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Sequencing and Analyses of the Hexaploid Wheat Chromosome 3B

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Because of its 17 Gb hexaploid genome, wheat genomics has been lagging behind the one of the other major crops. Two years after the establishment of the first physical map of the biggest wheat chromosome, the 3B, which represents 1 Gb, its complete sequencing is now underway (ANR project 3BSEQ). In order to prepare for its complete sequencing and analysis, we performed a pilot project on 18 Mb of large BAC contigs which allowed us to improve our understanding of the wheat genome composition and dynamics. Comparative and evolutionary analyses revealed that increase of the genome size, mainly mediated by transposable element amplification, was uneven and has led to the formation of small gene islands. In addition, it was accompanied by rearrangement of the ancestral gene content. Indeed, a significant amount of nonsyntenic genes are interspersed into a conserved ancestral grass gene backbone, revealing that, in our sample, about 50% of the annotated genes was unexpected based on synteny with model genomes.