IWGSC OPEN BUSINESS MEETING

Kellye Eversole
IWGSC Executive Director

Plant & Animal Genome Conference
San Diego, California, USA
12 January 2019
Congratulations to all of you!!!!

Science, 17 August 2018
Measuring the Impact of the IWGSC: Data Access

Cumulative Downloads: 112,723
Cumulative BLAST searches: 1,204,345
Measuring the Impact of IWGSC RefSeq v1.0

- Genome structure (9)
- Genome expression (4)
- Genetic diversity (18)
- Trait genomics (67)
- Genome enabled breeding (9)

2017

# of papers referencing use of IWGSC RefSeq related resources since January 2017: over 100 papers
Measuring the Impact of IWGSC RefSeq v1.0

> 260 papers*

- Genome structure (40)
- Genome expression (15)
- Genetic diversity (13)
- Trait genomics (161)
- Genome enabled breeding (36)

2018

* Incomplete number of 2018 papers published that referenced or used IWGSC RefSeq and associated resources
Measuring the Impact of IWGSC RefSeq v1.0: Publications

2017: >100 papers
2018: > 260 papers*

2017-2018: >372 papers & counting

* Incomplete number of 2018 papers published that referenced or used IWGSC RefSeq and associated resources
IWGSC 2019 Awards

- IWGSC Early Career Award: Carolina Sansaloni, CIMMYT

- IWGSC Leadership Awards:
  - François Quetier, Université d'Evry/ANR
  - Hélène Berges, CNRGV-INRA
  - Hirokazu Handa, Institute of Crop Science, NARO
  - Curtis Pozniak, University of Saskatchewan
Vision and strategy for IWGSC 2.0

Reference sequences with high quality functional annotations

Public, user-friendly, integrated databases and tools for all users

A wheat pan-genome representing worldwide diversity

An international, well connected and coordinated community
 IWGSC 2.0 activities

- IWGSC Exome Array based on the reference sequence

- Wheat pan-genome based on de novo sequencing and assembly of multiple wheat genomes (landraces and elite varieties) that cover the breadth of wheat diversity

- IWGSC Gold Standard: maintenance, updates, and integration of manual and functional annotation to the reference sequence

- User-friendly, integrated databases and tools to benefit public breeders and the full range of industry partners, from SME to large companies
Jacob Enk, Arbor Biosciences
Develop a wheat pan-genome that represents the breadth of worldwide wheat diversity

- Reference quality for 8-12 landraces
- Diversity panels at draft quality
- Haplotype database
- Skim-sequencing and high throughput genotyping of many lines
Eight landraces with less than 1% admixture @ 180-220X

- describe ancient wheat haplotypes

Additional lines (including elite varieties) @ 30-40X

- describe the modern genetic diversity (including alien introgressions)

BioRxiv: https://doi.org/10.1101/477455
IWGSC focus is primarily on high quality, reference sequences of landraces that represent the 8 areas of genetic diversity.

How can we integrate our activities with the 10-Genome project that focused mostly on elite varieties?

Is anyone else planning to sequence elite varieties with assembly statistics of at least 2Mb N50?

Can we get all sequences in the IWGSC repository at URGI?
Identification of gene family leaders for manual and functional annotation

Identification of individuals working on gene cloning or marker development

Michael Alaux: Discussion on how to provide updated gene annotations for inclusion in IWGSC RefSeq annotation v2.0.

IWGSC Wheat Genome Manual & Functional Annotation Workshop on Tuesday (1:30 to 5:30 pm, Pacific Salon 2)
Are there other issues to be discussed?
Thank you for your attention!

www.wheatgenome.org