



Human eye conditions: insights from the fly eye

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Abstract

The fruit fly *Drosophila melanogaster* has served as an excellent model to study and understand the genetics of many human diseases from cancer to neurodegeneration. Studying the regulation of growth, determination and differentiation of the compound eyes of this fly, in particular, have provided key insights into a wide range of diseases. Here we review the regulation of the development of fly eyes in light of shared aspects with human eye development. We also show how understanding conserved regulatory pathways in eye development together with the application of tools for genetic screening and functional analyses makes *Drosophila* a powerful model to diagnose and characterize the genetics underlying many human eye conditions, such as aniridia and retinitis pigmentosa. This further emphasizes the importance and vast potential of basic research to underpin applied research including identifying and treating the genetic basis of human diseases.

Introduction

The sequencing of the genome of the fruit fly *Drosophila melanogaster* in 2000 (Adams et al. 2000; Myers et al. 2000; Rubin and Lewis 2000) and subsequent comparative genomic studies showed that approximately 70% of human disease-associated genes have a single *Drosophila* homolog (e.g. Reiter et al. 2001; Yamamoto et al. 2014). This highlights the relevance of this model organism to study the function of conserved genes and their roles in human disease (Wangler et al. 2015). Indeed, studies of the genetic regulation of *Drosophila* development over the last 30 years have provided many crucial insights into the genetic basis and progression of a wide range of human conditions from cancer to neurodegeneration and aging (Burke et al. 2017; Kreipke et al. 2017; Michno et al. 2005; Sen and Cox 2017; Sonoshita and Cagan 2017).

The compound eye of *Drosophila* in particular has proven to be an excellent model for many diseases despite the noticeable anatomical differences between insect and

vertebrate eyes (Fig. 1; Table 1). The *Drosophila* eye consists of a regular array of several 100 individual light-sensing hexagonal structures called ommatidia (Cagan 2009; Hilbrant et al. 2014; Kumar 2012, 2018; Posnien et al. 2012), which together project a single image to the brain (Land 2005) (Fig. 1). The human “camera” eye also projects one image but from a single lens (Fig. 1). Although humans have a much narrower field-of-view than fruit flies, our eyes achieve higher spatial resolution and acuity (Borst 2009) because of thousands of sensory cells (rods and cones) packed tightly into the retina (Jonas et al. 1992), while each *Drosophila* ommatidia only has eight photoreceptors and 11 accessory cells (Treisman 2013) (Fig. 1). At the basic structural level, however, both insect and vertebrate eyes are made up of a lens to focus light, a neural retina with photoreceptors to sense the light and a pigmented epithelium to protect photoreceptor signaling from scattered or diffracted light (Charlton-Perkins et al. 2011; Sanes and Zipursky 2010) (Fig. 1). Moreover, decades of research have revealed that the development of *Drosophila* eyes is regulated by genetic pathways that are conserved between flies and humans, and consequently studies of *Drosophila* have taught us much about human eyes (Gehring 2005; Halder et al. 1995; Kumar and Moses 2001; Vopalensky and Kozmik 2009; Wawerski and Maas 2000).

In this review, we focus on how research on the genetic regulation of *Drosophila* eye development has informed our understanding of human eye development and highlight the

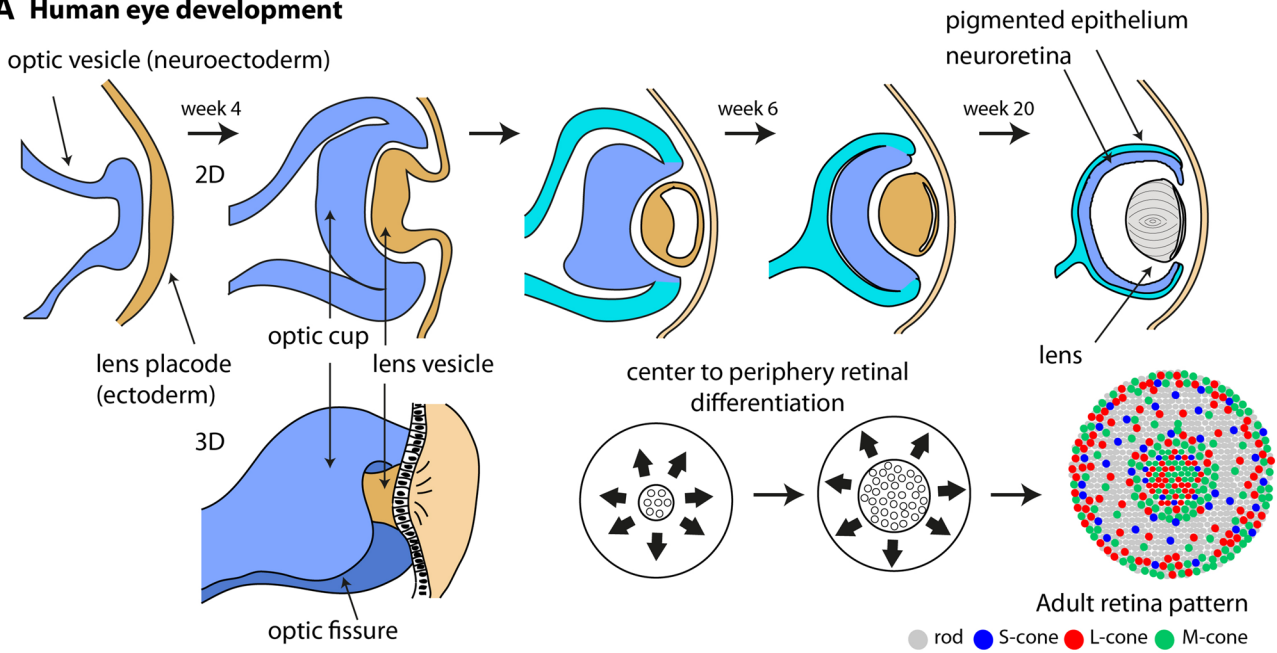
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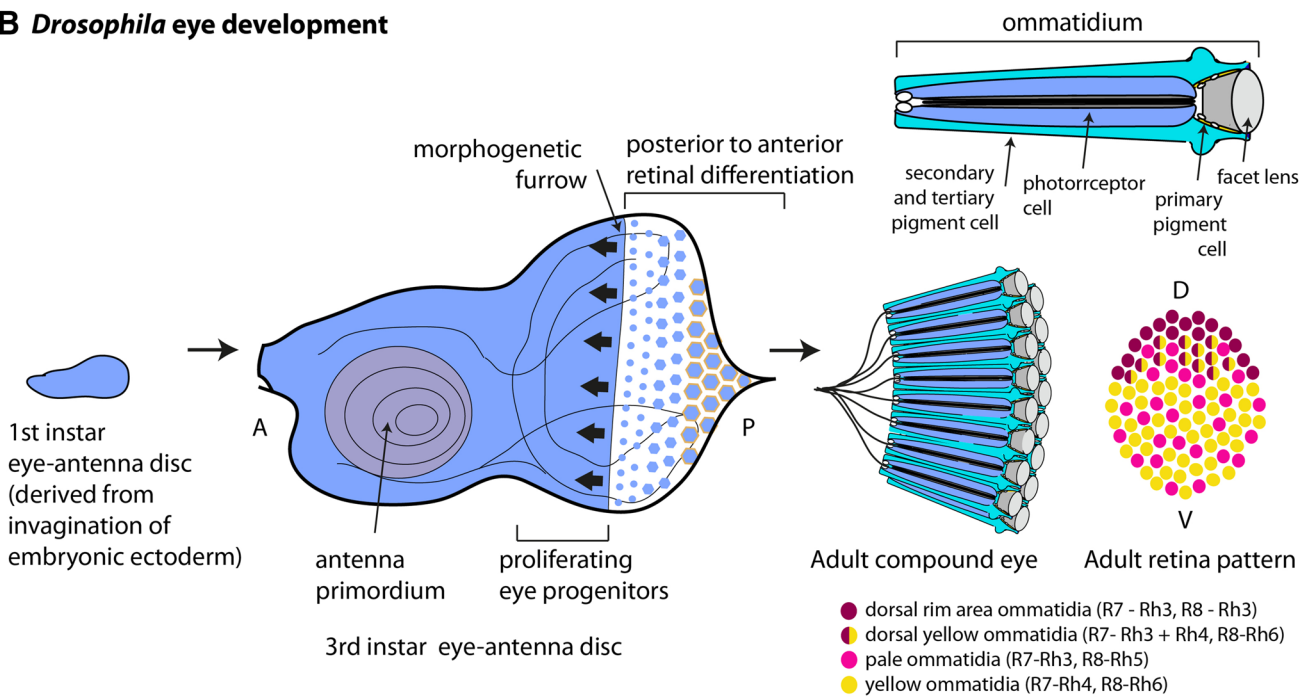
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A Human eye development



B Drosophila eye development



power and potential of research on fly eyes to better understand and potentially treat human conditions (Table 1).

Eye development

Selector genes of invertebrate and vertebrate eye development

The *Drosophila* eyes develop from evagination of the embryonic neuroectoderm to form two epithelial sacs, the so-called eye-antennal imaginal discs (Casares and

Fig. 1 Comparative overview of human and *Drosophila* eye development. Eye development from week 4 to week 20 of human embryogenesis **a**. At week 4 of development, the optic vesicles evaginate from the forebrain neuroectoderm inducing the adjacent ectoderm to form the lens placode. Between weeks 4 and 6, the optic vesicle invaginates on itself, forming the optic cup, which partially encapsulates the invaginating lens vesicle (interrupted posteriorly by the optic fissure). After week 6 and until week 20, the optic cup differentiates into two main layers, the neuroretina and the pigmented epithelium, while the lens vesicle thickens and forms the crystalline lens. The neural cells in the neuroretina differentiate from the center to the periphery of the optic disc, such that the adult retina pattern is set with circumferential bands or zones enriched in specific photoreceptors. Eye development and adult retina patterning of *Drosophila* **b**. The eye imaginal disc develops from an invagination of the embryonic ectoderm, being subdivided early to form precursor regions to the eye and antenna (1st larval instar imaginal disc). During the 3rd larval instar, differentiation of ommatidia into clusters of 8 photoreceptor cells progresses from the posterior to the anterior of the disc, as a band of apical cell constrictions termed the morphogenetic furrow sweeps across the tissue. The longitudinal structure of the adult ommatidium shows an apical facet lens lined basally by primary pigment cells and focusing into a central rhabdomere projected by the lateral membrane of the photoreceptor cells. The cluster of photoreceptor cells is surrounded by secondary and tertiary pigment cells. The adult retina is patterned dorso-ventrally into two main zones, a dorsal third consisting of the dorsal rim area and dorsal yellow ommatidia, and a ventral area with a stochastic pattern of yellow and pale ommatidia. Ommatidia in these areas have a specific repertoire of rhodopsin (Rh) gene expression in photoreceptors R7 and R8 (A— anterior, P—posterior, D—dorsal, V—ventral, R—photoreceptor, Rh—rhodopsin)

Almudi 2016; Green et al. 1993; Younossi-Hartenstein et al. 1993) (Figs. 1, 2). This region is characterized by the early expression of several conserved transcription factors, Orthodenticle (Otd)/Otx and the Pax6 homologues Twin of eyeless (Toy) and Eyeless (Ey) in the posterior region of the epithelial sac, which will give rise to the eye, ocelli, and head capsule, and Cut in the anterior region, which will mostly give rise to the antenna and maxillary palps (Czerny et al. 1999; Kenyon et al. 2003) (Fig. 2).

Much like in *Drosophila*, vertebrate eye development is centered on the activity of core selector genes, namely the Pax6 gene. Vertebrate Pax6 genes encode two alternatively spliced variants that differ in the presence of exon 5a. In contrast, *Drosophila* Pax6 and Pax6(5a) homologues arose as separate loci from a relatively recent gene duplication event (Aldaz et al. 2003; Jun et al. 1998). Like in vertebrates, the two *Drosophila* Pax6 genes, *ey* and *toy* (Czerny et al. 1999; Quiring et al. 1994), and two Pax6(5a) genes, *eyegone* (*eyg*) and *twin-of-eyegone* (*toe*) (Jang et al. 2003; Jun et al. 1998) have distinct roles in eye development. *ey* and *toy* promote primarily retinal specification, whereas *eyg* mainly promotes cell proliferation (Chao 2004; Dominguez et al. 2004). Each Pax6/Pax6(5a) orthologue also acts through distinct transcriptional mechanisms, with Ey acting as a transcriptional activator, while Eyg seems to act as a transcriptional repressor (Chao 2004; Dominguez

et al. 2004; Punzo 2004; Punzo et al. 2001; Yao and Sun 2005).

Based on its sufficiency for eye development in *Drosophila* and vertebrates, it was originally proposed that Pax6 functions at the highest level of a hierarchy of genes whose sequential expression leads to eye development (Gehring 1996). Indeed, three core members of this postulated hierarchy: *eyes absent* (*eya*) (EYA1, EYA2, EYA3), *sine oculis* (*so*, SIX1, SIX2 and SIX3), and *dac* (DACH1) have been identified in *Drosophila* and vertebrates, and share similar temporal expression patterns during eye development (Bonini et al. 1997; Chen et al. 1997; Pignoni et al. 1997; Shen and Mardon 1997; Treisman 1999; Zuber 2003). However, rather than acting in a simple linear pathway, it seems that positive transcriptional feedback organizes these core selector genes into an interconnected network (Desplan 1997). This regulatory structure appears critical to induce retinal tissue as evidenced by mis-expression experiments where core genes fail to induce ectopic eyes if any of the other critical factors is absent (Bonini et al. 1997). Positive transcriptional feedback is also needed for these genes to activate a second, independently regulated phase of gene expression, as many of these genes function at several stages of eye development. For instance, *ey*, *eya* and *so* are critical for growth of the eye primordium and initiation of differentiation (Bonini et al. 1993; Cheyette et al. 1994; Halder et al. 1998; Jang et al. 2003; Mardon et al. 1994; Pignoni et al. 1997), while *eya* and *so* are then also required for progression of photoreceptor differentiation (Pignoni et al. 1997), and *ey* is needed for rhodopsin gene expression (Papatsenko et al. 2001; Sheng et al. 1997).

Cellular differentiation

During the first larval stages of *Drosophila*, the epithelial cells are undifferentiated progenitor cells that proliferate continuously due to the combined activity of the genes *ey*, *homothorax* (*hth*), *toy*, *teashirt* (*tsh*), *tiptop* and *yorkie* (*yki*) (Figs. 1, 2) (Bessa et al. 2009; Bessa and Casares 2005; Datta et al. 2009; Laugier et al. 2005). The growth of the *Drosophila* eye is interconnected with the organization of both antero-posterior and dorso-ventral axes during development, such as established through the action of Wingless (Wg) and Notch (N) (Dominguez and de Celis 1998; Heberlein et al. 1998; Papayannopoulos et al. 1998). In particular, N induces proliferation by activating the expression of *eyg* (Dominguez et al. 2004). At the same time, the first wave of retinal determinants, mainly *ey* and *toy*, induce and reinforce the expression of other retinal determinants, *eya*, *so* and *dachshund* (*dac*) (Fig. 2) (reviewed in Casares and Almudi 2016; Davis and Rebay 2017).

The differentiation of the cells that form the ommatidia in *Drosophila* is a sequential process. A morphogenetic

Table 1 Genes that cause human eye conditions and their *Drosophila* orthologs

Human gene	Phenotype	References	<i>Drosophila</i> gene	Phenotype	References
<i>PAX6</i>	Aniridia, anophthalmia, microphthalmia	Glaser et al. (1992); Jordan et al. (1992); Ton et al. (1991)	<i>eyeless</i>	Reduced eyes	Patterson and Muller (1930)
<i>EYA1</i>	Congenital cataracts; anterior segment anomalies	Azuma et al. (2000)	<i>eyes absent</i>	Eye facets completely absent in strong alleles	Bonini et al. (1993)
<i>SIX1</i>	Cataracts; branchio-oto-renal syndrome; deafness	(Salam et al. 2000)	<i>sine oculis</i>	Eyes reduced to small groups of ommatidia, occasionally missing	Cheyette et al. (1994)
<i>SIX5</i>	Branchio-oto-renal syndrome; deafness	Hoskins et al. (2007)			
<i>SIX3</i>	Holoprosencephaly and microphthalmia	Wallis et al. (1999)	<i>optix</i>	Eye defects	Weasner et al. (2007)
<i>SIX6</i>	Optic disc anomalies with retinal and/or macular dystrophy	Aldahmesh et al. (2013); Yariz et al. (2015)			
<i>DACH1</i>	Microphthalmia, anophthalmia, and coloboma	Warburg (1993)	<i>dachshund</i>	Severely reduced or no eyes	Shen and Mardon (1997)
<i>MEIS2</i>	Cleft palate; cardiac defects; mental retardation	Crowley et al. (2010)	<i>homothorax</i>	Overgrowths of eye tissue; loss of ventral and dorsal head structures	Pichaud and Casares (2000)
<i>ATOH7</i>	Congenital blindness; nystagmus; shallow anterior chamber; massive retrolental mass; retinal nonattachment	Ghiasvand et al. (2011)	<i>atonal</i>	Neuroanatomy defective; adult photoreceptors missing	Jarman et al. (1995)
<i>OTX2</i>	Microphthalmia, syndromic 5; retinal dystrophy; early onset, with or without pituitary dysfunction; cone-rod retinal dystrophy-2	Freund et al. (1997); Ragge et al. (2005)	<i>oc</i>	Eyes somewhat reduced and body size dwarfed. Phototaxis normal	Benzer (1967)
<i>CRX</i>	Cone-rod dystrophy; retinitis pigmentosa; LCA	Freund et al. (1997); Freund et al. (1998); Sohocki et al. (1998)			
<i>CRB1</i>	Pigmented paravenous chorioretinal atrophy; retinitis pigmentosa-12, autosomal recessive	Freund et al. (1999); Freund et al. (1999)	<i>Crumbs</i>	Mild overgrowth of adult eyes	Ling et al. (2010)
<i>EYS</i>	Retinitis pigmentosa 25	Abd El-Aziz et al. (2008)	<i>Eyes Shut</i>	Rhabdomere defects	Zelhof et al. (2006)
<i>PAX2</i>	Optic nerve coloboma	Favor et al. (1996); Sanyanusin et al. (1995)	<i>D-Pax2</i>	Eyes small, rough, and glazed	Fu et al. (1998)
<i>SHH</i>	Holoprosencephaly	Roessler et al. (1996)	<i>hedgehog</i>	Eye small and narrow with about 150 facets	Heberlein et al. (1995); Lee et al. (1992); Renfranz and Benzer (1989)
<i>RHO</i>	Autosomal dominant retinitis pigmentosa	Bhattacharya et al. (1991); Dryja et al. (1991); Dryja et al. (1990)	<i>minaE</i>	Rhabdomeres 1–6 is smaller than normal; light-independent degeneration of R1-6 rhabdomeres	Colley et al. (1995); Kurada and O'Tousa (1995)
<i>PROMININ-1</i>	Autosomal recessive retinal degeneration	Maw et al. (2000)	<i>Prominin</i>	Defective photoreceptor morphogenesis; disrupted inter-rhabdomeral space	Zelhof et al. (2006)

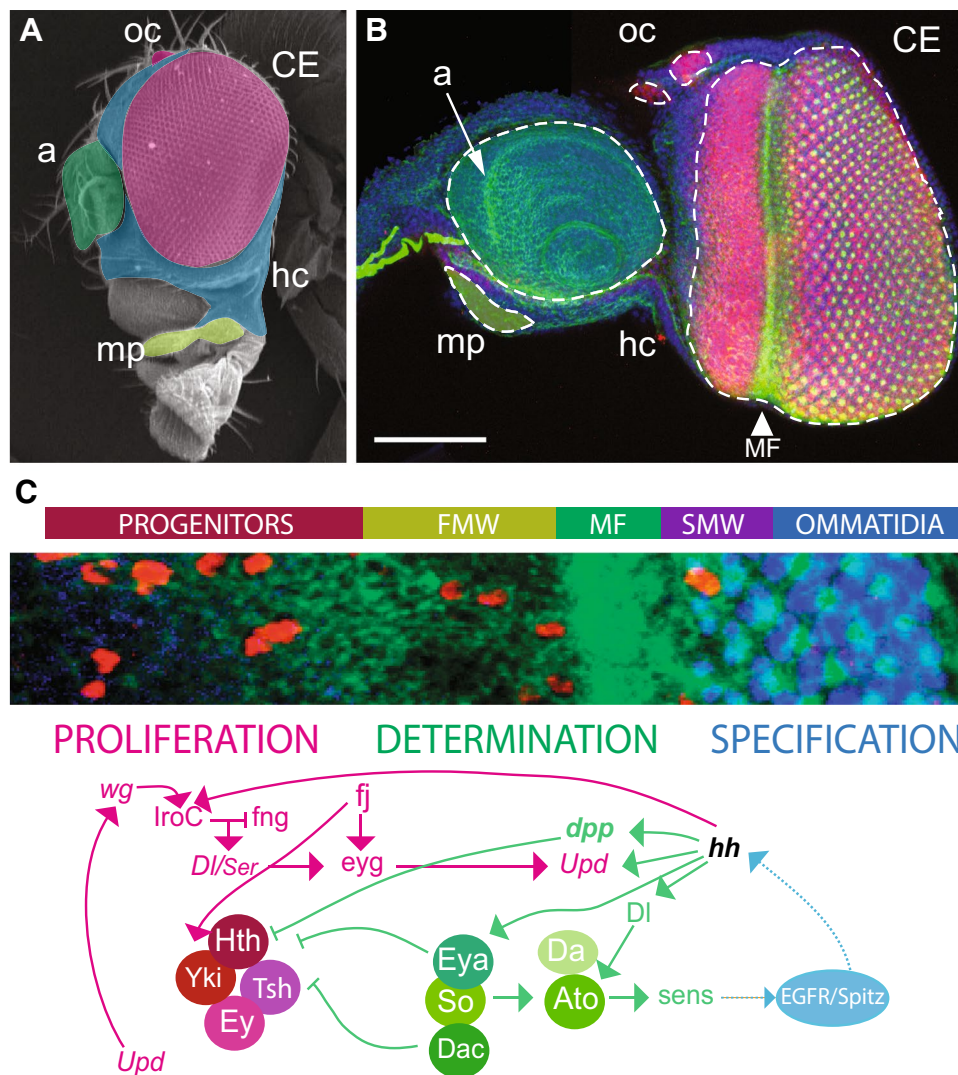


Fig. 2 *Drosophila melanogaster* eye determination and gene regulatory network. *Drosophila* adult head **a** and eye-antennal imaginal disc stained with anti-Eya (magenta), DAPI (blue) and phalloidin-AlexaFluor488 (Green) **b**. Color code represents the larval structures that will give rise to the structures of the adult head: compound eye (CE, magenta), ocelli (oc, dark magenta), antenna (a, dark green), maxillary palp (mp, light green), and head capsule (hc, blue). **c** Section of an eye imaginal disc showing the compartments where proliferation (most anterior), determination (around MF) and specification (posterior to MF) are occurring. From anterior to posterior (left to right): progenitors are characterized by high levels of proliferation (mitotic

cells in red), followed by synchronic cells at G1, the first mitotic wave (FMW), morphogenetic furrow (MF), and cells differentiating (second mitotic wave, SMW) into ommatidia most posteriorly. Mitotic cells are stained using an anti-PH3 antibody (red), MF is marked with Phalloidin-AlexaFluor488 (green) and photoreceptors are shown using anti-Elav, in blue. A simplified gene network showing the main molecules involved in the three processes is displayed. Color code highlights the process in which each molecule has its main role. Scale bar 50 μ m. All the panels show anterior to the left and posterior to the right

wave, designated as the morphogenetic furrow (MF, Figs. 1, 2), sweeps across the epithelium from the most posterior region towards the anterior promoting the recruitment and differentiation of the different types of cells that constitute the ommatidium (reviewed in Kumar 2011; Lee and Treisman 2002). During differentiation, the activity of Hedgehog ahead of the MF triggers N-dependent activation of the proneural gene *atonal* (*ato*) and restriction of its expression to a single cell in each proneural cluster, the R8 cell, which

differentiates into the first photoreceptor of the ommatidial cluster (Jarman et al. 1994, 1995) (Fig. 2). Similarly, in zebrafish, retinal neurogenesis has been shown to occur in a wave starting in the optic cup adjacent to the optic stalk and spreading outwards, and is dependent on expression of Sonic Hedgehog and the Ato homologue Ath5 (Masai et al. 2000; Neumann and Nuesslein-Volhard 2000). In primates, differentiation also follows sequential waves of gene expression, emanating from the center of the optic disc to

its periphery (Cornish et al. 2005; Hendrickson et al. 2008) (Fig. 1). Much like *Ato* in *Drosophila*, *Ath5* in mice seems to be essential to specify the first retinal neurons, the retinal ganglion cells (Brzezinski et al. 2012; Sun et al. 2003). In a recent study, gene replacement of *Drosophila* *Ato* with the mouse ortholog *Ath1* demonstrated its ability to recapitulate the correct specification of the initial photoreceptors in *Drosophila*, albeit with changes in the pattern of retinal differentiation (Weinberger et al. 2017). Furthermore, in zebrafish, the early differentiating red cones recruit undifferentiated cells to drive further cone cell differentiation, in a process analogous to R8 recruitment of other photoreceptors in *Drosophila* (Raymond and Barthel 2004). Therefore, the initial specification of photoreceptors from undifferentiated progenitor cells appears to have many similarities between flies and vertebrates (Fig. 1).

In flies, *Ato* activates the expression of *senseless* (*sens*), whereas in the two adjacent remaining cells, *Rough* inhibits *sens* to specify the R2 and R5 photoreceptors (Pepple et al. 2008). The rest of the photoreceptors are specified in a sequential manner, involving the activity of the epidermal growth factor receptor (EGFR) signaling pathway, much of which was first delineated in *Drosophila* by the analysis of mutants affecting photoreceptor differentiation (Freeman 1996, 1997; Kumar et al. 1998). During this specification process, photoreceptors are specialized by expression of specific color-detecting rhodopsins, a process that shares some similarities again between flies and vertebrates (Fig. 1).

In flies, the *Otx*-family transcription factor *Otd* regulates the transcriptional repressor *Defective Proventriculus* (*Dve*) to regulate rhodopsin gene expression in specific photoreceptor subtypes (Johnston et al. 2011; Yan et al. 2017). In mice, the genes *Nr2e3* and *Nrl* also act with *Otx*-family members, like *Crx*, the orthologue of fly *Otd*, to activate rod opsin expression and repress cone opsin expression (Cheng et al. 2004; Hennig et al. 2008; Kaewkhaw et al. 2015; Peng et al. 2005). Interestingly, like *Otd*, human *OTX1* and *OTX2* can induce *dve* expression in *Drosophila* photoreceptors, suggesting conserved mechanisms of *OTX*-mediated regulation of photoreceptor specification between flies and humans (Terrell et al. 2012). Differentiation of yellow and pale ommatidial subtypes in *Drosophila* is based on the stochastic expression of the PAS-bHLH transcription factor *Spineless*, which determines *Rh3* expression, and is counteracted by *Spalt-major* (*Sal*) and *Otd* to select expression of *Rh4* (Fig. 1) (Johnston et al. 2011; Tahayato et al. 2003; Wernet et al. 2006). Interestingly, in mice, *Sall3* (homolog of *sal*) has been shown to activate opsins and in humans expression of red versus green opsins also relies on a stochastic mechanism (de Melo et al. 2011; Nathans et al. 1989; Wang et al. 1992). Although different to that of *Drosophila*, this stochastic mechanism may share aspects of counter-regulation by *Sal* and *OTX* factors.

Overall, current research suggests that late photoreceptor specification by regulation of rhodopsin gene expression shares many conserved mechanisms between flies and vertebrates, which highlights this as an important area of focus for understanding human retinal diseases using the *Drosophila* model.

Insights into human eye conditions from *Drosophila*

Research on *Drosophila Pax6* genes and their impact on understanding eye developmental diseases

As mentioned above, in both flies and humans, oculogenesis is the product of a conserved gene regulatory network centered on the activity of *Pax6* (Gehring 2014; Quiring et al. 1994). The *Drosophila Pax6* gene, *ey*, was cloned first and functionally analyzed, and then shown to share a high level of sequence conservation with the *Small eye* gene in mice and the *Aniridia* gene in humans, all now collectively established as *Pax6* functional homologues (Halder et al. 1995; Quiring et al. 1994). Nearly 300 dominant mutations in the human *Pax6* locus have been described and most of these mutations lead to iris hypoplasia or total loss of the iris associated with cataracts and corneal changes, a condition designated as aniridia (Glaser et al. 1992; Hanson et al. 1994; Jordan et al. 1992; Verbakel et al. 2018). Other mutations in *Pax6* (and other functionally conserved genes in eye development) can also cause failed embryonic optic fissure closure in MAC (microphthalmia–anophthalmia–coloboma) spectrum diseases, like anophthalmia, characterized by absence of one or both eyes; microphthalmia, characterized by abnormally small eyes with various malformations, and colobomas, characterized by an opening in the iris, retina, choroid or optic disc (Glaser et al. 1994; Skalicky et al. 2013; Williamson and FitzPatrick 2014). Of the core eye regulators, apart from *Pax6*, mutations in *Six5*, for example, have been shown promote cataract formation in mice (Klesert et al. 2000; Sarkar et al. 2000) and mutations in *EYA1* have been associated with congenital cataracts (Azuma et al. 2000).

Despite the differences in development of the optic primordium between *Drosophila* and vertebrates, *Pax6/Ey* is necessary to induce eye formation, and ectopic expression of *ey* or mouse *Pax6* is sufficient to induce ectopic eyes (Halder et al. 1995). Additionally, a *Drosophila* eye enhancer of *ey* is capable of driving many features of endogenous *Pax6* expression in mice (Xu et al. 1999). These experiments have established the *Drosophila* model as suitable to study conserved *Pax6* functions in eye development and disease. It is, however, worth noting that based on the human and mice mutant phenotypes, *Pax6* in vertebrates seems more critical for lens development (Glaser et al. 1994).

The fly eye, which develops as an evagination of the embryonic ectoderm, much like the vertebrate lens vesicle, may thus bear greater similarities in genetic regulation to this structure than to the whole vertebrate eye (Charlton-Perkins et al. 2011) (Fig. 1). Of special mention in this respect is the highly conserved regulation of lens crystallin proteins by *Drosophila* Pax2 through the same binding sites as vertebrate Pax6 (Blanco et al. 2005; Kozmik et al. 2003). Lens crystallins are a family of ancient proteins, found even in jellyfish, where their expression in lentoid bodies relies on the activity of the ancestral PaxB transcription factor (Kozmik et al. 2003). Therefore, it appears that the Pax2 gene may have been co-opted into lens development in *Drosophila*, whereas vertebrate Pax6 has retained or reacquired that function. As such, *Drosophila* research into Pax2 regulation of *Crystallin* gene expression may prove essential to uncover mechanisms of vertebrate lens abnormalities in Pax6 mutations.

***Drosophila* contributions to understanding conserved aspects of the gene regulatory logic of eye development**

Drosophila research has been instrumental in understanding and modeling the gene regulatory logic underlying eye differentiation (Frankfort and Mardon 2002). Recently, this was again shown by rigorous spatiotemporal quantification and computational modeling that helped to reveal general principles about the logic of the Hedgehog, Notch and EGFR signals during eye growth and morphogenesis (Fried et al. 2016; Zhu et al. 2016). Indeed, the regulatory logic among genes involved in eye determination was shown to be very similar between flies and vertebrates. For example, switching off or dampening *ey/Pax6* expression is required for photoreceptor fate specification in both flies and vertebrates, as in both cases maintenance or prolonged high levels of Ey/Pax6 after eye determination have been associated with failures of neuronal differentiation (Belecky-Adams et al. 1997; Canto-Soler et al. 2008; Toy et al. 2002). To achieve this transition, the positive feedback loop that maintains anterior *ey* expression in eye precursors must be interrupted. In *Drosophila*, this inhibition results from rewiring the network such that Eya-So directly represses *ey* transcription in differentiating cells (Atkins et al. 2013). Interestingly, increasing the levels of Eya and So anterior to the MF reduces *ey* expression (Atkins et al. 2013). Dac appears to be crucial for this switching, as Dac is required for *ey* repression posterior to the MF and can cooperate with Eya and So to inhibit *ey* transcription in anterior cells (Atkins et al. 2013). One idea is that Dac joins Eya-So to switch the complex into a repressive activity (Davis and Rebay 2017). Although a direct repressive function has not been confirmed in *Drosophila*, this may be a conserved function of Dac, as mammalian DACH1 can recruit co-repressors and directly repress

target gene transcription (Chen et al. 2013; Chu et al. 2014; Li et al. 2003; Sundaram et al. 2008; Wu et al. 2003, 2006, 2008, 2009, 2011; Zhao et al. 2015). On the other hand, mammalian Eya is thought to convert repressive SIX–DACH complexes to activating EYA–SIX–DACH complexes (Li et al. 2002, 2003).

A second example of regulatory switching is the coordination of proliferation with specification in retinal progenitors. Competency to switch from proliferation to specification is initiated when Ey activates transcription of *eya* and *so*, which in turn reinforces *ey* expression and promotes *dac* transcription (Fig. 1) (Anderson et al. 2006; Atkins et al. 2013; Bonini et al. 1997; Chen et al. 1997; Halder et al. 1998; Niimi et al. 1999; Ostrin 2006; Pappu 2005; Pignoni et al. 1997; Salzer and Kumar 2009). Dac then terminates the pro-proliferative role of Hth–Yki complexes by inhibiting Hth expression and interfering with the ability of Hth–Yki to activate transcription of the pro-growth *bantam* microRNA (Fig. 2) (Bras-Pereira et al. 2015). Subsequently, Ey cooperates with Eya–So to activate *ato* transcription, which specifies the first photoreceptor to initiate ommatidial assembly (Fig. 2) (Jemc and Rebay 2007; Zhang et al. 2006; Zhou et al. 2014). This results in a mutual inhibition between the Ey–Hth–Tsh and Ey–Eya–So–Dac signaling networks, which drives precursors from asynchronous proliferation to coordinated differentiation.

As in the first switching example, Dac appears to be a key player in the transcriptional repression events that drive developmental transition. How these transitions are orchestrated at the level of chromatin regulation and transcriptional regulation is poorly understood. One idea stemming from *Drosophila* studies is that core eye determination factors recruit Polycomb group proteins (PcG) to promote switching from proliferative precursors to differentiating retinal cells. Indeed, deletion of repressive Polycomb Group genes leads to ectopic Hth and Tsh expression posterior to the MF, which is reminiscent of *eya*, *so*, or *dac* loss (Janody et al. 2004). Another intriguing observation is that mutation of *skuld* or *kohtalo*, two Trithorax Group genes, leads to inappropriate maintenance of Ey posterior to the MF (Janody et al. 2004). Consistent with this, Eya1 and Six1 recruit the SWI/SNF complex to activate downstream target transcription that drives cochlear neurogenesis (Ahmed et al. 2012), while Dach1 primarily associates with co-repressors, as discussed above.

The rewiring mechanisms of the retinal determination gene network discussed above are now beginning to give a better picture of developmental transitions, such as the transition from proliferative precursors to differentiating retinal cells. These mechanisms, namely the role of DACH1 in cell proliferation, are also beginning to be appreciated in the context of human cancer (Chen et al. 2013; Chu et al. 2014; Wu et al. 2006, 2009, 2011), but further studies in vertebrate

models are needed to investigate how these mechanisms may be impaired specifically in eye developmental diseases.

Retinal degeneration models

As highlighted earlier in this review, the *Drosophila* compound eye has little resemblance to the human eye morphologically and yet the gene regulatory networks governing their development are remarkably similar. At a cellular level, the fly and human retinas share many similarities, namely in the structure of photoreceptors and in the genetic and molecular bases of phototransduction, both of which are frequently affected in retinal disease.

Since the mid-70s genetic screens have been designed in *Drosophila* to identify mutations where the morphogenesis of the eye is normal, but photoreceptor cells degenerate from the onset of adult visual function (Harris and Stark 1977; Harris et al. 1976; Hotta and Benzer 1970; Steele and O'Tousa 1990; Yoon et al. 2000). These studies revealed mutants that lead to either a light-independent (Bentrop 1998; Dolph et al. 1993; Lee et al. 1996; Raghu et al. 2000) or light-dependent photoreceptor degeneration (Meyertohlen et al. 1987; Stark and Sapp 1987; Steele and O'Tousa 1990). This was of great relevance to understanding the mechanisms of many inherited degenerative diseases that cause blindness in humans, such as Retinitis Pigmentosa, a disease that affects 1 in 4000 people, and is associated with progressive degeneration from night blindness to full blindness, or Leber congenital amaurosis (LCA), the most early and severe form of inherited retinal dystrophy, accounting for at least 5% of inherited retinal diseases (Verbakel et al. 2018). Animal models have shown that retinal degeneration in these cases results from cell death via apoptosis (Chang et al. 1993; Chen et al. 1999; Liu et al. 1999).

Mutations in humans that cause Retinitis Pigmentosa have been mapped to more than 80 known genes, and the genetics of their inheritance is complex, from autosomal dominant or recessive to X-linked (Ali et al. 2017; Daiger et al. 2007; Kaplan and Rozet 2008; Verbakel et al. 2018). Mutations in the human rhodopsin genes account for nearly 25% of the autosomal dominant retinitis pigmentosa (ADPR) cases (Alemaghteh et al. 1993; Ali et al. 2017; Bhattacharya et al. 1991; Shokravi and Dryja 1993; Sung et al. 1993; Verbakel et al. 2018). Importantly, many of the mutations uncovered in *Drosophila* genetic screens affect the synthesis, maturation, intracellular transport, chemical recycling or degradation of the light-sensitive G protein-coupled receptor rhodopsins.

As in vertebrates, the phototransduction cascade in *Drosophila* is initiated by the photoactivation of a G protein-coupled receptor rhodopsin covalently linked to a chromophore, the carotenoid 3-hydroxyl, 11-*cis* retinal (Fig. 3). Light-stimulation induces isomerization of the chromophore

thereby inducing a conformational change of rhodopsin to metarhodopsin that allows its interaction with a Gq α protein, thereby inducing multiple downstream processes, namely metabolism of diacylglycerol and the ensuing regulation of calcium influx (Fig. 3) (reviewed in Wang and Montell 2007; Xiong and Bellen 2013). Phototransduction is terminated upon metarhodopsin phosphorylation by GPRK1 and upon Arrestin2 binding, which lead to endocytic internalization (Fig. 3). Early studies in *Drosophila* revealed that mutations in genes involved in the termination of metarhodopsin activity, including *arr2*, *rdgB*, *rdgC*, *norpA* and *Camta*, cause light-dependent retinal degeneration (Fig. 3) (Wang and Montell 2007). In these cases, cell death is light dependent because it depends on the light-induced association of metarhodopsin with arrestin, the internalised accumulation of which triggers apoptosis in photoreceptors (Alloway et al. 2000; Kiselev et al. 2000; Kristaponyte et al. 2012). Similar to what happens in *Drosophila*, the vertebrate rhodopsin mutant RhK296E, common in autosomal dominant retinitis pigmentosa (ADPR), forms a stable complex with arrestin and accumulates in the inner segment of photoreceptors (Chen et al. 2006), suggesting this is a conserved mechanism in retinal degeneration between flies and vertebrates. Other *Drosophila* and vertebrate mutants highlight toxicity due to internalised accumulation of rhodopsin, such as in genes affecting endolysosomal degradation or the autophagy pathway (Chinchore et al. 2009; Hara et al. 2006; Komatsu et al. 2006; Xu et al. 2004). Furthermore, dominant mutations in *Drosophila* Rh1 were isolated that cause photoreceptor degeneration only in the heterozygous state (Colley et al. 1995; Kurada and O'Tousa 1995), with many being identical to those found in ADRP patients, implying that degeneration is dependent on the existence of both wild-type and mutant rhodopsin and revealing that dominant mutant rhodopsin interferes with the maturation of wild-type rhodopsin (Colley et al. 1995). Toxicity due to incorrect folding or maturation of rhodopsin has also been implicated by mutations in the *Drosophila* chaperones calnexin and Xport, which lead to Rh1 accumulation in the ER and reduced Rh1 levels in rhabdomeres and thereby cause light-enhanced retinal degeneration (Rosenbaum et al. 2006, 2011).

Uncontrolled activity of rhodopsin can also result in retinal degeneration. Indeed, this is the case in the *Drosophila* Rh1 PP100 mutant, where the mutant opsin persistently binds arrestin and there is a constitutive activity of the phototransduction cascade (Iakhine 2004). In this case, loss of either arrestin or the Gq α rescues the degenerative phenotype. This mechanism may be relevant to autosomal dominant congenital night blindness, where a mild retinal degeneration is seen as a result of constitutively active forms of rod opsin (Dryja 2000).

The transcriptional mechanisms regulating the expression of rhodopsin genes are yet another important factor

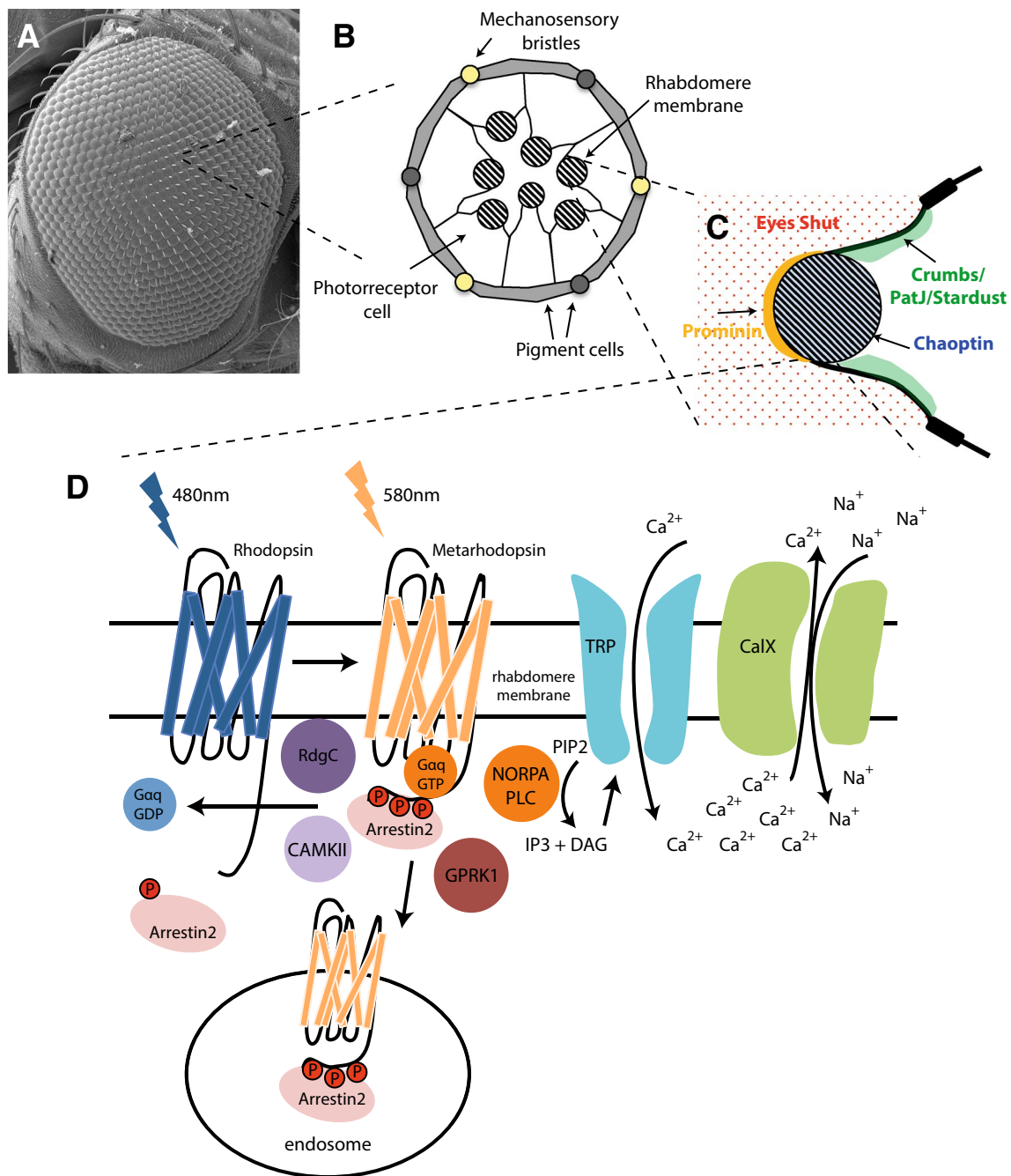


Fig. 3 The *Drosophila* phototransduction apparatus. The *Drosophila* compound eye **a** is composed of hundreds of ommatidia **b** each made up of a cluster of 8 photoreceptor cells surrounded by accessory cells. Each photoreceptor cell projects a microvilli dense membrane towards the center of the ommatidium, making up the light-sensitive rhabdomere **c**. The rhabdomere membrane is supported at its base by the Crumbs/PatJ/Stardust complex and at its core by the structural proteins Chaoptin, Prominin and Eyes Shut. Within the rhabdomere membrane **d**, the phototransduction cascade is initiated by the light-induced conformational change of rhodopsin into

metarhodopsin, which in turn is able to become phosphorylated by GPRK1, interact with a Gαq protein and bind Arrestin2. This initiates a series of other reactions, from the conversion of PIP2 into IP3 and DAG to the internalization of metarhodopsin–arrestin complexes. DAG is able to stimulate Ca²⁺ influx via TRP channels, which in turn can be counterbalanced by Ca²⁺/Na⁺ antiport by the CalX channel. Light-induced conformational change of metarhodopsin can promote its dephosphorylation by RdgC and phosphorylation of Arrestin2 by CAMKII, which promotes its dissociation, thus ensuing the recycling of rhodopsin's original state

commonly affected in retinal diseases. In *Drosophila*, the transcriptional activation of the Rh3 and Rh5 genes and transcriptional repression of Rh6 are orchestrated by the homeodomain protein Otd, and these functions can be partially complemented by the human Otd-related genes *OTX2* and *Crx*, both of which are expressed in human cones and rods and regulate many photoreceptor-specific genes (Terrell et al. 2012). Importantly, several homeodomain mutations in CRX lead to LCA and these mutations have been used in genetic complementation experiments with *Drosophila otd* to reveal differential effects of these mutations on rhodopsin gene expression and rhabdomeric structure (Terrell et al. 2012).

Concerning rhabdomeric structure, some *Drosophila* mutants have been particularly useful in elucidating how this impacts retinal degeneration. In particular, mutations affecting the Crumbs complex, formed by the proteins Stardust, Discs-lost/PATJ and Crumbs, were shown to disrupt the correct separation of the rhabdomere from the stalk membrane in photoreceptors (Fig. 3) (Berger et al. 2007; Hong et al. 2003; Pellikka et al. 2002; Richard et al. 2006). Furthermore, mutations affecting the GPI-anchored protein Chaoptin and the transmembrane protein Prominin along with its associated extracellular glycoprotein Eyes Shut prevent the separation of adjacent rhabdomeric membranes and disrupt the inter-rhabdomeral space (Fig. 3) (Cook and Zehhof 2008; Gurudev et al. 2014; Husain et al. 2006; Nie et al. 2012; Zehhof et al. 2006). These mutations result in light-dependent photoreceptor degeneration possibly as a direct consequent of loss of localisation of rhodopsin and other proteins to the rhabdomeric membrane. Indeed, these effects are similar to architectural defects seen in the rhabdomeres of null or strong mutants of *Drosophila* Rh1 (Kurada and O'Tousa 1995; Leonard et al. 1992). Importantly, Crumbs has been shown to interact and stabilize Myosin V and thereby promote trafficking of Rh1 to the rhabdomeres (Pocha et al. 2011). This mechanism may bear relevance to cases of autosomal recessive retinitis pigmentosa and LCA and autosomal dominant pigmented paravenous chorioretinal atrophy associated with mutations in the human *CRB1* gene (Cremers et al. 2002; den Hollander et al. 1999, 2001, 2010; Jacobson et al. 2003; Lotery et al. 2001; McKay et al. 2005), or in autosomal recessive retinal degeneration caused by mutation in human *PROMINI-1* (Maw et al. 2000), or *RP25*, the orthologue of *Drosophila Eyes Shut* (Abd El-Aziz et al. 2008; Alfano et al. 2016; Yu et al. 2016).

Critically, *Drosophila* research has contributed to high-light targets for therapeutical approaches to many of the degenerations reported above. The chemical transformations of dietary carotenoids into 3-hydroxyl, 11-*cis* retinal, were shown to be important modulators of light-induced retinal degeneration (Voolstra et al. 2010; Wang et al. 2010, 2012). Limiting de novo chromophore synthesis, via B-carotene/

vitamin-A dietary depletion, can greatly reduce rhodopsin levels, thus significantly rescuing light-induced retinal degeneration in mutants affecting the stability of the metarhodopsin–Arrestin2 complex (Alloway et al. 2000; Berger et al. 2007; Kiselev et al. 2000; Richard et al. 2006), and similarly in *crumbs*, *stardust* and *PATJ* mutant eyes (Johnson et al. 2002).

On the other hand, in cases of accumulation of immature rhodopsin, a *Drosophila* study has shown that boosting ER-associated degradation (ERAD), by overexpression of the ERAD factors Hrd1 and EDEM2, reduces mutant Rh1 levels in dominant RhG69D mutants, thereby delaying retinal degeneration (Kang and Ryoo 2009). Intriguingly, genetic inactivation of the ERAD effector chaperone VCP/ter94 in *Drosophila* or its chemical inhibition with Eeyarestatin I led to strong suppression of retinal degeneration caused by accumulation of the immature RhP23H mutant (Griciuc et al. 2010). These apparently conflicting observations hint at different mechanisms of dominance of Rh1 mutations and argue that manipulation of ERAD for therapeutic purposes should consider these differences carefully. Similar to the effects observed for the manipulation of ERAD, potentiating autophagy or lysosomal degradation pathways can effectively reduce rhodopsin accumulation and ameliorate retinal degeneration (Lee et al. 2013; Wang et al. 2009).

A possible mechanism underlying the degeneration upon subcellular rhodopsin accumulation is an overload of cytoplasmic Ca^{2+} influx (Orrenius et al. 2003). Cytoplasmic Ca^{2+} influx induces the dephosphorylation of metarhodopsin by CAMKII and, therefore, low levels of Ca^{2+} can lead to accumulation of internalized metarhodopsin–arrestin complexes and cause photoreceptor degeneration (Chinchore et al. 2009; Kiselev et al. 2000; Orem and Dolph 2002). This is also seen in loss of function mutations in TRP calcium channels, but simultaneous counterbalancing mutations in the Ca^{2+}/Na^{2+} exchanger CalX or the diacylglycerol Kinase, RDGA, can greatly suppress light-induced retinal degeneration, indicating that balanced Ca^{2+} levels are critical for photoreceptor survival (Fig. 3) (Raghu et al. 2000; Wang et al. 2005). Cytoplasmic Ca^{2+} influx during the photo-response is modulated by the levels of PIP2 and their effect on calcium channels. Interestingly, an altered PIP2 regeneration cycle in *Drosophila* photoreceptors, such as through mutations affecting the Diacylglycerol Kinase, RDGA, or the phosphatidate phosphatase, Lazaro, or overexpression of phospholipase D, can all modify light-induced neurodegeneration phenotypes (Garcia-Murillas et al. 2006; Inoue et al. 1989; Kwon and Montell 2006; LaLonde et al. 2006; Masai et al. 1993).

It has been suggested that dominant negative mutations in rhodopsin associated with retinitis pigmentosa could be especially amenable to gene therapy, as providing extra dosage of rhodopsin was shown to significantly ameliorate the

cell death observed in the Rh P23H mouse model (Lewin et al. 2014; Mao et al. 2011). However, too much rhodopsin overexpression was also shown to cause retinal degeneration in this case, indicating that rhodopsin augmentation needs to be tightly controlled for therapeutic purposes. In *Drosophila*, it was also noticed that expression of phosphorylation-deficient rhodopsin could offer protective effects in *norpA* mutant photoreceptors, indicating that modulation of rhodopsin phosphorylation is critical to prevent its high levels of toxic internalization in light-dependent retinal degeneration (Kristaponyte et al. 2012).

With the advent of CRISPR/Cas9 technology, it is now possible to realize many of these gene therapy changes, albeit cautiously considering possible off-target effects. Recently, AAV-mediated CRISPR/Cas9 targeting of *Nrl*, a rod-specific transcription factor, was shown to improve rod survival in a mouse Rh P374S mutant (Yu et al. 2017). Furthermore, CRISPR/Cas9 targeting of the Rh P23H allele has been achieved efficiently in a null background both in the mouse and pig retina, offering a great promise for gene therapy (Burnight et al. 2017; Latella et al. 2016). Alternatively, using an artificial transcription factor, it was recently possible to repress a mutant rhodopsin gene in pigs, while maintaining normal expression of the wild-type rhodopsin (Botta et al. 2016).

Future perspectives

The genetic basis of most eye conditions, for example, anophthalmia and microphthalmia, has only been characterized in less than 30% of cases (Chassaing et al. 2014; Williamson and FitzPatrick 2014). This low rate of diagnosis is caused in part by the polygenic nature of eye development and by the fact that many cases are caused by rare variants. This is exacerbated by a poor understanding of the function of most human genes. Further functional analysis of known disease-causing genes and screens for new candidates in *Drosophila* has great potential to improve diagnosis and better understand the underlying mechanisms (Wangler et al. 2017). This was exemplified recently by an elegant screen in *Drosophila* for lethal mutations in genes involved in sensory functions and cross-referencing with human exome data (Yamamoto et al. 2014). This study allowed the diagnosis of conditions in several individuals including a new role for *Crx* in bull's eye maculopathy where the phenotypic effect on photoreceptors was similar in flies and humans (Yamamoto et al. 2014). This was facilitated by the availability of sophisticated approaches for screening and powerful tools for genetic and phenotypic analysis in this model. Therefore, it is clear that the *Drosophila* eye will continue to be an excellent and economic model to study eye conditions as well as other diseases (Chow and Reiter 2017; Kumar 2018; Senturk and Bellen 2017; Yamamoto et al. 2014). This

can be enhanced by further collaborations between clinicians and researchers working on *Drosophila* (Wangler et al. 2015) as part of national and international initiatives such as the Undiagnosed Diseases Network (Gahl et al. 2016) and tools such as GeneMatcher (Sobreira et al. 2015a, b).

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Compliance with ethical standards

Conflict of interest On behalf of all authors, the corresponding author states that there is no conflict of interest.

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