International Wheat Genome
Sequencing Consortium

International Wheat Genome Sequencing Consortium

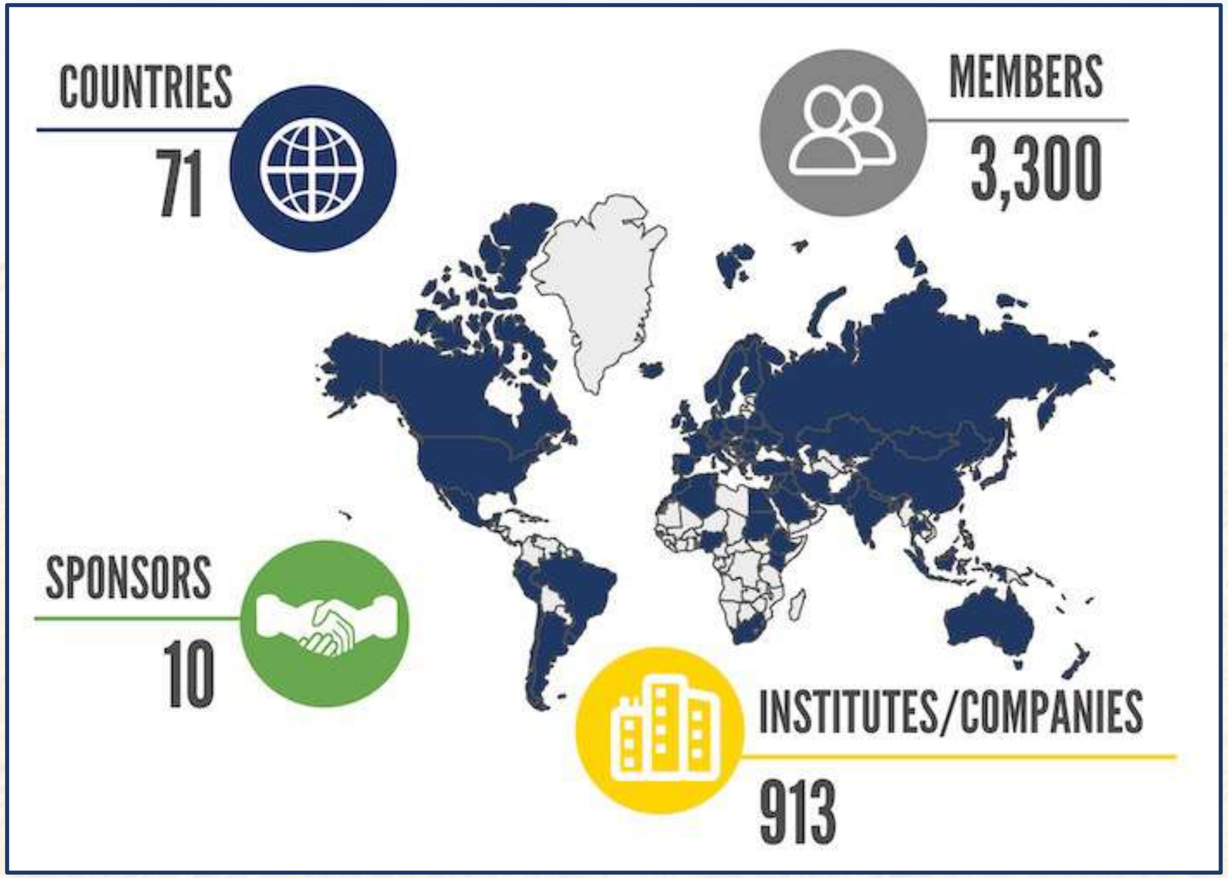
Dusti Gallagher

11 January 2022

PAG XXIX

IWGSC

The International Wheat genome Sequencing Consortium



COUNTRIES
71

MEMBERS
3,300

SPONSORS
10

INSTITUTES/COMPANIES
913

arbor biosciences

BASF
We create chemistry

CIMMYT
International Maize and Wheat Improvement Center

CURIO

FLORIMOND DESPREZ

INRAE

illumina®

KANSAS WHEAT

RAGT

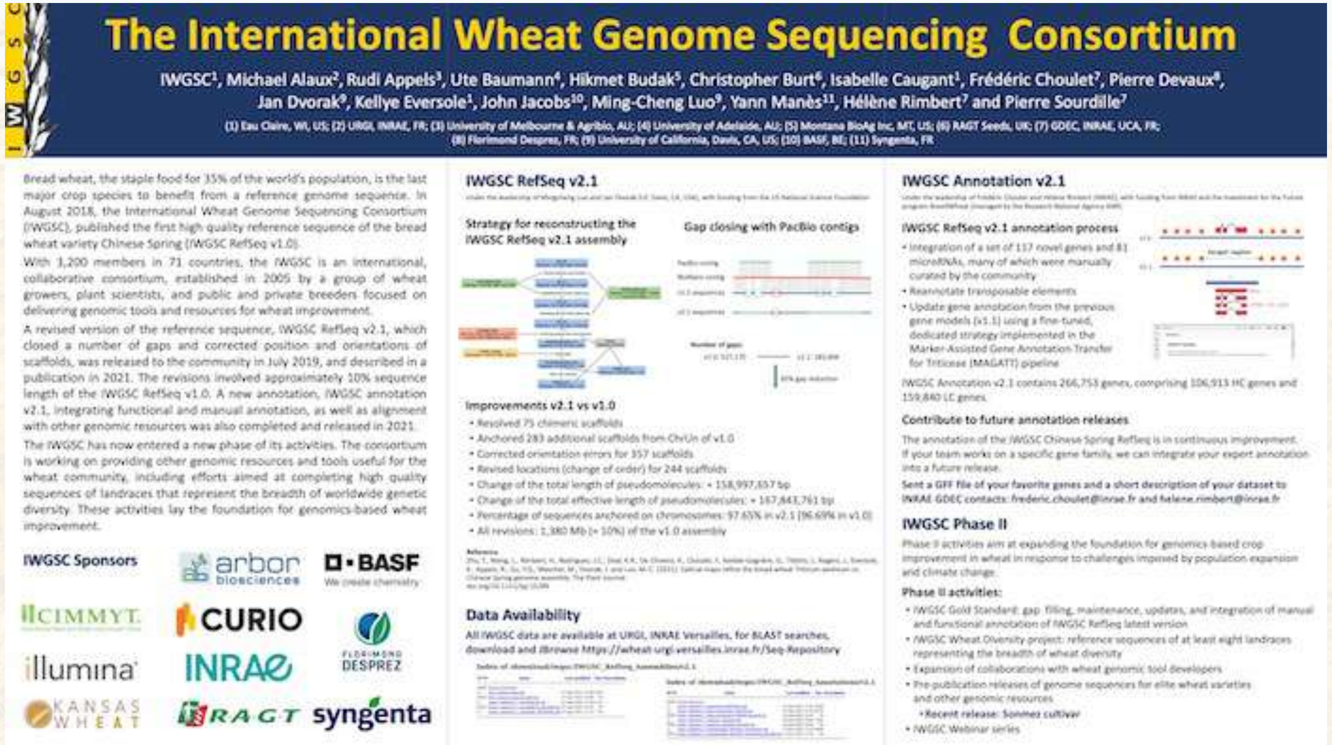
syngenta

IWGSC 2.0 Vision

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

IWGSC Poster

- Eposter https://pag.confex.com/pag/xxix/poster/eposterview.cgi?eposterid=55



The International Wheat Genome Sequencing Consortium

IWGSC[1], Michael Alaux[2], Rudi Appels[3], Ute Baumann[4], Hikmet Budak[5], Christopher Burt[6], Isabelle Caugant[1], Frédéric Choulet[7], Pierre Devaux[8], Jan Dvorak[9], Kellye Eversole[1], John Jacobs[10], Ming-Cheng Luo[9], Yann Manès[11], Hélène Rimbert[7] and Pierre Sourdille[7]

(1) Eau Claire, WI, US; (2) URGI, INRAE, FR; (3) University of Melbourne & Agribio, AU; (4) University of Adelaide, AU; (5) Montana BioAg Inc, MT, US; (6) RAGT Seeds, UK; (7) GDEC, INRAE, UCA, FR; (8) Florimond Desprez, FR; (9) University of California, Davis, CA, US; (10) BASF, BE; (11) Syngenta, FR

Bread wheat, the staple food for 35% of the world's population, is the last major crop species to benefit from a reference genome sequence. In August 2018, the International Wheat Genome Sequencing Consortium (IWGSC), published the first high quality reference sequence of the bread wheat variety Chinese Spring (IWGSC RefSeq v1.0).

With 1,200 members in 71 countries, the IWGSC is an international, collaborative consortium, established in 2005 by a group of wheat growers, plant scientists, and public and private breeders focused on delivering genomic tools and resources for wheat improvement.

A revised version of the reference sequence, IWGSC RefSeq v2.1, which closed a number of gaps and corrected position and orientations of scaffolds, was released to the community in July 2019, and described in a publication in 2021. The revisions involved approximately 10% sequence length of the IWGSC RefSeq v1.0. A new annotation, IWGSC annotation v2.1, integrating functional and manual annotation, as well as alignment with other genomic resources was also completed and released in 2021.

The IWGSC has now entered a new phase of its activities. The consortium is working on providing other genomic resources and tools useful for the wheat community, including efforts aimed at completing high quality sequences of landraces that represent the breadth of worldwide genetic diversity. These activities lay the foundation for genomics-based wheat improvement.

IWGSC Sponsors

arbor biosciences
BASF We create chemistry
CIMMYT
CURIO
Florimond Desprez
illumina
INRAE
Kansas Wheat
RAGT
syngenta

IWGSC RefSeq v2.1

Strategy for reconstructing the IWGSC RefSeq v2.1 assembly

Gap closing with PacBio contigs

Improvements v2.1 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: + 157,843,761 bp
- Percentage of sequences anchored on chromosomes: 97.65% in v2.1 (96.69% in v1.0)
- All revisions: 1,380 Mb (+ 10%) of the v1.0 assembly

Data Availability

All IWGSC data are available at URGI, INRAE Versailles, for BLAST searches, download and JBrowse https://wheat-urgi.versailles.inrae.fr/Seq-Repository

IWGSC Annotation v2.1

IWGSC RefSeq v2.1 annotation process

- Integration of a set of 117 novel genes and 81 microRNAs, many of which were manually curated by the community
- Reannotate transposable elements
- Update gene annotation from the previous gene models (v1.1) using a fine-tuned, dedicated strategy implemented in the Marker-Assisted Gene Annotation Transfer for Triticeae (MAGATT) pipeline

IWGSC Annotation v2.1 contains 266,753 genes, comprising 106,913 HC genes and 159,840 LC genes.

Contribute to future annotation releases

The annotation of the IWGSC Chinese Spring RefSeq is in continuous improvement. If your team works on a specific gene family, we can integrate your expert annotation into a future release.

Sent a GFF file of your favorite genes and a short description of your dataset to INRAE GDEC contacts: *frederic.choulet@inrae.fr* and *helene.rimbert@inrae.fr*

IWGSC Phase II

Phase II activities aim at expanding the foundation for genomics-based crop improvement in wheat in response to challenges imposed by population expansion and climate change.

Phase II activities:

- IWGSC Gold Standard: gap filling, maintenance, updates, and integration of manual and functional annotation of IWGSC RefSeq latest version
- IWGSC Wheat Diversity project: reference sequences of at least eight landraces representing the breadth of wheat diversity
- Expansion of collaborations with wheat genomic tool developers
- Pre-publication releases of genome sequences for elite wheat varieties and other genomic resources
  - Recent release: Sonmez cultivar
- IWGSC Webinar series

IWGSC Webinar Series

- Check out the schedule http://www.wheatgenome.org/IWGSC-Activities/Webinars

- Upcoming Webinar
  - Thursday 27 January
  - 11:00am EST
  - Recombination and chromatin landscapes in the wheat genome
  - **Presenter**: Ian Henderson, University of Cambridge, UK
  - **Registration**: https://attendee.gotowebinar.com/register/6306776026160905487

Thank you for your participation!

www.wheatgenome.org

wheat.genome

@wheatgenome