Poster

'Mechanisms of organ size variation: differential gene expression analysis during the development of two fly eyes of very different sizes'

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ABSTRACT

Motivation: Often, organs of related species differ in size in spite of having the same function and general structure. However, the mechanisms that control the variation of organ size, are in most part unknown. This project aims to understand some of those mechanisms that control organ size variation. We will use the eyes of Diptera (flies) as model, because, first, the eyes of flies can be found in a wide range of sizes; and second, eye development in the reference fly model Drosophila melanogaster is simple: the eye primordium is a flat epithelium formed initially by proliferative multipotent progenitors. Differentiation of these progenitors depends on the advance of a signalling wave that induces the differentiation of these progenitors into retinal cells. What are the mechanisms that vary during development of flies that have eyes formed by different cell numbers? We will investigate this problem in Drosophila melanogaster and Episyrphus balteatus, the eyes of which comprise about 20,000 and 100,000 cells.

Methods: To identify mechanisms of differential eye size we will compare the transcriptional profiles of eye promordia from Drosophila and Episyrphus at equivalent developmental times. To account for species-specific gene expression differences not related to eye-specific changes, we will compare the transcriptional profiles of wing primordia from both species. Total RNA is isolated from the primordia to generate sequencing libraries. Eye-specific differentially expressed genes will then be identified and characterized globally, using bioinformatic tools and selected genes will be analyzed by in situ hybridization in developing eye primordia using DIG-labelled RNA probes.

Prior knowledge of Drosophila eye development suggests a list of interesting candidate genes as potentially involved in eye size control: these are the Wnt-1 wingless (wg) and the BMP2/4 decapentaplegic (dpp). We expect that the patterns of them will vary from Drosophila to Episyrphus. These patterns will be examined through in situ hybridization in eye primordia.

In order to structure these data from transcriptomes into a genetic hierarchy (or a gene regulatory network), it would be necessary to establish regulatory relationships between transcription factors and relevant targets. To do so, we are carrying the ChIPmentation-sequencing experiments to identify the binding profile, genome wide, of a set of transcription factors that play essential roles in early eye development.

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