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Plant Breeding Symposium
Texas A&M University
2015

Texas A&M Plant Breeding Symposium
February 19, 2015
10:00 – 11:00 am

# **Genomic Selection**: Historical Context, Technical Details, Empirical Findings, and Perspectives

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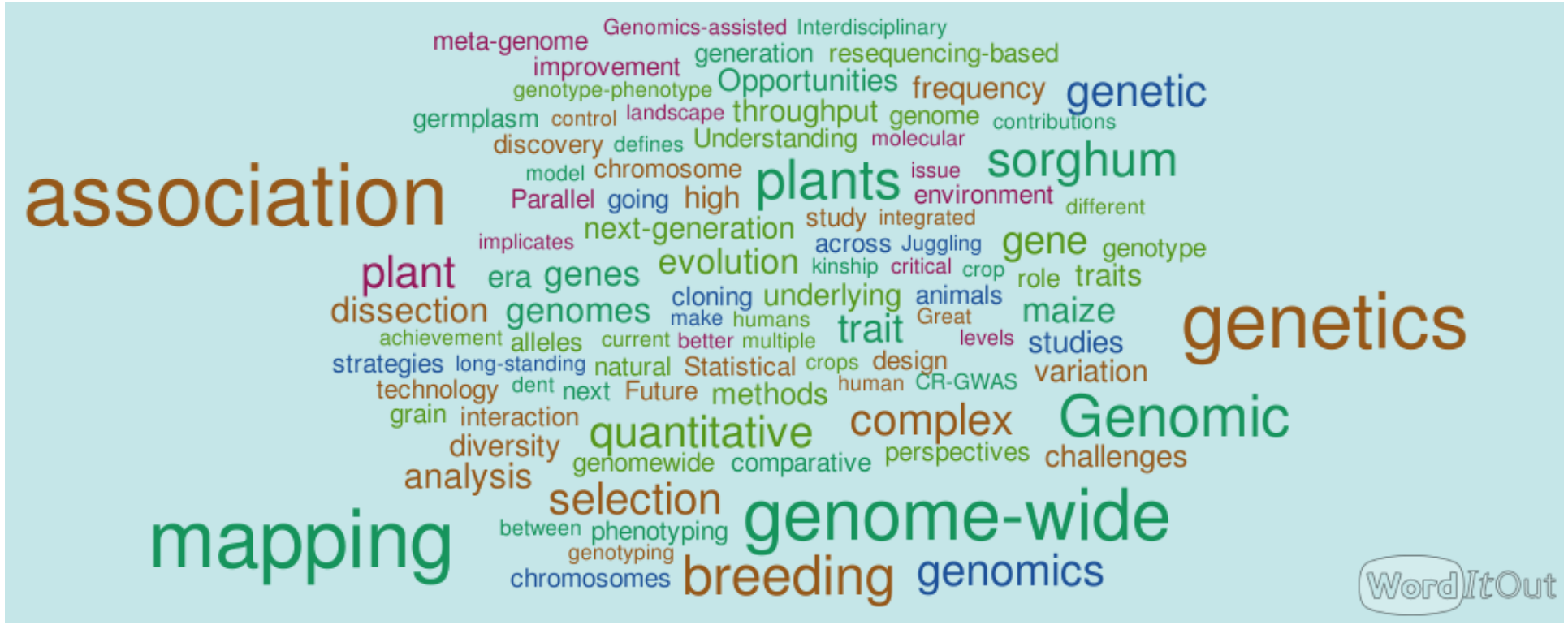
# Introduction

From 56 presentation titles



USDA United States Department of Agriculture
National Institute of Food and Agriculture
USDA/DOE Plant Feedstock Genomics for Bioenergy

Targeted Excellence K-STATE Kansas State University

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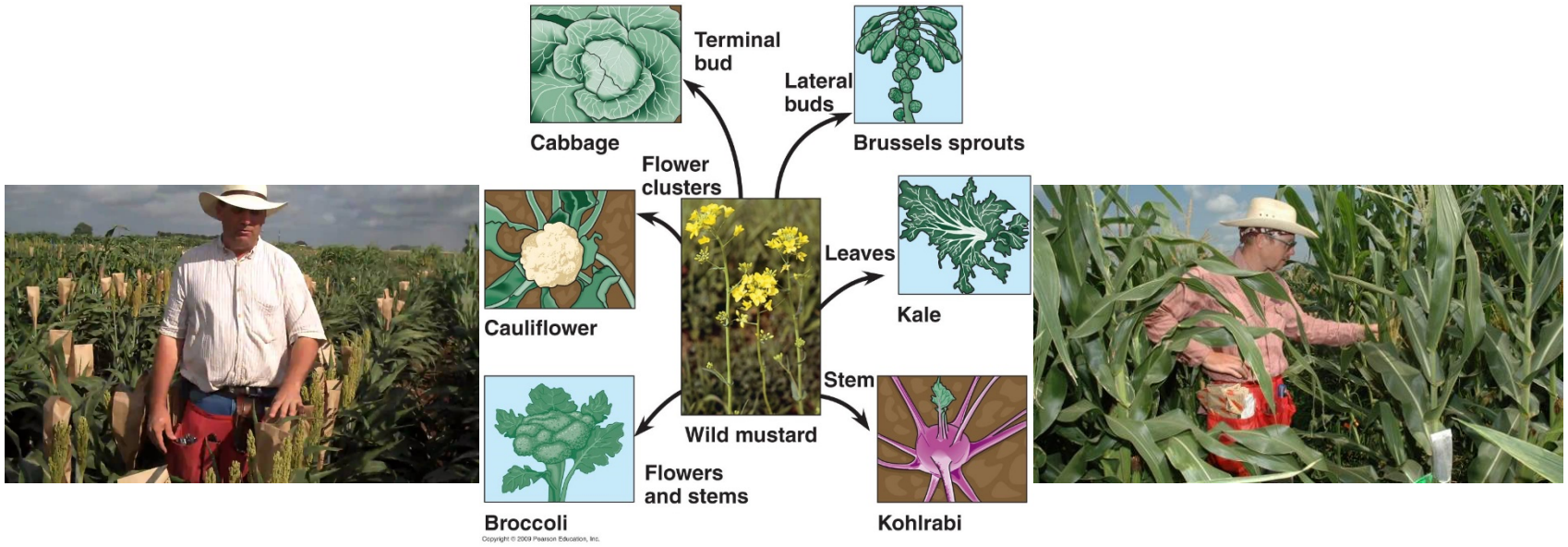
# Outline

- Genomic Selection
  - Historical Context & Technical Details
  - Breeder's 10 Tenets
- Empirical Findings
  - 44,733, 1,000, 300, 200, 100, 50, 50
- Perspectives
  - Optimizing GS following Breeder's Tenets

Historical Context

# *What is "Selection"?*

- Differential viability (survival) and fertility (reproduction) among genotypes. Natural selection *versus* artificial selection
- In plant breeding, selection changes allele frequencies and genotype frequencies.
- Selection happens at different stages of the breeding cycle.



Historical Context

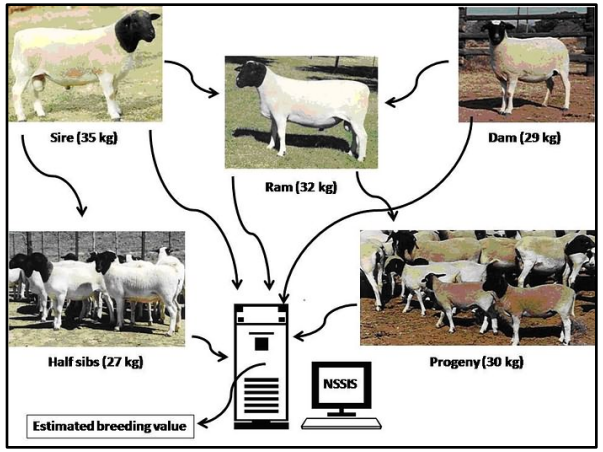
# *What is not "Genomic" Selection?*

- Selection based on observations (from the unreplicated trial)
- Selection based on rankings from the replicated, multi-environment trials
- Selection on best linear unbiased prediction of the phenotypes on the individual and its relatives

Parallel selection for non-shattering
Nature Genetics 44:720–724

Texas A&M AgriLife Extension
Service photo by Dr. Gaylon Morgan

Breeding value for weaning weight of a ram




GROOTFONTEIN
Agricultural Development Institute

Historical Context

# *What is not "Genomic" Selection?*

- Genotyping and selection based on known markers (*e.g.*, disease resistance, insect resistance, or major QTLs)
  - Assume we have identified the informative markers

- Genotyping and selection based on sum of estimated genotypic values across multiple QTLs
  - Assume we have detected multiple QTLs
  - Assume the summation across individual QTL effects provides a good estimate of the overall genotypic value
  - $\boldsymbol{G_Q} = \sum_{k=1}^{q} (\alpha_i^k + \alpha_j^k)$, where $\boldsymbol{q}$ is the number of declared QTLs

Historical Context

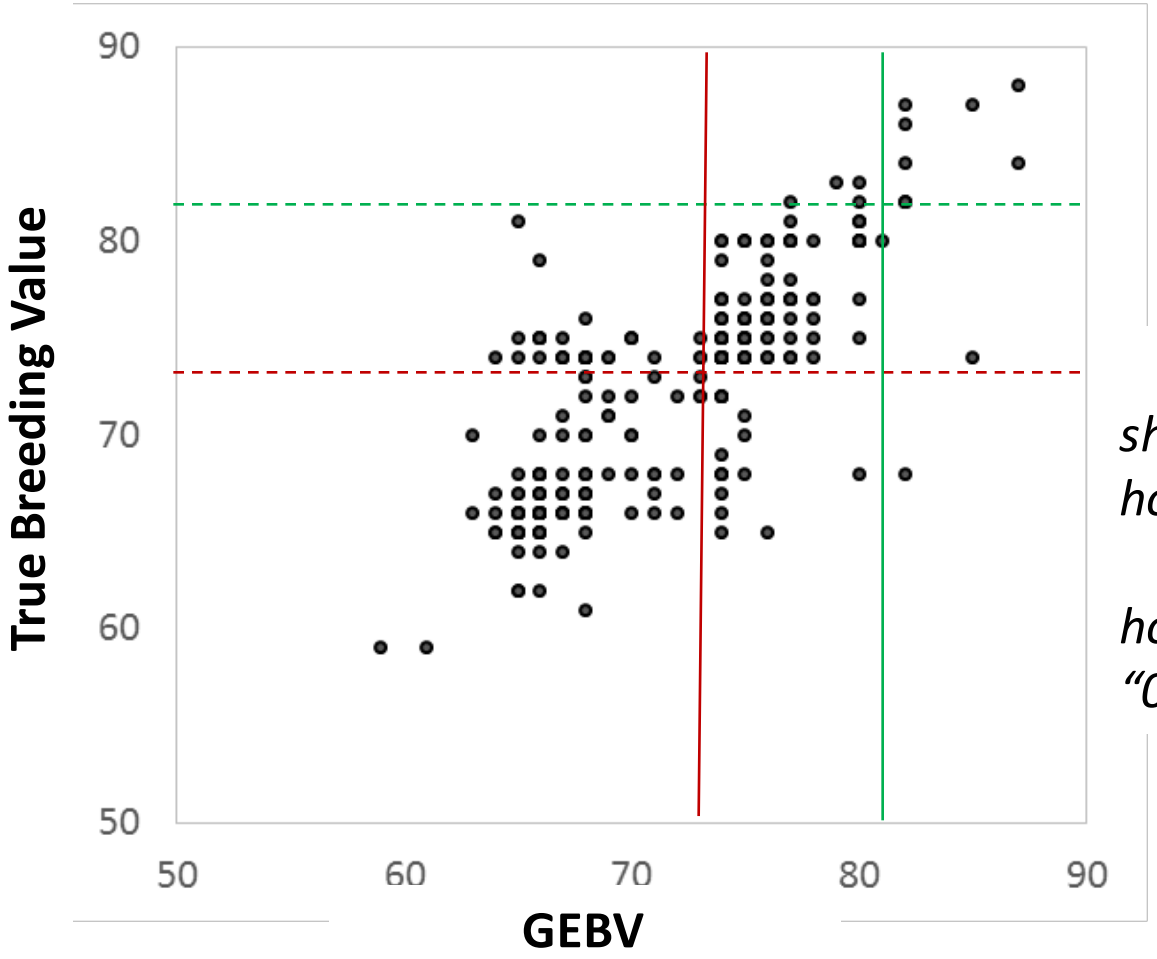
# *What is Genomic Selection?*

- Genotyping and selection based on Genomic Estimated Breeding Value (GEBV)
  - $G_{EBV} = \sum_{k=1}^{m} (\alpha_i^k + \alpha_j^k)$, where ***m*** is the number of genome-wide markers
  - Assume we can have accurate estimates of marker effects
  - Assume $G_{EBV}$ is a better estimate of the overall genotypic value than $G_Q$

- A procedure where genetic merits are predicted for unphenotyped individuals so that selection can be made
  - Model Training Genome-wide marker information across a group of phenotyped individuals is used in developing the prediction model
  - Prediction Prediction is made for a different group of unphenotyped individuals but with genome-wide marker information
  - Selection **Either** directly advance the breeding generation, **or** significantly narrow down the candidate pool before field evaluation

Technical Details

# *What is Genomic Selection?*

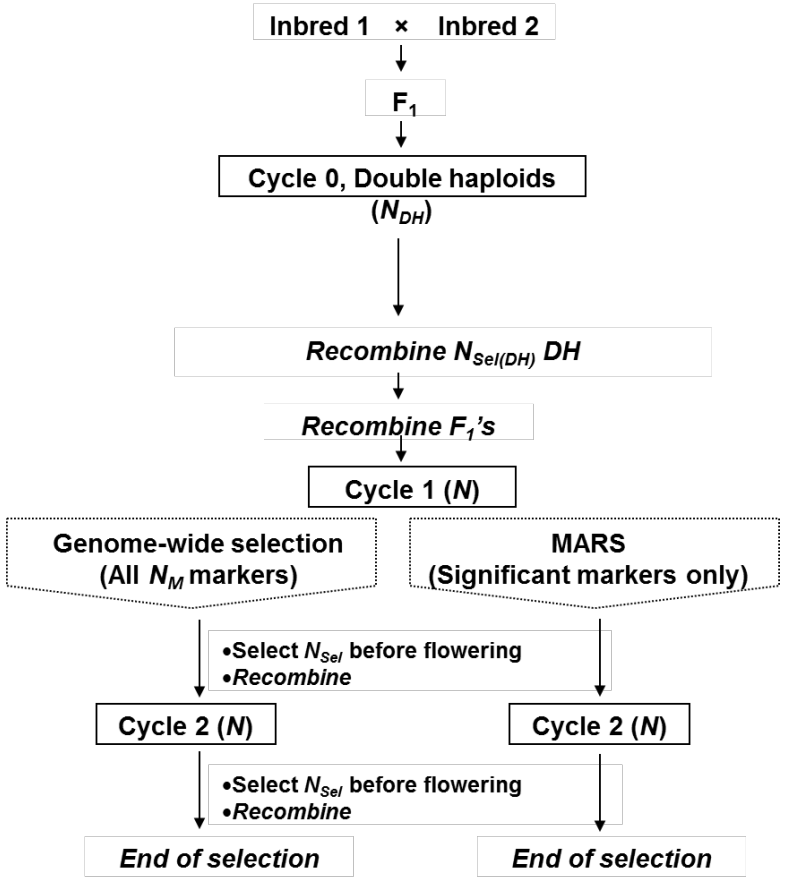



*r* = 0.77 in this case

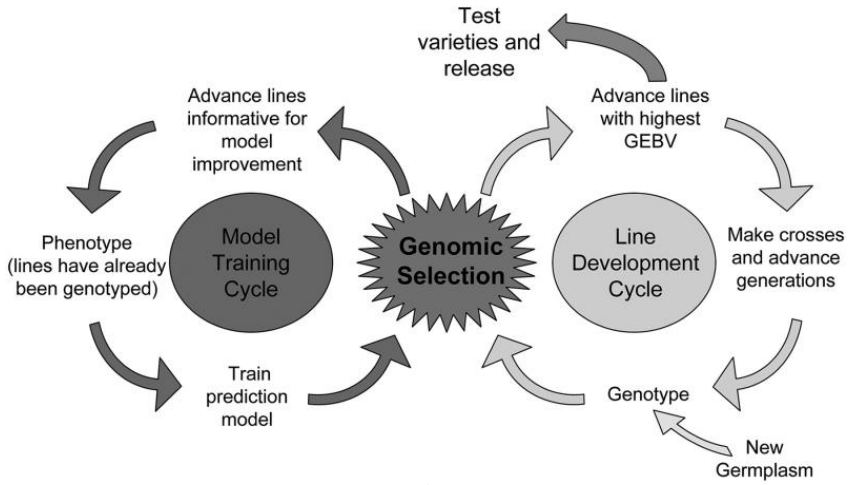
At the start,
*should you be thinking about how close your r is to "1"?*
or
*how different your r is from "0"?*

Technical Details

# *What is Genomic Selection?*




Bernardo and Yu, 2007. Crop Science 47:1082-1090.




Heffner *et al.* 2009. Crop Science 49:1-12.

It is all about having a step to improve the plant breeding process by better utilizing resources: time and cost.

Technical Details

# *What is Genomic Selection?*

Individuals

$$y = X\beta + Ig + e$$

$$V = Var(y) = A\sigma_g^2 + I\sigma_e^2$$

Markers

$$y = X\beta + Wu + e$$

$$V = Var(y) = WW'\sigma_u^2 + I\sigma_e^2$$

$W_{ij}=(M_{ij}-2p_i)/\mathrm{Sqrt}(2p_i(1-p_i))$

$$\begin{bmatrix}\hat{\beta}\\ \hat{g}\end{bmatrix} = \begin{bmatrix}X'X & X'\\ X & I+\frac{\hat{\sigma}_e^2}{\hat{\sigma}_g^2}A^{-1}\end{bmatrix}^{-1}\begin{bmatrix}X'y\\ y\end{bmatrix}$$

Connection

$$A\sigma_g^2 = WW'\sigma_u^2$$

$$\sigma_u^2 = \sigma_g^2/m,\ A = WW'/m$$

$$\begin{bmatrix}\hat{\beta}\\ \hat{u}\end{bmatrix} = \begin{bmatrix}X'X & X'W\\ W'X & W'W+\frac{\hat{\sigma}_e^2}{\hat{\sigma}_u^2}I\end{bmatrix}^{-1}\begin{bmatrix}X'y\\ W'y\end{bmatrix}$$

$$\hat{g} = A\frac{\hat{\sigma}_g^2}{\hat{\sigma}_e^2}\hat{V}^{-1}(y - X\hat{\beta})$$

$$\hat{u} = W'A^{-1}\hat{g}/m = W'(WW')^{-1}\hat{g}$$

$$\hat{\lambda}=\frac{\hat{\sigma}_e^2}{\hat{\sigma}_u^2}$$

Genomic Estimated Breeding Value (GEBV) of the individuals with only marker data

$$\hat{g}_{new} = W_{new}\hat{u} \qquad \boldsymbol{G_{EBV}}=\sum_{k=1}^{m}(\alpha_i^k + \alpha_j^k)$$

Technical Details

# *What is Genomic Selection?*

| Markers $y = X\beta + Wu + e$ | Marker Effect Estimates |
|---|---|
| $\begin{bmatrix}\hat{\beta}\\ \hat{u}\end{bmatrix} = \begin{bmatrix}X'X & X'W\\ W'X & W'W + \frac{\hat{\sigma}_e^2}{\hat{\sigma}_u^2}I\end{bmatrix}^{-1}\begin{bmatrix}X'y\\ W'y\end{bmatrix}$<br>$V = Var(y) = WW'\sigma_u^2 + I\sigma_e^2$<br>$\hat{\lambda} = \frac{\hat{\sigma}_e^2}{\hat{\sigma}_u^2}$ | $\hat{u}$ estimated from Training Population, and used for Prediction/Validation Population<br>Prediction Accuracy<br>$r_1 = Corr\,(y_{new}, \hat{g}_{new})$<br>$r_1 = Corr\,(y_{new}, \hat{g}_{new})/\sqrt{h^2}$ |

- What is the distribution of quantitative trait variants?
  - **GBLUP**, Single distribution $u \sim N(0, \sigma_u^2)$
  - **BayesA**, Different distributions $u_k \sim N(0, \sigma_{u_k}^2)$, $\sigma_{u_k}^2 \sim \chi^{-2}(v, s)$
  - **BayesB**, $\sigma_{u_k}^2$=0 with probability of π AND $\sigma_{u_k}^2 \sim \chi^{-2}(v, s)$ with probability of 1- π
  - **BayesC$_\pi$**, Mixture of $u$=0 probability of π AND $u \sim N(0, \sigma_u^2)$ with probability of 1- π; π estimated from the data
  - **Kernel-based methods**, capturing non-additive effects

Technical Details

# *What Can We Do with Genomic Selection?*

- Genomic selection has been extensively studied in recent years
  - Prediction accuracy, Different models, Different genetic architectures
  - Resources allocation: “Plant breeding is a number’s game.” “Genetic gain per unit time and cost.”
- Genomic selection has been well integrated into many plant breeding programs
  - Inbred development
  - Testcross evaluation
  - Parental selection for generating breeding populations
  - Hybrid prediction

Technical Details

# Emerging Areas of Research

- Genomic selection under G x E
  - Environmental covariates
  - Modeling G x E prior to genomic selection
  - Reaction norm model
  - **Integration of genomic selection and crop model**
- Genomic selection for exotic germplasm introgression
- *Genomic selection for germplasm enhancement?*

Breeders' Tenets

# Ten Things a Successful Plant Breeder Understands - Roger Boerma

10 Tenets

1. De ments
and
3. Ur type
and
4. Us year
6. Th ost
quar
7. M
geno
8. In ow
how
10. T

## Ten Things a Successful Plant Breeder Understands

H. Roger Boerma, Executive Director, Georgia Seed Development & Emeritus Professor, University of Georgia

4th Annual Meeting of the Nationa
8th Annual Meeting of the Plant Br
Minneapolis, MN - 6 August 2014

GEORGIA SEED DEVELOPMENT

# Bioenergy Crop Breeding and Genomics

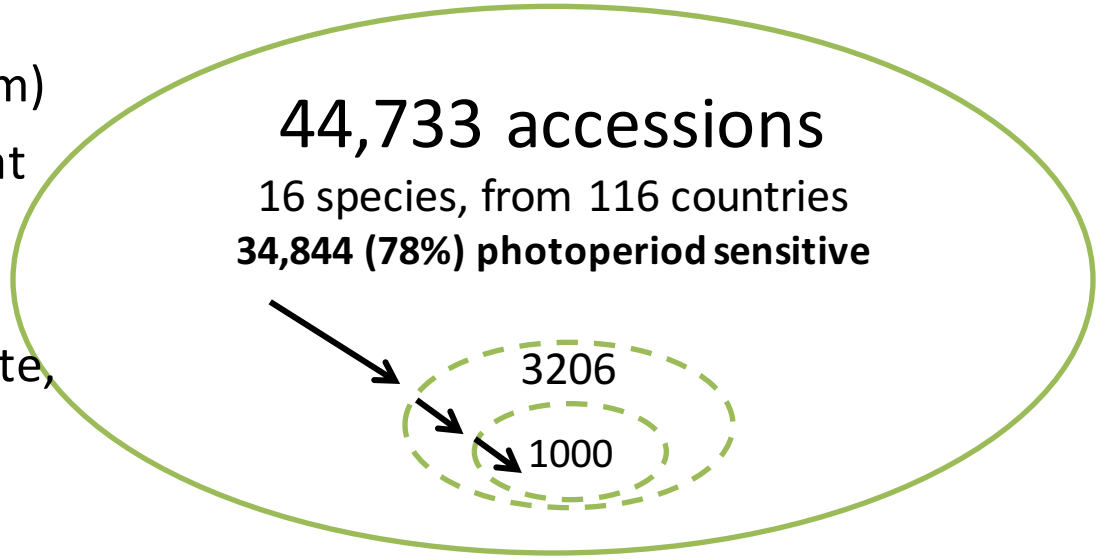
- New crops that not much breeding and genetics have been conducted in the past. But, many genomics and phenomics resources are available.
- **Genomics-Assisted Breeding**

➢ *How do we tap into the vast plant **germplasm** collections for biomass crop improvement?*

➢ *How do we increase the information contained in genotypic and phenotypic **data** for the selected germplasm so that this **information** can generate maximum **knowledge** to enrich our **understanding** of the **germplasm** and **genotype-phenotype relationship**?*

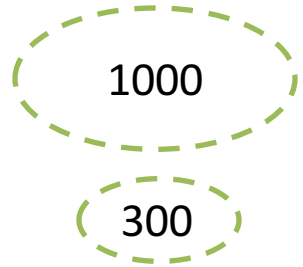
# Start Right with Available Germplasm Information

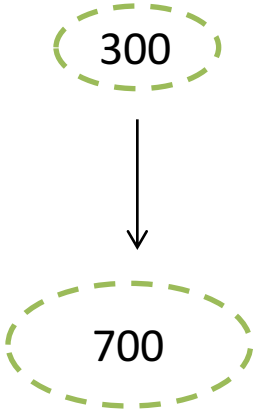
- Selection of the initial biomass sorghum accessions (base population)
  - Step 1: Flowering = 6, photoperiod sensitive; Plant height (280 ~ 400cm)
  - Step 2: Seed availability at GRIN for distribution
  - Step 3: Germplasm information: collection site, race, height uniformity, disease, lodging, etc.



# Selective Phenotyping

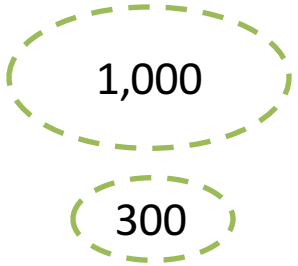
- Trait evaluation of only those individuals that contain the maximum genetic information
  - Genotyping a large set of accessions
  - Select a subset for a given sample size to maximize genetic information content (allele number, gene diversity, recombination break point, etc.)
  - Mapping power and resolution
  - Prediction accuracy



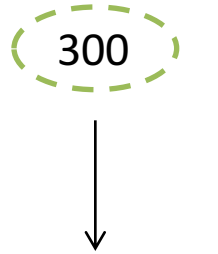
# Selective Phenotyping

Genotyping-By-Sequencing (GBS) of all




Choose most representative accessions & Phenotype

Build and evaluate genomic prediction models

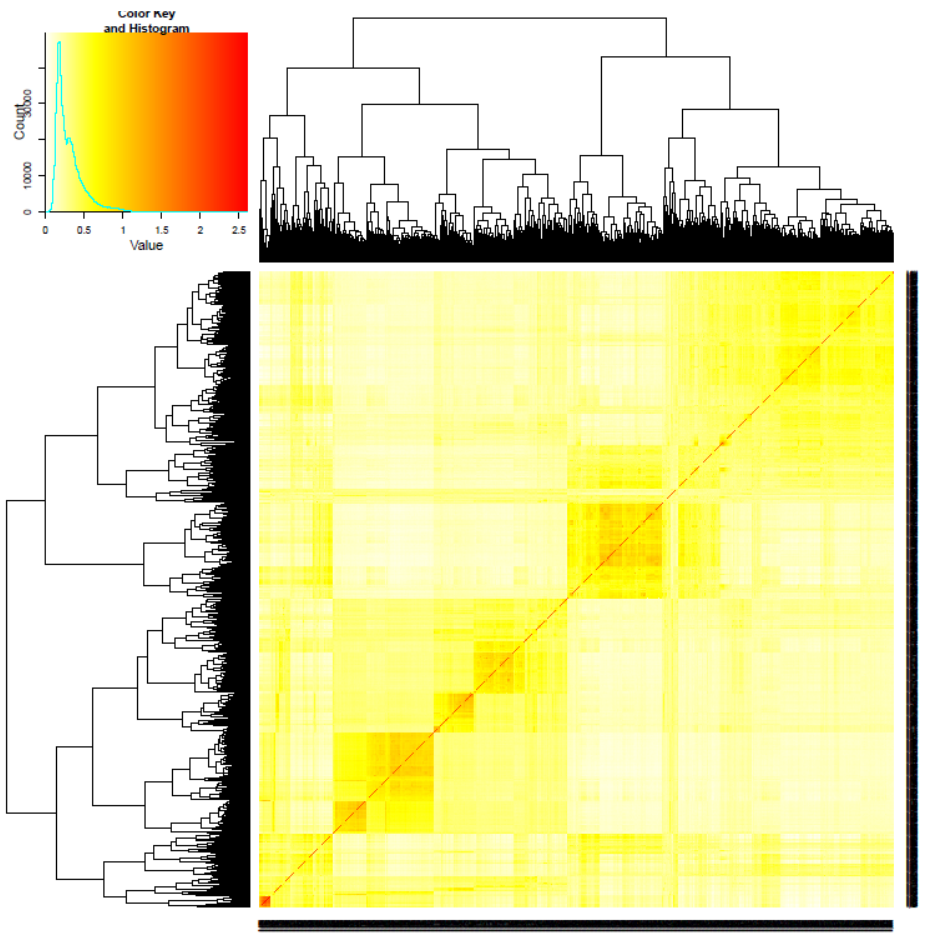



Predict genomic estimated breeding values of the rest

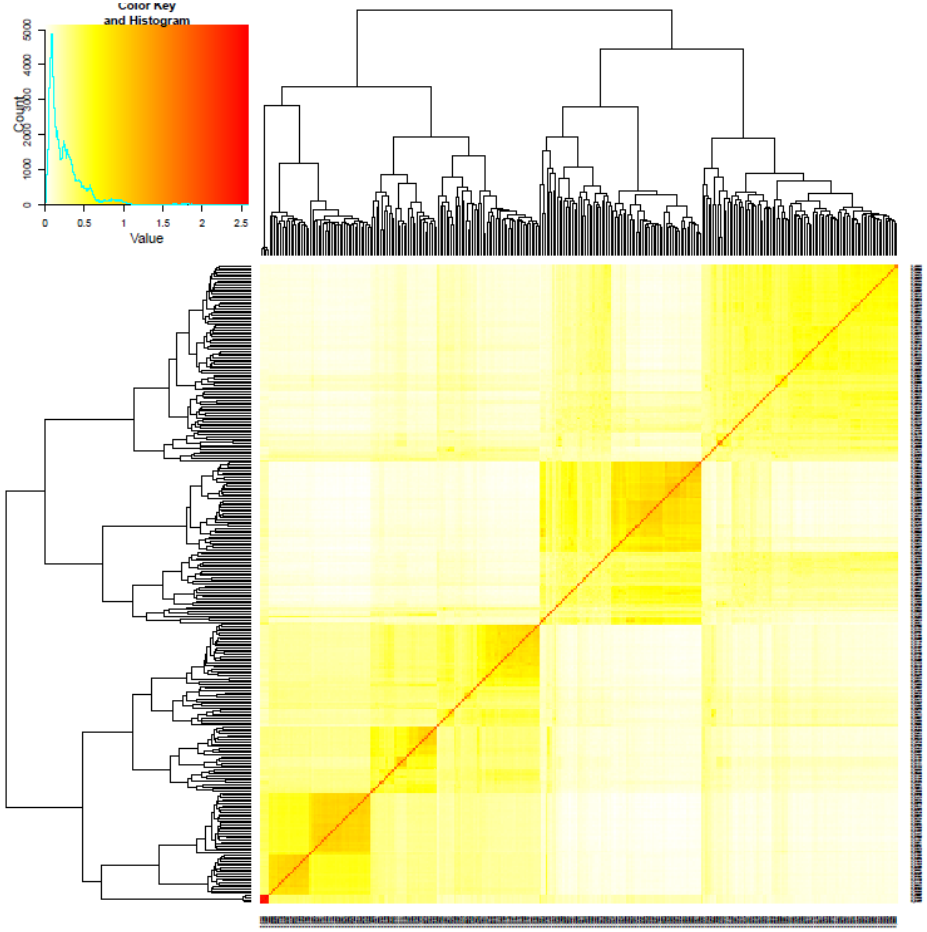
Empirical Findings

# Genetic Relationship

1000




300

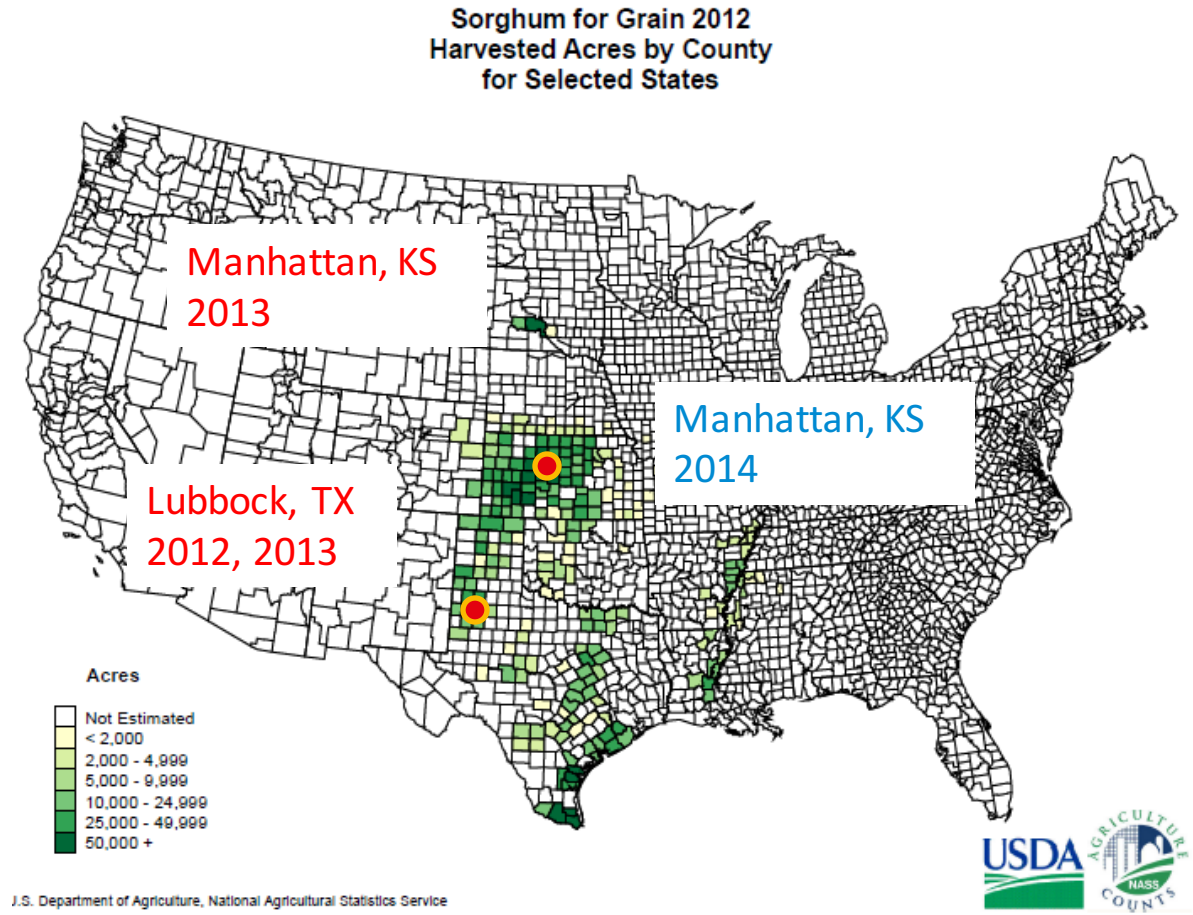


# Experiment Location

300

700

200



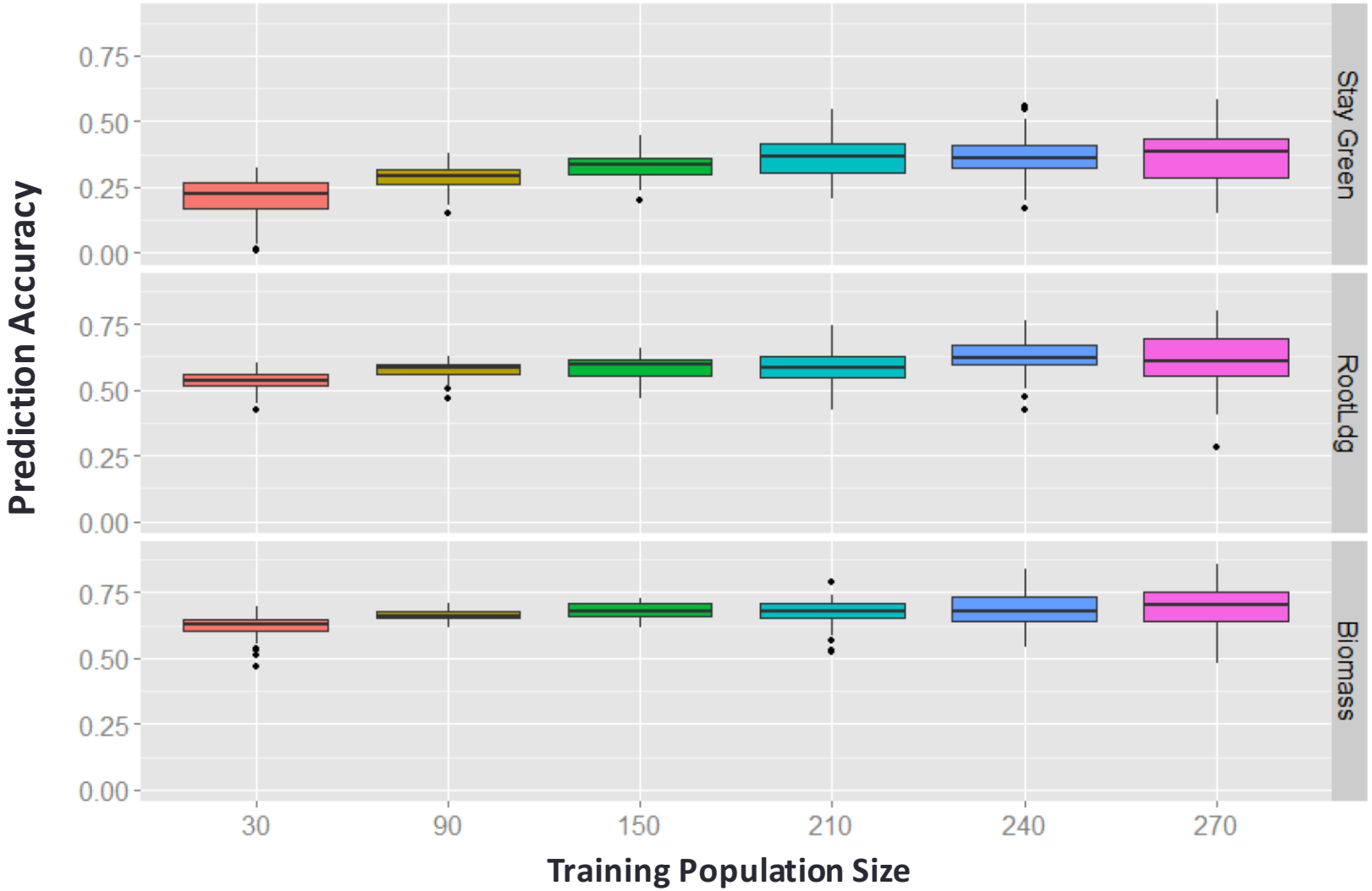

Two replications in each environment

Empirical Findings

300

# Prediction Potential

## Evaluated by Cross Validation

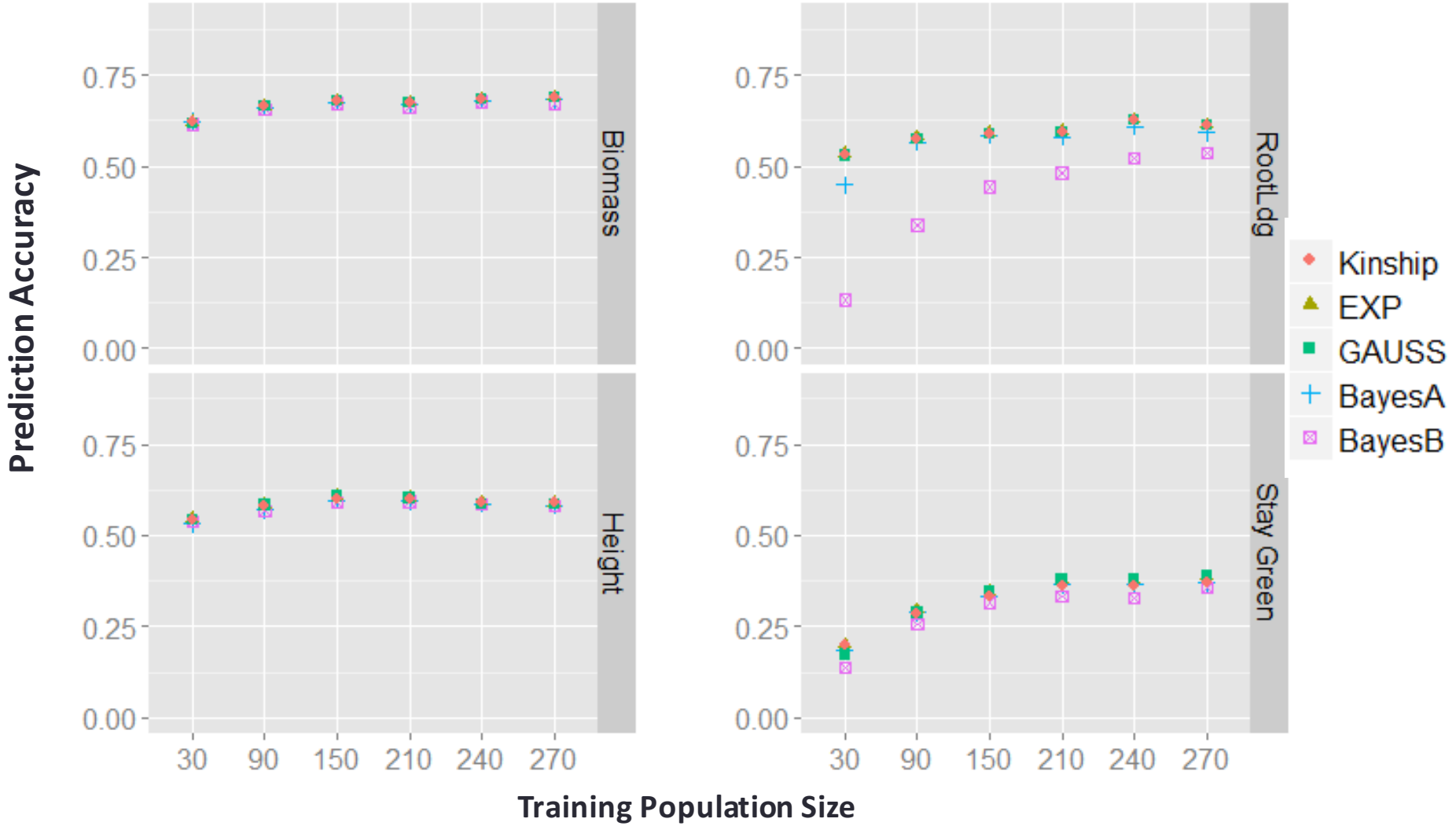


Empirical Findings

# Model Performance

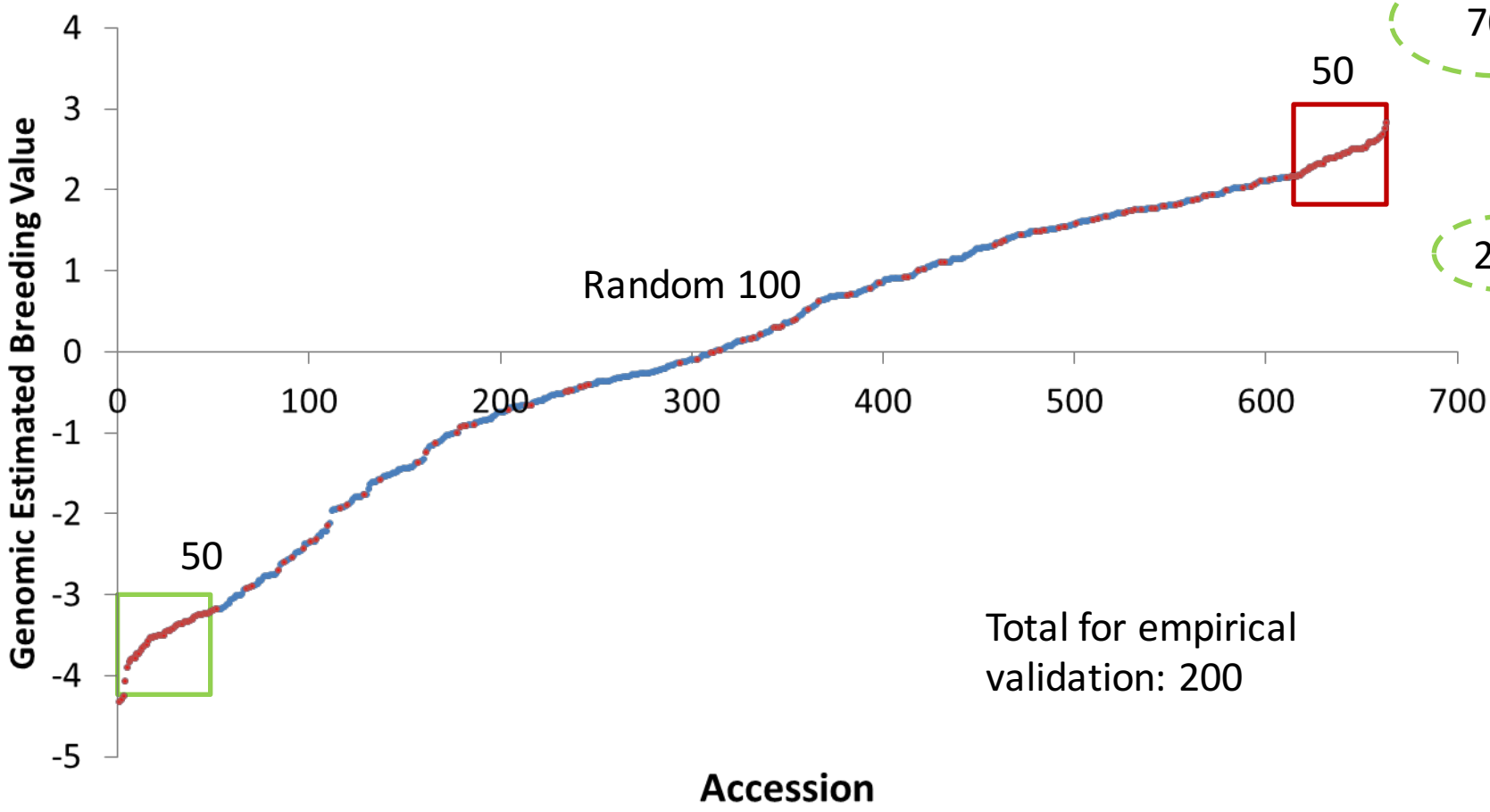
## Evaluated by Cross Validation

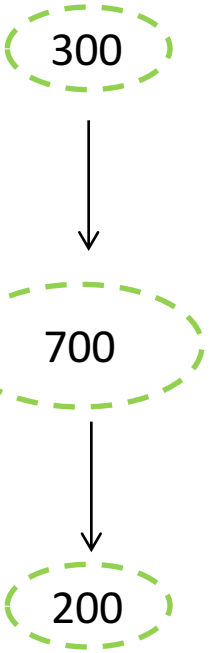
300



Empirical Findings

# Genome-wide Prediction of Unphenotyped Individuals

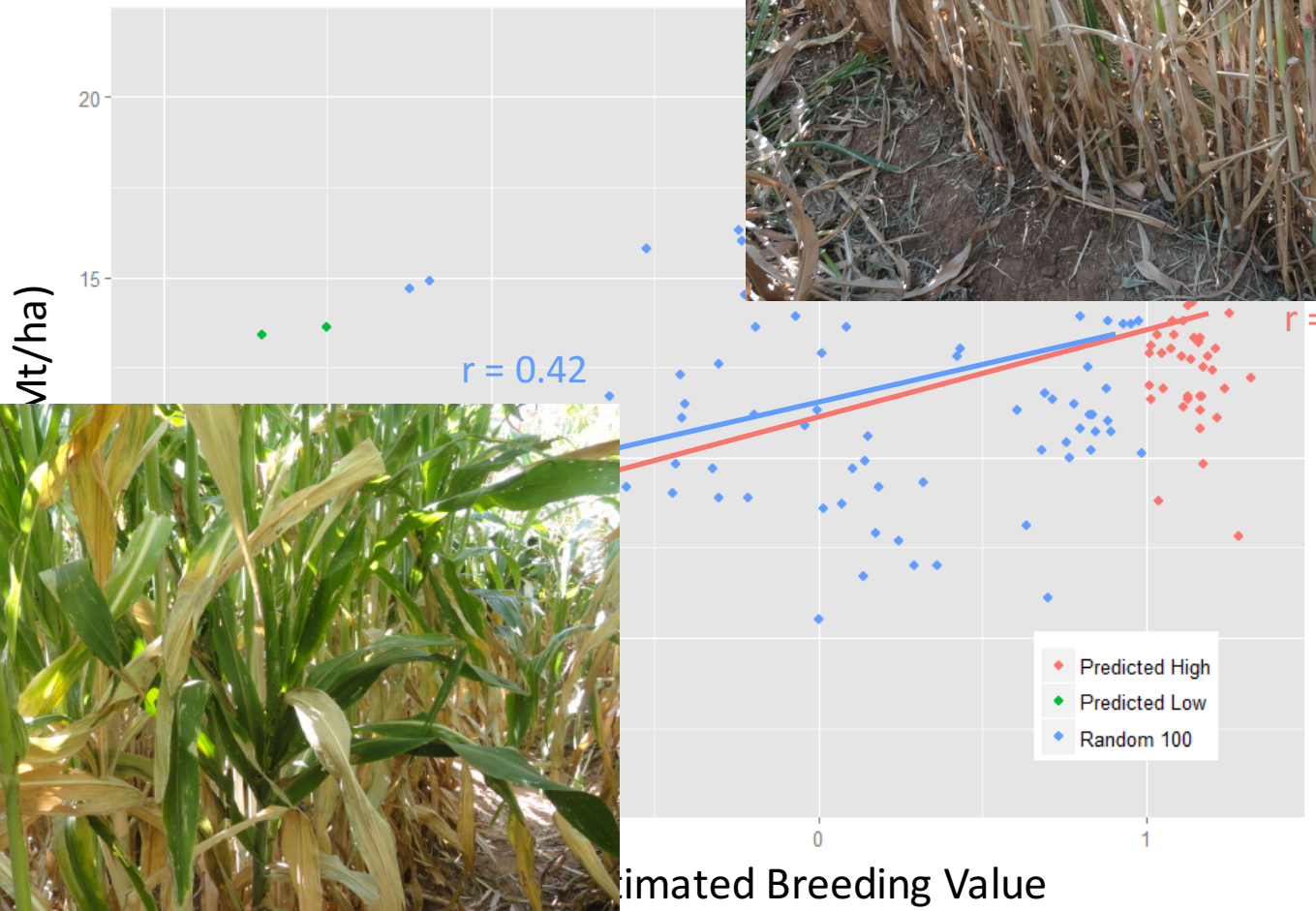



Total for empirical validation: 200

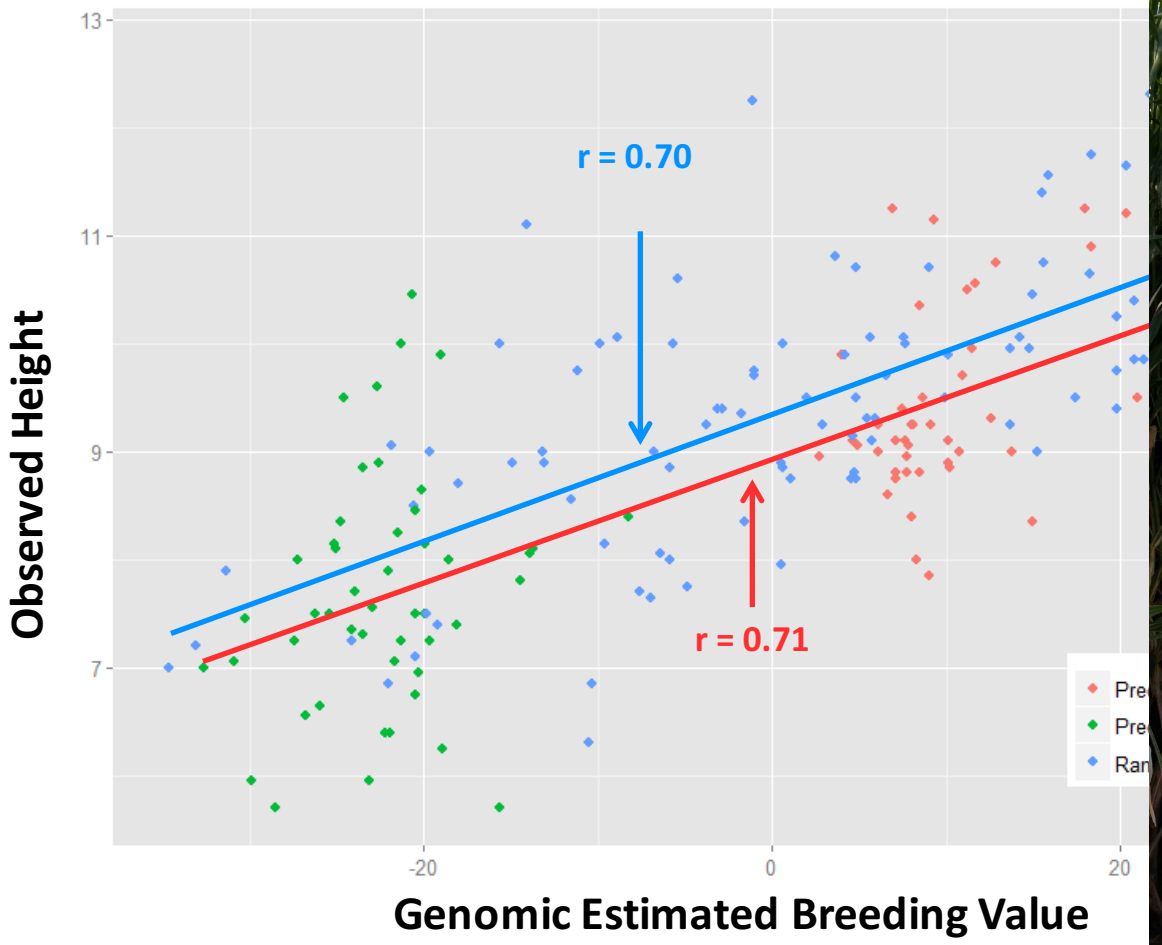
Empirical Findings

# Biomass



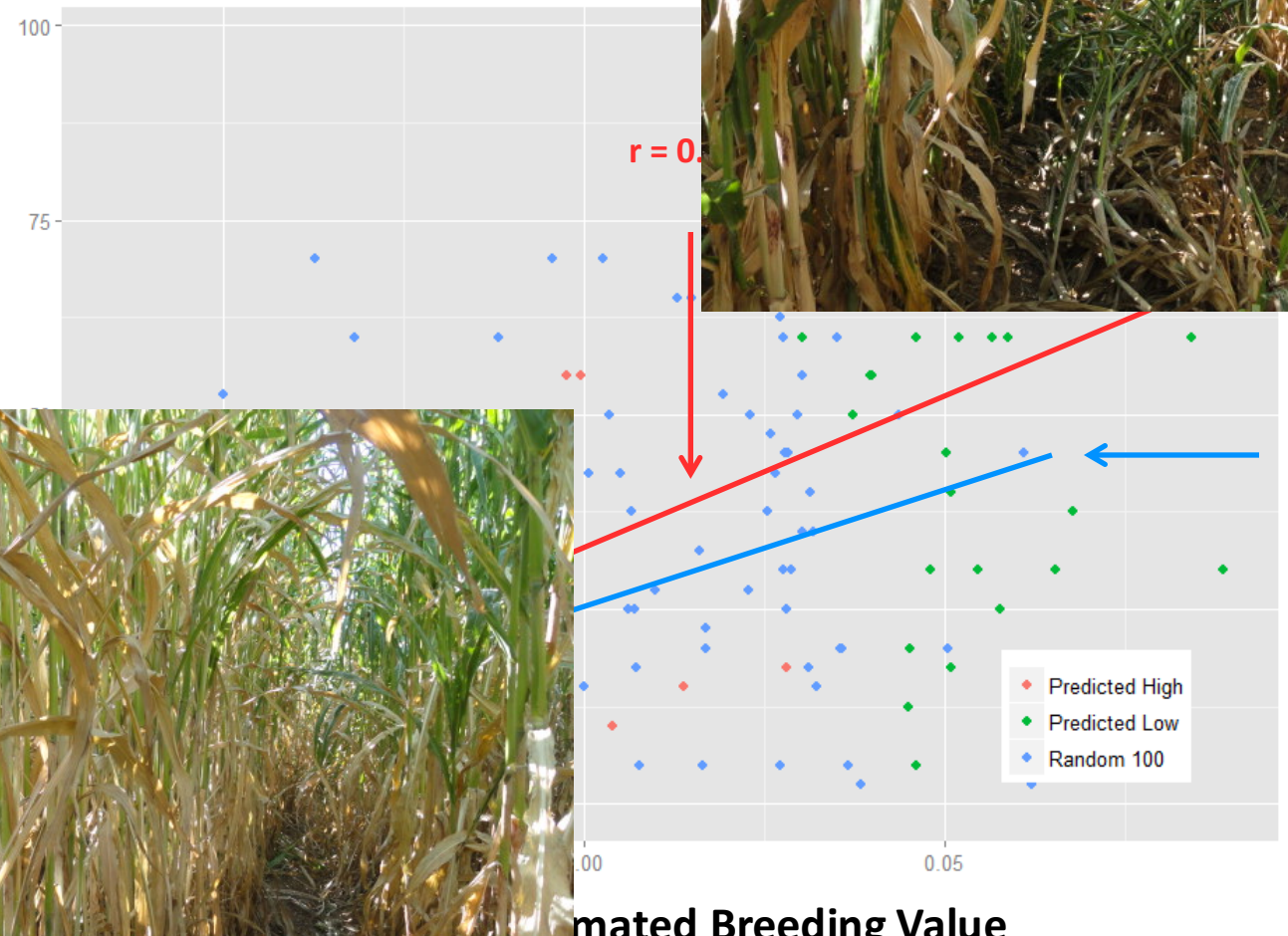
Empirical Findings

# Plant Height



Empirical Findings

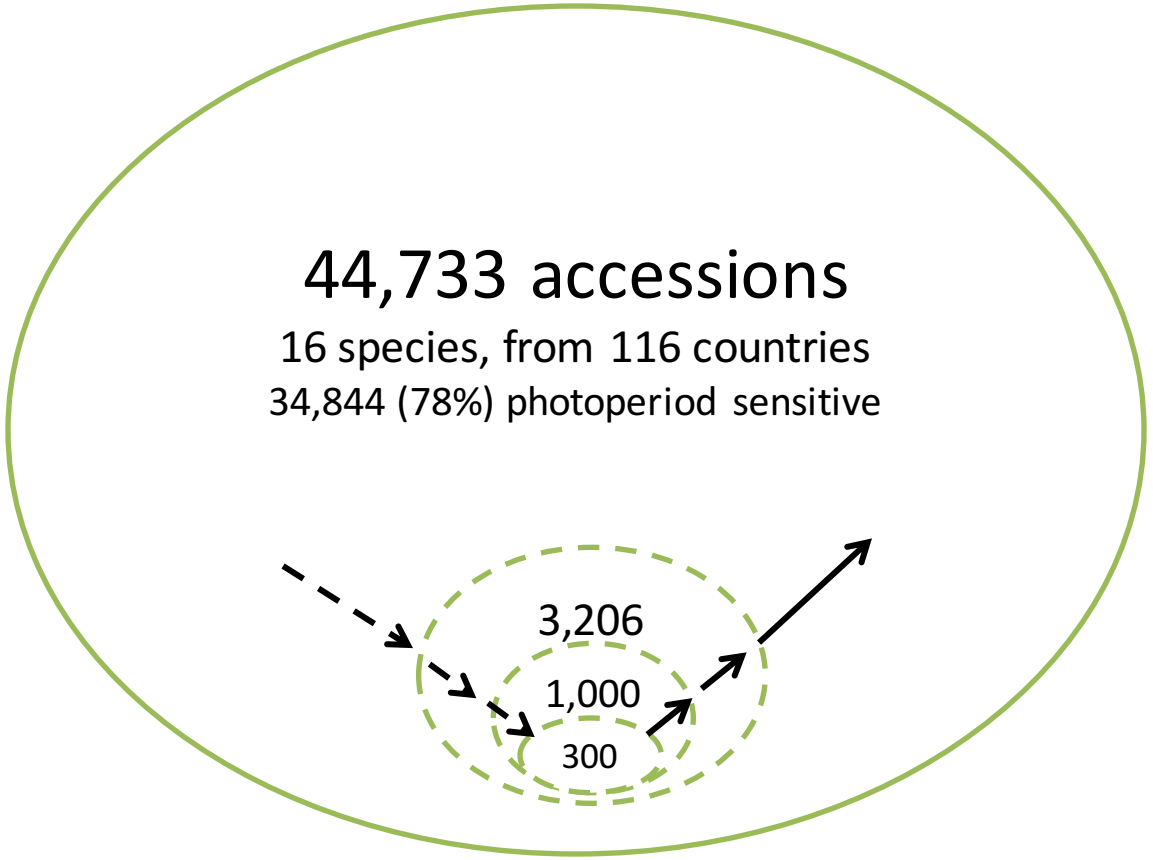
# Root Lo



Bioenergy crops
provide a great opportunity to
implement and test new strategies of
genomics-assisted breeding

Perspectives

# *Why did Things Work out Nicely?*




Germplasm Information
Genotyping-by-Sequencing
Selective Phenotyping
Genome-Wide Prediction
Genome-Wide Association Study

Breeder's Tenet 6: There is a large amount of **additive genetic variance** for most quantitative traits

Perspectives

# Base Population

- Breeder's Tenet 1: Definition and exploitation of **base population** of **environments** and **genotypes**
  - *Is it possible to define the base population of genotypes at the germplasm collection level?*
  - *Is it the right time to GBS all accessions of a species in a gene bank?*
  - *Are we saying that one can generate a potentially functional GS model?*

Perspectives

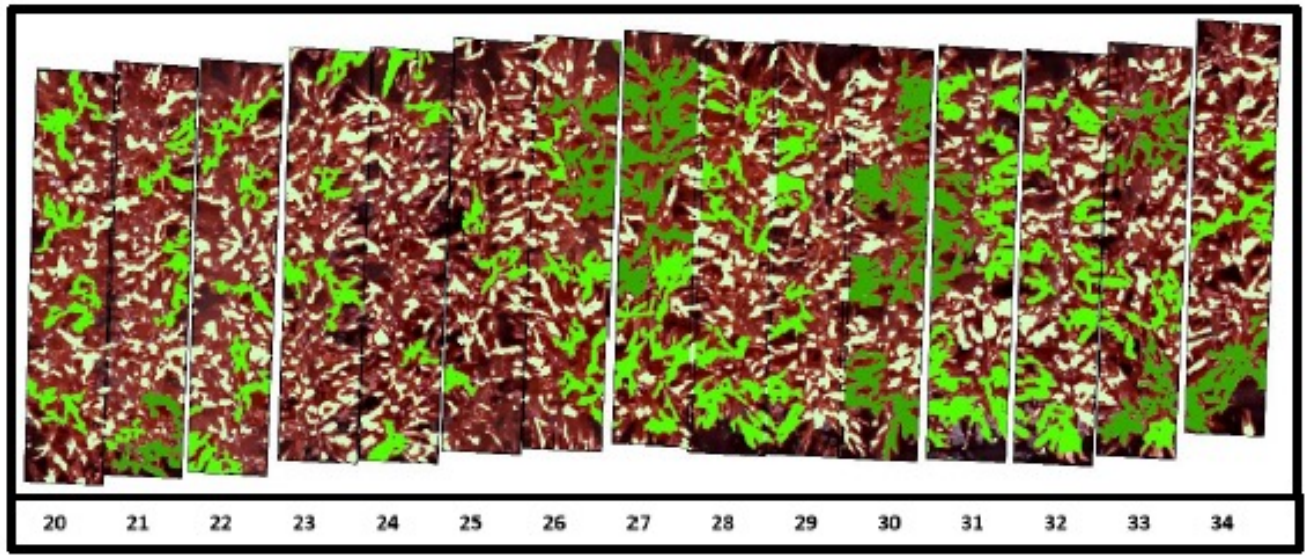
# Phenotyping

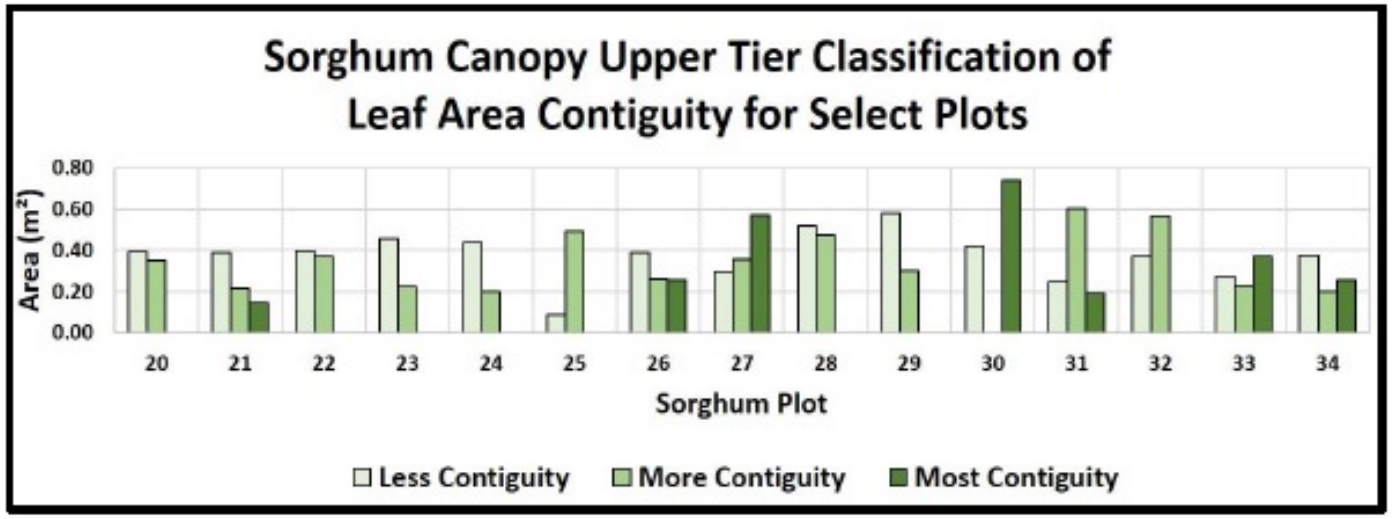
- Breeder's Tenet 3: **Uniform plots** strengthen the association between **phenotype** and **genotype**
- Breeder's Tenet 4. Use of **heritability** of a trait to achieve maximum **gain per year**
  - *Is it important to make sure our phenotypic data for training population reliable? Validation population?*
  - *Can we achieve higher accuracy with High Throughput Phenotying?*
  - *Will there be many startup companies that are focused on generating high accuracy field-level phenotypes?*

Perspectives

AgPixel

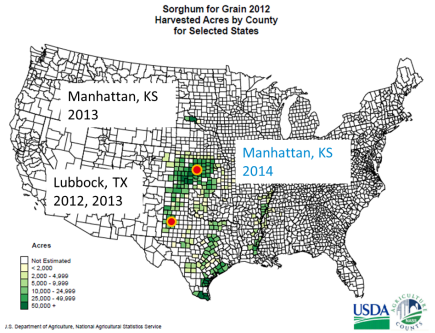
# High Throughput Phenotyping



Perspectives

# Environment

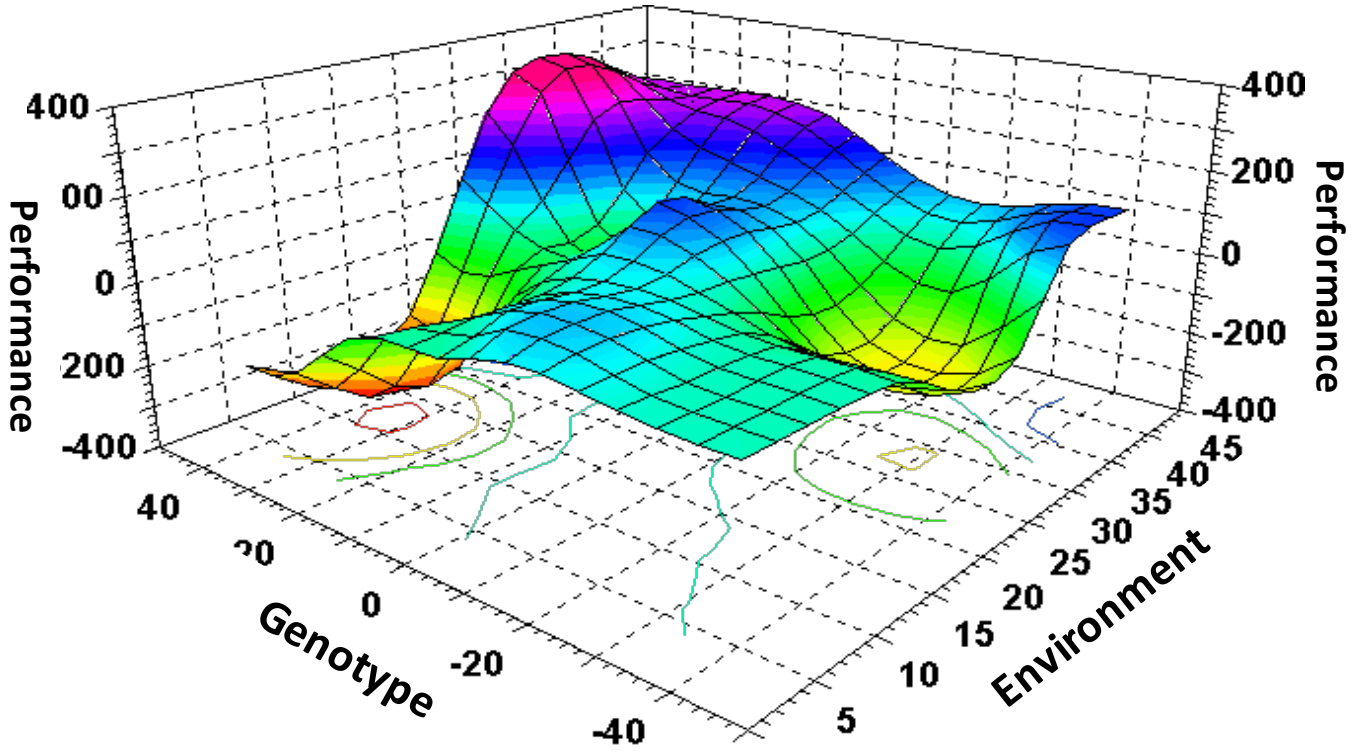



- Breeder's Tenet 8: Include **check genotypes** in breeding experiments and know how you will **analyze** an experiment before you plant it.
  - *Should we rely on environment variables to generate the kernel (variance-covariance) among different environments, particularly training and validation stage?*
  - *Should we include a small subset of training population to mark up the testing environments at validation stage?*

Perspectives

# Optimization

- Breeder's Tenet 1: Definition and exploitation of **base population** of **environments** and **genotypes**



Perspectives

# Optimization, Optimization

- *Are there better algorithms to "design" the training population? Testing sites?*
- *Should we consider this design under a "progressive" context so that the validation information can be used to update the prediction model?*
- *Are there options to "optimize" the validation set?*
- *Should we "embed" checks that capture the GxE dynamics so we are well prepared to deal with uncertainties?*

Perspectives

# Positive Perspectives

- *Is it possible to define the base population of genotypes at the germplasm collection level?*
- *Is it the right time to GBS all accessions of a species in a gene bank?*
- *Are we saying that one can generate a potentially functional GS model?*
- *Is it important to make sure our phenotypic data for training population reliable? Validation population?*
- *Can we achieve higher accuracy with High Throughput Phenotying?*
- *Will there be many startup companies that are focused on generating high accuracy field-level phenotypes?*
- *Should we rely on environment variables to generate the kernel (variance-covariance) among different environments, particularly training and validation stage?*
- *Should we include a small subset of training population to mark up the testing environments at validation stage?*
- *Are there better algorithms to "design" the training population? Testing sites?*
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- *Are there options to "optimize" the validation set?*
- *Should we "embed" checks that capture the GxE dynamics so we are well prepared to deal with uncertainties?*

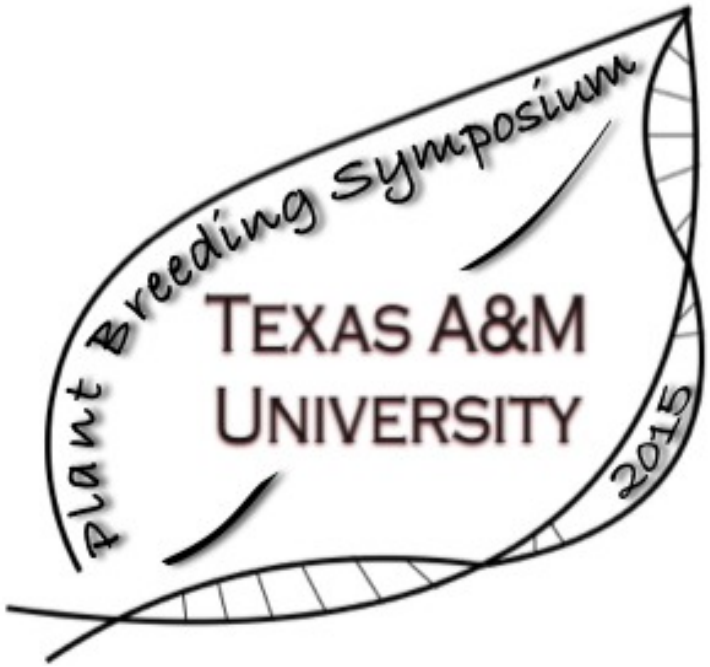
Yes to all these questions!

# Take-home Message

- Genomic Selection is more than a difficult-to-understand equation.

***What is Genomic Selection?***

- Genomic Selection is a tool/strategy in plant breeding. Itself and the whole process of plant breeding is being, and can be further optimized.




# Question & Answer Session

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