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Transcriptome Analysis of the Planarian Eye Identifies ovo as a Specific Regulator of Eye Regeneration

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SUMMARY

Among the millions of invertebrate species with visual systems, the genetic basis of eye development and function is well understood only in Drosophila melanogaster. We describe an eye transcriptome for the planarian Schmidtea mediterranea. Planarian photoreceptors expressed orthologs of genes required for phototransduction and microvillus structure in Drosophila and vertebrates, and optic pigment cells expressed solute transporters and melanin synthesis enzymes similar to those active in the vertebrate retinal pigment epithelium. Orthologs of several planarian eye genes, such as bestrophin-1 and Usher syndrome genes, cause eye defects in mammals when perturbed and were not previously described to have roles in invertebrate eyes. Five previously undescribed planarian eye transcription factors were required for normal eye formation during head regeneration. In particular, a conserved, transcription-factor-encoding ovo gene was expressed from the earliest stages of eye regeneration and was required for regeneration of all cell types of the eye.

INTRODUCTION

The vertebrate eye is a structure of striking complexity in form and function. Consequently, understanding the evolution and development of eyes has been a classic challenge. The human eye is also subject to numerous pathologies that are poorly understood, such as heritable retinopathies and age-related degeneration. Genetic studies in model invertebrates have the potential to advance the understanding of eye evolution and development, and of the functions of conserved genes associated with eye disorders.

The relevance of invertebrate models to vertebrate systems depends in part on whether homology exists between most bilaterian eyes, a difficult point to establish based on morphological studies alone. Establishing some degree of common ancestry between vertebrate and invertebrate (primarily Drosophila) visual systems has been a success of comparative molecular genetics. Two findings figure prominently in understanding the relationship between diverse animal eyes. First, two photoreceptor neuron categories, rhabdomeric (microvillar) and ciliary, exist throughout the Bilateria and rely on conserved R-opsin and C-opsin signal transduction pathways, respectively (Arendt, 2003). Second, embryonic development of multiple eye types involves Pax-6, Sine oculis, Eyes absent, and Otx gene family members. These observations have led to the suggestion that photoreceptor cell types were already present prior to the existence of the Bilateria, and that the common ancestor of the Bilateria utilized transcription factors for eye development still commonly used in extant eyes (Nilsson, 2009).

To explore many conserved features of eye biology, additional invertebrate model eyes must be established. The morphology, cell type composition, and set of gene activities present in ancestral bilaterian eyes remain largely unknown, and can only be inferred using data from multiple extant eyes belonging to diverse animal phyla. Invertebrate models are not yet established for extensive genetic study of several common aspects of eye biology not characteristic of Drosophila eyes, such as the formation of optic cups. Furthermore, many genes associated with eye disease have not yet been identified and studied in invertebrate models. Certain invertebrate species allow for study of regenerative repair of eye damage, an increasingly important therapeutic approach.

The planarian Schmidtea mediterranea is an emerging invertebrate model system that is highly amenable to gene function studies with RNAi. Planarians are ideal for the study of eye evolution because they are members of the Lophotrochozoa, the sister grouping of phyla to the Ecdysozoa (which includes Drosophila and Caenorhabditis elegans), and therefore exist at an important and understudied position in the animal phylogeny (Tessmar-Raible and Arendt, 2003). Planarian eyes are true cerebral eyes, as they connect via axon tracts to the brain (Agata et al., 1998), and express orthologs of Otx (Umesono et al., 1999), Sine oculis (Pineda et al., 2000), and Eyes-absent (Mannini et al., 2004). Planarians have rhabdomeric photoreceptor neurons (PRNs), pigment cells (PCs), and a pigmented optic cup structure - features that are common among cerebral eyes (Figure 1A). Photoreceptive organelles in the planarian eye face the optic cup in an inverse orientation, similar to the orientation...
of ciliary vertebrate photoreceptors with respect to the retinal pigment epithelium (RPE) (Figure 1A). Finally, planarians possess unique abilities to regenerate entire eyes, and replenish eye tissue throughout adulthood. These abilities require a population of adult regenerative cells (neoblasts) that includes pluripotent stem cells (Wagner et al., 2011).
Here we use eye purification and RNA-seq to identify most genes active in planarian eyes. These data demonstrate conserved features of the R-opsin signaling cascade, candidate rhodomeric microvillus-regulating genes, and unexpected similarities between rhodomeric and ciliary cell types. In addition, a high degree of similarity exists between the types of solute transporters expressed in planarian optic PCs and the vertebrate RPE, suggesting that optic pigment cells have an ancient role as an accessory eye cell type distinct from photoreceptors. We describe several conserved transcription factors expressed in the planarian eye that are functionally required for eye regeneration, including a central role for the conserved gene ovo in formation of all eye progenitors.

RESULTS

Planarian Eye Purification and the Eye Transcriptome

To obtain pure eye tissue for gene expression analysis, we developed a dissociation protocol for isolating ~200 morphologically intact planarian eyes in 1–2 hrs (Figure 1B). Greater than 96% of cells in the purified eye preparation were indeed eye cells, as determined using an opsin RNA probe for PRNs and melanin as a marker for PCs (Figure 1B). RNA from purified eyes was used to generate a cDNA library for quantitative RNA sequencing (RNA-seq). Animals were fed prior to eye harvesting to stimulate growth and incorporation of new cells in eyes. All genes previously described to be expressed in planarian eyes, and many phototransduction-related genes, displayed at least 4-fold enrichment in our eye reads compared to reads from control tissue (ventral, anterior tissue enriched for neurons), in terms of fragments per kilobase per million fragments mapped (FPKM) values (Figures 1C–1E) (See Experimental Procedures for details). 

Expression of Microvillus-Related Genes in Photoreceptor Neurons

Unexpectedly, orthologs of genes involved in the function and development of auditory hair cells displayed enriched expression in planarian eyes and were prominently represented in GO analysis (Figures 2B and 2C; Table S3). Like planarian photoreceptors, hair cells are sensory neurons with abundant apical microvilli. Microvilli are actin-based structures, and we identified enriched PRN expression of genes encoding actin (Smed-actin-1, and STIM (Smed-stim) (Figures 2B and S1), which regulate intracellular calcium levels (Smyth et al., 2010). PRNs also expressed genes encoding the cGMP pathway components guanylate cyclase (Smed-gucy-1, Smed-gucy-2), cGMP-dependent phosphodiesterase (Smed-cgs-pde), RGST/9 (Smed-rgs6/7/9), a cGMP-gated ion channel (Smed-cng), and a hyperpolarization-activated cyclic nucleotide-gated channel (Smed-hcn) (Figures 1E, 2B, and S1). Many of these components mediate signaling downstream of C-opsin in vertebrates (Arendt, 2003), but we were unable to identify an ortholog of C-opsin in planarians. GO analysis of the RNA-seq data indicated that Rhodopsin signaling, cGMP signaling, and intracellular calcium regulation were all enriched categories in the data set of eye-expressed genes (Table S3).

Expression of Microvillus-Related Genes in Photoreceptor Neurons

Unsurprisingly, orthologs of genes involved in the function and development of auditory hair cells displayed enriched expression in planarian eyes and were prominently represented in GO analysis (Figures 2B and 2C; Table S3). Like planarian photoreceptors, hair cells are sensory neurons with abundant apical microvilli. Microvilli are actin-based structures, and we identified enriched PRN expression of genes encoding actin (Smed-actin-1), the actin-regulating proteins Ezrin/Radixin/Moesin (Smed-erm), Clic (Smed-clc), Maguk (Smed-maguk), Gelsolin (Smed-gls), and the actin-based motor Myosin VI (Smed-myovI). These genes have all been shown to have roles in morphogenesis and function of vertebrate hair cells (Gagnon et al., 2006; Kitajiri et al., 2004; Mburu et al., 2006, 2010; Self et al., 1999). Auditory hair cells of human and mouse also express Usher syndrome genes, which function in morphogenesis of microvillus bundles (Frolenkov et al., 2004). Planarian PRNs also expressed genes encoding the cGMP pathway components guanylate cyclase (Smed-gucy-1, Smed-gucy-2), cGMP-dependent phosphodiesterase (Smed-cgs-pde), RGST/9 (Smed-rgs6/7/9), a cGMP-gated ion channel (Smed-cng), and a hyperpolarization-activated cyclic nucleotide-gated channel (Smed-hcn) (Figures 1E, 2B, and S1). Many of these components mediate signaling downstream of C-opsin in vertebrates (Arendt, 2003), but we were unable to identify an ortholog of C-opsin in planarians. GO analysis of the RNA-seq data indicated that Rhodopsin signaling, cGMP signaling, and intracellular calcium regulation were all enriched categories in the data set of eye-expressed genes (Table S3).
Figure 2. An In Situ Hybridization Screen of Genes with Enriched Expression in Planarian Eyes

(A) Schematic of tissue types in the head that appear in expression patterns. PRN expression domains curve toward the midline, and PC expression domains curve away from the midline.

(B) In situ hybridization of eye-enriched transcripts, grouped by predicted function. Full names and additional orthology information are given in Table S1.

(C) Plot of the log2 of fold enrichment (FPKM eye sample/FPKM control sample) for genes screened (see also Table S2). Values for rhabdomeric phototransduction and cGMP pathway genes are shown in Figure 1. Table shows FPKM values for genes in the eye sample and summarizes expression data from vertebrate (V), Drosophila (Dm), and planarian (Sm). PR, photoreceptor neuron; PC, optic pigment cell; HC, inner ear hair cell; asterisk indicates that planarian gene orthology could only be assigned to a broad gene family for which functions have been identified in the eyes of Drosophila or vertebrate.

Scale bar, 200 μm.

See Figures S1 and S2 as well.
been described to be expressed in *Drosophila* photoreceptors. Therefore, our analysis describes unexpected similarity between a rhabdomeric photoreceptor and auditory hair cells, identifying genes that are candidates to regulate microvillus-like apical membrane specialization.

**Genes of the Pigmented Optic Cup**

The vertebrate RPE supports photoreceptor function by providing organic molecules, maintaining extracellular ion concentrations, phagocytosing aging photoreceptor components, and absorbing light energy (Strauss, 2005). Many genes expressed in planarian PCs were orthologs of genes important for the support function of RPE cells. The metabolic rate of the vertebrate retina necessitates high levels of available glucose. Planarian PCs expressed orthologs of Glut3 (*Smed-glut3*) (Figures 2B and 2C) and MCT transporters (*Smed-mct-1* and *Smed-mct-2*) (Figures 2B and 2C), which transport glucose to the retina (Ban and Rizzolo, 2000) and remove lactic acid waste (Bergersen et al., respectively). Lactic acid uptake is coupled to proton uptake (Lin et al., 1994; Lin and Miller, 1991) and two genes encoding pH-regulatory proteins, a Na+/H+ exchanger regulatory cofactor (*Smed-nhe-rf*) and a sodium bicarbonate cotransporter (*Smed-nabct*), were expressed specifically in the planarian PCs (Figures 2B and 2C). High metabolic activity in the retina results in excess water production, which is eliminated using chloride gradients across the RPE (Strauss, 2005). Orthologs of the RPE-expressed chloride channels Bestrophin-1 (*Smed-best-a*) and Cfr (*Smed-cfr*) were strongly expressed in the PCs of planarian eyes (Figures 2B and 2C).

Planarians are similar to vertebrates, but differ from most other invertebrates, in the use of melanin as the primary eye shading pigment (Hase et al., 2006; Strauss, 2005). Among the most abundantly expressed genes in planarian PCs were those encoding orthologs of enzymes required for melanin synthesis in vertebrates, including Tyrosinase (Lapan and Reddien, 2011) (Figure 1D), Aromatic amino acid hydroxylase (Nishimura et al., 2007) (see “*tph*,” Figure 1D); and Dopa decarboxylase (*Smed-ddc*) (Figures 2B and 2C). PCs also expressed orthologs of Quinoid dihydropteridine reductase (*Smed-qdr*), which produces an essential cofactor of tyrosine/phenylalanine hydroxylase (*Schalleuter et al., 2008*); and Glutathione-S-transferase (*Smed-gst*), which catalyzes addition of glutathione during pheomelanin polymerization (del Marmol et al., 1996) (Figures 2B and 2C).

 Peroxide is generated by melanin-synthesizing enzymes and is required for melanin polymerization, but it can also cause cytotoxicity in melanocytic cells (Mastore et al., 2005). The GO category for “Response to hydrogen peroxide” was significantly enriched in the eye RNA-seq data (Table S3). Two orthologs of *catalase*, *Smed-cat-1* and *Smed-cat-2*, were expressed in the planarian PCs. Similar to *tyrosinase*, *Smed-cat-1* was one of the most strongly and specifically expressed genes in the planarian PCs (Figures 2B and 2C and Table S2). Glutathione-S-transferase might also function as an antioxidant enzyme in the eye (Giblin, 2000; Singhal et al., 1999). Therefore, planarian and vertebrate optic PCs express similar melanin-synthesizing enzymes and enzymes that protect from oxidative damage.

**Heterogeneity of the PRN and PC Populations**

Recently, planarian photoreceptor neuron heterogeneity has been described, with pro-hormones and *smad6/7-2* expressed in distinct domains of the PRN population (Collins et al., 2010; González-Sastre et al., 2012). *Smed-sox3*, *Smed-best-2*, *Smed-pcdhP-1*, and *Smed-pltcr* were expressed only in anterior photoreceptors (Figure S2A). *Smed-fzdP-1* was expressed primarily in dorsal and anterior photoreceptors, as well as progenitors near the eye (Figure S2A). *Smed-zfp-2*, *Smed-pectaire*, and *Smed_19866* were expressed only in posterior photoreceptors (Figure S2B). We also identified a gene, *Smed-actin-2*, expressed in a subset of pigment cup cells, indicating that heterogeneity also exists within this population (Figure S2C).

**Identification of an Eye-Specific Transcription Factor-Encoding Gene, *Smed-ovo***

Molecular regulators remain to be identified for key steps in planarian eye formation, including progenitor migration, homotypic cell aggregation, mesenchymal-to-epithelial transition, and cupping morphogenesis. In situ screening identified enriched expression in the planarian eye for many genes that are good candidates to encode proteins regulating these processes, including 14 kinases, 5 protocadherins, and 18 signaling receptors (Figures 2B, 2C, and S1).

Transcription factors that control eye development in both *Drosophila* and vertebrates have received close attention for their capacity to elucidate the evolution of eye development. Here, we have identified ten conserved genes predicted to encode transcription factors with enriched expression in planarian eyes (Figures 2B and 2C). The gene with the most prominently enriched expression was a member of the Ovo family of zinc finger transcription factor-encoding genes (Figure S3), which includes the *Drosophila* gene ovo (*shavenbaby*) and mouse ovo1-3 genes. Expression of *Smed-ovo* (ovo) was detected in both PRNs and PCs, as well as in mesenchymal cells posterior to the eye (Figure S3). At later regeneration time points ovo+ eye aggregates formed in the anterior blastema, while dispersed cells posterior to the eye remained visible. This pattern was similar to a recently defined population of regenera-

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ovo Expression Is Required for Eye Regeneration
RNAi of ovo followed by decapitation resulted in animals that failed to regenerate eyes (Figure 3D). These animals also lacked detectable tyrosinase mRNA and Arrestin protein (Figure 3E), and no eye structure could be detected by differential interference contrast microscopy (DIC) (Figure S4B). We studied ovo(RNAi) animals using six-1/2/eya co-expression to label all eye progenitors, and otxA/eya and sp6-9/eya co-expression to label PRN and PC progenitors, respectively (Lapan and Reddien, 2011). ovo RNAi resulted in failure to generate any eye aggregate (primordium), and loss of most eye progenitors (Figures 4A and 4B). We observed no defects that were unrelated to the eyes, consistent with the highly specific expression of this gene. For example, other cell types of the head, such as sp6-9′/eya′ cells of the head rim appeared unaffected (Figure 4A). Therefore, eyes and eye progenitors are strongly and specifically affected in ovo(RNAi) animals.

Formation of ovo+ Progenitors Requires Expression of Other Eye Transcription Factors
In gene regulatory networks involved in Drosophila and vertebrate eye development, several transcription factors that regulate eye formation are required for the expression of each other (Silver and Rebay, 2005; Zuber et al., 2003). We tested whether ovo+ progenitor cells are sensitive to expression of other planarian eye transcription factors. RNAi of six-1/2 and eya resulted in animals with greatly reduced or absent ovo signal in the eyes and eye progenitor region (Figures 4C and 4D). RNAi of the cell type-specific transcription factors otxA and sp6-9, required for PRN and PC regeneration respectively, also impacted the presence of ovo+ progenitors (Figures 4E and 4F). RNAi of otxA led to a 34% reduction in ovo+ cells; this reduction was primarily a result of loss of ovo+ PRN progenitors (Figures 4E and 4F), because most remaining ovo+ cells were sp6-9′. Similarly, RNAi of sp6-9 led to a 60% reduction in ovo+ cells, primarily a result of loss of ovo+ PC progenitors, because most remaining ovo+ cells were otxA+ (Figures 4E and 4F). These large decreases indicate that ovo-expressing cells, even in early stages of eye progenitor formation, are sensitive to the expression of six-1/2, eya, otxA, and sp6-9 transcription factors.

ovo Is Expressed in a Population of Eye Progenitors during Homeostasis and Is Required for Maintenance of Intact Eyes
The specificity of ovo expression for eyes and eye progenitors allowed us to ask for the first time whether subsets of neoblasts in uninjured animals are specialized for particular differentiation paths. In intact animals undergoing normal adult homeostasis, ovo was expressed not only in the eye but also in sparse cells posterior to the eye and anterior to the pharynx (Figure 5A). Adult planarians undergo perpetual tissue turnover (Newmark and Sánchez Alvarado, 2000), but the identity and origin of progenitors that replenish eyes in uninjured animals is unknown. ovo+ cells posterior to the eye in intact animals expressed eya and six-1/2 (Figure 5B), and those...
nearer to the eye also expressed markers for differentiated photoreceptor neurons (trpc-1) or PCs (tyrosinase) (Figure S5A). Therefore, ovo+ cells that exist posterior to the eye in intact animals have a gene expression profile seen elsewhere only in cells of the eye.

The localization of the ovo+ cells posterior to the eye in intact animals is consistent with the location of eye progenitors during regeneration following head amputation (Lapan and Reddien, 2011). Strikingly, these cells were eliminated within 1 day of irradiation (Figure S5A), a treatment known to specifically eliminate the dividing cells of the adult animal (the neoblasts) (Reddien and Sánchez Alvarado, 2004). Furthermore, many ovo+ cells in this prepharyngeal population expressed the neoblast-specific markers histone h2b (Figure 5C) and smedwi-1 (Figure S5B) (Reddien et al., 2005). It is unknown whether these ovo+ neoblasts are self-renewing or constantly produced from a more naive cell. These results suggest that eye progenitors constitutively exist in the neoblast population.

ovo RNAi in intact animals resulted in gradual loss of eyes, with pigment cups undetectable following two months of RNAi

n = 8 eyes + trails for all quantifications.

Error bars represent SD. ***p < .005. Scale bars, 50 μm (A, C, and E), and 20 μm (A, insets).

See Figure S4 as well.

Figure 4. ovo Is Required for Formation of Regenerative Eye Progenitors, and ovo+ Progenitor Presence Requires Other Eye Transcription Factors

(A and B) ovo RNAi eliminates regenerative eye progenitors as assessed by markers for PRN (otxA+/eya+), PC (sp6-9+/eya+), and general eye progenitors (six-1/2+/eya+). Arrows indicate double-positive cells.

(C and D) Most regenerative ovo+ progenitor cells are eliminated by six-1/2 and eya RNAi.

(E and F) sp6-9 RNAi eliminates most ovo+ pigment cell progenitors (ovo+ /otxA-), and otxA RNAi eliminates most ovo+ photoreceptor neuron progenitors (ovo+ /sp6-9-).
These un-amputated ovo(RNAi) animals also lacked six-1/2/eya+ cells in the region of putative homeostatic eye progenitors (Figures 5E and 5F). Reciprocally, homeostatic RNAi of six-1/2 and eya, in addition to causing loss of eye tissue, caused a loss of ovo+ cells in the prepharyngeal region (Figures 5G and 5H). Overall, these data suggest that ovo, six-1/2, and eya are expressed in a population of eye progenitors during homeostasis as well as regeneration and are required for maintenance of this population.

**Smed-soxB, Smed-foxQ2, Smed-klf, and Smed-meis Regulate Eye Differentiation and Morphogenesis**

RNAi of genes encoding four additional conserved transcription factors, Smed-soxB, Smed-foxQ2, Smed-klf, and Smed-meis (Figure S3) resulted in PRN aggregates that were smaller in cross-section than in the control (Figures 6A–6C). All of these genes were expressed in PRNs and eye progenitors during regeneration (Figure S6A). Photoreceptor aggregates in klf(RNAi) animals were also displaced posteriorly relative to the pigment cup and descended unusually far toward the interior of the animal along the D-V axis, embedding within the brain (Figures S7A and S7B).

Small eye phenotypes were not accompanied by an evident decrease in the number of ovo+ progenitors in these RNAi animals (Figures S6B, S6C, and S6F), suggesting that these genes function primarily following progenitor specification. Because contrast, posterior PRNs (pctaire) were not affected (Figure 6D). soxB RNAi did not significantly impact numbers of PC (sp6-9+/ovo+) or PRN (sp6-9/ovo+) progenitors (Figures 6E and 6F), and soxB is not abundantly expressed in the ovo+ progenitor population (Figure S6A). However, soxB+ eye signal is eliminated by ovo RNAi (Figure S6D). These data indicate that whereas ovo (along with six1/2, eya, and otxA) acts in general PRN progenitor specification (Figures 4A and 4E), soxB acts subsequently to promote differentiation of an anterior subset of PRNs.

Several RNAi phenotypes affected the pigment cup shape. Loss of photoreceptor cells by RNAi of PRN-specific genes, such as otxA, results in pigment cups with diminished apertures (Lapan and Reddien, 2011). Accordingly, in klf and foxQ2 RNAi animals, optic cups were more closed than in the control, or even completely circularized (Figures 6A and 6B), possibly explained if rhabdomeres provide support for optic cup opening. In meis+RNAi animals, however, optic cups were also elongated and often more than one cupped structure was visible in each eye - a defect not characteristic of photoreceptor cell loss (Figures 6B and S7C). Although meis expression was not detected in the pigment cup, meis transcripts are detectable in tyrosinase+ PC progenitors (Figure S7D). Meis1 loss in mouse also disrupts optic cup morphogenesis, with optic cup duplication observed (Hisa et al., 2004).

**Figure 5. ovo Is Expressed in a Population of Homeostatic Eye Progenitors**

(A) In starved intact animals, ovo is expressed in isolated dorsal cells between the eyes and pharynx. These cells are eliminated within 24 hr of irradiation.

(B) ovo+ cells posterior to the eyes in intact animals also express six-1/2 and eya.

(C) ovo+ cells posterior to the eyes in intact animals also express the neoblast marker histone h2b (60% ± 15%, x = 0.05).

(D) ovo(RNAi) animals that are not amputated fail to maintain eyes (n = 10/10).

(E and F) ovo(RNAi) animals that are not amputated fail to maintain six-1/2/eya+ cells posterior to the eyes (n = 4 animals). For image clarity only six-1/2 signal is shown.

(G and H) six-1/2(RNAi) and eya(RNAi) animals fail to maintain ovo+ cells posterior to the eyes (n = 4 animals).

See Figure S5 as well.
SoxB

**Figure 6. Smed-soxB, Smed-meis, Smed-klf, and Smed-foxq2 Are Required for Eye Regeneration**

(A) Eye regeneration defects at 7 days of regeneration in live RNAi animals.
(B) Detection of tyrosinase transcript and Arrestin protein reveals defects in optic cup formation and photoreceptor neuron regeneration. Arrow indicates duplicated optic cup in meis(RNAi) animal.
(C) Quantification of cross-section area ($\mu m^2$) of photoreceptor neuron aggregate (mean + SD, n = 8 eyes).
(D) soxB RNAi results in loss of anterior subtypes of photoreceptor neurons, but not posterior subtypes (n = 8 eyes for each condition).
(E and F) soxB RNAi does not affect numbers of ovo+ progenitors, nor the ratio of PC progenitors (sp6-9+/ovo+) to PRN progenitors (sp6-9+/ovo-).

Error bars represent SD, **p < .005. Scale bars, 200 $\mu m$ (A), 100 $\mu m$ (D), 20 $\mu m$ (B and E).
See Figures S6 and S7 as well.

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**Developing Eyes of Planarian Embryos Express Transcription Factors Involved in Eye Regeneration**

Most eye formation studies in other organisms are performed in developing embryos. Therefore, we investigated whether the transcription factors that govern planarian eye regeneration might also be expressed during planarian embryonic development (Figure 7A). Recent work has shown that beginning at stage 6, *Schmidtea polychroa* embryos have expression of *eya*, *six-1/2*, *otxA* in the eyes, and lack expression of *pax6A*, *rax*, and *dachsund* in the eye domain (Martin-Durán et al., 2012), similar to the case in regeneration. We found that from early stages of *Schmidtea mediterranea* embryonic eye formation, *ovo* was expressed in the eyes and in mesenchymal cells posterior to the eye that were reminiscent of regenerative progenitor eye trails (Figure 7B). Double FISH (fluorescent in situ hybridization) with *ovo* enabled us to determine whether regeneration-related eye genes were expressed in the embryonic eye primordium and/or presumptive earlier progenitors. Embryonic eyes expressed all known transcription factors that function during eye regeneration: *eya*, *six-1/2*, *otxA*, *sp6-9*, *klf*, *meis*, *foxQ2*, and *soxB* (Figure 7C). Regionalization of expression in the embryonic eye mirrored the case in regeneration (Lapan and Reddien, 2011); for instance, *otxA* was expressed in the lateral eye primordium whereas *sp6-9* was expressed in the medial eye primordium, and both were expressed in only a subset of *ovo+* trail cells (Figure 7C). Furthermore, neither the eye primordium (Martin-Durán et al., 2012) nor the *ovo+* trail cells (Figure 7D) expressed *pax6A*, *rax*, *dachsund*, or another Pax6 ortholog, *pax6B*. Therefore, findings regarding genetic regulation of eye regeneration are relevant to planarian embryonic development.

**DISCUSSION**

**Planarian Eye Formation in Regeneration, Homeostasis, and Embryogenesis**

The cellular events bridging the pluripotent state and cellular differentiation during planarian regeneration and homeostasis are poorly understood, and the eye is emerging as a system to study adult lineage specification in this animal (Lapan and Reddien, 2011). *ovo* is the first identified gene that is expressed in all eye progenitors and is specifically expressed in eye cells, and therefore is a marker that facilitates study of progenitor dynamics during various modes of planarian eye formation. Our investigations of *ovo* expression lead to three conclusions concerning planarian eye formation. (1) Isolated eye progenitors are present early in regeneration (by 2 days after decapitation),...
prior to the appearance of an aggregated eye primordium. Therefore, specification at a distance from the aggregated eye occurs from the onset of regeneration rather than only at later stages of eye growth (Lapan and Reddien, 2011). (2) Eye progenitors exist in uninjured intact animals in a dorsal prepharyngeal domain, similar to regenerative progenitors but at lower density. These data indicate that some neoblasts are specialized for specific lineages during normal tissue turnover conditions of adult life. (3) During embryogenesis, ovo7 cells are present in the eye and in a trail-like formation posterior to the eye.

Further experiments are required to formally determine whether, like regenerative progenitors (Lapan and Reddien, 2011), homeostatic and embryonic eye progenitors move toward the eye primordium. However, our ovo expression analyses indicate that migration of differentiating mesenchymal cells, rather than patterning of an epithelium, might be a feature of all modes of eye formation in planarians. Our findings advance the use of the planarian eye as a system for exploring the extent of similarity between embryonic, regenerative, and homeostatic modes of organ formation within a species and between species.

**Eye Purification and Transcriptome Analysis**

Canonical phototransduction cascades have been described for ciliary and rhabdomeric phototransduction based on functional investigations in vertebrates and *Drosophila*, respectively (Arendt, 2003). However, a diversity of phototransduction strategies likely exists among animals. For instance, horseshoe crab (*Limulus*) and *Drosophila* light sensation both begin with an R-opsin/PLC cascade, but *Drosophila* phototransduction culminates in Trp channel opening (Katz and Minke, 2009). By contrast, most evidence from *Limulus* indicates that opening of cyclic nucleotide-gated (CNG) ion channels (preceded by IP3-dependent intracellular calcium release and changes in cGMP levels) is responsible for photoreceptor depolarization (Garger et al., 2004). We observed robust expression for orthologs of nearly all central *Drosophila* phototransduction components in planarian photoreceptors, including two Trp channels. However, we also detected enrichment for intracellular calcium regulation and cGMP pathway-like components, including CNG channels. Based on the high levels of Trp channel gene expression, we hypothesize that these are the primary mediators of membrane depolarization following light detection. The roles of CNG channels in planarian eyes are unknown, but electrophysiological recordings combined with RNAi could be used to test possible functions, such as in the regulation of light response or light/dark adaptation.

The planarian pigmented optic cup has numerous similarities to the RPE of vertebrates. Melanin is not commonly found in protostome eyes; however, it is the primary pigment of both planarian PCs and the RPE. We expand upon this similarity by demonstrating that the enzymes used in melanin production and for protection from oxidative damage (a consequence of melanin production) are the primary mediators of membrane depolarization following light detection. The roles of CNG channels in planarian eyes are unknown, but electrophysiological recordings combined with RNAi could be used to test possible functions, such as in the regulation of light response or light/dark adaptation.
metabolite and solute transporters, consistent with a common function of these cell types as components of a transport epithelium. This similarity supports a model in which pigmented cells already existed as an accessory cell type separate from photoreceptor neurons in the ancestral bilaterian eye.

The RPE is commonly affected in eye diseases, including age-related macular degeneration (AMD), edema, and inherited retinal degeneration syndromes. A molecular explanation for pathogenesis is lacking for most of these diseases. Planarian PCs express orthologs of two RPE chloride channels underlying eye diseases. Best-1 is mutated in Best vitelliform macular dystrophy, and Cfrt mutations underlie vision defects in cystic fibrosis patients (Marmorstein et al., 2009; Xiao et al., 2010). Furthermore, RPE degeneration in AMD correlates with peroxide accumulation and declining Catalase function, which is also responsible for degeneration of other melanocytic cell types (Venza et al., 2012; Wood et al., 2009). catalase-1 is very abundantly and specifically expressed in the planarian pigment cup. Molecular similarities between Drosophila ocellar PCs and the vertebrate RPE have been difficult to identify (Charlton-Perkins and Cook, 2010). The planarian eye should therefore prove useful as an invertebrate model system for investigating orthologs of mammalian RPE genes involved in pathogenesis, as well as for inferring ancestral functions of ocellar PCs.

Transcription Factor Control of Planarian Eye Formation

Comprehensive sequencing of RNA from intact eyes identified three genes that encode transcription factors and that are expressed in all cells of the eye and their progenitors—six-1/2, eya, and ovo. The requirement for six-1/2 and eya in planarian eyes and eye progenitors is previously described (Lapan and Reddien, 2011; Mannini et al., 2004; Pineda et al., 2002) and both are homologs of well-known eye development genes (Figure 7E). We propose a model for eye regeneration in which six-1/2, eya, and ovo expression specifies all eye progenitor formation, with additional expression of otxA specifying PRNs and additional expression of sp6-9 and dlx specifying PCs (Figure 7F).

How do available planarian eye data impact models about transcriptional regulators governing eye formation in the common ancestor of the Bilateria? Planarian data support the inclusion of Otx and Eya as ancestral bilaterian eye genes, and of Six-1/2 as an ancestral eye gene for the protostomes (Figure 7E). Our data also support the possibility that Meis and SoxB family genes encode transcription factors with ancestral roles in eye biology. Meis genes regulate eye progenitor proliferation in Drosophila and vertebrates as well as optic cup morphology in mouse (Figure 7E) (Bessa et al., 2002; Heine et al., 2008; Hisa et al., 2004). The SoxB family sox-neuro and fish-hook genes are expressed in the Drosophila eye disc (Mukherjee et al., 2000), and Sox2 is required for neural progenitor maintenance and differentiation of retinal ganglion cells in vertebrates (Matsushima et al., 2011).

In contrast to Otx, Eya, Six-1/2, Meis, and SoxB, several transcription factors that have prominent roles in Drosophila and/or vertebrate eye formation—Pax6, Dachshund, Rax, and Six3—have no apparent role in planarian eye formation (Figure 7E) (Lapan and Reddien, 2011; Mannini et al., 2008; Martín-Durán et al., 2012; Pineda et al., 2002), a conclusion extended by our eye transcriptome and embryonic eye expression data. Therefore, planarian data does not support the argument that these genes are ancestral regulators of eyes. Loss of a role for any of these genes in eye biology during planarian evolution is clearly a reasonable possibility, especially in cases such as Pax6 where data from multiple other phyla support an eye role for the gene. In addition to the case of the planarian eye, however, the development of Drosophila larval ocellus, branchiostome eye cups, Limulus eyes, and Platyneiris adult eyes also does not depend on Pax6 (Vopalensky and Kozmik, 2009). Furthermore, orthologs of the Drosophila eye regulator Dachshund do not have major functions in mouse eye development (Davis et al., 2008), and an ortholog of the vertebrate eye regulator Rax is not known to be involved in Drosophila eye development (Arendt et al., 2004). Six3 family transcription factors predominate in vertebrate eye development, whereas most invertebrates depend on Six-1/2 (Vopalensky and Kozmik, 2009). Analysis of additional animal eyes will therefore be an important direction for further testing evolutionary hypotheses related to these genes and eye evolution.

We describe a number of transcription factors conserved among the Bilateria that regulate planarian eye formation, but for which the functions in other animal eyes has not been extensively investigated (Figure 7E). These include ovo, kif, and foxQ2. Our prior work also indicated prominent roles for dlx and sp6-9 in optic cup formation (Lapan and Reddien, 2011). One gene encoding an Ovo-like transcription factor, shavenbaby, is known to exist in Drosophila. This gene is well-studied in epidermal morphogenesis, but roles for this gene in the eye have not been reported. The chromosomal locus responsible for the blind-sterile phenotype in mouse contains the ovol2 gene (Li et al., 2002). These mice exhibit small eye size as well as early onset cataracts; however, other genes are contained in this locus and no causal role for ovol2 in this phenotype is known. Mouse ovol2 is expressed in the surface ectoderm of the ventral forebrain at E8.75-9.5 (Mackay et al., 2006), the site of optical eminence formation. Interestingly, ovol2 knockout mice die at E10.5 without displaying any sign of optic vesicle formation typical of this stage, despite the fact that D-V expression domains examined in the neural tube are maintained and overall embryonic development is not delayed (Mackay et al., 2006; Unezaki et al., 2007).

We demonstrate an unbiased technical approach to systematically survey the molecular basis of eye formation and function. This approach identified novel and conserved genetic features of eyes in planarians, further indicating the power of planarians as a system for study of animal eyes. Few transcription factors in animals display eye-specific expression and are required for formation of all eye cells, and ovo is a newly discovered one.

EXPERIMENTAL PROCEDURES

Tissue Isolation

Large axenial Schmidtea mediterranea were used for eye preparation. Animals were fed twice prior to eye harvest. Head tips were amputated...
posterior to the eyes and collected into CMFB + 1 mg/mL collagenase (Sigma) + 0.05% NAC and agitated. Freed eyes were rinsed and transferred to Trizol for RNA collection. For control (ventral anterior) tissue, heads were amputated above the pharynx and then coronal amputation was made to remove dorsal tissue, including eyes.

**cDNA Sequencing and Analysis**

Approximately 1 ug of RNA was used to construct Illumina libraries for 36bp single-end sequencing on the GAII platform. Libraries were constructed using Illumina reagents and according to commercial protocol. FPKM were calculated using the Cufflinks program Cuffdiff. See Extended Experimental Procedures for further detail.

**Gene Cloning**

For cDNA library generation, RNA from heads was isolated using Trizol purification, and used as template for first-strand reverse transcription with SuperScript III (Invitrogen). Cloning was otherwise performed as described (Lapan and Reddien, 2011).

**RNA Synthesis and RNome**

For probes used in RNome experiments, riboprobe template was produced with the same primers as were used for cloning, except that gateway adapters were not present on primers, and T7 promoter sequence was added to the 3’ primer. Probe synthesis and RNome were otherwise performed as described (Lapan and Reddien, 2011). In homeostasis RNome experiments, animals were fed dsRNA food every 4 days for 6 weeks.

**Histology and Imaging**

Whole-mount FISH and antibody staining was performed as described (Lapan and Reddien, 2011; Pearson et al., 2009). Embryos were killed in 2.7% HCl following manual decapsulation and were otherwise treated the same as adult worms for histologic analysis. Images were acquired with a Zeiss confocal microscope (LSM 700).

**ACCESSION NUMBERS**

The GenBank accession numbers for Smed-ovo, Smed-kif, Smed-foxQ2, Smed-mes, and Smed-soxB are JX091074, JX091075, JX091076, JX091077, and JX091078, respectively.

**SUPPLEMENTAL INFORMATION**

Supplemental Information includes an Extended Discussion, Extended Experimental Procedures, seven figures, and three tables and can be found with this article online at http://dx.doi.org/10.1016/j.celrep.2012.06.018.

**LICENSING INFORMATION**

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