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CONTROLLING HOMOLOGOUS AND HOMOELOGOUS RECOMBINATION IN BREAD WHEAT TO ENHANCE THE DEVELOPMENT OF ORIGINAL AND PRODUCTIVE WHEAT VARIETIES

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Crop improvement relies on the production of crosses between the most relevant accessions and the screening of the progeny for the most powerful descent gathering the best combination of genes of agronomical interest. Reshuffling of the genetic material between individuals and/or between species occurs through meiotic recombination with the formation of crossovers (COs). Meiotic recombination is a fundamental process for all sexual eukaryotes that is required to produce balanced gametes and therefore is essential to the fertility of species. Over the past decade, considerable progress has been made in deciphering meiotic recombination in plants. However, much of that work has focused on diploid model species and thus largely ignored possibilities of practical exploitation and/or disregarded the special features of crop genomes like polyploidy. As an allo-polyploid species, bread wheat (*Triticum aestivum* L.; $2n = 6x = 42$; AABBDD) must face two levels of control for recombination, between homologues and between homoeologues. Homologous recombination is a rare event (one CO/chromosome arm/meiosis) that locates in small regions (hot-spots) that are unevenly distributed along the chromosomes. In bread wheat, this reduces drastically the genes' admixture in the pericentromeric regions that nevertheless bear ~50% of the genes. In addition, negative linkages between antagonistic genes are often almost impossible to break. Finally, introgression of DNA fragments from related species that are frequently used to introduce biotic and abiotic resistance genes, fully blocks recombination leading to undesired linkage drag. Here, our latest results regarding understanding and improvement of recombination in bread wheat will be presented as well as their impact on breeding strategies.