Assembling a pseudomolecule for a wheat chromosome: the 3B experience

Frédéric Choulet, Adriana A. Alberti, Valérie Barbe, Sébastien Theil, Pierre Sourdille, François Balfourier, Jean-Marc Aury, Helene H. Berges, Jaroslav Dolezel, Hadi Quesneville, et al.

Assembling a Pseudomolecule for a Wheat Chromosome: The 3B Experience

Frédéric Choulet[1], Adriana Alberti[2], Valerie Barbe[2], Sébastien Theil[1], Pierre Sourdille[1], François Balfourier[1], Jean-Marc Aury[2], Hélène Bergès[3], Jaroslav Doležel[4], Hadi Quesneville[5], Patrick Wincker[2] and Catherine Feuillet[1]

[1]INRA GDEC, Clermont-Ferrand, France
[2]CEA - Genoscope, Evry, France
[3]INRA - CNRGV, Castanet Tolosan, France
[4]Institute of Experimental Botany, Olomouc, Czech Republic
[5]INRA - URGI, Versailles, France

We produced a reference sequence for the giant wheat chromosome 3B (900 Mb). The strategy established was based on the sequencing of 8452 BACs pooled by 10 using Roche/454 8 kb long paired-end reads combined with Illumina whole 3B shotgun (2x100 bp reads). Automated assembly, manual improvement of the scaffolding, gap filling, and BAC redundancy removal led to assemble 2808 scaffolds representing 833 Mb, estimated to cover 94% of the chromosome. The scaffold N50 was 949 kb and gaps represented only 7% of the sequence. Additionally, SNP markers were developed and genotyped in a mapping population and association panels. A high-density genetic map was constructed and marker positions were refined using Linkage Disequilibrium data. This allowed the construction of a single pseudomolecule comprised of 1358 ordered scaffolds representing 774 Mb i.e. 93% of the sequence.