Role of genetic and epigenetic modifications in changing the rules of homologous recombination in *Brassica*: a useful tool to increase genetic diversity

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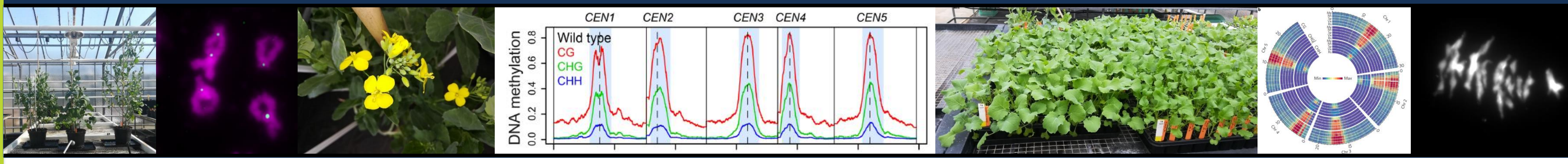


Social-economic context

Meiotic recombination between homologous chromosomes is the main tool used by breeders to improve oilseed rape varieties by combining alleles of interest. Meiotic recombination events, also called crossing-over (COs), are highly regulated in frequency, with only 1 to 3 events per homologous pair of chromosomes, and spatially, with almost no events in pericentromeric regions. However, these genomic regions are far from being deprived of genes and contain diverse agronomic traits (yield, tolerance to biotic or abiotic stresses). In this context, it is extremely important and timely to identify innovative ways that tinkers with recombination to efficiently improve this crop. Additionally, this research will enable to significantly improve *B. napus* genetic diversity that has been severely eroded by human selection in the last decades.

Scientific context

Brassica napus (AACC, 2n=38) is a natural allotetraploid species deriving from *B. rapa* (AA, 2n=20) and *B. oleracea* (CC, 2n=18). It has been shown that *Brassica* allotriploids AAC (*B. napus* x *B. rapa)* have a higher homologous recombination rate all along the A genome (including in pericentromeric regions) compared to their tetraploid and diploid progenitors (Leflon et al., 2010; Pelé et al., 2017). However, it is yet to be deciphered if this triploid feature may be maintained for several generations, thus enabling to further break the linkage disequilibrium. So far, the underlying molecular mechanisms at the origin of this feature remain largely unknown. Recent studies using *Arabidopsis* mutants demonstrated that DNA methylation and various histone conformations play an important role in the regulation of meiotic recombination (Yelina et al., 2015; Underwood et al., 2018). Despite the recombination patterns observed in these mutants differ from those identified in *Brassica* allotriploid, it is extremely likely that epigenetic modifications are involved. During my Ph. D., I will be be particularly interested in deciphering the role of epigenetics in changing the recombination landscape in *Brassica* allotriploids.

Objectives

I will explore the following questions:

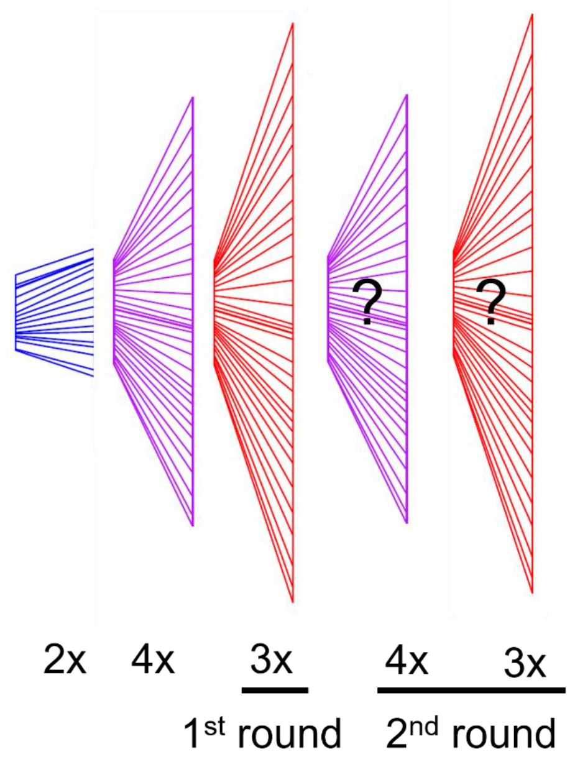
1) What is the role of epigenetic modifications (DNA methylation, histone modifications) in modifying the recombination rules in *Brassica* allotriploids?

2) How far can we break the linkage disequilibrium by performing successive generations at the allotriploid level in *Brassica*?

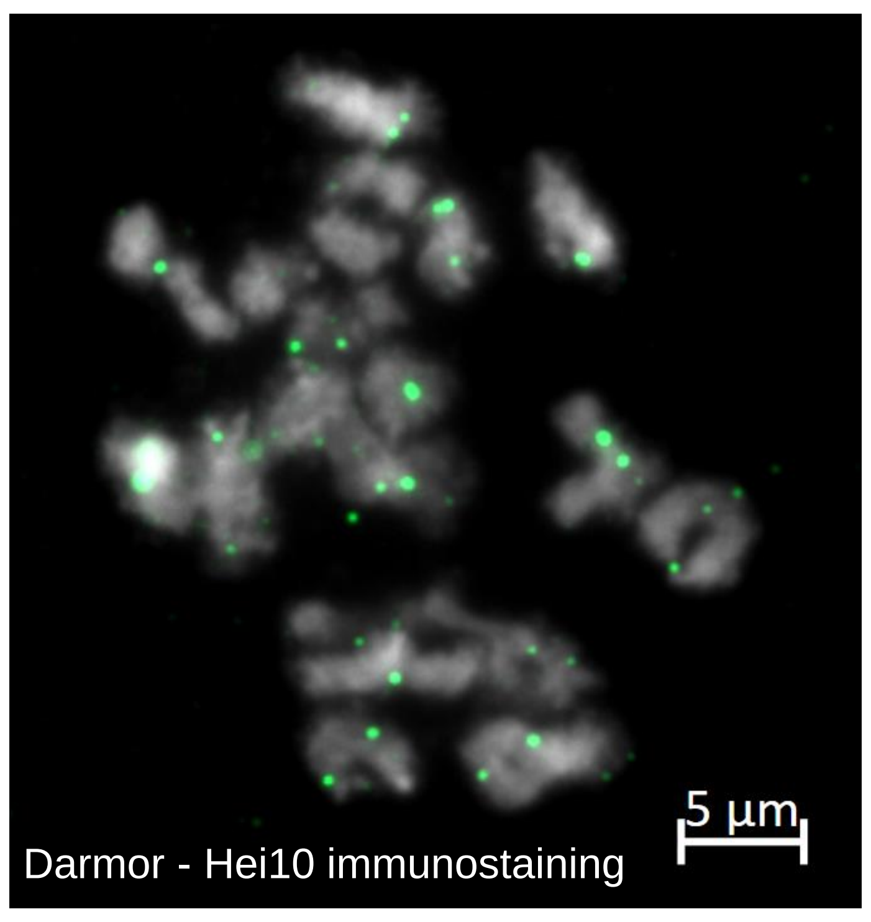
3) Do we revert this phenomenon when recovering an allotetraploid oilseed rape structure?

Results

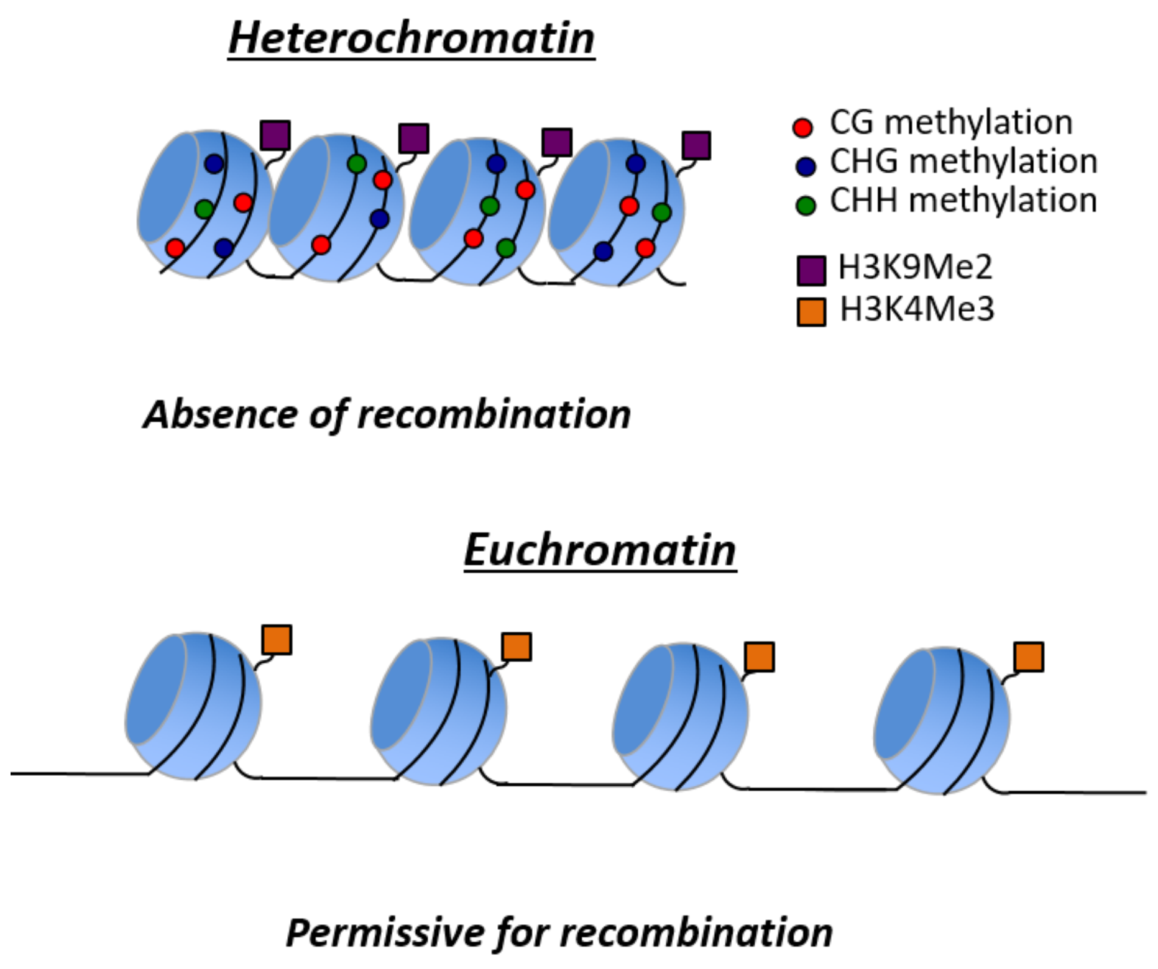
By using both immunostaining and genetic mapping approaches, I will test if the modified recombinations rules observed in Brassica allotriploids can be maintained or revert to normal.
By performing comparative epigenomics (BS and ChIP-seq) and transcriptomics (RNA-seq) between *Brassica* diploid, allotriploid and allotetraploid, I will explore the role of these features in changing the recombination landscape.



Genetic maps



Darmor - Hei10 immunostaining



Perspectives

Using complementary and multidisciplinary approaches (immunolocalization, molecular cytogenetics, comparative epigenomics and transcriptomics, and genetic mapping), my Ph. D. will increase our current knowledge on the molecular mechanisms that may modify the recombination rules in *Brassica*.
This Ph. D. will be of high interest to breeders by offering new ways to increase the low *B. napus* genetic diversity and by facilitating the combination of beneficial alleles, even in normally cold recombination regions.

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