

Maximizing meiotic crossovers

Meiotic crossovers shuffle parental genetic information, providing novel combinations of alleles on which natural or artificial selection can act. However, meiotic crossovers are relatively rare and non-homogenously distributed in the genome, with notably almost universal suppression in proximity to centromeres. Another key feature of meiosis compared to mitosis is the monopolar orientation of sister kinetochores, which is required for proper segregation of homologs at meiosis I.

Using the model plant *Arabidopsis thaliana*, we revealed multiple mechanisms that limit meiotic crossovers. Mutation of the corresponding genes led to a spectacular more-than-10-fold increase in genome-wide recombination, without a dramatic effect on chromosome segregation and fertility. However, no crossover increase was observed in proximity to centromeres.

In parallel, we performed a forward genetic screen in *Arabidopsis thaliana*, specifically designed to identify the components imposing monopolar orientation of sister kinetochores, based on their ability to restore fertility in haploid plants. The findings show that cohesion dynamics and SUMOylation enforce monopolar orientation at meiosis I. The study of meiotic crossovers in these mutants with weakened cohesin/mono-orientation showed that crossovers are strongly enhanced in proximity to the centromeres, compared to wild-type. This suggests that crossovers are actively suppressed in the proximal regions by a cohesin-based mechanism.

Altogether, this shows that crossovers are naturally constrained well below their possible maximum, open possibilities to manipulate crossover rate for plant breeding, and raises the question of the evolutionary forces that limit meiotic crossover.