

Newsletter N° 2/2019

IWGSC Newsletter – May to August 2019

The IWGSC

- Membership:
 - The IWGSC has 2400 members in 68 countries, working at 749 institutions/companies.
- Sponsors:
 - o In July, <u>BASF joined the IWGSC</u> as a sponsoring partner.
 - o Currently, the IWGSC has <u>8 sponsors</u>.
 - Sponsor support is essential to ensure continuation of Phase II activities. Please inform us if you know of any potential sponsors (research institutes, universities, governmental agencies, or companies).

Projects

• <u>IWGSC Wheat Diversity project</u>: the aim is to characterize the breadth of worldwide wheat diversity.

In this project, the genomes of eight to twelve landraces, representing the full breadth of genetic diversity in wheat (as described by <u>Balfourier</u>, <u>et al.</u>), will be sequenced at high quality. These, in conjunction with the IWGSC RefSeq, will serve as the foundation for the diversity panel and haplotype map. Lower quality genome sequences of other landraces and elite lines will be added as available. Proposals are under preparation and will be submitted to funding entities in the near future.

• IWGSC Exome Array project:

Arbor Biosciences has launched a full-service offering which includes the myBaits^R Expert Wheat Exome capture panel and a Curio Genomics bioinformatics analysis through the myReads NGS services or as stand-alone products. The bioinformatics service provides whole genome alignment as well as variant calling from Chinese Spring or other cultivars of hexaploid wheat. Arbor Biosciences' partnership with the IWGSC and Curio Genomics will continue as Arbor plans to develop new iterations of the exome panel and data analysis pipeline as further understanding of the wheat genome grows. The kit covers hexaploid and tetraploid cultivars of wheat. Pricing for the panel and services will be announced this fall.

IWGSC RefSeqv2.0

An improved version of the reference wheat genome has been completed under the leadership of Mingcheng Luo and Jan Dvorak (UC Davis, CA, USA) with funding from the US National Science Foundation. IWGSC RefSeq v1.0 was improved using whole genome optical maps and contigs assembled from whole-genome-shotgun (WGS) PacBio SMRT reads. Optical maps were used to detect and resolve chimeric scaffolds, anchor unassigned scaffolds, correct ambiguities in positions and orientations of scaffolds, create super-scaffolds, and estimate gap sizes more accurately. PacBio contigs were used for gap closing. Pseudomolecules of the Chinese Spring 21 chromosomes were re-constructed to develop a new reference sequence, IWGSC RefSeq v2.0. The data are available at IWGSC RefSeq v2.0. The data are available at IWGSC data repository hosted by URGI-INRA under Toronto protocol.

IWGSC RefSeq Annotation v2.0

Targeted annotation of IWGSC RefSeq v2.0 is currently under way.

<u>A call for contributions</u> has been sent out to the community for manually and functionally annotated genes (deadline was 31 August). These curated genes will be integrated in IWGSC RefSeq Annotation v2.0, expected to be released in 2020.



Continued manual and functional annotation of the reference is essential. To facilitate high quality functional annotation, we continue to seek experts willing to take the lead in the functional annotation of gene families in wheat, contact <u>Kellye Eversole</u> if you would like to be involved.

Data Repository at URGI

- The IWGSC RefSeq v2.0 assembly is available for <u>download</u> and <u>BLAST</u>. The data are being released in advance of publication to the scientific community under the terms of <u>Toronto agreement</u> which affords the data producers the right to publish the first whole genome analyses of the data.
- How to access the data:

Access does require registration. For specific access terms, see the <u>IWGSC General Data</u> Access agreement .

- Individuals who have not signed the IWGSC Data Access Agreement should FIRST register on the IWGSC website and sign the Agreement; URGI login details will be provided subsequently for access to the data.
- Individuals who have already signed the IWGSC Data Access Agreement can go directly to the URGI website to access the data using their URGI login details. If you have forgotten your URGI credentials, please send an email to urgi-support@inra.fr.

People:

Leader spotlight on <u>Jaroslav Doležel</u>

Upcoming Meetings/Workshops

- 22-24 October 2019: <u>International Conference on Wheat Diversity and Human Health</u>, Istanbul, Turkey. Hikmet Budak will give a talk entitled "The International Wheat Genome Sequencing Consortium phase II: Towards a diversity platform that represents the breadth of global wheat diversity" on Thursday 24 October at 10:10 am.
- 11-15 January 2020: <u>Plant and Animal Genome conference PAG XXVIII</u>, San Diego, CA, USA:
 - o IWGSC Main Workshop: 11 January 2020, 8:00-10:10am
 - o IWGSC Business Meeting: 11 January 2020, 6:20-8:00 pm.
 - o IWGSC Second PAG Workshop: 14 January 2020, 1:30-5:00 pm

Publications/resources

- 2018 Annual Report
- Press releases:
 - o 22 July: BASF joins the IWGSC
 - 16 July: <u>Arbor Biosciences Partners with Curio Genomics for Analysis of IWGSC</u> Wheat Exome
- Kellye Eversole's interview on the show "Constant Wonder" on BYU radio.
- Book Announcement: <u>Advances in breeding techniques for cereal crops</u>
- Set of slides for members to use in their presentations Updated September 2019
- Animated video: <u>The Bread Wheat Genome Sequence A Tool for Breeders to Improve Wheat and Contribute to Food Security</u>

And don't forget to follow us on <u>Twitter</u> and <u>Facebook</u> and <u>LinkedIn</u>