Genomic Selection for Dwarf Bunt Resistance in Wheat

22nd International Workshop on Bunt and Smut Diseases of Cereals

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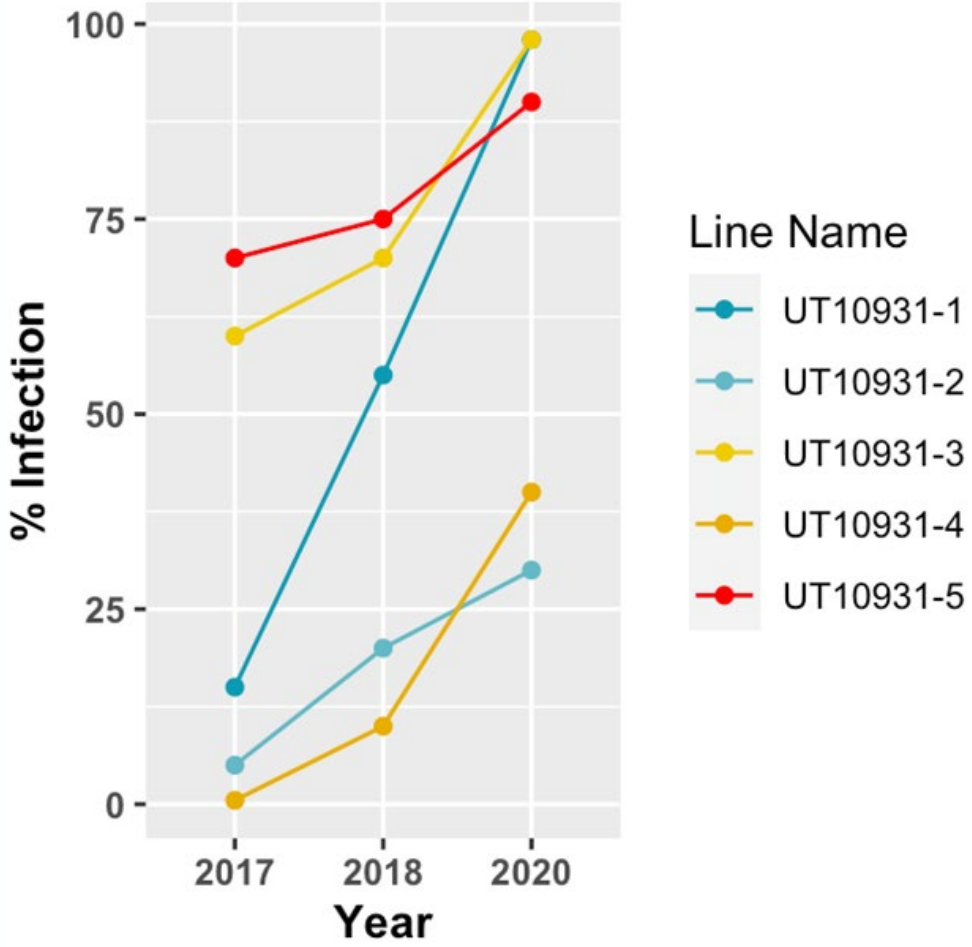
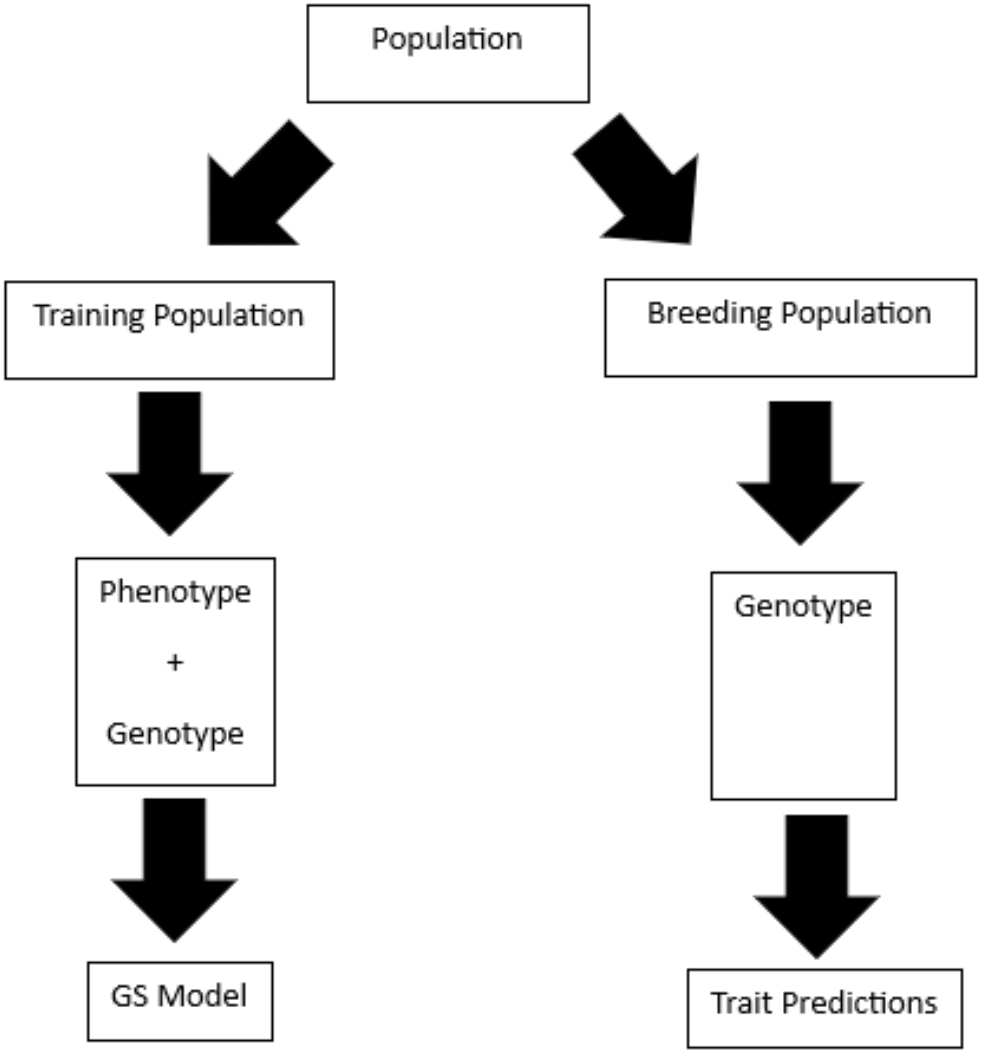
Disease History and Significance

- Scientific name : *Tilletia controversa*
- Common name : dwarf bunt
- First identified as a problem
  - 1930's in Utah
- Importance of management
  - Organic production : 30% of Utah acreage
- USU varieties
  - Relief 1934
  - PI 178383

Objective

- Test genomic selection's ability to predict dwarf bunt resistance in winter wheat
- Good vs poor infection
- Emergence, weather, snow cover




Population
Training Population
Breeding Population
Phenotype
+
Genotype
Genotype
GS Model
Trait Predictions

Wheat Population

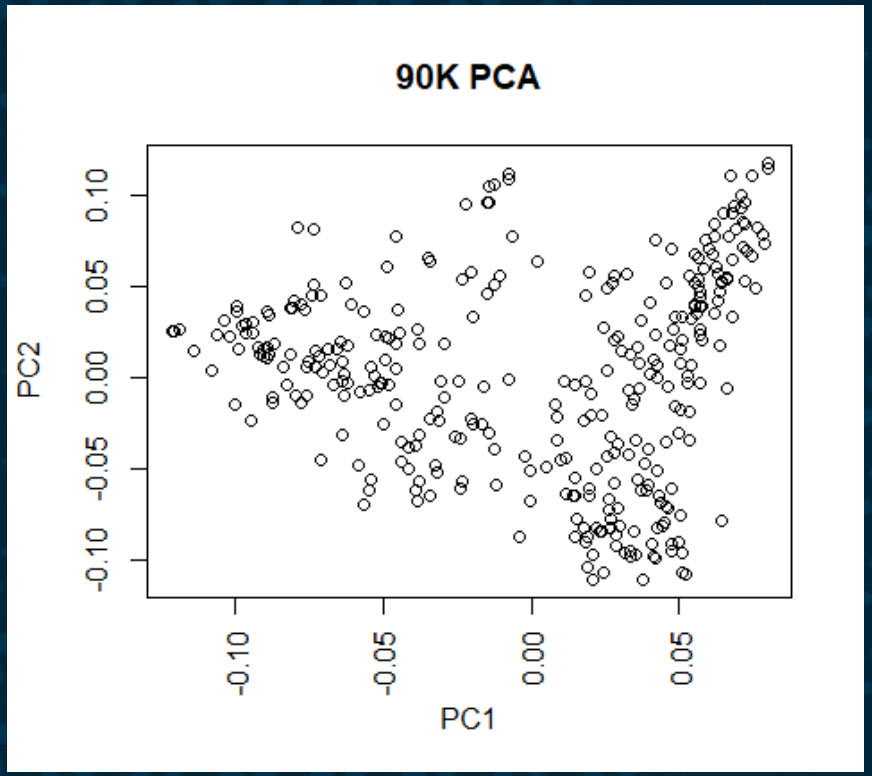
- 384 diverse inbred lines of winter wheat with varying levels of resistance
- Public sector programs from Intermountain West
- Comprise the “Training Population”
- Genotypic data : two types of SNP genotyping platforms
- Phenotypic data : 2022 and 2023 dwarf bunt ratings

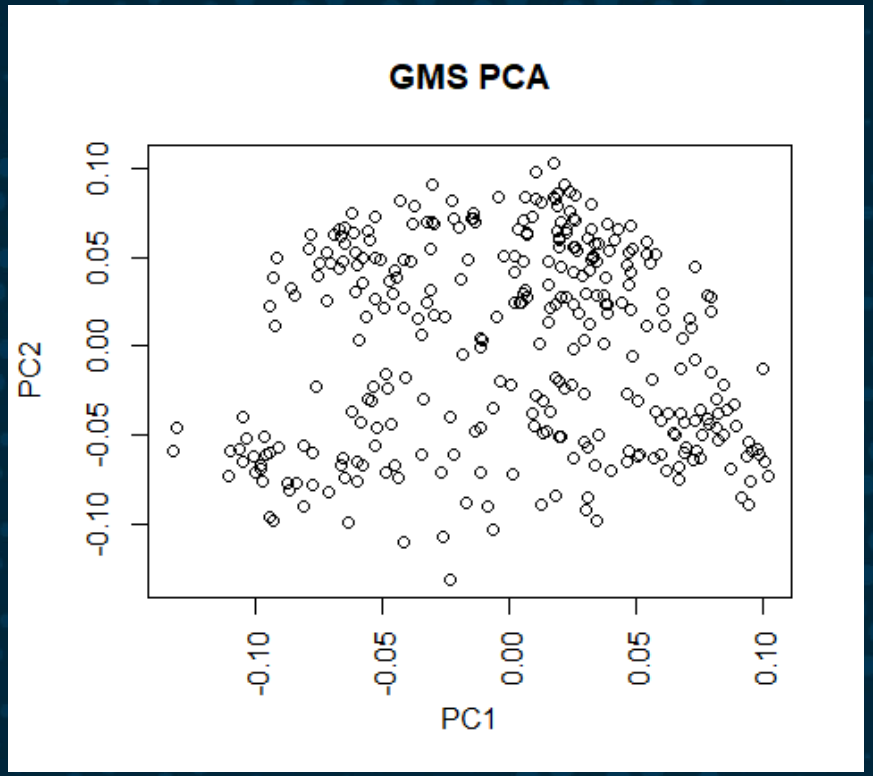
How does genomic prediction accuracy differ between SNP genotyping platforms?

- Genotyping by Multiplexed Sequencing (GMS) : 1519 SNPs
  - Dr. Deven See : USDA Pullman, Washington USA

- 90k Illumina iSelect SNP chip : 3330 SNPs

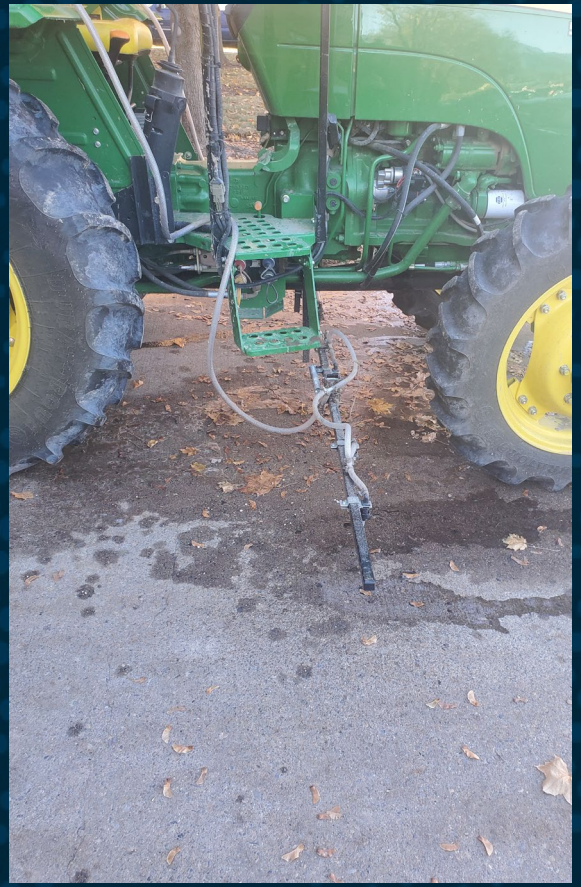
Principal Component Analysis





Phenotypic Data

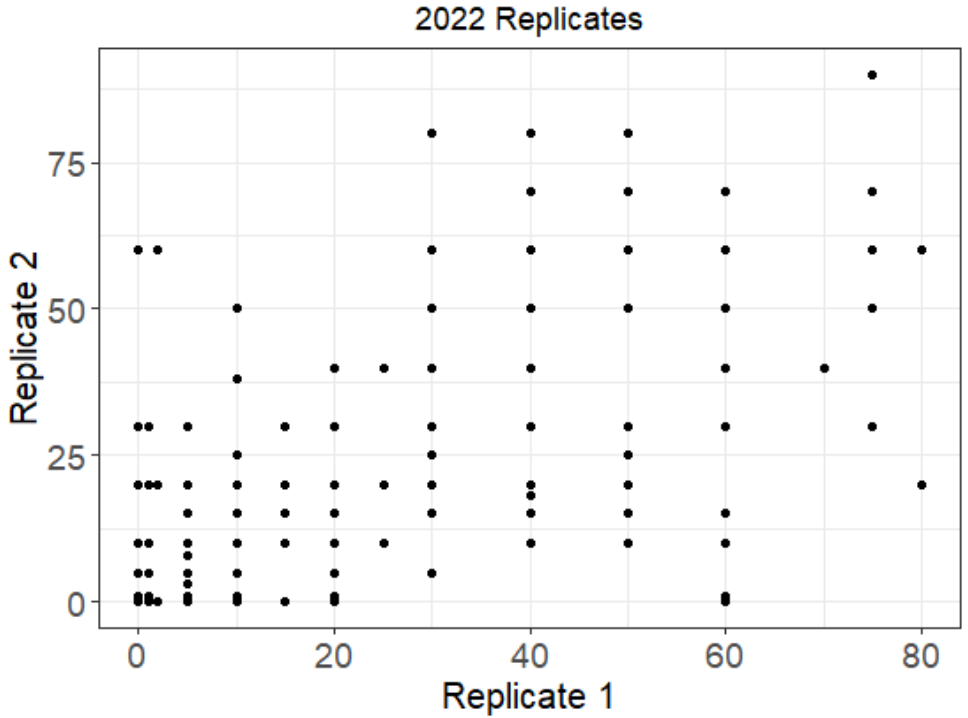
- Disease ratings
  - Ratio of infected vs uninfected spikes

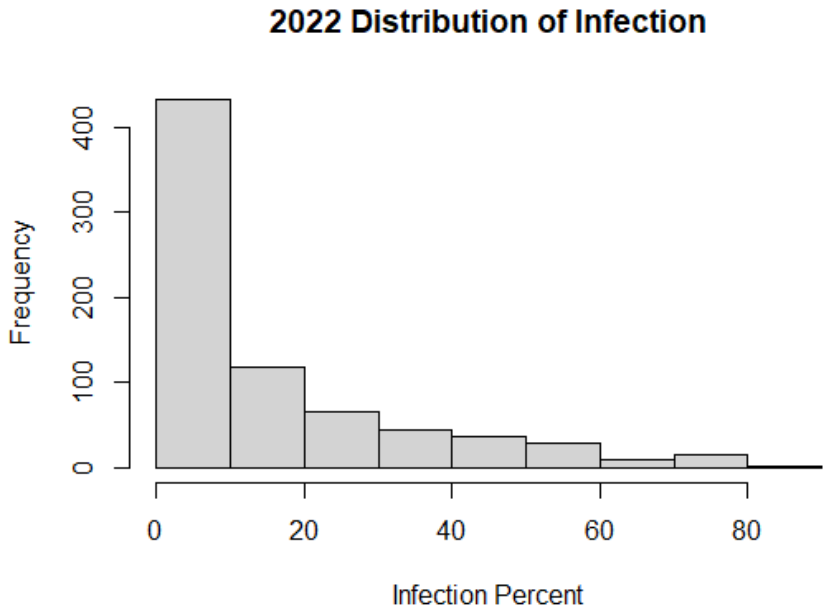


Trial Inoculation

- Dwarf Bunt spores are inoculated with 1g of spores per 1.2m row

Dwarf Bunt Infection Data



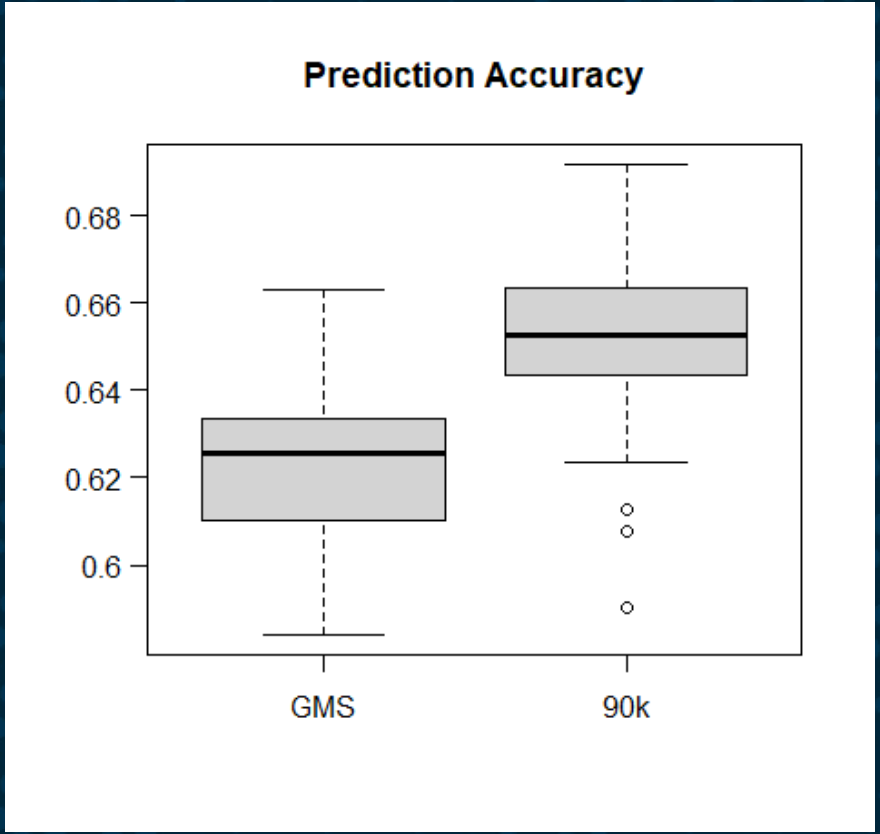


Analysis

- Line mean heritability of 0.84
  - Calculated from replicated field data
  - Values from 0 to 1

$$\frac{V_g}{V_g + (V_e / n.rep)}$$

Prediction Accuracy



Conclusion and Future Work

- High line mean heritability : Replicates show similar infections
- High prediction accuracy : Model reliably predicts infection
- Future work
  - Additional PCA analysis
  - Collect 2023 dwarf bunt infection data
  - Repeat analysis for 2023 data
  - Genome Wide Association Study
  - Models incorporating high effect markers as fixed effects

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USDA United States Department of Agriculture

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