**vhnf1 integrates global RA patterning and local FGF signals to direct posterior hindbrain development in zebrafish**

Rafael E. Hernandez1,2, Holly A. Rikhof1, Ruxandra Bachmann1,* and Cecilia B. Moens1,†

1Howard Hughes Medical Institute and Division of Basic Sciences, Fred Hutchinson Cancer Research Center, 1100 Fairview Avenue North, PO Box 19024, Seattle, WA 98109, USA
2Medical Scientist Training Program and Molecular and Cellular Biology Program, University of Washington, Seattle, WA 98195, USA

*Present address: Département de Pédiatrie, Hôpitaux Universitaires Genevois, 6 rue Willy Donze, 1211 Genève, Switzerland
†Author for correspondence (e-mail: cmoens@fhcrc.org)

Development 131, 4511-4520
Published by The Company of Biologists 2004
doi:10.1242/dev.01297
Accepted 8 June 2004

**Summary**

The vertebrate hindbrain is transiently divided along the anterior-posterior axis into seven morphologically and molecularly distinct segments, or rhombomeres, that correspond to Hox expression domains. The establishment of a proper ‘hox code’ is required for the development of unique rhombomere identities, including specification of neuronal fates. valentino (val), the zebrafish ortholog of mafB/Kreisler (Kr), encodes a bZip transcription factor that is required cell autonomously for the development of rhombomere (r) 5 and r6 and for activation of Hox group 3 gene expression. Recent work has demonstrated that the expression of val itself depends on three factors: retinoic acid (RA) signals from the paraxial mesoderm; fibroblast growth factor (Fgf) signals from r4; and variant hepatocyte nuclear factor 1 (vhnf1, also known as tfc2), a homeodomain transcription factor expressed posterior to the r4-5 boundary. We have investigated the interactions between these inputs onto val expression in the developing zebrafish hindbrain. We show that RA induces val expression via activation of vhnf1 expression in the hindbrain. Fgf signals from r4, acting through the MapK pathway, then cooperate with Vhnf1 to activate val expression and subsequent r5 and r6 development. Additionally, vhnf1 and val function as part of a multistep process required for the repression of r4 identity in the posterior hindbrain. vhnf1 acts largely independently of val to repress the r4 ‘hox code’ posterior to the r4-5 boundary and therefore to block acquisition of r4-specific neuronal fates in the posterior hindbrain. However, vhnf1 is not able to repress all aspects of r4 identity equivalently. val is required downstream of vhnf1 to repress r4-like cell-surface properties, as determined by an ‘Eph-ephrin code’, by repressing ephrin-B2a expression in r5 and r6. The different requirements for vhnf1 and val to repress hoxb1a and ephrin-B2a, respectively, demonstrate that not all aspects of an individual rhombomere’s identity are regulated coordinately.

**Key words:** Rhombomere, Hindbrain, Retinoic acid, vhnf1, valentino, mafB, Fibroblast growth factor, hox

**Introduction**

The rhombomeres of the vertebrate hindbrain are a series of seven transient segments first distinguished by expression of molecular markers and later as morphological segments giving rise to distinct neuronal fates (Lumsden and Krumlauf, 1996; Moens and Prince, 2002). The acquisition of proper anteroposterior (AP) identity and subsequent neuronal development in the hindbrain is established by the Hox genes that are expressed in nested, rhombomere-restricted domains and that play a role in the specification of AP axis identities across metazoan phyla (Wilkinson et al., 1989). Although the functions of Hox genes in specifying rhombomere identity are well established, the genetic events leading to the deployment of Hox gene expression remain to be fully elucidated. This work focuses on the genetic hierarchy that establishes appropriate Hox gene expression in the caudal hindbrain, where specification of rhombomere (r) 5 and r6 identity involves the activation of Hox paralog group 3 (hox3) expression and the repression of hox1 gene expression.

Previous work has shown that the transcription factors MafB and Krox20 are direct regulators of Hox gene expression in r5 and r6. Kreisler (Kr) and valentino (val), the mouse and zebrafish orthologs of mafB, respectively, are required for normal r5 and r6 development (Cordes and Barsh, 1994; McKay et al., 1994; Moens et al., 1996; Moens et al., 1998; Prince et al., 1998) and MafB has been shown to activate hoxb3 and hoxa3 expression directly in transgenic mice (Manzanares et al., 1997; Manzanares et al., 1999a; Manzanares et al., 2001; Manzanares et al., 2002). Krox20 is required for the maintenance of r3 and r5 identity (Schneider-Maunoury et al., 1997) and cooperates with Kr to regulate hoxb3 directly in r5 (Manzanares et al., 2002). Furthermore, hox3 genes are both necessary and sufficient for the development of somatic motoneurons in the hindbrain (Gaufo et al., 2003; Guidato et al., 2003).

Since mafB/Kr/val plays an important and conserved role in the control of r5 and r6 specification, significant effort has been made to understand how its expression is established in the
developing hindbrain. Several inputs onto \textit{mafB/Kr/val} expression have been identified: retinoic acid (RA) signaling is necessary for acquisition of all hindbrain fates posterior to \textit{r3}, including expression of \textit{mafB/Kr/val}, as determined by pharmacologic and genetic disruption of RA production or activity (Dupe and Lumsden, 2001; Gavalas and Krumlauf, 2000; Linville et al., 2004; Wendling et al., 2001). Transplantation and genetic mosaic analyses have suggested that the relevant source of RA for posterior hindbrain patterning appears to be the trunk paraxial mesoderm (Begemann et al., 2001; Gould et al., 1998). Secondly, \textit{variant hepatocyte nuclear factor1} (vhnf1; \textit{tcf2} – Zebrafish Information Network), a homeodomain transcription factor expressed throughout the posterior hindbrain and anterior spinal cord, was identified in a genetic screen in the zebrafish as a positive regulator of \textit{val} (Sun and Hopkins, 2001). Finally, work in zebrafish showed that \textit{r4} is a source of \textit{Fgf3} and Fgf8, which are required for the patterning of surrounding rhombomeres, including the initiation of \textit{val} expression (Maves et al., 2002; Walshe et al., 2002). Wiellette and Sive (2003) have recently demonstrated that Fgfs and Vhnf1 synergize to drive the expression of both \textit{val} and krox20 in \textit{r5}.

Specification of \textit{r5} and \textit{r6} identities requires not only the activation of \textit{r5}- and \textit{r6}-specific gene expression, but also the repression of \textit{r4}-specific gene expression. Recent work in the zebrafish has shown that Vhnf1 represses \textit{hoxb1a} in a \textit{val}-independent manner (Wiellette and Sive, 2003), while other work in the mouse has shown that \textit{hox3} genes, which are targets of \textit{MafB/Kr/Val}, are required for \textit{hoxb1} repression (Gaufo et al., 2003). The role of \textit{MafB/Kr/Val} itself in the repression of \textit{hoxb1} is controversial; while some posterior expansion of \textit{hoxb1} expression in mouse \textit{Kr} mutants and zebrafish \textit{val} mutants has been reported (McKay et al., 1994; Prince et al., 1998), little expansion of a \textit{Hoxb1-r4} reporter transgene was observed in \textit{Kr} mutants (Manzano et al., 1999b).

We have investigated how global RA signals, local FGF signals and \textit{vhnf1} expression are integrated to specify \textit{r5} and \textit{r6} in the developing zebrafish hindbrain. We show that RA signals are essential for the activation of \textit{vhnf1} expression and that Vhnf1 acts downstream of RA signaling to drive \textit{val} expression. Secondly, we show that Vhnf1 strictly requires \textit{r4}-derived Fgf signals, probably through the Map kinase cascade, to initiate \textit{val} expression. Vhnf1 therefore integrates local \textit{r4}-Graf signals with global positional information provided by RA to specify \textit{r5} and \textit{r6} identities. We have also investigated how Vhnf1 and Val contribute to the repression of \textit{r4}-specific gene expression in the \textit{r5-6} territory. We find that repression of \textit{r4} gene expression in the \textit{r5-6} territory is initially established in a \textit{vhnf1}-independent manner, but that \textit{vhnf1} is then rapidly required to reinforce this restriction. By contrast, \textit{val} plays a relatively minor and late role in the repression of \textit{hoxf1/r4-identity}. Thus, specification of \textit{r5} and \textit{r6} identity is achieved through temporally and genetically distinct steps that establish and then maintain repression of \textit{r4} identity, as well as activating \textit{r5}- and \textit{r6}-specific gene expression. Furthermore, we find that different aspects of rhombomere identity, specifically those determining neuronal identity and those determining cell-surface character, are regulated independently. As a consequence, cells with very different ‘\textit{hox} codes’ can mix freely in genetic mosaics because they share an ‘\textit{Eph-ephrin} code.’

**Materials and methods**

**Zebrafish stocks, RNA in-situ hybridization, antibody staining and genetic mosaics**

Zebrafish strains and mutant alleles used in this study were *AB* for wild-type, \textit{valh335} (Moens et al., 1998), \textit{vhnf1hi2169} (Sun and Hopkins, 2001), \textit{acerebellar} (\textit{ace}) (Reifers et al., 1998) and \textit{neckless} (\textit{nls}) (Begemann et al., 2001).

Two color in RNA in-situ hybridization was performed essentially as described (Prince et al., 1998), except that in some cases BM-Purple (Roche) and Iodo-Nitrotetrazolium Violet (Sigma) were used as alkaline phosphatase substrates. For \textit{cyp26b1} a probe was synthesized by linearizing IMAGE clone 3722563 (Invitrogen) with \textit{SalI} and transcribing with SP6. Whole-mount immunohistochemistry, using the 3A10 antibody to detect Mauthner cells, was performed as described (Hatta, 1992), except a biotinylated secondary antibody and the ABC kit (Vector Labs) were used prior to detection with FITC-Tyramide (Perkin-Elmer). Genetic mosaic analysis was performed essentially as described (Moens and Fritz, 1999).

**Generation of \textit{Val}-monoclonal antibody, immunoblot analysis and genotyping**

A GST fusion protein, where GST was fused to the full open reading frame of \textit{Val}, was used to generate monoclonal antibodies in the FHCRC Biologics Facility. Immunoblotting was performed with hybridoma supernatant (1:4) essentially as described (Waskiewicz et al., 2001), except that NuPAGE sample buffer and 10% NuPAGE gels (Invitrogen) were used. Three embryo equivalents were loaded per lane.

Genotyping of embryos with respect to \textit{val} was performed as described (Moens et al., 1998). Genotyping for \textit{nls} was performed similarly with the primers 5'-GCTCCCAAGTAAAGTCTGACCT-3' and 5'-GGTTGGTCGAGAATGGACAGACAGA-3', followed by digestion with excess \textit{PstI}, which cuts the mutant allele.

**Morpholino injections, mRNA overexpression and pharmacological treatments**

Embryos lacking both \textit{Fgf3} and Fgf8 function were generated as described (Maves et al., 2002). mRNA for injections was generated using the mMessage mMachine kit (Ambion) and the following plasmids linearized with the indicated enzymes and used at the given final concentration: pCS2+\textit{vhnf1} (Sun and Hopkins, 2001), \textit{NotI}, 50 ng/\textit{l}; \textit{Pcs2}+\textit{fgf3} (Maves et al., 2002), \textit{NotI}, 25 ng/\textit{l}; \textit{psP64-T-cAMek} (Umbhauer et al., 1995), \textit{SalI}, 20 ng/\textit{l}; \textit{noggin-GFP} \textit{NotI}, 20 ng/\textit{l} (D. Kimelman, personal communication). For experiments involving the injection of more than one mRNA, total mRNA injected was normalized with \textit{eGFP} mRNA.

Pharmacological treatments of dechorionated embryos were performed in agarose- (1.2% in embryo medium) coated dishes as follows: AGN193109 (Agarwal et al., 1996) 10 \textmu M in 2% DMSO in embryo medium, all-trans \textit{RA} (Sigma) at given final \textmu M concentration in 0.1% ethanol in embryo medium.

**Results**

\textit{vhnf1} acts downstream of retinoic acid to drive \textit{val} expression

Both retinoid signaling and the transcription factor Vhnf1 have been shown to be required for \textit{val/mafb/Kr} expression in the posterior hindbrain (Gavalas and Krumlauf, 2000; Sun and Hopkins, 2001). Since the pattern and timing of \textit{vhnf1} expression resembles that of other RA-controlled genes in the hindbrain, such as \textit{hoxb1b} (Alexandre et al., 1996), we asked whether the requirement of RA for normal \textit{val/mafb/Kr} expression might be indirectly mediated via the control of \textit{vhnf1} expression by RA.
To determine if RA is sufficient for the induction of\textit{vhnf1} expression, we treated embryos with all-trans RA from 8.2 hours postfertilization (hpf) (70% epiboly) to approximately 10.7 hpf (2-3 somite stage). Embryos treated with all-trans RA exhibited a dose-dependent expansion of\textit{vhnf1} expression along the AP axis compared with solvent-treated controls (Fig. 1A,B and data not shown). To determine if\textit{vhnf1} expression requires RA signaling, zebrafish embryos were treated with the pan-retinoic acid receptor antagonist AGN193109 (Agarwal et al., 1996; Johnson et al., 1995) beginning at 4.5 hpf, prior to the onset of gastrulation, until approximately the 3 somite stage (11 hpf). $10^{-5}$ M AGN193109, which blocks expression of\textit{val} and other hindbrain markers caudal to r4 (Linvile et al., 2004) resulted in a severe reduction or complete loss of neural expression in all treated embryos ($n=103$, Fig. 1D). Furthermore,\textit{neckless (nls)} mutant embryos, which lack Raldh2, the final enzyme in the biosynthesis of all-trans RA (Begemann et al., 2001), exhibited reduced levels of\textit{vhnf1}, which blocks expression of\textit{val} in all treated embryos ($n=51/51$\textit{nls}–/– embryos vs. 5/98 wild-type siblings). The effect was most striking at the end of gastrulation, when\textit{nls}– embryos (Fig. 1F) had virtually no\textit{vhnf1} expression compared with the robust\textit{vhnf1} expression of their wild-type siblings (Fig. 1E).\textit{vhnf1} expression in\textit{nls}– embryos partially recovered by early somite stages (11 hpf), consistent with previous studies suggesting that RA signaling is attenuated, but not fully blocked, in zebrafish\textit{raldh2} mutants (Grandel et al., 2002).

To determine if\textit{vhnf1} functions downstream of RA to activate\textit{val/mafB/Kr}, we overexpressed\textit{vhnf1} in combination with $10^{-5}$ M AGN193019 treatment to block RA signaling. Solvent (DMSO)-treated embryos had essentially normal\textit{val} expression at 11.7 hpf (Fig. 1G), whereas only 2% of embryos treated with $10^{-5}$ M AGN193019 ($n=63$) had cells with strong\textit{val} expression (Fig. 1H). Overexpression of\textit{vhnf1} restored robust\textit{val} expression in 88% of embryos ($n=126$, Fig. 1J), demonstrating that\textit{vhnf1} functions downstream of RA in controlling\textit{val} expression. Together, these data demonstrate that RA probably contributes to the specification of r5 and r6 by inducing\textit{vhnf1} expression in the caudal hindbrain and therefore indirectly regulating\textit{val}.

\textbf{vhnf1 and Fgfs cooperate to drive\textit{val} expression}

Other work has shown that\textit{val} expression in r5 and r6 also depends on\textit{fgf3} and\textit{fgf8}, which are strongly expressed in r4 (Maves et al., 2002; Walsh et al., 2002). Expression of\textit{vhnf1} in the hindbrain does not require\textit{fgf3} and\textit{fgf8} expression in r4, and vice versa (data not shown and see below) (Wiellette and Sive, 2003). Therefore, we were interested in how Fgfs and\textit{vhnf1} interact to drive\textit{val} expression.

In order to determine if\textit{vhnf1} requires Fgf signaling for its ability to drive\textit{val}, we overexpressed\textit{vhnf1} in wild-type (wt) embryos and embryos lacking Fgf3 and Fgf8 function. In wt embryos, overexpression of\textit{vhnf1} by mRNA injection expanded the\textit{val} expression domain anteriorly (Fig. 2A,B) to include the r2-r4 territories. By contrast, overexpression of\textit{vhnf1} in embryos lacking Fgf3 and Fgf8 function did not drive\textit{val} expression in either its endogenous domain of r5 and r6 or ectopically in more anterior rhombomeres (Fig. 2C). These data demonstrate that activation of\textit{val} by\textit{vhnf1} strictly depends on Fgf signaling.

We hypothesized that if Fgfs and\textit{vhnf1} synergize to drive\textit{val} expression, then overexpression of\textit{fgf3} and\textit{vhnf1} together would drive broad ectopic expression of\textit{val} in zebrafish embryos. We overexpressed\textit{vhnf1} and\textit{fgf3} either alone or together and assessed\textit{val} expression by both in-situ hybridization and immunoblotting at the mid-gastrula stage (8.25 hpf, 80% epiboly), just prior to the normal onset of\textit{val} expression. Overexpression of\textit{fgf3} alone did not result in ectopic\textit{val} expression (Fig. 2E), nor did it result in a significant anterior expansion of\textit{vhnf1} expression (data not shown);
overexpression of vhnf1 alone mildly upregulated val (Fig. 2F).
By contrast, overexpression of fgf3 and vhnf1 together caused a
dramatic upregulation of val expression throughout the
embryo (Fig. 2G), correlating with a dramatic increase in Val
protein as assessed by immunoblotting (Fig. 2D’-G’). This
result is specific and not simply the result of dorsalization
by ectopic fgf3, since co-injection of vhnf1 with noggin,
a dorsalizing BMP antagonist (Furthauer et al., 1999;
Zimmerman et al., 1996), did not induce robust val expression
(Fig. 2H,I,H’). Similarly, wnt8-orf1 (Lekven et al., 2001),
another classic posteriorizing factor, failed to cooperate with
vhnf1 to induce robust val expression (data not shown).
Wiellet and Sive (Wiellet and Sive, 2003) obtained similar
results using a combination of vhnf1 overexpression and Fgf-
bead implantation. Our data demonstrate that vhnf1 and Fgf
signaling are capable of globally activating val expression
along the entirety of the anterior-posterior axis in both the
epiblast and hypoblast.

One of the key downstream effectors of Fgf signaling is the
Ras-Map kinase (MapK) signaling cascade (Powers et al.,
2000). To determine if Fgf signaling through MapK synergizes
with vhnf1 to drive val, we coexpressed vhnf1 with a
constitutively active MapK/ERK kinase (caMek) mRNA
(Umbhauer et al., 1995). caMek alone did not drive val
expression (Fig. 2I) but cooperated with vhnf1 to drive val
expression in a manner similar to that of Fgf (Fig. 2K).

The normal expression of val in r5 and r6 is dependent on a
positive autoregulatory loop (Giudicelli et al., 2003; Moens et
al., 1998). In order to determine if the vhnf1-fgf3 interaction
we observed is dependent on this positive autoregulatory loop,
we repeated the vhnf1-fgf3 overexpression experiments in
embryos from a val+/− intercross. We found that strong
expression of val at 8.5 or 12 hpf correlated with wt or
heterozygous genotype (94%, n=98, Fig. 2L), while nearly all
embryos with little to no val expression were mutant (88%,
n=51, 2M). These data suggest that val autoregulation is
required for vhnf1 and fgfs to drive robust val expression.

Vhnf1 controls some aspects of rhombomere
identity independently of Val

The above data and that of others demonstrate that RA activates
vhnf1, which in cooperation with Fgfs is both necessary and
sufficient to drive expression of val in r5 and r6. To determine
whether vhnf1 performs all its functions in hindbrain
development through its regulation of val, or whether the
functions of val and vhnf1 are in part separable, we carefully
compared molecular and neuroanatomical markers of
rhombomere identity in val−/− and vhnf1−/− embryos. If the
principal role of vhnf1 in specifying hindbrain fates is the
initiation of val expression, val− and vhnf1− embryos should
exhibit identical phenotypes.

Both val and vhnf1 mutant embryos failed to develop a
recognizable r5-r6 territory. This is exemplified by the loss of
r5 krox20 expression (Fig. 3A-C), of hox3 gene expression and
of r5-6 specific abducens motoneurons (data not shown) in
both mutants. However, there are subtle differences in the
two mutant phenotypes. For example, in val mutants the remnant
of r5 krox20 expression is always in the dorsalmost hindbrain
(Fig. 3B), while vhnf1 mutants often have fewer krox20-
positive cells than do val mutants and many of the cells are
located ventrally (Fig. 3C). Furthermore, the r5-6 region of val
mutants is about the length of a single rhombomere (Moens et
al., 1996), while that of vhnf1 mutants is the same as in wild-
type embryos (data not shown). This is unexpected if vhnf1
performs all its functions through val.

A stark difference between vhnf1− and val− embryos became
apparent when we examined the expression of r4 markers. The
transcription factor hoxb1a is initially expressed posterior to the

Fig. 2. vhnf1 and Fgfs cooperate to drive val expression. (A-C) vhnf1
requires Fgfs to drive val expression in the hindbrain. At 18 hpf val
(blue) is normally expressed in r5 and r6 (A); krox20 expression in r5
and r5 and eng3 at the mid-hindbrain boundary (MHB) is in red.
After injection of vhnf1 mRNA (50 pg), val expression expands
anteriory to approximately the level of r2 (B). By contrast, vhnf1
overexpression in fgf3−/−fgf8− embryos does not drive val expression
(C). (D-I) vhnf1 and fgfs cooperate to drive val expression. val (blue)
is not normally expressed at 8.25 hpf (D), and injection of fgf3
mRNA (25 pg) alone is not sufficient to induce val (E). vhnf1 mRNA
alone will induce a low level of val (F), while vhnf1 and fgf3 together
induce val at a high level (G). Injection of noggin-gfp mRNA (20 pg)
causes a dorsalization similar to fgf3 but when injected alone (H) or
with vhnf1 mRNA (I) it does not induce val. (D’-I’) Val protein is
upregulated similarly to transcript levels at 8.25 hpf following
mRNA injection (as in D-I), as detected by anti-Val immunoblot of
lysed embryos. (J,K) Overexpression of caMek mRNA (20 pg) alone
does not induce val expression (J) but like fgf3 can cooperate with
vhnf1 to do so (K). (L,M) Robust upregulation of val downstream of
fgf3 and vhnf1 requires val autoregulation. 12 hpf val+/− and val−/−
embryos expressing vhnf1 and fgf3 exhibit robust val expression (L),
while little or no val is detected in val+/− embryos (M). A-C, are
dorsal views with anterior to the left. D-M are optical cross sections
near the dorsal midline.
...and Hopkins, 2001) compared with wt and vhnf1− expression just posterior to r4. Shortly thereafter (11.7 hpf) vhnf1− embryos were initially normal in gastrulation (Maroon et al., 2002; Maves et al., 2002), was expression, which is normally restricted to r4 at the end of expansion and upregulation of hoxb1a embryos (B) compared with the variable dorsal and ventral expression in vhnf1− embryos (C). (D-L) Repression of hoxb1a (blue) in r5 and r6 requires multiple genes. hoxb1a is initially downregulated posterior to r4 (asterisks) at 10.7 hpf in wt (D), val− (E) and vhnf1− (F) embryos. By 11.7 hpf hoxb1a expression is largely restricted to r4 in wt (G) and val− (H) embryos but is upregulated posterior to r4 in vhnf1 mutants (I). At 18-20 hpf hoxb1a is clearly expanded in vhnf1 mutants (L) and mildly expanded in val mutants (K) compared with wt (J). (M-R) fgf3 (blue) expression is similar between wt (M), val− (N) and vhnf1− (O) embryos at 10.5 hpf. By 11.7 hpf fgf3 is normally only highly expressed in r4 (P), while in vhnf1 mutants (R) its expression expands posteriorly. (S-U) Expression of the RA-metabolizing enzyme cyp26b1 is restricted to r4 and r3 at 12 hpf in wt (S) val− (T) and vhnf1− (U) embryos. Expression of fgf8 is also limited to r4 and anterior by 12 hpf in wt (V) val− (W) and vhnf1− (X) embryos. (Y-AA) A single pair of Mauthner cells is present in r4 of wt (Y) and val− (Z) embryos, while supernumerary Mauthner cells are detected in 58% of vhnf1− embryos (AA; arrowhead). A-C are lateral views with anterior to the left and dorsal to the top. D-AA are dorsal views with anterior to the left. krox20 expression in r3 and r5 is in red (D-X). The mid-hindbrain boundary (MHB) is marked by pax2.1 (blue, J-L; red, M-O) or en3 (red, P-R).

r3-4 boundary and is subsequently upregulated in r4 and downregulated posteriorly (Prince et al., 1998). Expression of hoxb1a at 10.5 hpf was essentially unchanged in val− and vhnf1− embryos compared with wt (Fig. 3D-F), with all embryos demonstrating an upregulation of hoxb1a in r4, and a slightly lower level of expression just posterior to r4. Shortly thereafter (11.7 hpf) vhnf1− embryos showed a pronounced posterior expansion and upregulation of hoxb1a expression (Fig. 3I) (Sun and Hopkins, 2001), compared with wt and val− embryos (Fig. 3G,H). At 18 hpf, expansion of hoxb1a expression in vhnf1 mutants persisted in the domain that would normally adopt r5-6 fates (Fig. 3L). By contrast, the hoxb1a expression in val− embryos expanded only very weakly posterior to r4 (Prince et al., 1998) and in a more limited domain compared with that of vhnf1− embryos (compare Fig. 3K,L). Similarly, fgf3 expression, which is normally restricted to r4 at the end of gastrulation (Maroon et al., 2002; Maves et al., 2002), was initially normal in vhnf1− embryos (Fig. 3M-O). However, fgf3 expression expanded posteriorly over the subsequent few hours in vhnf1 mutants compared with wt and val mutants (Fig. 3P-R).

While some r4 markers behave differently in vhnf1 and val mutants, other r4 markers are unaffected in either mutant. cyp26b1, which encodes a retinoic acid-degrading enzyme, is expressed in r4 beginning at tailbud stage and expands to include r3 by 12 hpf (R.E.H. and C.B.M., unpublished). fgf8 is expressed in a domain anterior to the r4-5 boundary at 12 hpf (Reifers et al., 1998). Surprisingly, neither marker was expanded posterior to r4 in either val or vhnf1 mutants at a stage when hoxb1a was strongly expanded in vhnf1 mutants (Fig. 3S-X).

Wiellette and Sive (Wiellette and Sive, 2003) reported that the Mauthner cell, a large identified reticulospinal neuron characteristic of r4, is duplicated in more posterior segments in vhnf1 mutants. Our finding that the transformation to r4 identity in vhnf1 mutants was incomplete based on marker gene expression led us to reexamine Mauthner cell specification. We found that only 58% of mutants had one or more supernumerary Mauthner cells, consistent with an incomplete transformation (n=19, Fig. 3AA). val mutants never had supernumerary Mauthner cells (n=19, Fig. 3Z), consistent with only a very weak anterior transformation.

Taken together, our marker analysis demonstrates that vhnf1 function in hindbrain patterning is only partially executed through its activation of val. Both vhnf1 and val are required for upregulation of r5 and r6 markers, but vhnf1 functions largely independently of val to repress some aspects of r4...
identity. However, even in the absence of *vhnf1* function the r5-6 territory appears to be specified properly initially, including transient restriction of r4-specific genes. *vhnf1*, but not *val*, is strongly required to maintain repression of some, but not all, r4 markers, and the partial transformation of the r5-6 region of *vhnf1* mutants to r4 identity correlates with a variable gain of r4-specific neurons.

**vhnf1** and **val** mutant cells behave equivalently in genetic mosaic analysis

Individual rhombomeres have specific cellular surface characteristics and the involvement of individual genes in the acquisition of this aspect of rhombomere identity can be determined by genetic mosaic analysis. Previous work has shown that *val* is required cell autonomously for the acquisition of r5 and r6 identity (Moens et al., 1996). Similarly, *vhnf1* mutant cells were excluded from r5 and r6 of wild-type hosts (Fig. 4B, n=20, compare with control in Fig. 4A), only occasionally contributing to the r5-6 boundary of the host hindbrain. Conversely, wild-type cells typically formed compact clusters within the presumptive r5-6 of *vhnf1*– hosts (arrowheads in Fig. 4C, n=29) and the clusters of cells located in the presumptive r5 expressed krox20. These dense clusters were unilateral, consistent with a failure of the transplanted wild-type cells to make a characteristic division that requires single cells to insert themselves across the midline (Geldmacher-Voss et al., 2003; Kimmel et al., 1994). These data demonstrate that *vhnf1* is required cell autonomously for cells to acquire r5 and r6 identities.

Our marker analysis demonstrated that *vhnf1*– and *val*– embryos have unique molecular phenotypes: based on Hox gene expression, the r5-6 region of *vhnf1*– embryos is strongly transformed to r4 identity, while this region of *val* mutants has an indeterminate hox-less ‘rX’ identity. Therefore we anticipated that *vhnf1*– and *val*– cells would behave differently in genetic mosaics. Specifically, we predicted that while neither *val*– nor *vhnf1*– cells can contribute to r5 and r6 of wild-type hosts (as observed above), *val*– cells lying in the expanded r4-like domain of a *vhnf1* mutant host would adopt ‘rX’ identity and would therefore be unable to contribute. Similarly, we predicted that r4-like *vhnf1*– cells lying in ‘rX’ of a *val*– host would be excluded from this territory. However, we did not observe this to be the case. *vhnf1*– cells transplanted into a *val*– host embryo (Fig. 4D, n=15), and conversely *val*– cells transplanted into a *vhnf1*– host embryo (Fig. 4E, n=17), were able to contribute throughout the hindbrain, including the respective mis-specified r5-6 regions (brackets in Fig. 4D,E). These data suggest that, although the presumptive r5-6 regions of *vhnf1*– and *val*– embryos have distinct molecular identities at the level of hoxb1a and fgf3 expression, the cellular surface characteristics of *vhnf1*– and *val*– cells in this region of the hindbrain are identical.

Cell sorting in the hindbrain is probably controlled by repulsive interactions between Ephs and Ephrins (Cooke et al., 2001; Mellitzer et al., 1999; Xu et al., 1999). Therefore, we determined whether the cell-surface properties of *val*– and *vhnf1*– cells observed in our mosaic analysis were reflected in Eph and ephrin expression patterns. In spite of marked differences in hoxb1a and fgf3 expression in the two mutants, Eph and ephrin expression were very similar. In both *vhnf1*– and *val*– embryos, expression of EphB4a in r5 and r6 and of EphA4 in r5 was greatly reduced (Fig. 4F-H and data not shown); this reflects changes in krox20 and hox3 expression, which were also similar in the two mutants. By contrast, ephrin-B2a, which is normally not expressed in r5 or r6, was expanded in both *val*– and *vhnf1*– embryos (Fig. 4I-K) (Cooke et al., 2001). The similar cell-sorting behavior of *vhnf1*– and *val*– cells in genetic mosaics would not have been predicted by the examination of Hox expression alone. These results demonstrate that rhombomere-specific neuronal identity as determined by a ‘hox code’ can be unlinked from rhombomere-specific cell-surface properties as determined by an ‘Eph-ephrin code’.
Ectopically expressed \( \text{vhnf1} \) represses \( \text{hoxb1a} \) and \( \text{r4-ephrin-B2a} \) in a \( \text{val} \) dependent manner

The expression of \( \text{hoxb1a} \) and \( \text{ephrin-B2a} \) in \( \text{vhnf1} \) mutants suggests that \( \text{vhnf1} \) normally represses the expression of these two genes. Since \( \text{ephrin-B2a} \) expression is significantly expanded in \( \text{val} \) embryos while \( \text{hoxb1a} \) is not, we hypothesized that \( \text{vhnf1} \) repression of \( \text{ephrin-B2a} \) requires \( \text{val} \) while \( \text{vhnf1} \) repression of \( \text{hoxb1a} \) does not. In order to test this hypothesis, we overexpressed \( \text{vhnf1} \) in embryos from an intercross of heterozygous \( \text{val} \) fish and then assessed the expression of \( \text{hoxb1a} \) and \( \text{ephrin-B2a} \) by in-situ hybridization.

Consistent with \( \text{vhnf1} \) playing a role in the repression of \( \text{hoxb1a} \) and \( \text{ephrin-B2a} \), we observed that wild-type embryos injected with \( \text{vhnf1} \) mRNA showed repression of \( \text{hoxb1a} \) (88%, \( n=114 \)) and \( \text{ephrin-B2a} \) (88%, \( n=91 \)) in \( r4 \) at about 5-9 somites (11.5-13 hpf). Many of these embryos had nearly a complete loss of the \( r4 \) \( \text{hoxb1a} \) or \( \text{ephrin-B2a} \) domain, with only a few \( \text{hoxb1a} \) (Fig. 5B) or \( \text{ephrin-B2a} \) (Fig. 5F) positive cells remaining between two-fused \( krox20 \) stripes. However, essentially no homozygous \( \text{val} \) embryos showed repression of \( \text{hoxb1a} \) (6%, \( n=51 \), Fig. 5D) or \( \text{ephrin-B2a} \) (0%, \( n=33 \), Fig. 5H) in \( r4 \) following overexpression of \( \text{vhnf1} \).

These data demonstrate that, as predicted, \( \text{val} \) is required for the repression of \( \text{ephrin-B2a} \). Furthermore, although \( \text{val} \) is not required to repress \( \text{hoxb1a} \) in the \( r5-6 \) region (Fig. 3H), it is required to repress \( \text{hoxb1a} \) when \( \text{vhnf1} \) is overexpressed in \( r4 \). This suggests that in addition to \( \text{Val} \) cooperating with \( \text{Vhnf1} \) to repress \( \text{hoxb1a} \), another factor, expressed in \( r5/6 \) but not in \( r4 \), may cooperate with \( \text{Vhnf1} \) in the \( r5/6 \) region to repress \( \text{hoxb1a} \) in a manner that is partially redundant with \( \text{val} \).

Discussion

Our data, together with that of others, suggest a model (Fig. 6) in which RA signaling activates \( \text{vhnf1} \) expression posterior to the \( r4-5 \) boundary. The expression of \( \text{Vhnf1} \) is sufficient to repress the \( r4 \) ‘\( \text{hox} \) code’ posterior to \( r4 \), including expression of \( \text{hoxb1a} \), which specifies \( r4 \) neurons. \( \text{Vhnf1} \) cooperates with \( \text{Fgf} \) signals from \( r4 \) to initiate the expression of \( \text{val} \) in \( r5 \) and \( r6 \). Subsequently \( \text{Val} \) activates the expression of \( \text{hox3} \) genes and others to specify \( r5-6 \)-specific neuronal development. Furthermore, though \( \text{Val} \) is not strictly required to repress the majority of \( r4 \)-specific \( \text{hox} \) gene expression in the \( r5-6 \) territory, it is required to both repress \( r4 \) and upregulate \( r5-6 \) cell-surface characteristics via an ‘\( \text{Eph-ephrin} \) code’.

The data presented in Fig. 1 demonstrates that this is probably due to a primary effect of RA on \( \text{vhnf1} \) expression, since RA is both required and sufficient for \( \text{vhnf1} \) expression, and \( \text{vhnf1} \) can rescue \( \text{val/mafB/Kr} \) expression in embryos in which RA signaling is blocked.

\( \text{vhnf1} \) integrates global RA patterning with \( r4 \)-derived \( \text{Fgf} \) signals

Previous work showed that \( \text{val/mafB/Kr} \) expression is reduced or lost after RAR antagonist treatment or genetic ablation of RA biosynthesis (Gavalas and Krumlauf, 2000; Linville et al., 2004). The data presented in Fig. 1 demonstrates that this is probably due to a primary effect of RA on \( \text{vhnf1} \) expression, since RA is both required and sufficient for \( \text{vhnf1} \) expression, and \( \text{vhnf1} \) can rescue \( \text{val/mafB/Kr} \) expression in embryos in which RA signaling is blocked.

**Fig. 5.** When overexpressed, \( \text{vhnf1} \) requires \( \text{val} \) for its ability to repress both \( \text{hoxb1a} \) and \( \text{ephrin-B2a} \) in \( r4 \). Overexpression of \( \text{vhnf1} \) by mRNA injection (25 pg) represses \( \text{hoxb1a} \) (blue) in \( r4 \) of wild-type (B) but not \( \text{val} \) mutant embryos (D). Similarly, injection of \( \text{vhnf1} \) mRNA represses \( \text{ephrin-B2a} \) in \( r4 \) of wild-type (F) but not \( \text{val} \) mutant embryos (H). Dorsal views of 11.5-13 hpf embryos, anterior to the left, with \( krox20 \) in red.

**Fig. 6.** A model for the functions of \( \text{vhnf1} \) and \( \text{val} \) in directing hindbrain development. RA activates \( \text{hoxb1b} \) and \( \text{hoxb1a} \) expression to initiate an \( r4 \) development program, including the specification of Mauthner neurons. An unknown factor, ‘\( X \)’, initially represses \( \text{hoxb1a} \) in \( r5 \) and \( r6 \), independent of \( \text{vhnf1} \). RA activates \( \text{vhnf1} \) expression, which reinforces repression of \( \text{hoxb1a} \) expression in \( r5 \) and \( r6 \), possibly in cooperation with an unknown co-factor, which may or may not be the same ‘\( X \)’ above. Repression of \( \text{hoxb1a} \) by \( \text{Vhnf1} \) blocks acquisition of \( r4 \) neuronal fates in \( r5 \) and \( r6 \), but \( \text{Vhnf1} \) must act through \( \text{Val} \) to drive \( r5-6 \) neuronal development, including abducens cranial motor neurons (CMNs). Furthermore, \( \text{Val} \) is required for the acquisition of \( r5-6 \)-specific cell-surface characteristics by both activating \( r5-6 \) \( \text{EphB4a} \) expression and repressing \( r4 \)-like \( \text{ephrin-B2a} \) expression in \( r5 \) and \( r6 \). Finally, \( \text{Val} \) contributes to the maintenance of \( \text{hoxb1a} \) repression at later stages, possibly through activation of \( \text{hox} \) group 3 genes.
It remains unclear whether the activation of vhnf1 by RA is direct, as has been determined for some Hox genes (Dupe et al., 1997; Gould et al., 1998; Marshall et al., 1994), or if it acts through a more indirect mechanism. Members of the steroid nuclear receptor superfamily, including RARs, can bind a DR1 motif upstream of murine Vhnf1, and the DR1 is required for full reporter activity in cultured cells, but it is unclear if this element mediates retinoic acid responsiveness (Power and Cereghini, 1996). Pbx proteins, which function as DNA-binding partners for Hox proteins, are also required for normal hindbrain expression of vhnf1 (Waskiewicz et al., 2002). Since Pbx proteins are not known to be required for RA synthesis or to be regulated by RA, their requirement for vhnf1 expression is likely to be either independent or downstream of RA signaling. A careful analysis of the vhnf1 promoter will help elucidate which proteins directly regulate vhnf1 in the hindbrain.

**vhnf1 and Fgfs synergize to drive val expression**

We have shown that vhnf1 and Fgfs cooperate to drive val expression and specify r5 and r6 fates. Using Fgf-coated beads, Wiellette and Sive (Wiellette and Sive, 2003) demonstrated a similar synergy between Fgf and vhnf1. Our results support and extend their findings, by showing that unlike RA signals, Fgf signals are strictly required for vhnf1 to induce val expression, since vhnf1 cannot drive val expression in an embryo lacking fgf3 and fgf8. Furthermore, we demonstrate that Fgf signaling through the MapK pathway is sufficient to cooperate with vhnf1 in inducing val expression, and that robust upregulation of val by Vhnf1 and Fgfs requires a positive autoregulatory loop that is dependent on Val function.

The control of val expression by vhnf1 is probably conserved across vertebrates. vhnf1 is expressed in the hindbrain of mouse embryos in a similar domain to that in zebrafish, but its requirement for hindbrain development has not been determined because homozygous mutant mice have defects in visceral endoderm development and die prior to gastrulation (Coffinier et al., 1999). Inactivation of vhnf1 in the embryonic tissues or CNS alone will be required to test the requirement for vhnf1 in mammalian hindbrain patterning.

At this point it is unclear whether vhnf1 acts directly or indirectly to regulate expression of val, and little is known about the direct regulation of the val locus. The classical *kreisler* mutation, an inversion approximately 30 kb upstream of the transcriptional start of *Kr/MafB*, disrupts a regulatory element that is specifically required for expression in r5 and r6 but not sites outside the hindbrain (Cordes and Barsh, 1994; Eichmann et al., 1997). This and other data (Hamada et al., 2003) suggest that elements controlling the hindbrain expression of val/mafB/Kr are rather distant from the gene. We have identified a consensus Hnf1-binding site (CTGTATACATAACA) within a highly conserved island of homology (85% identity over 500 base pairs) approximately 22.5 kb upstream of the *MafB/Kr* gene of humans and mice (data not shown). However, we have as yet been unable to identify a corresponding island in the available genomic sequence from either *fugu* or zebrafish. Further analysis is necessary to determine if this potential Hnf1 binding site has any role in regulating hindbrain expression of *val/mafB/Kr*.

Although our data and that of Wiellette and Sive (Wiellette and Sive, 2003) show that Fgfs synergize with Vhnf1 to drive val expression, the mechanism underlying this effect is unclear. Our data suggest that Fgf signaling through the MapK cascade promotes Vhnf1 protein activity. We considered the possibility that MapKs may directly regulate Vhnf1 by phosphorylation. However, Vhnf1 is a poor substrate for Erk2 in an in-vitro assay and has only marginal consensus MapK phosphorylation sites (data not shown). More indirect mechanisms, in which MapK-signaling activates other proteins or expression of intermediate target genes, remain to be investigated.

**Different aspects of rhombomere identity are regulated independently by Val and Vhnf1**

The specification of r5 and r6 identities requires both the activation of r5- and r6-specific genes and the repression of r4-specific genes. Our data demonstrate that while vhnf1 and val probably function in a linear pathway to activate r5- and r6-specific genes, the repression of r4-specific genes is more complex. Vhnf1 functions through Val to repress *ephrin-B2a* and thus repress r4-specific cell-surface properties, but it does not require Val to repress *hoxb1a* and thus repress r4-specific neuronal differentiation. As a result, vhnf1 and val mutants have different ‘hox codes’ and patterns of neuronal differentiation, but have similar ‘Eph-ephrin codes’ and cell behaviors in genetic mosaics. These results show that different aspects of segment identity, in this case neuronal phenotype and cell-surface character, can be regulated independently.

**vhnf1 and val participate in a multistep process to repress the r4 ‘hox code’**

Wiellette and Sive (Wiellette and Sive, 2003) propose that a sweep of r4 identity from posterior to the r3/4 boundary is subsequently restricted to r4 by the expression of vhnf1. However, the expansion of r4 fates in vhnf1 mutants is not complete, suggesting that multiple factors are required for the restriction of r4 fates.

Our analysis of r4 marker expression shows that *hoxb1a* expression is transiently downregulated posterior to r4 in vhnf1 mutants, as in wt embryos. Thus, an unknown factor functions to repress the earliest *hoxb1a* expression in the presumptive r5/6 territory. After the onset of its expression, vhnf1 rapidly becomes the primary repressor of *hoxb1a* expression. However, vhnf1 does not repress all r4-specific gene expression as predicted by Wiellette and Sive (Wiellette and Sive, 2003), since *fgf8* and *cytochrome b* are restricted anterior to the r4/5 boundary even in vhnf1 mutants. As a result, the expanded r4 territory in vhnf1 mutants has different molecular identity from r4 proper. Consistent with this incomplete transformation, the duplication of r4-specific Mauthner cells in vhnf1 mutants is not fully penetrant. Together, these results show that r4 is distinguished from the more posterior hindbrain by more than simply the expression of vhnf1 posterior to the r4-5 boundary.

Once the repression of *hoxb1a* is strongly established by Vhnf1, the expression of vhnf1 recedes from the hindbrain. This coincides with the period that *hoxb1a* expands slightly in *val* embryos (Prince et al., 1998), suggesting that Val is required at later stages to maintain repression of *hoxb1a* in r5 and r6. Val may function to repress *hoxb1a* by activating *hox3* genes, which have been shown to be required for the maintained repression of *hoxb1* in the mouse (Gaufo et al., 2003).
**val** is required for the repression of the r4 ‘Eph-ephrin’ code and the establishment of r5-6 cell adhesive properties

Wiellette and Sive (Wiellette and Sive, 2003) suggested that vhnf1 may function non-autonomously through an unknown signal to specify the most anterior r5 fates, because they did not observe vhnf1 expression extending to the r4-5 boundary. We have seen that the domain of vhnf1 expression does include the entire r5 domain of krox20 expression (Fig. 1A). Furthermore, our mosaic analysis demonstrates that vhnf1 is required cell-autonomously for the acquisition of r5 and r6 fates (Fig. 4B,C), since vhnf1− cells are excluded from r5 and r6 of wild-type hosts.

In the absence of either val or vhnf1, cells in the r5-6 region acquire the same cell-surface properties as determined by reciprocally transplanting cells between the two mutants (Fig. 4D,E). This is in direct contrast to the distinct molecular phenotypes of the two mutants, including hoxb1a expression, but correlates with their similar patterns of Eph and ephrin expression. Cooke and colleagues (Cooke et al., 2001) demonstrated that cell sorting in val mosaics was attributable to repulsive signals between val− ephrin-expressing cells and wt Eph-expressing cells; the same mechanism probably explains the cell sorting we observed in vhnf1 mosaics. The similar effects on Eph and ephrin expression in val and vhnf1 mutants, and our observation that vhnf1 requires val to repress ephrin-B2a when it is overexpressed, suggest that vhnf1 functions through val to specify the cell-surface character of the r5-6 region, including repression of r4-specific adhesive character (i.e. ephrin-B2a).

Together, our data support a multistep model for the initial restriction of r4 identity and the specification of r5-6 development (Fig. 6). r4 identity is initially restricted by the repression of hoxb1a in the presumptive r5-6 region by an unknown, val-independent mechanism. vhnf1 expression is activated by RA up to the r4-5 boundary and strictly reinforces the restriction of hoxb1a to r4, thereby limiting the expression of fgf3 and development of r4-specific Mauthner neurons. Vhnf1 also cooperates with Fgfs expressed in r4 to activate the expression of val and the r5-6 program of development. val subsequently drives the expression of r5-6 specific Hox genes and the development of r5-6-specific neurons. Although val is not strongly required for the repression of hoxb1a expression, it is required for the repression of r4-like cell-surface characteristics that drive cell sorting as mediated by Eph and ephrin expression. The different requirements for vhnf1 and val in the specification of ‘hox’ code and ‘Eph-ephrin code’ demonstrate that the mechanisms that specify segmental neuronal identity and differential cell-surface characteristics between rhombomeres in the hindbrain can be independently regulated. Previous work showing that Eph and ephrin expression are regulated by krox20 and val/mab2/Kr rather than by Hox genes (Cooke et al., 2001; Theil et al., 1998) had predicted that cell-surface characteristics could be regulated independently from other aspects of segment identity. However, due to cross-regulation between krox20, val and Hox genes, Hox expression and Eph-ephrin expression are generally coupled, so this prediction has not been tested. Our discovery of an instance in which Hox expression and Eph-ephrin expression are unlinked has allowed us to show directly that neuronal identity corresponds with ‘hox code’, while cell sorting behaviors correspond with ‘Eph-ephrin code’.

We wish to thank A. Waskiewicz and J. Stout for making the anti-Val antibody. We also thank a number of colleagues for providing reagents: N. Hopkins for the vhnf1 mutant and expression constructs, P. Ingham for the neckless mutant, J. Smith for the caMek expression construct, D. Kimelman for the noggin-off expression construct. Allergan, Inc. provided the AGN193109 antagonist. Finally, we wish to thank L. Maves, T. Schilling, S. Collins and current and former members of the Moens lab for their input during the course of this work, including helpful comments on the manuscript. R.E.H. was supported by NIH Training Grants 2T32 HD07183 and NIGMS T32 07266, a Cora May Poncin Scholarship and an ARCS-WSRF Fellowship. R.B. was supported by a grant from the Swiss NSF and from the Fondation Eugenio Litta. This work was supported by NIH grant HD37909 and NSF grant 18N-9816805. C.B.M. is an assistant investigator with the Howard Hughes Medical Institute.

References


