The International Wheat genome Sequencing Consortium

Board of Directors
Role: Overall strategy and organization
Up to 10 directors including at least 1 Outside Director

Leadership Team
Role: Daily Management
Members: Appels, Baumann, Budak, Eversole, Paux & Praud

Coordinating Committee
Role: Scientific strategy
Members: Sponsors & Leaders of IWGSC Projects & Initiatives

Members
Role: Participation & input
Members: Open to anyone

COUNTRIES 68
MEMBERS 2400
SPONSORS 10
INSTITUTES/COMPANIES 734
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
Roadmap to the wheat Genome Sequence

Illumina sequencing of individual chromosomes

- Chromosome Survey Sequence (CSS) v2 (2014)
- Whole genome mate pairs
- IWGSC CSS v3 (2016)

Physical maps of individual chromosomes

- MTP sequencing
  - 100%
- Pseudomolecule assembly
  - 62%
- Chromosome 3B (2014)
- 20 chromosomes (2016)

NRGene-Illumina WGS

- IWGSC Whole Genome Assembly v0.4 (2016)

BioNanoGenomics optical, RH, HiC maps

- Genetic, LD maps
- MTP sequence tags...

IWGSC Reference Genome Sequence v1.0 (2017)
Concerted integration of resources: RefSeq v1.0

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

<table>
<thead>
<tr>
<th>Metric</th>
<th>Value</th>
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<tbody>
<tr>
<td>total size</td>
<td>14.5 Gb (genome size ~15.5 -&gt; 94%)</td>
</tr>
<tr>
<td>completeness</td>
<td>97-99%</td>
</tr>
<tr>
<td>contig N50</td>
<td>52 kb</td>
</tr>
<tr>
<td>scaffold N50</td>
<td>7 Mb</td>
</tr>
<tr>
<td>superscaffold N50</td>
<td>23 Mb</td>
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21 pseudomolecules:

<table>
<thead>
<tr>
<th>Metric</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>total size</td>
<td>14.1 Gb (97%)</td>
</tr>
<tr>
<td>superscaffolds</td>
<td>1601 (avg 76 per chr.)</td>
</tr>
</tbody>
</table>
All data publicly available at URGI

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

Data also available at Ensembl Plants, NCBI and GrainGenes
Measuring the impact of IWGSC RefSeq v1.0

476,595 BLAST searches
22,935 downloads

2017

# of papers referencing use of IWGSC RefSeq related resources since January 2017: over 100 papers

- Genome structure (9)
- Genome expression (4)
- Genetic diversity (18)
- Trait genomics (67)
- Genome enabled breeding (9)
Vision and strategy for IWGSC 2.0

- Reference sequences with high quality functional annotations
- Public, user-friendly, integrated databases and tools for all users
- A wheat Pan-genome representing the worldwide diversity
- An international, well connected and coordinated community

International Wheat Genome Sequencing Consortium
IWGSC 2.0 activities

- IWGSC Exome Array based on the reference sequence

- Wheat pan-genome 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: maintenance, updates, and integration of manual and functional annotation to the reference sequence

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