Sequencing and analyses of the hexaploid wheat chromosome 3B

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Sequencing and analyses of the hexaploid wheat chromosome 3B

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Because of its large (17 Gb, 5x the human genome and 40x the one of rice), polyploid (3 homoeologous A-, B- and D-genomes within a same nucleus) and highly repetitive (>80% of DNA corresponding to transposable elements) genome, the development of 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 (Paux et al. Science 2008), its complete sequencing is now underway (ANR project 3BSEQ) by combining Roche 454 sequencing of pools of contiguous BACs and Whole Chromosome Shotgun sequencing by Solexa/Illumina. High throughput marker development and functional analyses based on RNASeq, tiling array and copy number variants detection are also planned in the framework of this project. In order to prepare for its complete sequencing and analysis, we performed a pilot project on 18 Mb of contiguous sequences which allowed us to improve our understanding of the wheat genome composition and evolution. Comparative and evolutionary analyses revealed a large amount of nonsyntenic genes interspersed into a conserved ancestral grass gene backbone, suggesting that the wheat gene content has been extensively rearranged probably through transposable element-mediated gene capture. Finally, bioinformatics tools and databases has been developed in order to manage automatic annotation and analyses of such a large amount of data.