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.