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**Temat pracy: Impact of DNA interhomolog polymorphism on meiotic crossover formation at the genome-wide and recombination hotspot scale in *Arabidopsis thaliana***

(Wpływ polimorfizmu DNA pomiędzy homologami na formowanie meiotycznych crossing-over w skali całogenomowej i na poziomie gorących miejsc rekombinacji u *Arabidopsis thaliana*)

Meiotic crossover recombination is a fundamental process relying on reciprocal exchanges of DNA fragments between homologous chromosomes, which enables to create novel allelic combinations in hybrid organisms. During meiotic recombination, the DNA polymorphism between parental chromosomes can be detected and influence the crossover frequency and distribution along chromosomes. However, this effect remains still poorly understood.

To investigate the relation between polymorphisms and recombination at the genome-wide scale, I optimized the genotyping-by-sequencing (GBS) method that enables crossover mapping in different *Arabidopsis thaliana* hybrids. Comparison of crossover distributions in wild type and in *msh2* mutants, defective in DNA mismatch recognition, revealed the remodeling of crossover landscapes from the diverse pericentromeres towards the less-polymorphic subtelomeric regions in the *msh2* mutant.

Furthermore, I also developed a new tool to study crossover distribution at the hotspot level in *Arabidopsis*, called *seed-typing*. It provides both, a precise measurement of the crossover frequency and mapping of crossover breakpoints at the fine scale. Taking advantage of this approach, I identified highly polymorphic ChP interval with three recombination hotspots: *Aro*, *Coco* and *Nala*. Our results demonstrate that the hotspot centres are practically devoid of polymorphisms but the presence of SNPs around hotspots stimulate their crossover activity. We also show that structural changes surrounding the interval have no effect on the crossover frequency unless they directly involve recombination hotspots. We also confirmed lack of short-distance hotspot competition in *Arabidopsis* using a line with a natural deletion in *Coco* and after deleting a part of *Coco* by CRISPR/Cas9. The detailed protocol for efficient generation of desired mutations in different *Arabidopsis* accessions is also included in this dissertation.

The relation between polymorphisms, MSH2 and recombination was investigated by crossover mapping in the *msh2* background at the hotspots level. It revealed an interesting trend that more polymorphic hotspots are less active after disabling mismatch recognition system (i.e., in the *msh2* mutant). The direct effect of polymorphisms was examined in lines, which are heterozygous only within the tested interval. They showed higher crossover rates when compared to inbred lines. This effect was not observed in sibling plants carrying the *msh2* mutation, which highlights that MSH2 promotes crossover recombination in hotspot polymorphic regions.

**Key words:** Meiosis, meiotic hotspot, polymorphism, MSH2, *Arabidopsis*