Pigment cell gene regulatory networks in the *Ciona robusta* nervous system

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Project Summary

The development of the central nervous system (CNS) depends on complex gene regulatory networks orchestrating the specification, patterning and differentiation of neural cell types. We would like to take advantage of the unique characteristics of a simple chordate, the ascidian *Ciona robusta*, to investigate the molecular mechanisms underlying cell specification within CNS, with a cellular resolution unprecedented in chordate models. The *Ciona* anterior sensory vesicle, considered to be homologous to the forebrain of vertebrates, contains two distinct pigment cell-containing sensory organs, the otolith and the ocellus. The otolith is a single cell containing a melanin granule and involved in negative geotactism while the ocellus in a complex organ involved in light detection. Transcriptome profiling of PCPs isolated by Fluorescence-Activated Cell Sorting (FACS) performed by our group, has allowed to unravel the regulation of transcription downstream of FGF signaling in this lineage. The plethora of genes, drived by FGF signaling, identified in this study and partially characterized, represent a richness still not completely explored, to understand the gene regulatory network involved in differentiation of single cells inside the nervous system.

AIM of this PHD project is to use CRISPR/Cas9 technologies to knock out a number of genes identified in the previous microarray analysis and study the differential transcriptomic and behavioral response with the final goal to understand how gene activity can instruct each developing brain cell to move around, change shape, and connect to other cells and which are the networks controlling neuronal specification, morphology of the cells inside the *Ciona* sensory vesicle with special attention to pigment cell differentiation.