal cells of the neural plate

In principle, Barhl2 overexpression may decrease neural plate formation by inhibiting neural induction, inhibiting neuroectodermal cell proliferation or increasing neuroectodermal cell death or by some combination of these.

The neuroectodermal expression pattern of Barhl2 argues against a role for Barhl2 as a direct inhibitor of neural induction. We assessed whether Barhl2 regulates neuroectodermal cell proliferation. Embryos injected with Xbarhl2AS were immunostained using an antibody against phosphorylated histone H3, which specifically recognizes mitotic chromosomes (Saka and Smith, 2001). We did not observe a significant change in the number of mitotic cells on the Xbarhl2AS-injected side compared with the control side (Fig. 3A, part a). When similarly injected embryos were allowed to develop from the gastrula stage onwards in hydroxyurea (HU), which effectively blocks DNA replication and cell division (Newport and Dasso, 1989), Xbarhl2AS-injected side exhibited a typical increase in the Xsox3 expression domain compared with the control size (Fig. 3A, part b). These observations argue against a role for Barhl2 as a modulator of cell proliferation at these early stages.

Therefore we tested whether the overexpression of Barhl2 decreased neural plate formation by increasing apoptosis in neuroectodermal cells. Apoptosis can be inhibited by
overexpression of the human BCL2 gene, which encodes the apoptosis inhibitor BCL2 (Yeo and Gautier, 2003). We injected BCL2 and followed the establishment of neural and epidermal territories using Xsox3 and XK81. As we had observed with injections of Xbarhl2AS, we saw an increase in the size of the neural plate and a decrease in the size of epidermis on the BCL2 injected side along the entire AP axis of the embryos (Fig. 3A, part c, data not shown) (Yeo and Gautier, 2003), consistent with the possibility that Xbarhl2AS increases neural plate development by decreasing apoptosis there.

We injected different quantities of mouse Barhl2, Xbarhl2 or, as a control, RNA encoding GFP or XPax6, and followed apoptosis by TUNEL analysis in Xenopus neuroectoderm (Fig. 3B,C). We observed a reproducible increase of 2.6 in the number of TUNEL-positive nuclei on the injected side of stage 15 embryos treated with mouse Barhl2 or Xbarhl2 compared with the control side (Fig. 3B,C). No difference was detected when RNA encoding GFP or XPax6 was injected as a control (data not shown), or with ventral injections of mouse Barhl2 (n=53, data not shown). Interestingly, we observed a specific pattern of apoptotic nuclei in embryos injected with the lowest dose of mouse Barhl2: over 50% of the TUNEL-positive cells were located within a narrow stripe bordering the midline of the posterior neural plate (Fig. 3B, part c), suggesting that these cells were most sensitive to the apoptosis-promoting effect of Barhl2. We did not detect any increase in the frequency of apoptotic cells in embryos dorsally injected with Barhl2ÁFIL (Fig. 3C), showing that Barhl2 transcriptional activity is strictly necessary for the pro-apoptotic effect of Barhl2. Finally we co-injected mouse Barhl2 and BCL2, and studied these embryos by TUNEL analysis. As shown in Fig. 3C, there was no significant difference between the number of apoptotic nuclei in embryos injected with both mouse Barhl2 and BCL2, when compared with the controls, confirming that Barhl2 overexpression promotes apoptosis.

To see if the pro-apoptotic effect of Barhl2 correlated with the observed phenotype of Barhl2-overexpressing embryos, we studied the expression of Xsox3 in embryos injected with mouse Barhl2, BCL2 or mouse Barhl2 together with BCL2 at the same doses as those used for TUNEL analysis. We observed that hbc12 expression rescued the Barhl2-induced phenotype in over 60% of the embryos at this stage (Fig. 3D).

Thus, Barhl2 can induce apoptosis in dorsal cells through its transcriptional regulatory function. Cells localized along the midline appear to be most sensitive to the pro-apoptotic activity of Barhl2, and the reduction in neural plate territory caused by Barhl2 overexpression can be rescued by overexpression of the apoptotic inhibitor Bcl2.

**Inhibition of endogenous Barhl2 activity partially inhibits endogenous apoptosis**

To assess the normal function of Barhl2 pro-apoptotic activity we first used the TUNEL assay to follow endogenous apoptosis from stage 12 to stage 18. At stage 12, apoptotic nuclei were mainly detected around the blastopore and along the axial midline as it forms (Fig. 4A, part a) (Hensey and Gautier, 1998; Yeo and Gautier, 2003). At stage 15, the apoptotic cells were detected in two stripes along the midline (Fig. 4A, part b). At stage 18, we observed apoptotic cells in the neural groove and in the anterior part of the neural plate (Fig. 4A, parts c,d). As described by others, we observed an asymmetric pattern of
apoptotic cells between the right and left sides of the embryo. Double in situ hybridization analysis with Xshh (Fig. 4A, part e), which is expressed in midline structures and the prechordal plate (Ekker et al., 1995), and Xpax6 (Fig. 4A, part f), which is expressed in the forebrain (Hirsch and Harris, 1997), suggested that this anterior neural plate area containing apoptotic cells could correspond to the domain of Xbarhl2 expression. In agreement with this hypothesis, we observed a dramatic expansion of the Xpax6 expression domain, most strikingly in the dorsal diencephalic area where its expression overlaps with that of Xbarhl2, in embryos injected with Xbarhl2AS (Fig. 4A, part g). These data are consistent with the possibility that Barhl2 can promote apoptosis at these early developmental stages.

We examined whether inhibition of Barhl2 activity could change the level of endogenous apoptosis. Using the TUNEL assay, we compared apoptosis in stage 15 wild-type embryos and embryos injected with Xbarhl2AS. When Barhl2 activity was inhibited in this way, we observed a reproducible decrease in the number of apoptotic cells per embryo (Fig. 4B), strengthening the hypothesis that Barhl2 normally acts on a cell survival pathway.

The zygotic apoptotic program in the Xenopus embryo comes into play at the onset of gastrulation, when Xbarhl2 transcripts are first detected. We assessed whether Barhl2 pro-apoptotic activity was dependent on the endogenous apoptotic program. Embryos were injected with Xbarhl2, GFP or Xbarhl2, together with Xbarhl2AS. Apoptosis was measured in extracts from stage 8 to stage 13 embryo using an ELISA assay for cytoplasmic histone-associated mono- and oligonucleosomes that are specifically released during the apoptotic process (Veenstra et al., 1998). As shown in Fig. 4C, we observed, from stage 10.5 onwards, a steady increase in the apoptotic enrichment factor (EF) that is the number of dying/dead cells in a specimen over the number of dying/dead cells in the control GFP-injected embryos (Fig. 4C, EF=9 at stage 13). Co-injection of Xbarhl2AS with Xbarhl2 completely inhibited apoptosis. The measured EF in embryos injected with Xbarhl2 and Xbarhl2AS was less then one (Fig. 4C, EF=0.8 at stage 13), in agreement with our observation that Xbarhl2AS can partly inhibit endogenous apoptosis.

Cellular stress, including that caused by the overexpression of transcription factors, can trigger apoptosis in an unspecific way (Kumar and Cakouros, 2004). As a control, we measured the apoptotic EF in embryos injected with Xpax6. We observed only a slight increase in the apoptotic EF in the Xpax6-injected embryos (Fig. 4C, EF=1.2 at stage 13). We conclude that the apoptotic response of cells upon Barhl2 overexpression is not due to an unspecific stress response.

We followed the presence of activated Caspase 3, the
Neurulating Cell death occurs along the forming axial structures in expressing cells (Adams, 2003). To assess which cells undergo an increase in the number of both chordin- and Xshh-expressing cells, we followed the development of the prospective notochord and the floorplate territories in embryos in which Barhl2 expression was experimentally modified.

We used chordin as a marker of axial mesoderm territory (Sasai et al., 1994). The pattern of chordin expression was normal at stage 10 in both mouse Barhl2- and Xbarhl2AS-injected embryos, showing that the Spemann’s organizer developed normally (Fig. 5A). At stage 15, we observed the disappearance of chordin-expressing cells in mouse Barhl2-injected embryos (Fig. 5B, part b). Conversely, in Xbarhl2AS-injected embryos, the area of expression of chordin was broader (Fig. 5B, part c). To test if the increase in chordin-expressing area might be due to a decrease in the pro-apoptotic effect of Barhl2, we injected human BCL2 instead of the morpholino. Similar to what we observed with Xbarhl2AS, we did not detect any defect in chordin expression at stage 10 (Fig. 5A, part d), but an increase in the area of chordin expression at stage 15 (Fig. 5B, part d).

A series of anterior-to-posterior transverse sections from stage 15 stage embryos injected with Xbarhl2AS confirmed an increase in the size of the chordin-expressing area that was greater at the anterior end of the embryos (Fig. 5C, parts a-g). Observations of serial frozen sections of control and Xbarhl2AS-injected embryos indicated that this increase is not due to a change in the size of chordin-expressing cells (Fig. 5C, parts h,i). We confirmed these results with transverse sections of similarly treated stage 18 embryos (Fig. 5D), and found that the axial territory failed to develop in Barhl2-overexpressing embryos (Fig. 5D, part b). Conversely, there was a surplus of chordin-expressing cells in embryos in which Barhl2 activity was inhibited (Fig. 5D, part c).

Chordin acts as a BMP inhibitor. An increase in the number of chordin-expressing cells should generate an overall decrease in BMP signaling. We followed changes in the expression pattern of Xvent2 that is under the control of BMP signaling (Onichtchouk et al., 1996). As shown in Fig. 5E, in stage 12 mouse Barhl2-injected embryos Xvent2 area of expression was shifted dorsally towards the midline compared with control embryos (Fig. 5E, part b). Whereas in stage 12 Xbarhl2AS-injected embryos, the Xvent2 expression area was shifted ventrally (Fig. 5E, part c). We concluded that Barhl2 indirectly modulates BMP signaling.

We studied the expression of Shh that is expressed in the prospective notochord and in the floorplate (Fig. 5F). One side injection of mouse Barhl2 caused a decrease of about 50% in the size of the floorplate (Fig. 5F, parts b,f), while a similar injection of Xbarhl2AS caused an increase in this territory (Fig. 5F, parts c,g). We confirmed the increase in the number of Xshh-expressing cells in the mesoderm and the neuroectoderm by examination of sections (Fig. 5F, part i). The Gli transcription factors mediate the effects of the Shh signaling. We followed the expression of gli1, which is a direct target of Shh signaling, and gli3, which is repressed by Shh. Embryos injected with Xbarhl2AS showed increased Shh activity in the posterior neural plate, as judged by an increase in the area of gli1 expression on the injected side (Fig. 5F, part j) and a decrease in gli3 expression (Fig. 5F, part k).

In embryos where apoptosis was inhibited by injecting BCL2, we observed a similar enlargement of the Xshh territory of expression (Fig. 5F, parts d,h), and an increase in Shh activity in the posterior neural plate, indicated by an increase in gli1 expression (Fig. 5F, part l).

We conclude that endogenous Barhl2 normally plays an important role in limiting the number of cells expressing chordin and cells expressing Xshh and indirectly in regulating BMP and Shh signaling.

Discussion

The Barhl2 DNA binding homeodomain protein is normally part of a pathway regulating apoptosis in early Xenopus neurodevelopment

EPCD affects proliferating and early differentiating cells and mainly occurs during neuroulation, neural crest formation and eye induction and formation (reviewed by de la Rosa and de Pablo, 2000; Kuan et al., 2000; Yeo and Gautier, 2004). Here, we provide evidence that the highly conserved Barhl2 gene is part of a pathway that regulates EPCD. Overexpression of Barhl2 through injection of RNA into the dorsal part of the embryo induces an increase in apoptosis that cannot be attributed to nonspecific cellular stress response. Inhibition of Barhl2 activity diminishes endogenous apoptosis and
Fig. 6. A neurula stage graft of notochord and floorplate rescues Barhl2 gain-of-function phenotype. (A) Notochord and floorplate explants from stage 12-14 β-galactosidase (100 pg)-injected donor embryos were grafted in the presumptive neural plate midline of wild-type or mouse Barhl2 (25 pg)-injected embryos. (B-D) The embryos were analyzed at stage 40. β-Galactosidase activity is revealed in blue. (B) Control embryo (top) and control embryo grafted with wild-type explants (bottom). (C) Mouse Barhl2-injected embryos (n=40). (D) Mouse Barhl2-injected embryos grafted with explants from β-galactosidase-injected wild-type donors (n=41).

Barhl2-regulated apoptosis plays a role in limiting the size of the forming axial neural organizer

As morphogenetic gradients of both BMP and Shh are essential for outgrowth and patterning of the neural plate, the number of cells producing these morphogens must be tightly regulated. Barhl2-regulated apoptosis appears as part of the system that controls both the size and correct establishment of the axial organizer during the rapid growth of the gastrulating embryo. A similar role for apoptosis has been described in vertebrate limb development. There a Shh-producing polarizing region acts as an organizing center and apoptosis regulates the number of Shh-expressing cells (Sanz-Ezquerro and Tickle, 2000). The location, size and shape of an organizing center determines the size, shape and orientation of the target tissue (Agarwala et al., 2001). Xbarhl2AS-injected embryos phenotype is similar to the phenotype seen in BMP4 loss-of-function (Dale and Jones, 1999; Gamse and Sive, 2000) and in Bcl2 gain-of-function (Yeo and Gautier, 2003) experiments. Conversely, Barhl2 overexpression causes a ventralization phenotype similar to that seen in BMP4 gain-of-function experiments (Dale and Jones, 1999; Gamse and Sive, 2000). A neurula stage graft of notochord and floor-plate cells into an mouse Barhl2 overexpressing embryo partially rescues the formation of head structures, strongly arguing that the Barhl2 gain-of-function and loss-of-function phenotypes are mainly caused by interference with correct signaling from the forming neural organizing centers (see Fig. 7).

During gastrulation and early neurulation, polarized cell movements from the mesoderm are key regulators in elongating the AP axis of the Xenopus embryo (Keller, 2002; Wallingford et al., 2002). Interference with these cell movements can generate defects similar to those we observe by inhibiting Barhl2 activity (Leise and Mueller, 2004), raising the possibility that interference with these cell movements contributes to the Barhl2 loss-of-function phenotype. However, such interference cannot produce an increase in the number of chordin- and Shh-expressing cells, and alteration in apoptosis may secondarily play a part in the convergent extension movements.

Barhl2 could act directly on a survival program or indirectly on a survival pathway

During development, higher animals cells require signals from other cells to avoid apoptosis (reviewed by Raff, 1996). Our data suggest that Barhl2 could act either directly though transcriptional regulation of a cell death program, or indirectly...
through transcriptional modulation of the survival pathways controlling EPCD.

Studies in C. elegans and Drosophila have demonstrated the importance of transcriptional control of developmental cell death (Kumar and Cakouros, 2004). Hox-dependent regulation of apoptosis, for example, appears to be a conserved mechanism in vertebrate development. Bix3, a Xenopus homeobox gene, regulates apoptosis during development, but this activity does not depend on its ability to regulate transcription (Trindade et al., 2003). Hoxa13 may be involved in eliminating cells located between the forming digits in mice (Stadler et al., 2001), and a direct role for Engrailed genes in the regulation of apoptosis has been suggested in mesencephalic dopaminergic neurons (Alberi et al., 2004).

Targeted deletion of Barhl1, the closest homologue of Barhl2 in vertebrates, caused degeneration of mouse cochlear hair cells. Analysis of this phenotype showed that Barhl1 plays an essential role in the maintenance of cochlear hair cells whereas it had little role in specification and differentiation of these cells (Li et al., 2002). The BH3-only protein, Egl-1, a pro-apoptotic member of the Bcl2 family is transcriptionally controlled in C. elegans (Metzstein and Horvitz, 1999). Therefore, Barhl2 could directly or indirectly regulate the transcription of a gene that encodes a BH3-only protein.

In the neural plate, Shh regulates apoptosis in various ways: it acts as a cell survival signal (Charriér et al., 2001; Chiang et al., 1996; Litingtung and Chiang, 2000), and has a apoptotic promoting activity in chick ventral neuronal precursors and floor-plate cells (Oppenheim et al., 1999). Similarly, several BMPs have been shown to promote apoptosis on developing neural cells (Golden et al., 1999; Mabie et al., 1999). Therefore, Barhl2 could modulate directly or indirectly the cellular production of these apoptosis-modulating signals and/or their cellular responses, and indirectly control cell survival of the chordin- and shh-expressing cells. It is foreseeable that determining if this new function is conserved and/or for the Barhl1, a gene belonging to a new subfamily of mammalian homeobox genes, is expressed in migrating neurons of the CNS. Hum. Mol. Genet. 9, 1443-1452.


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