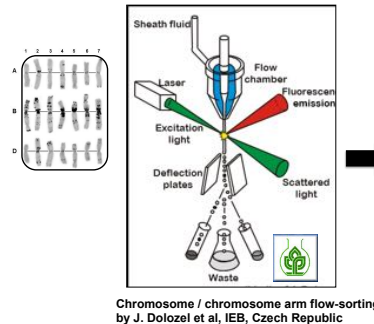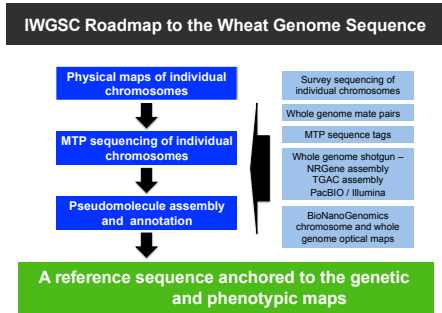# The International Wheat Genome Sequencing Consortium

IWGSC[1], Kellye Eversole[2], Jane Rogers[3] and Isabelle Caugant[1]

(1) Lee's Summit, MO, USA; (2) IWGSC, Bethesda, MD, USA; (3) IWGSC, Cambridge, UK

www.wheatgenome.org

In 2005, the International Wheat Genome Sequencing Consortium (IWGSC) was created to facilitate and coordinate an international initiative to accelerate wheat improvement by delivering to breeders and scientists a gold standard reference genome sequence anchored to the genetic maps. The strategy adopted by the IWGSC has focused on the production of physical maps anchored to genetic maps for each of the 21 individual bread wheat chromosomes and subsequent sequencing of minimal tiling paths of mapped BACs. To complement and complete the BAC-based sequences, the IWGSC has produced additional chromosome-specific and whole genome resources. These include a chromosome-based survey sequence of the genome that has provided early access to genic sequences and underpinned the development of extensive genotyping and population genetic tools and resources. By integrating the new data resources with the BAC-based sequences, the IWGSC expects to complete the reference sequence of hexaploid bread wheat cv. *Chinese Spring* by 2019.
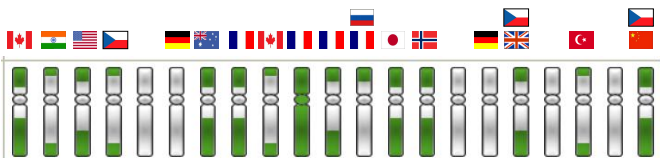
IWGSC Roadmap to the Wheat Genome Sequence

Physical maps of individual chromosomes

MTP sequencing of individual chromosomes

Pseudomolecule assembly and annotation

A reference sequence anchored to the genetic and phenotypic maps

Survey sequencing of individual chromosomes

Whole genome mate pairs

MTP sequence tags

Whole genome shotgun – NRGene assembly / TGAC assembly / PacBIO / Illumina

BioNanoGenomics chromosome and whole genome optical maps

Chromosome / chromosome arm flow-sorting by J. Dolozel et al, IEB, Czech Republic

BAC libraries for 4 chromosomes and 34 chromosome arms: 2,713,728 BAC clones For access see cnrgv.toulouse.inra.fr

Illumina chromosome arm shotgun libraries for survey sequence

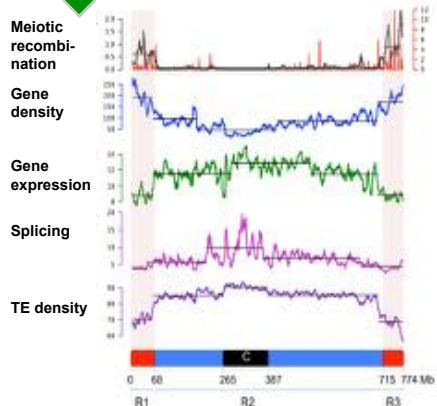Chromosome-specific BioNanoGenomics optical maps for pseudomolecule assembly and QC

Bread Wheat Physical Maps

1A 2A 3A 4A 5A 6A 7A 1B 2B 3B 4B 5B 6B 7B 1D 2D 3D 4D 5D 6D 7D
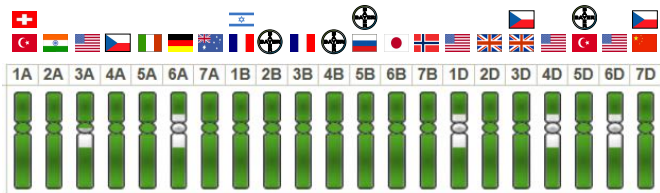
Bread Wheat MTP Sequencing

First chromosome reference sequence of 3B reveals structural and functional variation

Meiotic recombination

Gene density

Gene expression

Splicing

TE density

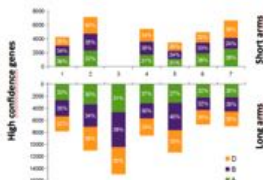0 60 265 387 715 774 Mb
R1 R2 R3

Bread Wheat Survey Sequence

First chromosome-based draft sequence of the bread wheat genome (CSS): Science 18 July 2014: Vol. 345 no. 6194. DOI: 10.1126/science.
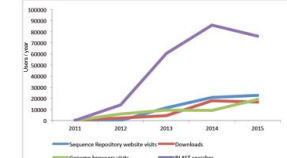
- 10.2 Gb assembled sequences
- 128 Mb (1DS) – 639 Mb (3B) per chromosome
- N50 contig length after repeat masking = 5.9 kb (1.7 kb - 8.9 kb)
- 99,386 annotated genes assigned to chromosomes

Foundation for SNP Chips: Illumina 90k and Affymetrix 420K; and chromosomal assignment of new whole genome sequence assemblies from NRGene, The Genome Analysis Centre and UC Davis based on Illumina + PacBio sequences.

Gene distribution across the bread wheat genome

Data Resources

The IWGSC data repository at URGI INRA Versailles provides access to chromosome physical maps and survey sequences in g-browse formats, with links to mapped tag sequences, genetic markers, gene annotations and gene ordering based on the Genome Zipper and POPSeq data. A J-Browse viewer has also been developed for the annotated chromosome 3B reference sequence and will be available for other chromosomes as well.

wheat-urgi.versailles.inra.fr

Use of IWGSC data since the CSS release in 2011