



HAL
open science

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.

► To cite this version:

Frédéric Choulet, Adriana A. Alberti, Valérie Barbe, Sébastien Theil, Pierre Sourdille, et al.. Assembling a pseudomolecule for a wheat chromosome: the 3B experience. 22. Conference on Plant and Animal Genome, Jan 2014, San Diego, Californie, United States. hal-02743902

HAL Id: hal-02743902

<https://hal.inrae.fr/hal-02743902v1>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Frédéric Choulet¹, Adriana Alberti², Valerie Barbe², Sébastien Theil¹, Pierre Sourdille¹, François Balfourier¹, Jean-Marc Aury², Hélène Bergès³, Jaroslav Doležel⁴, Hadi Quesneville⁵, Patrick Wincker² and Catherine Feuillet¹

¹INRA GDEC, Clermont-Ferrand, France

²CEA - Genoscope, Evry, France

³INRA - CNRGV, Castanet Tolosan, France

⁴Institute of Experimental Botany, Olomouc, Czech Republic

⁵INRA - 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.