

The International Wheat Genome Sequencing Consortium

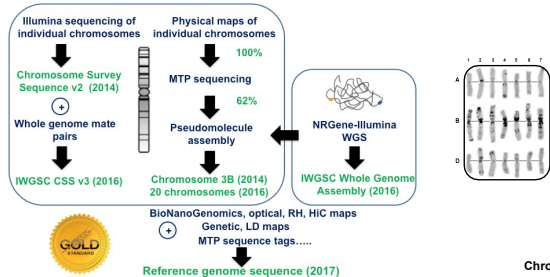
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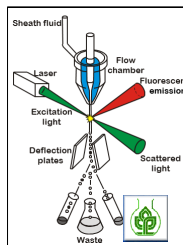
www.wheatgenome.org

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 genetic maps. The IWGSC strategy focused initially on producing 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. A genome-wide chromosome-based survey sequence provided early access to genic sequences and, more recently, a whole genome sequence assembled with the NRGene DeNovoMAGIC™ software has been integrated with the BAC-based resources (sequences, physical maps, WGP tags) and long range marker maps (genetic maps, Hi-C, radiation hybrid maps) to produce the IWGSC v1.0 of the reference sequence of hexaploid bread wheat cv. *Chinese Spring*.

Roadmap to the Wheat Genome Sequence



Chromosome-based resources



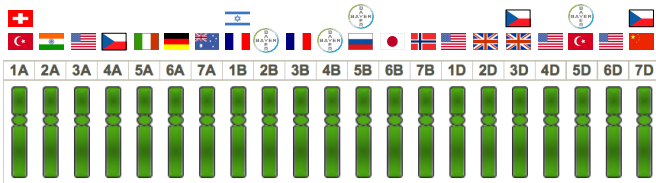
Chromosome / chromosome arm flow-sorting by J. Dolozel et al, IEB, Czech Republic

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

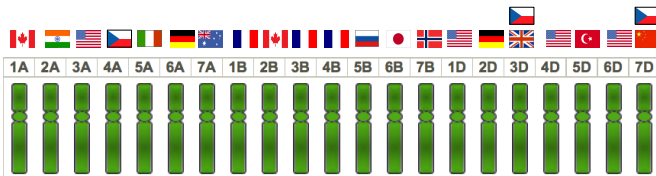
Illumina chromosome arm shotgun libraries for survey sequence (CSS)

Chromosome-specific BioNanoGenomics optical maps for pseudomolecule assembly and QC (7A, 7B and 7D)

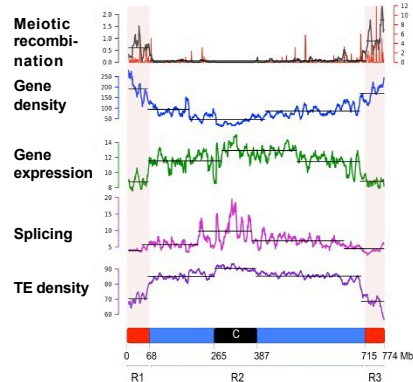
Bread Wheat Physical Maps



Bread Wheat Pseudomolecules



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

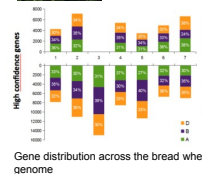


Bread Wheat Survey Sequence



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 sequence
- N₅₀ contig length = 5.9 kb
- ~ 100,000 annotated genes assigned to chromosomes



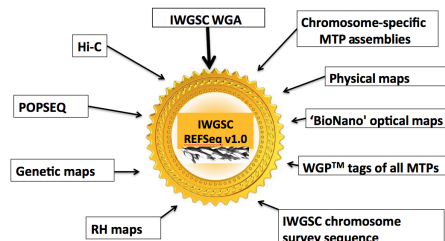
Used for Illumina 90k and Affymetrix 420K SNP Chips and chromosomal assignment of POPSEQ and whole genome sequence assemblies.

Bread Wheat Reference Genome Sequence

The IWGSC Chinese Spring Bread Wheat Reference Sequence v1.0 has been assembled by integrating a *de novo* assembly of Illumina short sequence reads built with NRGene DeNovoMAGIC™ software (IWGSC WGA) with whole genome and chromosome-based map resources. A pre-publication release of the sequence scaffolds ordered using POPSEQ and Hi-C was made in June 2016 (IWGSC WGA v0.4).

IWGSC REFSeq v1.0 assembly:

- 14.5 Gb assembled sequence; 14.1 Gb assigned to chromosomes; 262 Mb gaps (N_s)
- N₅₀ super-scaffold 22.8 Mb; N₅₀ scaffold = 7.1 Mb (max 46 Mb).



Data Resources

IWGSC project data are available via the IWGSC Sequence Repository at URGI INRA Versailles: hkp://wheat-urgi.versailles.inra.fr

Thanks to IWGSC sponsors

