Genomic Selection for Fusarium Head Blight Resistance in Barley

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NDSU NORTH DAKOTA STATE UNIVERSITY

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University of Nebraska Lincoln

U.S. Wheat & Barley
Scab Initiative

UNIVERSITY OF MINNESOTA
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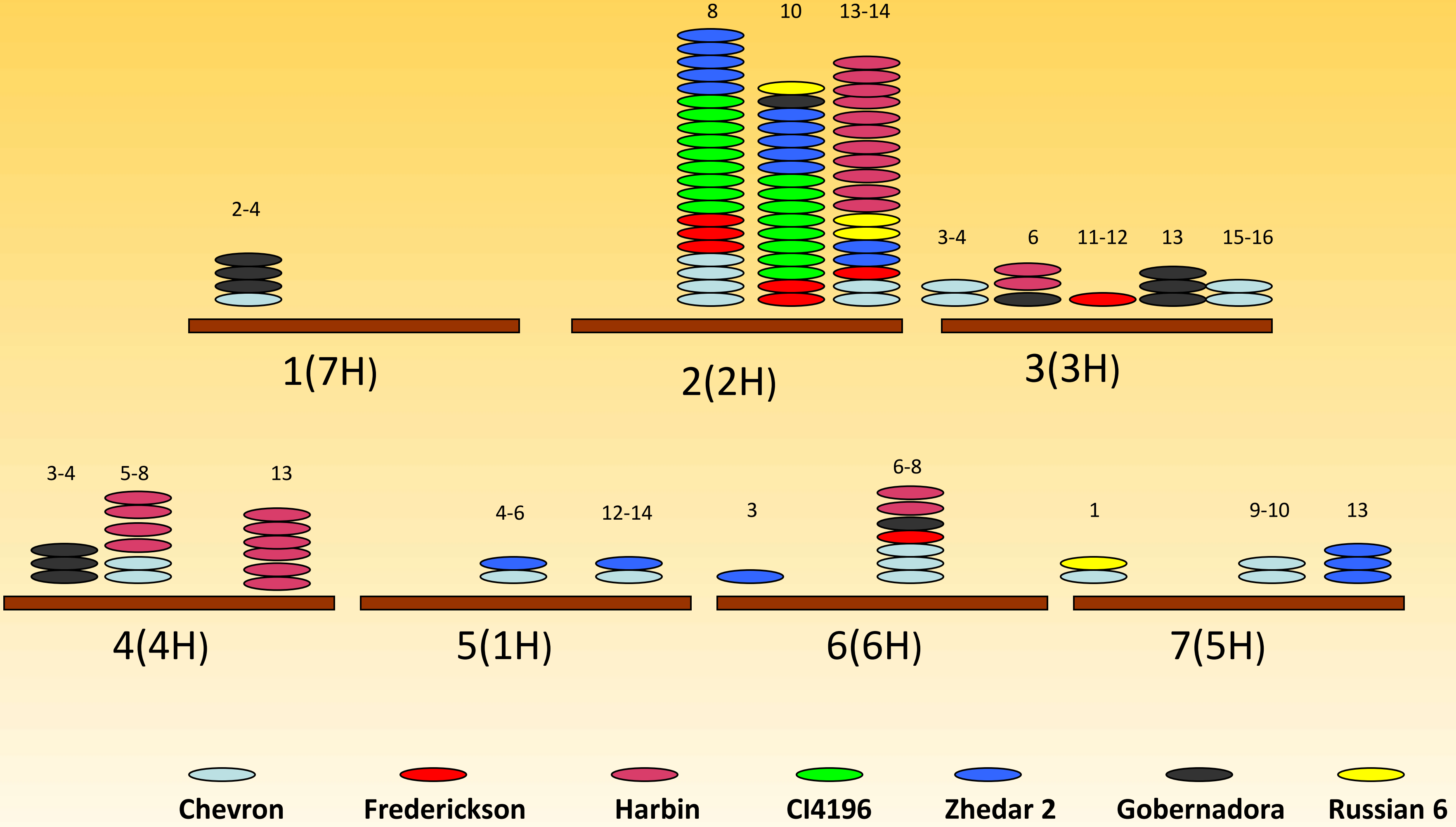
FHB QTL – *Bi-Parental Mapping*

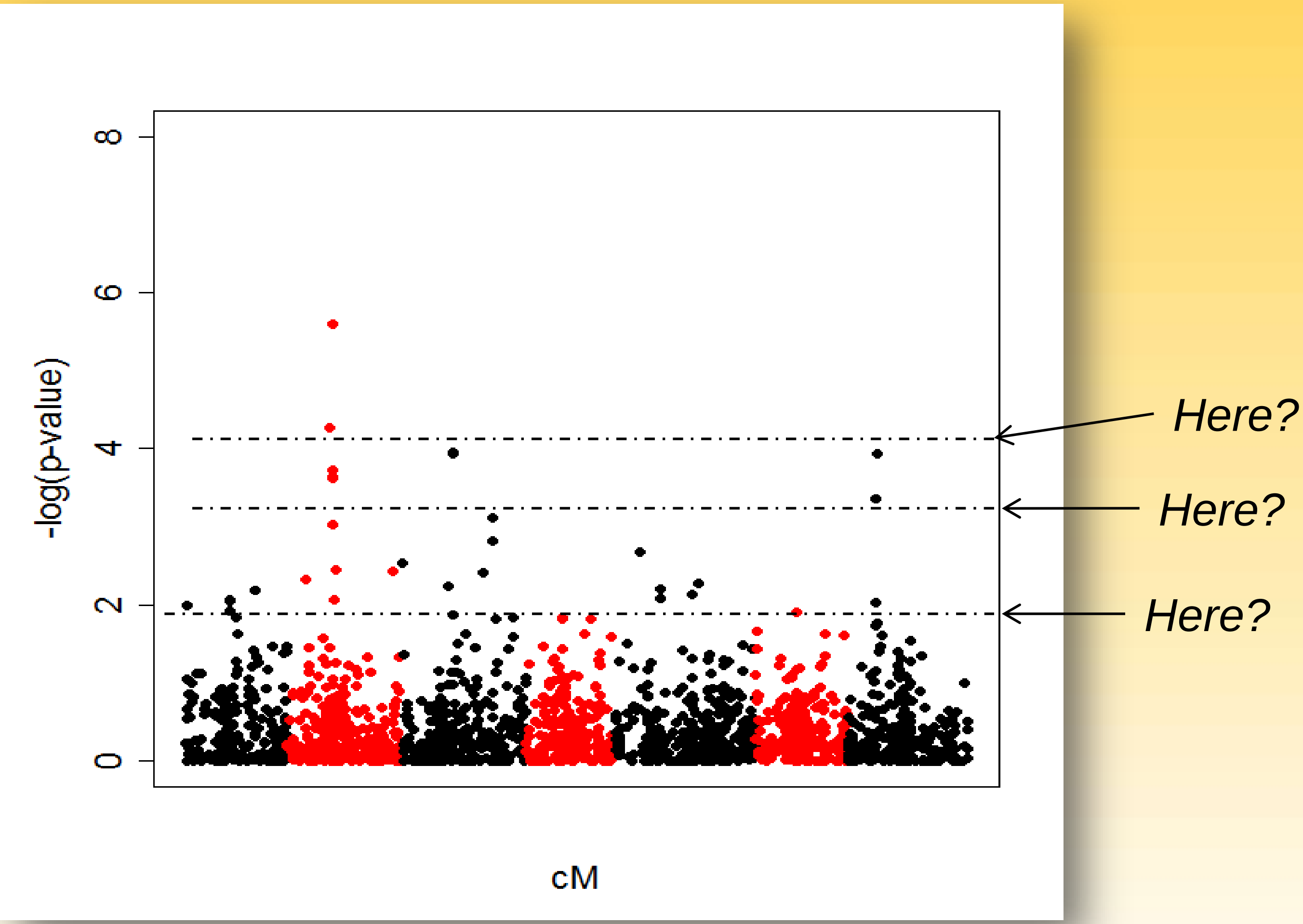


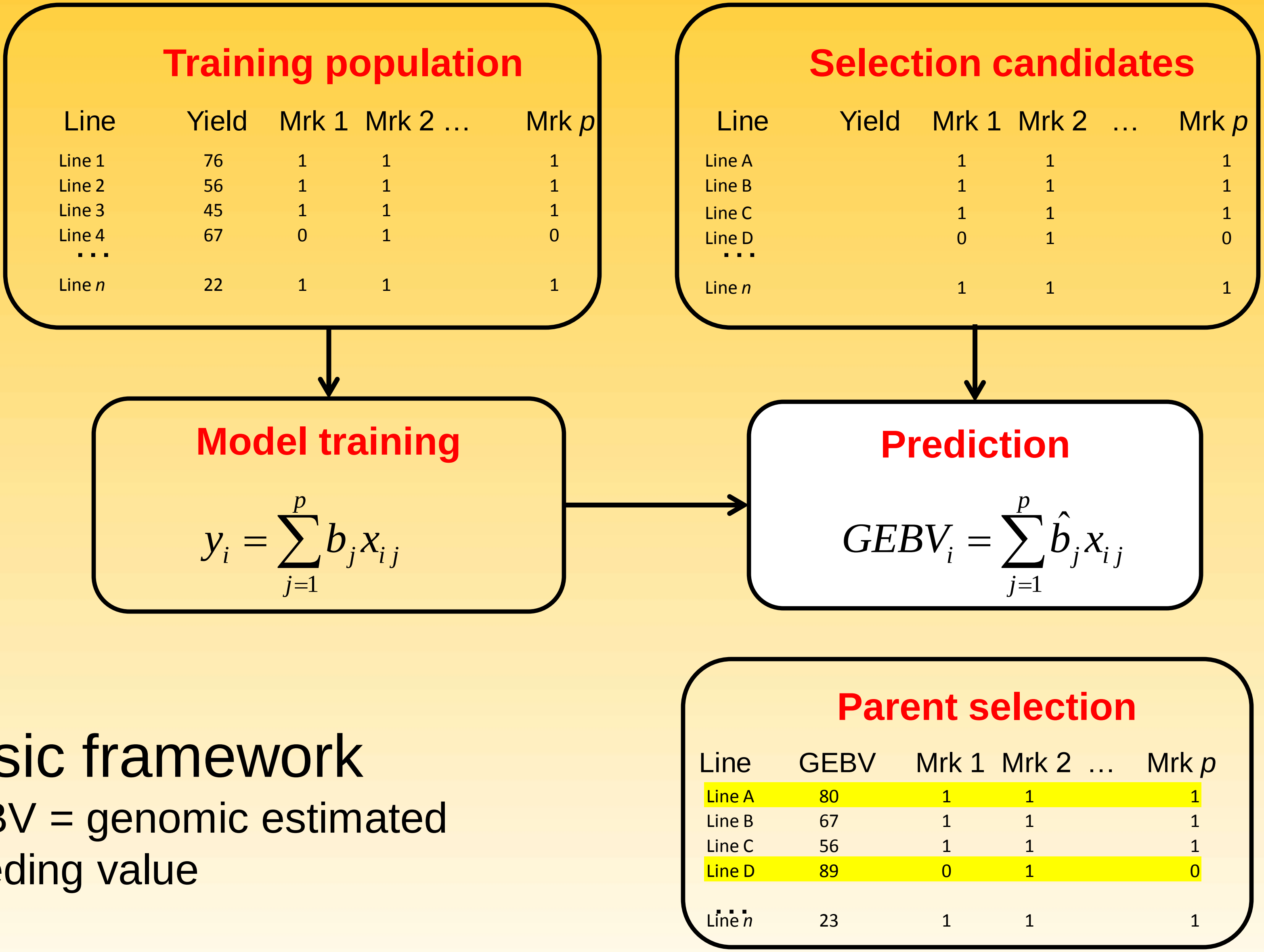
FHB and DON QTL – Association Mapping

- Robust QTL identified in both CAP I and CAP II
- DON and FHB sometimes coincident
- Relatively small allelic effects

Trait	Chrom	cM	bin	r^2
FHB	2H	50-56	6-7	0.010
FHB	4H	24-36	4-7	0.020
FHB	6H	42-61	5-7	0.011
FHB	6H	124-127	14	0.017
DON	1H	88	9-12	0.007
DON	2H	125-132	11-13	0.020
DON	3H	52-65	4-7	0.027
DON	4H	3	1	0.009
DON	4H	21-36	2-5	0.015
DON	4H	40-61	5-7	0.008
DON	5H	190-192	13-15	0.012
DON	6H	42-67	5-7	0.007

In traditional marker-assisted selection choice of markers is somewhat arbitrary





Training population

Line	Yield	Mrk 1	Mrk 2	…	Mrk *p*
Line 1	76	1	1		1
Line 2	56	1	1		1
Line 3	45	1	1		1
Line 4	67	0	1		0
…					
Line *n*	22	1	1		1

Selection candidates

Line	Yield	Mrk 1	Mrk 2	…	Mrk *p*
Line A		1	1		1
Line B		1	1		1
Line C		1	1		1
Line D		0	1		0
…					
Line *n*		1	1		1

Model training

$$y_i = \sum_{j=1}^{p} b_j x_{ij}$$

Prediction

$$GEBV_i = \sum_{j=1}^{p} \hat{b}_j x_{ij}$$

Parent selection

Line	GEBV	Mrk 1	Mrk 2	…	Mrk *p*
Line A	80	1	1		1
Line B	67	1	1		1
Line C	56	1	1		1
Line D	89	0	1		0
…					
Line *n*	23	1	1		1

Basic framework

GEBV = genomic estimated breeding value

Implementing Genomic Selection

Why switch now?

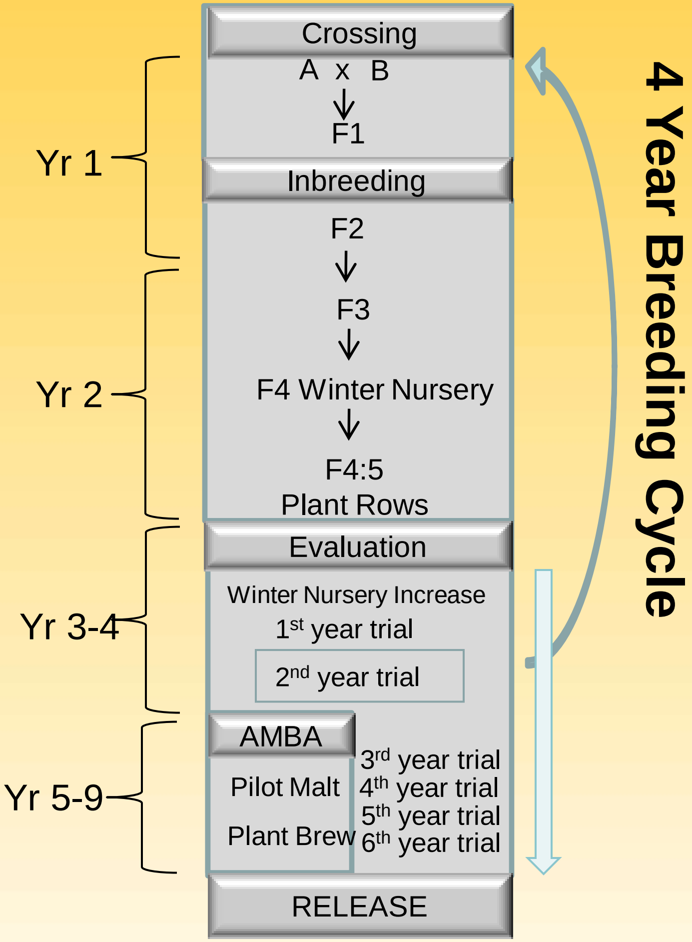
- Relatively slow progress via phenotypic selection
- Large cost of phenotyping
- Limited throughput (plot area, time, people)
- FHB genetics (quantitative, small effects)
- Decreasing cost of genotyping
- USDA Genotyping Laboratories
- Promising results from simulation and cross validation of GS

Genomic Selection for Fusarium Head Blight Resistance in Barley

- **Conventional Phenotypic Selection**
- Fitting and Validating Models
- Implementing Selection
- Evaluating Selection Accuracy & Gain

Phenotypic Selection

Current Scheme



Yr 1

Crossing

A x B

↓

F1

Inbreeding

Yr 2

F2

↓

F3

↓

F4 Winter Nursery

↓

F4:5

Plant Rows

Evaluation

Yr 3-4

Winter Nursery Increase

1st year trial

2nd year trial

Yr 5-9

AMBA

Pilot Malt

Plant Brew

3rd year trial

4th year trial

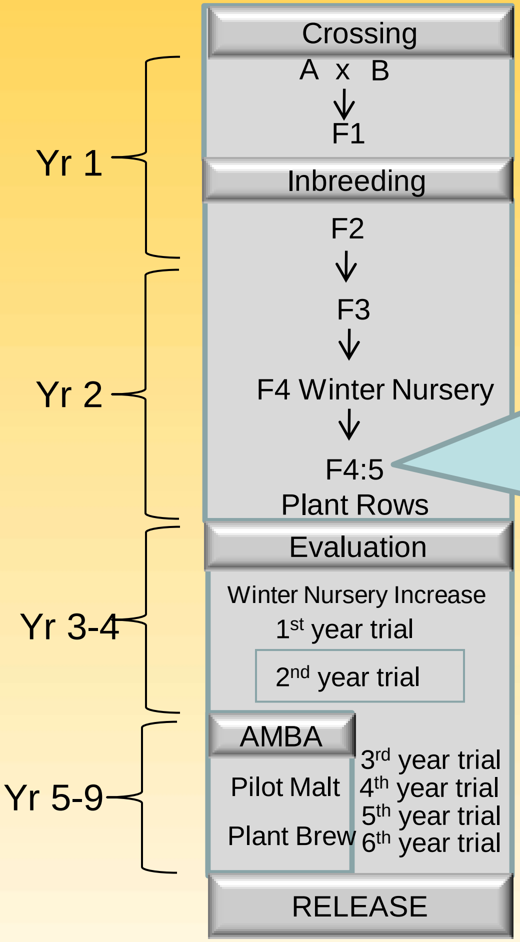
5th year trial

6th year trial

RELEASE

4 Year Breeding Cycle

Current Scheme



Crossing

A x B

↓

F1

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F2

↓

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F4:5

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Field Screening for FHB

In 2010 evaluated over 13,000 single row plots for FHB severity

Phenotypic Selection Costs (per sample/plot)

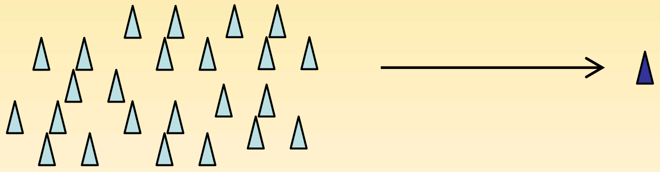
Seedling Disease Assay	$2
Single Plant Off-Season Nursery	$4
FHB Severity (head rows)	$5
DON	$10
Yield	$15
Malting Quality	$100

Genomic Selection for Fusarium Head Blight Resistance in Barley

- Conventional Phenotypic Selection
- **Fitting and Validating Models**
- Implementing Selection
- Evaluating Selection Accuracy & Gain

Model Cross-Validation Studies

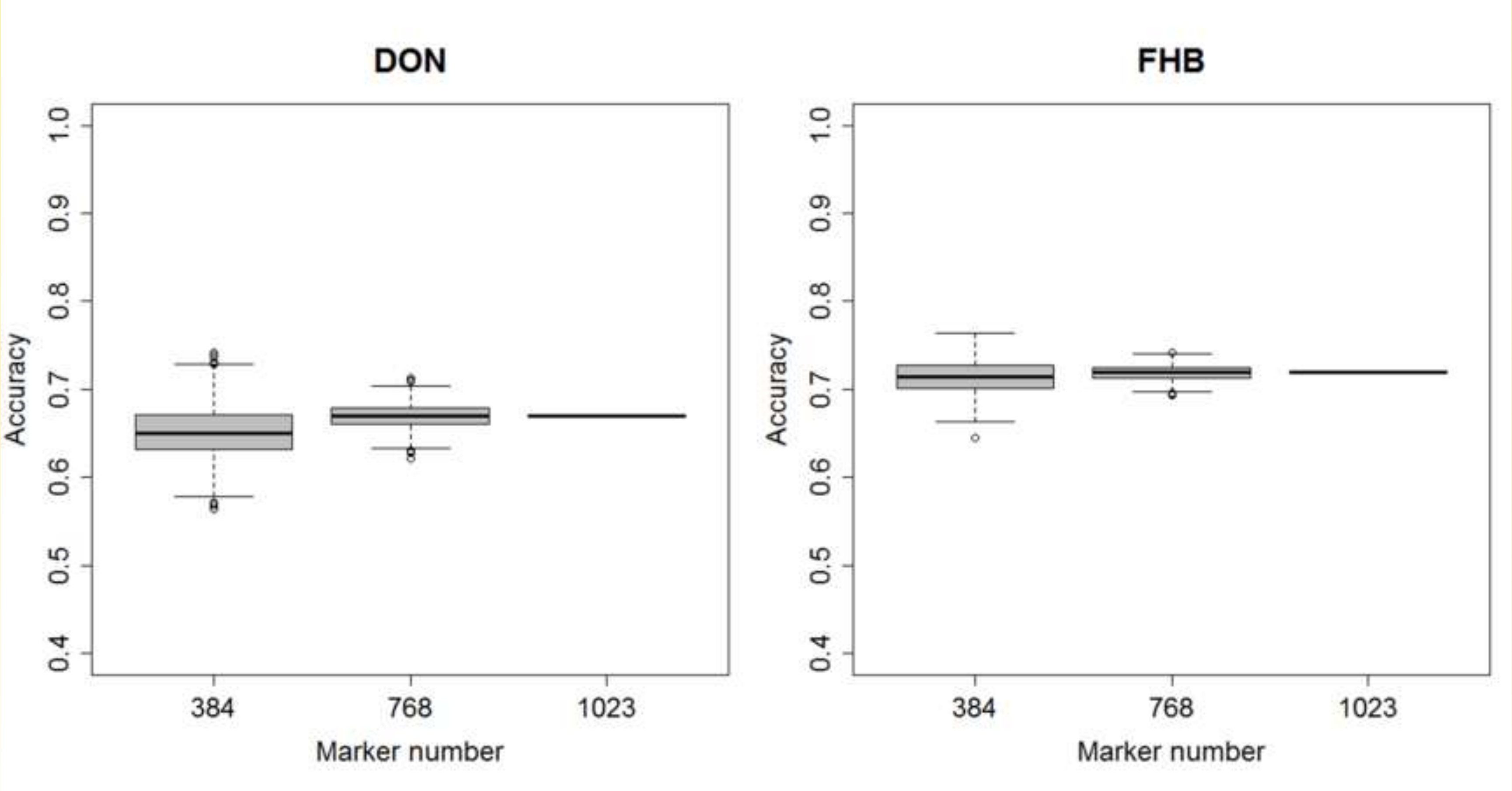
- Model for estimating marker effects
- Number of markers
- Size of training population
- Composition of training population



Train Model

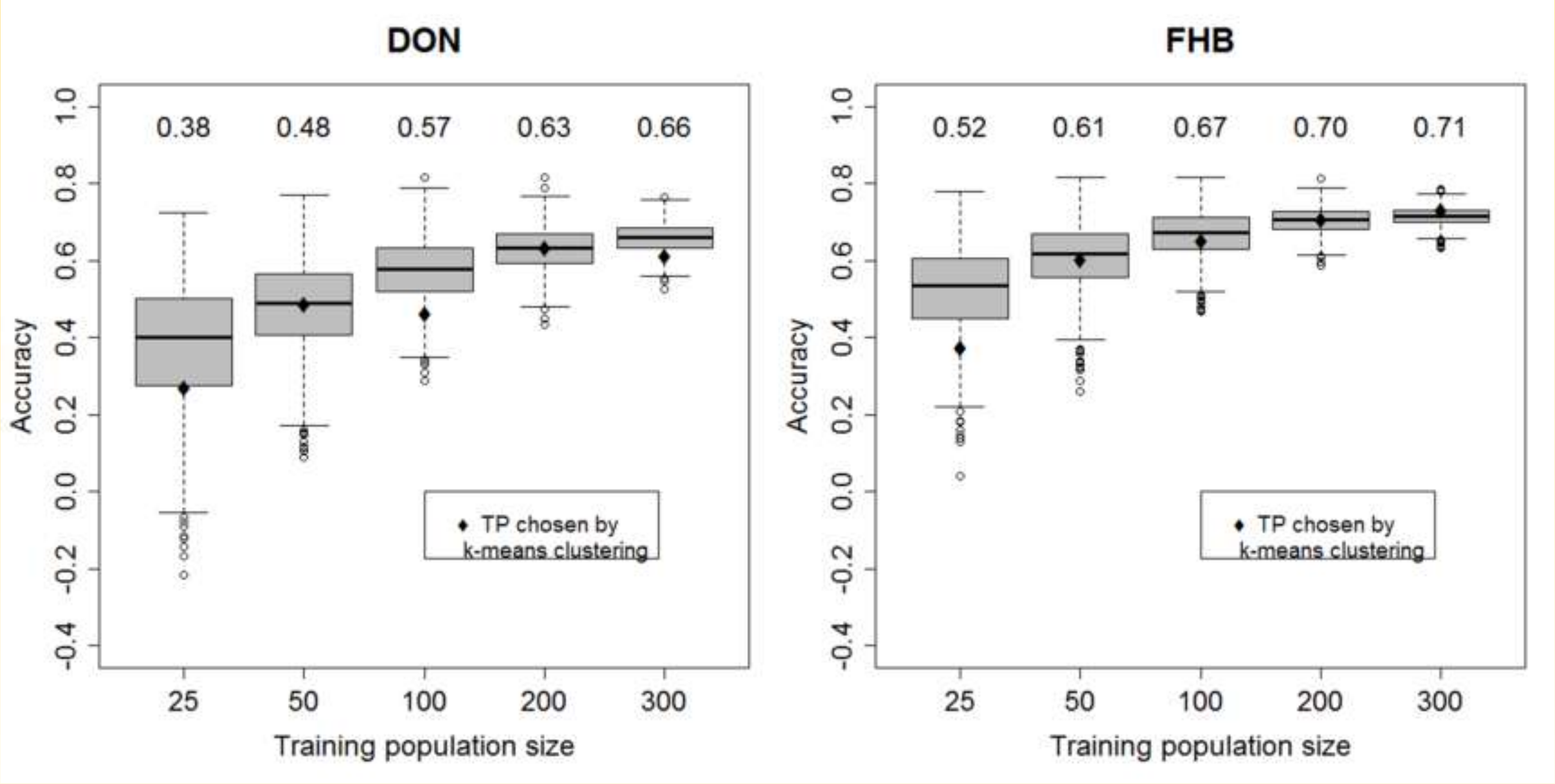
Predict Individual

More markers are better, but 384 is enough



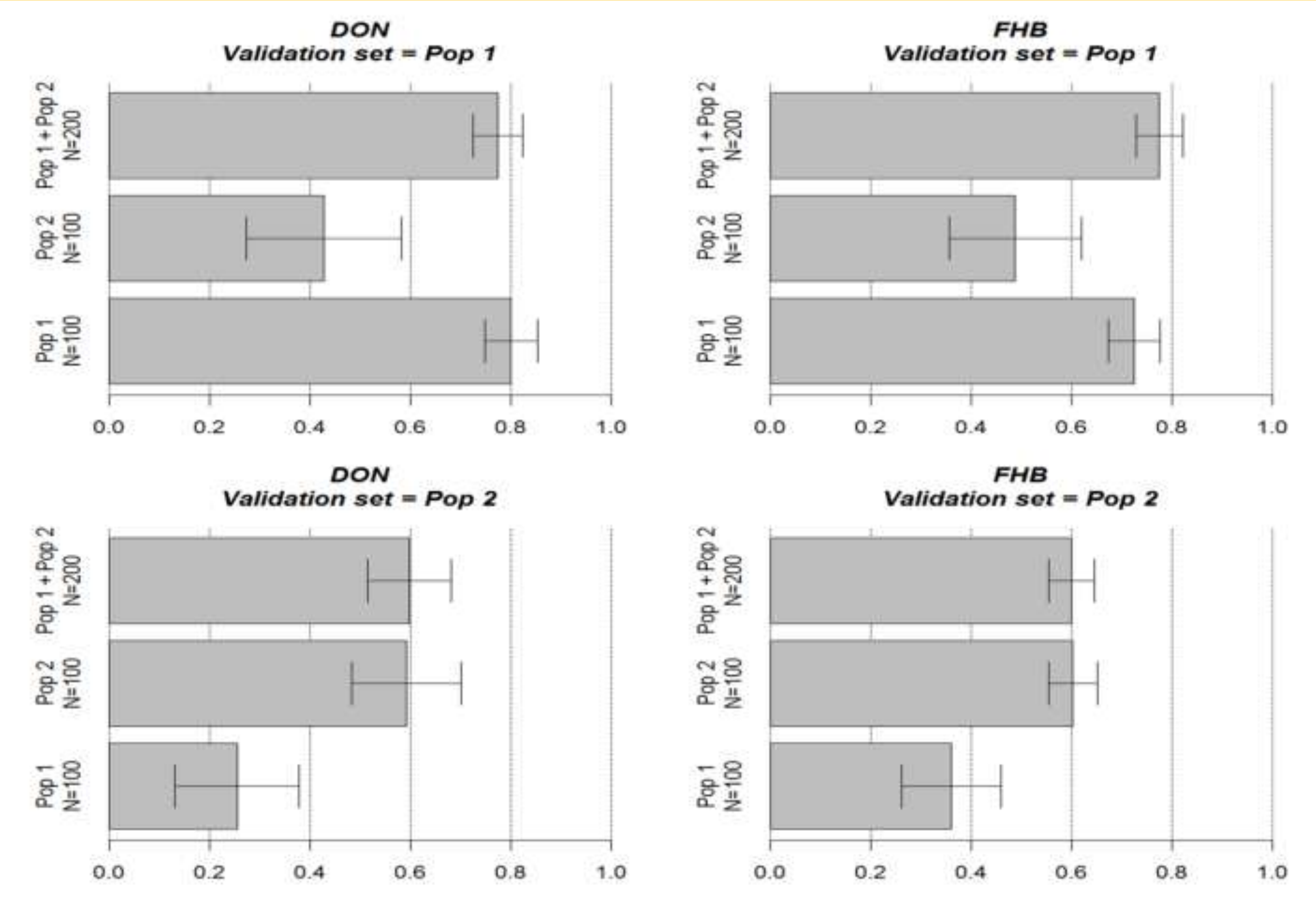
Training population 691 six-row barley lines from CAP

Large populations are better (at least 300)



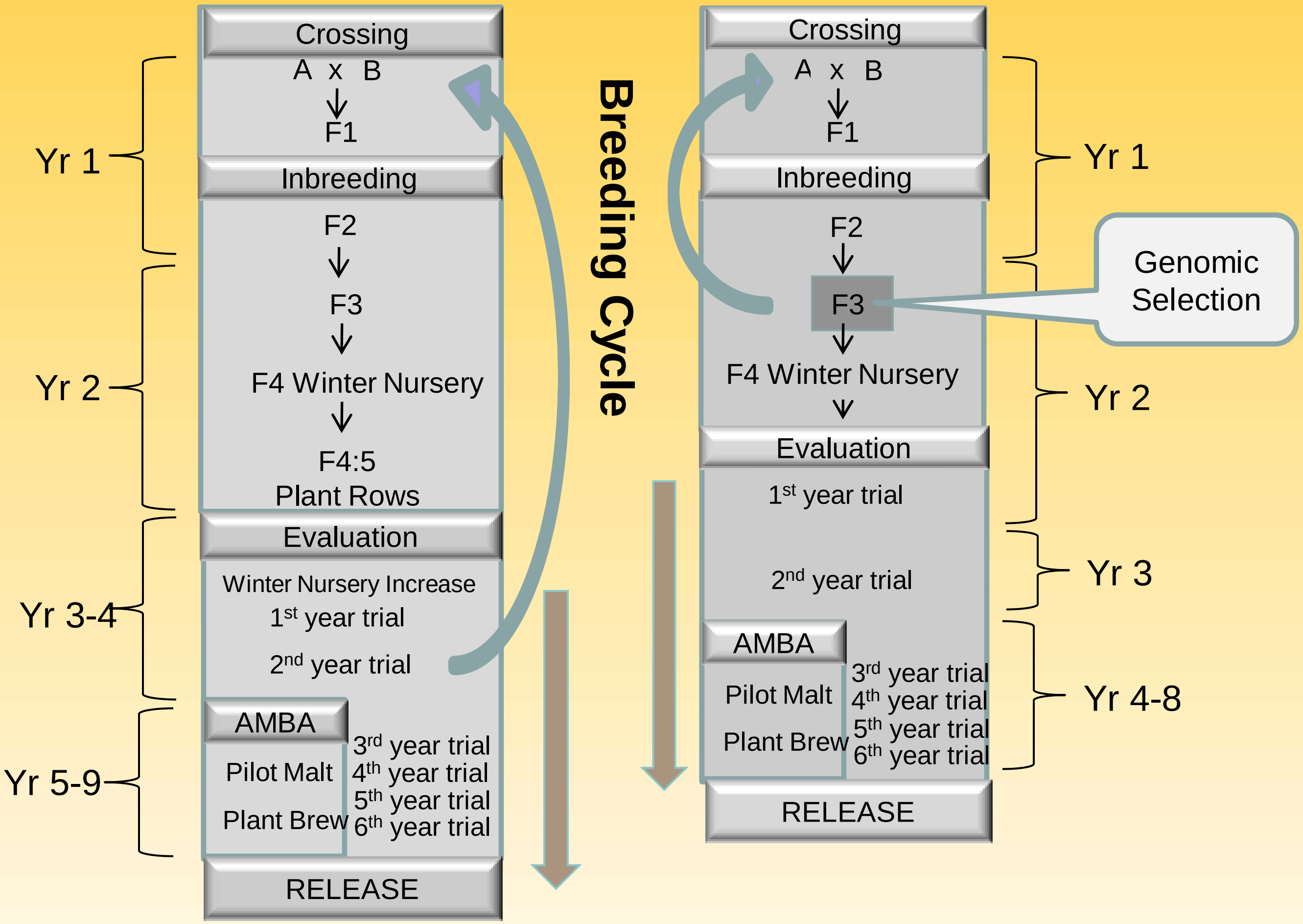
Training population 691 six-row barley lines from CAP

Training population composition effects model accuracy



Genomic Selection for Fusarium Head Blight Resistance in Barley

- Conventional Phenotypic Selection
- Fitting and Validating Models
- **Implementing Selection**
- Evaluating Selection Accuracy & Gain



Current Scheme

Yr 1
Crossing
A x B
↓
F1
Inbreeding
Yr 2
F2
↓
F3
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F4 Winter Nursery
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1st year trial
2nd year trial
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AMBA
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3rd year trial
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6th year trial
RELEASE

Breeding Cycle

Genomic Selection

Crossing
A x B
↓
F1
Inbreeding
Yr 1
F2
↓
F3
↓
F4 Winter Nursery
↓
Genomic Selection
Evaluation
Yr 2
1st year trial
Yr 3
2nd year trial
Yr 4-8
AMBA
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3rd year trial
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RELEASE

FHB Genomic Selection Project

Parents

UM | Busch Ag | NDSU

Crosses

UM | B A | NDSU

UM B A | B A NDSU | UM NDSU

1440 progeny = 6 cross types x 10 crosses per type x 24 progeny per cross

384 SNPs selected from BOPA1&2 optimized for PIC and genome distribution

Training Data set CAPI, II, II from three programs

Ridge Regression Model

Shiaoman Chao, Jean-Luc Jannink, Aaron Lorenz,
Rich Horsley, Blake Cooper, Gary Hanning,

GS Predicted Values

Lacey	-2.38	6.42	0.08	-117.00	-5.87	-0.22	0.09	-5.68	0.18	3.56	406.87
Quest	-17.76	-1.04	2.04	36.25	11.35	0.51	0.06	-2.10	8.96	1.13	226.05
Tradition	-10.32	5.49	9.01	-141.00	37.33	-0.02	-2.01	-4.59	2.94	4.55	569.52
MIN	-26.62	-4.82	-10.49	-203.16	-29.51	-1.82	-1.87	-8.90	-4.88	-0.36	-292.99
MAX	7.11	9.54	24.54	62.29	55.02	1.30	2.53	6.44	21.87	14.29	930.77
AVE	-9.05	1.49	8.61	-63.01	10.09	0.09	0.15	-1.48	9.38	5.01	362.50
	Freq Wt										
x	**DON_f**	**FHB**	**Aa**	**Bg**	**Dp**	**protein**	**hd**	**ht**	**plump**	**st**	**yield**
G10W037.06	-26.036785	-0.08	12.36	-87.88	4.28	-0.57	-1.04	1.08	7.67	8.15	-80.55
G10W037.05	-12.634535	4.48	15.75	-34.40	-12.60	-1.09	-0.74	-1.21	11.55	13.24	5.52
G10W037.04	-20.93098	2.63	12.06	-61.65	6.66	-0.43	-1.04	0.50	1.84	9.81	-267.73
G10W037.03	-13.563582	0.34	17.90	-144.02	26.45	0.59	-0.71	1.65	9.15	8.53	160.00
G10W037.02	-12.336345	2.80	14.67	-8.61	-6.75	-0.34	-0.84	-0.26	7.73	9.87	53.24
G10W037.01	-12.814291	0.05	10.35	-50.78	-11.23	-0.13	-1.25	-0.78	4.36	9.31	78.35
G10W036.24	-3.2181708	5.28	8.30	-127.83	12.26	-0.15	-0.80	-5.54	9.28	5.60	823.17
G10W036.23	-7.0848412	2.56	1.89	-59.88	12.59	0.23	-0.89	-3.85	12.20	3.46	598.09
G10W036.22	-1.5979616	5.61	13.03	-136.51	18.48	-0.35	-0.65	-6.43	6.31	6.86	814.85
G10W036.21	-9.1445027	3.58	9.66	-85.16	23.14	0.04	-0.46	-6.59	5.41	3.64	408.84
G10W036.20	-5.1177605	4.06	9.25	-44.29	13.89	0.22	-0.45	-4.70	5.71	3.58	509.14
G10W036.19	-15.336236	-0.48	6.11	-28.36	27.26	0.92	-0.34	-1.25	8.98	1.29	331.65
G10W036.18	-5.4771292	3.91	6.87	-52.88	23.73	0.26	-0.77	-4.12	11.92	3.21	477.44
G10W036.17	-2.5725907	6.66	8.70	-150.35	23.64	-0.35	-0.88	-6.77	6.63	4.33	723.18
G10W036.16	-9.4996327	1.96	4.86	-45.28	14.34	0.67	-0.41	-4.11	7.18	2.43	382.44

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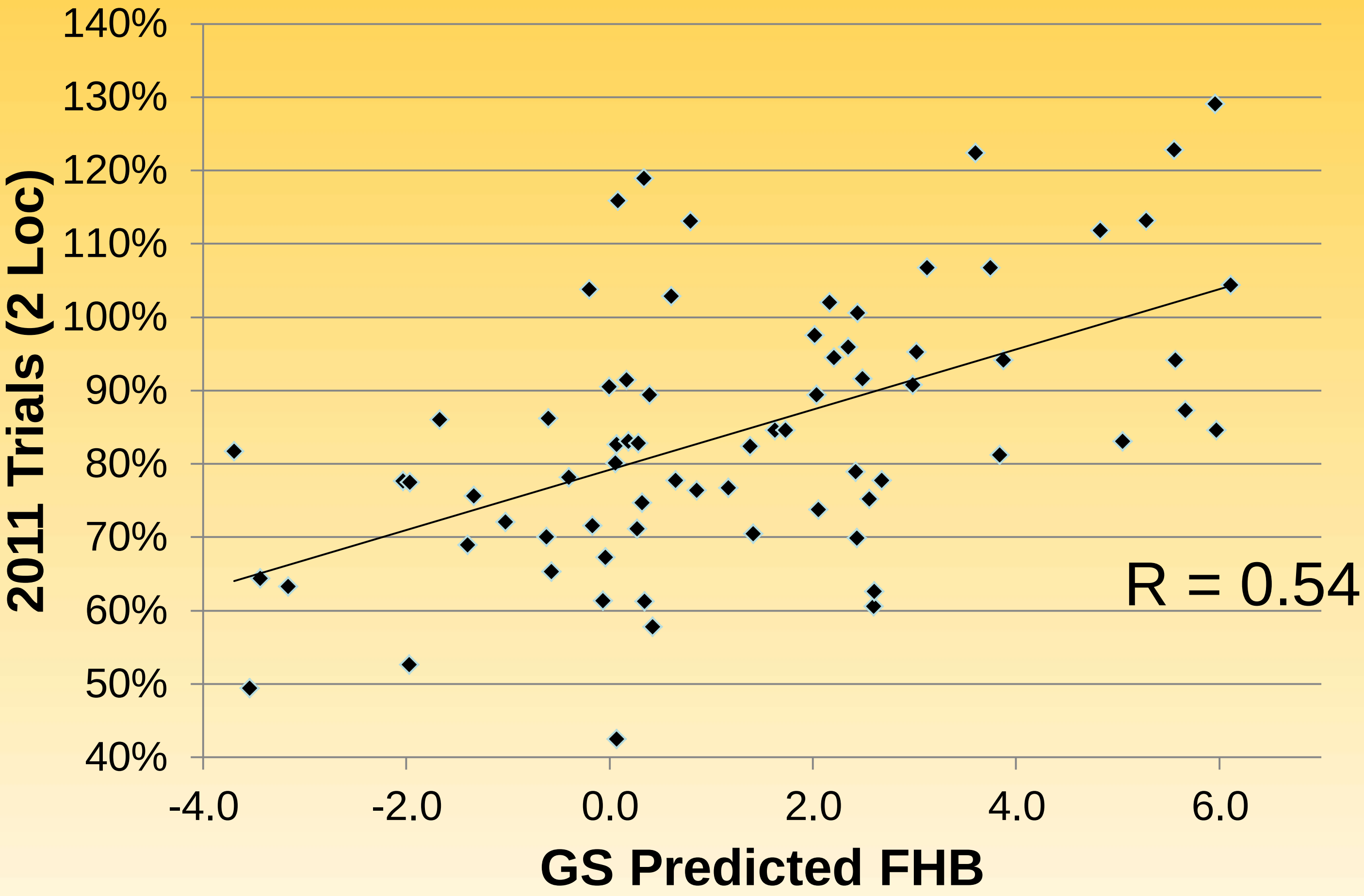
- **Evaluating Selection Accuracy & Gain**

Evaluation of Cycle 1

Fall 2009	Crosses among parents (UM, BA, NDSU)
Winter 2009/10	F1
Summer 2010	F2
Fall 2010	F3 GS (384 SNP markers)
Winter 2010/11	F4 New Zealand Off Season Nursery
Summer 2011	Yield Trials, FHB Screening, Malting Quality


140%
130%
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100%
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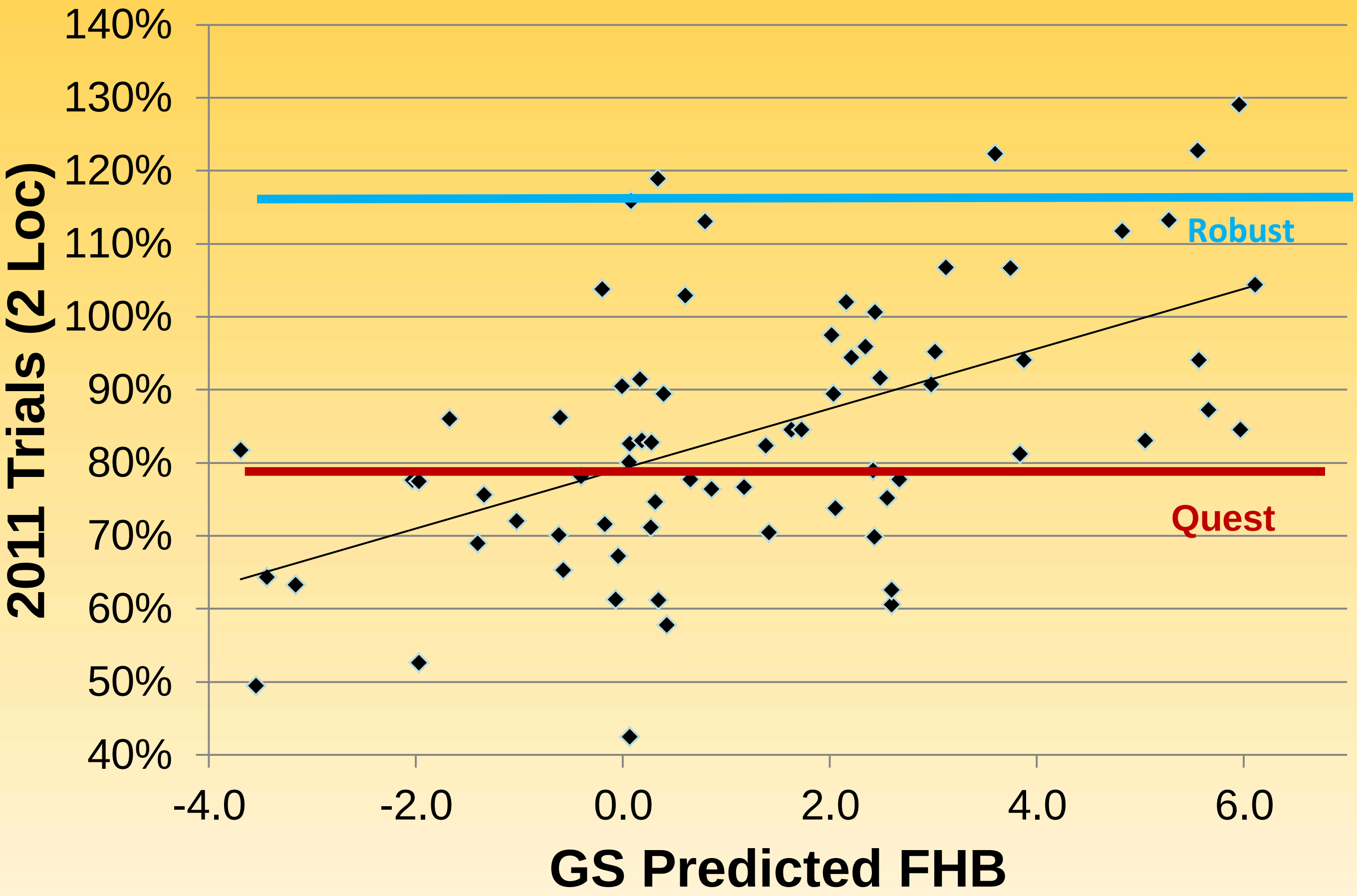
80%
70%
60%
50%
40%
2011 Trials (2 Loc)
-4.0
-2.0
0.0
2.0
4.0
6.0
GS Predicted FHB
R = 0.54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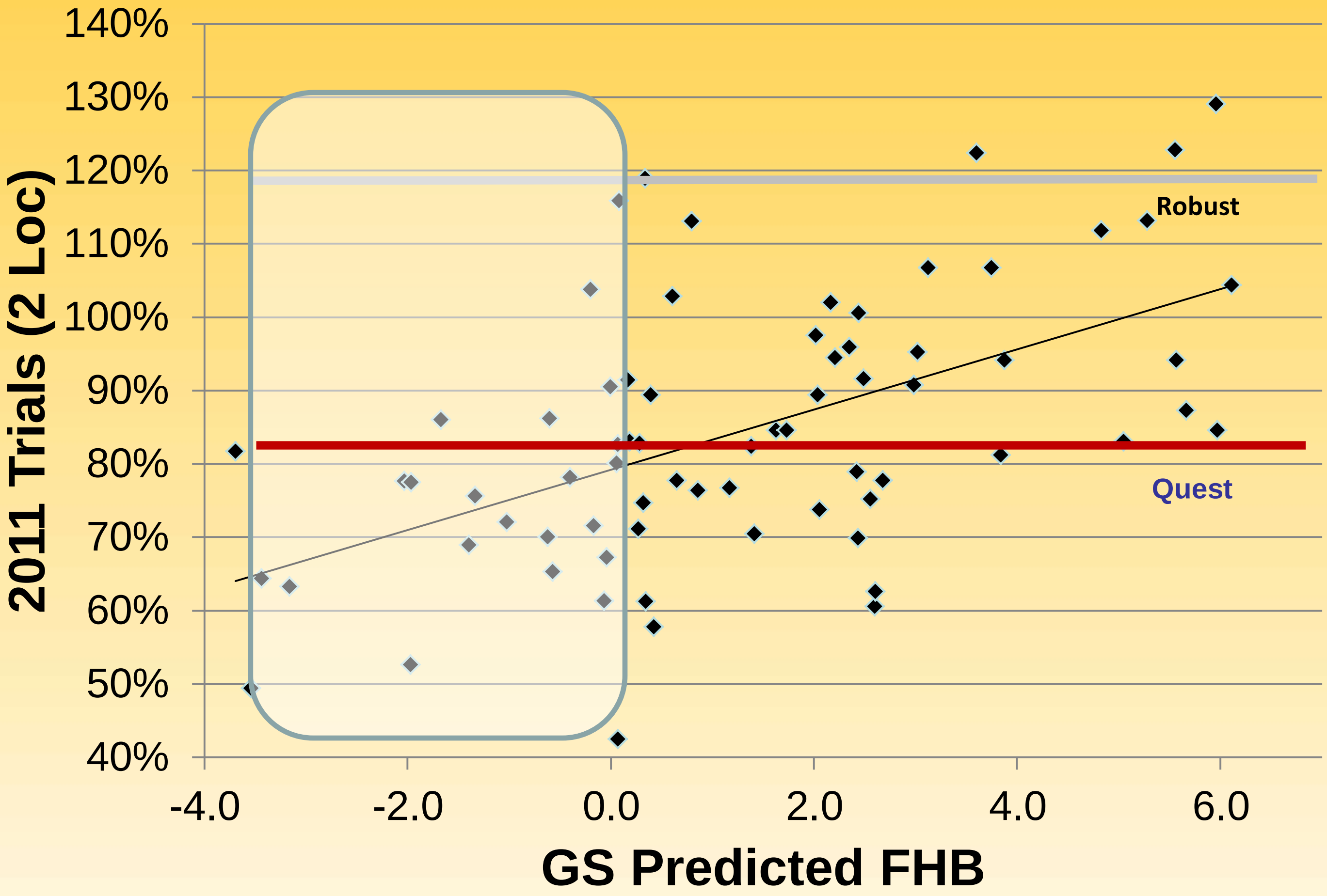
80%
70%
60%
50%
40%
2011 Trials (2 Loc)
-4.0
-2.0
0.0
2.0
4.0
6.0
GS Predicted FHB
Robust
Quest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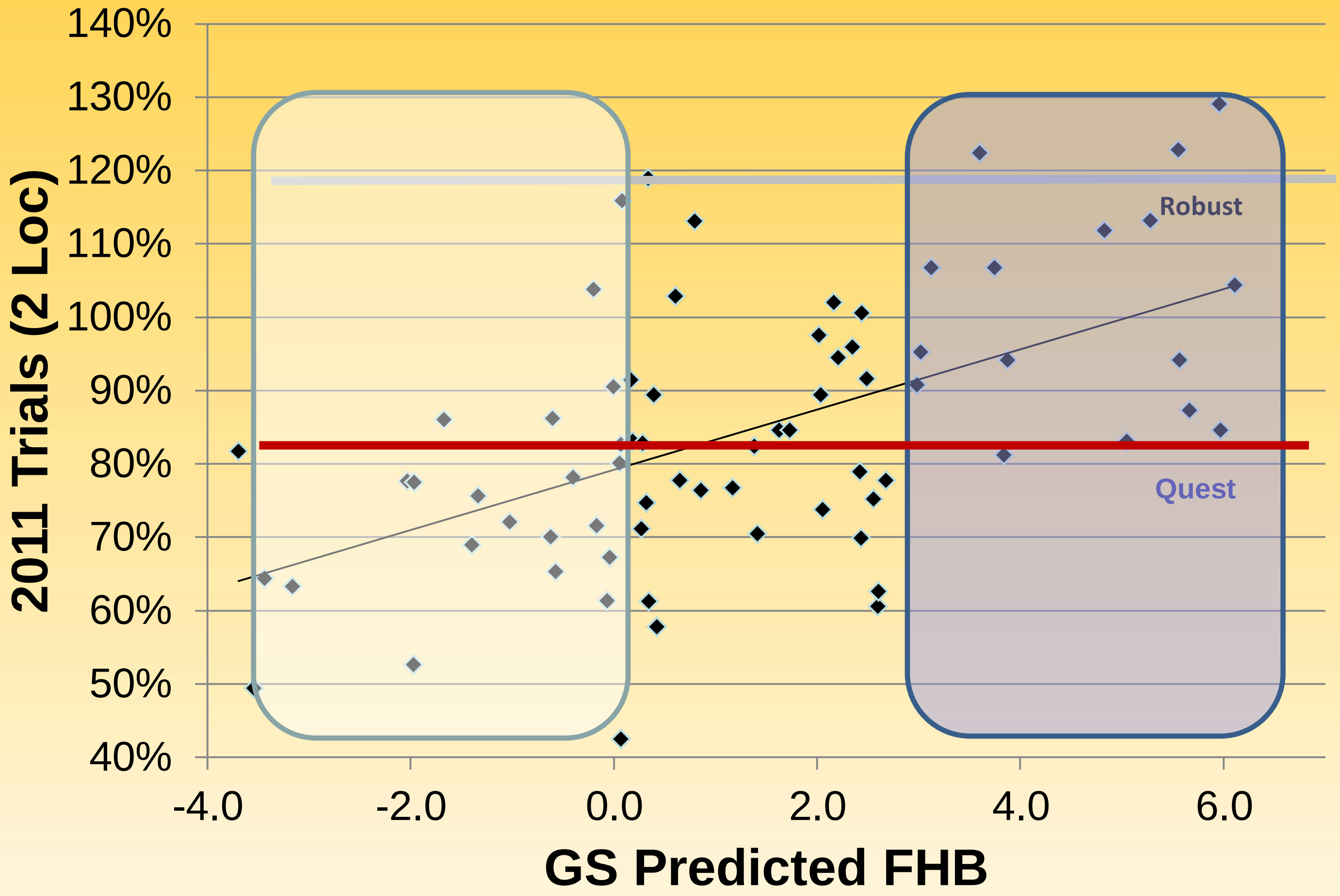
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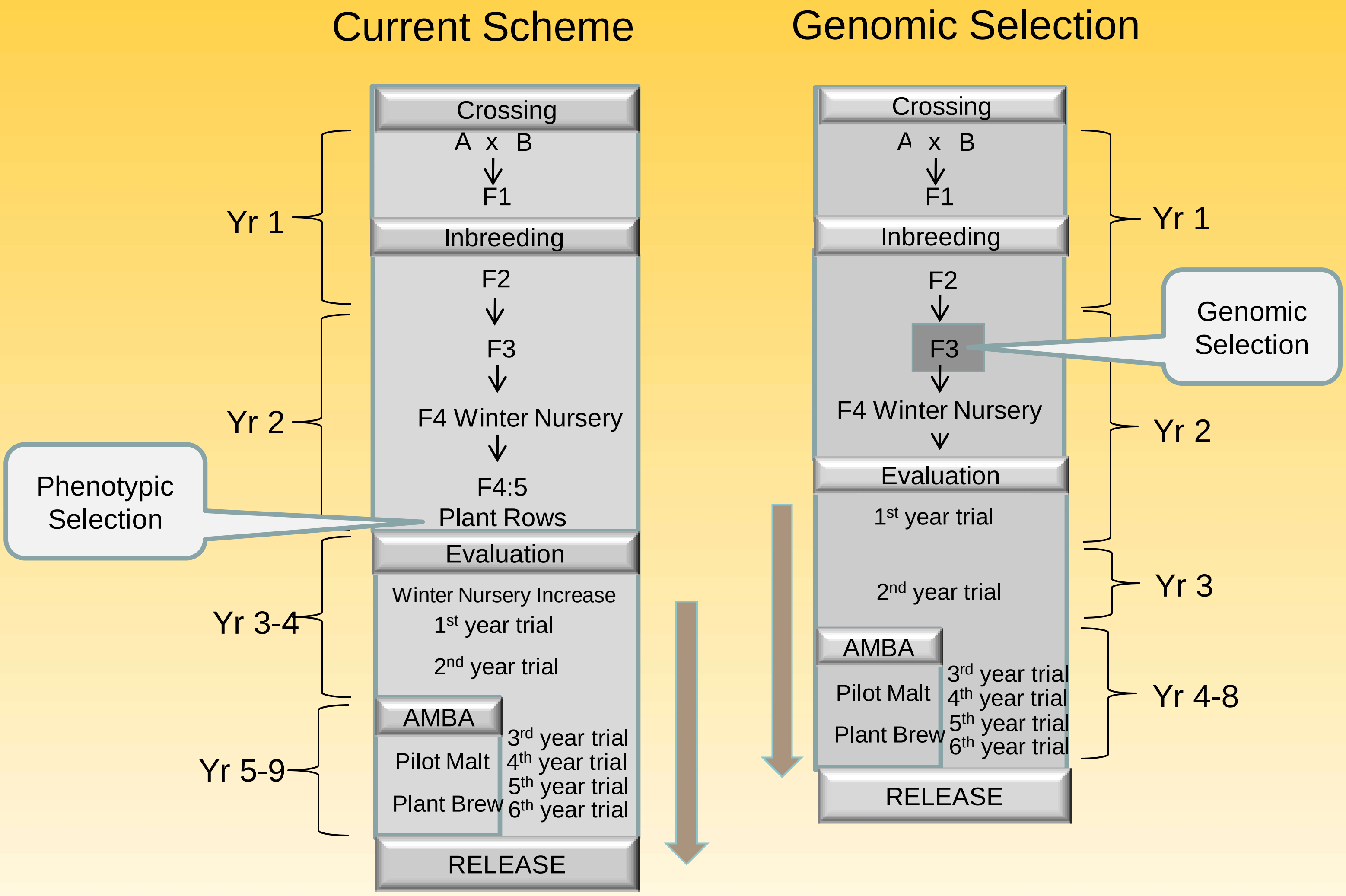


Current Scheme

Yr 1

Crossing

A x B

↓

F1

Inbreeding

Yr 2

F2

↓

F3

↓

F4 Winter Nursery

↓

F4:5

Plant Rows

Phenotypic Selection

Yr 3-4

Evaluation

Winter Nursery Increase

1st year trial

2nd year trial

Yr 5-9

AMBA

Pilot Malt

Plant Brew

3rd year trial

4th year trial

5th year trial

6th year trial

RELEASE

Genomic Selection

Yr 1

Crossing

A x B

↓

F1

Inbreeding

Yr 2

F2

↓

F3

Genomic Selection

↓

F4 Winter Nursery

↓

Evaluation

1st year trial

Yr 3

2nd year trial

Yr 4-8

AMBA

Pilot Malt

Plant Brew

3rd year trial

4th year trial

5th year trial

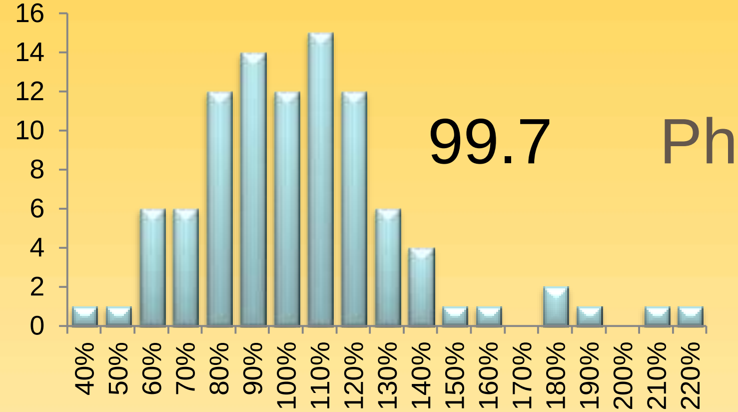
6th year trial

RELEASE

Phenotypic versus Genomic Selection

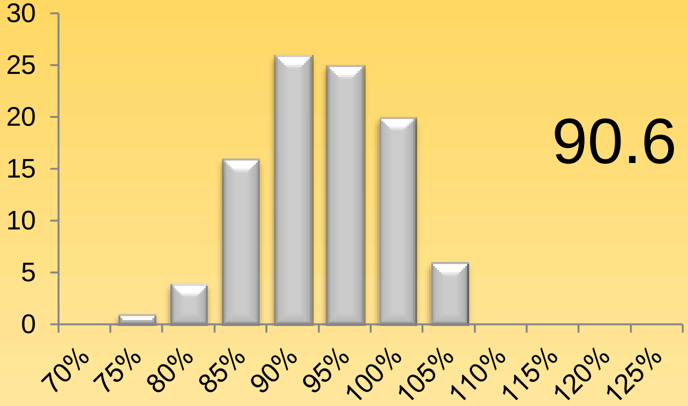
FHB

Yield

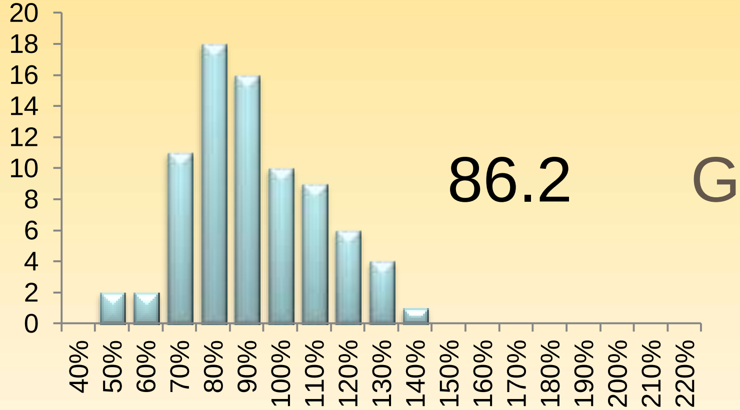


99.7

Phenotypic

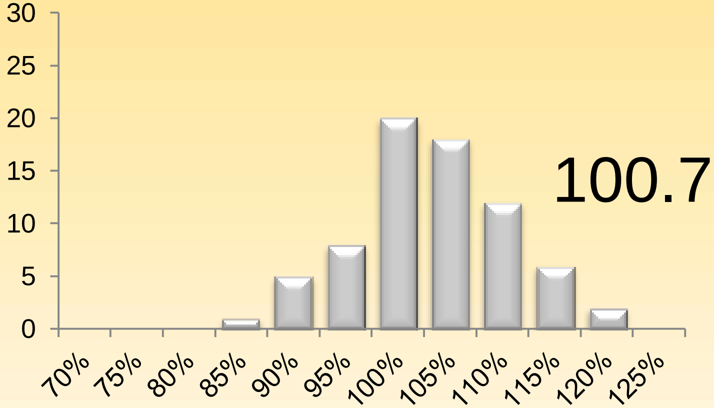


90.6



86.2

Genomic



100.7

Summary

Enhancing FHB resistance in barley is a good target for genomic selection approach.

We can reduce breeding cycle to 1 year.

Training populations of 500 or more and 384 markers should be sufficient to both increase gain per year and reduce overall cost of selection.

Join me..........?

Focus on phenotyping

Assemble training data sets

Use a database

Work closely with genotyping centers.

Collect data to measure gain/impact

Acknowledgements

Barley Project
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University of Minnesota
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Yanhong Dong
Brian Steffenson
Galen Thompson

SMALL GRAINS INITIATIVE

UNIVERSITY OF MINNESOTA

Minnesota Agricultural
Experiment Station

U.S. Wheat & Barley
Scab Initiative

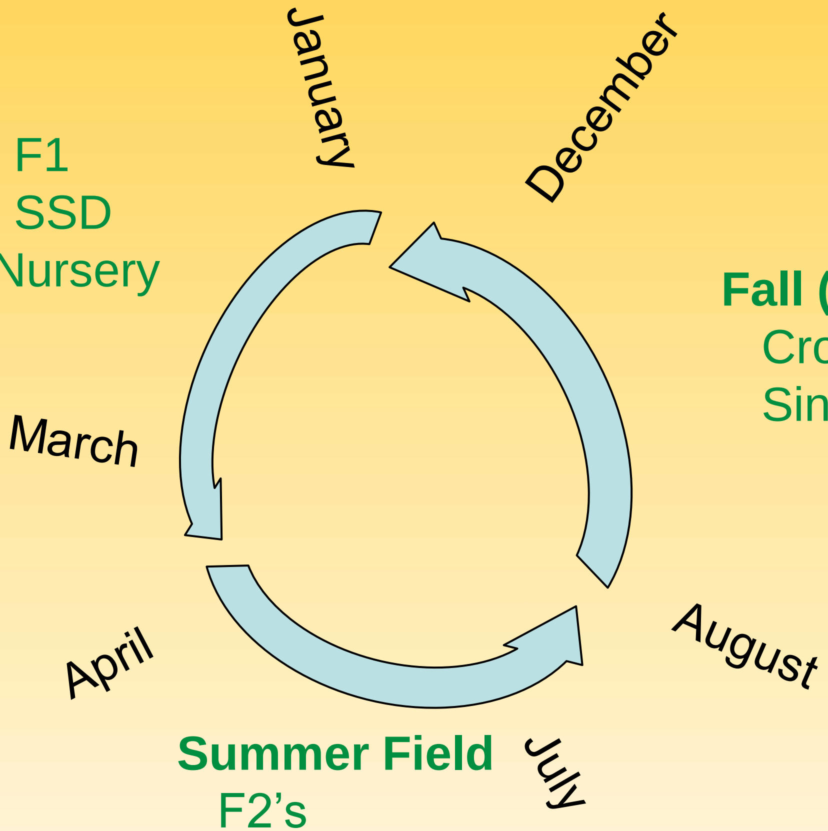
USDA ars

American
Malting
Barley
Association

BARLEY CAP

Barley Breeding Cycle

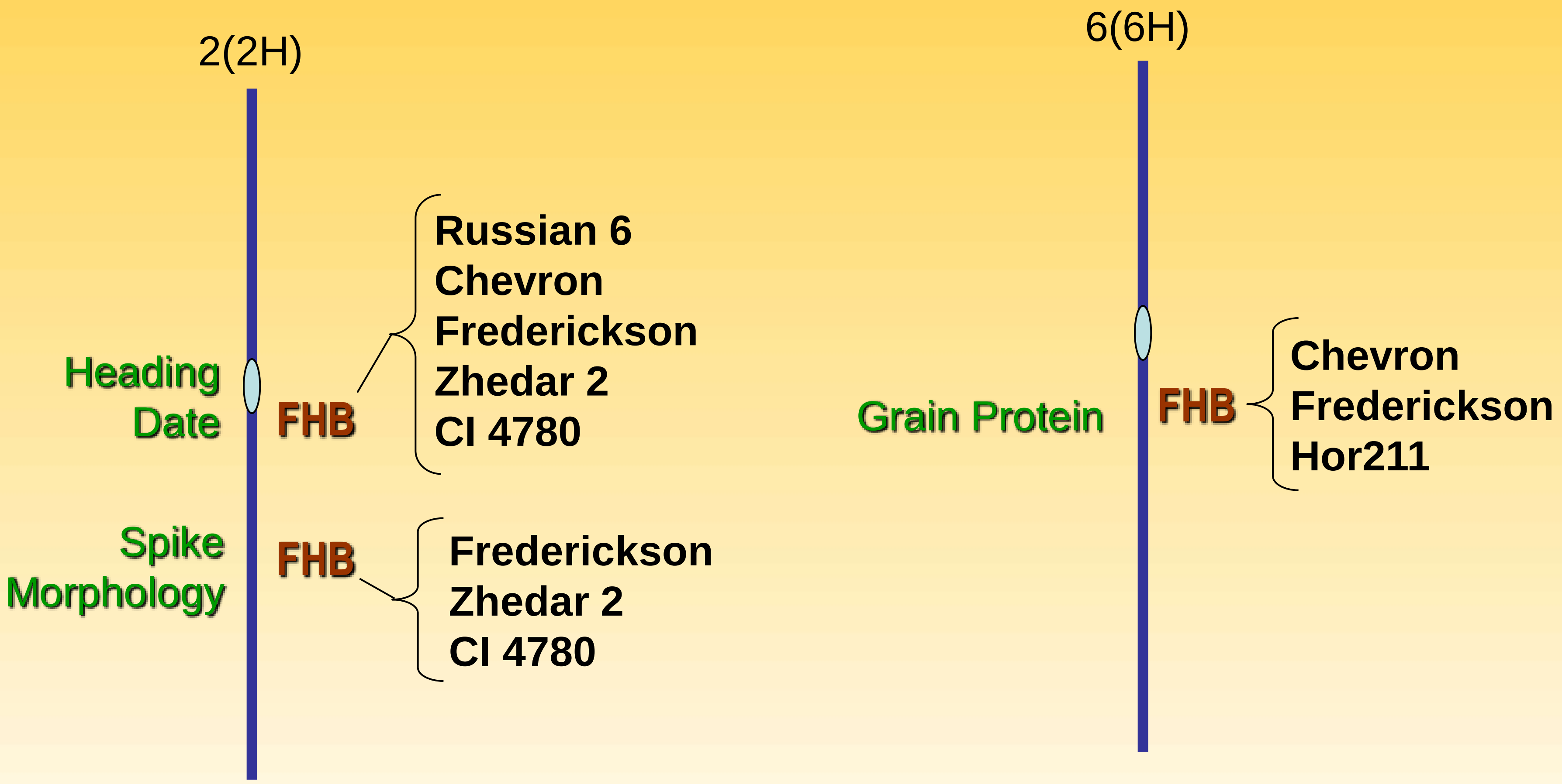
Winter
- Greenhouse F1
- Greenhouse SSD
- Off-Season Nursery



Fall (Greenhouse)
- Crossing block
- Single Seed Decent (SSD)

Summer Field
- F2’s
- Head Rows
- Yield Trials

Unfavorable Linkages with FHB Resistance



2(2H)

Heading Date — FHB

- Russian 6
- Chevron
- Frederickson
- Zhedar 2
- CI 4780

Spike Morphology — FHB

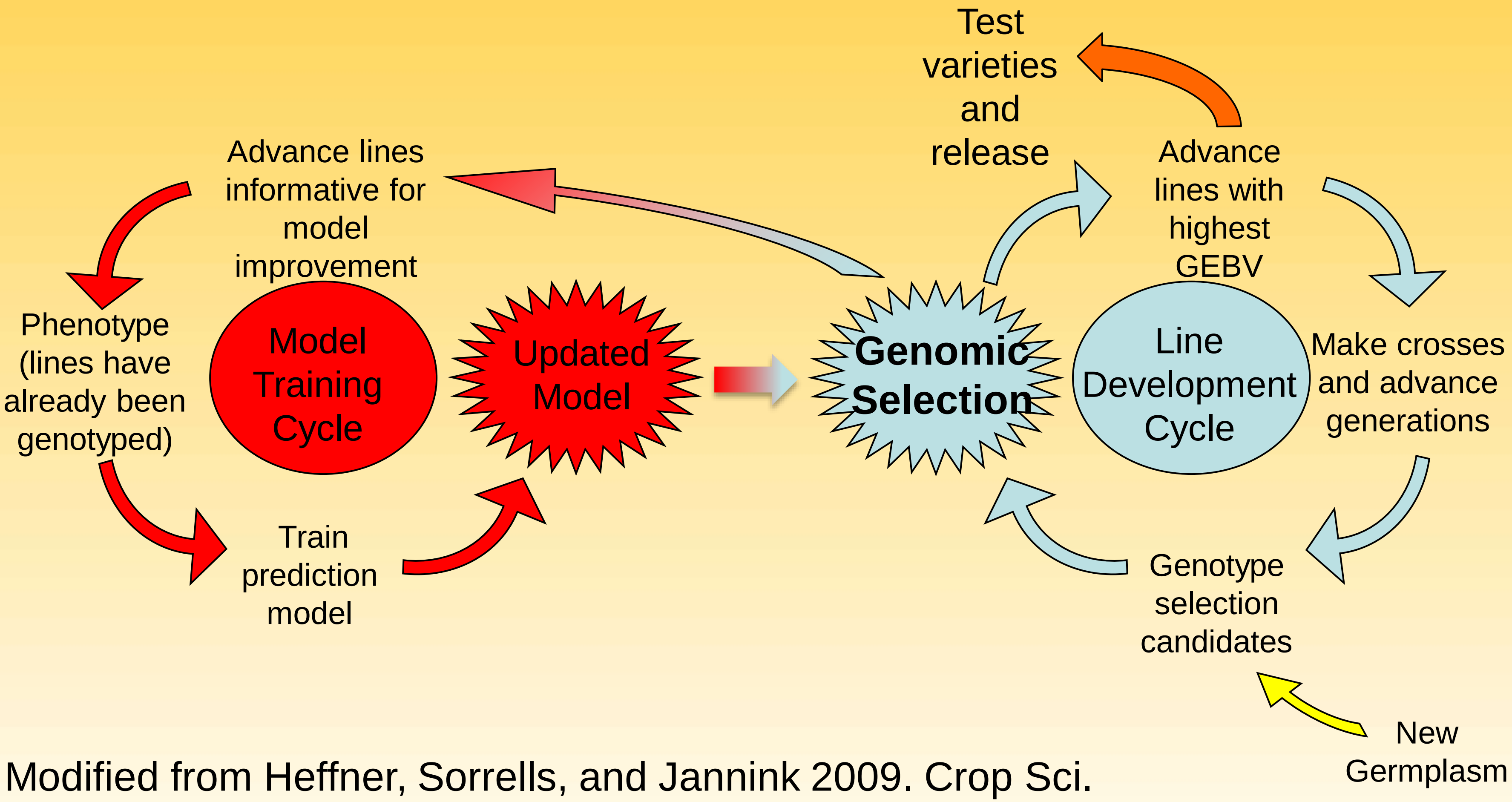
- Frederickson
- Zhedar 2
- CI 4780

6(6H)

Grain Protein — FHB

- Chevron
- Frederickson
- Hor211

The Genomic Selection Cycle



Test varieties and release

Advance lines informative for model improvement

Advance lines with highest GEBV

Phenotype (lines have already been genotyped)

Model Training Cycle

Updated Model

Genomic Selection

Line Development Cycle

Make crosses and advance generations

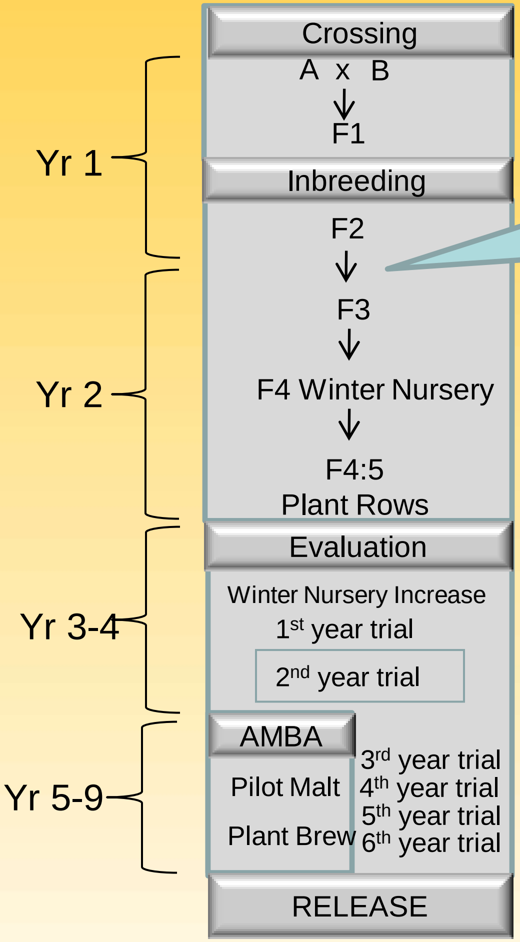
Train prediction model

Genotype selection candidates

New Germplasm

Modified from Heffner, Sorrells, and Jannink 2009. Crop Sci.

Current Scheme



Yr 1

Yr 2

Yr 3-4

Yr 5-9

Crossing

A x B

↓

F1

Inbreeding

F2

↓

F3

↓

F4 Winter Nursery

↓

F4:5
Plant Rows

Evaluation

Winter Nursery Increase

1st year trial

2nd year trial

AMBA

Pilot Malt

Plant Brew

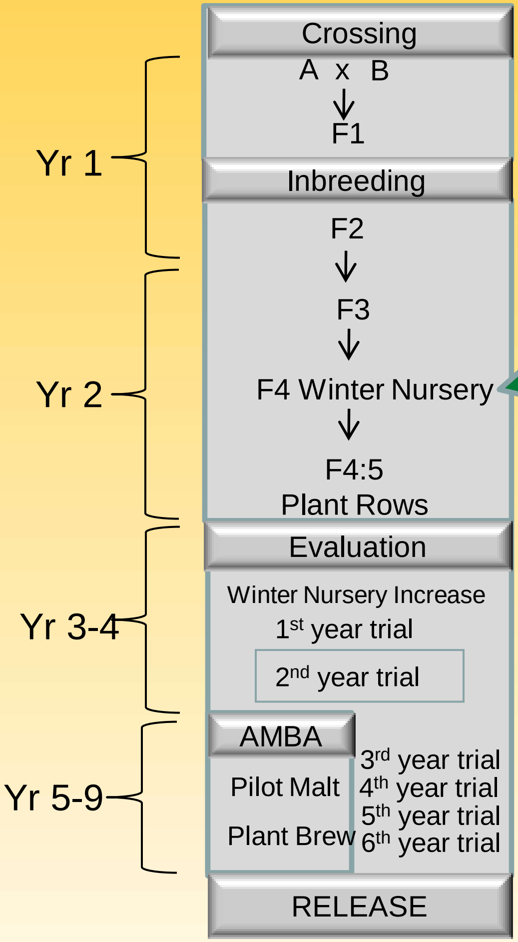
3rd year trial
4th year trial
5th year trial
6th year trial

RELEASE

<u>F2-F3 Limited Selection</u>

Visual head selection
Greenhouse seedling disease assays
Traditional MAS – single QTL

Current Scheme



Yr 1

Yr 2

Yr 3-4

Yr 5-9

Crossing

A x B

↓

F1

Inbreeding

F2

↓

F3

↓

F4 Winter Nursery

↓

F4:5

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2nd year trial

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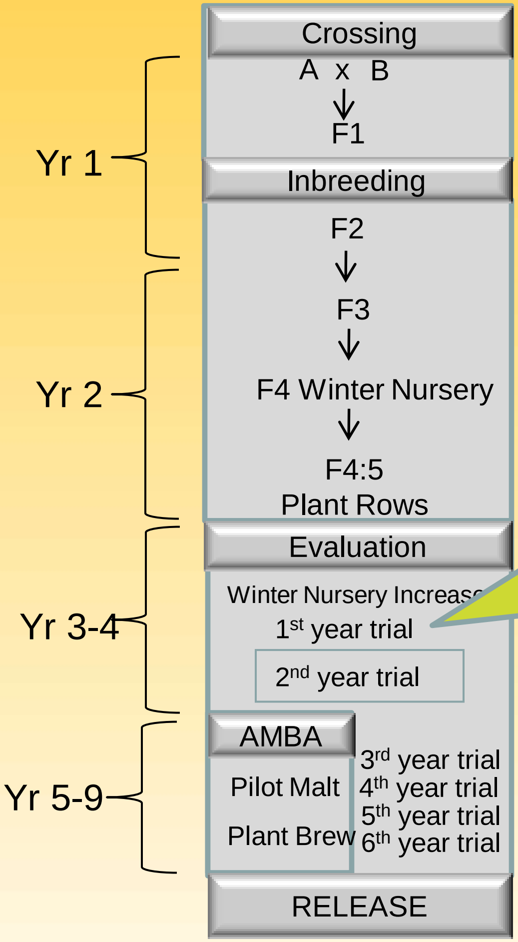
5th year trial

6th year trial

RELEASE

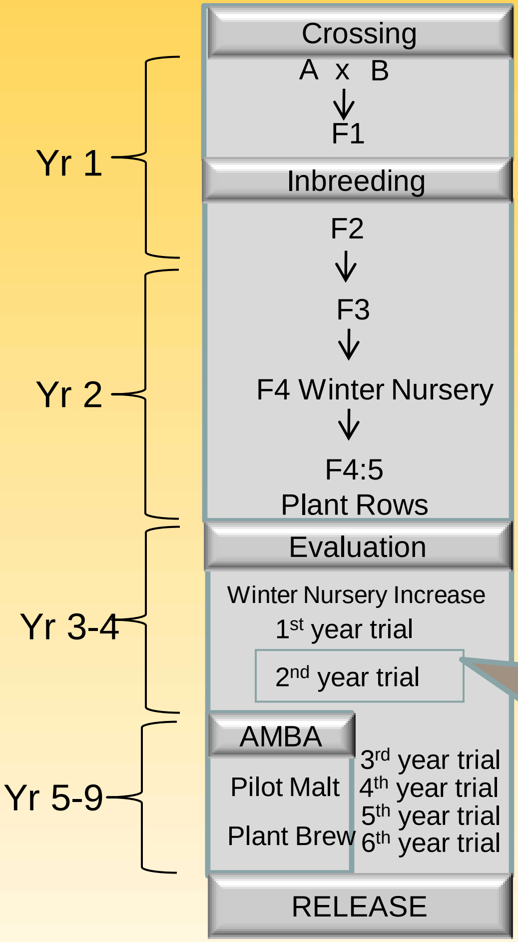
Single Plant Selection

Current Scheme



Replicated Preliminary Yield Trials (3 locations)

Current Scheme



Yr 1

Crossing

A x B

↓

F1

Inbreeding

F2

↓

Yr 2

F3

↓

F4 Winter Nursery

↓

F4:5

Plant Rows

Yr 3-4

Evaluation

Winter Nursery Increase

1st year trial

2nd year trial

Yr 5-9

AMBA

Pilot Malt

Plant Brew

3rd year trial

4th year trial

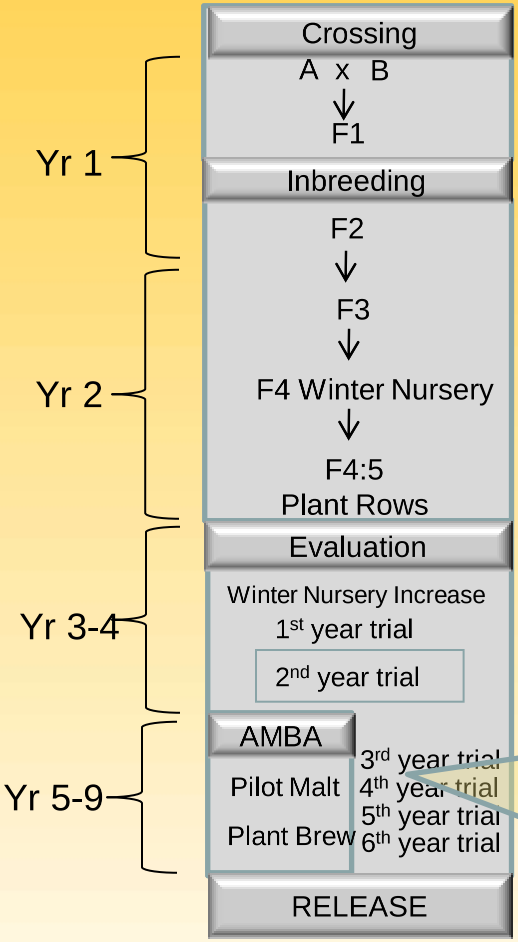
5th year trial

6th year trial

RELEASE

Replicated 2nd Year Yield Trials (5 locations)

Current Scheme



Yr 1

Crossing

A x B

↓

F1

Inbreeding

F2

↓

F3

↓

F4 Winter Nursery

↓

F4:5

Plant Rows

Yr 2

Evaluation

Winter Nursery Increase

1st year trial

2nd year trial

Yr 3-4

AMBA

Pilot Malt

Plant Brew

3rd year trial

4th year trial

5th year trial

6th year trial

Yr 5-9

RELEASE

USDA Malt Quality Lab – Yield Trials

Industry (AMBA) Pilot Malt Trials

Plant Scale Brewing

Selection Accuracy as Effected by Training Population

Evaluation of Cycle 1

6 populations randomly selected lines

Cross	n	Correlation	Heritability
1	24	0.60	0.165
2	21	0.58	0.360
3	22	0.33	0.429
4	23	0.32	0.376
5	21	0.04	0.315
6	19	0.14	0.424
All	130	0.35	0.426

Evaluation of Cycle 1 Selected Breeding Lines

Location	Correlation	Accuracy
Saint Paul	0.38	
Crookston	0.46	
2 Locations	0.54	

72 lines selected from among 25 crosses for low DON and high yield

Correlation (r) between GEBV : Observed Phenotype

Accuracy = r/H H^2 = heritability

Genotyping Logistics

Harvest F2 (field)	July 30
Plant F3 (greenhouse)	August 16
Harvest Plant Tissue	August 30
DNA Extraction/Genotyping	Sept 20
GS Predictions / Parent Selection	Sept 27
Crossing	Oct 4