

The Characterization of the Retinal Determination Network in *Drosophila melanogaster* in order to Optimize the Diagnosis and Treatment of Human Retinal Disease

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In *Drosophila melanogaster*, the development of the compound eye is organized by a network of highly conserved transcriptional regulators called the retinal determination (RD) network, which is crucial to normal fly and human development. The RD network is composed of the *eyeless* (*ey*), *twin of eyeless* (*toy*), *eyes absent* (*eya*), and *sine oculis* (*so*) genes which act in transcriptional complexes to regulate each other and are part of a group of downstream genes that direct aspects of eye development. *Eya* plays the role of transcriptional coactivator as well as a protein phosphatase while *ey*, *toy*, and *so* encode paired and/or homeodomain transcription factors. All four genes are necessary and sufficient for retinal development in *Drosophila* and the encoded proteins physically interact and act synergistically to regulate development of several organ systems. Despite their importance in animal development, the mechanisms of *ey*, *toy*, *eya*, and *so* are poorly understood. The aim of our study was to uncover *eya* and *so* function posterior to the MF, specifically their effects on the development of accessory cells during pupal development. However, prior to studying this, it was necessary to study the interaction between *eya* and *so* expression as this allowed us to know whether any change of downstream genes' expression at the posterior MF was due to the modified *eya* expression, rather than the *so* knockout. The study allowed us to uncover the specific roles of *ey*, *toy*, *eya*, and *so* and using this information we can better diagnose and treat human retinal disease.

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