Note:

Slide 2-39 are for 1-hr research talk

Slide 40-50 are for a short talk to growers' association



The past, present and future of quantitative genetics in plant breeding

CJ Yang Aug 2, 2023

Self introduction



Wisconsin

2012-2018

Indiana 2009-2012 BSc Biotech, Math





Edinburgh 2019-now Postdoc



Freising 2018-2019 Postdoc



Talk outline



Talk outline



Talk outline



Introduction – Plant Breeding



Wallace et al (2018)

- Domestication
- Improvement
- Experimental design

- Marker assisted selection (MAS)
- Genomic selection (GS)
- Phenomic selection (PS)
- Biology-Breeding
- Functional variants
- Gene editing (GE)
- Machine learning (ML/AI)

Introduction – Genetic Gain

Breeder's equation (Lush 1937)

Rate of genetic gain

 $R = h^2 S$

 $\Delta R = \frac{h\sigma_g i}{t}$



 $R = h\sigma_g i$

 $\Delta R = \frac{sel. accuracy \times genetic \ variation \times sel. intensity}{time}$ Framework for quantitative genetics











Primitive Technology 101: Domestication

This earliest form of <u>plant breeding</u> is known as <u>domestication</u>, where plants were selected to be more productive, easier to harvest, or more aesthetically or gastronomically pleasing (Flint-Garcia 2013).

Primitive Technology 101: Domestication

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Teosinte (left) and maize (right) in Homestead, FL, 2013-2017.

Primitive Technology 101: Domestication

Domestication reduced the genetic variances and changed the genetic correlations.



Yang et al (2019), see also Chen et al (2020, 2021) and Samayoa et al (2021)

Shuffling genetic diversity



Selection reduces genetic diversity.

Rely on exotic sources (wild/landrace) for novel alleles, e.g. stress tolerance/resistance. Linkage drag is a challenge.

Shuffling genetic diversity



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Selection bias



- Simulation study by Gorjanc et al (2016)
- Selection within exotic is slow.
- Selection within exotic x elite reconstitutes the elite genome.

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Origin Specific Genomic Selection (OSGS)

How do we improve selection in exotic x elite?

Can we target favorable exotic alleles?

OSGS GS u(-) Favorable Elite elite alleles Х (+) Favorable Exotic exotic alleles **Favorable alleles** New elite lines

А 7H 1H 2H 3H 5H 6H 4H 0.10 0.05 effect 0.00 -0.05 -0.10 0 20 0 20 0 02 00 0 0 Genetic Position (cM) в С 1250 57:43 1000 100 Predicted count 750 a (0.85) 50 500 â, (0.78) â, (0.53) 250 0.00 0.10 -50 50 -0.100 100

effect

Yield in a barley NAM family (BC1)

Yang et al (2020)

Observed

Origin Specific Genomic Selection (OSGS)



- Simulation with 60:40 split in favorable alleles between the elite and exotic parents.
- OSGS prevents selection on the favorable alleles from the elite parent.

Origin Specific Genomic Selection (OSGS)



- Simulation with 60:40 split in favorable alleles between the elite and exotic parents.
- OSGS prevents selection on the favorable alleles from the elite parent.
- The advantage of OSGS diminishes in BC population.

Vertical farming of purslane





- Rich in Omega-3.
- Novel crop in the UK.
- Not adapted to the UK climate.

Purslane cultivation



Short vs long day

- Evaluate and optimize growing conditions (recipes).
- Green = 4 weeks, golden = 3 weeks.





Extension activities with purslane







- Royal Highland Show (state fair).
- Taste test, survey, flyer, talk, demonstration.
- Other work: PhD student, nutritional profiling, variety registration, market development.

Research vision

Basic science

- Breeding program design
- Innovative strategy
- Technology evaluation
- Method development

Applied science

- Small grains breeding
- Cultivar delivery
- SunGrains
- Population development

Research vision

Basic science	 Applied science
 Breeding program design 	 Small grains breeding
 Innovative strategy 	 Cultivar delivery
 Technology evaluation 	SunGrains
 Method development 	 Population development

Research: lab, field, greenhouse, statistics, simulation, programming	ch: lab, field, ouse, statistics, tion, programming Funding: federal, state, industry, commodity board		Collaboration: projects, grants, interdisciplinary	
Dissemination: publication talks, posters, websites, social media, outreach	emination: publications, s, posters, websites, al media, outreach		stakeholders, es, growers,	

Research vision

	Basic science)		Applied so	cience
	Breeding program	n design			• Small g	rains breeding
	 Innovative strategy 				Cultivar delivery	
	Technology evaluation	ation			• SunGra	ins
	Method developm	ent]		• Populat	ion development
Research: lab, field, greenhouse, statistics, state, indu		Funding: fe state, indus	deral, stry,	Collat projec	oration: cts, grants,	
simu	lation, programming	commodity	board	interd	isciplinary	Training: capacity
Dissemination : publications, talks, posters, websites, seed			ement: stakeholders,		olders,	building, independ
			industries, growers,			

talks, posters, websites, social media, outreach

seed industries, growers, consumers

How can we improve breeding strategy to deliver higher rate of genetic gain?



An example with 2-part strategy (Gaynor et al 2017)

- Isolate breeding program into PI and PD.
- Allows us take advantage of GS and SB.

Questions to follow:

- Trade-off between speed and genetic diversity?
- Trade-off between speed and prediction accuracy?
- Compatibility with crop types?
- How does it work for different traits?
- Is there indirect selection (SSD/SB, epigenetics)?
- Any uptake in real-world breeding?

Higher genetic gain in 2P at a cost of depleting genetic variance.

Optimal Contribution Selection (OCS) to sustain the genetic gain.





Gorjanc et al (2018)

OSGS in cultivar development

In general,

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Polygenic traits = Genomic Selection (GS)
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Oligogenic traits = Marker Assisted Selection (MAS)

Recall from earlier slides...



- Introgression of polygenic traits.
- E.g. tolerance to abiotic stresses (drought, heat, salinity).
- Important traits for climate change.

Improvement to OSGS

Currently, OSGS has only been shown in single trait in bi-parental populations.



Traits: multi-trait mixed model

Parents: parental probability or haplotype approach

Improvement to OSGS

Currently, OSGS has only been shown in single trait in bi-parental populations.



Traits: multi-trait mixed model

Parents: parental probability or haplotype approach

The SNP-BLUP model is $y = X\beta + Wu + \varepsilon$. And we assume $u \sim N(0, I\sigma_u^2)$.



- Does the normality assumption still hold when the two parents are vastly different?
- Is there any bias introduced by the model?

The following is a conventional mixed model for genomic BLUP (gBLUP).

 $y = X\beta + Zg + \varepsilon$ $g \sim N(0, K\sigma_g^2)$ K = MM'

In phenomic selection, the genomic markers (*M*) are replaced by phenome.



- Phenome can be near-infrared spectra (NIRS), image data, etc.
 - Part of the phenome is heritable.
 - Phenome is cheap(?).
 - Phenome captures G x E x M.

Current states of phenomic selection



•

- Maize lines (elite, landrace populations).
- PS vs GS depends on populations and traits.

Opportunities in phenomic selection

Compare GS and PS for different traits.



Predictions from PS are biased toward information within the predictors, Dallinger et al (2023).



Evaluate PS across developmental time points.



Simulation is an important part of GS, how can we do that for PS?



Summary

Quantitative genetics, plant breeding



Many thanks to the Search Committee, Department of Crop and Soil Sciences, NCSU for the opportunity to present the talk!

Wisc + Others John Doebley Ali York Qiuyue Chen Wei Xue Natalia de Leon Claudia Calderón Jim Holland L Fernando Samayoa Ed Buckler M Cinta Romay Peter Bradbury Many more...

SRUC Ian Mackay Wayne Powell Rajiv Sharma Nicola Rossi Emma Irving David Marshall <u>OSGS</u> Gregor Gorjanc Sarah Hearne

MAGIC

Rodney Edmondson Hans-Peter Piepho

<u>DUS</u> Joanne Russell Luke Ramsay Bill Thomas

<u>RALLY</u> Funmi Ladejobi Richard Mott

<u>RL</u>

Scottish Society for Crop Research

<u>Computing</u> UK Crop Diversity

https://cjyang-work.github.io/

XXX 🔀



in cjyang90

Quantitative Genetics and

Small Grains Breeding

CJ Yang Aug 3, 2023

Self introduction



Wisconsin

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Indiana 2009-2012 BSc Biotech, Math





Edinburgh 2019-now Postdoc



Freising 2018-2019 Postdoc





Research background



Research background



Background – Small Grains Breeding

- Small grains: wheat, barley, oats, rye, triticale, etc.
- 6% of NC total crop production value in 2022 (<u>USDA NASS</u>).
- Winter wheat ranked fifth with a production value of \$202 millions.
- Primary use: flour.
- Other uses: feed, malt, cover crop.
- Availability of crop insurance?
- Line breeding, GS, hybrid?
- SunGrains (NC, AR, FL, GA, LA, SC, TX): cooperative breeding, royalty.

Soft red winter wheat







ASSOCIATES www.uswheat.org

https://kswheat.com/news/which-wheat-for-what

www.wheatfoods.org



https://www.uswheat.org/working-with-buyers/wheat-classes/

- Low protein content (8.5-10.5%)
- Flour for cake, pastry, dessert, etc.

Research and breeding vision



Research and breeding vision



- Link between basic and applied science test and apply innovations.
- Incorporate end users' interest into breeding.
- Create new markets.
- Maintain/develop healthy relationship with industry/public breeders, growers.
- Train future breeders.
- Learn the process and ensure continuity.

Relevant research areas



polygenic introgression.



