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Proposal

A commonly observed pattern in visual ecology is the tuning of the sensory system to available light in the environment. This is accomplished by the duplication, diversification, and differential expression of visual system genes. Proteins involved in the visual system can reside in the lens, which is composed of crystallins. Crystallin genes have undergone extensive duplications and deletions, but it remains unknown how they have diversified with respect to changes in lens morphology and function across diverse environments. Salamanders are an excellent model to study visual systems because of their diverse life cycle modes and extreme transitions in habitat across ontogeny. The life cycles of salamanders not only include the typical metamorphic life cycle of a frog, but also permanently aquatic and terrestrial lineages. Representatives occupy a plethora of habitats that vary in light environment and media type therefore the visual systems of salamanders have undergone repeated transitions in visual media, often across development.

Our study objective is to understand if crystallin genes involved in the visual system vary from larva to an adult, and whether it results from heterochrony or ontogeny. If paedomorphic adults and larva share the same trend in differential gene expression, this implies a developmental truncation via heterochrony, but if the paedomorphic and metamorphic adults maintain a similar developmental pattern, then it is an effect of ontogeny (being an adult).

To understand the diversity of crystallin genes I deep transcriptome sequenced the whole eyes of 17 species representing six salamander families. Through this analysis I uncovered dozens of previously unknown crystallin genes. The study I am proposing would be the first study to examine the diversity of salamander crystallins, and use a newer, more gene-specific method, transcriptomics, to map genes to known crystallins across a fine gradient of development. I can also take advantage of the fact that salamanders exhibit alterative life cycle modes, with paedomorphic salamanders not metamorphosing.

Thus far, I sequenced whole-eye transcriptomes for eight species of *Eurycea*, and then used short read (3’end) sequencing of the transcripts of over 100 *Eurycea* representing larvae and adults of 12 lineages including seven biphasics and five paedomorphs. Instead of using CLC Genomics Workbench to run RNA-Seq analyses, I want to examine my data with other mapping options. I expect to find a precipitous decline in crystallin genes from the larval to the adult stage in both paedomorphic and metamorphic salamanders.