

MSC proposal 3
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Do cryptic species differ in genome size

Evolutionary change occurs through alterations of the genetic code, and we have made great advancements in sequencing and comparing genomes. However, one additional way to drive adaptive change is through “facultative” parts of the genome, meaning genes and regions that are not found in all individuals or tissues. These facultative pieces are not seen in classical comparative genomics, because these typically use a single reference and only compare the pieces that overlap among samples. Thus, to discover these variable parts, we need to measure genome size.

On the Western Atlantic coast there are three species of snails in the genus *Melampus*: *M. bidentatus*, *M. jaumei* and *M. gundlachi*. These three species occur in overlapping and interconnected ranges and experience a range of physiological conditions in salinity and temperature. We are interested in the genomic basis of adaptations to cope with this.

In this project we will use the Feulgen method to measure genome size in a variety of individuals from different populations and in different tissues. The Feulgen method is not new, but has been recently improved and used in a number of species. It is based on staining cells and measuring the size and intensity of the regions containing DNA. This project will give the student experience with several laboratory and analytical skills including:

- Preparation of tissue samples
- Microscopy
- Statistical analyses to compare genome size and environmental variables (performed in R)

Work will be performed with the support of the Dennis lab, and in collaboration with Prof. Jean-François Flot at the University of Brussels.



Note: If there is high interest in this topic, a second student could use the same methods to understand genome variation in different lines of cowpeas. These are very important crop strains, especially in drought prone area. We currently have several mutant lines that have been irradiated to produce novel adaptive abilities. This irradiation likely made drastic changes in the genome, and Feulgen methods are the first step in this important food resource.

