Prep1.1 has essential genetic functions in hindbrain development and cranial neural crest cell differentiation

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Summary

In this study we analysed the function of the Meinox gene prep1.1 during zebrafish development. Meinox proteins form heterotrimeric complexes with Hox and Pbx members, increasing the DNA binding specificity of Hox proteins in vitro and in vivo. However, a role for a specific Meinox protein in the regulation of Hox activity in vivo has not been demonstrated. In situ hybridization showed that prep1.1 is expressed maternally and ubiquitously up to 24 hours post-fertilization (hpf), and restricted to the head from 48 hpf onwards. Morpholino-induced prep1.1 loss-of-function caused significant apoptosis in the CNS. Hindbrain segmentation and patterning was affected severely, as revealed by either loss or defective expression of several hindbrain markers (foxb1.2/mariposa, krox20, pax2.1 and pax6.1), including anteriorly expressed Hox genes (hoxb1a, hoxa2 and hoxb2), the impaired migration of facial nerve motor neurons, and the lack of reticulospinal neurons (RSNs) except Mauthner cells. Furthermore, the heads of prep1.1 morphants lacked all pharyngeal cartilages. This was not caused by the absence of neural crest cells or their impaired migration into the pharyngeal arches, as shown by expression of dlx2 and snail1, but by the inability of these cells to differentiate into chondroblasts. Our results indicate that prep1.1 has a unique genetic function in craniofacial chondrogenesis and, acting as a member of Meinox-Pbc-Hox trimers, it plays an essential role in hindbrain development.

Key words: Vertebrate, Zebrafish, Hox, Pbx, Meis, Prep, Rhombomere, Segmentation, Neural Crest, Pharyngeal arch, Morpholino

Introduction

Segmentation is an essential, evolutionarily conserved, step in embryonic development that allows the generation and determination of different parts of the body. The Hox genes are key players in segmental determination through their combined expression in individual segments (Krumlauf, 1994; Moens and Prince, 2002). Spatial-specific and temporal-specific gene expression is regulated by mechanisms generated by combinatorial interactions of individual transcription factors. The segmentation of the vertebrate hindbrain, for example, relies on the rhombomere-specific expression of a subset of Hox genes. Hox gene products, in turn, gain high specificity for DNA target sequences by interacting with Pbc (Pbx in vertebrates) members of the TALE family of homeodomain proteins (Burglin, 1997; Kamps et al., 1990; Nourse et al., 1990). Four Pbx genes have been identified in mammals and five in zebrafish (Mann and Chan, 1996; Moens and Prince, 2002; Waskiewicz et al., 2002).

A further subfamily of homeodomain transcription factors, which are also members of the TALE family, is involved in the Hox regulation machinery. These are the Meinox proteins (Burglin, 1997). In vertebrates, the Meinox subfamily include Meis and Prep proteins, whereas a single member occurs in Drosophila (Hth) and Caenorhabditis (UNC-62) (Van Auken et al., 2002). The interaction between Meinox and Pbc proteins leads to the nuclear import of the former, which lack a nuclear localization signal, and prevents the nuclear export of the latter (Abu-Shaar et al., 1999; Berthelsen et al., 1999). Because Pbc uses different surfaces to interact with Hox and Meinox proteins, Pbc-Hox and Meinox-Pbc molecular interactions direct the formation of Meinox-Pbc-Hox trimers. Such trimeric complexes recognize a split, 16-bp sequence on the regulatory regions of target genes (Ferretti et al., 2000; Jacobs et al., 1999; Ryoo et al., 1999). Moreover, Meinox proteins are important in stabilizing Pbc members. For example, Hth is required to maintain the level of the Pbc protein Exd in D. melanogaster (Kurant et al., 2001) and overexpression of dominant negative Meis derivatives reduce the level of Pbx proteins in higher vertebrates and zebrafish (Capdevila and Belmonte, 1999; Choe et al., 2002; Mercader et al., 1999; Waskiewicz et al., 2001), whereas overexpression of Prep1 in mammalian cells increases the level of Pbx proteins (Longobardi and Blasi, 2003).

A total of 14 hox paralogs (11 in the mouse), 2 pbx, 3 meis and 2 prep genes are expressed in zebrafish hindbrain (Moens and Prince, 2002). The inactivation of pbx4/azarus (lzr) in...
zebrafish leads to a phenotype that is characterized by embryonic death at 6-7 days post-fertilization (dpf) with major developmental defects, in particular in hindbrain segmentation and cranial neural crest determination (Pöpperl et al., 2000). This phenotype closely resembles that of the mouse Pbx1-null mutant (Selleri et al., 2001) because, in both cases, major developmental defects are observed in the cartilages arising from the second branchial arch. In zebrafish, elimination of hindbrain-expressed Pbx proteins (Pbx2 and Pbx4) uncovers a hindbrain ground state in which rhombomeres 2 to 6 (r2-r6) acquire an r1 identity (Waskiewicz et al., 2002). In Xenopus, zebrafish and chicken, the role of Meis proteins has been investigated by overexpression and dominant-negative mutant approaches (Dibner et al., 2001; Mercader et al., 1999; Salzberg et al., 1999; Vlachakis et al., 2001; Waskiewicz et al., 2001). However, the specific role of individual Meis or Prep proteins is unknown.

Prep1 was identified as a protein that copurifies with several Pbx proteins in human cells, and Prep2 was identified from a search of the human genome sequence and cloned subsequently (Berthelsen et al., 1998a; Berthelsen et al., 1998b; Fognani et al., 2002; Haller et al., 2002). Together, they form a subgroup of Meinox proteins that share ~80% overall amino acid sequence identity. By contrast, the Meis and Prep proteins share high amino acid sequence conservation only in specific domains (Fognani et al., 2002). An additional difference between Prep and Meis might lie in HoX proteins binding activity. Vertebrate Meis associates in vitro with Hox9-Hox13, which increases the DNA-binding specificity of the Meis-Hox complex (Shen et al., 1997); no such properties appear to be present in Prep1 (Thorsteinsdottir et al., 2001). Whereas prep1.1 and prep1.2 are expressed almost ubiquitously in zebrafish, at least in early developmental stages up to 24 hpf (Choe et al., 2002), the expression of meis genes is more restricted (Biemar et al., 2001; Waskiewicz et al., 2001). However, both Meis and Prep bind to Pbx proteins, need Pbx for nuclear localization and prevent export of Pbx from the nucleus.

In the present investigation we have studied the functional role of the prep1.1 gene during early zebrafish development using antisense morpholino technology. We demonstrate that prep1.1 is necessary for histogenesis of the pharyngeal skeleton and, interacting with Pbc, is crucial for hindbrain patterning. In addition, our results support the idea that segmentation of the hindbrain and pharyngeal arches are independent processes.

Materials and methods

Characterization and radiation hybrid-panel mapping of prep1.1

We screened the Genbank database for a zebrafish expressed sequence tag (EST) that contained an open reading frame (ORF) that encoded a polypeptide homologous to human PREP1. One of the clones matching the criteria, fc13f10, was obtained from RZPD (Berlin) and sequenced completely. Sequence analysis of this EST revealed an ORF encoding a protein of 433 amino acids that contained two HR domains and one TALE homeodomain (Fig. 2A). Sequence comparison and phylogenetic reconstruction showed that the fc13f10 ORF is more similar to human PREP1 than to its parologue PREP2 (Fig. 1A); for this reason the zebrafish fc13f10 EST was called prep1.1.

To determine the position of prep1.1 onto the zebrafish genetic map we used the Zebrafish/Hamster Radiation Hybrid Panel (Goodfellow T51 panel, Invitrogen). The panel was screened by PCR using primers 5'-TCAACAGAGGCTATCAAAAG-3' and 5'-GTGCGCTGACGTCATAAAC-3', and 125 ng template, 100 nM each primer. 100 µM each dNTP, 2 mM MgCl2 and 1.25 units Taq DNA Polymerase (Promega). Thirty five cycles of PCR were completed: 94°C for 30 seconds, 95°C for 30 seconds, 72°C for 30 seconds. The retention profile of the PCR reaction was placed by the RH Instant Mapper program (http://134.174.23.167/zonrhmapper/instantMapping.htm) at 1894 cRay on chromosome 9, between meiotic SSLP markers z416 (796 cRay, 48.7 cM) and z6663 (2071 cRay, 48.7 cM).

RNA constructs and microinjections

To create the prep1.1-deletion constructs (Fig. 2A), the full-length prep1.1 cDNA (RZPD clone MPMGp6092025Q8) was dissected by PCR amplification. The primers used to prepare prep1.1ΔHR1-2 cDNA, in which HR1-2 (Meis family Homology Regions 1 and 2) are deleted, were:

5'-caggatccCATTTTGAATATGAGGCTGC-3'
5'-ggaggactCATGACAGTGTTGCAACC-3'
5'-ggaggactTTGTGGTTTGTGGCATTGG-3'
5'-ggaggatctGTCGCTGACGTCTAAACC-3'

The primers used to amplify prep1.1ΔHD cDNA, in which the homedomain (HD), were:

5'-caggatccCATTTTGAATATGAGGCTGC-3'
5'-ggaggactTTCACAGAGGACTCTAAAGC-3'
5'-ggaggatctCCCCGAAGAAACTCCAAGTCC-3'
5'-ggaggatctGTCGCTGACGTCTAAACC-3'

The primer used to prepare full coding prep1.1 cDNA, which lack 5' and 3' non-coding ends, were:

5'-caggatccCATTTTGAATATGAGGCTGC-3'
5'-ggaggatctGTCGCTGACGTCTAAACC-3'

In each case, BamHI and BglII sites are underlined. Constructs were subcloned in BamHI sites of pc2S+ and pc2S+GFP plasmid vectors and sequenced. For microinjection of mRNAs, plasmids containing coding sequences were linearized, and sense-strand capped mRNAs synthesized using SP6-dependent mMessage mMachine kit (Ambion). Subsequently, mRNAs were purified, tested by agarose-gel electrophoresis, diluted in PBS and microinjected into fertilized embryos at the one-cell stage. The amount of mRNA injected was determined by measuring the diameter of the drop injected. To confirm that mRNA cause no nonspecific effects during embryogenesis, control embryos were also injected with an mRNA encoding green fluorescent protein (GFP).

Morpholino antisense oligonucleotides were obtained from Gene Tools. The sequences of morpholinos used were as follows:

prep1.1-MOa, 5'-TGGACACAGACTGGGACGCCATCAT-3' (fluorescein tagged at 3' end); prep1.1-MOb, 5'-GCCAACCTGCCACCTGGGACCATATT-3';

pbx2-MO, 5'-GATCATCCATAATCTTTTGGCCG-3';

negative control-MO, 5'- CCTCTTACCTCAGTCTACATTTA-3' (fluorescein tagged at 3' end).

The pbx2-MO has been described (Waskiewicz et al., 2002). The stock solution was diluted to working concentrations of 0.5-3.0 mg ml⁻¹ in Danieau solution [58 mM NaCl, 0.7 mM KCl, 0.4 mM MgSO4, 0.6 mM Ca(NO3)2, 5 mM HEPES pH 7.6], before injection into the yolk of embryos at the one-cell stage. For the rescue experiment, prep1.1-MOb was co-injected with synthetic prep1.1 mRNA. To test the capacity of prep1.1-MOa to block translation, zebrafish eggs were injected with 25 pg of prep1.1-GFP mRNA and 2 ng of prep1.1-MOa (directed against the start codon and fluorescein tagged at the 3' end). The embryos were then fixed at 80% epiboly and GFP expression tested using anti-GFP antiserum (Biocat). Lack of staining in embryos co-injected with prep1.1-GFP and prep1.1-MOa, confirmed the specific targeting.
and abnormal phenotypes classified either as S (spacehead-like) (Abdelilah et al., 1996), P (posteriorized) and Izr (lacarceus) (Pöpperl et al., 2000). Injection of 10 pg of prep1.1-GFP mRNA had no significant effect on the phenotype, whereas the maximum effect was reached with 50 pg. By contrast, injection of 50 pg of prep1.1-∆HR-GFP, which encodes a Prep1.1 derivative that is not translocated to the nucleus (see Fig. 2), did not affect the phenotype. The embryos referred to in this Table are different from those in Figs 4-7.

### RT-PCR

Total RNA was extracted from ~100 frozen embryos at each developmental stage and from dissected ovaries using TRIzol (Gibco), purified with DNasel and quantified by agarose-gel electrophoresis. mRNA was then retrotranscribed and amplified with the Access RT-PCR System kit (Promega) using oligos specific for either prep1.1 (5'-CTCTTTTTCCTCTCTCTGCT-3' and 5'-CTCTTTTTCCTCTCTCTGCT-3') or β-actin (5'-TGGTTCCTCAATGGTG-3' and 5'-TTTCCTCTTGATGTCACGGAC-3'), which resulted in a 560-bp cDNA product.

### Cell extracts and immunoblotting

After dissection, 100 zebrafish embryos were resuspended in 60 µl lysis buffer (10 mM HEPES pH 7.9, 30 mM KCl, 1.5 mM MgCl2, 1 mM DTT, 0.5 mM PMSF, 1 mM Na2S2O5), kept in ice for 10 minutes and lysed with TritonX-100 to a final concentration of 0.1%. The nuclei were washed and the cell debris collected by centrifugation. The supernatant was removed into a new tube, added 0.1% and the nuclei were washed and the cell debris collected by centrifugation. The supernatant was removed into a new tube, added 0.1% TritonX-100 to a final concentration of 0.1%. The nuclei were washed and the cell debris collected by centrifugation. The supernatant was removed into a new tube, added 0.1%

### Immunochemistry

#### Cartilage staining

Larvae were fixed overnight in 4% buffered p-formaldehyde, rinsed in distilled water and stained overnight in a 0.1% Alcian blue solution. Larvae were then cleaned by washing sequentially in 3% hydrogen peroxide and 70% glycerol, and whole mounted.

#### Immunohistochemistry and histology

**Cartilage staining**

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#### Whole-mount in situ hybridization

Embryos were fixed in 4% buffered p-formaldehyde. RNA in situ hybridizations were performed essentially as reported in (Thisse et al., 1993). DIGoxigenin and fluorescein-labelled antisense probes were synthesized from cDNAs of prep1.1 (RZPD clone MPMGp609C2025Q8), krox20 (Oxtoby and Jowett, 1999), tmc2 (Puschel et al., 1992), tmc2 (Puschel et al., 1992), tmc2 (Puschel et al., 1992), tmc2 (Puschel et al., 1992). Iset1 (Korzh et al., 1993), snail1 (Krauss et al., 1993), foxb1.2/mariposa (Moens et al., 1996), foxb1h and foxb1a (McClintock et al., 2001), foxb2 and foxb2 (Prince et al., 1998), dtx2 (Akimenko et al., 1994), col2a1 (Sachdev et al., 2001) and myoD (Weinberg et al., 1996). Results of the hybridizations were analyzed statistically using Chi-square analysis.

#### Immunohistochemistry

Antibody staining of whole-mounted embryos with acetylated tubulin, RMO-44 and Zn5, was performed essentially as described by (Abdelilah et al., 1996; Piotrowski and Nüsslein-Volhard, 2000; Waskiewicz et al., 2001), respectively.

#### Detection of apoptotic cell death

For a preliminary analysis of cell death, embryos were stained with the vital dye acridine orange (acridinium chloride hemi-zinc chloride; Sigma) (Abrahams, 1999). Embryos were incubated for 10–15 minutes in 5 µg ml−1 acridine orange, washed twice for 5 minutes in Fish Water (60 mg l−1) Instant Ocean) and observed under a microscope (Leica MZFLIII) using a green filter set to reveal labelled cells undergoing cell death. For further analysis, apoptosis was detected by terminal transferase dUTP nick-end labelling (TUNEL), as previously described (Williams et al., 2000).

#### Retrograde labelling

RSNs were revealed by retrograde labelling from the spinal cord of 3- and 5-day-old larvae, as described (Alexandre et al., 1996). Labelled brains were dissected free of surrounding larval tissues, mounted in 50% glycerol in PBS and visualized by epifluorescence with a compound microscope (Leica Diaplan) using a Texas-red filter.

### Image acquisition and elaboration

Subcellular dynamics of Prep1.1-GFP constructs were visualized,

### Table 1. Results of microinjection experiments

<table>
<thead>
<tr>
<th>Construct injected</th>
<th>Amount injected</th>
<th>Injected/survived</th>
<th>Abnormal phenotype</th>
<th>Type</th>
<th>Wild-type phenotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>prep1.1- MOa</td>
<td>3 ng</td>
<td>141/129</td>
<td>129 (100%)</td>
<td>S</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>prep1.1- MOa</td>
<td>2 ng</td>
<td>101/96</td>
<td>90 (93.8%)</td>
<td>S</td>
<td>6 (6.2%)</td>
</tr>
<tr>
<td>prep1.1- MOa</td>
<td>2 ng</td>
<td>113/106</td>
<td>104 (98.1%)</td>
<td>S</td>
<td>2 (1.9%)</td>
</tr>
<tr>
<td>prep1.1- MOa</td>
<td>1 ng</td>
<td>107/79</td>
<td>70 (88.6%)</td>
<td>S</td>
<td>9 (11.4%)</td>
</tr>
<tr>
<td>prep1.1- MOa + prep1.1- MOb</td>
<td>0.5 + 0.5 pg</td>
<td>93/90</td>
<td>90 (100%)</td>
<td>S</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>prep1.1- GFP mRNA + prep1.1- MOb</td>
<td>50 pg + 2 pg</td>
<td>135/121</td>
<td>55 (45.5%)</td>
<td>S</td>
<td>66 (54.5%)</td>
</tr>
<tr>
<td>pbx4-MO</td>
<td>2 pg</td>
<td>144/132</td>
<td>128 (97%)</td>
<td>Izr</td>
<td>4 (3%)</td>
</tr>
<tr>
<td>prep1.1-GFP mRNA + pbx4-MO</td>
<td>10 pg + 3 pg</td>
<td>53/45</td>
<td>44 (98%)</td>
<td>Izr</td>
<td>1 (2%)</td>
</tr>
<tr>
<td>prep1.1-GFP mRNA + pbx4-MO</td>
<td>10 pg + 6 pg</td>
<td>55/34</td>
<td>34 (100%)</td>
<td>Izr</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Control MO</td>
<td>2 ng</td>
<td>46/43</td>
<td>0 (0%)</td>
<td>-</td>
<td>43 (100%)</td>
</tr>
<tr>
<td>prep1.1 mRNA</td>
<td>100 pg</td>
<td>62/44</td>
<td>25 (56.8%)</td>
<td>P</td>
<td>19 (43.2%)</td>
</tr>
<tr>
<td>prep1.1 mRNA</td>
<td>50 pg</td>
<td>46/55</td>
<td>18 (51.4%)</td>
<td>P</td>
<td>17 (48.6%)</td>
</tr>
<tr>
<td>prep1.1-GFP mRNA</td>
<td>100 pg</td>
<td>34/19</td>
<td>11 (57.9%)</td>
<td>P</td>
<td>8 (42.1%)</td>
</tr>
<tr>
<td>prep1.1-GFP mRNA</td>
<td>50 pg</td>
<td>87/72</td>
<td>43 (59.7%)</td>
<td>P</td>
<td>29 (40.3%)</td>
</tr>
<tr>
<td>prep1.1-GFP mRNA</td>
<td>10 pg</td>
<td>50/43</td>
<td>1 (2.3%)</td>
<td>P</td>
<td>42 (97.7%)</td>
</tr>
<tr>
<td>prep1.1AHD-GFP mRNA</td>
<td>50 pg</td>
<td>40/35</td>
<td>15 (42.9%)</td>
<td>P</td>
<td>20 (57.1%)</td>
</tr>
<tr>
<td>prep1.1AHR1-2-GFP mRNA</td>
<td>50 pg</td>
<td>28/27</td>
<td>0 (0%)</td>
<td>S</td>
<td>27 (100%)</td>
</tr>
</tbody>
</table>

Each row represents one experiment with the same batch of mRNA and/or morpholino (MO). Embryos injected at the one-cell stage were observed at 24 hpf and abnormal phenotypes classified either as S (spacehead-like) (Abdelilah et al., 1996), P (posteriorized) and Izr (lacarceus) (Pöpperl et al., 2000). Injection of 10 pg of prep1.1-GFP mRNA had no significant effect on the phenotype, whereas the maximum effect was reached with 50 pg. By contrast, injection of 50 pg of prep1.1AHR-GFP, which encodes a Prep1.1 derivative that is not translocated to the nucleus (see Fig. 2), did not affect the phenotype. The embryos referred to in this Table are different from those in Figs 4-7.
Results

prep1.1 mRNA expression pattern

Previous studies have documented the occurrence of prep1.1 transcripts in zebrafish embryos from the earliest developmental stages to 25 hpf, which implies that prep1.1 mRNA is laid down maternally (Choe et al., 2002; Waskiewicz et al., 2001). Our RT-PCR analysis shows that prep1.1 cDNA could be amplified from total RNA of mature ovaries and embryos at all stages studied, from 2 cells to larval day 4 (Fig. 1B), which confirms the occurrence of maternally expressed prep1.1 mRNA in zebrafish embryos. Transcripts of prep1.1, revealed with an anti-sense probe, were distributed ubiquitously in the embryo up to 24 hpf (Fig. 1C-G), whereas no labelling was detected with a sense probe (not shown). However staining in the trunk and tail, was already weaker at 24 hpf, markedly reduced at 48 hpf (Fig. 1H) and had completely disappeared by 72 hpf (Fig. 1I). At 72 hpf, labelling was limited to the head, predominantly in the brain and otic vesicles, the latter representing the posteriormost boundary of prep1.1 expression. Hence, prep1.1 transcripts were initially spread throughout the embryo, but became restricted to the head in later developmental stages.

Prep1.1 may be translocated to the nucleus from gastrulation onwards in the whole embryo

Prep1.1 is a cofactor in transcriptional regulation, so its presence in the nucleus is a prerequisite for its activity. To determine the timing and regulation of the nuclear localization of Prep1.1, we injected fertilized eggs with 10 pg of prep1.1-GFP mRNA, a dose that did not alter the phenotype (Table 1) but allowed the subcellular localization of the fluorescent protein to be tracked directly in live embryos. We found that Prep1.1-GFP localized in the cytoplasm at early developmental stages and that its nuclear import began during the blastula period. In particular, the fluorescent protein was exclusively cytoplasmic during the high stage (not shown) but soon after, during the sphere stage, was traced both to the cytoplasm and nucleus (Fig. 2B). Then, from 30% to 50% epiboly, Prep1.1-GFP became predominantly nuclear (Fig. 2C) and, at the beginning of gastrulation, was almost exclusively localized to the nucleus (Fig. 2D). An identical pattern was observed after injection of prep1.1ΔHD-GFP mRNA (Fig. 2I), which encodes a GFP-linked derivative of Prep1.1 that lacks the homeodomain (Fig. 2A). Conversely, injection of prep1.1ΔHR-GFP mRNA, which encodes a GFP-linked Prep1.1 derivative that lacks HR1 and HR2 Pbx-binding regions, resulted in the restriction of the fluorescent product to the cytoplasm (Fig. 2J). Incidentally, this also excluded the possibility that the nuclear localization of Prep1.1-GFP was influenced by the GFP moiety. On the basis of these results we conclude that (1) the mechanisms required for the nuclear translocation of Prep1.1 are fully effective at the onset of gastrulation in the whole embryo, and (2) as for other Meinox proteins, the Pbx-binding region, but not the homeodomain, is required for its nuclear import.

Prep1.1 nuclear translocation involves Pbx4

The nuclear transport of Meinox proteins is a highly conserved mechanism requiring the formation of Pbx-Meinox complexes that are translocated to the nucleus because of a nuclear-localization signal in the Pbx homeodomain (Abu-Shaar et al., 1999; Berthelsen et al., 1999). Pbx4/Lzr is the Pbx member with higher levels of expression during zebrafish embryogenesis (see Fig. 2K) (Waskiewicz et al., 2002), indicating that it might be the most important partner of Prep1.1 in early development. To determine whether the two proteins interacted during embryogenesis, we examined the subcellular localization of Prep1.1-GFP in live embryos in which pbx4 expression was repressed using a pbx4 antisense probe
morpholino. The fact that the phenotype of nearly all embryos injected with 2 ng of pbx4-MO at the one-cell stage was altered, proved the effectiveness of the morpholino treatment (Table 1). The specificity of the effects produced by the pbx4-MO was demonstrated by the observation that pbx4 morphants displayed morphological anomalies (Fig. 3I) and impaired expression patterns of molecular markers (see below), identical to those observed in the lzr mutant (Pöpperl et al., 2000). We found that in embryos that received 2-6 ng of pbx4-MO and 10 pg of prep1.1-GFP mRNA, the fluorescent protein was translocated to the nucleus with the same temporal pattern in both pbx4-MO-treated embryos and untreated siblings (Fig. 2E-G). But, importantly, in all pbx4 morphants a significant amount of Prep1.1-GFP was traced to the cytoplasm in stages when it was restricted mostly to the nucleus in the controls (Fig. 2D,G). This provided evidence that Pbx4 is involved in the nuclear transport of Prep1.1. Moreover, the nuclear signal (Fig. 2D,G) provided evidence that Pbx4 is involved in the nuclear transport of Prep1.1. This suggested that maternal Pbx4, which is still present at 10 hpf in pbx4/lzr homozygous mutants (Waskiewicz et al., 2002), was responsible of the residual nuclear import of Prep1.1-GFP.

prep1.1 inactivation affects the levels of both Pbx2 and Pbx4

Hth/Meis/Prep proteins influence the subcellular localization (Abu-Shaar et al., 1999; Berthelsen et al., 1999) and the stability of their Exd/Pbx partners (Kurant et al., 2001; Waskiewicz et al., 2001; Longobardi and Blasi, 2003). Because this indicates that Prep1.1 interacts with Pbx4 and, possibly, other Pbx proteins, we asked whether Prep1.1 might affect the levels and localization of Pbx proteins. To this purpose, we performed an immunoblot analysis, using a pan-Pbx antibody (Pöpperl et al., 2000), to test cytoplasmic and nuclear extracts of wild-type and prep1.1-MO-treated embryos at 24 hpf. As a control, we employed human Pbx1a and Pbx1b cotranslated in vitro with human Prep1. The pan-Pbx antibodies identified the 47×10^3 and 39×10^3 Mr bands expected for the two Pbx proteins (Fig. 2K). Moreover, the same two bands were also identified in extracts from human HEK cells, whereas a species of ~38×10^3 Mr was revealed in an extract from mouse testis (Wagner et al., 2001). When tested with the zebrafish extracts, the pan-Pbx antiserum revealed two major bands with mobilities that matched the electrophoretic migration of in vitro translated mouse Pbx1b (38.5×10^3 Mr) and Pbx1a (46.5×10^3 Mr). This pattern is identical to that obtained by Waskiewicz et al. (Waskiewicz et al., 2002) in identifying Pbx2

Fig. 2. Subcellular localization of Prep1.1-GFP. (A) Full-length zebrafish prep1.1, as sequenced from the EST fc13f10, is represented with the Meis family homology regions (HR1 and HR2) in blue and the homeodomain homology region (HD) in red. The positions of the morpholinos (MOs) relative to the cDNA sequence are indicated by orange bars. prep1.1 constructs, with GFP coding sequence in green, are also shown. prep1.1-MOab inactivates endogenous, full-length mRNA but not the full-coding constructs. (B-J) Subcellular localization of Prep1.1-GFP chimeric proteins. (B-D,H) In a wild-type embryo injected with 10 pg of prep1.1-GFP mRNA, Prep1.1-GFP, which is cytoplasmic at the high stage (not shown), is translocated to the nucleus from the sphere stage onwards. Starting from the shield stage, the fluorescent protein is restricted mostly to the nucleus. (E-G) In an pbx4 morphant injected with 6 ng pbx4-MO and 10 pg prep1.1-GFP mRNA, Prep1.1-GFP is also translocated to the nucleus from the sphere stage onwards, but significant amounts are detected in the cytoplasm in all subsequent stages. (L,J) In wild-type embryos, Prep1.1ΔHD-GFP, a derivative lacking the homeodomain, is translocated normally to the nucleus (I), whereas Prep1.1ΔHR-GFP, a derivative lacking the Meis homology region is not (J). (B-D,H) and (E-G) are from the same wild-type and pbx4 morphant embryos, respectively. (K) Western blot of extracts from 24 hpf zebrafish embryos. The left panel is a control blot to assess the migration of two Pbx proteins, mPbx1a and mPbx1b, of known molecular weight and antibody specificity. The two proteins, which are recognized specifically by the pan-Pbx antibody, were translated in vitro with hPrep1 in a rabbit reticulocyte system. The middle panel is another control using nuclear extracts (NE) and cytoplasmic extracts (CE) of either human HEK293 cells or mouse testis. The right panel shows the immunoblotting analysis of NE and CE from wild-type zebrafish embryos at 24 hpf and following injection of prep1.1-MOab. The migration of Pbx2 and Pbx4 (arrows) is inferred on the basis of the Mr of the bands, and observation of the identical pattern elsewhere (Waskiewicz et al., 2002). A pan-Pbx antibody (Pöpperl et al., 2000) was used throughout.
and Pbx4. Both species were more abundant in NEs than CEs and, importantly, all the bands were much more intense in extracts from wild-type embryos than prep1.1 morphants. As the assay was standardized by loading an equal amount of protein and by Ponceau staining of the gel (not shown), it appears that suppression of prep1.1 expression caused a significant decrease of the concentration of Pbx2 and Pbx4 in both nucleus and cytoplasm. This is consistent with the possibility that Prep1.1 stabilizes and increases the nuclear localization of different Pbx proteins.

**Effects of prep1.1 mRNA inactivation and overexpression**

It has been shown that appropriate amounts of antisense morpholinos injected into zebrafish embryos at the one-cell stage might repress the expression of both maternal and zygotic genes (Nasevicius and Ekker, 2000). Hence, as the first step in investigating the functional role of prep1.1 during early embryonic development we adopted the morpholino approach to examine the phenotypic effects induced by prep1.1 inactivation. We used two different morpholinos, complementary to either the initial 25 bp of the translated region (MOa) or a 25-bp sequence from the 5’-untranslated region (MOb) of prep1.1 mRNA (Fig. 2A). Embryos that received either prep1.1-MOs developed normally, both morphologically and temporally, up to early somitogenesis. However, at the 15-somite stage (16.5 hpf), cell death was apparent in the form of an opacity in the neuroectoderm. The effects of the two morpholinos were indistinguishable, dose-dependent and synergistic: 2-3 ng of either morpholino injected separately or 0.5 ng of each injected in combination, modified the phenotype of virtually all embryos treated (Table 1). One-day old morphants were characterized by a prominent area of degeneration, which was clearly visible bilaterally both inside and outside the CNS at the level of the hindbrain (Fig. 3B,C,E,F). Morphant embryos were impaired in motor coordination, so that most were unable to exit from the shell. At 5 dpf, the morphant embryos had small heads and eyes, and atrophic pectoral fins; they lacked jaws and a recognizable swim bladder and displayed an abnormal distribution of melanocytes and pericardial edema (Fig. 3H). The morphant embryos did not survive after 6–7 dpf.

We next investigated the effects of Prep1.1 overexpression by injecting one-cell stage embryos with either 50 pg or 100 pg of prep1.1 mRNA. Embryos injected with either dose developed normally beyond gastrulation, but the phenotype of >50% of the treated embryos was markedly affected at 24 hpf (Table 1). Injection of 50 pg prep1.1 mRNA induced two main
phenotypes in ~50% of embryos, both characterized by a shortening of the head, as evidenced by a decreased distance between the eye and the otic vesicle (Fig. 3R). Most of these embryos had a phenotype in which the eyes were closer to another but still distinct, whereas a few exhibited a more severe phenotype that was characterized by a single cyclopic eye. In situ hybridization with a krox20 antisense probe showed that the hindbrain was unaffected (Fig. 3T) but a pax6.1 probe revealed a strong reduction of the forebrain (Fig. 3V). Similar effects were observed in embryos treated with 50 pg of prep1.1ΔHD-GFP mRNA, encoding a GFP-linked Prep1.1 derivative lacking the homeodomain (Table 1), but in this case most embryos were cyclopic. This indicates that deletion of the homeodomain does not impair but rather increases the activity of Prep1.1, reminiscent of the finding that deletion of the PREP1 homeodomain might enhance the transcriptional activity of mammalian PBX1-HOXB1-PREP1 complexes (Berthelsen et al., 1998b). Moreover, embryos that received 100 pg of prep1.1 mRNA, displayed a even more extreme phenotype, characterized by the absence of eyes and a marked reduction of all head structures. Conversely, overexpression of prep1.1ΔHR-GFP mRNA, which encodes a GFP-linked Prep1.1 derivative that lacks the HR1 and HR2 regions, had no phenotypic consequences (Table 1). This indicates that, as with other members of the Meinox family (Choe et al., 2002), the Pbx-interacting domain is crucial to Prep1.1 activity. In summary, the results of the overexpression of prep1.1 in zebrafish closely resemble those obtained in Xenopus in which the overexpression of meix3 causes caudalization of anterior neural tissue (Salzberg et al., 1999; Dibner et al., 2001).

To verify the specificity of the morpholinos, we checked whether the mutant phenotype was rescued by coinjecting MOb with a prep1.1-expressing mRNA. To this purpose, we used an mRNA (prep1.1-GFP mRNA) that encodes wild-type Prep1.1 linked to GFP, so that expression of the chimeric protein could be ascertained visually in the embryos. This experiment could be devised for two reasons: first, when overexpressed in zebrafish embryos, Prep1.1-GFP and Prep1.1 produced qualitatively and quantitatively identical effects (Table 1), indicating that the activity of the chimeric protein was not significantly affected by the GFP moiety; second, because the prep1.1-MOb was complementary to a sequence in our morphants, this phenotype could be caused by the idea of an important role of Meinox proteins in this process (Choe et al., 2002; Waskiewicz et al., 2002). Hence, we first checked whether the expression of hoxb1b was altered in prep1.1 morphants. We observed that expression of this gene was indistinguishable in wild-type and prep1.1-MO-injected embryos (Fig. 4A,B). Because expression of hoxb1b is also unaffected by eliminating both pbx2 and pbx4 (Waskiewicz et al., 2002), it appears that neither Prep1.1 nor Pbx proteins are involved in the regulation of this gene.

We then investigated the effects of prep1.1 knockdown on the expression of foxb1.2/mariposa and pax6.1, two genes that depict hindbrain segmentation by outlining rhombomere boundaries (Moens et al., 1996; Choe et al., 2002). As shown in Figs. 4 (Fig. 4C,D,G,H), prep1.1 knockdown caused the loss of the six clear-cut boundaries (from r1-r2 to r6-r7), evidenced by the expression of these two genes in wild-type embryos. By contrast, in pbx4 morphants (Fig. 4I) pax6.1 expression revealed that hindbrain segmentation was indistinct rostrally but remained clearly identifiable in the three caudal boundaries (from r4-r5 to r6-r7). This agrees with the expression pattern of pax6.1 in embryos that express ectopically a dominant negative derivative of pbx4 (Choe et al., 2002), and correlates with the fact that in mutants such as lzr (Pöpperl et al., 2000) and MZ/lzr (which lacks both maternal and zygotic pbx4) (Waskiewicz et al., 2002), mariposa expression is eliminated rostrally but maintained in the three caudal boundaries. However, expression of mariposa in the hindbrain was suppressed completely by injecting MZ/lzr embryos with a pbx2 morpholino (Waskiewicz et al., 2002). Because suppression of mariposa expression can be caused by the simultaneous depletion of Pbx2 and Pbx4, we asked whether, in our morphants, this phenotype could be caused by prep1.1 knockdown disrupts hindbrain segmentation

In zebrafish, Pbx proteins are essential for hindbrain development (Waskiewicz et al., 2002), but overexpression of wild-type and dominant-negative Meis proteins also support the idea of an important role of Meinox proteins in this process (Choe et al., 2002; Vlachakis et al., 2001). As both the morphological inspection and TUNEL analysis showed that the hindbrain is significantly affected in prep1.1 morphants, we addressed the role of prep1.1 in hindbrain development by analysing the effects of its knockdown on the expression of several hindbrain markers. The results were compared to those observed in mutants that lack Pbx proteins (Pöpperl et al., 2000; Waskiewicz et al., 2002) and embryos treated with a pbx4 morpholino.

In zebrafish, hoxb1b is indispensable for normal segmentation of the hindbrain (McClintock et al., 2001), and the onset of its expression represents the initial step of hindbrain patterning (Waskiewicz et al., 2002). Hence, we first checked whether the expression of hoxb1b was altered in prep1.1 morphants. We observed that expression of this gene was indistinguishable in wild-type and prep1.1-MOb-injected embryos (Fig. 4A,B). Because expression of hoxb1b is also unaffected by eliminating both pbx2 and pbx4 (Waskiewicz et al., 2002), it appears that neither Prep1.1 nor Pbx proteins are involved in the regulation of this gene.

Neural degeneration in prep1.1 morphants is caused by apoptosis

Visual inspection of prep1.1 morphants revealed a pronounced process of degeneration that started during early somitogenesis and peaked at about 24-36 hpf. Staining with the vital dye acridine orange showed a major increase in cell death in prep1.1 morphants. Although this occurred principally in the CNS, in particular the hindbrain and spinal cord, it was also significant in other tissues (Fig. 3K). By contrast, acridine orange staining was inconsistent in wild-type embryos and pbx4 morphants (Fig. 3J,L). To establish whether cell death induced by prep1.1 inactivation was due to apoptosis, the embryos were analyzed by in situ TUNEL assay to detect DNA fragmentation. As shown in Fig. 3 (Fig. 3N,P) TUNEL labelling was evident throughout the brain of prep1.1-MOb-treated embryos, especially in the hindbrain, but was limited in the brains of controls (Fig. 3M,O). Therefore, we, conclude that the pronounced cell death induced by prep1.1 inactivation was due primarily to apoptosis.
knockdown-mediated reduction of Pbx proteins. However, this was not the case, because injection of pbx4 mRNA did not rescue mariposa expression in prep1.1 morphants (26 morphants observed, 21 deficient, data not shown).

Further evidence of impaired hindbrain segmentation in prep1.1 morphants was provided by the expression of pax2.1. In wild-type embryos, pax2.1 is expressed in segmental clusters of commissural interneurons, arranged in two longitudinal rows extending from the hindbrain to the whole spinal cord (Jiang et al., 1996; Mikkoła et al., 1992; Schier et al., 1996). Injection of prep1.1-MOb caused the selective disappearance of pax2.1-expressing cells in the region from r2 to r6 (Fig. 4E,F), whereas injection of pbx4-MO did not affect the wild-type phenotype (data not shown).

We next investigated the effects of prep1.1 knockdown on the expression of a series of markers that specify rhombomere identity. In wild-type embryos at 24 hpf, hoxb1a is expressed in r4, krox20 is expressed in r3 and r5, hoxa2 is expressed highly in r2 and r3 and at lower levels in r4 and r5, and hoxb2 is expressed highly in r3 and r4 and at a lower level in r5 (Prince et al., 1998). Injection of prep1.1-MOb suppressed the expression of hoxb1a in r4 (Fig. 4J,K). Because expression of hoxb1a, like that of mariposa, is suppressed by depletion of both Pbx2 and Pbx4 (Waskiewicz et al., 2002), we checked the effects of Pbx4 overexpression on hoxb1a pattern in prep1.1 morphants. Although hoxb1a expression was rescued in a significant number of embryos, it always remained at minimal levels (Fig. 4T). Hence, it appears that the hoxb1a phenotype of the morphants was caused by the combined effects of prep1.1 knockdown and reduced Pbx protein concentration. Nonetheless, the fact that hoxb1a expression was only minimally rescued by pbx4 overexpression demonstrates that prep1.1 is crucial for the regulation of hoxb1a.

In prep1.1 morphants, krox20 expression was abolished in r3, but not in r5 (Fig. 4Q). This effect was rescued by coinjection of prep1.1 mRNA plus prep1.1-MOb (Fig. 4R), which confirms the morpholino specificity. Disappearance of
krox20 expression in r3 was also observed in lzar and MZlzar mutants (Pöpperl et al., 2000; Waskiewicz et al., 2002) and in embryos injected with pbx4-MO (Fig. 4S). However, krox20 expression in r3 was not rescued by pbx4 mRNA overexpression in prep1.1 morphants (Fig. 4U), indicating that prep1.1 and pbx4 are both crucial for expression of krox20 in r3. By contrast, depletion of both pbx4 and pbx2 suppressed krox20 expression in r3 and r5 (Waskiewicz et al., 2002). In prep1.1-injected embryos, expression of both hoxa2 and hoxb2 was reduced markedly along the whole expression domain (Fig. 4L-O), which resembles the phenotype of lzar mutants (Pöpperl et al., 2000). In MZlzar mutants, hoxa2 expression is similarly reduced, and eliminated entirely following injection with a pbx2 morpholin (Waskiewicz et al., 2002). Thus, the expression of krox20 and hoxa2 appears to be more susceptible to the elimination of the two pbx genes than to prep1.1 knockdown.

**prep1.1 knockdown affects the migration of facial nerve motor neurons and causes disappearance of all reticulo-spinal neurons except Mauthner cells**

In vertebrates, the position of the motor nuclei of cranial nerves mirrors the rhombomeric organization of the hindbrain (Lumsden and Keynes, 1989). Because hindbrain segmentation and expression of rhombomere-specific genes were severely perturbed in prep1.1 morphants, we asked whether the patterning and localization of these nuclei was also affected. We examined the expression of islet1 (isl1), which is widely expressed in early postmitotic neurons (Korzh et al., 1993) and whose expression pattern in the motor nuclei of cranial nerves has been described in detail in zebrafish embryos (Chandrasekhar et al., 1997; Higashijima et al., 2000). In wild-type embryos at 48 hpf, isl1 was detected in all motor nuclei of the hindbrain and ganglia of cranial nerves (Fig. 5A,C). In prep1.1 morphants (Fig. 5B,D), the number of neurons that expressed isl1 neurons in cranial nerve nuclei was not changed significantly, but their distribution was altered. In particular, the motor neurons of the facial nerve (nVII) were not located in the region that corresponded to r6 and r7 as in controls (Fig. 5A), but were spread in an elongated nucleus extending from r4-r6 (Fig. 5A-D). In zebrafish, the nVII motor neurons originate in r4 and migrate caudally to r6 and r7 (Higashijima et al., 2000). Therefore, the presence of this aggregate indicates that their migration is impaired in prep1.1 morphants. The altered migration of nVII motor neurons to caudal regions of the hindbrain correlated well with the downregulation of hoxb1a in r4. In fact, knockdown of hoxb1a inhibits migration of nVII motor neurons (McClinock et al., 2002; Cooper et al., 2003). Further evidence of abnormal neuronal organization in the hindbrain of prep1.1-MO-injected embryos was revealed with antisera to acetylated tubulin. As shown in Fig. 5K,L, neuropils and commissural tracts of the rhombomeric segments were clearly distinguishable in the controls but barely detected in prep1.1 morphants. By contrast, the ganglion and sensory root of the trigeminal nerve (nV), were apparently unaffected by prep1.1 inactivation, confirming the results of isl1 expression.

RSNs are a population of individually identifiable neurons that have a rhombomere-specific localization and are sensitive to alterations in the expression of hox genes (Alexandre et al., 1996). A striking feature of prep1.1 morphants at both 3 and 5 dpf, is the disappearance of most retrogradely labelled RSNs apart from a pair of large, bilateral neurons that project contralaterally. These are identifiable as Mauthner cells that
normally develop in r4. Given that general defects of the CNS might lead to the impossibility of backfilling RSNs, we also examined the presence and morphology of RSNs at 48 hpf using the RMO-44 antibody. The results confirmed the retrograde labelling analysis and showed that the projection of the RMO-labelled cells in prep1.1 morphants was identical to that of Mauthner neurons in wild-type embryos (Fig. 5LJ). The results of this experiment demonstrate that Prep1.1 is necessary for the development of all RNSs except Mauthner cells.

Head cartilage defects in prep1.1 morphants
As described above, prep1.1 morphants lacked the jaw, indicating a defective development of neural-crest derivatives. To analyze the cranial skeletal defects induced by prep1.1 inactivation, we examined the skull morphology using Alcian Blue staining. Five-day-old morphants lacked all neural crest-derived cartilages of the pharyngeal arches (Fig. 6C,D). The skull consisted of the neurocranium only in which the ethmoid plate and trabeculae cranii, which are thought to derive from the neural crest, were misshaped and reduced significantly in size, whereas the mesodermally-derived elements were affected much less. The phenotype induced by the prep1.1-MOb could be substantially rescued by co-injection of prep1.1 mRNA (data not shown). The occurrence of the cartilaginous neurocranium indicates that the lack of pharyngeal cartilages was not the consequence of a generalized block in the chondrogenic process, but the result of either patterning or specification defects. In pbx4 morphants, the pharyngeal skeleton displayed the same defects as in lzf mutants (Pöpperl et al., 2000). In such embryos (Fig. 6G,H), all the branchial cartilages were missing, and the skeletal elements of the mandibular and hyoid arches were present but improperly shaped and abnormally fused.

The defects of the pharyngeal skeleton in prep1.1 morphants might be due to either the absence or defective migration of neural crest cells, or to their inability to differentiate into cartilage cells. To address this issue we first examined the expression of the neural crest cell marker dlx2 (Akimenko et al., 1994). In wild-type embryos, dlx2 is expressed in three distinct streams of cranial neural crest cells that migrate to the mandibular (m), hyoid (h) and five branchial (b) arches (Fig. 7A). dlx2 is also expressed in post-migratory neural crest cells within the arches (Fig. 7C). In embryos injected with prep1.1-MO, dlx2-positive cranial neural crest cells behaved like those of wild-type embryos, gathering in three migrating streams that eventually populated the pharyngeal arches (Fig. 7B,D). The correct pattern of neural crest cell migration in prep1.1 morphants, was further confirmed with the snail1 marker (Fig. 7E,F), which is expressed in the head mesenchyme, in neural crest cells that give rise to the pharyngeal skeleton and in paraxial mesoderm cells that originate muscle cells (Thisse et al., 1993). The fact that dlx2-positive and snail1-positive postmigratory cells were distributed similarly in separate clusters in the pharyngeal region in both prep1.1 morphants and wild-type embryos indicated that pharyngeal segmentation occurred normally in the morphants (Fig. 7C-F). Indeed, staining with the Zn5 antibody, confirmed that formation of the endodermal pouches and segmentation of the pharyngeal region took place correctly in prep1.1 morphants (Fig. 7G,H).

Col2a1, which is expressed in differentiating chondrocytes, is essential for normal chondrogenesis in zebrafish and mammals (Vandenberg et al., 1991; Yan et al., 2002). Therefore, we examined whether the expression of col2a1 was altered in postmigratory neural crest cells of prep1.1 morphants. We found that col2a1 was expressed in the mesenchyme that will give origin to the neurocranium in prep1.1 morphants, though to a lesser degree than in wild-type embryos. However, it was not expressed in the pharyngeal arches (Fig. 7I-L).

Neural crest cells are known to pattern the muscles of the pharyngeal region (Noden, 1983). In zebrafish, pharyngeal chondroblasts and myoblasts differentiate synchronously, which indicates interdependence of their patterning (Schilling and Kimmel, 1994). In both chinless (chn) (Schilling et al., 1996b) and jellyfish (jef) (Yan et al., 2002) mutants, neural crest cells migrate normally to the pharyngeal region but fail to differentiate into chondrocytes. However, the pharyngeal musculature is absent in chn mutants but develops normally in jef mutants, which indicates that chondrogenesis is not a prerequisite for the differentiation of the pharyngeal musculature. To determine whether prep1.1 knockdown affected the pharyngeal musculature we examined the
expression of *myoD*, the early marker of myogenesis, in *prep1.1* morphants. At a stage in which all head muscles of wild-type larvae express *myoD*, expression of *myoD* in the head of the morphants was detected in the eye muscles and in few lateral elements, seemingly opercular muscles, but not in the pharyngeal region (Fig. 7M,N).

In zebrafish, there are two independent phases of expression of the homeobox gene *goosecoid* (*gsc*), a gene that is required for cranio-facial development in mammals (Clouthier et al., 2000; Zhu et al., 1997): an early phase in cells anterior to the presumptive notochord; and a late phase at 2-3 dpf in the brain and in neural crest derivatives of the mandibular and hyoid arches (Schulte-Merker et al., 1994). In zebrafish, expression of *gsc* in mandibular and hyoid arches is dependant on Hoxa2 function (Hunter and Prince, 2002). To assess whether *gsc* expression was affected by *prep1.1* knockdown we used transgenic zebrafish that contain a GFP construct driven by a gsc promoter, which express GFP in the embryonal brain and mandibular cartilage (Doitsidou et al., 2002). Knockdown of *prep1.1* in transgenic larvae suppressed GFP expression in the first pharyngeal arch but not in the anterior telencephalic area. Embryos are in dorsal (A,B,I-N) and lateral (C-H,O,P) views, with anterior to the left. b, branchial arch; ba, branchial arches; bm, branchial muscles; h, hyoid arch; m, mandibular arch; me, Meckel’s cartilage; n, notochord oc, otic capsule; om, opercular muscles; ov, otic vesicle; sr, superior rectum of the eye; te, telencephalon.

Quantitative data: (picture) *probe*, defective/total; (B) *dlx2*, 1/18; (D) *dlx2*, 0/22; (F) *snail1*, 4/25; (H) *zn5*, 4/18; (I) *col2a1*, 18/21; (L) *col2a1*, 18/19; (N) *myoD*, 16/18; (P) *gsc*, 4/5.

Discussion

In the present work we describe the effects of the morpholino-induced inactivation of the *prep1.1* gene in zebrafish embryos. Four major features are characteristic of *prep1.1* morphants: (1) prominent apoptotic cell death, which becomes evident at the 15-somite stage in the neuroectoderm and peaks at 24-36 hpf in the CNS, particularly in the hindbrain; (2) loss of expression of several genes, in particular *hox* members, in specific rhombomeres; (3) defective hindbrain patterning; and (4) lack of all neural crest-derived cartilages in the head skeleton. Moreover, using a *pbx4*-MO, that reproduced faithfully the *lzr* phenotype, we provide evidence that Prep1.1 and Pbx4 interact in certain developmental processes but act independently in others.

The maternal expression of *prep1.1* and its ubiquitous distribution in zebrafish embryos up to 24 hpf indicated...
its involvement in early embryogenetic processes. This assumption was confirmed by our finding that inactivation of prep1.1 induced prominent apoptosis, which becomes clearly visible during somitogenesis. Accordingly, the time course of the nuclear translocation of Prep1.1-GFP, demonstrated that the mechanisms required for the nuclear import of Prep1.1, which is a prerequisite for its activity, are fully functional by the end of gastrulation. Like other Meinox proteins, Prep1.1 lacks a nuclear-localization signal and relies on Pbc partners for translocation to the nucleus (Berthelsen et al., 1999).

Because Pbx4 and Pbx2 are the main Pbc members that are expressed early in zebrafish embryogenesis (Pöpperl et al., 2000; Waskiewicz et al., 2002), they appear to be the major Prep1.1 partners in early zebrafish development. Indeed, this is supported by the observation that Prep1.1-GFP remains mostly cytoplasmic in both pbx4 and pbx2/pbx4 double morphants. However, in such morphants, the finding that some Prep1.1-GFP was associated with the nucleus, is consistent with the occurrence of maternal Pbx4 in early developmental stages (Waskiewicz et al., 2002).

As evidenced by immunoblotting analysis, Prep1.1 affects the levels of Pbx2 and Pbx4 and, possibly, of other Pbx members. The effect is probably post-transcriptional and might be caused by a longer half-life of Pbx proteins when they form dimers with either Prep and Meis. In fact, in Drosophila, Exd is destabilized and degraded in the absence of Hth (Kurant et al., 2001), and lack of Prep1 in mice coincides with a strong, widespread reduction of the levels of all Pbx proteins (E.F. and F.B., unpublished). Moreover, overexpression of Prep1 in mouse teratocarcinoma cells increases the half-life and, therefore, the level of Pbx proteins (Longobardi and Blasi, 2003). As simultaneous depletion of Pbx2 and Pbx4 also causes a series of molecular and morphological effects that are similar to the phenotypes observed in prep1.1 morphants (Waskiewicz et al., 2002), such a phenotype might be due to the reverberating effects of Prep1.1 suppression on the levels of Pbx proteins. However, this was apparently not the case. In fact, the inability of pbx4/lzr mRNA to rescue apoptosis, expression of mariposa in rhombomeric boundaries, expression of krox20 in r3 and branchial cartilage formation in prep1.1 morphants, reveals a direct role of prep1.1 in embryo development other than the mere stabilization of Pbx proteins.

Suppression of prep1.1 induces apoptosis

Meinox proteins control differentiation through a wide array of interactions with different homeodomain transcription factors. Thus, the apoptotic process observed in prep1.1 morphants might be caused by the programmed cell death of cells that fail to differentiate (Ishizaki et al., 1995). It is noteworthy that the morphological phenotype of prep1.1 morphants shares similarities with the spacehead class (group II) of zebrafish mutants described by Abdelilah et al. (Abdelilah et al., 1996). In particular, the onset of apoptosis coincides temporally and spatially in prep1.1 morphants and spacehead mutants. Interestingly, it was proposed that the genes affected in spacehead mutants are involved in either the differentiation or maintenance of neural cell types, suggesting that cells that are unable to conclude their differentiation process are fated to death by apoptosis (Abdelilah et al., 1996). Links between Meinox partners such as mouse HoxA1 and HoxB1 (which are the orthologous of zebrafish Hoxb1b and Hoxb1a, respectively) and apoptosis have been established recently (Barrow et al., 2000; Lohmann et al., 2002). Thus, the prominent apoptotic process observed in prep1.1 morphants might be related to an impaired activity of Hox proteins due to prep1.1 inactivation.

Suppression of prep1.1 affects the expression of genes crucial for hindbrain development

Our results show that prep1.1 morphants exhibit major changes of gene expression patterns in the hindbrain. First, although expression of hoxb1b, the orthologue of mouse Hoxa1, is not affected, hoxb1a, the orthologue of mouse Hoxb1, which is normally expressed in r4, is absent. Moreover, we show that the expression of hoxa2 and hoxb2 is strongly reduced. Meinox proteins form functionally active heterotrimeric complexes with Pbx and Hox and these complexes are functionally important in vivo in the expression of at least hoxb2 in r4 and r6-r8 (Jacobs et al., 1999; Ryoo et al., 1999; Ferretti et al., 2000). However, the Meinox protein involved has not been identified. In zebrafish, hoxb1a expression in r4 requires pbx2/4 and hoxb1b (Cooper et al., 2003; Waskiewicz et al., 2001; Waskiewicz et al., 2002). Because prep1.1 is required for full expression of hoxb1a in r4, the expression of this gene might also require the formation of a heterotrimeric complex between prep1.1, pbx2/4 and hoxb1b gene products. Although the role of heterotrimeric complexes was not apparent in initial investigations of Hoxb1 expression (Jacobs et al., 1999; Ferretti et al., 2000), we have observed that, in mice, the r4 Hoxb1 enhancer extends slightly more 3’ than previously defined, and heterotrimeric Meinox-Pbc-Hox complexes might be required for Hoxb1 expression (E. Ferretti, R. Krumlauf and F. Blasi, in preparation).

In the mouse, expression of Hoxb2 depends on krox20 in r3 and r5, and on the heterotrimeric Meinox-Pbx-Hox complex in r4 (Jacobs et al., 1999; Ryoo et al., 1999; Ferretti et al., 2001). Here, we show that hoxb2 expression requires prep1.1 in r2, r4 and r3. The effect observed in r3 is probably due to the absence of krox20, whereas in r4 it might depend directly on the lack of prep1.1 as well as the induced decrease of pbx4. In conclusion, because the absence of prep1.1 results in the absence of hoxb1a, prep1.1 inactivation causes the decrease/absence of all factors that are required for activity of the hoxb2 enhancer Krox20 in r3 and the heterotrimeric complex in r4. The lack of expression of krox20 in prep1.1 morphants is also reflected by the absence of hoxa2 expression in r3. Conversely, in prep1.1 morphants krox20 is expressed normally in r5, in which hoxa2 and hoxb2 are absent. These results show unique properties of the Prep1.1 protein in the specification of r2-r5.

prep1.1 is crucial for hindbrain patterning

The vertebrate hindbrain exerts a key function in patterning the developing head through its segmental rhombomeric structure and its ability to generate neural crest cells. Rhombomeres direct the proper organization of cranial ganglia, branchiomotor nerves and the migration of neural crest cells (Trainor and Krumlauf, 2000). Our results show that Prep1.1 is crucial for hindbrain patterning. This is illustrated in prep1.1 morphants by the loss of the segmental expression patterns of mariposa and pax6.1 throughout the hindbrain, and the absence of pax2.1-positive commissural interneurons in the
r2-r6 region. Unlike Prep1.1, Pbx4 is necessary for hindbrain segmentation only anteriorly to the r4-r5 boundary. In fact, in our Pbx4 morphants, and in embryos expressing a dominant negative derivative of pbx4 (Choe et al., 2002), pax6.1 segmentation is lost anteriorly but not posteriorly to the r4-r5 boundary. This is in accord with the loss of rhombomere segmentation anterior to the r4-r5 boundary in lzr mutants revealed by mariposa expression (Pöpperl et al., 2000).

On the basis of the effects of prep1.1, pbx4 and pbx2 inactivation on hindbrain patterning (Fig. 4) (Waskiewicz et al., 2002), and of the deficiencies in hox gene expression in the hindbrain (Fig. 4), it can be deduced that Prep1.1 regulates the process of rhombomeric segmentation and specification by acting with Pbx4 rostral to the r4-r5 boundary, and with Pbx4 and Pbx2 caudal to that boundary.

Another striking effect of prep1.1 inactivation on hindbrain development is the lack of RSNs except Mauthner cells. This feature indicates that Prep1.1 is necessary for early differentiation and/or survival of most RSNs. By contrast, pbx4 would be required subsequently for the acquisition of the identity of RSNs, as shown in lzr mutants in which all RSNs located posteriorly to r2 display r2 identity (Pöpperl et al., 2000). Although r4 identity is disrupted in prep1.1 morphants, as evidenced by the absence of hoxb1a expression, the occurrence of r4-specific Mauthner cells is not incongruous. In fact, Mauthner cells appear normally at 7.5 hpf, so their differentiation is independent of hoxb1a, whose expression starts ~2 hours later (Prince et al., 1998; McClintock et al., 2001). Indeed, the development of Mauthner cells requires hoxb1b, which is expressed first at 6 hpf in the presumptive r4 (Alexandre et al., 1996; McClintock et al., 2001) and is normally expressed in prep1.1 morphants. Being independent of prep1.1, the development of Mauthner cells might require another Meinox member. This possibility is indicated by the disappearance of Mauthner neurons in embryos that express a dominant negative derivative of Pbx4 (Choe et al., 2002), and is supported by the high level of expression of other Meinox genes in r4 during somitogenesis (Waskiewicz et al., 2001).

**prep1.1 is indispensable for the development of the pharyngeal skeleton**

The selective lack of all neural crest-derived cartilages of the head skeleton and pharyngeal muscles are major traits shared by prep1.1 morphants and chn mutants (Schilling et al., 1996b).

It is noteworthy that none of the 109 (Piotrowski et al., 1996; Schilling et al., 1996a) and 48 (Neuhauss et al., 1996) mutants with cranio-facial abnormalities that were obtained in large-scale screens for mutations that affect early zebrafish development lacked specifically all the cartilages derived from the neural crest. Thus prep1.1 is the only gene so far identified that is indispensable for the development of the whole pharyngeal skeleton and it might be involved in a common genetic pathway with chn. In prep1.1 morphants, as in chn mutants (Schilling et al., 1996b), the particular phenotype is caused neither by a general defect in the process of chondrogenesis because the mesodermally derived cartilages of the neurocranium are present, nor to the lack and unsuccessful migration of neural crest cells into the pharyngeal arches, as evidenced by dlx2 and snail1 labelling (Fig. 7). Hence, it appears that cartilage precursors of the pharyngeal arches lack the capacity to differentiate into chondrocytes in the absence of prep1.1. It has been shown that segmentation of the pharyngeal endoderm is required for the correct patterning of the cartilages of the pharyngeal arches. Indeed, in lzr mutants, in which endodermal pouches do not form, only deformed and fused mandibular and hyoid cartilages develop (Pöpperl et al., 2000). Moreover, in van gogh (vgo) mutants, in which only the first endodermal pouch develops, the cartilages of the mandibular and hyoid arches do occur, whereas those of the posterior (P3-P7) arches are highly reduced (Piotrowski and Nüsslein-Volhard, 2000). However, in prep1.1 morphants, the pharyngeal region is segmentated normally and the pharyngeal endoderm is patterned correctly. Hence, our results indicate that in prep1.1 morphants the absence of all pharyngeal cartilages is caused either by a primary specification defect of neural crest cells or by the lack of competence/signals necessary for chondrogenic differentiation of specified cells. The fact that in lzr and vgo mutants pharyngeal cartilaginous structures do occur, albeit heavily reduced and improperly shaped, indicates that endodermal segmentation is not indispensable for chondrogenesis, although it affects profoundly its patterning. Hence, the very process of differentiation of neural crest cells into chondrocytes within the pharyngeal arches appears to be independent of endodermal segmentation. The complete lack of P3-P7 cartilages in lzr mutants and pbx4 morphants might, thus, be explained by the failure of a process that requires the Prep1.1-Pbx4 partnership. If this hypothesis is correct, chondrogenesis in P1 and P2 would require Prep1.1 and a Pbc partner other than Pbx4, consistent with the occurrence of mandibular and hyoid cartilages in lzr mutants. Thus, pharyngeal endodermal segmentation would need Pbx4, whereas chondrocyte differentiation in all pharyngeal arches would require Prep1.1 in association with Pbx4 in P3-P7 and another Pbc partner, possibly Pbx2, in P1 and P2. Indeed, the homeotic transformation of the cartilages of the hyoid arch into those of the mandibular arch in lzr mutants (Pöpperl et al., 2000), confirms that Pbx4 is required for P2 cartilage identity but not for its histogenesis. Finally, the defective hindbrain segmentation in the presence of a normally segmentated pharyngeal endoderm in prep1.1 morphants, supports the hypothesis (Piotrowski and Nüsslein-Volhard, 2000) that the two processes are independent and based on different molecular mechanisms.

Our data show that Prep1.1 is uniquely involved in essential aspects of embryo development, in particular hindbrain patterning, cell differentiation and apoptosis. Some effects might be ascribed to the interaction with either Pbx4 or Pbx2 and appear to be dependent on transcriptional effects on Hox genes. The presence of at least two Prep and three Meis proteins in zebrafish embryos (Waskiewicz et al., 2001), and the fact that the Prep proteins are expressed ubiquitously in early development, might indicate redundant functions. Indeed, in vitro experiments have failed to show differences in the ability of different Meinox proteins to interact with Pbx or to produce ternary complexes with Hox members. However, the results of prep1.1 inactivation demonstrate some specificity, indicating the occurrence of mechanisms based on different specific combinations of Meinox and Pbc proteins. The functional inactivation of prep1.1 in zebrafish is the first attempt to dissect the function of the various Meinox proteins in development. Further work will undoubtedly highlight the role of the other Meinox proteins.
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