Every sexually reproducing organism possesses a double set of genes, with one set inherited from the father and the other from the mother. The process of creating gametes, egg cells or sperm cells in humans, occurs during meiosis, which reduces the genetic material by half. As a result, when the gametes are combined, the offspring organism inherits a double set of genes.

Crossovers occur during meiosis, serving two primary functions. Firstly, they facilitate the exchange of genetic material between parental chromosomes, known as meiotic recombination. This makes siblings genetically different, even though they have the same parents. In addition, crossovers play an important role in the proper segregation of chromosomes into daughter cells, which is crucial for the proper functioning of gametes. Improper segregation of chromosomes can lead to many genetic diseases.

The number and location of crossovers are tightly controlled. They occur at recombination hotspots that show increased recombination frequency when compared to genome average. Analysis of historical recombination maps of two rice subspecies has shown that the vast majority of hotspots are located in different locations, despite their close relation. What exactly determines the location of recombination hotspots and how their evolution occurs in plants has been studied only to a very limited extent. Therefore, in this project, we will study the hotspot conservation in the pericentromeric region by creating recombination maps for hybrids of *Arabidopsis thaliana* accessions that are evolutionarily distant from each other. In addition, we will examine how structural differences between different Arabidopsis lines contribute to changes in the location and conservation of meiotic hotspots. Analysis of our results will identify genetic factors underlying hotspot distribution.

The activity and localization of recombination hotspots depend on both genetic and epigenetic factors, making the number and distribution of crossovers along a chromosome not random. Therefore, the second goal of this project is to explore the possibility of changing the activity of hotspots by locally modifying the state of chromatin. Specifically, we will aim to develop a system that can reduce the activity of specific hotspots in the centromeric region, making it possible to control the sites of crossover events.

These studies will provide conclusions about hotspot distribution and conservation between very different Arabidopsis hybrids. In addition, we will elucidate to what extent chromatin state affects meiotic recombination at the level of recombination hotspots within pericentromeric regions. Our results will contribute to the development of novel strategies in intelligent crop breeding.