Rb deficiency during Drosophila eye development deregulates EMC, causing defects in the development of photoreceptors and cone cells

Milena K. Popova¹, Wei He¹, Michael Korenjak², Nicholas J. Dyson² and Nam-Sung Moon¹,*

¹Department of Biology, Developmental Biology Research Initiative, McGill University, Montreal, Quebec H3A 1B1, Canada
²Massachusetts General Hospital Cancer Research Center and Harvard Medical School, Charlestown, MA 02129, USA

*Author for correspondence (nam.moon@mcgill.ca)

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Summary
Retinoblastoma tumor suppressor protein (pRb) regulates various biological processes during development and tumorigenesis. Although the molecular mechanism by which pRb controls cell cycle progression is well characterized, how pRb promotes cell-type specification and differentiation is less understood. Here, we report that Extra Macrochaetae (EMC), the Drosophila homolog of inhibitor of DNA binding/differentiation (ID), is an important protein contributing to the developmental defects caused by Rb deficiency. An emc allele was identified from a genetic screen designed to identify factors that, when overexpressed, cooperate with mutations in rbf1, which encodes one of the two Rb proteins found in Drosophila. EMC overexpression in an rbf1 hypomorphic mutant background induces cone cell and photoreceptor defects but has negligible effects in the wild-type background. Interestingly, a substantial fraction of the rbf1-null ommatidia normally exhibit similar cone cell and photoreceptor defects in the absence of ectopic EMC expression. Detailed EMC expression analyses revealed that RBF1 suppresses expression of both endogenous and ectopic EMC protein in photoreceptors, thus explaining the synergistic effect between EMC overexpression and rbf1 mutations, and the developmental defect observed in rbf1-null ommatidia. Our findings demonstrate that ID family proteins are an evolutionarily conserved determinant of Rb-deficient cells, and play an important role during development.

Key words: rbf1, Retinoblastoma, emc, ID, Development

Introduction
Retinoblastoma tumor suppressor protein (pRb) is an evolutionarily conserved protein whose activity controls various biological processes. The best-characterized function of pRb is to regulate cell cycle progression (Dyson, 1998). Inactivation of Rb family proteins in multicellular organisms, such as insects and mammals, often leads to additional rounds of cellular division during development (van den Heuvel and Dyson, 2008). One of the key molecular targets of Rb family proteins is the E2F transcription factor that regulates the expression of genes that are involved in DNA synthesis and cell cycle progression. In quiescent cells, Rb family proteins physically bind to E2F and act as transcriptional corepressors. In cycling cells, Rb family proteins are regulated by cyclin-dependent kinases, thus coupling the expression of E2F target genes to different phases of the cell cycle. As a result, in most cancer cells where Rb family proteins are functionally inactive, expression of E2F target genes is no longer regulated in a cell cycle-dependent manner (Sherr, 1996). Importantly, in addition to E2F, pRb tumor suppressor proteins physically interact with and regulate the activities of other cell cycle regulators such as S-phase kinase-associated protein 2 (Skp2) and anaphase-promoting complex (APC) (Bimne et al., 2007; Ji et al., 2004). A recent study demonstrated that, like E2F, Skp2 is required for the tumorigenesis in pRb heterozygous mice (Wang et al., 2010), demonstrating that the tumors generated by pRb deficiency are the result of deregulation of multiple factors such as E2F and Skp2.

In addition to the role of pRb during cell cycle progression, evidence from mouse studies indicates that pRb also participates in cell-type specification and differentiation processes. Various developmental defects in the nervous, muscular and hematopoietic systems have been identified in pRb knockout mice (Lipinski and Jacks, 1999). More recently, pRb was shown to regulate the cell-fate choice of mesenchymal progenitors during development, and to influence the identity of cell lineages susceptible to tumorigenesis (Calo et al., 2010). At the molecular level, pRb has been shown to physically associate with transcription factors that are directly involved in cell-fate specification. For example, pRb physically binds to MyoD to promote expression of muscle-specific genes and to Runx2 to promote osteogenic differentiation (Gu et al., 1993; Thomas et al., 2001). Despite these findings, the exact molecular mechanism by which the inactivation of pRb interferes with cell-type specification and differentiation processes remains unclear.

One factor that was shown to have both physical and genetic interactions with pRb is inhibitor of DNA binding/differentiation 2 (ID2). ID family proteins contain helix-loop-helix (HLH) domains for protein–protein interactions but lack a DNA binding domain. Therefore, they function as dominant-negative proteins to other transcription factors with a HLH domain (Lasorella et al., 2001). Genetic studies in mice demonstrated that the Id2 mutation suppresses numerous developmental defects observed in pRb knockout mice (Iavarone et al., 2004; Lasorella et al., 2001).
2000). Moreover, ID2 ablation was shown to delay tumor onset and decrease the number and size of early focal lesions observed in pRb heterozygous mice (Lasorella et al., 2005). These findings support the idea that pRb normally limits the activity of ID2 during development, and that deregulated ID2 activity contributes to the tumorigenesis of pRb-deficient cells. A possible molecular explanation for these genetic interactions was previously provided by the observation that the hypophosphorylated form of pRb physically binds to ID2 (Iavarone et al., 1994; Lasorella et al., 1996), suggesting that pRb might prevent ID2 from interacting with other transcription factors. Currently, it is not known whether the genetic interaction between pRb and Id2 is caused by the physical interaction between their products.

*Drosophila melanogaster* serves as a useful model system to investigate the in vivo function of a gene in a developmental context. *Drosophila* encodes two Rb family proteins, RBF1 and RBF2 (van den Heuvel and Dyson, 2008). Although the effect of *rspb* mutations on cell cycle progression and survival are well characterized, their role in differentiation is less understood. Genome-wide transcriptome analysis clearly demonstrated that RBF1 and RBF2 directly bind to and regulate expression of many genes that potentially have consequences on differentiation (Dimova et al., 2003; Stevaux et al., 2005). However, no obvious cell cycle- or cell death-independent developmental defects have been associated with *rspb* single or double mutant flies. A recent study demonstrated that *rspb* mutations can cooperate with *warts* mutations to interfere with photoreceptor differentiation (Nicola et al., 2010). Moreover, a genetic screen designed to discover mutations that can cooperate with *rspb* mutations identified Rhinoceros as a protein that cooperates with RBF1 to promote R8 photoreceptor development (Steele et al., 2009). Perhaps, the *rspb* mutation itself might not be sufficient to cause a visible phenotype, but it might cause important changes that render cells more susceptible to other genetic alterations.

We sought to identify factors that can specifically cooperate with *rspb* mutations. We reasoned that the identification of such factors could help us to determine pathways deregulated by the loss of Rb family proteins, and to understand how Rb-deficient cells respond to additional genetic changes. This idea led us to conduct a mis-expression genetic screen in *Drosophila* to identify factors that, when overexpressed, induce an eye phenotype specifically in an *rspb* mutant background. An Exelixis stock that can induce overexpression of Extra Macrochaetae (EMC) was identified from this genetic screen. Interestingly, EMC is the *Drosophila* homolog of ID family proteins, suggesting that the relationship between Rb and ID family proteins is evolutionarily conserved. Overexpression of EMC in the eye of a hypomorphic *rspb* allele, *rspb*120a, induced formation of ommatidia with abnormal numbers of cone cells and photoreceptors. Interestingly, similar developmental defects were observed in a substantial fraction of *rspb*-null mutant ommatidia without overexpressing EMC. The molecular aspect of the ommatidial defects was elucidated, at least in part, by the observation that RBF1 post-transcriptionally regulates the expression of both endogenous and ectopic EMC proteins. Our findings provide evidence suggesting that ID family proteins are an important determinant of developmental defects caused by Rb deficiency in both flies and mammals.

**Results**

In an attempt to identify factors that can cooperate with *rspb* mutations, a genetic screen that utilizes a viable hypomorphic allele of *rspb*, *rspb*120a was designed. Although cell cycle and cell death defects have been found in *rspb*120a mutant larvae, the adult eyes of *rspb*120a appear relatively normal (Fig. 1B) (Du and Dyson, 1999; Moon et al., 2006). We reasoned that *rspb*120a represents a hypersensitized genetic background where factors that can cooperate with *rspb* mutations could be identified. This led us to establish tester stocks where any UAS-transgenes can be expressed in wild-type and *rspb*120a backgrounds in an eyespecific manner (see Materials and Methods). The Exelixis stock collection at Harvard Medical School was used as the source of UAS-transgenes. A subset of Exelixis collection was generated by inserting XP vectors at random sites in the *Drosophila* genome (Thibault et al., 2004). An XP vector carries two UAS enhancer elements that can be activated by Gal4 to bidirectionally overexpress genes neighboring the insertion site. Because one of the two UAS elements in the vector is flanked by Flip-recombinase target (FRT) sequences, and our tester stocks express eye-specific Flip-recombinase (see Materials and Methods), we presumed that the gene primarily mis-expressed in our screen is downstream of the UAS element not flanked by FRT sequences. After crossing our tester stocks to the XP collection, we identified stocks that produced *rspb*120a mutant eye-specific phenotypes (Fig. 1A). We screened approximately 3500 stocks and identified 11 that had a reproducible effect in the *rspb*120a mutant background. Although to a lesser extent, most stocks identified from the screen had a small effect in the wild-type background. Among the 11 stocks identified, *d09015* produced the most specific effect in the *rspb*120a mutant eyes (Fig. 1B). *d09015* in the *rspb*120a mutant background induced roughness and reduction in overall size of the eye. We also noted that *d09015* in both wild-type and the *rspb*120a backgrounds produced eyes in which bristles were missing. Immunostaining against Cleaved Caspase 3 (C3) revealed that the level of cell death normally observed in *rspb*120a eye discs was largely unaffected by *d09015*, indicating that the specific eye phenotype induced by *d09015* in the *rspb*120a background was not caused by an excessive amount of cell death (Fig. 1C). This result indicates that *d09015* contains an XP insertion next to a gene that, when overexpressed, cooperates with *rspb* mutations to interfere with *Drosophila* eye development. We decided to further characterize *d09015* because of the specificity of its effect in the *rspb*120a background.

The insertion sites of the Exelixis collection have been sequenced (Thibault et al., 2004). According to the information provided, *d09015* has an XP insertion on the second chromosome, upstream of a micro-RNA cluster mir-310 to mir-313. However, we quickly realized that *d09015* carries a transgene that segregates with the third chromosome. This led us to sequence the integration site of the XP vector. The sequencing result revealed that *d09015* carries an XP insertion 72 bp upstream of *emc*, a helix-loop-helix (HLH) motif-containing gene (Fig. 2A). We tested whether mis-expression of *emc* is capable of recapitulating the eye phenotype generated by *d09015* by taking advantage of a previously characterized UAS-*emc* transgene (Adam and Montell, 2004). We used the same tester stocks to drive expression of *emc* in the control and *rspb*120a eyes. As shown in Fig. 2B, similarly to *d09015*, overexpression of *emc* produced an eye phenotype in an
rbf1120a-specific manner. Moreover, similarly to d09015, emc overexpression produced adult eyes with no bristles in both control and rbf1120a backgrounds. Because d09015 is homozygous lethal, we performed a genetic complementation test to determine whether d09015 is an emc allele. We crossed d09015 flies to a known emc allele, emc1, that carries a point mutation in the HLH domain. The d09015/emc1 transheterozygous flies displayed the extra macrochaetae phenotype (Fig. 2C), indicating that d09015 is allelic to emc. These results indicate that the effect of d09015 on rbf1120a mutant eyes is the result of emc overexpression.

A recent study demonstrated that emc is required for R7 photoreceptor and cone cell development (Bhattacharya and Baker, 2009). This prompted us to investigate the cellular defect caused by d09015 in rbf1120a eyes. Pupal eye discs 42 hours after puparium formation (APF) were co-immunostained with anti-ELAV and anti-Cut antibodies to visualize photoreceptors and cone cells, respectively (Fig. 3A). We could not detect any obvious neuronal or cone cell defects in the control background in the presence or absence of d09015. ELAV and Cut staining patterns were also relatively normal in the rbf1120a background, although we occasionally detected a few ommatidia with an abnormal number of cone cells (data not shown). By contrast, in the rbf1120a background where emc was overexpressed through d09015, we frequently detected ommatidia with less than four cone cells per cluster (Fig. 3A, yellow arrows). Moreover, we also noticed that the ommatidia associated with cone cell defects also displayed an irregular pattern of ELAV staining. To better examine the ELAV staining pattern, pupal eye discs were co-immunostained with anti-ELAV and anti-Chaoptin antibodies (Fig. 3B). Chaoptin is specifically expressed in photoreceptors and localizes to the plasma membrane (Reinke et al., 1988). The co-immunostaining for ELAV and Chaoptin allowed us to count the number of photoreceptors per ommatidium. Normally, each ommatidium contains eight ELAV-positive photoreceptors. As shown in Fig. 3B, ommatidia in rbf1120a mutant eyes expressing emc frequently contained less than eight photoreceptors. Importantly, the same defects were observed when the UAS-emc transgene was used to overexpress emc in the rbf1120a mutant background (data not shown). To understand the nature of the photoreceptor defect, third-instar eye imaginal discs were immunostained for cell-type specific proteins: Senseless for R8, Rough for R2 and R5, and Lozenge (Lz) for R1, R6 and R7 photoreceptors. Photoreceptors are specified in sequence during Drosophila eye development: R8 is the first to be specified, followed by R2/R5, R3/4, R1/6, and R7 is the last photoreceptor to be determined. The Senseless expression pattern was not altered by EMC overexpression either in wild-type or rbf1120a mutant eye discs (supplementary material Fig. S1A). The Rough expression pattern was disrupted in rbf1120a mutant eye discs by overexpressing EMC; however, the majority of ommatidia clusters contained two Rough-expressing cells, suggesting that R2 and R5 photoreceptor specification was not greatly affected (supplementary material Fig. S1A). Interestingly, Lz expression was significantly delayed in rbf1120a mutant eye discs overexpressing EMC, and was absent in several photoreceptor clusters in the posterior region of the eye disc (Fig. 3C). Overall, EMC overexpression can interfere with a subset of photoreceptors and cone cell development when the function of RBF1 is compromised.

In mammals, there are four emc homologs, Id1–Id4. As mentioned in the Introduction, physical association between pRb and ID2 has been previously reported (Iavarone et al., 1994). Therefore, we tested whether RBF1 could also physically interact with EMC by performing a co-immunoprecipitation assay in S2 cells. However, we could not detect any appreciable protein–protein interaction between the two proteins. Similar results were obtained with protein extracts prepared from Drosophila adult heads (supplementary material Fig. S2 and see Discussion). Because RBF1 is a repressor of transcription, we next asked whether expression levels or patterns of EMC staining are altered in rbf1 mutant cells. Immunostaining of larval eye imaginal discs containing rbf1-null, rbf1A4, mutant clones revealed that the intensity of EMC staining was stronger in rbf1 mutant cells,
addition, Lz expression was also delayed in rbf1^{114} mutant clones at the third-instar larval stage (supplementary material Fig. S1B). To be able to clearly count the number of photoreceptors per ommatidium, immunostaining with anti-ELAV and anti-Chaoptin antibodies was carried out (Fig. 5B). A number of rbf1^{114} ommatidia appeared to contain an abnormal number of photoreceptors. To determine the frequency of this phenotype, we counted the number of photoreceptors within each ommatidium. For this analysis, we only examined ommatidia that were entirely composed of either rbf1^{114} or wild-type cells. As shown in Fig. 5C, 99% of control ommatidia contained eight photoreceptors per cluster (n=599), as expected. As for those ommatidia entirely composed of rbf1^{114} photoreceptors, more than one third of ommatidia contained less than eight photoreceptors per ommatidium (n=641), indicating that RBF1 is required for proper formation of the ommatidial cluster.

Considering the role of rbf1 in survival, it is possible that the decrease in the number of photoreceptors is due to an increased level of cell death. To examine this possibility, we repeated the clonal analysis with eye discs expressing a baculoviral cell death inhibitor, p35. During Drosophila eye development, a wave of programmed cell death at the pupal stage eliminates the surplus of cells that are not incorporated into ommatidia. Any excess of cells that survive this process end up occupying interommatidial space, and can be visualized by anti-Disc Large (Dlg) immunostaining. Normally, there should be only one tertiary pigment cell occupying each side of hexagonal ommatidia. As shown in Fig. 6A, we could detect extra interommatidial cells in the eye discs expressing p35; confirming that programmed cell death was indeed inhibited (Fig. 6A). This was particularly true in rbf1^{114} clones where more than one row of interommatidial cells could be observed. Co-immunostaining with anti-ELAV and anti-Cut antibodies revealed that the ommatidial defect was still present, despite cell death being suppressed (Fig. 6B). In fact, we even found some ommatidia with the correct number of cone cells displaying an abnormal pattern of ELAV staining, suggesting that p35 might actually enhance the phenotype (Fig. 6B, asterisk). We therefore performed immunostaining with an anti-Chaoptin antibody to quantify the photoreceptor defects (Fig. 6C,D). As shown in Fig. 6D, more than 80% of rbf1^{114} ommatidia contained less than eight photoreceptors when cell death was inhibited (n=451). In addition, ommatidia with less than seven photoreceptors appeared to be more frequent than rbf1^{114} mutant ommatidia without p35 expression. This result demonstrates that the defects observed in rbf1^{114} ommatidia are not likely to be the result of an increased level of cell death.

To determine whether RBF1 controls EMC expression by regulating emc transcription, we took advantage of the emc^{w5c} allele where β-galactosidase (β-Gal) is expressed under the control of the endogenous emc promoter. We generated rbf1^{114} mutant clones in eye discs that carried a copy of the emc^{w5c} chromosome (Fig. 7). Immunostaining for β-Gal and EMC revealed that the promoter activity of emc was reduced in the same rbf1^{114} mutant clone where EMC protein expression was increased. This result suggests that, if anything, RBF1 promotes the transcription of emc, and that the mechanism by which RBF1 suppresses EMC expression is post-transcriptional.

We also generated a GFP-tagged EMC construct (GFP–EMC) to monitor the expression of ectopically expressed EMC protein. Importantly, GFP–EMC overexpression in the control and rbf1^{120a} tester stocks recapitulated the same adult eye

![Fig. 2.](image-url) The d09015 allele is an emc allele that contains an XP vector insertion 72 bp upstream of the emc transcription start site. (A) Representation depicting the XP vector insertion in the d09015 allele. Sequencing the genomic DNA of the d09015 allele revealed that the XP vector is inserted 72 bp upstream of the emc transcription start site. (B) SEM images of Drosophila adult male eyes of the tester alleles and of the tester alleles crossed to a previously published UAS-emc transgenic allele. Note that UAS-emc is capable of inducing an eye phenotype specifically in the rbf1^{120a} background. (C) Dorsal views of a d09015 heterozygous adult fly and a d09015/emc^{w5c} trans-heterozygous adult fly. Note the extra bristles in the trans-heterozygous d09015/emc^{w5c} adult fly.

particularly in the posterior region of the eye disc (Fig. 4A). The pattern of EMC staining led us to suspect that EMC is specifically deregulated in the differentiating photoreceptors. Co-immunostaining of eye discs with anti-EMC and anti-ELAV antibodies confirmed that the level of EMC is increased in the rbf1^{114} mutant photoreceptors (Fig. 4B).

Deregulated EMC expression in the rbf1 mutant clones prompted us to look closely at the ommatidial development in rbf1^{114} mutant clones. Because the overexpression of EMC can cooperate with hypomorphic rbf1 mutations (Fig. 3), we asked whether a similar developmental defect could be observed in an rbf1-null background where EMC expression is normally deregulated. In fact, cone cell defects for another rbf1-null mutant allele have been recently described (Steele et al., 2009). Immunostainings for Cut, a cone cell marker, confirmed that cone cell defects were present in rbf1^{114} mutant clones (Fig. 5A). More importantly, similar to observations with EMC overexpression in the rbf1^{120a} background, we frequently detected irregular patterns of ELAV staining in rbf1^{114} ommatidia with cone cell abnormalities (Fig. 5A, arrows). In
phenotype induced by the untagged EMC, indicating that the GFP tag does not interfere with EMC function (data not shown). We first expressed GFP–EMC in the wild-type background using the same Gal4 driver used in the genetic screen. Confocal images of the apical plane of the eye disc immunostained with anti-ELAV antibody revealed that GFP–EMC expression was suppressed in differentiating photoreceptors (Fig. 8A). We observed that the GFP signal was weaker in ELAV-expressing cells than in cells anterior to the morphogenetic furrow (MF) and cells between the ELAV-positive clusters. We did, however, occasionally detect some ELAV-positive cells that expressed a relatively high level of GFP–EMC (supplementary material Fig. S3). In fact, the same driver preferentially expresses GFP in ELAV-positive cells. We then expressed GFP–EMC in eye discs containing rbf1D14 mutant clones to ask whether RBF1 participates in suppression of GFP–EMC expression. We performed the experiment at 18°C to minimize the expression level of GFP–EMC, hoping to limit the overall activity of ectopic EMC. However, we still observed irregularities in the pattern of ELAV staining in the rbf1D14 clones (Fig. 8B). Considering the phenotype observed in the rbf1120a background, this observation was not unexpected (Fig. 3). On the other hand, the ELAV staining pattern in the wild-type clones was normal, demonstrating again the synergistic effect of EMC overexpression and rbf1 mutation. Importantly, we could more frequently detect ommatidia that contained one or more ELAV-positive cells expressing a high level of GFP–EMC in rbf1D14 clones compared with the neighboring control clones (Fig. 8B, yellow arrows). Although we did not quantitatively measure the intensity of the GFP signal, we counted the number of ommatidia that contained one or more ELAV-positive cells.

Fig. 3. The d09015 allele in the rbf1D128a background induces cone cell and photoreceptor defects. (A) Pupal eye discs (42 hours APF) of control and rbf1D128a tester flies by themselves or crossed with the d09015 allele were stained with anti-ELAV (white) and anti-Cut (red) antibodies. ELAV is a marker for photoreceptors and Cut is a marker for cone cells. Note that the abnormalities in the cone cell staining pattern in the rbf1D128a mutant flies that overexpress EMC (d09015) are often associated with irregular ELAV staining patterns (yellow arrows). The merged image was generated by overlaying the anti-ELAV image with the anti-Cut image taken at a different focal plane in the same field of vision. (B) Pupal eye discs (42 hours APF) of indicated genotypes were stained with anti-ELAV (blue) and anti-Chaoptin (red) antibodies. Chaoptin is a glycoprotein specifically expressed in photoreceptors and localized to the membrane. Note the irregular pattern and abnormal number of photoreceptors in rbf1D128a tester flies crossed to d09015. (C) Third-instar eye discs of indicated genotypes were stained with anti-ELAV and anti-Lz antibodies. Note that Lz expression is delayed in rbf1D128a eye discs overexpressing EMC and is missing in several photoreceptor clusters at the posterior region (yellow arrowheads). The position of the MF is marked by white arrows.

Fig. 4. Expression of endogenous EMC protein is increased in rbf1 mutant photoreceptors. Mosaic clones of an rbf1-null allele, rbf1114, were generated in third-instar larval eye discs using eyFLP. The rbf1114 mutant clones are marked by the lack of GFP signal. (A) Anti-EMC antibody (red) was used to compare the expression pattern of EMC in the wild-type and rbf1 mutant clones. The position of the MF is marked by white arrows. The yellow arrow indicates a small rbf1114 clone where EMC expression was increased. (B) Posterior region of an eye disc containing rbf1114 mutant clones. The disc was co-stained with anti-EMC (red) and anti-ELAV (blue) antibodies. Note the overlap between EMC and ELAV signals in the rbf1114 mutant clones, indicating that EMC expression was deregulated in the rbf1114 mutant photoreceptors.
that displayed a strong GFP signal (see Materials and Methods). We found that 11% of wild-type photoreceptor clusters (n=903) and 49% of rbf1null photoreceptor clusters (n=610) had at least one ELAV-positive cell expressing a high level of GFP–EMC, showing a four-fold increase in rbf1null clones (Fig. 8C). This result indicates that RBF1 is needed for correctly suppressing EMC expression in differentiating photoreceptors. This finding is also significant because it provides a molecular explanation for the synergistic effect between EMC overexpression and rbf1 mutation. We concluded from these results that EMC expression is post-transcriptionally regulated during Drosophila eye development and that RBF1 plays an important role in this process.

Discussion

We report here that elevated levels of EMC, the Drosophila homolog of the ID family proteins, cooperate with rbf1 mutations to interfere with Drosophila eye development. Analysis of this interaction led us to discover that rbf1-null mutant eyes exhibit intrinsic ommatidial defects, and that RBF1 is required to limit EMC expression in a cell-type-specific manner. Our study suggests that the genetic interaction between Rb and Id family genes is evolutionarily conserved, and that in Drosophila, Rb family proteins influence the post-transcriptional regulation of EMC protein levels.

The function of pRb tumor suppressor proteins on differentiation is one of the less understood biological processes that pRb regulates. It is still unclear whether some of the differentiation defects associated with pRb deficiency are secondary consequences of deregulating cell cycle progression and/or survival. For example, a recent study demonstrated that myogenic defects caused by pRb deficiency could be rescued by inhibiting cell death or autophagy, indicating that the important biological process affected in this context was not differentiation (Ciavarra and Zacksenhaus, 2010). By contrast, our study strongly supports the idea that Rb family proteins do have specific functions in differentiation. Not only have we demonstrated that rbf1 mutations in flies can lead to specific differentiation defects, but also uncovered that, like in mammals, the ID family of proteins are likely to be an important determinant of differentiation in Rb-deficient flies. Our results suggest that, similarly to their role in cell cycle progression and survival, the function of Rb family proteins in differentiation seems to be evolutionarily conserved. Perhaps, ID family proteins are targets of Rb family proteins in differentiation, similar to the way that E2F is a target in cell cycle progression and survival.

Analysis of rbf1-null pupal eye discs shows that RBF1 is required for proper formation of the ommatidial cluster. Although the exact molecular mechanism underlying the cone cell and photoreceptor defects is unclear, we believe that an increased amount of cellular division or cell death is probably not the cause of the phenotype. Previous studies have demonstrated that rbf1-null cells do not reenter the cell cycle once they start to express ELAV (Firth and Baker, 2005). In addition, we demonstrated that
the inhibition of cell death does not suppress the defect. In fact, it appears to enhance the phenotype. Perhaps, rbf1 mutant photoreceptors that fail to properly differentiate are normally eliminated by apoptosis. In this context, apoptosis serves as a quality control mechanism to ensure proper formation of ommatidia. An alternative explanation for the enhancement of the phenotype is that the surplus of surviving rbf1 mutant cells produced by p35 expression somehow affects ommatidial integrity. Either way, we believe that the enhancement of the ommatidial defect induced by p35 expression occurs at the pupal stage because we could not detect any discernible enhancement of cell-type specification defect at the larval stage (data not shown). Although we focused our effort on analyzing Drosophila eye development, rbf1 mutant flies probably possess additional developmental defects previously overlooked.

Although the phenotype observed in rbf1 hypomorphic eyes overexpressing EMC is similar to that seen in the rbf1-null mutant, rbf1<sup>Δ14</sup>, we could not directly demonstrate that the deregulated EMC activity is required for the developmental defects observed in rbf1-null ommatidia. To test this, we would need to generate double mutant clones of rbf1 and emc. However, because emc itself is required for proliferation and differentiation during Drosophila eye development (Bhattacharya and Baker, 2009), we could not experimentally test this idea. We attempted to reduce the overall level of EMC expression in eye discs containing rbf1<sup>Δ14</sup> clones by introducing a single copy of d09015 or emc<sup>05c</sup> chromosome. However, we did not observe any appreciable changes in the ommatidial phenotype. What we do know is that elevated expression of EMC itself is not sufficient to produce the ommatidial defect described in this study. We used a strong eye-specific Gal4 driver, GMR-Gal4, to increase the

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**Fig. 6.** The developmental defect in the rbf1<sup>Δ14</sup> mutant ommatidia is not suppressed by blocking cell death. (A) Mosaic clones of rbf1<sup>Δ14</sup> were generated as described in Fig. 5. To block cell death, baculoviral p35 proteins were expressed using GMR-p35. Pupal eye discs (42 hours APF) were immunostained with anti-ELAV (blue) and anti-Dlg (red) antibodies. Inhibition of cell death was evidenced by the extra number of interommatidial cells that were present in both wild-type and rbf1<sup>Δ14</sup> mutant clones. (B) Pupal eye discs of the genotype described in A were immunostained with anti-ELAV (blue) and anti-Cut (red) antibodies. The merged image was generated by overlaying the anti-ELAV image with the anti-Cut image taken at a different focal plane in the same field of vision. Yellow arrows point out ommatidia with abnormal numbers of cone cells. Asterisks indicate ommatidia with the correct number of cone cells displaying an abnormal pattern of ELAV staining. (C) Pupal eye discs of the same genotype were stained with anti-ELAV (blue) and anti-Chaoptin (red) antibodies. (D) Control (n=451) and rbf1<sup>Δ14</sup> mutant (n=599) ommatidia were analyzed to determine the number of photoreceptors per ommatidium. The table indicates the raw of number of ommatidial clusters with indicated number of photoreceptor cells. The bar graph shows the percentages of ommatidia, with the number of photoreceptors indicated on the x-axis.

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**Fig. 7.** RBF1 does not repress emc transcription. Mosaic clones of rbf1<sup>Δ14</sup> were generated in third-instar larval eye discs that carried an emc enhancer trap allele, emc<sup>05c</sup>. β-Gal expression in the emc<sup>05c</sup> allele was controlled by the endogenous emc promoter. Immunostaining of the eye disc with anti-EMC and anti-β-Gal antibodies showed that RBF1 normally promotes the transcription of emc while repressing EMC protein expression. The position of the MF is marked by white arrows.
expression level of EMC in wild-type photoreceptors, higher than what was observed in the rbf1^{A14} clones. However, we failed to observe any discernible eye phenotypes, indicating that factors other than EMC must participate to produce the developmental defect observed in rbf1^{A14} mutant clones (data not shown). Recently, Rhinoceros and the hippo/warts pathway have been shown to cooperate with rbf1 mutations to control differentiation processes in the Drosophila eye (Nicolay et al., 2010; Steele et al., 2009). A better understanding of how these factors cooperate with rbf1 mutations will help us to determine additional factors that contribute to the developmental defect. We are currently in the process of analyzing other alleles identified from the genetic screen, hoping to identify additional alleles that can interfere with proper ommatidial development. Nevertheless, given the similarity of the phenotypes observed between rbf1^{A120a} eyes overexpressing EMC and rbf1^{A14} eyes, EMC is likely to contribute to the developmental defect observed in rbf1^{A14} eyes.

One of surprising findings from our study is that the genetic interaction between rbf1 and emc is not simply due to the physical interaction between their gene products. In mice, it is generally thought that ID2 is hyperactivated in pRb knockout mice because pRb physically binds to ID2 and limits its function. However, we found no evidence that RBF1 stably interacts with EMC. We tested this hypothesis by expressing epitope-tagged RBF1 and EMC in S2 Drosophila tissue culture cells and by expressing GFP-tagged EMC in Drosophila eyes. In the experimental conditions where transfected RBF1 (S2 cells) or endogenous RBF1 (in flies) co-immunoprecipitated endogenous dE2F2, we could not detect any appreciable binding of ectopically expressed EMC proteins. We also tested physical interaction between endogenous proteins, but the result was the same (supplementary material Fig. S2). Nevertheless, two observations suggest that the increase in EMC expression in rbf1^{A14} mutant photoreceptors is the result of a change in the post-transcriptional regulation of EMC. First, the enhancer trap allele of emc revealed that RBF1 normally promotes (rather than suppresses) emc transcription (Fig. 5). Second, expression of the GFP–EMC construct induced by the Act5C-Gal4 driver was also regulated by RBF1. A previous study has demonstrated that pRb proteins physically interact with Cdh1-containing APC and participate in ubiquitylation of Skp2 upon cell cycle exit (Binne et al., 2007). In another study, ID family proteins have been shown to be ubiquitylated by Cdh1-containing APC during the process of neuronal differentiation (Lasorella et al., 2006). These studies raise the interesting possibility that RBF1 might promote ubiquitylation of EMC during photoreceptor differentiation. Supporting this notion, we have discovered that EMC protein expression is also increased in fizzy-related (fzr, the Drosophila homolog of cdh1) mutant clones in the posterior region of the eye disc, similar to observations in rbf1^{A14} clones (supplementary material Fig. S4). Although this result does not directly demonstrate that RBF1 controls ubiquitylation of EMC proteins, it does show that EMC protein stability is regulated during Drosophila eye development by an ubiquitin-dependent mechanism. Our failure to detect any appreciable physical interaction between RBF1 and EMC could...
suggestion that the RBF1–Fzr–EMC protein complex might be unstable, and/or that EMC is rapidly targeted for degradation upon ubiquitylation, making it difficult to detect by the co-immunoprecipitation assay.

Previous studies have identified many transcriptional targets of pRb whose expression is deregulated in cancer cells. Often, these genes play an important role during pRb-deficient tumorigenesis. Perhaps, identification and characterization of genes whose expression is post-transcriptionally deregulated in pRb-deficient cells will further improve our understanding of the function of pRb during tumorigenesis.

Materials and Methods

Drosophila stocks

Unless otherwise specified, all fly crosses were performed at 25°C. The rbf1 mutants, rbf1120a and rbf1144, have been previously described (Du and Dyson, 1999). UAS-EMC and emc1-7 were obtained from Denise Montell (Johns Hopkins School of Medicine, Baltimore, MD) (Adam and Montell, 2004) and the emc allele was obtained from Bloomington Stock Center. The UAS-GFP–EMC allele was generated as follows: using complementary DNA (cDNA) generated from yw third-instar eye imaginal discs, sequences starting at the translation start site and ending at the 3’ UTR of emc were isolated by PCR and cloned into the pENTR vector (Invitrogen). The gateway system was used to transfer the emc sequence to pAGW vector (Drosophila Genomic Resource Center), which was then injected into yw embryos.

The genotype of flies containing rbf1 mutant clones was as follows: rbf1144FRT19A/GFPsnapshot FRT19A, eyFLP/+; rbf1120a FRT19A/GFPsnapshot FRT19A, eyFLP/GMR-p35; rbf1144 FRT19A/Gal80snapshot FRT19A, eyFLP/+; Act5C<CD2<Gal4, UAS-GFP–EMC/+.

Genetic screen and identification of d09015

To sustain high levels of UAS-transgene expression in both early and late stages of Drosophila eye development, the following tester stocks were generated and used in the genetic screen:

yw eyFLP, Act5C<CD2<Gal4, UAS-GFP/CyO, GFPsnapshot-Gal4

rbf1120a FRT19A/FLP+FRT19A, GFPsnapshot-Gal4 ; Act5C<CD2<Gal4, UAS-GFP/CyO, GFPsnapshot-Gal4

Males of individual X chromosomes from the Exelixis Drosophila collection (Harvard Medical School) were crossed to virgin females of the rbf1120a tester stock and the adult eyes of F1 male progeny were monitored for any discernible abnormality. Selected alleles were then counter-screened against the wild-type tester stock to determine whether the abnormality was specific to rbf1120a, d09015 was identified as one of the alleles that can induce an rbf1120a-specific eye phenotype. According to the annotated information, d09015 contains an Xp insertion on the second chromosome; however, we noticed that the insertion was present on the third chromosome. We therefore PCR-amplified the region of insertion (https://drosophila.med.harvard.edu/~qli/node/32609) and sequenced it to determine whether d09015 had the Xp insertion 72 bp upstream of the emc transcription start site.

Immunostaining and microscopy

The following antibodies were obtained from Developmental Studies Hybridoma Banks: anti-Dlg, anti-ELAV, anti-Cut, anti-Chaoptin (2B810), anti-Lz, anti-Rough and anti-f-Gal. The anti-EMC antibody was a generous gift from Yuh Nung Jan (University of California, San Francisco, CA) (Brown et al., 1995) and the anti-Senseless was from Hugo Bellen (Baylor College of Medicine, Houston, TX) (Nolo et al., 2000). The anti-C3 antibody was from Cell Signaling. For immunostaining of third-instar larval or pupal eye discs, discs were dissected and fixed with 4% paraformaldehyde for 20 minutes (30 minutes for pupal eye discs) at room temperature. Subsequently, discs were washed twice with 0.3% PBST (0.3% Triton X-100 in PBS) for 5 minutes and once with 0.1% PBST. Discs were then incubated with the primary antibody in 0.1% PBST with 5% normal goat serum at 4°C on a rotator for 16 hours. After washing five times with 0.1% PBST, discs were incubated with secondary antibody or antibodies. After washing, discs were mounted in glycerol for confocal microscopy imaging (Zeiss LSM).

Image processing of pupal eye discs

To combine pupal eye disc images at two different focal planes, confocal images at different planes were taken in the same field of vision. The channel denoting the photoreceptors from one plane and the channel denoting the cone cells at another plane were selected and merged to facilitate visualization of cone cells and photoreceptors in the same ommatidium.

Function of RBF1 during development

Quantification

After generating rbf1 mutant clones and immunostaining pupal eye discs (42 hours APF) with anti-ELAV and anti-Chaoptin antibodies, confocal microscopy images were taken. Areas of the pupal eye discs that contained large clones of control and mutant photoreceptors were imaged for subsequent analysis. We selected the focal plane where wild-type ommatidia containing eight photoreceptors could be readily detected. We then counted the number of photoreceptors per ommatidium in wild-type and rbf1144 mutant clones and determined the number of ommatidia that contained a certain number (8, 7, 6, etc.) of photoreceptors in each genetic background. Mosaic ommatidia that included both wild-type and rbf1144 mutant photoreceptors were excluded from analysis. We calculated the percentages of ommatidia (x-axis in Fig. 5C and Fig. 6D) that contained a given number of photoreceptors (y-axis in Fig. 5C and Fig. 6D).

To count ommatidia that contained one or more ELAV-positive cells expressing high levels of GFP–EMC, confocal images of the apical plane of numerous imaginal discs were taken. The boundaries of the photoreceptor clusters were determined by ELAV staining. If a cluster contained a distinct nuclear GFP signal that was distinguishably stronger than the neighboring cells within and outside the cluster, it was scored as an ommatidium that contained a photoreceptor expressing a high level of GFP–EMC.

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Supplementary material available online at


References


