Seedlings (n=4000)

GBS and GS

n=(1000)
n=(100)

(2-3 Years)
Phenotype
Update GS

Cross

Update GS Model

Repeat Cycle
Genomic Selection Model
Development and Validation

- 6364 SNP markers with less than 5% missing data used for model and minor allele frequency >0.05
- 2600 Plants genotyped
- Due to missing data, 1000 to 2600 data points per trait
- Validation by forming model with 90% of data to predict 10%, 10 resamplings without replacement

Credit: Jared Crain
$h^2 = 0.41$

$r = 0.6$, $RMSE = 17.33$
$h^2 = 0.25$

$r = 0.75$, RMSE = 0.63
$h^2 = 0.35$

$r = 0.43, \text{RMSE} = 0.11$
$h^2 = 0.24$

$r = 0.78$, RMSE = 0.03

Percent Fertility

Predicted value vs. Observed value scatter plot.