Proper differentiation of photoreceptors and amacrine cells depends on a regulatory loop between NeuroD and Six6

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SUMMARY
Timely generation of distinct neural cell types in appropriate numbers is fundamental for the generation of a functional retina. In vertebrates, the transcription factor Six6 is initially expressed in multipotent retina progenitors and then becomes restricted to differentiated retinal ganglion and amacrine cells. How Six6 expression in the retina is controlled and what are its precise functions are still unclear. To address this issue, we used bioinformatic searches and transgenic approaches in medaka fish (Oryzias latipes) to characterise highly conserved regulatory enhancers responsible for Six6 expression. One of the enhancers drove gene expression in the differentiating and adult retina. A search for transcription factor binding sites, together with luciferase, ChIP assays and gain-of-function studies, indicated that NeuroD, a bHLH transcription factor, directly binds an ‘E-box’ sequence present in this enhancer and specifically regulates Six6 expression in the retina. NeuroD-induced Six6 overexpression in medaka embryos promoted unorganized retinal progenitor proliferation and, most notably, impaired photoreceptor differentiation, with no apparent changes in other retinal cell types. Conversely, Six6 gain- and loss-of-function changed NeuroD expression levels and altered the expression of the photoreceptor differentiation marker Rhodopsin. In addition, knockdown of Six6 interfered with amacrine cell generation. Together, these results indicate that Six6 and NeuroD control the expression of each other and their functions coordinate amacrine cell generation and photoreceptor terminal differentiation.

KEY WORDS: Neurogenesis, Retinal development, Transcription regulation, Medaka

INTRODUCTION
The vertebrate retina is a layered structure composed of six neuronal and one glial cell type, which are organised in three cellular layers: the ganglion cell layer, comprising retinal ganglion (RGC) and displaced amacrine cells, the inner nuclear layer (INL), which contains bipolar, horizontal and amacrine interneurons and Müller glial cells, and the outer nuclear layer (ONL), where rod and cone photoreceptors are located (Rodieck, 1998).

These cell types differentiate from common multipotent retinal progenitors in a loosely conserved temporal order, where RGCs are always the first to be generated. Although secreted factors, such as Fgf5 and Shh, are crucial for the onset and propagation of retinal differentiation (Esteve and Bovolenta, 2006; Martínez-Morales et al., 2005), combinations of proneural basic helix-loop-helix (bHLH) and homeodomain (HD)-type transcription factors (TFs) determine the intrinsic properties of retinal precursors and regulate their differentiation into specific cell types (Hatakeyama and Kageyama, 2004; Wang and Harris, 2005). For example, Ath5, a bHLH-TF, renders postmitotic retinal precursors competent to generate RGCs and activates the expression of HD-TFs such as Brn3 and Islet 1, which are required for RGC differentiation (Hatakeyama and Kageyama, 2004). Similarly, the bHLH TF NeuroD is expressed in postmitotic retinal cells that originate amacrine and photoreceptor cells, although with notable variations among vertebrate species (Liu et al., 2008; Moore et al., 2002; Ochocinska and Hitchcock, 2007; Ochocinska and Hitchcock, 2009; Yan and Wang, 1998). Co-expression of the HD-TF Crx drives NeuroD-positive progenitors toward the photoreceptor fate, activating rod- or cone-specific determinants (Hennig et al., 2008). Although similar TF combinations have also been determined for the remaining retinal neurons (Hatakeyama and Kageyama, 2004; Wang and Harris, 2005), the precise transcriptional network required for the full differentiation of each retinal cell type is still poorly understood and probably involves additional components.

Six3 and Six6 are two highly related members of the Six/sex oculis family of HD-TFs. Both genes act as transcriptional repressors by interacting with members of the Groucho family of transcriptional co-repressors (Beccari et al., 2009; Marco-Ferreres et al., 2009) but there is also evidence for their role as transcriptional activators (Jeong et al., 2008; Liu et al., 2006; Reichman et al., 2010). In most vertebrate species, both genes are strongly expressed starting at the gastrula stages in the anterior neural plate, where they are required for early forebrain specification. Overexpression of either gene induces ectopic retinal tissues and increases retinal neuroblast proliferation (Del Bene et al., 2004; Loosli et al., 1999; Lopez-Rios et al., 2003; Zuber et al., 1999). In vertebrates, genetic inactivation of Six3 causes loss of brain structures anterior to the midbrain, including the eyes (Lagutin et al., 2003). Six6-null mice instead present strong pituitary defects and retinal hypoplasia, often associated with the absence of the optic chiasm and nerves (Li et al., 2002). Possibly owing to these early defects, the function of Six3 and Six6 during retinal neurogenesis has been barely explored. Both TFs are initially expressed in the entire retinal neuroepithelium, Six6 with
a ventroanteriorhigh to dorsoposteriorlow gradient. Thereafter, Six3 become mostly localised to the amacrine, horizontal and RGC cells, whereas Six6 withdraws from most differentiating precursors but is retained in RGC, amacrine and progenitor cells of the ciliary margin (Bovolenta et al., 1998; Conte and Bovolenta, 2007; Kawakami et al., 1996; Li et al., 2002; Manavathi et al., 2007). Although Six3 alone has no effect, its co-expression with NeuroD or the related Math3 increases the number of amacrine cells (Inoue et al., 2002). Six3 might also be involved in photoreceptor differentiation as its HD interacts with specific DNA elements in retinogenesis. Here, we took advantage of this model and an ideal model to study the possible function of Bovolenta, 2007), the expression of subfunctionalisation of the functions in retinal cell type specification is unknown.

Probably owing to teleost genome duplication and subfunctionalisation of the Six3/6 paralogue genes (Conte and Bovolenta, 2007), the expression of Six6 in medaka fish starts later in development than in other vertebrate species (Conte and Bovolenta, 2007; Lopez-Rios et al., 2003), making the medaka fish an ideal model to study the possible function of Six6 during retinogenesis. Here, we took advantage of this model and investigated Six6 function in the retina, looking, as a starting point, for the elements that regulate Six6 expression. Combining phylogenetic footprinting with bioinformatic prediction of DNA binding sites, we identified and characterized a highly conserved Six6 retinal enhancer that is functionally recognised by NeuroD. NeuroD-mediated activation of Six6 in vivo promotes unorganized retinal progenitor proliferation and unexpectedly impairs photoreceptor differentiation, with no apparent changes in other retinal cell types. Notably, knockdown of Six6 decreases NeuroD expression levels and alters markers of photoreceptor and amacrine cell differentiation. Therefore, we propose that Six6 and NeuroD control each other’s expression and function to coordinate the terminal differentiation of photoreceptors and the genesis of amacrine cells.

MATERIALS AND METHODS

Sequence analysis

The available vertebrate Six6 and NeuroD genomic sequences were retrieved from public databases (http://genome.ucsc.edu; http://genome.jgi-psf.org/) and aligned to identify putative regulatory modules on the basis of sequence conservation (Conte and Bovolenta, 2007). The TRANSFAC, Jaspar and rVISTA tools were used to predict modules on the basis of sequence conservation (Conte and Bovolenta, 2007). The TRANSFAC, Jaspar and rVISTA tools were used to predict putative binding sites for known TFs (Bryne et al., 2008; Matys et al., 2003).

DNA constructs

A 7 kb genomic fragment upstream of the coding sequence of the medaka fish (Oryzias latipes) Six6, including the first 9 coding nucleotides, was isolated from genomic DNA using specific primers (see Table S1 in the supplementary material) and cloned in frame with a nuclear eGFP reporter gene into the pSKII-I-Sce-eGFP vector to create the cl construct. Four deleted constructs, pSKII-I-Sce-Six6-7kbΔXhol-Nsil (cIV), pSKII-I-Sce-Six6-7kbΔXhol-Nsil (cIV), pSKII-I-Sce-Six6-7kbΔXhol-SphI (cV) and pSKII-I-Sce-Six6-7kbΔXhol-HindIII (cVI), were obtained by digestion with the indicated enzymes. The sequence containing only the retinal enhancer b (RE-b) was isolated by PCR amplification from the medaka and mouse genomes with specific primers (see Table S1 in the supplementary material) and cloned upstream of the tyrosine kinase promoter in the pSKII-I-Sce-Tk-eGFP vector (cVII-cVIII and cIXV-cXV constructs). One kilobase of the 3’UTR of Six6 (named D) was amplified by PCR and cloned downstream of eGFP into an HpaI site of the cl construct to generate cII. For Luciferase assays, 1.7 kb of the cIXV genomic sequence containing the B and C clusters and including 9 nucleotides of the coding region was cloned in frame with the Luciferase reporter into the pGL3 basic vector (cIX). The B cluster, isolated by restriction enzyme digestion (EcoRV or SmaI), and the RE-b, obtained by PCR amplification, were inserted in sense and antisense orientation into the polylinker of pSKII-I-Sce-Tk-eGFP (cX and cXI) and pGL3 promoter vector (cXII and cXIII). Mutations in the NeuroD binding site of the constructs were generated by PCR and cloned in a similar manner (cXVI; see Table S1 in the supplementary material). Constructs were verified by automated sequencing (Secugen, S.L., Madrid).

Establishment of transgenic lines

The Cab inbred medaka strain was used throughout the study. Stages were determined according to Iwamatsu (Iwamatsu, 2004). Transgenesis and monitoring of eGFP expression in the living lines was performed as described (Conte and Bovolenta, 2007). Three independent stable transgenic lines were generated for all tested constructs.

Isolation of NeuroD cDNA

The NeuroD cDNA was obtained by RT-PCR from total RNA of embryos collected at different developmental stages using specific primers.

mRNAs and morpholino injections

In vitro synthesis of the mouse or medaka NeuroD and Six6 mRNAs was performed as described (Esteve et al., 2003). NeuroD mRNAs were injected at 10-100 ng/µl, which induced a dose-dependent phenotype. Selected working concentrations were 50-75 ng/µl for NeuroD and 75 ng/µl for Six6. Control embryos were injected with 15 ng/µl of eGFP mRNA. A morpholino (MO; Gene Tools LLC, Oregon, USA) was designed against the 5’UTR of Six6: 5’-GGCTTCTCCAGTTTG-3; a control MO carrying five mismatches was used as a control. The specificity and inhibitory efficiency of MO-Six6 was determined by co-injecting the MO with a synthetic 5’UTR-Six6+eGFP mRNA. eGFP intensity was quantified with ImageJ, as previously reported (Esteve et al., 2004; Ruiz et al., 2009). MO-Six6 at 90 µM fully abrogated eGFP fluorescence. MO was injected into one blastomere at the two-cell stage. At least three independent experiments were performed for each marker and condition.

Wholemount in situ hybridization

Wholemount in situ hybridizations were performed, photographed and sectioned as described (Conte and Bovolenta, 2007). Antisense and sense riboprobes for the medaka Six6, Otx2, Crx, Rhodopsin, Pax6, NeuroD, CycD1 (Cdcn1) and Meis2.2 were used. The mRNA localization was revealed using the NBT/BCIP (purple precipitate), NBT (light blue precipitate) or Fast Red (red fluorescent precipitate) substrates.

Immunohistochemistry

Embryos were processed for immunocytochemistry as described (Esteve et al., 2004; Ruiz et al., 2009). The following primary antibodies were used: anti-phospho-Histone-H3 (1/1000; Roche Diagnostics), rabbit anti-Pax6 (1/1000, PRB-278P Cowance), rabbit anti-Six3 (raised against the mouse Six3 RLOHQAIGPGMRSLAEPEG C-terminal sequence) and a rabbit polyclonal anti-Otx2 (1/300, Abcam, ab21990) raised against the 250-289 human amino acid sequence. This peptide shows 90% and 68% identity with Otx2 and Crx, respectively, suggesting that the antisem might recognize both proteins. The secondary antibodies were from Molecular Probes (used at 1/1000 dilution).

Transient transfection and Luciferase assays

Dissociated cell cultures were prepared from chick retinas as described (Lopez-Rios et al., 2008). In each experiment, cultured cells were cotransfected with the cIX, cXII, cXIII and cXVI constructs (100 ng), the expression vectors (100 ng; pcDNA3/Aith3, pcDNA3/Aith5, pcDNA3/ NeuroD, pcDNA3/E47, or pcDNA3 alone) and the RL-TK plasmid with Renilla Luciferase (10 ng) as a transfection efficiency control. Cells were harvested 48 hours after transfection. Reporter activities were measured using the Dual-Luciferase Reporter Assay System (Promega). Each assay was performed in duplicate. Results are shown as mean ± s.d. for at least three independent assays.
Electrophoretic mobility shift assays

Electrophoretic mobility shift assays (EMSA) were performed as described (Martinez-Morales et al., 2003). Recombinant mouse NeuroD-myc was synthesized in vitro using a TNT kit (Promega). In supershift assays, reactions included 2.5ng/µl of rabbit anti-myc polyclonal antibody or 2.5ng/µl of rabbit anti-HA polyclonal antibody (Sigma-Aldrich). The oligonucleotide primers used for the EMSA are shown in Table S1 in the supplementary material.

Chromatin immunoprecipitation

ChIP assays were performed with a commercial kit (Millipore) following the manufacturer’s instructions. P19 cell line was transfected with the chick Six6 promoter alone or with a myc-tagged mouse NeuroD. Chromatin was immunoprecipitated with 2 µg of either rabbit α-myc antibody (Sigma) or a goat IgG (Sigma). DNA was analysed by PCR (Roche) to amplify regions containing the putative NeuroD binding sites on chick or mouse Six6 promoters. Fold enrichment is expressed as the ratio of myc to control IgG signal.

RESULTS

Six6 hypothalamic and retinal expression is controlled by different HCNE

Phylogenetic footprinting based on the alignment of orthologous genomic sequences from related teleost species has been successfully used to identify the regulatory code of the Six3.2 gene (Conte and Bovolenta, 2007). We applied a similar strategy to identify cis-regulatory elements controlling Six6 expression, focusing particularly on the retina. The sequence of the medaka Six6 loci was retrieved from public databases using the Six6 coding sequence (AM353044) as a query. Alignment of about 20 kb flanking the Six6 gene with the corresponding regions from fugu, tetraodon and stickleback (Fig. 1A,B) identified four clusters (named A-D; Fig. 1B,C) of highly conserved non-coding elements (HCNE). Three of them (A-C) lie in the first 7 kb upstream of the Six6 coding region, whereas an additional cluster (D; Fig. 1B,C) was identified in the 3 kb downstream region (Fig. 1A). To address their regulatory potential, the 7 kb genomic fragment was amplified from medaka genomic DNA and fused with a nuclear eGFP reporter to generate construct I (cl) (Fig. 1C). cl was then assayed for possible enhancer activity in medaka embryos, as previously reported (Conte and Bovolenta, 2007). Three stable cl transgenic lines showed comparable and robust eGFP expression only in the retina. The expression began at stage 24 and was thereafter observed in this region with a pattern that matched endogenous Six6 expression (Fig. 1D-F; see Fig. S2A in the supplementary material). eGFP fluorescence was observed with progressively increasing intensity, first in the retinal neuroepithelium (Fig. 3A-B) and then in the RGC and amacrine cells (Fig. 1C; Fig. 3C,F,H). Because cl did not recapitulate Six6 hypothalamic expression (Fig. 1D), we asked whether the cluster of HCNE contained in the 3 kb fragment downstream of Six6 was needed to drive expression in this region. Fusion of this amplified fragment downstream of eGFP in construct cl (cII; Fig. 1C) was sufficient to observe reporter expression in the hypothalamus, although a weak signal was
detected also in the cerebellum (Fig. 1G), suggesting that additional repressor elements might refine Six6 spatial expression, as reported for Six3.2 (Conte and Bovolenta, 2007).

To identify which, if any, of the HCNE contained in the cI construct was responsible for Six6 expression in the retina, we generated a series of constructs (cIII-cVI) where HCNE were progressively deleted (Fig. 1C). Embryos carrying constructs cIII-cV showed the same pattern of reporter expression observed with cI, whereas no eGFP fluorescence was observed in those carrying cVI (Fig. 1D), restricting the region responsible for expression to a stretch of about 180 base-pairs (bp) corresponding to the first HCNE of cluster B (Fig. 1B-D). This region appeared necessary and sufficient to drive expression in the retina as stably transfected embryos carrying the cVII construct, where HCNE-b was combined with the minimal tyrosine kinase promoter, efficiently expressed eGFP with the expected retinal pattern. The HCNE-b was therefore named retinal enhancer b (RE-b).

NeuroD specifically binds and activates the Six6 RE-b

To determine potential trans-acting factors, we next analysed RE-b from different vertebrates with TRANSFAC and Jaspar softwares (Bryne et al., 2008; Cartharius et al., 2005). This analysis identified a highly conserved consensus E-box binding site within the RE-b (Fig. 2A,B). E-boxes bind TFs of the bHLH family, including the proneural genes Ath3, Ath5 and NeuroD, which have been implicated in the specification of RGC, amacrine and photoreceptor precursors (Hatakeyama and Kageyama, 2004), where Six6 is also expressed (Conte and Bovolenta, 2007) (see Fig. S2A-C,E in the supplementary material). We thus asked whether these factors could activate the Six6 retinal enhancer in Luciferase reporter assays in cultures of dissociated cells from embryonic day 5 (E5) chicken retinas. Cells were transiently transfected with the reporter construct containing the chick RE-b coupled to the Luciferase gene (cXII) together with different combinations of mouse Ath3, Ath5, NeuroD and E47, a ubiquitously expressed bHLH protein that forms heterodimers with other family members, enhancing their
activity (Longo et al., 2008; Naya et al., 1995). Notably, in all the tested combinations, only the presence of NeuroD led to a significant activation of reporter expression (see Fig. S1 in the supplementary material). This activation was particularly evident when NeuroD was cotransfected with E47 (Fig. 2A; see Fig. S1 in the supplementary material), in line with the notion that these two factors form particularly stable heterodimers (Longo et al., 2008). This activation was no longer observed when transfections were repeated with a reporter construct carrying three point-mutations in the E-box of the RE-b (cXVI; Fig. 2A,B). The specificity of NeuroD binding was confirmed by EMSA and ChIP assays. NeuroD-myc protein formed a complex with a P32-labelled oligonucleotide derived from the RE-b and containing the E-box binding site (Fig. 2B,C). The migration of the complex was specifically retarded by anti-myc antibodies and binding to the probe was competed by an excess amount of the same unlabelled oligonucleotide, but not by increasing concentrations of its mutated version (Fig. 2C). In line with this finding, anti-myc antibodies, but not a control IgG, immunoprecipitated chick RE-b in P19 cells transfected with NeuroD-myc and the chick Six6 promoter (Fig. 2D). NeuroD-myc immunoprecipitated the mouse RE-b from P19 chromatin (Fig. 2D) with the same specificity, further proving that Six6 RE-b is a direct target of NeuroD.

**NeuroD overexpression expands the domain of Six6 expression causing an increase in cell proliferation**

Together, these studies identified NeuroD as a strong candidate to regulate Six6 expression in the retina. Consistent with this possibility, the distribution of NeuroD and Six6 mRNAs partially overlapped in the embryonic wild-type retinas (see Fig. S2 in the supplementary material). As shown in different vertebrate species (Conte and Bovolenta, 2007; Lopez-Rios et al., 1999; Toy and Sundin, 1999), medaka Six6 mRNA is localised to the entire retinal neuroepithelium at the beginning of neurogenesis, albeit its levels are slightly lower in the region where NeuroD-positive cells begin to accumulate (see Fig. S2A-D in the supplementary material). These results were also confirmed by the presence of nuclear eGFP reporter expression in cells of cl transgenic retinas (Six6 cI>eGFP) where NeuroD mRNA was localised in the cytoplasm (Fig. 3A,B). The photoreceptor progenitor nature of these NeuroD- and Six6-positive cells was further confirmed by the expression of Crx/Otx2 (see Materials and methods), established photoreceptor markers (Nishida et al., 2003) (Fig. 3D,E). However, Six6 expression was progressively downregulated in photoreceptors (Fig. 3B; see Fig. S2C,E in the supplementary material), whereas a strong Six6 and
NeuroD colocalisation was maintained in an amacrine cell subpopulation (Fig. 3C; see Fig. S2E,F in the supplementary material).

To understand if NeuroD-directed regulation of Six6 occurs in vivo, we tested whether NeuroD overexpression could expand the Six6 expression domain in both wild-type and transgenic embryos. In contrast to the restricted expression observed in control eGFP-injected embryos (Fig. 3F,H), injections of NeuroD mRNA (50-75 ng/µl) in Six6 c5>eGFP transgenic embryos activated eGFP expression in most of the retinal neuroepithelium (stage 38; Fig. 3G,I). Likewise, NeuroD overexpression in wild-type embryos expanded Six6 mRNA distribution, which, in the most affected embryos, was also observed in layers where it is normally absent (Fig. 3K,M). No ectopic Six6 expression was observed in regions other than the retina, supporting a tissue-specific NeuroD-mediated activation of Six6.

Notably, NeuroD mRNA overexpression caused abnormal eye development in most embryos (75±5%; n=1750). In the majority of the affected embryos (54±3%), the eyes were slightly larger and shifted ventroanteriorly with absent or reduced ventral retinal pigmented epithelium (Fig. 3G,K,M) and optic stalks, which acquired neural retina characteristics. As an extreme phenotype, cyclopic eye positioned in the anterior-most of the embryo (see Fig. 20±3% (n=1750) injected with high NeuroD concentrations (~100 ng/µl). No central nervous system (CNS) regions other than the eyes were affected in NeuroD-injected embryos, at least on the basis of morphological inspection.

Gain of Six6 (also known as Optx2) function in Xenopus leads to an increase in cell proliferation (Zuber et al., 1999), explained by the finding that Six6 directly represses the expression of cyclin inhibitors like p27Kip1 (Li et al., 2002). If the NeuroD phenotype is mostly mediated by direct Six6 activation, we should expect a similar increase in cell proliferation and this increase should be abrogated by the injection of a Six6-specific morpholino (olSix6-MO). In line with this idea, the number of retinal cells immunostained with anti-PH3 antibodies, a marker for mitotic cells, was significantly increased in NeuroD-treated embryos (Fig. 4A,B,J). Notably, PH3-positive cells were not confined to the ventricular surface of the neuroepithelium or the ciliary marginal zone (CMZ), as observed in controls (Fig. 4A), but were dispersed within the thickness of the retina (Fig. 4B). Similarly, CycD1 mRNA, an additional proliferation marker, localised only to the CMZ in stage 38 control retinas, expression was still observed in the ventral retina of NeuroD-injected embryos at the same stage (Fig. 4D-G). The co-injection of Six6-MO (90 μM) together with NeuroD mRNA was sufficient to bring both proliferation and CycD1 expression back to the level observed in controls (Fig. 4C,H,I,J). Notably, Six6-MO did not counterbalance the tendency to cyclopia induced by a high concentration of NeuroD (data not shown) nor the optic stalk defects observed even with lower NeuroD doses (Fig. 4C,H, arrows).

Together, these data indicate that NeuroD-mediated activation of Six6 controls retinal cell proliferation, whereas ectopic activation of other NeuroD target genes are responsible for optic stalk defects.
zebrafish or *Xenopus* and which of the putative NeuroD activities could be specifically counterbalanced by Six6-MO, thus confirming a possible physiological role of Six6 as a downstream target of NeuroD.

NeuroD-mediated overexpression of Six6 led to a disorganised growth of the eye where, in the most severe cases, specific cell layers were indistinguishable (Fig. 3G,K; see Figs S3 and S4 in the supplementary material). To overcome this problem, we selected for analysis only those NeuroD-injected embryos where retinal layers could still be recognised (54±3%). Analysis of the expression of Pax6, Meis2.2, Otx2 and Six3, markers for RGC, amacrine, bipolar and horizontal cells, respectively, did not show any statistically significant defects in NeuroD overexpressing embryos when compared with age-matched controls (Fig. 5A-B’,D-E’,G-H; see Fig. S4A-D,G in the supplementary material). By contrast, Rhodopsin expression, a marker for differentiated photoreceptors, was markedly reduced or totally absent in NeuroD-overexpressing retinas (40%; n=30; Fig. 5J-K’). This reduction did not reflect a complete loss of the photoreceptor lineage, as Crx-positive postmitotic photoreceptor precursors (Garelli et al., 2006) were still observed (see Fig. S4E,F in the supplementary material). Rhodopsin expression was completely rescued when Six6-MO was co-injected with NeuroD (Fig. 5L,L’), indicating that these alterations involve Six6 activity. As observed before, Six6-MO did not counterbalance the tendency to cyclopia induced by NeuroD nor the apparent extension of the retina into the optic stalk, frequently observed in both NeuroD and Six6-MO plus NeuroD-injected embryos (Fig. 5C,F,J,L).

**Six6 and NeuroD act in a regulatory loop to control photoreceptor differentiation and amacrine cell specification**

The data reported above suggest that high Six6 levels interfere with Rhodopsin expression and thus with photoreceptor maturation. If this was the case, interference with Six6 expression alone should force photoreceptor differentiation ahead of time. Surprisingly, analysis of Six6-MO-injected embryos at stages 30-34, when photoreceptor differentiation is still ongoing, revealed the opposite effect. Approximately 67% of the morphants (n=40) expressed a very low level of or no Rhodopsin at stage 34, whereas a milder reduction was observed only in 35% of the misMO-injected control embryos (Fig. 6A,B). At stage 38, 31% of the morphant embryos showed a Rhodopsin decrease, suggesting that reduced Six6 levels interfere with the onset of photoreceptor terminal differentiation but not their specification because, as observed in NeuroD-injected retina, Crx expression appeared unaltered (Fig. 6C,D).

To explain this apparently contradictory result, we hypothesized that Six6 and NeuroD might act in a regulatory loop, where Six6 would initiate and/or maintain NeuroD expression and both genes would be required, directly or indirectly, to regulate Rhodopsin levels. In line with this hypothesis, the appearance of the first NeuroD-positive cells around stage 27 was delayed (see Fig. S5A in the supplementary material) and the overall NeuroD expression levels were decreased in the retina of Six6-MO-injected embryos (Fig. 6E,F; 40%, n=60) as compared with misMO-injected controls. At later developmental stages, the decrease was also evident in both the amacrine and photoreceptor layers, but whereas Crx-positive photoreceptor precursors were normally generated, Pax6 and Six3-positive amacrine precursors were significantly diminished (see Fig. S4H-L in the supplementary material). Conversely, Six6 overexpression increased NeuroD mRNA levels in the retina (60%; n=30; Fig. 6G,H; see Fig. S5 in the supplementary material), which was ectopically observed in the optic stalk (Fig. 6H) and throughout the thickness of the retinal neuroepithelium in embryos with the strongest phenotype (see Fig. S5B in the supplementary material). In a lower proportion of embryos (25%), Six6 mRNA induced ectopic patches of pigmented cells in the brain with an associated ectopic expression of NeuroD (Fig. 6H,J,L), suggesting that Six6 can initiate NeuroD expression in tissues other than the retina. In agreement with what was observed after NeuroD-mediated Six6 overactivation, Six6 mRNA

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**Fig. 5. NeuroD-induced activation of Six6 specifically reduces photoreceptor differentiation.** (A-L’) Frontal sections from stage 38 control, NeuroD and NeuroD plus MO-Six6-injected embryos. Embryos were hybridized with the following probes: Pax6 and Meis2.2 (amacrine and ganglion cells; A-F’); Otx2 (bipolar cells; G-I’); Rhodopsin (differentiated photoreceptors; J-L’). NeuroD-injected embryos show a strong reduction of Rhodopsin expression, which is counteracted by MO-Six6 coinjection. No major alterations were observed in the distribution of other cell type markers. Arrows in C,F,I,L indicate optic stalk defects. A’-L’ are magnified views of the boxed areas in A-L. Scale bars: 50 μm.
injection did not affect the generation of amacrine cells while strongly reducing \textit{Rhodopsin} but not \textit{Crx} expression (Fig. 6M,N; data not shown). Together, these results suggest that \textit{Six6}, together with \textit{NeuroD}, is necessary but, by itself, is not sufficient to specify amacrine cells. Furthermore, the mutual regulation of \textit{Six6} and \textit{NeuroD} contributes to photoreceptor differentiation.

**DISCUSSION**

Generation of neuronal diversity is largely initiated by the cooperation between TFs of proneural bHLH and HD types. Proneural genes act as general determinants driving proliferating precursors towards a neuronal phenotype in broad domains of the CNS (Guillemot, 2007; Powell and Jarman, 2008) but their activity precursors towards a neuronal phenotype in broad domains of the CNS (Guillemot, 2007; Powell and Jarman, 2008) but their activity is made context specific by the interaction with locally expressed HD-TFs. According to this general principle, we have shown that \textit{NeuroD}, a widely expressed proneural gene, regulates \textit{Six6} expression exclusively in the retina. \textit{Six6}, in turn, is sufficient to activate \textit{NeuroD} expression, even ectopically. Physiologically, this regulatory loop appears to control retinal photoreceptor maturation and amacrine cell specification. These conclusions are based on genomic and functional experiments in the medaka fish where the late onset of \textit{Six6} expression provides a unique opportunity to study time-specific functions of \textit{Six6} in the retina.

\textit{Six6} is strongly expressed in the retina and hypothalamus of all vertebrate species so far analysed (Aijaz et al., 2005; Conte and Bovolenta, 2007; Conte et al., 2005; Gallardo et al., 1999; Jean et al., 1999; Lopez-Rios et al., 1999). We previously used a two-step genome comparison strategy, followed by a highly reproducible transgenic analysis to dissect the regulatory code of \textit{Six3.2} (Conte and Bovolenta, 2007). Using the same approach, we have demonstrated that only two clusters of HCNE (B and D) are sufficient to reproduce the entire expression domain of \textit{Six6} in the medaka fish. The B element is responsible for the retinal expression, whereas the D cluster, alone or in combination with the 5’ regulatory region, is responsible of the hypothalamic expression.

The pattern of the eGFP reporter was highly reproducible in all injected embryos (roughly 97%, albeit with intensity differences, thus excluding chromosome position effects) and verified by the establishment of three independent stable transgenic lines for each of the tested constructs, supporting that clusters B and D contain functionally important cis-regulatory sequences. Despite their conservation, clusters A and C did not activate eGFP reporter expression, although subtle regulatory activities below the resolution of our analysis cannot be excluded. Alternatively, their conservation might reflect other important roles in the control of gene transcription, including the regulation of chromatin structure (Glazko et al., 2003; Gomez-Skarmeta et al., 2006) or, in the particular case of module C, minimal promoter functions. Proper \textit{Six6} expression might additionally require a yet unidentified repressor, similar to that described for \textit{Six3.2} (Conte and Bovolenta, 2007), which could normally silence the ectopic eGFP signal observed in the cerebellum upon injection of the downstream hypothalamic enhancer.

The strong sequence conservation indicates an evolutionary conserved role for both the B and D regions. However, we focused our attention on and demonstrated the functional relevance only of the RE-b, a 200 bp region contained in the upstream B cluster. This enhancer, independently of its species origin, was sufficient to recapitulate endogenous \textit{Six6} expression in the retina of medaka fish embryos and in chick retinal cultures, strongly supporting its functional relevance from teleost to mammals. Although binding sites for other TFs are likely to be present in this region, we identified only a strongly conserved consensus E-box. A recent study showed that Lhx2 and Pax6, two TFs involved in the specification of the eye anlage (Porter et al., 1997; Zuber et al., 2003), act synergistically to activate the early expression of \textit{Six6} in the mouse optic vesicles (Tetreault et al., 2009). Consistent with the late expression of \textit{Six6} in medaka (Conte and Bovolenta, 2007; Lopez-Rios et al., 2003), binding sites for these two TFs were not found in the \textit{Six6} promoter.
Different subfamilies of bHLH proteins can form heterodimers and recognize the same canonical E-box sequence (Hernandez et al., 2007; Powell and Jarman, 2008). We cannot exclude that a number of bHLH might compete to occupy the conserved Six6 E-box and control different phases of Six6 expression, as reported for Ath5 regulation in RGCs (Hernandez et al., 2007). Nevertheless, our results support a highly specific role of the NeuroD-E47 heterodimer in the binding and transactivation of the E-box in the Six6 enhancer. Indeed, E47 alone or the related Ath5 and Ath3 had no effects, although their expression also partially overlaps with that of Six6 in the retina (Brown et al., 1998; Brown et al., 2001; Inoue et al., 2002; Kanekar et al., 1997). This specificity is further supported by our EMSA, ChIP and in vivo studies. NeuroD mRNA injections lead to an increased and ectopic expression of Six6 in the entire retina but in no other CNS regions, strongly arguing for a temporal and tissue-specific NeuroD-mediated regulation of Six6. This observation is also consistent with the possible existence of repressors that antagonise NeuroD-mediated expansion of Six6 outside the retina or, alternatively, with the existence of a retinal-specific positive cofactor. On the contrary, Six6 overexpression results in the activation of NeuroD expression, even ectopically. Notably, forced expression of Six6 alone or in combination with Groucho co-repressors generates ectopic retina-like tissue in the forebrain (Lopez-Rios et al., 2003), similar to that observed here. Together, these results suggest that Six6 might indirectly regulate NeuroD, for example, by normally repressing a NeuroD negative regulator. Alternatively, Six6 might work as transcriptional activator as recently suggested by the observation that the protein can activate the promoter of the gene encoding the RdCVF (rod-derived cone viability factor), a trophic factor expressed in rods (Reichman et al., 2010). These possibilities are not mutually exclusive and might be context-dependent, involving differential transcriptional networks in amacrine and photoreceptor cells, which might be refined by the availability of other co-factors. For example, E47, although ubiquitously expressed, might be particularly abundant in amacrine cells, whereas other bHLH cofactors, such as Hes6 (Bae et al., 2000), might be abundant in photoreceptors.

Six3 and Six6 loci might have arisen from the duplication of a common ancestor (Gallardo et al., 1999), which implies the possible existence of similar regulatory elements. Co-expression of Six3 and NeuroD increases amacrine cell numbers (Inoue et al., 2002), and protein-protein interaction between Six3 and NeuroD has been reported (Tessmar et al., 2002). Despite some parallels with Six6, we could not find sequence conservation by comparing the regulatory elements that drive late retinal expression of Six3.2 (Conte and Bovolenta, 2007) with that identified for Six6. Accordingly, no difference in Six3 expression was observed in the medaka fish retinas upon NeuroD overexpression, further confirming the specificity of NeuroD-Six6 regulation.

NeuroD promotes neuronal cell fate acquisition and links cell cycle withdrawal with terminal differentiation in different neural cell populations (Lee et al., 1995; Farah et al., 2000; Chae et al., 2004). In the retina, its function has been linked with the generation of amacrine and photoreceptor cells (Inoue et al., 2002; Kanekar et al., 1997; Moore et al., 2002; Morrow et al., 1999; Yan et al., 2005; Yan and Wang, 2004). Six6 activity, instead, has been mostly associated with undifferentiated proliferating precursors (Li et al., 2002; Zuber et al., 1999). It was therefore somewhat surprising to find that NeuroD directly activates Six6 expression. NeuroD overexpression combined with MO-mediated inhibition of Six6 confirmed this relationship and proved that the phenotypic alterations of NeuroD overexpression in part resembled those reported for Six6 gain-of-function in other vertebrates (Bernier et al., 2000; Zuber et al., 1999), as expected for a direct regulation of NeuroD over Six6. Our overexpression studies uncovered additional and previously unnoticed defects caused by NeuroD gain-of-function, which were not antagonised by Six6-MO and thus probably mediated by additional NeuroD targets. These defects included the ventral displacement of the eye, the loss of the ventral retinal pigmented epithelium and, most notably, the transformation of the optic stalk in tissue with neural retina characteristics. These defects culminated with cyclopia and retinal hyperplasia in the most-affected embryos. This is in striking contrast with the results of NeuroD overexpression in Xenopus, where the eyes were reduced in size owing to precocious neuronal differentiation (Kanekar et al., 1997; Lee et al., 1995). Defects somewhat similar to those observed here have been instead described as a consequence of the overexpression of the related Xenopus Ath3 (Takebayashi et al., 1997). Given the redundant function of NeuroD and Ath3 (Inoue et al., 2002), it is possible that, in medaka fish, NeuroD has acquired functions exerted by Ath3 in other species.

Although we initially observed a regulation of Six6 by NeuroD, the overall picture that emerged from our studies suggests that NeuroD and Six6 undergo a mutual regulation. Alignment of the NeuroD loci from different teleost species identified a number of conserved putative Six6 binding sites (Marco-Ferrerés et al., 2009) in the putative regulatory region of NeuroD (see Fig. S6 in the supplementary material). However, ChIP and Luciferase assays failed to validate the functional relevance of these putative binding sites (see Fig. S6 in the supplementary material), suggesting, although not definitively proving, that Six6 regulates NeuroD expression in the retina indirectly. An indirect regulatory mechanism might be particularly appropriate for photoreceptor precursors where the two genes are only transiently co-expressed. Otx2 and Crx, which colocalise with both Six6 and NeuroD, are possible candidates, especially because Otx2 function has already associated with NeuroD regulation (Hennig et al., 2008).

Taken together, our data suggest the following plausible model (Fig. 7). Six6 expressed in multipotent progenitors activates the expression of NeuroD in a cell subpopulation, which become committed to generate photoreceptors and a subset of amacrine cells (Masland, 2001). Six6 is necessary but not sufficient for
amacrine cell generation. Its knockdown significantly decreases amacrine cell number, whereas its direct or indirect (NeuroD-mediated) overexpression does not significantly modify it, suggesting that additional factors, for example the related Six3 (Inoue et al., 2002), are required for amacrine cell generation. In committed photoreceptors, NeuroD and Six6 are both required to initiate the differentiation program, which seems particularly sensitive to both low and high Six6 levels. Although in adult human retinas SIX6 protein is abundantly localized to the ONL (Aijaz et al., 2005), the Six6 mRNA (which does not necessarily reflect protein concentration) felt below detectable levels as photoreceptors began to differentiate, indicating that a significant amount of Six6 is required, directly or indirectly, to initiate Rhodopsin expression. This might be then maintained by the cooperative activity of NeuroD with other factors, including Otx2 or possibly Six3 (Manavathi et al., 2007). Indeed, an ordered sequence of E-boxes and putative Six3 and Six6 binding sites are highly conserved in the Rhodopsin promoter, although our preliminary observations indicate that knockdown of Six6 has only a modest effect on eGFP reporter expression when a Xenopus Rhodopsin promoter eGFP construct was co-injected in medaka fish embryos (Fadool, 2003) (data not shown). This suggests that Six6-mediated regulation of Rhodopsin expression is probably indirect. Why sustained high levels of Six6 might have a repressive effect on Rhodopsin expression is unclear but it might involve repression and/or sequestration of other transcription factors.

In zebrafish, NeuroD conditionally overexpressed at late stages of differentiation increases photoreceptor generation, whereas its downregulation does not affect their specification (Ochocinska and Hitchcock, 2009). In line with the latter observation, the reduced levels of NeuroD observed in Six6 morphants did not interfere with photoreceptor precursor generation but, contrary to what was observed in zebrafish, early medaka NeuroD or Six6 overexpression did not increase photoreceptor number. This indicates that additional and NeuroD-independent mechanisms must specify this fate. These are probably operative only at late stages of neurogenesis when NeuroD is conditionally overexpressed in zebrafish.

Previous works had shown that Six6 plays an important role in retinal proliferation (Li et al., 2002; Zubet et al., 1999); however, the possible functions of this HD-TF during retinal cell specification remained unknown. Our study uncovered a novel role of Six6 in amacrine and photoreceptor differentiation in cooperation with NeuroD. This cooperation, together with the observation that Lhx2 and Pax6 regulate SIX6 expression in mammals (Tetreault et al., 2009), constitutes a starting point towards the full identification of the transcriptional network controlling mammalian SIX6 function. This, in turn, might help define the molecular causes of human inborn eye defects such as anophthalmia, microphthalmia and coloboma, which have been associated with genetic alterations of the SIX6 locus (Ahmad et al., 2003; Gallardo et al., 1999; Gallardo et al., 2004).

Competing interests statement
The authors declare no competing financial interests.

References


### Table S1. Oligonucleotides used in this study

<table>
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<tr>
<th>Primer name</th>
<th>Sequence (5’-3’)</th>
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<tr>
<td>pSKII-LsceolSix6-7kb F</td>
<td>AATGGCATTTGACATAAGGCC</td>
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<tr>
<td>pSKII-LsceolSix6-7kb R</td>
<td>CTAAACAAGTGCGAGAGATGTC</td>
</tr>
<tr>
<td>olSix6 RE-b F</td>
<td>ATGAACAGCTTGGGTACGAGAAAGG</td>
</tr>
<tr>
<td>olSix6 RE-b R</td>
<td>CCGCAACTTGGAGAGATGTC</td>
</tr>
<tr>
<td>mSix6 RE-b F</td>
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</tr>
<tr>
<td>mSix6 RE-b R</td>
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<tr>
<td>mSix6 Nd BS (ChIP) –1621 to –1248 R</td>
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ol, Oryzias latipes; m, mouse; c, chick.