



Newsletter N° 1/2020

IWGSC Newsletter – January to April 2020

In those difficult times, we hope that you, your family, friends and colleagues are safe and well.

The IWGSC

- Membership:
The IWGSC has 2,800 members in 70 countries, working at 828 institutions/companies.
- Sponsors:
 - Currently, the IWGSC has [8 sponsors](#).
 - Read the sponsor highlight on [Syngenta](#), a supporter of the IWGSC since 2011.
 - Sponsor support is essential to ensure continuation of activities. Please inform us if you know of any potential sponsors (research institutes, universities, governmental agencies, or companies).

Projects

- IWGSC-Arbor Biosciences Exome Array project
The Arbor Biosciences [myBaits® Expert Wheat Exome capture](#) panel, developed in collaboration with the IWGSC is available. The panel utilizes over two million probes to cover 250 megabases of high confidence exons in the genome and is compatible with both hexaploid and tetraploid cultivars of wheat. To learn more about the Wheat Exome Panel and its utility for hexaploid, tetraploid, and diploid cultivars of wheat, [watch the webinar](#).
- IWGSC-Arbor Biosciences Promoter Capture project
Arbor Biosciences is working on the design of a promoter capture under the leadership of IWGSC Coordinating Committee member, Jorge Dubcovsky. We expect it to be available soon.
- IWGSC-Arbor Biosciences Expansion Modules
Plans are underway for Arbor Biosciences to develop add-on modules for the exome panel. These will include new manual and functional annotations of IWGSC RefSeq v1.0, the updated and annotated RefSeq v2.1 expected later this year, and genome-wide SNPs.
- IWGSC Wheat Diversity project
In this project, the genomes of eight to twelve landraces, representing the full breadth of genetic diversity in wheat (as described by [Balfourier, et al.](#)), will be sequenced at high quality. These, in conjunction with the IWGSC RefSeq v1.0 and subsequent versions, 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. Recent pilot studies and reports from barley and polyploid sequencing projects are guiding the development of our strategy for tackling the IWGSC wheat diversity project. Efforts to secure funding are underway. Jane Rogers, previous IWGSC director of sequencing, is working with the IWGSC on the project and, as usual, is providing extremely valuable guidance.
- IWGSC RefSeqv2.0 and RefSeq Annotation v2.0
[An improved version](#) of the reference wheat genome, completed under the leadership of Coordinating Committee members Mingcheng Luo and Jan Dvorak, is available at the [IWGSC data repository hosted by URGI-INRA](#) under Toronto protocol. Additional improvements and

corrections are being made by the team at UC Davis. Fred Choulet and H  l  ne Rimbart from INRAE are leading the integration of targeted annotation of IWGSC RefSeq v2.0 as well as the manual and functional annotations contributed by the community for RefSeq v1.0. Thus, we expect that an even better assembly and the updated annotation will be released this year. Jane Rogers is providing assistance to the IWGSC on this matter as well.

- IWGSC RefSeq Annotation beyond 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 [Kellye Eversole](#) and [Fred Choulet](#) if you would like to be involved.

Data Repository at URGI

- The IWGSC RefSeq v2.0 assembly is available for [download](#) and [BLAST](#). The data are being released in advance of publication to the scientific community under the terms of [Toronto agreement](#) 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 [IWGSC General Data 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:

- Leadership Awardee: [Vijay Tiwari](#)
- Early Career awardee: [Harriet Benbow](#)
- Sponsor Highlight: [Jan Gielen, senior scientist at Syngenta](#)

Webinars

- 22 January 2020: the IWGSC kick started its webinar series with "[Understanding abiotic stress signalling in wheat through \(phospho\)proteomics](#)" presented by Ive De Smet (Ghent University, Belgium).
- 25 March 2020: Jacob Enk (Arbor Biosciences) presented the webinar "[Comprehensive Cost-Effective Exome Sequencing with Arbor Biosciences Wheat Exome Panel](#)",

Mark your calendar with those upcoming webinars:

- 30 April 2020: "[Extending the Curio Genomics Platform for the Wheat Research Community: DNA Sequences to Analysis Results](#)" presented by Shawn Quinn (Curio Genomics)
- 27 May 2020: "[Genome-wide analysis of a wheat transcription factor family: the power of bioinformatics resources](#)" presented by Rainer Melzer and Susanne Schilling (University College Dublin, Ireland)
- 29 June 2020: Curtis Pozniak (University of Saskatchewan, Canada) will present a webinar on the 10-genome project
- 15 July 2020: Cristobal Uauy (John Innes Center, UK) will present a webinar on gene functional characterization in crops

Workshops

- PAG ASIA 2020: Due to COVID-19 concerns, PAG Asia 2020 has been cancelled, and accordingly the IWGSC workshop will not be held. PAG ASIA 2021 is now scheduled for 9-11 June 2021.
- PAG 2021: The IWGSC intends to hold two workshops, as usual, at the Plant and Animal Genome Conference PAG XXIX in January 2021. Stay tuned for the announcement of calls for speaker and early career award recipient abstracts.

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