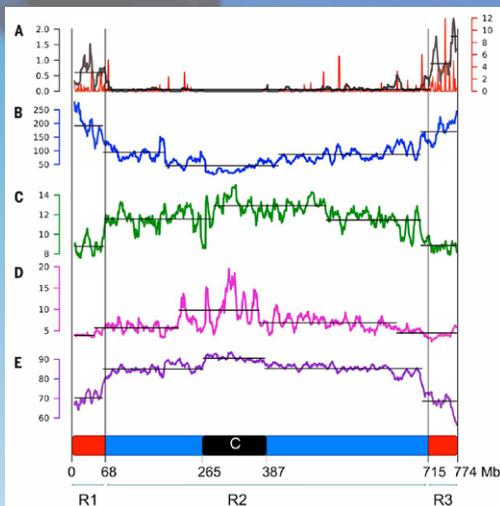


Structural and functional partitioning of bread wheat chromosome 3B

Publication of the first reference sequence of the biggest bread wheat chromosome. Thanks to an international collaboration, coordinated by INRA jointly with CEA (Genoscope), CNRS and Université d'Evry in France, this major achievement will allow the identification of numerous genes of agronomic interest, and accelerate wheat improvement.

We produced a reference sequence of the 1-gigabase chromosome 3B of hexaploid bread wheat. By sequencing 8452 bacterial artificial chromosomes in pools, we assembled a sequence of 774 megabases carrying 5326 protein-coding genes, 1938 pseudogenes, and 85% of transposable elements. The distribution of structural and functional features along the chromosome revealed partitioning correlated with meiotic recombination. Comparative analyses indicated high wheat-specific inter- and intrachromosomal gene duplication activities that are potential sources of variability for adaptation. In addition to providing a better understanding of the organization, function, and evolution of a large and polyploid genome, the availability of a high-quality sequence anchored to genetic maps will accelerate the identification of genes underlying important agronomic traits.



Structural and functional partitioning of wheat chromosome 3B.

We present a reference sequence of chromosome 3B that can be used to precisely delineate structural and functional features along a chromosome and establish correlations between recombination intensity, gene density, gene expression, and evolution rate. Our results indicate that during evolution, regions with distinct features become delineated along chromosome 3B, including relatively small distal regions that are preferential targets for recombination, adaptation, and genomic plasticity. Whether our observations reflect a general pattern for the wheat genome will need to be confirmed by the analysis of other chromosome reference sequences. Already, some of the features have been confirmed at the whole-genome level.

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