

Meiosis is a type of cell division aiming to produce reproductive cells. It is reductive, which means that the daughter cells have 50% of the genetic material of the parent. In order to achieve this division with success, genetic material exchange has to happen between the homologous chromosomes. These genetic exchanges, also called crossovers, are relatively rare events. Moreover, they do not happen randomly. Nowadays, we know that crossovers are initiated by programmed DNA double strand breaks. They can be generated by different processes and they can influence each other's positions. In addition, crossovers presence along chromosomes is sensitive to the level of divergence between homologous chromosomes. Crossover formation have been studied for a long time. However, we still do not know exactly how the crossover site is designated.

Using the information gathered up to now, we offer MutL γ as a candidate for the function of crossover designation. Indeed, Arabidopsis MutL γ complex is present, on chromosomes, in the same number as the average crossover number. Furthermore, our preliminary results show that this complex can be limiting for crossover formation. As a matter of fact, in our experimental conditions we see a decrease in the crossover number when MutL γ is depleted. Also, when we increase both the level of divergence between homologous chromosomes and the amount of MutL γ , we observe a relative increase in crossover rate.

The aim of this proposal is to test if the candidate we offer, MutL γ , is responsible for crossover designation. We hypothesize that MutL γ has a dosage effect on crossover rate, and that its activity is driven by the level of divergence between homologues. In other words, the crossover rate would positively correlate to the amount of MutL γ . And, MutL γ pro-crossover activity would be higher when the sequence of the homologous chromosomes presents more differences at the sequence level. It is important to point out that the outcome of this work can have very interesting agri-food applications. Actually, figuring out the factor responsible for genetic mixing can enable breeders to decide crossover positions. Having this tool in hands, crop breeding should become more efficient, faster and cheaper leading ultimately to reduction in food production costs.