



2017 Kernza / IWG Meeting Summary

Day1: Breeding, Genetics and Genomics Breakout Group

2nd Annual International Kernza Meeting

University of Minnesota, St. Paul

July 6, 2017

Moderator: Lee DeHaan

Recorder: Kayla Altendorf

Topic 1: A discussion about progenitors, genome

1. Kevin Dorn: Dasypyrum has the most sequence data and there are sections of that sub genome in wheatgrass that cannot be explained.
2. D genome is least diverse.
3. Distribution of genes across the genome - clear where the centromeres are. A little bit more well distributed than barley.
4. Genome is available for all to use

Topic 2: A discussion about seed size

1. As we select for increasing seed size, has the spikelet morphology changed?
 - a. Lee DeHaan: Initially there was a positive correlation between longer heads and larger seeds, but it is shifting. Selecting for seed size originally resulted in big heads, but then some plants showed smaller heads with large seed sizes, and those genes displaced gigantism in the breeding program.
 - b. Earliness genes are increasing in frequency at TLI. Seeds that develop before it gets hot and dry are larger than those that are heat stressed.
 - c. Other thoughts: lower fertility is a result of aborted seed, not necessarily lack of fertilization.

Topic 3: Early planting of wheatgrass

1. Some folks are exploring early spring planting for increased cropping system flexibility and to get strong establishment going into winter (important for winterhardiness and yield).
2. Selection for earliness - reduces vernalization requirement.
3. No desire to remove vernalization requirement.

4. Vernalization is a well-studied trait in grass species, there are multiple candidate genes to explore in wheatgrass.

Topic 4: If you could know the genetic control of any trait what would you choose?

1. Height
 - a. Lee DeHaan: Identify genes that reduce height without limiting yield; eg. a dwarfing gene that increases yield
 - b. In a selfed population at TLI, Lee found height QTL almost always negatively associated with yield
2. Yield persistence
 - a. Lee DeHaan: Selected plants in a parent nursery - best plants over time, almost all lodged entirely except a few, made a crossing block with these
 - b. Food science crossing blocks - yields are similar the first year, some yielded absolutely nothing in the second year.
 - c. The most elegant solution to this problem would be genetic, but we need to figure out what is causing it first. A question for the agronomists or physiologists! If it is caused by too much tillering, we can select against it, for example.
 - d. Kathryn Turner: What if we transplanted wheatgrass plants in competitive environments (maybe of wheatgrass or another species) to test how they fare. Maybe some genotypes handle the competition better than others.
3. Kevin Dorn: Candidate genes from other species
 - a. What would be a good story, something we could explain easily based on our knowledge of other species? Significant trait, with most genetic information from wheat and barley, on a gene for gene basis, fewest # of candidate QTL.
 - b. Flowering is well established and conserved trait in other grass species.
 - c. Maybe a trait is interesting to explore but it might not be super useful if it can be fixed easily via phenotypic selection.
4. Maturity
 - a. Should we explore developing classes of wheatgrass? Potentially for maturity? Or end use/quality?

Topic 5: Genomic selection, QTL

1. UMN breeding program uses a 2 year cycle, re-training the model every year. TLI completes 1 cycle per year. Both breeding programs are maintaining a phenotypic selection pipeline just in case.
2. Is there utility in adding data from different environments? GBS data could be merged with Lee's data to improve genomic selection model.
 - a. Jim Anderson: Barley has combined all the data from different genomic selection breeding populations. They found that as long as you have a good representation of your own germplasm in the model, it doesn't help to have data from other breeding programs. But it is important to note: barley is extremely inbred, very narrow genetic base, opposite of wheatgrass.

3. Will our heyday with variability continue? Rare genes likely becoming more frequent with selection.
4. Rapid response from selection for yield (or seed size) brought Lee to believe it was simply controlled, but now with info from Steve Larson about the # of QTL, maybe it's more complex than we thought. This is generally the thought regarding other traits that are simply controlled in other species (e.g. threshability – Larson found several QTL).

Topic 6: Data Sharing

1. David Crain: Data sharing database - phenotypic and genotypic data, it may be a good idea to try combining them and explore the utility. Contact David for access!
2. We need uniform phenotyping methods (maybe a methods paper?)

The summary that was shared with the group:

Traits on which to focus:

1. Yield persistence – understand mechanism
2. Height
3. Shattering and threshability
4. FHB
5. Seedling vigor – for the agronomists!
6. Traits to compare with other species
7. Self incompatibility (hybrid breeding)

Other topics:

1. Database and data sharing
2. Phenotyping methods – need to be on the same page
3. We need a physiologist – yield persistence question
4. Resources – more money, better computer programs to handle complexity of wheatgrass
5. Breeding classes