The International Wheat genome Sequencing Consortium
2005 – Goal & Vision

Goal

• Lay a foundation to accelerate wheat improvement
• Increase profitability throughout the industry

Vision

• High quality annotated genome sequence, comparable to rice
• Physical map-based, integrated and ordered sequence
High Quality Reference Sequence of Bread Wheat: IWGSC RefSeq v1.0

Science, 17 August 2018
IWGSC RefSeq v1.0 – Metrics

- **total size**: 14.5 Gb (genome size ~15.5 → 94%)
- **completeness**: 97-99%
- **contig N50**: 52 kb
- **scaffold N50**: 7 Mb
- **superscaffold N50**: 23 Mb

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**21 pseudomolecules:**
- **total size**: 14.1 Gb (97%)
- **superscaffolds**: 1601 (avg 76 per chr.)
Under the leadership of Mingcheng Luo and Jan Dvorak (UC Davis, CA, USA), with funding from the US National Science Foundation

Data available at the IWGSC data repository hosted by URGI-INRA (registration required) in advance of publication under the terms of the Toronto agreement.

**Improvements v2.0 vs v1.0**

- Resolved 75 chimeric scaffolds
- Anchored 283 additional scaffolds from ChrUn of v1.0
- Corrected orientation errors for 357 scaffolds
- Revised locations (change of order) for 244 scaffolds
- Change of the total length of pseudomolecules: + 158,997,657 bp
- Change of the total effective length of pseudomolecules: + 167,843,761 bp
- Percentage of sequences anchored on chromosomes: 97.65% in v2.0 (96.69% in v1.0)

**All revisions: 1,380 Mb (≈ 10%) of the v1.0 assembly**
All data available at URGI

- IWGSC RefSeq assembly v1.0
- IWGSC RefSeq assembly v2.0 (under Toronto protocol)
- IWGSC RefSeq annotation v1.1 including genes and RNAseq mapping
- IWGSC RefSeq annotation v1.0 including structural annotation (genes, transposable elements, ncRNAs), functional annotation, RH maps, GBS maps, optical maps)
- Physical maps for all chromosomes
- MTP BAC WGP™ sequence tags for all chromosomes, except 3B

Data also available at Ensembl Plants, NCBI and GrainGenes
IWGSC 2.0 Vision

Enhance breeding through an increased understanding of the molecular basis of traits and their allelic diversity
IWGSC 2.0 priorities

- IWGSC Exome Array based on the reference sequence

- IWGSC Wheat Diversity project based on de novo sequencing and assembly of multiple wheat genomes (landraces and elite varieties) that cover the breadth of wheat diversity

- IWGSC Gold Standard: gap filling, maintenance, updates, and integration of manual and functional annotation of IWGSC RefSeq v1.0

- User-friendly, integrated databases and tools to benefit public breeders and the full range of industry partners, from SME to large companies
IWGSC Sponsors

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