

## **Unraveling the genetic basis of crossover variation in *Arabidopsis thaliana* by exploiting a broad diversity**

Meiosis occurs in all eukaryotes (a group that includes human, animals and plants) during their sexual cycle and is the process that leads to the formation of haploid gametes *prior* fertilization. This process is fundamental for evolution as it is during meiosis that occurs genetic reshuffling. In other words, this is the reason why offspring is genetically different even if sharing the same parents. Moreover, genetic reshuffling is widely used in agriculture to generate new varieties to improved pest resilience for instance. Genetic reshuffling is due to crossovers that result in reciprocal exchanges between parental chromosomes. However, it is known that crossovers do not randomly take place but are tightly regulated, both in terms of number (no more than 2-3 events per chromosome pair) and localization along chromosomes.

Nevertheless, extensive variations are observed both between and within species. Piotr Ziółkowski, the leader of the laboratory in which the proposed project will be conducted, has spared no effort in the last years to better understand the reason of such a variation in the model plant *Arabidopsis thaliana*. From this work, he notably deciphered that variation of crossover number relates to differences in sequence of specific genes between accessions. However, to date, very few accessions were screened. Moreover, it is unknown whether similar genetic mechanisms regulate variation in crossover localization along chromosomes.

The main aim of the proposed project is to identify novel genetic regulators of crossover variation (number and localization) in plants. For this purpose, we will use a broad diversity of *A. thaliana* accessions that originate from around the world. This powerful population will be then screened for variation in crossover number and localization with tools specifically developed for *A. thaliana*. Finally, Quantitative Trait Loci (QTL) analyses and, for the first time, Genome-Wide Association Studies (GWAS), will be performed to associate crossover variation with differences in sequence of specific genes between accessions. These analyses will provide us novel candidate genes influencing crossovers formation in plants as well as tools for plant breeders to accelerate generation of new varieties by facilitating combination of desirable traits.