Antagonism between Gdf6a and retinoic acid pathways controls timing of retinal neurogenesis and growth of the eye in zebrafish

Leonardo E. Valdivia1,‡, Dayna B. Lamb2, Wilson Horner2, Claudia Wierzbicki1, Amanuel Tafessu2, Audrey M. Williams2, Gaia Gestri1, Anna M. Krasnow1, Terra S. Vleeshouwer-Neumann2, McKenzie Givens2, Rodrigo M. Young1, Lisa M. Lawrence1,*, Heather L. Stickney1, Thomas A. Hawkins1, Quenten P. Schwarz1,‡, Florencia Cavodeassi1,§, Stephen W. Wilson1,** and Kara L. Cerveny1,2,¶, **

ABSTRACT

Maintaining neurogenesis in growing tissues requires a tight balance between progenitor cell proliferation and differentiation. In the zebrafish retina, neuronal differentiation proceeds in two stages with embryonic retinal progenitor cells (RPCs) of the central retina accounting for the first rounds of differentiation, and stem cells from the ciliary marginal zone (CMZ) being responsible for late neurogenesis and growth of the eye. In this study, we analyse two mutants with small eyes that display defects during both early and late phases of retinal neurogenesis. These mutants carry lesions in gdf6a, a gene encoding a BMP family member previously implicated in dorsoventral patterning of the eye. We show that gdf6a mutant eyes exhibit expanded retinoic acid (RA) signalling and demonstrate that exogenous activation of this pathway in wild-type eyes inhibits retinal growth, generating smaller eyes with a reduced CMZ and fewer proliferating progenitors, similar to gdf6a mutants. We provide evidence that RA regulates the timing of RPC differentiation by promoting cell cycle exit. Furthermore, reducing RA signalling in gdf6a mutants re-establishes appropriate timing of embryonic retinal neurogenesis and restores putative stem and progenitor cell populations in the CMZ. Together, our results support a model in which dorsally expressed gdf6a limits RA pathway activity to control the transition from proliferation to differentiation in the growing eye.

KEY WORDS: Retinoic acid, BMP, Gdf6a, Ciliary marginal zone, Neurogenesis, Retinal stem cells, Zebrafish

INTRODUCTION

The balance between cell proliferation and differentiation is spatially and temporally regulated during development, ensuring the generation of tissues with the correct proportion of differentiated cells (Schmidt et al., 2013; Urbán and Guillermot, 2014). In the vertebrate retina, this process begins when retinal progenitor cells (RPCs) successively exit the cell cycle to generate retinal ganglion cells (RGCs), cone photoreceptors, interneurons, rod photoreceptors and Müller glia (Cepko, 2014). This progression of fate specification and the timing of neurogenic decisions require cells to integrate intrinsic information and extrinsic signals (Cepko, 2014; Cerveny et al., 2012). Cell cycle regulators and a variety of transcription factors are implicated in the cell-autonomous progression from RPC to post-mitotic neuron, and secreted signals can influence the transition from proliferation to differentiation (Agathocleous and Harris, 2009; Bassett and Wallace, 2012).

In vertebrate eyes, neurogenesis proceeds in waves. In zebrafish, neuronal differentiation spreads across the developing retina from a ventronasal patch of RPCs cells adjacent to the optic stalk (Rappaport, 2006). This spread of neurogenesis is preceded by comparable waves of expression of neurogenesis-related genes including the proneural gene atoh7 and the paired-class cone-rod homeobox gene crx (Masai et al., 2000; Shen and Raymond, 2004). Differentiation of distinct neuronal types continues to propagate circumferentially in successive waves, ultimately filling the central retina by 48 hours post fertilisation (hpf). After this point, neurogenesis occurs radially, with new neurons added to the eye in successive rings from a peripheral area of the retina termed the ciliary marginal zone (CMZ). The CMZ contains a stem cell niche that allows continued growth and neurogenesis in the eye (Centanin et al., 2011; Stenkamp, 2007).

Retinal neurogenesis occurs in a context where extrinsic signals impart nasotemporal and dorsoventral (DV) positional identity to newly generated neurons. In fish, the opposing actions of Fgf and Shh initiate nasotemporal patterning (Hernandez-Bejarano et al., 2015) whereas opposing Bmp and Hedgehog (Hh) signals (Yang, 2004) establish DV identities. For instance, Gdf6a (BMP13 homologue) and other BMPs are expressed in dorsal domains and influence dorsal identity within the retina (French et al., 2009; Gosse and Baier, 2009; Kruse-Bend et al., 2012; Williams et al., 2008). Mutations in gdf6 genes have also been linked to other ocular anomalies, including microphthalmia and coloboma (Asai-Coakwell et al., 2013; den Hollander et al., 2010; French et al., 2009). It is likely that the connection between axial patterning signals and positional identity is maintained within the CMZ as newly generated RGCs must integrate into existing circuitry and project to topographically appropriate target regions within the brain.

The RA signalling pathway also influences retinal development. RA-synthesising enzymes are expressed predominantly in the ventral retina and RA signalling is required for morphogenesis of the ventral eye, including choroid fissure closure (Lupo et al., 2011; Marsh-Armstrong et al., 1994). Expression of the RA synthesis enzyme aldha1a3 is expanded dorsally in eyes of gdf6a morphant...
embryos (French et al., 2009) raising the possibility that interactions between RA and Gdf6a signals occur during retinal development.

In this study, we sought to identify signals that regulate eye growth and found that, in addition to their roles in DV patterning, opposing Gdf6a and RA signals influence proliferation and differentiation of RPCs. Through a forward genetic screen in zebrafish, we identified two point mutations in gdf6a that lead to reduction in size of the CMZ and subsequent small eye phenotypes. These phenotypes are accompanied by an expansion of RA pathway activity within the CMZ and precocious differentiation of RPCs. We find that activating the RA pathway in wild-type eyes phenocopies gdf6a mutants and that abrogation of RA signalling ameliorates the gdf6a mutant phenotype. Together, our results show that signals that impart DV identity in the eye also regulate production of neurons and retinal growth, revealing an unappreciated link between the pathways that regulate patterning, proliferation, and stem/progenitor cell maintenance in the developing eye.

RESULTS
gdf6a mutants exhibit small eyes independent of apoptosis

Clutches of 72 hpf embryos from families of zebrafish carrying N-ethyl-N-nitrosurea (ENU)-induced mutations (Valdivia et al., 2011) were examined for ocular abnormalities, including microphthalmia. We recovered two non-complementing, recessive mutations, u768 and u900, that when homozygous led to small eyes with ventrally displaced lenses and, in some cases, coloboma (Fig. 1A). Although both homozygous mutant phenotypes are fully penetrant, u900 mutants displayed increased levels of retinal apoptosis at around 30 hpf (Fig. S1B), blocking cell death with the pan-caspase inhibitor Z-VAD-FMK reduced apoptotic levels but did not rescue the subsequent small eye size, corroborating previously published data (French et al., 2013) (Fig. S1C).

Functional studies have also implicated Gdf6a in patterning the DV axis of the retina (French et al., 2009; Gosse and Baier, 2009; Rissi et al., 1995). However, the u768 allele exhibits overtly normal expression of DV markers at 24 hpf (Fig. 1E) suggesting that the small eye phenotype arises in this mutant allele in the absence of major defects in the establishment of axial patterning of the retina. Together, these data suggest that a mechanism other than programmed cell death and/or abnormal retinal patterning is responsible for the small eye phenotype in gdf6a mutants.

The CMZ is reduced in gdf6a mutants

As the CMZ is the primary source of new neurons and retinal growth in fish larvae (Centanin et al., 2011; Raymond et al., 2006), we examined expression of markers for subdomains of the CMZ in gdf6a mutants. The number of apoptotic retinal cells between 24 and 36 hpf was similar to wild type (gdf6a<sup>+/+;</sup>野生型=0.12; n=13 embryos of each genotype; Fig. 1D; Fig. S1A), and retinal neurons appeared healthy, suggesting that cell death is not the main driver of the small eye phenotype in this mutant. Although gdf6a<sup>u900</sup> mutants displayed increased levels of retinal apoptosis at around 30 hpf (Fig. S1B), blocking cell death with the pan-caspase inhibitor Z-VAD-FMK reduced apoptotic levels but did not rescue the subsequent small eye size, corroborating previously published data (French et al., 2013) (Fig. S1C).

In this study, we sought to identify signals that regulate eye growth and found that, in addition to their roles in DV patterning, opposing Gdf6a and RA signals influence proliferation and differentiation of RPCs. Through a forward genetic screen in zebrafish, we identified two point mutations in gdf6a that lead to reduction in size of the CMZ and subsequent small eye phenotypes. These phenotypes are accompanied by an expansion of RA pathway activity within the CMZ and precocious differentiation of RPCs. We find that activating the RA pathway in wild-type eyes phenocopies gdf6a mutants and that abrogation of RA signalling ameliorates the gdf6a mutant phenotype. Together, our results show that signals that impart DV identity in the eye also regulate production of neurons and retinal growth, revealing an unappreciated link between the pathways that regulate patterning, proliferation, and stem/progenitor cell maintenance in the developing eye.

RESULTS
gdf6a mutants exhibit small eyes independent of apoptosis

Clutches of 72 hpf embryos from families of zebrafish carrying N-ethyl-N-nitrosurea (ENU)-induced mutations (Valdivia et al., 2011) were examined for ocular abnormalities, including microphthalmia. We recovered two non-complementing, recessive mutations, u768 and u900, that when homozygous led to small eyes with ventrally displaced lenses and, in some cases, coloboma (Fig. 1A). Although both homozygous mutant phenotypes are fully penetrant, u900 mutants consistently display smaller eyes than u768 mutants (Fig. S1D).

Both mutants carry lesions in gdf6a, a gene that is expressed dorsally both in the developing retina (French et al., 2009; Gosse and Baier, 2009) and the CMZ (Fig. 1B). Using bulk segregant analysis, complementation testing, and sequencing, we identified u768 as a missense mutation that results in the substitution of a threonine for an absolutely conserved alanine at position 350 in the Gdf6a protein (Fig. 1C). It is likely that this mutation generates a hypomorphic Gdf6a protein. Sequencing identified u900 as a nonsense mutation that converts the codon for Gln179 to a Stop (gdf6a<sup>u900;</sup>野生型=1.76; n=13 embryos of each genotype; Fig. 1D; Fig. S1A), and retinal neurons appeared healthy, suggesting that cell death is not the main driver of the small eye phenotype in this mutant. Although gdf6a<sup>u900</sup> mutants displayed increased levels of retinal apoptosis at around 30 hpf (Fig. S1B), blocking cell death with the pan-caspase inhibitor Z-VAD-FMK reduced apoptotic levels but did not rescue the subsequent small eye size, corroborating previously published data (French et al., 2013) (Fig. S1C).

Functional studies have also implicated Gdf6a in patterning the DV axis of the retina (French et al., 2009; Gosse and Baier, 2009; Rissi et al., 1995). However, the u768 allele exhibits overtly normal expression of DV markers at 24 hpf (Fig. 1E) suggesting that the small eye phenotype arises in this mutant allele in the absence of major defects in the establishment of axial patterning of the retina. Together, these data suggest that a mechanism other than programmed cell death and/or abnormal retinal patterning is responsible for the small eye phenotype in gdf6a mutants.

The CMZ is reduced in gdf6a mutants

As the CMZ is the primary source of new neurons and retinal growth in fish larvae (Centanin et al., 2011; Raymond et al., 2006), we examined expression of markers for subdomains of the CMZ in gdf6a mutants. The number of apoptotic retinal cells between 24 and 36 hpf was similar to wild type (gdf6a<sup>+/+;</sup>野生型=0.12; n=13 embryos of each genotype; Fig. 1D; Fig. S1A), and retinal neurons appeared healthy, suggesting that cell death is not the main driver of the small eye phenotype in this mutant. Although gdf6a<sup>u900</sup> mutants displayed increased levels of retinal apoptosis at around 30 hpf (Fig. S1B), blocking cell death with the pan-caspase inhibitor Z-VAD-FMK reduced apoptotic levels but did not rescue the subsequent small eye size, corroborating previously published data (French et al., 2013) (Fig. S1C).

Functional studies have also implicated Gdf6a in patterning the DV axis of the retina (French et al., 2009; Gosse and Baier, 2009; Rissi et al., 1995). However, the u768 allele exhibits overtly normal expression of DV markers at 24 hpf (Fig. 1E) suggesting that the small eye phenotype arises in this mutant allele in the absence of major defects in the establishment of axial patterning of the retina. Together, these data suggest that a mechanism other than programmed cell death and/or abnormal retinal patterning is responsible for the small eye phenotype in gdf6a mutants.
gdf6a mutants and found striking differences compared with wild-type eyes as early as 2.5 days post fertilisation (dpf). The most peripheral col15a1b-expressing region, which contains presumptive stem cells (Cerveny et al., 2010; Gonzalez-Nunez et al., 2010), is reduced in gdf6au768 mutants with fewer col15a1b-positive cells in the dorsal CMZ and virtually no col15a1b expression in the ventral CMZ (Fig. 2A,B). Similarly, all other subdomains of this germinal zone—proliferating progenitors (expressing ccnd1), specified precursors (expressing the transcription factor atoh7), and differentiating neurons (expressing the cyclin-dependent kinase inhibitor cdkn1c) (Cerveny et al., 2010)—are reduced (Fig. 2C-H). Additionally, altered patterns of gene expression were observed in the CMZ of gdf6au900 eyes (Fig. S2).

To characterise the mutant CMZs further, we examined expression of Tg[vsx2:GFP]. vsx2 encodes a homeodomain transcription factor expressed throughout the CMZ, in Müller glia and in a subset of bipolar cells (Vitorino et al., 2009). Consistent with fewer cells within the CMZ, we observed a smaller vsx2:GFP-expressing region with only a few cells separating the retinal margin and atoh7:GAP-RFP-expressing RGCs in 60 hpf gdf6au900 mutant retinae (Fig. 2I,J).

Consistent with decreased growth from a smaller CMZ, gdf6a mutant eyes contained fewer proliferative cells in both S phase [marked by bromodeoxyuridine (BrdU) staining] and M phase [marked by phospho-histone H3 (PH3) staining] of the cell cycle (Fig. 2K-N) by 2.5 and 3 dpf (Fig. 2O; n=10 embryos for each genotype). These findings indicate that reduced Gdf6a function is correlated with decreased cell proliferation in the CMZ.

To gauge expression levels of CMZ markers quantitatively, we used real-time PCR (qPCR) in dissected mutant and wild-type sibling larval retinae. Both mutant alleles show nearly identical reduction in transcript levels of genes expressed in proliferating progenitors (ccnd1) and committed precursors (e.g. atoh7) (Fig. 2P). Although in situ hybridisation clearly shows fewer col15a1b-positive cells, qPCR detected only a modest reduction in transcript levels. Not all genes analysed, however, showed decreased expression. A control gene, nr2f5, encoding a transcriptional target of RA signalling (Love and Prince, 2012) was elevated nearly 2.5-fold in gdf6a mutant eyes (Fig. 2P), suggesting increased RA pathway activity.

Fig. 2. gdf6a mutants exhibit decreased expression of stem, progenitor and committed cell genes and reduced proliferation within the CMZ. 
(A-H) Lateral views of whole-mount eyes from 3 dpf embryos (genotype bottom left) showing expression (purple) of various genes (indicated bottom left) in the CMZ. (A,B) col15a1b, a marker of the peripheral putative stem cell compartment, is expressed in the sibling CMZ (A), but reduced in the dorsal and nearly absent in the ventral CMZ of the gdf6au768 eye (B). (C,D) ccnd1 is highly expressed in proliferating progenitors of wild-type CMZs (C), but reduced in gdf6au768mutant eyes (D). (E-H) atoh7 and cdkn1c are expressed in committed precursors in wild-type CMZs (E,G) but in the gdf6au768 mutant eyes they are strongly downregulated (F,H). (I,J) Transverse sections of 3 dpf sibling and gdf6au900 eyes carrying the vsx2:GFP (green) and atoh7:GAP-RFP (red) transgenes highlighting a reduced CMZ in the gdf6au900 mutant (white arrows). (K-N) Coronal sections immunostained for markers of proliferation (green; BrdU incorporation in K,L or PH3 in M,N) and then counterstained with SYTOX Orange (red nuclei). (O) Graph showing numbers of PH3+ mitotic retinal cells in eyes of gdf6a mutant and sibling embryos. All PH3+ cells in ten whole-mount 60 hpf eyes were counted and graphed with standard error bars (95% confidence limits; Student’s t-test, \*\*\*P<0.0004). (P) Graph showing real-time PCR quantification of gene expression changes of col15a1b, ccnd1, atoh7 and nr2f5 in 3 dpf dissected mutant and wild-type retinas normalised to β-actin. Wild-type values for each gene were set to 1 and mutant fold changes were plotted relative to this value (±s.e.).
**gdf6a mutants display RA pathway activity throughout the peripheral CMZ**

RA synthesis and target genes are ectopically activated throughout the circumference of the peripheral-most compartment of the CMZ of gdf6a mutants. Expression of two genes involved in RA synthesis, retinol dehydrogenase (rdh10a) and a retinaldehyde dehydrogenase (aldh1a3), is increased and expanded dorsally in the gdf6a mutant mice (Fig. 3, top two rows). Consequently, and as expected from qPCR experiments, n2f5 is expressed in more cells of the presumptive CMZ (Fig. 3, middle row). Consistently, gdf6a mutant mice carrying an RA-responsive YFP transgene (Perz-Edwards et al., 2001) exhibit expanded YFP expression in the peripheral compartment of the CMZ (Fig. S3). Genes likely to limit RA activity, such as the cytosolic RA binding protein crabp2a (Cai et al., 2012) and the RA-degrading enzyme cyp26a1 (Isken et al., 2008), are expressed in fewer cells in gdf6a mutant eyes (Fig. 3, bottom row). Together, these data indicate that RA signalling is enhanced in the CMZ of gdf6a mutants.

**Enhanced RA pathway activity inhibits eye growth**

We next asked whether excessive RA affects eye size. We first tested whether all wild-type retinal progenitors respond to RA. Embryos carrying the Tg[RARE:YFP] RA reporter transgene (Perz-Edwards et al., 2001) were incubated with 13-cis RA, which can be locally converted to all-trans RA by UV-driven photo-isomerisation to activate the RA pathway (Xu et al., 2012). In 24-36 hpf wild-type embryos, only ventral retinal cells activate the RA pathway reporter transgene in the absence of exogenous all-trans RA (Fig. 4A). UV-mediated activation of RA signalling, however, demonstrated that most, if not all, RPCs are capable of responding to RA mediated activation of RA signalling, however, demonstrated that most, if not all, RPCs are capable of responding to RA.

We next investigated whether pharmacological activation of the RA pathway using AM580, a retinoic acid receptor alpha (RARα) agonist (Gianni et al., 1996), affects eye development similarly to gdf6a mutants. Embryos incubated in AM580 consistently displayed smaller eyes with fewer PH3+ cells (Fig. 4I-M). Pairwise t-test comparisons indicate that both gdf6a mutant and AM580-treated embryos contain significantly fewer PH3+ cells than sibling or DMSO-treated wild-type embryos (Fig. 4M). Permutation testing of relative means (untreated gdf6a/+68 mice and AM580-treated/DMSO-treated wild types) revealed that the proportion of PH3+ cells in gdf6a mutants relative to the number of PH3+ cells in sibling eyes is not statistically different from the proportion of PH3+ cells in AM580-treated eyes relative to wild type (P=0.56; Fig. S4). In addition, RA upregulation is correlated with reduced expression of markers for putative stem and progenitor cells within the CMZ (Fig. 4C-H).

**Inhibition of the RA pathway restores the CMZ in gdf6a mutants**

To evaluate the extent to which misregulation of RA pathway activity contributes to the imbalance in proliferation and differentiation, and subsequent growth of gdf6a mutant eyes, we asked whether reducing RA pathway activity could restore the CMZ in gdf6a mutant retinae. When clutches of embryos from a gdf6a+/768 carrier in-cross were incubated with the panRAR inverse agonist BMS493 (Germain et al., 2009), mutant eyes contained more cells expressing col15a1b, ccnd1 and atoh7 in the peripheral retina (Fig. 5A-F). We also quantified transcript levels for CMZ markers in BMS493-treated eyes relative to DMSO-treated eyes and confirmed in situ hybridisation data that ccnd1 and atoh7 levels were increased (Fig. 5G). Because changes in col15a1b detected by qPCR were modest, we measured the percentage area of col15a1b-positive cells in control and BMS-treated eyes and found that treated eyes contained a nearly 40% larger col15a1b-positive area than did controls (Fig. S5C). Sibling eyes with the same treatment exhibited a noticeable expansion of col15a1b in the ventral retina (Fig. S5B). Together, these data suggest that RA limits expression of CMZ...
markers in gdf6a mutants and contributes to CMZ maintenance during normal development.

Retinal precursors precociously generate neurons in gdf6a mutants

The reduced CMZs in gdf6a mutants could result from changes in cell cycle kinetics within the CMZ and/or altered timing of cell cycle exit and transition of post-mitotic cells into the mature retina. To distinguish between these possibilities, all S-phase cells were first labelled with BrdU for 4 h prior to fixation. Next, BrdU incorporation in cells that had progressed to M phase (PH3+) was evaluated. Wild-type progenitors can progress from S-phase to M-phase in as little as 2.5 h (Cerveny et al., 2010), and so this labelling regime results in 100% of PH3+ cells being labelled by BrdU. In both wild-type sibling and gdf6au768 mutant eyes, we found that all PH3+ cells were also BrdU+ (Fig. 6A,B; n=16 eyes), suggesting that cell cycle kinetics were not dramatically changed in mutant CMZ.

RPCs exit the cell cycle and differentiate in a stereotypical pattern (Cepko et al., 1996; Harris, 1997), with proliferative RPCs ultimately restricted to the CMZ by ∼2.5 dpf (Stenkamp, 2007). To characterise the precocious production of neurons in gdf6a mutants, we analysed the onset and progression of expression of atoh7 and crx, which both exhibit dynamic, fan-shaped ventral-nasal to dorsal-temporal patterns of expression (Masai et al., 2000; Neumann and Nuesslein-Volhard, 2000; Shen and Raymond, 2004). By ∼28 hpf, atoh7 is expressed in a small patch of ventral RPCs in wild-type eyes (Fig. 6A,B; n=16 eyes), suggesting that cell cycle kinetics were not dramatically changed in mutant CMZ.

RPCs exit the cell cycle and differentiate in a stereotypical pattern (Cepko et al., 1996; Harris, 1997), with proliferative RPCs ultimately restricted to the CMZ by ∼2.5 dpf (Stenkamp, 2007). To gauge the balance between proliferation and differentiation after the onset of retinal neurogenesis in gdf6a mutants, we labelled all S-phase cells with BrdU for 10 h beginning at ∼50 hpf. With this labelling regime, only a small proportion of cells in wild-type eyes (primarily RGCs) are BrdU negative and are likely to have exited the cell cycle prior to BrdU treatment (Fig. 6C; red cells; Ohnnuma et al., 1999). By contrast, all layers of gdf6a mutant retinae contained a much larger proportion of BrdU-negative cells (Fig. 6D, white arrows). We observed this striking pattern of precocious cell cycle exit and differentiation in all embryos (n=60 total genotyped embryos; 14 gdf6au768 mutants). These data indicate that the pace of neurogenesis is accelerated in gdf6a mutant retinae.

To characterise the precocious production of neurons in gdf6a mutants, we analysed the onset and progression of expression of atoh7 and crx, which both exhibit dynamic, fan-shaped ventral-nasal to dorsal-temporal patterns of expression (Masai et al., 2000; Neumann and Nuesslein-Volhard, 2000; Shen and Raymond, 2004). By ∼28 hpf, atoh7 is expressed in a small patch of ventral RPCs in wild-type eyes (Fig. 6E) whereas a larger proportion of ventral and central RPCs express atoh7 in gdf6a mutant eyes (Fig. 6F). Likewise, expression of crx, which is initially transcribed in the ventral-nasal and ventral-central retina at ∼36 hpf in wild-type eyes (Fig. 6G), is more broadly expressed in gdf6a mutant eyes (Fig. 6H), similar to wild-type crx expression at 48 hpf (compare Fig. 6H and 6I). Quantitative PCR in gdf6au768 mutant retinas corroborated the upregulation of atoh7 and crx (1.5- and 2-fold greater, respectively), as well as of the RA-target gene nr2f5 (2.5-fold greater) (Fig. 6K).
To explore the dynamic production of atoh7-positive neurons in gdf6a mutants, we imaged living Tg[atoh7:GFP] embryos. Initiation of GFP fluorescence occurred at the same time in gdf6a<sup>m0906</sup> mutants and siblings (Fig. 6L,M, top panels), but the number of GFP-expressing cells increased more rapidly and RGC axons extended earlier in mutant retinae (Fig. 6L,M, lower panels; Movies 1, 2), supporting the idea of expedited differentiation in gdf6a mutants.

**Precocious RA-mediated differentiation depletes retinal progenitors**

Because RA pathway activity is enhanced in gdf6a mutant retinae, we examined whether RA could modulate cell cycle exit and neurogenesis of RPCs by pharmacologically activating or inhibiting RA signalling and then examining atoh7 and Tg[atoh7:GFP] expression. Similar to gdf6a mutant retinae, wild-type embryos incubated in AM580 exhibited significantly more atoh7<sup>+</sup> cells (Fig. 7A-F). At 28 hpf, ~2% of the wild-type retinal volume was GFP<sup>+</sup>, whereas it was more than doubled in both gdf6a mutant and AM580-treated wild-type retinae (Fig. 7C,D,K). By 40 hpf, 3% of wild-type retinal volume was GFP<sup>+</sup>, but this percentage was nearly AM580-treated wild-type retinae (Fig. 7C,D,K). By 40 hpf, 3% of AM580-treated wild-type and treated wild type versus DMSO-treated wild type). (E,F) The number of embryos with staining pattern similar to that shown is indicated as a fraction in lower right corner of images. (G) qPCR quantification of relative gene expression levels for gdf6a<sup>u768</sup>, atoh7<sup>+</sup>, and sibling eyes contained similar GFP<sup>+</sup> retinal volumes whereas DMSO-treated gdf6a<sup>u768</sup> mutant eyes contained substantially larger GFP<sup>+</sup> retinal volumes (Fig. 7I,J,L; P = 0.001 for BMS614-treated u768 mutants versus DMSO-treated u768 mutants). Further suggesting that precocious neurogenesis underlies the gdf6a mutant phenotype, we found that mutant eyes contain a higher proportion of GFP<sup>+</sup> neurons in the RGC layer by 80 hpf (Fig. 7M-O; Fig. S6) and more GFP<sup>+</sup> cells in the inner nuclear layer, suggesting that more atoh7-positive cells are generated earlier (Fig. 7N, white arrows). Together, these observations suggest that RA can promote cell cycle exit and the production of atoh7-positive neurons in developing retinae.

**DISCUSSION**

This study reveals that opposing activities of Gdf6a from the dorsal retina and RA from the ventral retina influence RPCs as they transition from proliferation to differentiation, ultimately regulating eye size. Our data demonstrate that in addition to previously demonstrated roles in DV patterning, the combined action of these pathways regulates when RPCs exit the cell cycle. Our genetic and pharmacological manipulations illustrate that Gdf6a-mediated inhibition of RA pathway activity modulates the timing of retinal neurogenesis and suggest that RA-mediated precocious differentiation of the RPC pool might underlie the microphthalmic phenotype in vertebrates carrying GDF6 mutations.

**Gdf6a regulates retinal growth**

Our study adds to others linking eye defects to abrogation of Gdf6 function in fish, mice and humans (Asai-Coakwell et al., 2007, 2013; den Hollander et al., 2010; Gosse and Baier, 2009; Hanel and Hensey, 2006), but the mechanisms connecting loss of gdf6a to microphthalmia have remained unclear. It has been suggested that apoptosis contributes to the small eye phenotype in gdf6a mutants (den Hollander et al., 2010; Gosse and Baier, 2009). Our study and another (French et al., 2013), provide evidence that microphthalmia occurs independently of cell death in gdf6a mutants. Pronounced differences in eye size are observed in...
mutants, which exhibit levels of retinal apoptosis comparable to wild type, and in gdf6au900 embryos when apoptosis is blocked. Despite these differences in apoptosis, both gdf6a alleles exhibit similar changes in gene expression, proliferation and differentiation. Moreover, analyses of gdf6au768 mutants suggest that abnormal initiation of retinal DV patterning is not a prerequisite for gdf6a-linked microphthalmia.

Gdf proteins regulate cell cycle exit and differentiation through various mechanisms
Members of the BMP family regulate cell fate, proliferation, differentiation, and apoptosis during embryonic development. As a result, BMPs and their antagonists have been implicated in control of tissue and organ size (Beites et al., 2009; Sartori et al., 2013). The presence of fewer proliferating cells and the accelerated expression of differentiation genes in the early retinæ of gdf6a mutants suggest that the BMP-related protein Gdf6a is part of a genetic circuit that balances progenitor cell proliferation and differentiation to control eye size in zebrafish. In mammals, GDF11 and GDF8 (MSTN) balance proliferation and differentiation in different contexts. Both act as auto-inhibitory feedback signals to directly and reversibly regulate cell cycle exit of neuronal progenitors in the olfactory epithelium (Wu et al., 2003) and myoblasts (McPherron and Lee, 1997), respectively. GDF11 also modulates retinal size in mice but
through a different mechanism. During early neurogenesis, expression of GDF11 and its inhibitor, follistatin, influence the timing of expression of Atoh7 (also known as Math5) without affecting expression of cell cycle regulators (Kim et al., 2005). Despite diverse mechanisms by which these GDF proteins act, they promote similar consequences for timing of cell cycle exit and differentiation.

**Gdf6a-antagonised RA pathway activity regulates cell cycle exit and differentiation**

Our study reveals that a key role for Gdf6a is to limit RA activity in RPCs. We show that enhancing RA activity accelerates the production of neurons from RPCs and this presumably depletes the pool of proliferative precursors. Such a role for RA is consistent with studies showing that RA promotes neuronal differentiation in vitro (reviewed by Janesick et al., 2015). In the vertebrate retina, RA can skew the fate of post-mitotic photoreceptor precursors towards rod and red-sensitive cone fates (Hyatt et al., 1996; Kelley et al., 1999; Mitchell et al., 2015; Stevens et al., 2011) and in vitro studies of oligodendrocyte precursors suggest that the timing of differentiation is modulated by retinoid signalling (Barres et al., 1994). Similarly, our data indicate that RA influences the timing of cell cycle exit and neuronal differentiation in the developing central retina and CMZ. Consequently, unlike other Gdfs that regulate timing of neurogenesis by promoting cell cycle exit (Gokoffski et al., 2011; Kim et al., 2005; Wu et al., 2003), our data suggest that Gdf6a is permissive for proliferation and, in balance with RA signalling, governs the timing of differentiation in the retina to preserve the pool of progenitors needed for multiple rounds of neurogenesis.

Although our data suggest that antagonism between Gdf6a and RA regulates RPC behaviours, Gdf6a could also interact with other signalling pathways to influence proliferation and differentiation. For instance, Fgf signalling maintains a subpopulation of RPCs in a proliferative state (Wong et al., 2015), and Hedgehog signalling is implicated in RPC proliferation and differentiation decisions (Borday et al., 2012; Locker et al., 2006; Masai et al., 2000). Cross-talk and integration between these pathways and BMP have been demonstrated in many diverse progenitor cell populations, including those in the developing neural tube (e.g. Horner and Caspary, 2011; Sasai et al., 2014).

**Intersection between morphogenetic and neurogenic effects of Gdf6a**

In addition to the requirement for Gdf6a to establish and maintain dorsal retinal character, we suggest an additional role for Gdf6a during eye development. Our data suggest that Gdf6a modulates RA pathway activity, which in turn influences the probability of RPC

Fig. 7. RA pathway activation accelerates retinal neurogenesis. (A-F) Lateral views of eyes of wild-type (A,B) or Tg[atoch7:GFP] (C-F) embryos treated with AM580 (B,D,F) or vehicle control (DMSO; A,C,E) fixed at the times indicated to the left of the rows, and showing expression of either atoh7 (purple; A,B) or immunostained for GFP (green; C-F). (G-J) Lateral views of eyes of gdf6au768 mutants expressing the atoh7: GFP transgene treated with BMS614 (H,J) or vehicle control (DMSO; G,I), fixed at the times indicated to the left of the rows, and immunostained for GFP (green). Note that GFP expression does not extend beyond its ventral/ nasal initiation site in the BMS614-treated eye at 28 hpf. (K,L) Graphs showing average proportional volume of retina containing atoh7:GFP-positive cells at 28 and 40 hpf in the conditions indicated along the x-axes for activation (K) and suppression (L) of RA pathway, plotted with standard error bars (95% confidence limits; n=5 embryos for each condition). (M,N) Transverse cryosections of wild-type sibling (M) and gdf6au900 (N) eyes at 80 hpf showing expression of the atoh7:GFP transgene (green) and counterstained nuclei with DAPI (red). White arrows show ectopic GFP-positive cells in the inner nuclear layer. (O) Graph of the average number of atoh7:GFP-positive cells per area of retina in wild-type and gdf6au900 mutant eyes (n=6; standard error bars, 95% confidence limits; Student’s t-test **P=0.0014).
cell cycle exit by regulating proliferative versus neurogenic divisions. Bolstering this idea, we observed enhanced and accelerated expression of the HHLH transcription factor-encoding gene atoh7, which is required for RGC production (Kay et al., 2001). Furthermore, we show that normal timing of atoh7 expression is restored when RA pathway activity is downregulated in gdf6a mutants. Two observations from studies in medaka fish also support a connection between RA, atoh7 expression, and eye size. First, a global analysis of the regulatory inputs driving retinal neurogenesis identified a potential positive role for RA upstream of atoh7 expression (Souren et al., 2009), and, second, a study that expanded atoh7 expression throughout the developing retina generated smaller eyes (Sinn et al., 2014).

How might an imbalance between RA and Gdf6a contribute to the small eyes in gdf6a mutants? We observe a smaller CMZ in mutant eyes as well as in eyes in which the RA pathway is activated early in development. Consequently, the failure of gdf6a eyes to grow robustly could be due to problems in both establishment of the CMZ and generation of neurons from the CMZ. Although studies have begun to examine the origins of the CMZ (Heermann et al., 2015; Kwan et al., 2012), how this stem cell niche is established and maintained is not clear. One possibility is that in gdf6a mutants, precocious differentiation of RPCs depletes the pool of progenitors that ultimately populate the CMZ, thus generating a smaller CMZ.

Coupled with the possibility of fewer stem and progenitor cells in the CMZ of gdf6a mutants, defective Gdf6a/retinoid signalling within the CMZ is likely to further limit eye growth by exhausting the stem cell/progenitor population. Many signalling pathways required during early eye development, including BMP and RA pathways, remain active within the CMZ (Harris and Perron, 1998; Sharma et al., 2005; Shawi and Serluca, 2008). Previous work from our laboratories supports a model for differentiation dynamics within the zebrafish CMZ with at least two sets of environmental signals coexisting. One set of signals promotes proliferation of stem and progenitor cells and the other limits proliferation of rapidly cycling precursors by encouraging differentiation (Cerveny et al., 2010). Although a molecular basis for this so-called ‘environmentally driven differentiation’ has yet to be established, our current work suggests that Gdf6a and RA are two secreted signals that establish an appropriate balance between proliferation and differentiation in the CMZ. Together, our results support a model in which dorsally secreted Gdf6a balances RA pathway activity, controlling the transition from proliferation to differentiation during eye growth.

MATERIALS AND METHODS
Zebrafish lines
Eggs were collected by natural spawning, raised at 28.5°C in either fish water or E3 embryo medium (Nüsslein-Volhard and Dahm, 2002) and staged according to Kimmel et al. (1995). Transgenic and mutant lines are listed in supplementary Materials and Methods. To prevent pigment formation, 0.003% phenylthiourea (PTU, Sigma) was added to the fish water between 20 and 24 hpf.

ENU mutagenesis and eye screening
Mutagenesis was performed in wild-type male AB/TL fish by four rounds of 3 mM ENU treatment as previously described (Valdivia et al., 2011; van Eeden et al., 1999). Eyes of F3 larvae were screened for morphological abnormalities.

Genetic mapping, cloning and genotyping
The gdf6a

\( \text{gdf6a}^{AT} \)

mutation was mapped by bulk segregant analysis with simple sequence length polymorphisms to LG16 (Telbott and Schier, 1999). Markers Z13555 and Z45043 flanked a ∼2 Mb interval containing gdf6a.
white balance was digitally adjusted using the exposure option in Photoshop CS6. For quantifying TUNEL<sup>+</sup>, PH3<sup>+</sup> and PH3<sup>+/BrdU</sup> cells, images were blind-counted using ImageJ. To quantify the volume of retinae containing GFP<sup>+</sup> cells, the fluorescence of each z-plane of confocal stacks (~60 µm) was thresholded, images compiled and a contour surface drawn for both the entire eye and the fluorescent portion using the surface contour feature and either manual selection (for the entire eye) or auto selection (for GFP fluorescence) of Imaris. For eye and section size measurements, images taken from a lateral view at fixed magnification were opened in ImageJ. The freeshare selection tool was used to select to outline the circumference of each eye and then the measure function was used to calculate the area. Data were exported to R or Prism (GraphPad) for statistical analysis and graphing. Either permutation testing with 10,000 shuffle tests or Student’s t-tests with 5% cut-offs were used as indicated in the Results and figure legends. See supplementary Materials and Methods for details of permutation testing.

**Time-lapse imaging**

Confocal time-lapse imaging was performed on a Leica SP8 confocal microscope in an air chamber heated to 28.5°C. Once anaesthetised with MS-222 (Sigma), embryos were immobilised in 1.2% low melting point agarose. Photoactivation was performed with a single pulse of UV light (360-375 nm) illuminating the entire eye for 30 s, using a Zeiss 510 NLO two-photon microscope with 5 mW of power. Embryos were mounted in 1.2% low melting point agarose (Sigma), and imaged from a lateral view using water immersion objectives. Z-stacks were collected at intervals of 20 min for 9 h, beginning at 28.5 hpf.

**Pharmacological manipulation of apoptotic or RA pathways**

To block apoptosis, embryos were incubated with either 200 or 400 µM of the pan-caspase inhibitor Z-VAD-FMK (Promega) from 14 to 31 hpf (Williams et al., 2000). The drug was washed out and embryos were either fixed or incubated in fish water until 3 dpf and then fixed.

To activate RA pathway activity, embryos were soaked in 25 nM AM580 (Sigma), a pan-retinoic acid receptor (RAR) agonist, beginning at 24 hpf for the times indicated in figure legends. To inhibit the pathway, embryos were soaked in either 15 µM BMS493 (Sigma), an RARz inverse agonist, or 15 µM BMS614 (Tocris), an RARz antagonist, for 14-36 h from the 12-14 somite stage, which is after initial dorsal-ventral patterning of the eye and brain. After drug treatments, embryos were washed twice with embryo medium and then incubated until fixation with 4% paraformaldehyde at 28, 40 or 60 hpf. For optical manipulation of RA activity, Tg(RARE:YFP)<sup>+</sup> embryos were soaked in 5 nM 13-cisRA (Sigma; Xu et al., 2012) at 24 hpf for 1 h in the dark and then mounted in 1.2% low melting point agarose. Photoactivation was performed with a single pulse of UV light (360-375 nm) illuminating the eye for 30 s, using a Zeiss 510 NLO two-photon microscope with 5 mW of power. Embryos were fixed at 33 hpf in 4% paraformaldehyde and immunostained for GFP.

**Quantitative real-time PCR**

Quantitative RT-PCR was performed with total RNA extracted from dissected fixed retinae at 28 hpf and 3 dpf. Briefly, embryos were fixed in 4% paraformaldehyde overnight and transferred to RNase-free PBS, after two washes for 5 min each. Embryo tails were genotyped using KASP assays (Kettleborough et al., 2013). Heads were pooled by genotype and retinae dissected manually using insect pins. RNA was extracted using RecoverAll Total Nucleic Acid Isolation Kit for FFPE (Ambion) from 40 retinas for each condition (wild-type sibling versus mutant at each time point). RNA quality control was performed with the Experion LabChip (Bio-Rad). cDNA was synthesised and amplified with the Transplex Whole Transcriptome Amplification Kit (Sigma), and quantified using a Nanodrop 2000c. Quantitect primers (Qiagen) were used to amplify col1a1b (QT0215941), ccdn1 (QT02178519), atoh7 (QT02188459), wnt7b (QT02125424), adlb1a3 (QT02116113), cxr1 (QT02229584), cdh1c (QT02052253) and β-actin (QT02174907). Real-time PCR was performed on a BioRad iCycler using GoTaq qPCR Master Mix (Promega). Fold change in RNA levels was calculated using the ΔΔCt method, and expression normalised to β-actin levels (Livak and Schmittgen, 2001).

**Acknowledgements**

We thank members of the Cerveny and Wilson labs for helpful discussions and Chester Ismay for help with R and statistical analyses.

**Competing interests**

The authors declare no competing or financial interests.

**Author contributions**


**Funding**

This study was supported by the National Eye Institute of the National Institutes of Health [R15 EY03745-01 to K.L.C.]; M. J. Morduck Charitable Trust grants (to K.L.C.); Cancer Research UK [C11768/A11631 to K.L.C. and S.W.W.]; the BecaS Chile scholarship program-CONICYT (L.E.V.); Medical Research Council grants [G0900994 and MR/L003775/1 to S.W.W. and G.G.]; Wellcome Trust grants [088175, 089227, 104682] to S.W.W.; the European Commission Seventh Framework Programme (EU FP7) (Z-HEALTH (S.W.W.)); and a Biotechnology and Biological Sciences Research Council grant [BB/H012516/1 to S.W.W.]. Deposited in PMC for immediate release.

**Supplementary information**

Supplementary information available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.130922/-/DC1

**References**


