Overcoming the polyploid gap in *Nasonia* parasitoid wasps

Polyploidy is the condition of having more than the usual number of chromosome sets. Becoming polyploid is highly detrimental because it causes immediate problems of infertility, gene expression changes, and abnormal cell biology. Until recently it was considered a “cellular catastrophe” and an “evolutionary dead end”. However, polyploidization has happened many times via whole genome duplication in the evolutionary tree (including for humans!). It is now known to be a major evolutionary driver, having provided benefits such as additional gene copies for more complex gene networks, increased speciation, and increased hardiness. This introduces a major evolutionary mystery, how do polyploids overcome disadvantages to derive benefits, the so-called polyploid gap?

Polyploidy is difficult to study in animals because there are few species that can be intentionally polyploidized. Those that can be are sterile so studies cannot be conducted beyond the first generation. The parasitoid wasp *Nasonia vitripennis* is exceptional, because there is a naturally occurring polyploid line, ways to make polyploids by targeting single genes, and potentially ways to make polyploids through whole genome duplication. Polyploids also have limited fecundity, so the evolution of polyploid lineages can be studied over many generations.

The student will investigate how polyploidization detriments are managed by different polyploid backgrounds and how detriment and advantage changes over time. Based on previous results, there is the potential to develop various objectives into a full Master’s project. These include 1) mechanisms for differential mating success of polyploid males 2) mechanisms for differential reproductive success of polyploid females and 3) gene expression differences among polyploid backgrounds to explain likelihood of evolutionary success versus extinction. The student will use a large range of skills to including 1) insect (*Nasonia*) culture 2) life history assays 3) various molecular techniques such as RNAi injection to create different polyploid lines; flow cytometry to track the ploidy of individuals; RNA extraction for transcriptomics; qPCR for expression analyses 3) bioinformatics and statistical data analyses.

**Methods:** Insect (*Nasonia*) culture; Life history assays; RNAi injection; Flow cytometry; RNA extraction; qPCR; Bioinformatics and statistics

---

**Staff member:** Leo Beukeboom
**Contact:** lw.beukeboom@rug.nl

**Daily supervisor:** Kelley Leung
**Contact:** k.leung@rug.nl

**Expertise group:** Evolutionary Genetics, Development & Behaviour

**Type of project:** ☒ Bioinformatics  ☐ Fieldwork  ☐ Laboratory  ☐ Theoretical
**MSc program:** ☒ Biology  ☒ Ecology and Evolution  ☒ Marine Biology
 ☐ Biomedical Sciences  ☒ Behavioural and Cognitive Neurosciences

**ECTS:** ☒ 30  ☒ 40  ☐ Language: ☐ Dutch  ☒ English

**Start date:** Fall 2021  **Location:** GELIFES - Linnaeusborg

---

2021-2022