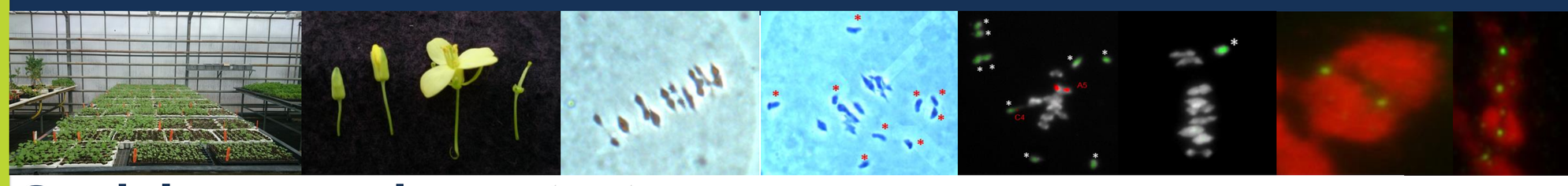
Impact of genomes evolution and ploidy level on frequency and distribution of recombination events in Brassica



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Social-economic context

Meiotic homologous recombination by crossovers (COs) is the main mechanism responsible for mixing genetic diversity by producing new allelic combinations in hybrids generated. However, rarely more than two COs occur between homologous chromosomes per meiosis and their distribution is not homogenous in all chromosomic regions limiting the loci separation. Thus, there is an high interest in the control of recombination in plant breeding.

Scientific context

Although CO number and distribution along the chromosomes are strictly regulated, it was recently established in Brassica that ploidy level have an impact on homologous recombination. Indeed, it was shown that, in allotriploid hybrids (AAC, 2n=29), resulting from crosses between *Brassica napus* (AACC, 2n=38) and *B. rapa* (AA, 2n=20), COs get a boost between the homologous A07 chromosomes compared to diploid hybrids (AA, 2n=20). In addition, it was demonstrated that this recombination rate increase was linked to the chromosome nature and particularly to the chromosome C09.

Objectives

The aim of this study is to determine the possibility to change the CO frequency and distribution as well as the origin of these variations. To that purpose, the questions raised in my PhD work are:

(1) What about the impact of ploidy level on CO rate and distribution?

(2) Does male and female meiosis have an impact on these variations?

(3) What are the C chromosomes involved in these variations?

(4) Does the evolution in polyploid context (C from *B. napus* or *B. oleracea*) impact recombination control?

Results

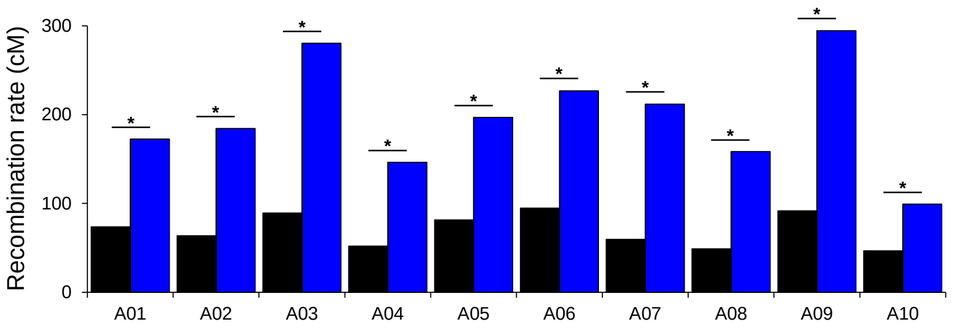

Figure 1 : Recombination rate in cM between the 10 A homologous chromosomes from A_1A_2 (black) and $A_1A_2C_O$ (blue) hybrids. Linkage groups significantly different for CO rates between the A_1A_2 and $A_1A_2C_O$ hybrids are indicated with a black stars (χ^2 test, $\alpha < 0.05$).

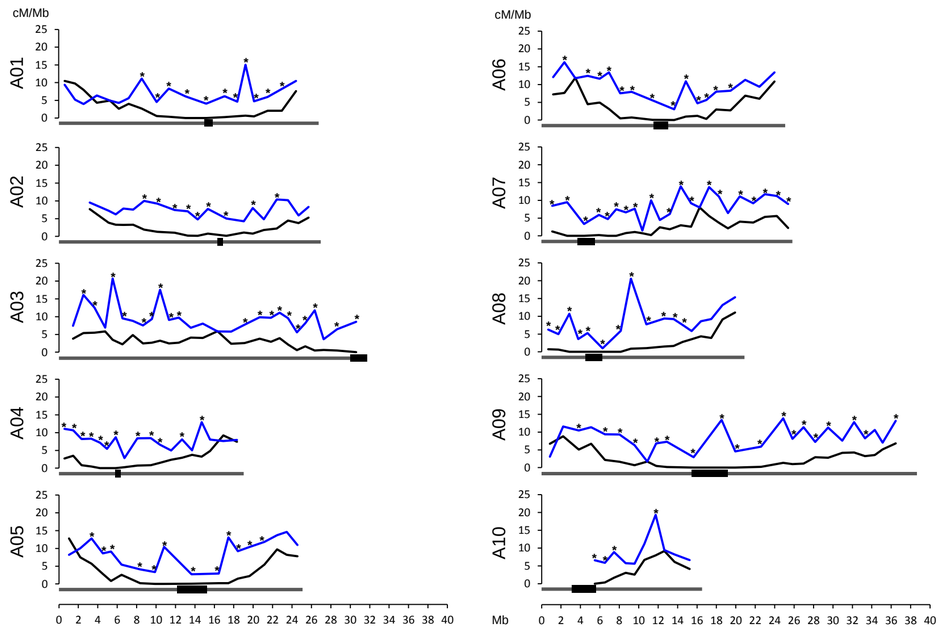

Figure 2 : COs distribution from A_1A_2 (black) and $A_1A_2C_O$ (blue) hybrids along the 10 A homologous chromosomes. Chromosomes are represented on x axis by grey bars and superimposed blackbox represent estimated pericentromeric regions. Intervals with significantly different CO rates between A_1A_2 and $A_1A_2C_O$ hybrids are indicated with a black stars (χ^2 test, $\alpha < 0.05$).

To address these questions, progenies were derived from 14 F1 hybrids either diploid (AA), diploid with different C chromosome combinations or triploid (AAC) hybrids. Recombination was assessed from 3000 COs per hybrid by genotyping of 204 SNPs well distributed along the 10 A chromosomes.

We showed that the presence of the 9 C chromosomes unpaired modifies the CO rate (figure 1) and distribution (figure 2) between the 10 A homologous chromosomes. New recombining regions were detected notably near pericentromeric regions whatever the genetic background and the sex meiosis.

Between triploid hybrids, significant variations for CO rate were observed depending on the sex meiosis (female > male).

Finally we determine that the C09 chromosome is responsible for all these changes, only when it comes from *B. oleracea* highlighting a change of homologous recombination control since *B. napus* formation.

Perspectives

For the first time, we showed that it is possible to change the distribution of COs. Several researches are under way to determine the CO type (interfering or not) and the (epigenetic) mechanisms involved. These results will be largely used in breeding programs as well as in the understanding of meiosis control in evolution.

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