

Newsletter N° 2/2017

IWGSC Newsletter – May to August 2017

Dear IWGSC Members and Friends.

The IWGSC

- Membership
 The IWGSC has 1,800 members, working in 536 institutes/companies in 62 countries.
 Check out the map.
- Sponsors
 Currently, the IWGSC has <u>15 sponsors</u>. We are pleased to welcome the University of Adelaide! 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).
 - T-shirt
 You will definitely want a T-shirt with the IWGSC RefSeq logo on it! Order your T-shirt by 22
 October and pick it up at PAG 2018 (with no shipping fee!) Not going to PAG? No problem, contact Mollie Hogan and we will arrange to ship it to you.

Projects

- An analysis of the wheat genome sequence is being prepared for publication, along with accompanying papers that will be submitted concurrently to a range of journals.
- Since July, IWGSC RefSeq v1.0 sequence and annotation can be viewed in a JBrowse at the IWGSC Sequence Repository <u>hosted at URGI</u>. 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 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 <u>download and BLAST</u> at the IWGSC Repository hosted by URGI since January.
- All data are being made available before publication in accordance with the <u>Toronto</u>
 <u>Agreement</u> under which the IWGSC reserves the right to publish the first global analyses of
 the data. For specific access terms, see the <u>IWGSC General Data Access agreement</u>.

People

• Leader Spotlight: Martin Mascher

Meetings/Workshops



- 7-9 August 2017: VIII Chinese Wheat Genomics and Molecular Breeding Conference, Shijiazhuang, China. Rudi Appels made a presentation on "The wheat genome in the 21st century".
- 15 September 2017, Okayama, Japan: Workshop to celebrate the centennial anniversary of the discovery of chromosome number and polyploidy in wheat. Hirokazy Handa, IWGGC Coordinating Committee member will make a presentation on the reference genome sequence of hexaploid wheat.
- 13-17 January 2018, San Diego, USA: <u>PAG XXVI</u> the IWGSC will organize two workshops and a business meeting.
- 22 March 2018, Clermont-Ferrand, France: International Wheat Innovation Workshop

Press release

• 18 July: <u>Sébastien Praud appointed to Board of Directors</u>

Publications/resources

- Article: The Wheat Genome Sequence Odyssey published on the Global Engage website
- New books: Achieving sustainable cultivation of wheat (Vol 1&2)
 - Two reference books on wheat, focused on ways to improve wheat cultivation at each step of the value chain, from breeding to post-harvest storage. <u>Read more</u>
 - IWGSC members get 20% off when ordering online with the code IWGSC20
 - Achieving sustainable cultivation of wheat volume 1
 - Achieving sustainable cultivation of wheat volume 2
- IWGSC poster Updated July 2017
- Set of slides for members to use in their presentations Updated August 2017

And don't forget to follow us on **Twitter Facebook** and **LinkedIn**.