

## Research Project

### Loss of heterozygosity during asexual reproduction.

#### Third-party funded project

**Project title** Loss of heterozygosity during asexual reproduction.

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Loss of Heterozygosity during Asexual Reproduction

#### Summary

Sexual reproduction is a widespread phenomenon in nature. Numerous reviews and theoretical studies have discussed this as a paradoxical situation because everything else being equal, sexual reproduction has high costs. However, the widespread existence and persistence of sexual reproduction combined with the observation that asexual lineages are usually young indicates that sexual reproduction has evolutionary advantages that outweigh its costs. A number of potential advantages have been suggested, among them A) that sexual lineages can purge deleterious mutations more effectively, B) that sexual lineages have a higher potential to evolve in a changing environment, and C) that asexual lines have a lower fitness than commonly expected, because they are faced with an ongoing loss of heterozygosity due to ameiotic recombination. This can occur as either reciprocal (crossover) or nonreciprocal (gene conversion) exchange in apomictic germ-line cells. This latter idea is at the centre of this proposal.

Asexual lines often emerge from sexual ancestors, raising the question of why asexuals do not out-compete their sexual relatives. It has been suggested that the loss of heterozygosity (LOH) and its associated loss of fitness may reduce the long-term advantages of asexual reproduction. Recently, LOH has been discovered in asexually reproducing *Daphnia*. Building on this finding, we here propose two sub-projects to quantify LOH and its fitness consequences during the asexual reproduction of *D. magna*, taking advantage of recently developed genomic tools.

Sub-project A will focus on the estimation of LOH in single generations. Using a high density SNP and INDEL array, we will quantify LOH in several mother-daughter pairs. This approach will not entirely exclude selection: selection during early development against offspring (embryos) with LOH would remain unnoticed. Therefore, we will complement it with a genome-wide analysis of Mendelian ratios of the codominant markers. Selection against recessive deleterious alleles would distort these ratios and would, in combination with a genetic map, allow us to estimate their number and distribution in the genome. From this one can estimate how much LOH is underestimated due to early selection.

Sub-project B will examine the fitness consequences of LOH in asexually propagating lines with and without competition. Furthermore, this project attempts to assess the effect of inbreeding load on LOH under competitive conditions. These experiments will enable us to estimate the longer-term consequences of LOH in asexual populations.

This proposed research will provide further insights into the evolution of asexuality, the maintenance

of sexual recombination and the genetic mechanisms at work during reproduction. It also promises to increase our understanding of the effects and distributions of deleterious alleles in the genome and of the evolution of genome structure in asexuals.

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