

Interaction between epigenetic and nutritional factors in the maintenance of high variation in an exaggerated sexually selected trait

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Background:

Exaggerated secondary sexual traits represent some of the most astounding examples of sexual dimorphism and intra-specific variation in nature (Darwin, 1871). In some species, these traits can reach degrees of expression so high that the individuals bearing them become almost unrecognizable as members of the same species (Toubiana and Khila, 2016). It is known that sexual selection promotes trait exaggeration in males through increased mating success, while natural selection constrains them due to survival costs (Andersson, 1994). Paradoxically though, exaggerated secondary sexual traits are often highly variable within populations despite strong selection. Which mechanisms are responsible for the development and the maintenance of this variation is still an open question in developmental and evolutionary studies (Lavine et al., 2015).

Hypothesis: Phenotypic variation in exaggerated traits is controlled by the interaction between phenotypic plasticity, genetic variation, and epigenetic factors.

Model system: We use an emerging model system, the pond skater *Microvelia longipes* (Figure), which exhibits a variable and exaggerated secondary sexual trait consisting of the extreme growth of male legs (allometric coefficient greater than 3; one of the highest known).

Tools: We have five distinct natural populations from South America breeding in our lab. Using artificial selection, we have also established inbred lines with either large or small males. We recently obtained a high quality genome of *Microvelia longipes*. We have generated a complete set of transcriptomic data on various lines with various growth phenotypes. Finally, we have established gene function studies using RNAi in this species (Santos et al., 2015).



Objective of the project:

Build a dataset of methylation profiles of animals raised in poor or rich nutritional conditions. We know that an inbred line (same genotype) gives large males in rich and small males in poor nutritional condition, respectively. The master's student will generate three replicates of individuals raised in poor and rich nutritional condition, respectively. These individuals will then be used to extract DNA and perform a methylome analysis using *Bisulfite* sequencing. The student will finally map the methylome data to the genome of *Microvelia longipes* to determine the effect of nutritional condition on the profiles of methylation. This experiment will allow us to know for which loci the methylation status changes depending on nutritional condition, and how this change translates into differences in growth.

Conclusions:

This project will contribute to our understanding of how large variation in exaggerated sexually selected traits develops and evolves in the face of strong selection. Furthermore, this project will improve our understanding of the relationship between environmental epigenetic mechanisms in shaping the phenotype in natural populations.

References:

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