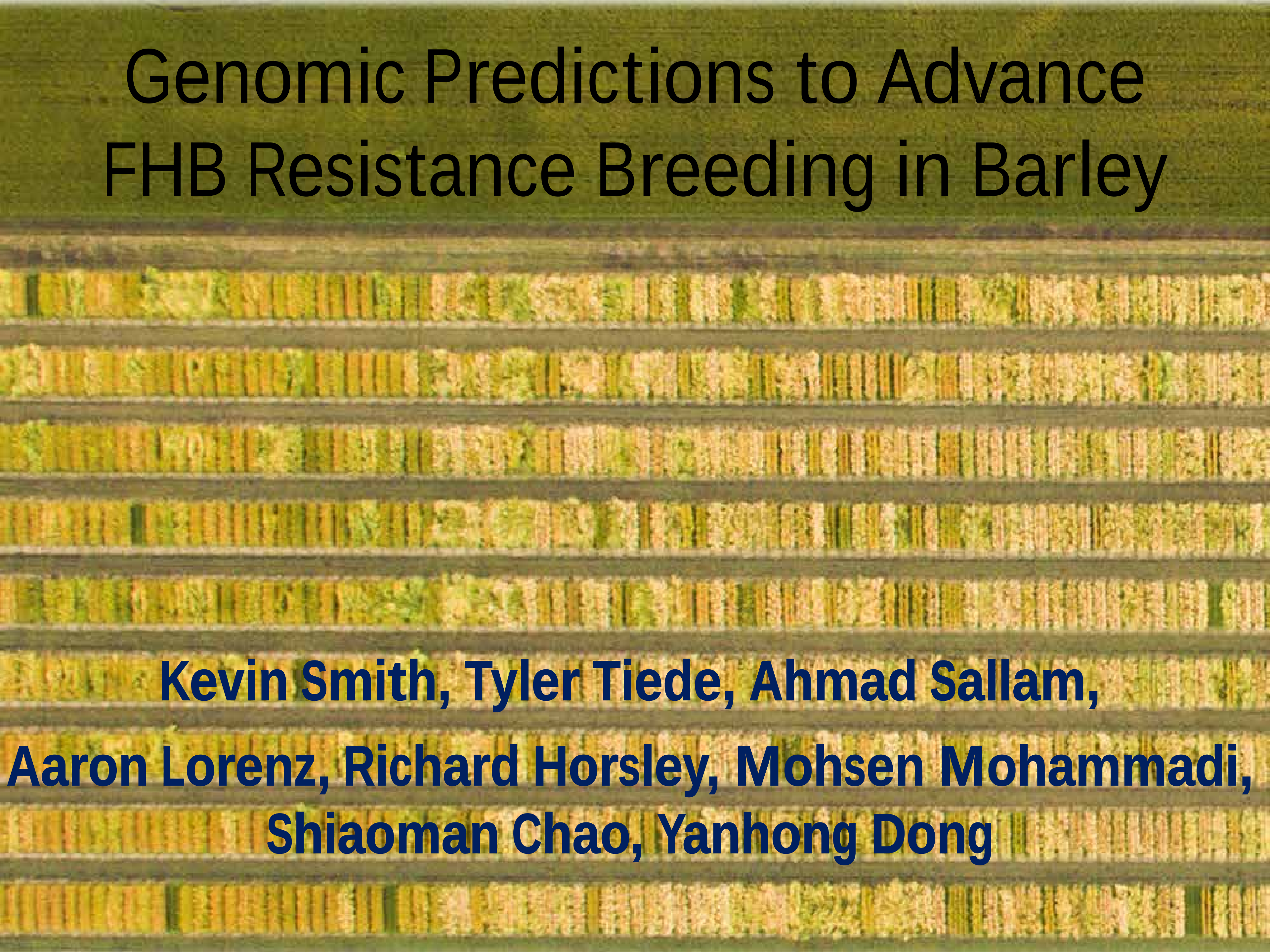


Genomic Predictions to Advance FHB Resistance Breeding in Barley

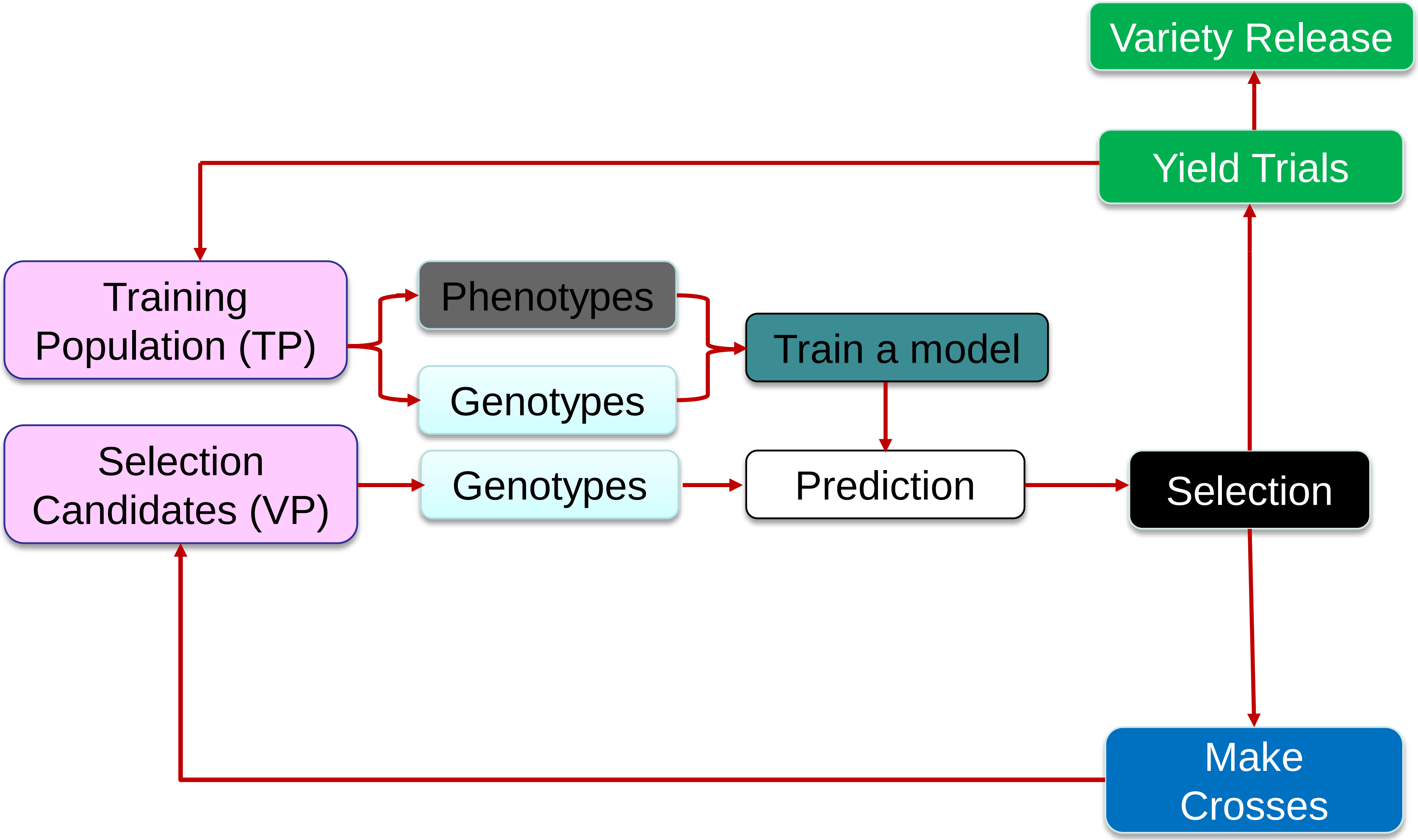
Kevin Smith, Tyler Tiede, Ahmad Sallam,
Aaron Lorenz, Richard Horsley, Mohsen Mohammadi,
Shiaoman Chao, Yanhong Dong

Photo: Brian Steffenson

Genomic Predictions to Advance FHB Resistance Breeding in Barley

Comparing Phenotypic Selection to Genomic Selection
Optimizing Training Population
Realized Gains
Predicting Variance

Genomic selection (GS)


Variety Release

Yield Trials

Training Population (TP)

Phenotypes

Genotypes

Train a model

Selection Candidates (VP)

Genotypes

Prediction

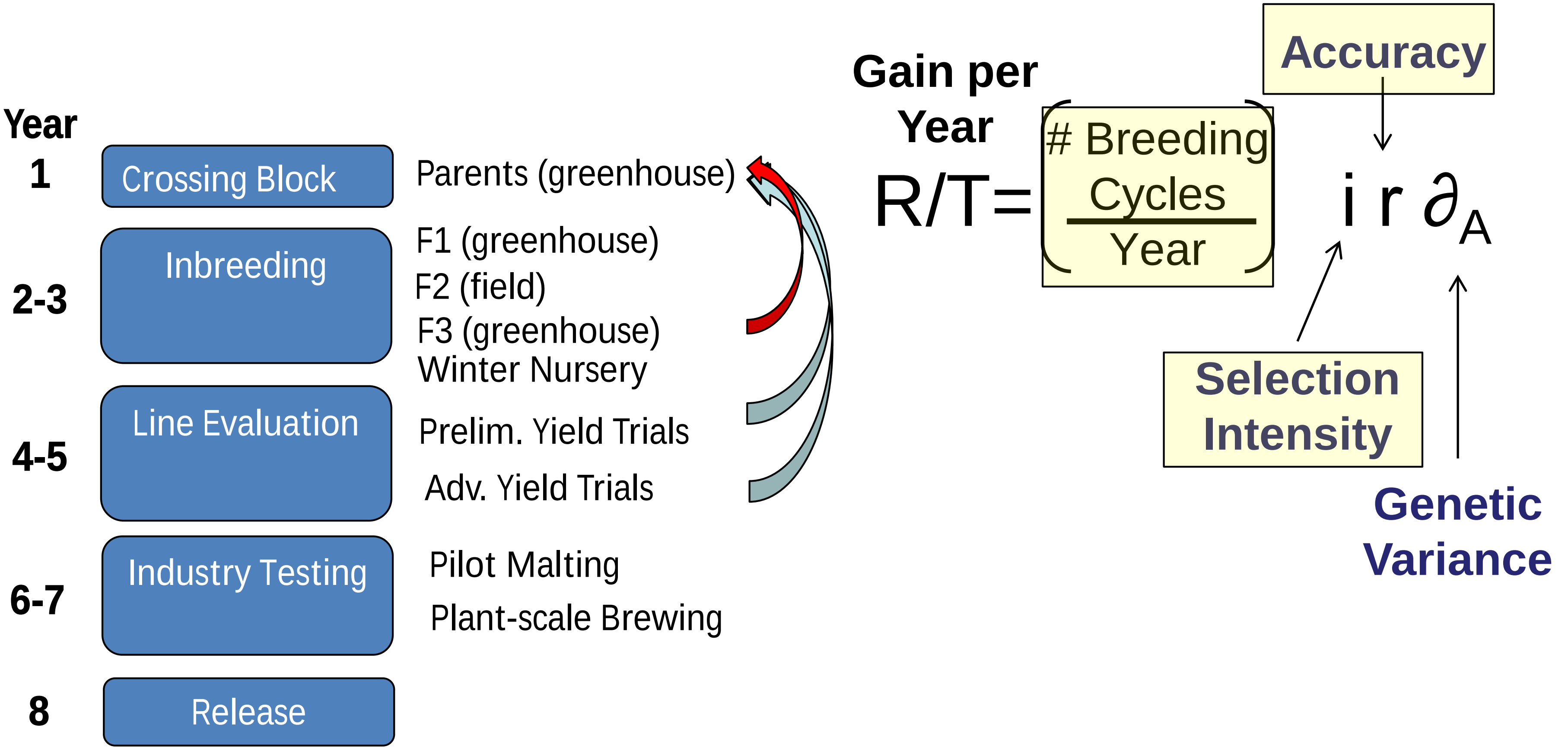
Selection

Make Crosses

Genomic Prediction Accuracy

Marker Density / Distribution
Training Population Size
Prediction Model
Training Population Composition
Training Population Environments (GxE)

Genomic Selection



Year		
1	Crossing Block	Parents (greenhouse)
2-3	Inbreeding	F1 (greenhouse) F2 (field) F3 (greenhouse) Winter Nursery
4-5	Line Evaluation	Prelim. Yield Trials Adv. Yield Trials
6-7	Industry Testing	Pilot Malting Plant-scale Brewing
8	Release	

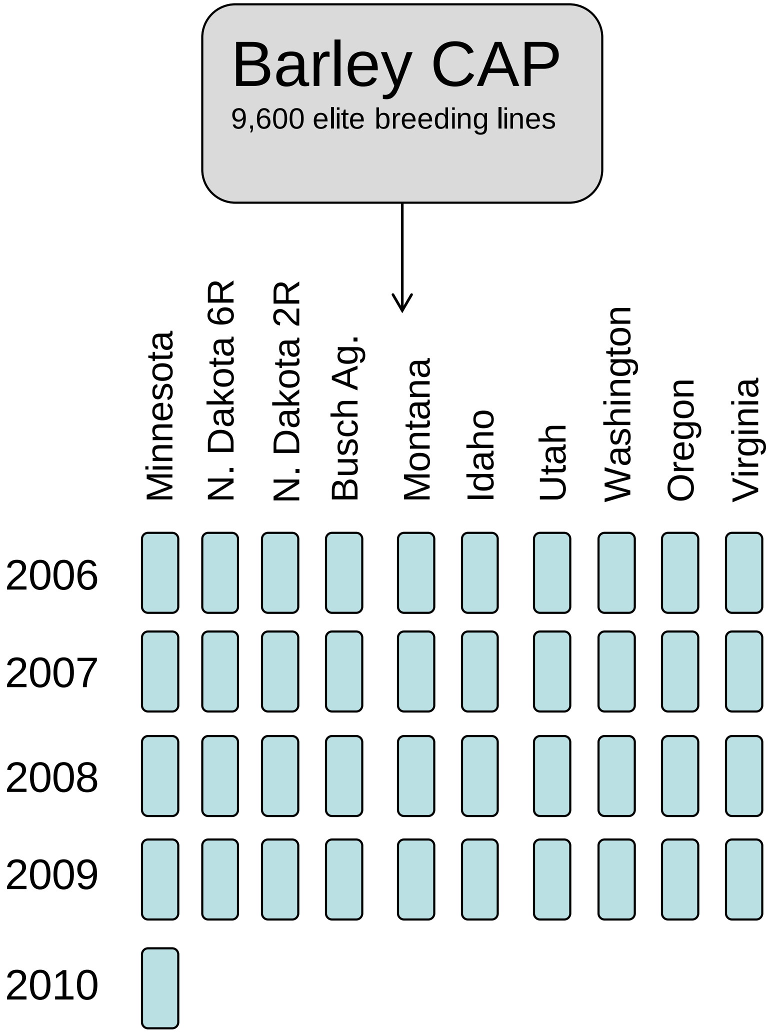
Gain per Year

$$R/T = \left(\frac{\#\ \text{Breeding Cycles}}{\text{Year}}\right) \quad i\ r\ \partial_A$$

Accuracy

Selection Intensity

Genetic Variance



Barley CAP

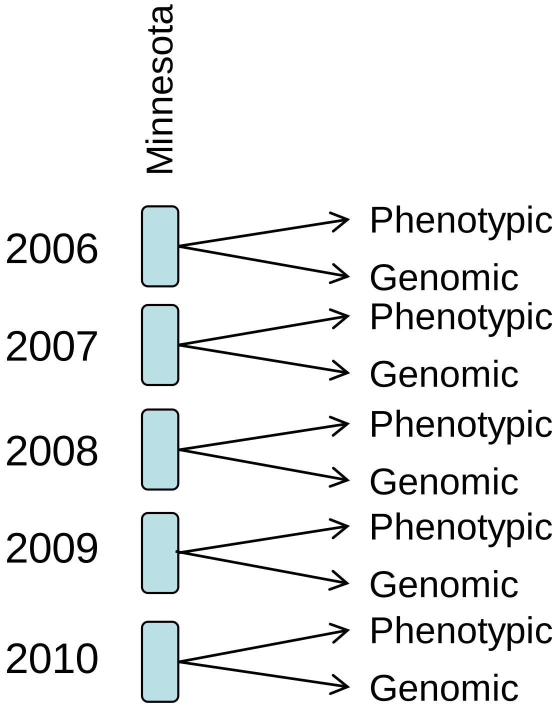
9,600 elite breeding lines

Minnesota
N. Dakota 6R
N. Dakota 2R
Busch Ag.
Montana
Idaho
Utah
Washington
Oregon
Virginia

2006
2007
2008
2009
2010

Barley CAP
10 Breeding Programs
96 entries per program per year
4 years
Genotyped: 3,072 SNP markers
Phenotyped: over 40 traits (FHB and DON)

Comparing Phenotypic (PS) to Genomic (GS) Selection



Selection Candidates (96 per year)

Selected Individuals (10 per year)

Minnesota

2006
Phenotypic
Genomic

2007
Phenotypic
Genomic

2008
Phenotypic
Genomic

2009
Phenotypic
Genomic

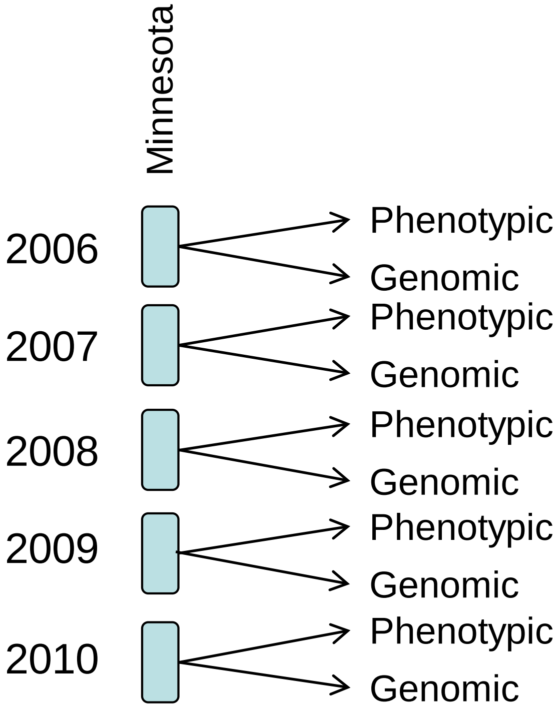
2010
Phenotypic
Genomic

Phenotypic Selection
2 trials in misted/inoculated nurseries
2 replicate per trial

Genomic Selection
Training Pop 186 breeding lines (parents to SC)
3 trials in misted/inoculated nurseries
1 replicate per trial
3072 SNP markers
RR-BLUP

Comparison Experiment
4 trials in misted/inoculated nurseries
1 replicate per trial wit repeated checks

Comparing Phenotypic (PS) to Genomic (GS) Selection



Selection Candidates (96 per year)

Selected Individuals (10 per year)

Minnesota

2006
Phenotypic
Genomic

2007
Phenotypic
Genomic

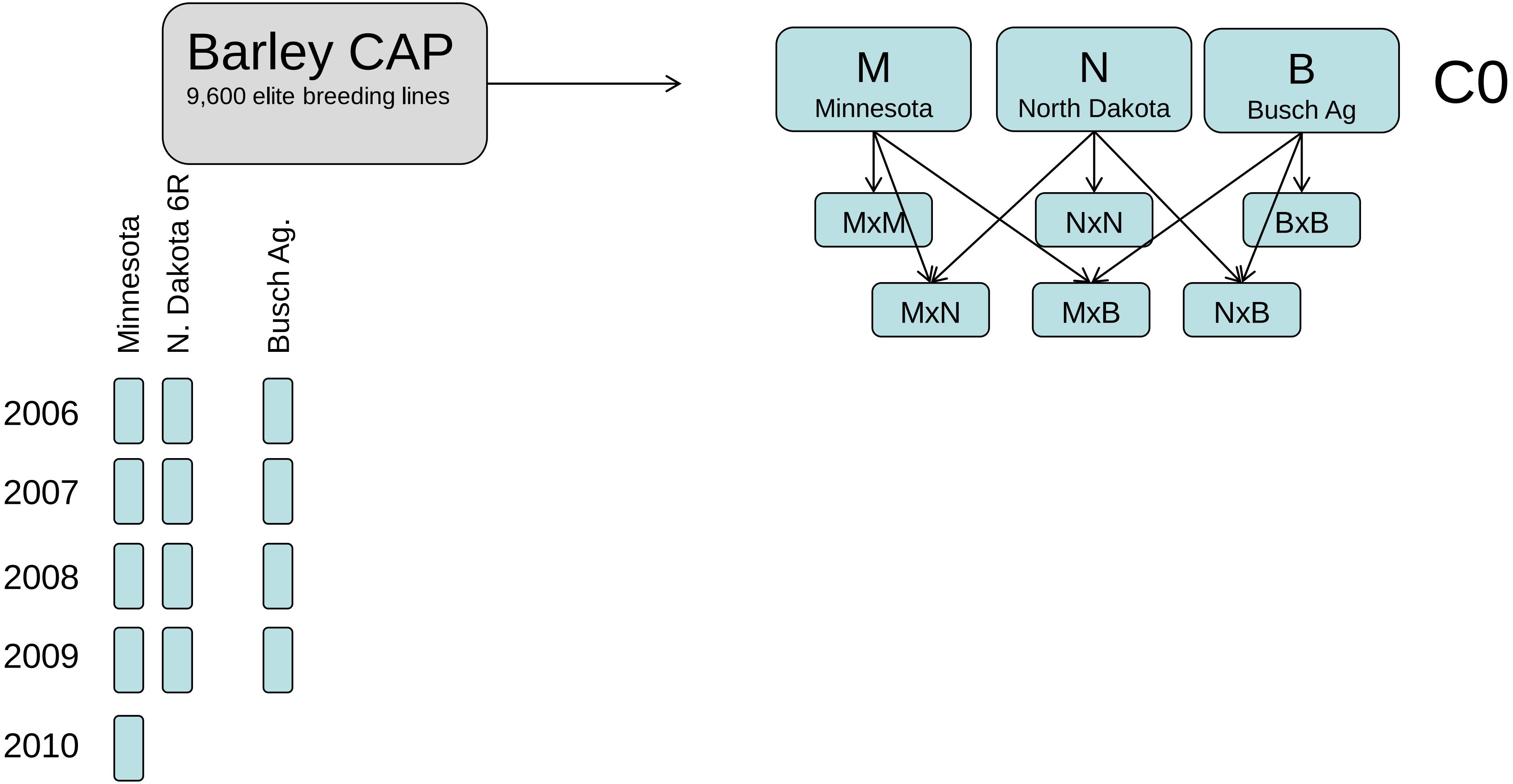
2008
Phenotypic
Genomic

2009
Phenotypic
Genomic

2010
Phenotypic
Genomic

Selection Method	**FHB severity (%)**	**DON (ppm)**
Sel. Candidates	19.6a	29.1a
Genomic	17.1 b	22.3 b
Phenotypic	17.5 b	23.5 b

Sallam et al., 2016 (in review)



Barley CAP

9,600 elite breeding lines

Minnesota | N. Dakota 6R | Busch Ag.

2006

2007

2008

2009

2010

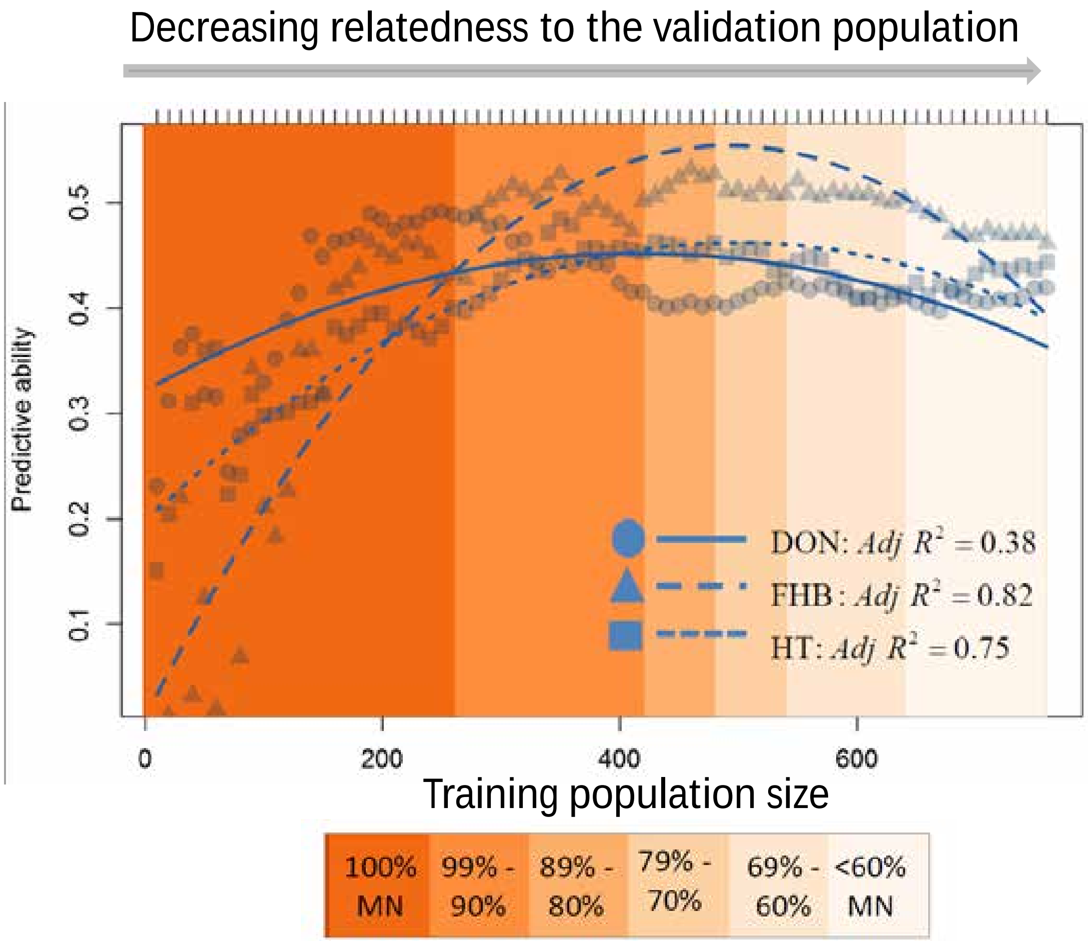
M
Minnesota

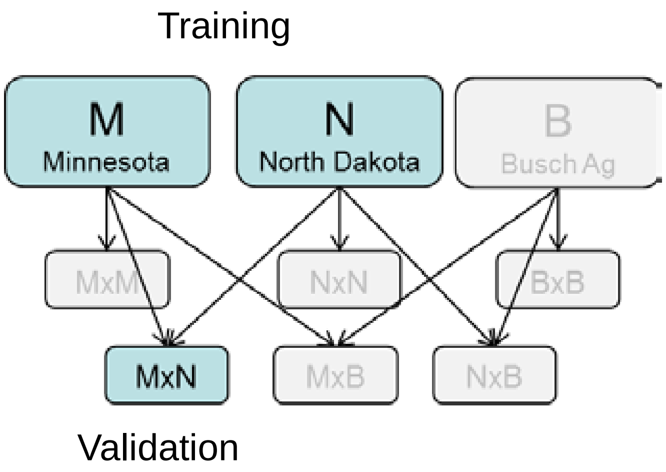
N
North Dakota

B
Busch Ag

C0

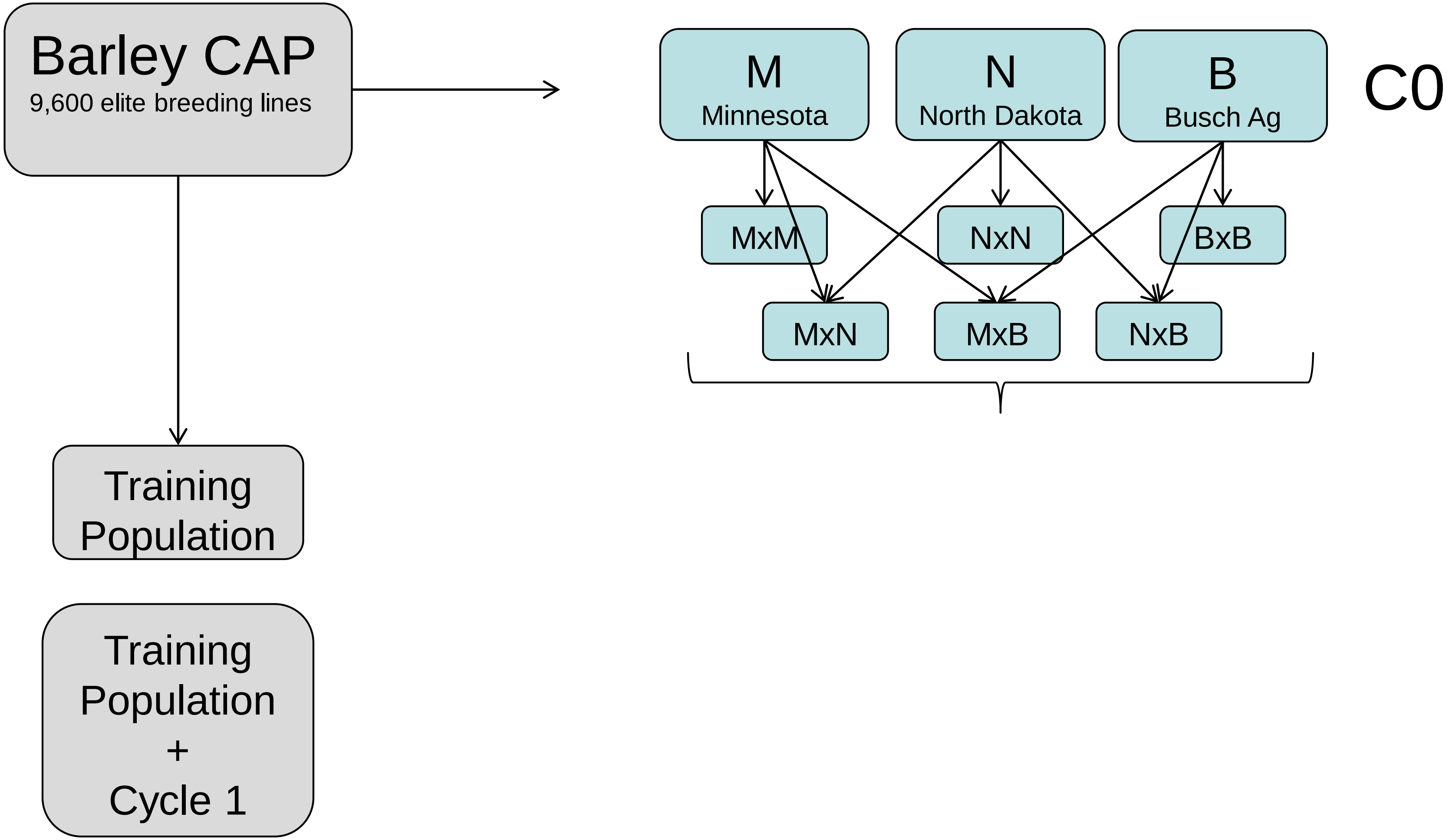
Training Population Composition





Lorenz and Smith, 2015 Crop Sci

Prediction accuracy is greatest when the training population is related to the validation population



Barley CAP

9,600 elite breeding lines

M
Minnesota

N
North Dakota

B
Busch Ag

C0

MxM

NxN

BxB

MxN

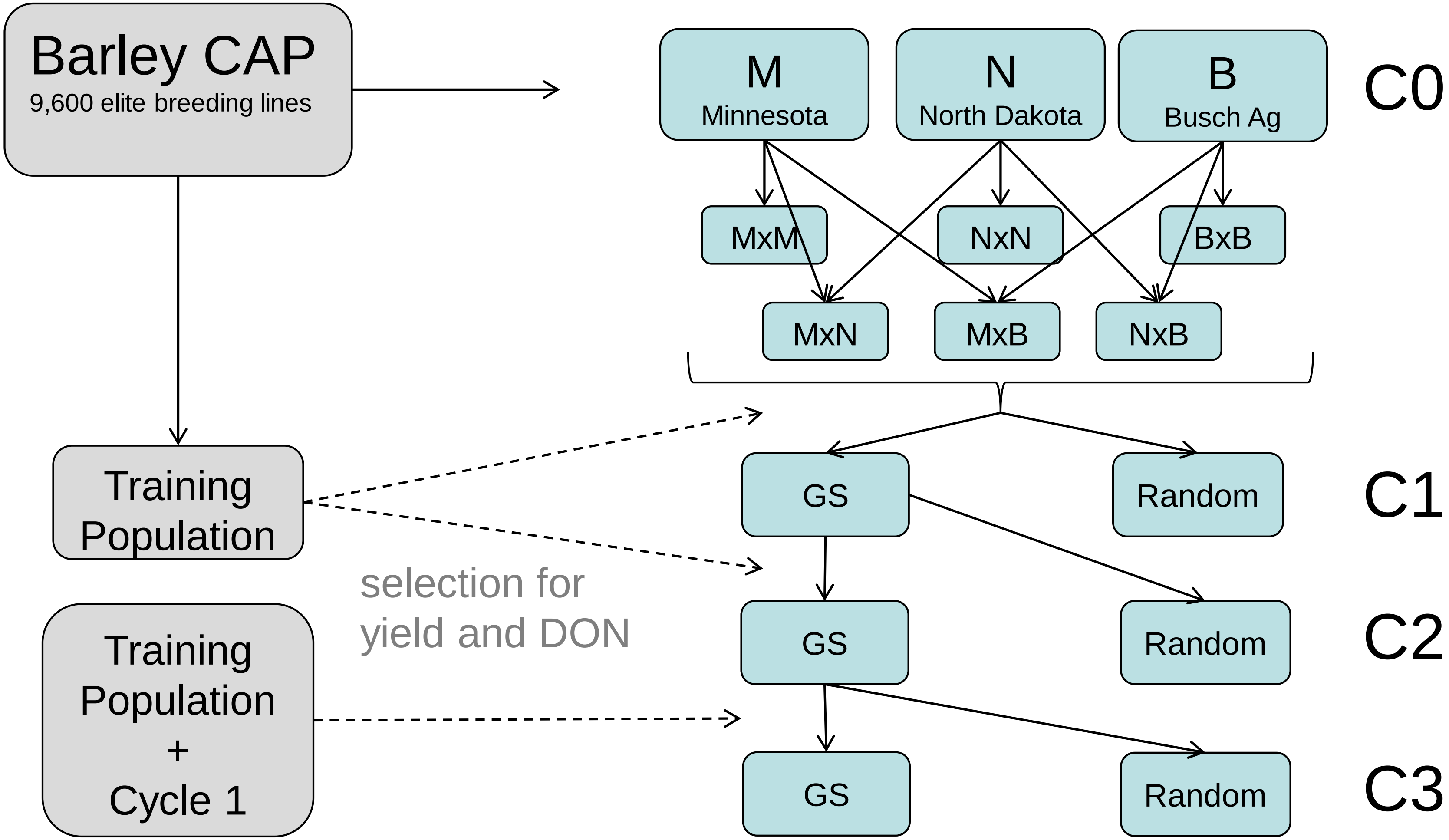
MxB

NxB

Training Population

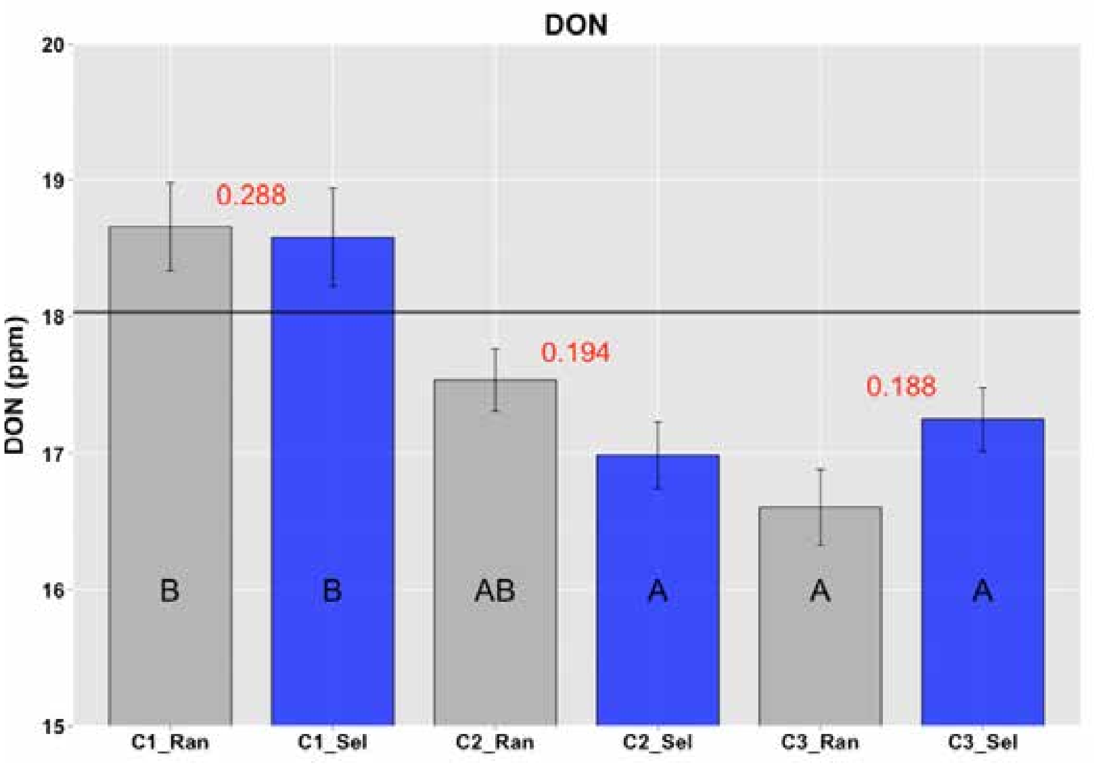
Training Population
+
Cycle 1

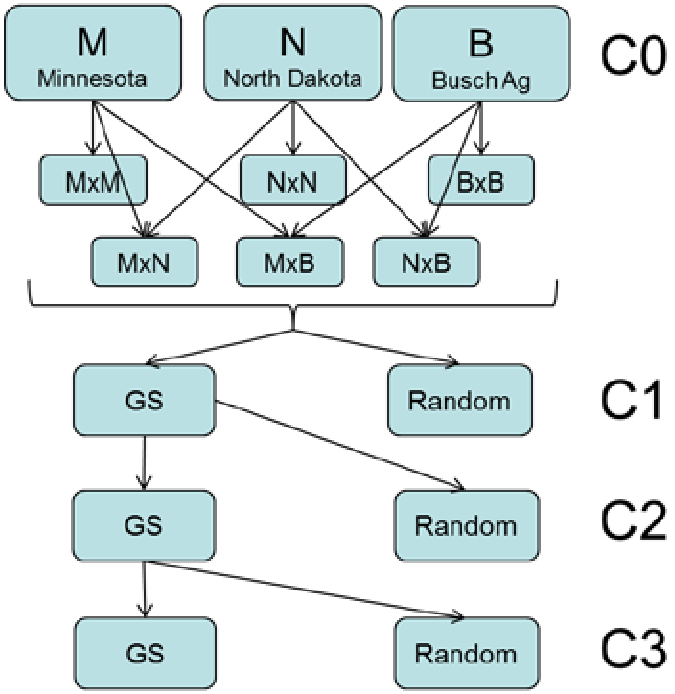
Gain From Selection (3 cycles)



selection for yield and DON

Gain From Selection for DON (3 cycles)




M
Minnesota

N
North Dakota

B
Busch Ag

C0

MxM
NxN
BxB
MxN
MxB
NxB

GS
Random
C1

GS
Random
C2

GS
Random
C3

Tiede et al, (in prep)

Implementing Genomic Selection

Year		
1	Crossing Block	Parents (greenhouse)
2-3	Inbreeding	F1 (greenhouse) F2 (field) F3 (greenhouse) Winter Nursery
4-5	Line Evaluation	Prelim. Yield Trials Adv. Yield Trials
6-7	Industry Testing	Pilot Malting Plant-scale Brewing
8	Release	

Early Generation - FHB

<u>Phenotypic Evaluation</u>

Disease Nurseries

Yield trials

Malting Quality

Implementing Genomic Selection

Year		
1	Crossing Block	Parents (greenhouse)
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8	Release	

Genomic Predictions

Phenotypic Evaluation

Disease Nurseries

Yield trials

Malting Quality

Implementing Genomic Selection

Year		
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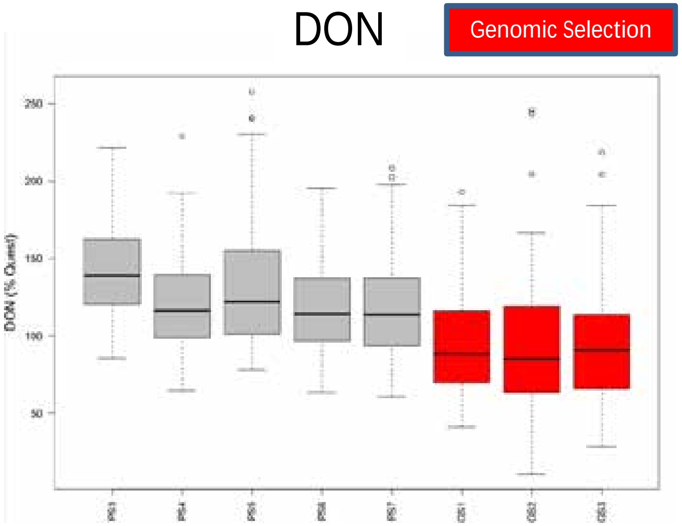
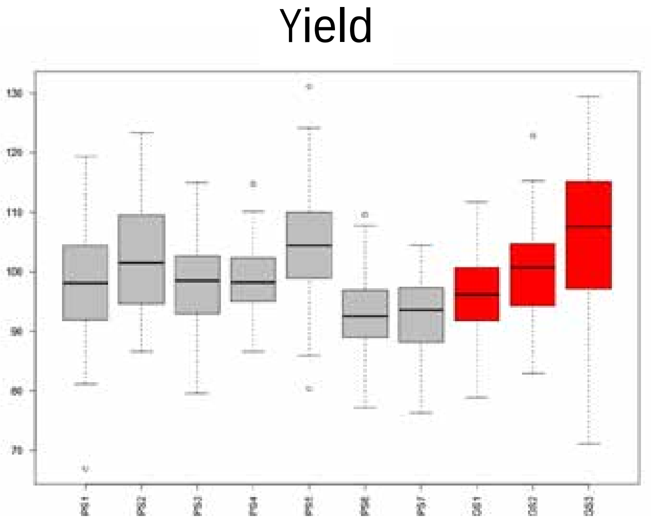
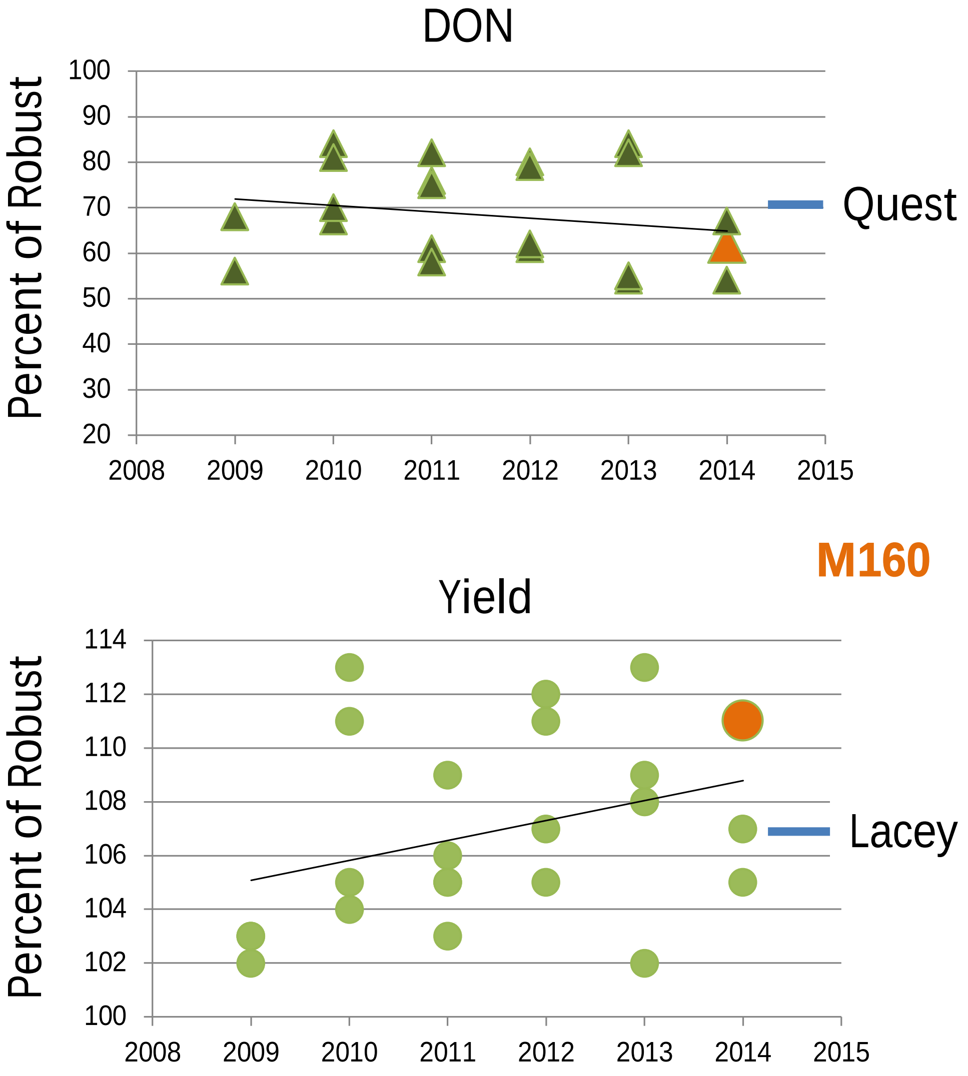
2-3	Inbreeding	F1 (greenhouse) F2 (field) F3 (greenhouse) Winter Nursery
4-5	Line Evaluation	**Prelim. Yield Trials** Adv. Yield Trials
6-7	Industry Testing	Pilot Malting Plant-scale Brewing
8	Release	



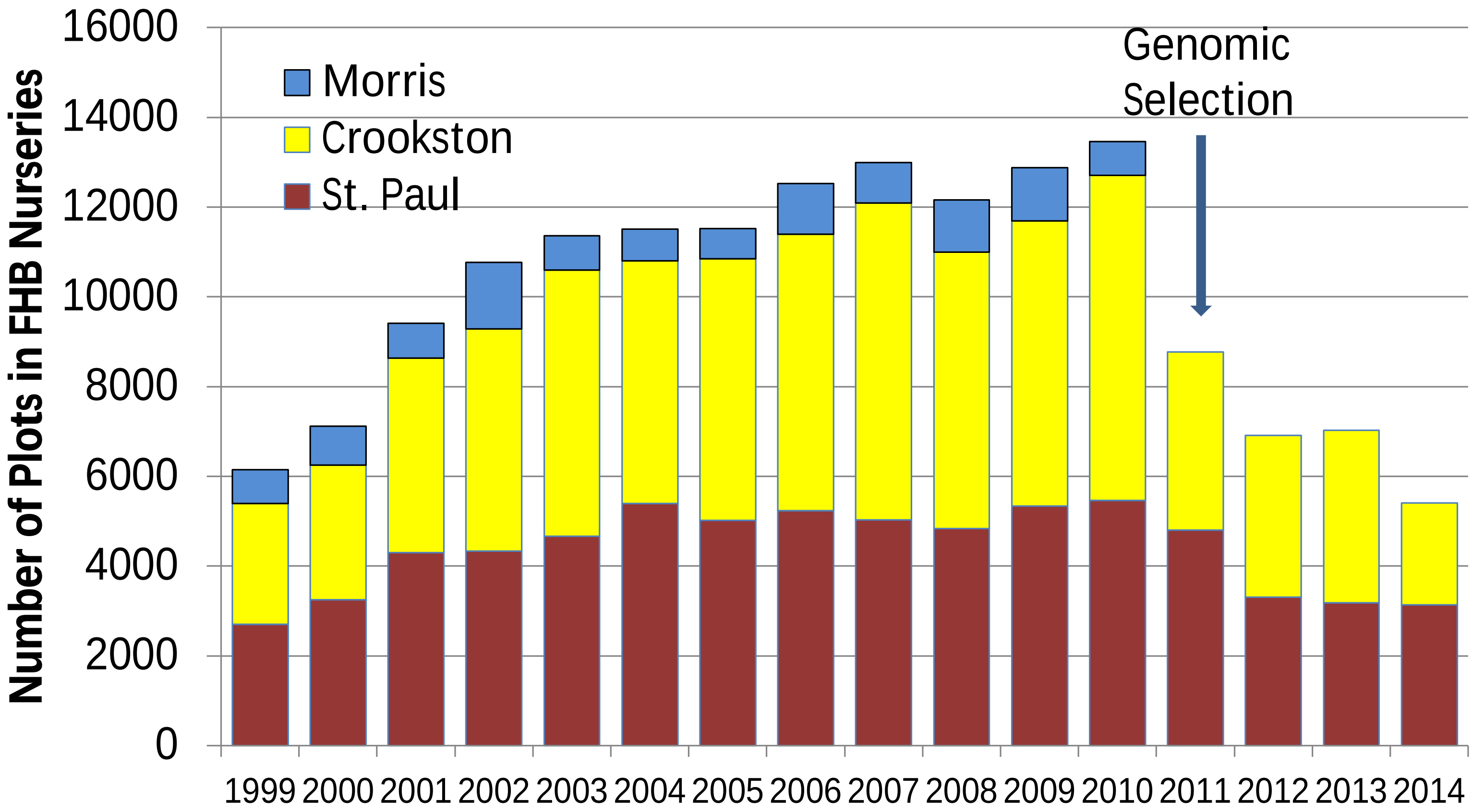


Implementing Genomic Selection

Year		
1	Crossing Block	Parents (greenhouse)
2-3	Inbreeding	F1 (greenhouse) F2 (field) F3 (greenhouse) Winter Nursery
4-5	Line Evaluation	Prelim. Yield Trials Adv. Yield Trials
6-7	Industry Testing	**Pilot Malting** Plant-scale Brewing
8	Release	



Genomic selection has reduced the field resources for disease screening



Genomic Selection

Year		
1	Crossing Block	Parents (greenhouse)
2-3	Inbreeding	F1 (greenhouse) F2 (field) F3 (greenhouse) Winter Nursery
4-5	Line Evaluation	Prelim. Yield Trials Adv. Yield Trials
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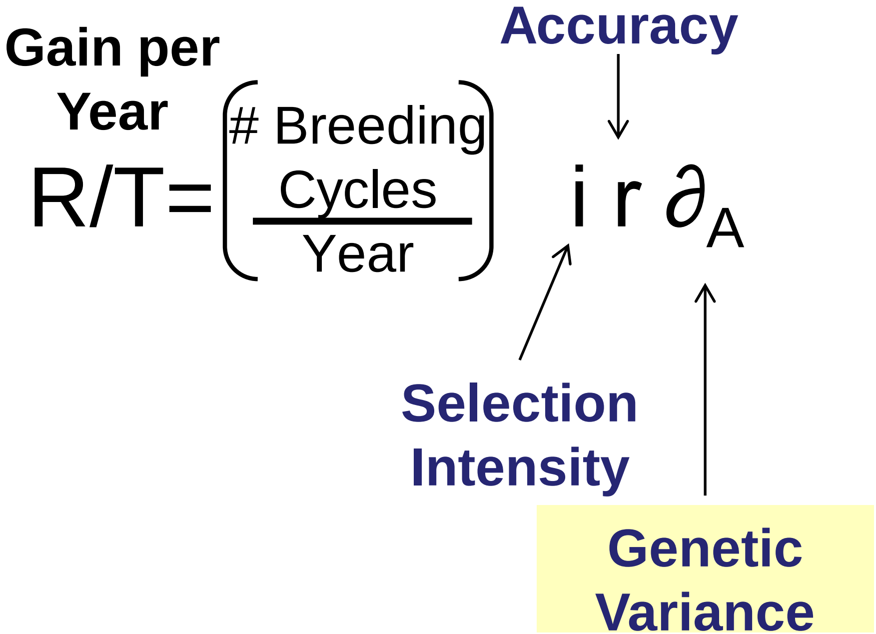


Gain per Year

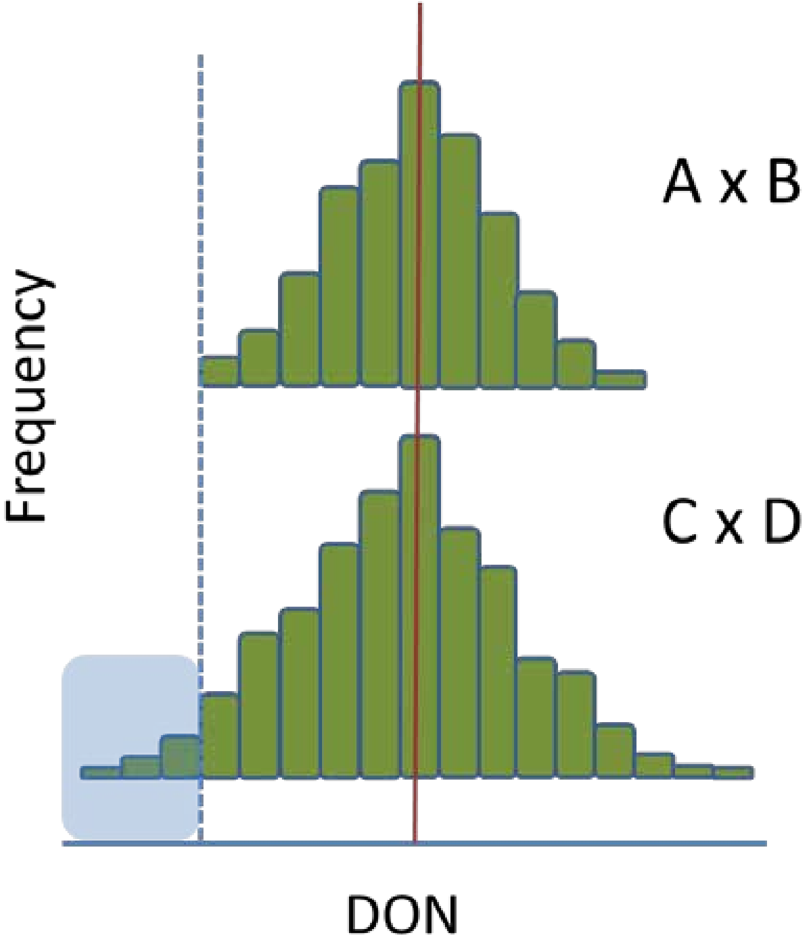
$$R/T = \left(\frac{\text{\# Breeding Cycles}}{\text{Year}} \right) \; i \; r \; \partial_A$$

Accuracy

Selection Intensity

Genetic Variance

Maximizing Genetic Variance



Both crosses have the same mid-parent and population mean

…. but different variances

Maximizing Genetic Variance

PopVar: R package that predicts the genetic variance of crosses between two parents

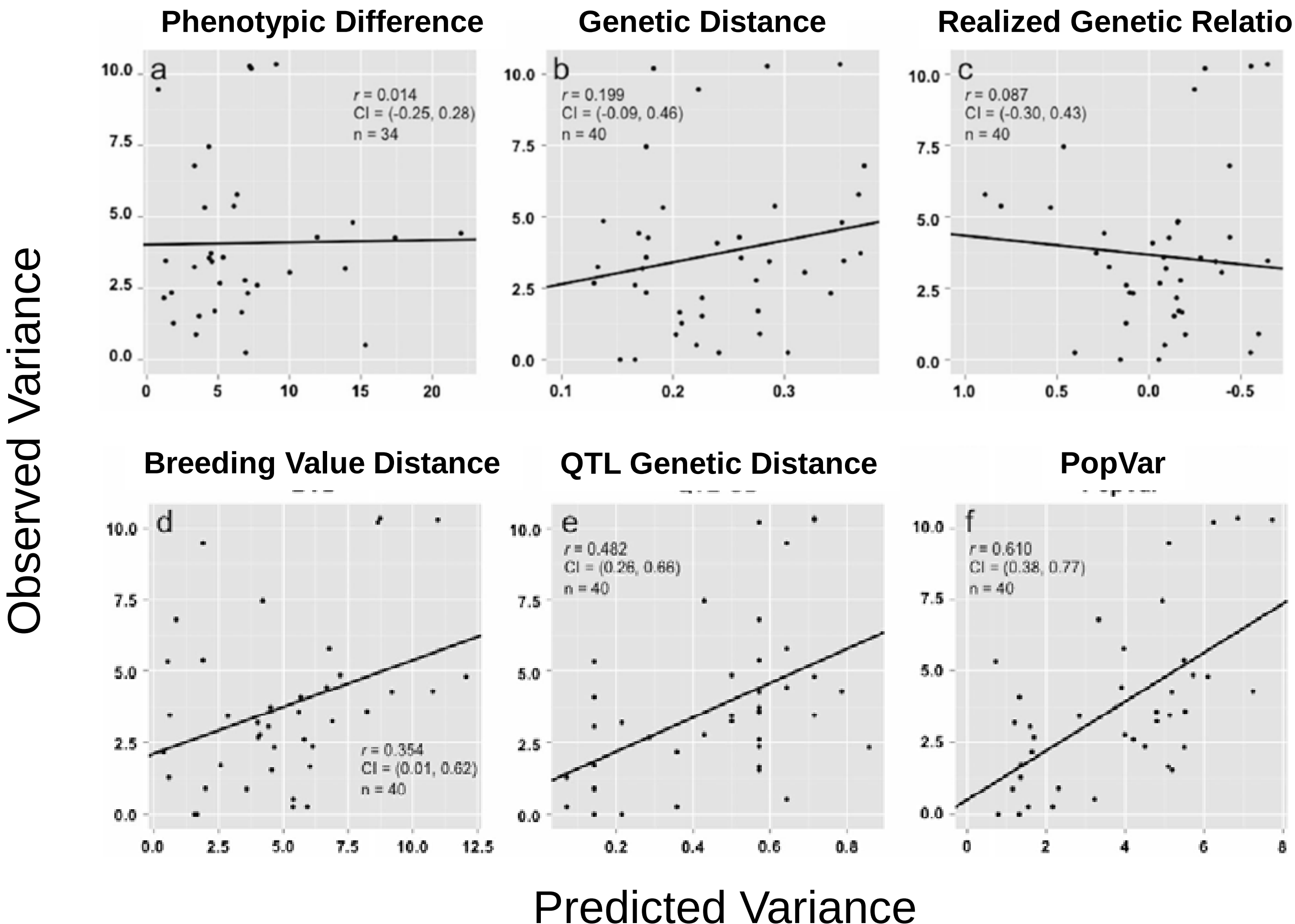
- Training Population -> estimate marker effects
- Genotype Parents
- Simulate RIL progeny for each cross combination
- Obtain GEBV for each progeny
- Calculate predicted variance & mean of best 10%
- Calculates correlation among GEBVs for multiple traits

Mohammadi et al., 2015 Crop Sci 55:2068–2077.

Predicting the Genetic Variance of FHB Severity

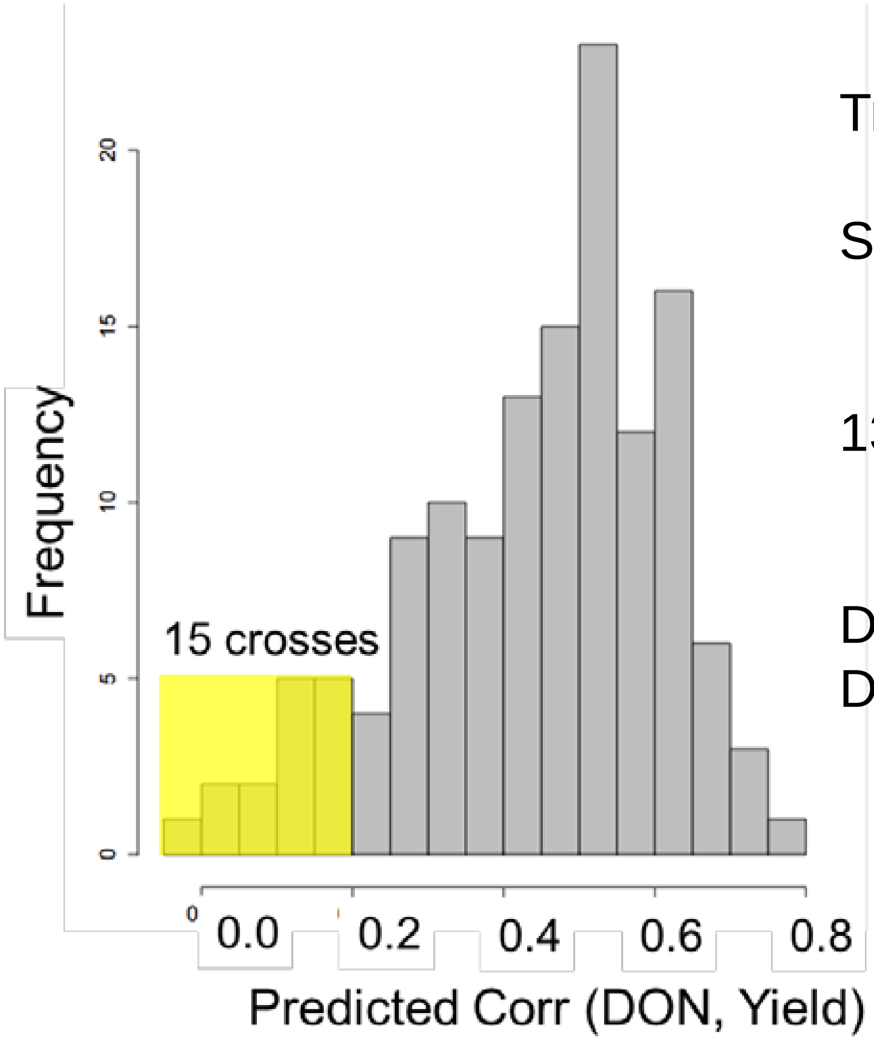
40 bi-parental breeding populations evaluated 2003–2010
FHB severity data collected in misted and inoculated nurseries
2 Locations, 2 reps per location, RCB design

Predicting the Genetic Variance of FHB Severity



Tiede et al., 2015. Mol. Breeding

Using PopVar to reduce negative trait correlation



Training Pop = 168 MN breeding Lines

Simulate ALL 13,600 cross combinations
DON range: 16–31 ppm (cross means)

136 populations (1% lowest DON)
DON range: 16-19 ppm (cross means)

Distribution of correlations between DON and yield

Tiede et al., 2015. Mol. Breeding

Take Home

- GS is about as effective as PS for selecting for FHB severity and DON
- Optimizing the training population - greatest opportunity to improve selection accuracy
- Implementing GS allows reallocation of resources
- Potential to use genome-wide marker effects to predict favorable parent combinations.
- Future expanding the number of traits that are predicted

Project Members / Key Collaborators

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Shiaoman Chao, USDA Fargo;
Joshua Butler, Busch Ag. Res., Inc
Jean-Luc Jannink, USDA

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American
Malting
Barley
Association

MnDrive

USDA | NIFA | Triticeae CAP

USDA ars

SMALL GRAINS INITIATIVE

UNIVERSITY OF MINNESOTA

Minnesota Agricultural
Experiment Station