

## Master thesis project opportunity

### How inversions can aid adaptation: Experimental evolution of artificial inversions in fission yeast

**Background:** Chromosomal inversions have multiple consequences. On the one hand, they reduce recombination rates, which can maintain combinations of alleles for loci that are located within the inversion, which can be beneficial if these alleles complement each other, for example for local adaptation or in divergence between the sexes. For example, sex chromosomes are thought to evolve by consecutive incorporations of inversions that suppress recombination. On the other hand, inversions have negative effects, because meiosis between inverted and non-inverted haplotypes will result in nonfunctional chromosomes.

The occurrence of large inversions that are segregating in many taxa indicates that selection for their presence and maintenance in populations can be favoured. Genomic rearrangements can maintain adaptive phenotypes, involving many genes acting together like a so-called supergene, and it has been demonstrated that they can be involved in environmental adaptation. However, many details about how inversions arise, extend and are affected by selection are still unknown.

**Project:** You will use molecular genetics techniques for the generation of *de-novo* inversions in *Schizosaccharomyces pombe* (fission yeast), that will be used to study their effect on recombination rates and adaptation.

You will use laboratory techniques such as fluorescence microscopy and flow cytometry to analyse the progeny of your newly generated strains to

1. Study the effect of new inversions in germination rates and recombination rates for the regions within and around the inversions
2. Understand the effect of divergent selection on the maintenance of inversions

If you are interested in this research, please contact Cristina Berenguer Millanes at [berenguer@bio.lmu.de](mailto:berenguer@bio.lmu.de) and/or Bart Nieuwenhuis at [nieuwenhuis@bio.lmu.de](mailto:nieuwenhuis@bio.lmu.de)

#### Background reading:

Kirkpatrick, M. (2010). How and why chromosome inversions evolve. *PLoS Biology*, 8(9). <https://doi.org/10.1371/journal.pbio.1000501>

Kirkpatrick, M. (2017). The evolution of genome structure by natural and sexual selection. *Journal of Heredity*, 108(1), 3–11. <https://doi.org/10.1093/jhered/esw041>

Wellenreuther, M., & Bernatchez, L. (2018). Eco-Evolutionary Genomics of Chromosomal Inversions. *Trends in Ecology and Evolution*, 33(6), 427–440. <https://doi.org/10.1016/j.tree.2018.04.002>

