The *Aegilops tauschii* pangenome: A tool for harnessing wild wheat genetic diversity

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Q&A session

Presenter: Andrea Gonzalez, PhD student, Wulff Lab, King Abdullah University of Science and Technology (KAUST), Kingdom of Saudi Arabia

The webinar recording is available on the IWGSC YouTube channel at: https://youtu.be/zwPvpWDLtyo

Q: What iteration should be selected with a ram size of up to 450 GB?

It is unclear what analyses you are referring to.

Q: Did you use R package for data?

Timestamp: 42:42

Q: Why lineage 3 under-represented among the 44 selected?

Timestamp: 47:00

Q: This question refers to k-mer GWAS. Why does the vertical axis always start at 6 rather than 0?

Timestamp: 43:20

Q: Did you try GWAS for L1 and L2 independently?

Timestamp 57:07

Q: Very interesting work. Thank you very much. There are some reports that tauschii genes would not express at hexaploid level. What is your plan to link directly with hexaploi?

In Gaurav et al., 2022 we describe the creation of a SHW library that captures 70% of the Ae. tauschii diversity. This library can be used to check the expression and phenotype of particular genes in the hexaploid background.

Q: Some reports said L3 is a hybrid between L1 and L2. Based on your results is this correct?

Timestamp 51:52

Q: In your opinion, What are the major barriers to look deep into Aegilops Taushii genome at this point and what is the way forward using this D genome for wheat improvement, in terms of techniques and resources?

Timestamp 45:10

Q: What target major wheat disease you considered to study the disease resistance traits?

Timestamp: 56:19

Q: Can you elaborate why L3 lineage is so closely related to L2 lineage phylogenetically?

In the phylogeny from Figure 1 in Guarav et al., 2022, L3 is most closely related to L1. However, the separation from the outgroup indicates that L3 is a basal and differentiated lineage.

Q: Can you indicate if the genome annotation has already been carried out for these high-quality pan-reference genomes? And, if there is a plan to release these genomic resources soon?

Timestamp 50:23

To add to the love response, we are collaborating with Gurcharn Brar and Curtis Pozniak to annotate the L1, L2 and L3 reference genomes. The pangenome resource will be released shortly. Stay tuned to the OWWC website for updates.

Q: Was AUS18911 the only line to have both genes-r33 andTA1662? are there other accessions which have both?

Timestamp 53:58

Q: Do trichomes contain insect-feedants such as polyphenols?

Timestamp: 44:17

Q: I don't see linages 1-3 from the fertile crescent was there any reason for that?

There are a few L1 and L2 accessions collected from sites within the Fertile crescent. Our collection reflects what we have been able to obtain from public good germplasm banks and collaborators. It is likely that Ae. tauschii is less prevalent in the Fertile Crescent.

Q: Where are these new references located? are they publicly available yet?

Timestamp 50:23

Q: I missed the beginning of the webinar. How was the GWAS for the trait done with the kmer count?

Timestamp 48:24

Q: Any thoughts on k-mer Vs Haplotype based association mapping for quantitative traits like FHB and cold tolerance ?

We haven't conducted a side-by-side comparison of k-mer vs haplotype-based GWAS. Refer to Sehgal et al., 2020, for a study on grain yield using haplotype-based GWAS in wheat. Another useful review is: https://www.mdpi.com/2073-4425/14/7/1439/review_report

Q: Is there any specific phenotypic trait/s which make/s that 5 lines (leanage 3 I assume) different from other groups/leanages

Lineage 3 was differentiated based on genetic analyses, specifically k-mer-based Bayesian clustering analyses using STRUCTURE (Guarav et al., 2022). Phenotypic or geographical differentiation of the lineages is not reliable since there are no characteristic traits that we are aware of that uniquely define them.