The intersection of genomics and wheat breeding for developing superior cultivars and hybrids

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Q&A session

Presenter: P. Stephen Baenziger, University of Nebraska-Lincoln, Lincoln, NE, USA

The webinar recording is available on the IWGSC YouTube channel at https://youtu.be/5q8DLF_2NY8

Q: How are the locations selected in a breeding program? Like what should be the main criteria, esp. in cereals?

> Pick your climatic zones and then try to have one to two location per zone. The Nebraska zones are obvious because the prairie grasses have the same three zones. The grasses were developed long before farming. Please clarify and restate the question.

Q: what are the merits of genotyping by sequencing (GBS) and the use of customized chip arrays. In what situations, would you suggest to use each?

> Timestamp: 49'

Q: Heat shock mitigated varieties are available? Last month in my country, heat stock attack all of the country of Bangladesh!

It is hard to select for conditions that are unique, so you have to be opportunistic. If a line does better than others, learn why.

Q: Do you suggest having a fixed % of entries to be promoted in segregating generations. for ex. x% from F4 to F5

> Timestamp: 52'
> Always do what is needed and what opportunities allow. The total program is set and you can allocate lines amongst the program trials as you can. Consistency is important.

Q: How often do you incorporate the environmental data and do you use subsets of locations or testing sites with common envirotypes for narrower ("customized") adaption?

> We are getting better at this, but we use the data more as a way to understand what we see in the field. We can do a better job.

Q: The major setback of wheat farming in Sub- Saharan Africa is heat street and moisture, I don't know whether the presenter have addressed related work on this issue. And how can this challenge be addressed permanently?

I did not address this directly in my talk and it is not may area of expertise. Hybrids are more climate resilient than varieties.

Q: What are the phenotyping tools/ techniques that he is using?
Timestamp: 55'30"

Q: What is the key for successful hybrid breeding?
In my view, you need a way to make experimental hybrids, a way to mass produce the hybrid seed, and a way to identify heterosis.

Q: Why MNCs are not interested in Hybrid breeding in wheat?
What is an MNC? If you mean, multinational corporations, they are interested in hybrids. If you do not know it now, just wait. The big companies are all getting ready.

Q: Which genomic selection model are you using? GBLUP?
Vikas Belamkar is the right person to ask. We have published some of our work in G3 if you need more information.

Q: Are you using environmental covariables in your phenotypic models? Do you think envirotyping will help breeding in the future?
timestamp: 57'50"

Q: what is reliability of genomic selection of crops having cross pollination probability?
Not sure I understand this question, but genomic selection is used heavily in hybrid crops such as maize.

Q: Breeding resistant wheat cultivars takes place in the epidemiological zone? How is this done in the case of rust and the pathogen races may change in the same uredinial generation stage through anastomoses in the same season and so on during the following seasons
This is not my area of expertise, but a key goal is to have sufficient variation in your program so that if there is a race change, you still have resistant sources. You need to keep diverse resistance sources so that not everything is lost in one season. You can also stack genes in hopes that slows down the race changes.

Q: Will increased seasonal variability and frequency of extreme events due to climate change require changed breeding goals?
The goal is always the same, adapted lines. However, extreme events make it much harder to find lines that consistently do well.

Q: Hi, XX, breeder from QC, Canada. We don't use genomic selection (yet). To use this strategy, I would worry about:
- **computation challenge you discussed, and**
- **turnaround time for lab+sequencing+computation. Any suggestion, based on your experience?**
Timing is everything. The turnaround time is based upon having a good pipeline. As soon as we plant our fields, we send the DNA off for genotyping. It usually takes 3 months for processing and then we get the DNA data back. We will have three months before heading, so that is when we process the genomic data.

Q: How are you modeling several traits for the genomic prediction? A complex model accounting for all the traits producing one GEBV or individual models per trait, and then selecting across traits?

> The way to approach this would be through a selection index. When you have multiple traits, you have to weight your selection criteria and your index can handle multiple traits.

Q: What is your advice for breeders who still want to practice breeding as an 'Art", in spite of availability of genomic resources?

> I never refer to plant breeding as an art, but if you mean as a creative enterprise, then my advice is to think about your plants and want they have a strength and what weaknesses they need to overcome. Also use all the information you have to understand how your plants respond to how they are grown. Remember no amount of technology can replace a skilled vision.

Q: Are you changing the vernalization and photoperiod responsive genes composition of the germplasm of your breeding program in view of global warming? How are you combining these genes in hybrids?

> Because the climate changes are slower than my breeding cycle, I think you will find selecting will adapt your lines to climate change. I am not purposely selecting for or against vernalization and photoperiod but expect nature will help me make the right selections. The problem will be if the climate becomes more erratic, so you need lines that are insensitive some years and sensitive in other years. This will make it very hard to breed.