IWGSC Newsletter – September 2017 to 09 January 2018

The IWGSC

- Membership
  As of end 2017, the IWGSC has 2,100 members, working in 610 institutes/companies in 64 countries. Check out the map.

- Sponsors
  The IWGSC has currently 15 sponsors. Sponsor support is essential to ensuring continuation of activities. Please inform us if you know of any potential sponsors (research institutes, universities, governmental agencies, or companies).

- Staff
  After more than seven years of working with the IWGSC as a leader of a sequencing centre or directly as part of the IWGSC staff team, Jane Rogers, the IWGSC deputy director and head of sequencing, retired at the end December 2017. Although Jane was instrumental in helping the IWGSC develop its strategic roadmaps during the first 5 years of the consortium, she officially joined the Coordinating Committee in 2009 to develop physical maps for several chromosomes after she established The Genome Analysis Centre (TGAC). In 2010, she agreed to lead the IWGSC chromosome survey sequencing initiative which, for the first time, provided the chromosomal location of genes with an idea of the order along the chromosome for many of the genes. This intermediate product released in draft in 2011 and in a final version in 2014, was published in a special issue in *Science* in July of that year. Jane joined the staff of the IWGSC in 2013 to lead the strategy for reference sequencing and the completion of the physical maps. She led the IWGSC-Bayer CropScience project which developed Whole Genome Profiling (WGP™) physical maps for three chromosomes and two chromosome arms. She also led the IWGSC-Bayer CropScience WGP™ tag sequencing project and the IWGSC RefSeq project. The entire wheat community owes a debt of gratitude to Jane as it is doubtful that we would be where we are today without her leadership. It is hard to imagine the IWGSC without Jane officially involved but she has left us with a great foundation upon which to continue our work.

- Phase II
  With the completion of IWGSC RefSEq v1.0, the Consortium is moving into phase II activities. As approved by the Coordinating Committee (CC), these include:
  - Pan-genome based on *de novo* sequencing and assembly of multiple wheat genomes (landraces and elite varieties) that cover the breadth of wheat diversity (under the leadership of Sébastien Praud (IWGSC Board Member) and Etienne Paux (IWGSC CC Member).
  - Pan-genome database, visualization, and tools that will benefit public breeders and the full range of industry partners, from SME to large companies (under the leadership of an IWGSC industry-led task force)
  - IWGSC Exome Array based on the reference sequence (with leadership from Burkhard Steuernagel (IWGSC CC member)
  - Pipeline for including community-based manual and functional annotation in annual annotation updates
  - Continued development and maintenance of an integrated database for the wheat genome sequence.

Projects
- An analysis of the reference wheat genome sequence (IWGSC RefSeq v1.0) has been submitted to a journal and is under review; a number of companion papers have been or will be submitted soon to several journals.

- Since July, IWGSC RefSeq v1.0 sequence and annotation v1.0 can be viewed in a JBrowse at the IWGSC Sequence Repository [hosted at URGI](#). The JBrowse displays the pseudomolecules and scaffolds with the automated annotation generated by the IWGSC of the genes, transposable elements and ncRNAs. Also available are mapped markers, and alignments of nucleic acid and protein evidence supporting the annotation.

- In May, the [IWGSCReference Sequence v1.0 annotation](#) was made available through the IWGSC Sequence Repository hosted by URGI. The annotation includes gene models generated by integrating predictions made by INRA-GDEC using *TriAnnot* and PGSB using their customised pipeline (previously MIPS pipeline). The integration was undertaken by the Earlham institute (EI), who have also added UTRs to the gene models when supporting data were available. Gene models have been assigned to high confidence (HC) or low confidence (LC) classes based on completeness, similarity to genes represented in protein and DNA databases, and repeat content. The automated assignment of functional annotation to genes has been generated by PGSB based on high throughput protein function annotation with human readable description (AHRD) parameters. In addition, annotated transposable elements (TEs) and non-coding RNAs are available.

- Reminder: the IWGSC RefSeq v1.0 has been available for [download and BLAST](#) at the IWGSC Repository hosted by URGI since January 2017.

- All data are being made available before publication in accordance with the [Toronto Agreement](#) under which the IWGSC reserves the right to publish the first global analyses of the data. For specific access terms, see the [IWGSC General Data Access agreement](#).

- All data will be made available without restriction upon publication of the IWGSC RefSeq v1.0 main paper.

People
- Leader Spotlight: [Cristobal Uauy](#)
- Early Career Awardee: [Joanna Melonek](#)

Meetings/Workshops
- 13-17 January 2018, San Diego, USA: [PAG XXVI](#)
    - [Main Workshop](#), Saturday 13 January, 8:00-10:10 am, room Town and Country, organized by Sébastien Praud and Kellye Eversole – [Speaker profiles](#)
    - Business meeting, Saturday 13 January, 6:30-8:30 pm, Tiki Pavilion
    - [Standards and Protocol workshop](#), Tuesday 16 January, 1:30-5:10 pm, room Pacific salon 3, organized by Frédéric Choulet, Jane Rogers, and Kellye Eversole
    - the IWGSC will present two posters: : # 0995 & 0994
- 19-22 March 2018, Clermont-Ferrand, France: [Eucarpia 2018](#), Eucarpia Cereal section meeting, jointly organized with the 2nd International Wheat Innovation Workshop (IWIW2
- 14-15 June 2018, Rome, Italy: [Wheats&Women International](#) Conference .

Publications/resources
- Article: [The Wheat Genome Sequence Odyssey](#) published on the Global Engage website
- Set of [slides](#) for members to use in their presentations – Updated August 2017