### Evaluation of genomic selection methods for dwarf bunt resistance in wheat

Margaret Krause, Tyler Gordon, David Hole, Jianli Chen

XXI International Workshop on Bunt and Smut Diseases 6 May 2021

### Why quantitative resistance?



the evolution of the pathogen to overcome host resistance

## Why quantitative resistance?



### Why genomic selection?



## Why genomic selection?

### Molecular Markers and Selection for Complex Traits in Plants: Learning from the Last 20 Years

Rex Bernardo 🔀 Crop Sci. 48:1649-1664

#### Marker assisted selection (MAS):

- Requires identification (significance testing) and validation of traitassociated markers
- Difficult to implement in breeding when trait is controlled by many QTL
- QTL analyses often miss small-effect loci
- Estimated QTL effects are usually inflated

### Genomic selection (GS)<sup>1</sup>:

- Significance testing not required
- Can select on small-effect loci
- Requires many markers



<sup>1</sup>Meuwissen et al. 2001

## Why genomic selection?



#### GS in practice:

- Reduced breeding cycle time
- Reduced cost of phenotyping
- Increased genetic gain

Poland J, Rutkoski J. 2016. Annu. Rev. Phytopathol. 54:79–98

# Testing genomic selection for dwarf bunt resistance

To evaluate the potential of GS to improve breeding for dwarf bunt resistance, we need a dataset with:

- Dwarf bunt phenotypes
- Genome-wide markers

Genetic characterization and genome-wide association mapping for dwarf bunt resistance in bread wheat accessions from the USDA National Small Grains Collection

Tyler Gordon, Rui Wang, David Hole, Harold Bockelman, J. Michael Bonman & Jianli Chen 🖂

Theoretical and Applied Genetics 133, 1069–1080(2020) Cite th

- **Phenotypes:** 246 accessions score in the field for dwarf bunt incidence in Logan, UT for three years
- Genotypes: 90 K iSelect SNP assay (19,281 markers)

# Testing genomic selection for dwarf bunt resistance

GBLUP model (vanRaden, 2008)

 $y = 1\mu + Zu + e$ 

**y** is vector of genomic estimated breeding values (GEBVs)



#### **Cross validation**



**"Prediction accuracy"**: Pearson's correlation between predicted and observed dwarf bunt incidence

## Genomic selection when majoreffect genes are known



effects

Allele

Accession	Bt gene	Origin	BLUE	DB- 6D1	DB- 6D2	QDB.ui- 6DLª	QDB.ui- 7AL <sup>b</sup>	QDB.ui- 7DS <sup>c</sup>
PI 345106		Serbia	3.9	+	-	-	-	-
PI 345428		Montenegro	4	-	-	-	-	-
PI 476212		USA	4	+	-	-	-	+
PI 560601		Turkey	3.8	+	-	-	-	-

QTL explained 9-15% of the phenotypic variation Gordon et al. 2020

# Genomic selection outperforms marker assisted selection, but accuracies are reduced when predicting less-related material



# Next steps

## Assemble and evaluate genomic selection training population that targets:

- Relatedness to Intermountain West wheat breeding programs
- Germplasm with intermediate phenotypes





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Looking forward to working with all of you!!!

I will start at Utah State University on July 1<sup>st</sup>

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