

Paleogenomics in Triticeae for translational research



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ABSTRACT

Recent access to Triticeae genome sequences as well as high resolution gene-based genetic maps recently offered the opportunity to compare modern Triticeae genomes and model their evolutionary history from their reconstructed founder ancestors. *In silico* paleogenomic data have revealed the evolutionary forces that have shaped present-day Triticeae and allowed to gain insight into how wheat, barley, rye genomes are organized today compared to their grass relatives (rice, sorghum, millet and maize).

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1. Triticeae genome evolution

Based on the BLAST-derived orthologous relationships and using DRIMM-synteny [1] to define syntenic groups as well as ANGES [2] to define ancestral gene order, the grasses has been proposed to derive from AGK (Ancestral Grass Karyotype) structured in $n = 7$ protochromosomes (or CARs for Conserved Ancestral Regions) containing 8581 ordered protogenes, dating back to 90 million years ago (hereafter mya), Fig. 1 [3]. In this scenario grasses derived from this $n = 7$ ancestor that went through a whole genome duplication (hereafter WGD, R for 'round' of WGD) to reach a $n = 14$ (A1-A14 CARs) AGK intermediate, Fig. 1. Ancestral small-scale shuffling events took place between the duplicated blocks in the $n = 14$ AGK with two telomeric/centromeric fusions (involving

A2-A4-A6 and A3-A7-A10 protochromosomes, black arrows Fig. 1), three inversions (in A5/A3 and A2 protochromosomes) as well as two translocations (between A4-A8 and A3-A12 protochromosomes) to reach a $n = 12$ AGK post-duplication intermediate containing 16464 protogenes (Fig. 1) [3]. Modern grass (maize, millet and sorghum) genomes were proposed to have derived from this duplicated intermediate (*i.e.* their genome consists then in a mosaic of A1-A5, A2-A4, A2-A6, A3-A7, A3-A10, A8-A9, A11-A12 paralogous ancestral blocks) through distinct ancestral chromosome fusion patterns. The modern rice genome [4] has retained the chromosome number of 12, derived from the post-duplication $n = 12$ AGK intermediate, making this genome as a reference karyotype for comparative genomics investigation in grasses (Fig. 1) [3].

The development of NGS (next generation sequencing) approaches and technologies (Solexa, SOLid, 454) allowed high-throughput WGS (whole genome shotgun) based sequencing of both simple and complex (*i.e.* high repeat content as well as polyploid) genomes. Table 1 provides information regarding the Triticeae genomes and sequence-based genetic maps available to

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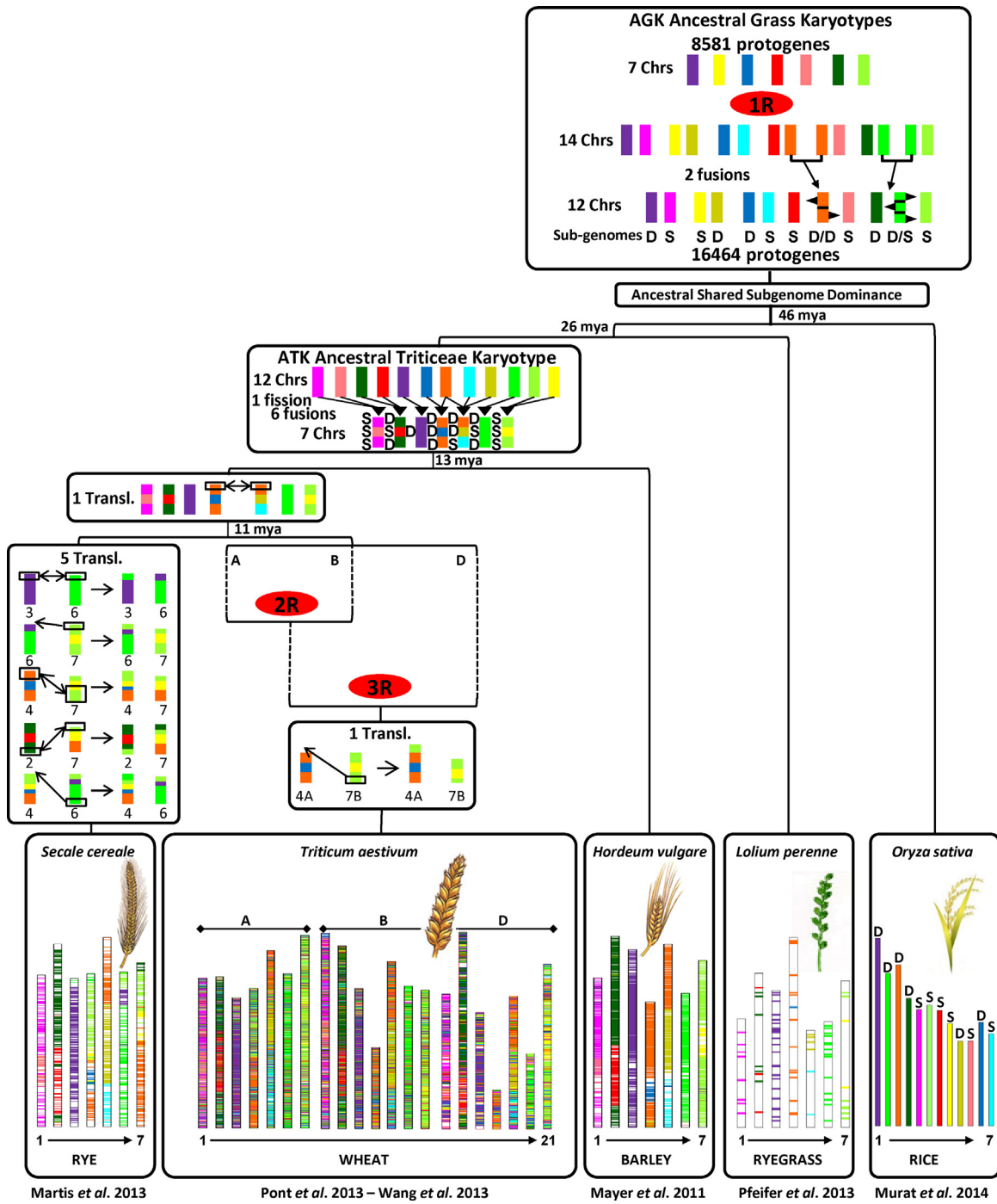


Fig. 1. Triticeae genome paleohistory scenario. The present-day Triticeae genomes (bottom) are represented with color codes to illuminate the evolution of segments from their founder ancestors (top) with seven protochromosomes (referenced as AGK and ATK). WGD events that have shaped the structure of the different Triticeae genomes during their evolution from their common ancestors are indicated in red (i.e. 1R, 2R and 3R). Evolutionary genome shuffling events such as chromosomal fusions and translocations are indicated in boxes with black arrows. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

Table 1
Triticeae genome data sets used in paleogenomics studies.

| | Species | Name | Chr | Size (Mbp) TE (%) | Mapped genes/markers | Syntenic genes | Chr. equation | WGD |
|-----------|--------------------------|----------|-----|-------------------|-----------------------|----------------|-------------------------------------|-----|
| Reference | <i>Oryza sativa</i> | Rice | 12 | 372/39 | 41046 [4] | RG | $2 \times 7 - 2$ | 1R |
| Outgroup | <i>Lolium perenne</i> | Ryegrass | 7 | 2600/>80 | 762 [10] | 84 | $2 \times 7 - 2 + 1 - 6$ | 1R |
| | <i>Triticum aestivum</i> | Wheat | 21 | ~17,000/>80 | 40267 [9]/124201 [15] | 24725 | $(2 \times 7 - 2 + 1 - 6) \times 3$ | 3R |
| Triticeae | <i>Hordeum vulgare</i> | Barley | 7 | ~5000/>80 | 15719 [6] | 5430 | $2 \times 7 - 2 + 1 - 6$ | 1R |
| | <i>Secale cereale</i> | Rye | 7 | 7917/>80 | 2940 [8] | 1205 | $2 \times 7 - 2 + 1 - 6$ | 1R |

RG refers to Reference Genome indicating that rice has been used as reference genome for the paleogenomics analysis of Triticeae genomes.

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