Understanding transcription factors involved in the development of the eye and nervous system.

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Abstract

DNA binding proteins such as transcription factors (TF) are key determinants of cellular state and have been shown to control cell differentiation. Evaluating the specificity profile of DNA binding proteins is a nontrivial challenge that hinders the ability to decipher gene regulatory networks or engineer molecules that act on genomes. They work as master regulators and selector of genes, taking control over processes in the development of diverse phenotypes. The intrinsic affinity of each TF to a specific binding site is important to establish and understand the role they play in multiple phases of development. The TF family know as sine oculis homeobox (SIX) are evolutionary conserved TF that are found in diverse organism that range from flies to humans. They play a pivotal role in development of the cell population that gives rise to head, retina, ear, nose, brain, kidney, muscle and gonads. Mutation seen in flies and mammal's versions of these genes have adverse consequences on the development of different tissues and organs and have been seen in high level expression during tumorigenesis in several cancer. In flies the formation of ectopic eyes have been observe when expressing TF members of the SIX family. *Optix* is a transcription factors that is involve in a numerous developmental stages of the eye and nervous systems. However, the direct gene targets of *optix* and its possible effects on gene regulation and cis-regulatory sequences hasn't been discovered. My current work in the Rodriguez-Martinez Lab is to: **Determine what are the intrinsic DNA binding preferences of the transcription factor optix and other SIX family members? What are the direct gene targets of optix and the role it may have?** and **How do cis-regulated elements vary across species and role they may have?** Based on this, we want to determine the intrinsic DNA-binding preferences of *optix*. We are currently working on cloning, over-expressing and purifying full-length optix and *optix* DNA-binding domain, the homeodomain (HD). We will determine the in vitro DNA-binding specificity of optix protein using Cognate Site Identification by high-throughput SELEX. Our results will enable us to bioinformatically predict the genomic intrinsic targets of optix and to better understand its role in wing color patterning.