

# Understanding the genetic basis of predator induced phenotypic plasticity in tadpoles

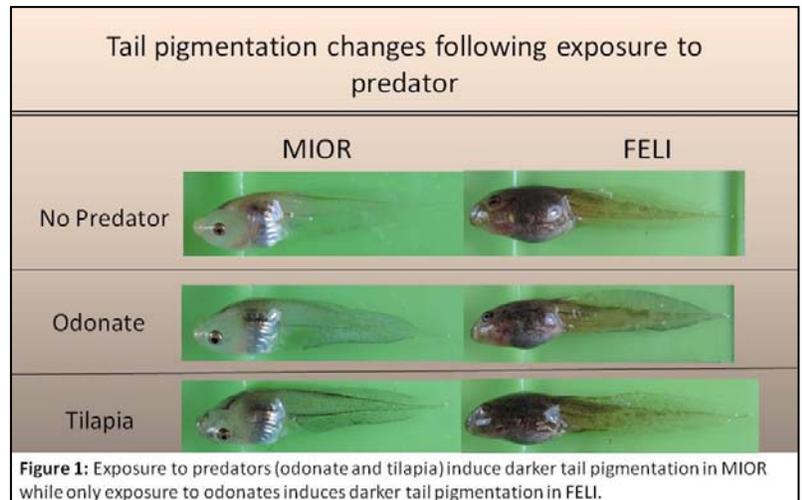
This project provides an outstanding opportunity for a student to learn bioinformatic techniques necessary to analyze genome-level data. The skills obtained are highly applicable to a wide variety of biological research and industrial careers, such as those in conservation and medical sciences.

## Project Description

Phenotypic plasticity, the ability for one genotype to express different phenotypes (e.g., morphology) under different environmental conditions, is important for maintaining biodiversity. Although phenotypic plasticity in traits has been well documented in a variety of organisms, the underlying genetic basis behind it remains poorly understood. Through this project we have a unique opportunity to be one of the first groups to study the genetic basis of phenotypic plasticity.

Tadpoles display plasticity in many traits such as tail pigmentation, tail length, body length, behavior, growth rate, and developmental rate when exposed to predators. We conducted an experiment where we exposed two tadpole species to three treatments: no predator control, dragonfly larva predator, and fish predator. We then collected tadpoles 4, 24 and 96 hours after being exposed to predators and sequenced their transcriptomes from their RNA.

Unlike a genome which provides every possible gene that could be expressed by an organism, the transcriptome provides us with the genes that are actively being expressed at that time point in response to the different predators.



## Project Goals:

- Understand the timing of gene expression important for phenotypic responses.
- Compare the expression differences invoked by two different predators.
- Identify convergent and conserved genes that induce phenotypic responses between the two species.

## Student Responsibilities

- The student will use genome databases to identify the function of genes in the transcriptome sequences.
- The student will contrast gene expression and gene functions in different transcriptome samples.
- Bioinformatic methods and techniques that will be used by the student will include: R statistical programming, Galaxy bioinformatic pipeline, and the BLAST2GO software.

## Location

Temple University, Center for Biodiversity, SERC, Main Campus, Philadelphia  
(VU students may choose to work remotely from Amsterdam)

## Supervisor Information

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