

# Genetic factors in *Arabidopsis thaliana* meiotic recombination: Mapping new crossover modifiers and characterizing MutL complexes

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Meiotic crossover recombination events are indispensable for proper chromosome segregation and genetic information mixing. A better understanding of crossover designation and distribution processes is of high interest for breeding and crop improvement. In this work, I use forward and reverse genetics to identify and characterize meiotic crossover recombination factors.

In the first chapter, I briefly introduce the state of the art on meiotic cell division, pro and anti-crossover pathways, and other factors and phenomena that affect crossover frequency and distribution.

In the second chapter, I explore the differences in crossover distribution and frequencies, the correlation between SNP density and crossover frequency, and map for recombination quantitative loci in 5 *Arabidopsis* bi-parental populations. These populations were obtained from crosses between the reference accession Col-0 and 5 accessions that originate from 5 different climates.

In the third and final chapter, I characterize the effect of MutL genes expression level on *Arabidopsis* crossover rates in specific genomic intervals. For this, I used mutant lines and two different levels of overexpression. My major conclusions are: 1. *Arabidopsis* MLH1 and MLH3, but not PMS1, affect recombination frequency in the tested intervals. 2. MLH1 and MLH3 display a dosage stabilization behavior, where both loss of function and excessive overexpression are detrimental to *Arabidopsis* fertility. 3. Cytogenetic characterization shows that MLH1 is indispensable for crossover formation and crossover assurance.