Chromosome 3B, a Model to Study the Structure, Function and Evolution of the Wheat Genome

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Improvement of bread wheat quality and yield in the context of sustainable agriculture has to be achieved in the next decades to meet human needs by 2050. Significant advances in the understanding of the wheat plant biology as well as in the management and exploitation of genetic resources are necessary to address this challenge. Genomic analyses can support this effort through a better understanding of the organisation, function, and evolution of this large and complex genome. Recent advances in wheat genomics already have led to better marker-assisted selection and to the positional cloning of a number of genes of agronomic interest. However, this knowledge remains too limited and larger scale studies are needed now to develop more efficient tools and strategies to support wheat improvement. While the size and the complexity of the wheat genome do not allow yet detailed studies at the scale of the whole genome, recently it has become possible to work on single chromosomes.

This project aims to exploit the first physical map of chromosome 3B of bread wheat that is under construction currently in the coordinating laboratory as a model to study the structure, function, and evolution of the wheat genome. This unique resource will allow us to address a number of important biological questions, such as:

1- The organisation of the gene space and the duplication of the genome. These studies focus on characterizing the gene islands (distribution along the chromosome, gene density within and outside islands), identifying ancestral genome duplications through comparative analyses with rice, and studying their impact on gene function and evolution.

2- The recombination and its effect on genome evolution. Analyses will be performed in different genetic contexts (homology, homoeology, ploidy) and at different scales (whole chromosome, saturated deletion bins and targeted sequenced regions) to study the recombination frequency and distribution as well as the effect of recombination on gene and genome evolution. Moreover, linkage disequilibrium and its use in association genetics will be evaluated.

3- The mechanisms of rearrangements that have shaped the wheat genome during evolution. As a model, we will study the evolution of the disease resistance locus *Rph7* in grasses. Rearrangement mechanisms leading to deletion and/or translocation of genes as well as gene sequence evolution at this locus will be studied through intraspecific (rice sub-species; wheat homoeologous chromosomes) and interspecific (barley, *Brachypodium*, rye-grass, maize, sorghum) comparative analyses.