

Structural and Evolutive Analysis of Ancestral Chromosomes Fusion Points within the Hexaploid Wheat Genome

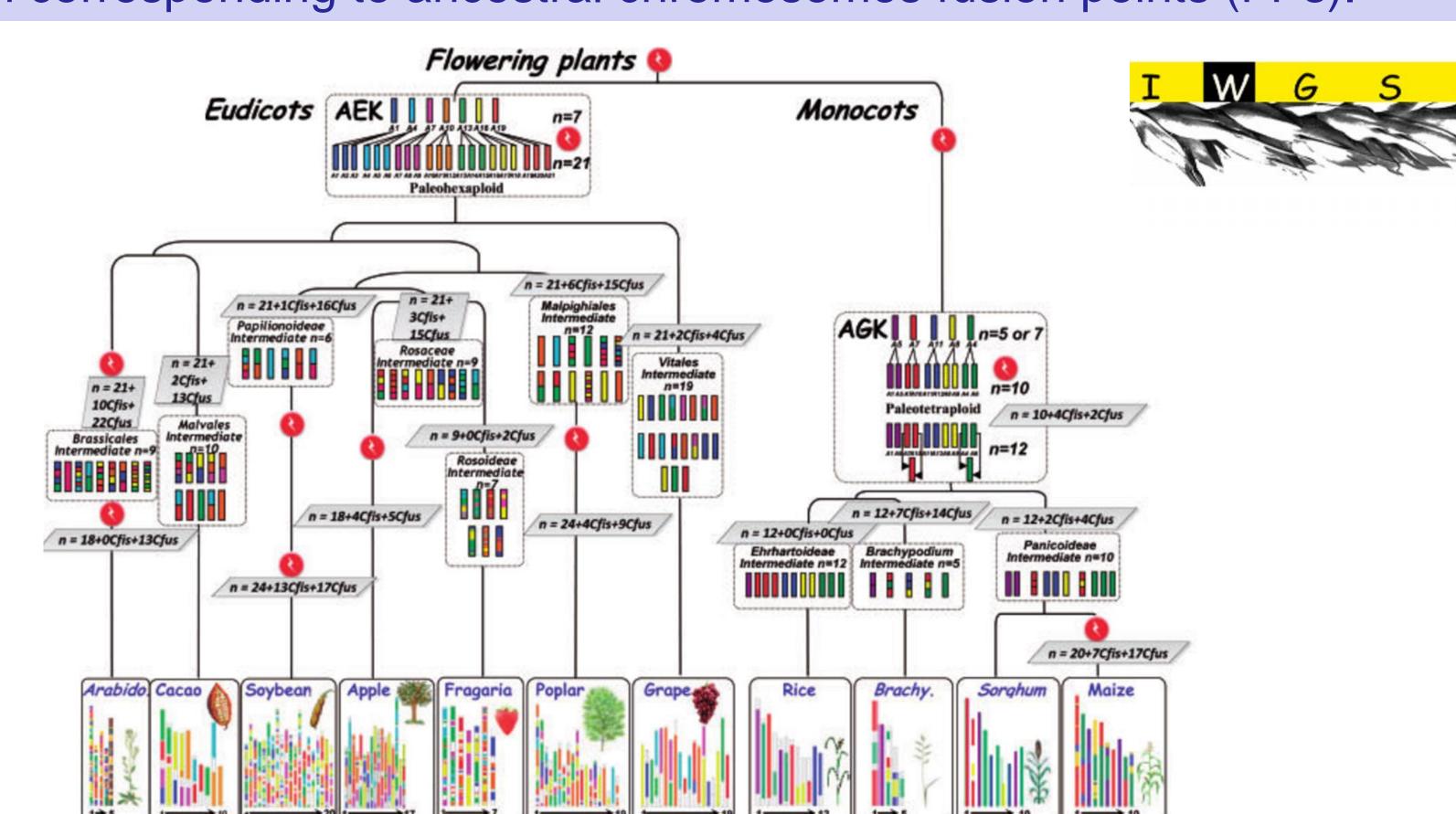
Arnaud Bellec¹, Joëlle Fourment¹, Nadège Arnal¹, Elisa Prat¹, Stéphane Cauet¹, Nathalie Rodde¹, Caroline Pont², Florent Murat², Jérôme Salse², Hélène Bergès¹ // ¹ INRA-CNRGV, Toulouse, France – ² INRA GDEC, Clermont-Ferrand, France // arnaud.bellec@inra.fr

Whole genome duplications (WGDs) are a major evolutionary driving force shared by multiples branches of the tree of life. However, chromosomes number increase over time have been balanced by chromosomes fusions (CFs). In plants, two major mechanisms of CFs have been found through genomes sequences comparisons and ancestral karyotype reconstruction. For monocots, models have highlighted the nested chromosome fusions (NCFs) mechanism. However, molecular mechanisms driving chromosomes fusions that have led to present monocots karyotypes are still largely unknown.

Based on this ascertainment, we aimed characterizing wheat genomic loci corresponding to ancestral chromosomes fusion points (FPs).

Strategy: searching for Synteny Break Points between rice and wheat to find chromosomes fusion sites

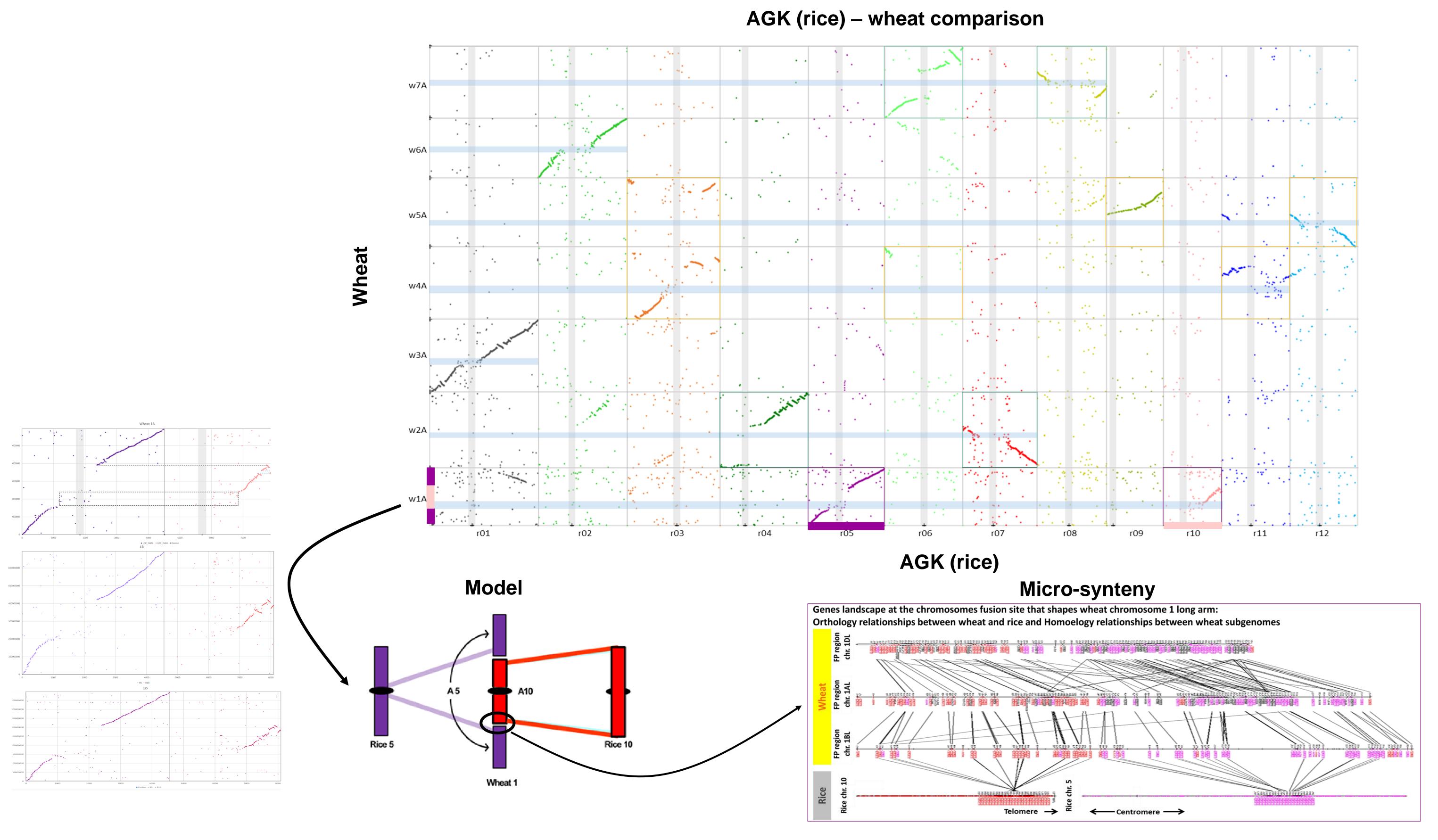
- (i) Reconstruction of ancestral karyotypes of monocots
- (ii) Definition of the synteny relationship between wheat and rice that do not share studied fusion point and corresponds to the ancestral grass karyotype (AGK)
- (iii) Screening of wheat chromosome specific BAC libraries and wheat sequences produced in the frame of the IWGSC (www.wheatgenome.org/)



Results: Chromosomes fusions are highlighted by plotting rice genes (http://rice.plantbiology.msu.edu/) on IWGSC Triticum aestivum sequence (v1.0 available at https://wheat-urgi.versailles.inra.fr/).

Here we present results for subgenome A (+ chromosomes 1B and 1D). Centromeres localizations are positioned in grey for rice chromosomes and light blue for wheat chromosomes.

The 5 CFs are observed. They correspond to scenarios ranging from a single NCF (chr 2A) to complex additions of rearrangement events (Chr 4A/5A).



Conclusions:

- Orthology relationships between wheat and rice genomes have been established highlighting chromosomes fusions and rearrangements that have shaped the wheat genome
- Homoelogy relationships between wheat subgenomes ABD at genes levels at chromosomes fusion point on the wheat chromosome group 1 long arm have been defined
- Based on wheat chromosomes structures and breakage points localizations on the rice genome, various scenarios of chromosomes fusion and evolution including centromeres fates are proposed









