Application of Genomic Selection in commercial corn breeding and crop improvement

Klaus Koehler Dow AgroSciences

Abstract:

In a breeding program, variety testing presents a significant part of the Cost. This cost is expected to increase. At the same time the cost of genotyping is being reduced annually while the amount of information (data points per sample) is being dramatically increased.

As tools are being developed to predict the performance of a genotype and its correlation to its field performance is more and more improved, genomic prediction is becoming a more and more desirable component of a routine breeding program. It will have a significant change on plant breeding.

The fist generations of a breeding cycle typically are characterized by low heritability which results in low heritability of selection in early breeding stages. The question is how much precision is needed in genomic selections to become a viable alternative to actual testing.

The presentation will show results from a genomic prediction experiment in a DAS cooperation project with Purdue. While the overall accuracy of prediction of untested lines is still relatively low for yield, the correlation between two years of testing for yield is even lower in the study. Genomic prediction shows higher correlation with yield in 2012 than actual yield trials in 2011.

This indicates that genomic prediction has the potential to better predict the performance of a genotype in a future year than previous year yield trials.

APPLICATION OF GENOMIC SELECTION IN COMMERCIAL CORN BREEDING AND CROP IMPROVEMENT

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Solutions for the Growing World

Dow AgroSciences

- Global Headquarters in Indianapolis, Indiana
- Annual Sales: >$ 7 billion in 2013
- Achieved milestone of $1 in seed sales in 2011
- Fastest growing seed company
- Employs 7000+ employees globally
- Serving markets in more than 150 nations
- Backing and leverage of a $60 B+ parent company

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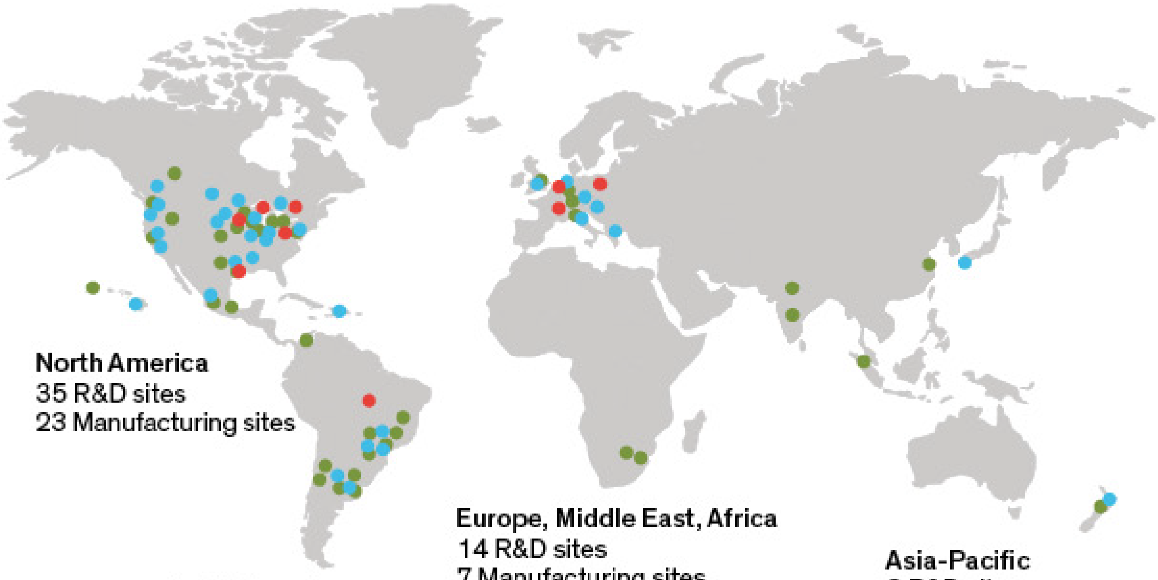
Global Operations



North America
35 R&D sites
23 Manufacturing sites

Latin America
10 R&D sites
20 Manufacturing sites

Europe, Middle East, Africa
14 R&D sites
7 Manufacturing sites

Asia-Pacific
3 R&D sites
5 Manufacturing sites

- ● **Recent Strategic Seed and Trait-related Bolt-on Acquisitions**
- ● **R&D Sites**
- ● **Manufacturing Sites**

Dots represent locations, not the number of sites in each location.

Rapid worldwide expansion.

Facilities in more than 40 countries
and products sold in more than 130 countries.

More than 7,000 employees worldwide.

Genomics and Corn breeding

- In corn breeding **yield testing** represents **half of breeding budget**:

  in search for **yield**, **stability** and related traits that **reward the farmer**

- **Field testing** will stay **expensive** (sophisticated equipment, land values, commodity pricing is up)
- **Genotyping** is becoming **cheaper** (currently less than 1/3 of yield test per candidate line)
- **Genomic pre-selection** will **change plant breeding**:
  - > **Increase response to selection** (=better mean of population to select)
  - > **Change allocation** of program for **first years field testing**
  - > **We must** as much as possible **integrate into our routine breeding cycle**
- Can Genome-based selection provide better advancements?

The reality of breeding ….

… and how we can improve

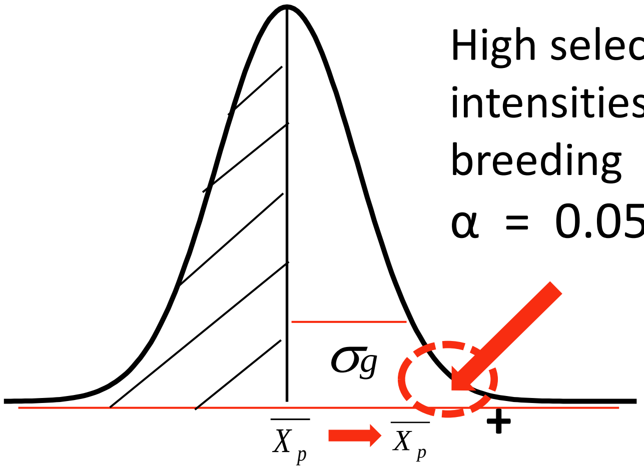
- **Understand the important genetics for inheritance** of **major** selection **traits**
  - > **Yield and yield related (quantitative traits – many controlling loci – small effects)**
  - > Typical breeding programs have **low heritability** (repeatability) of the **most important phenotypic trait = yield, especially** in **first year(s) of testing**: many entries - few replications = lower accuracy of selection

Multi- stage Select for:

☐ Hybrid yield

☐ Inbred per-se

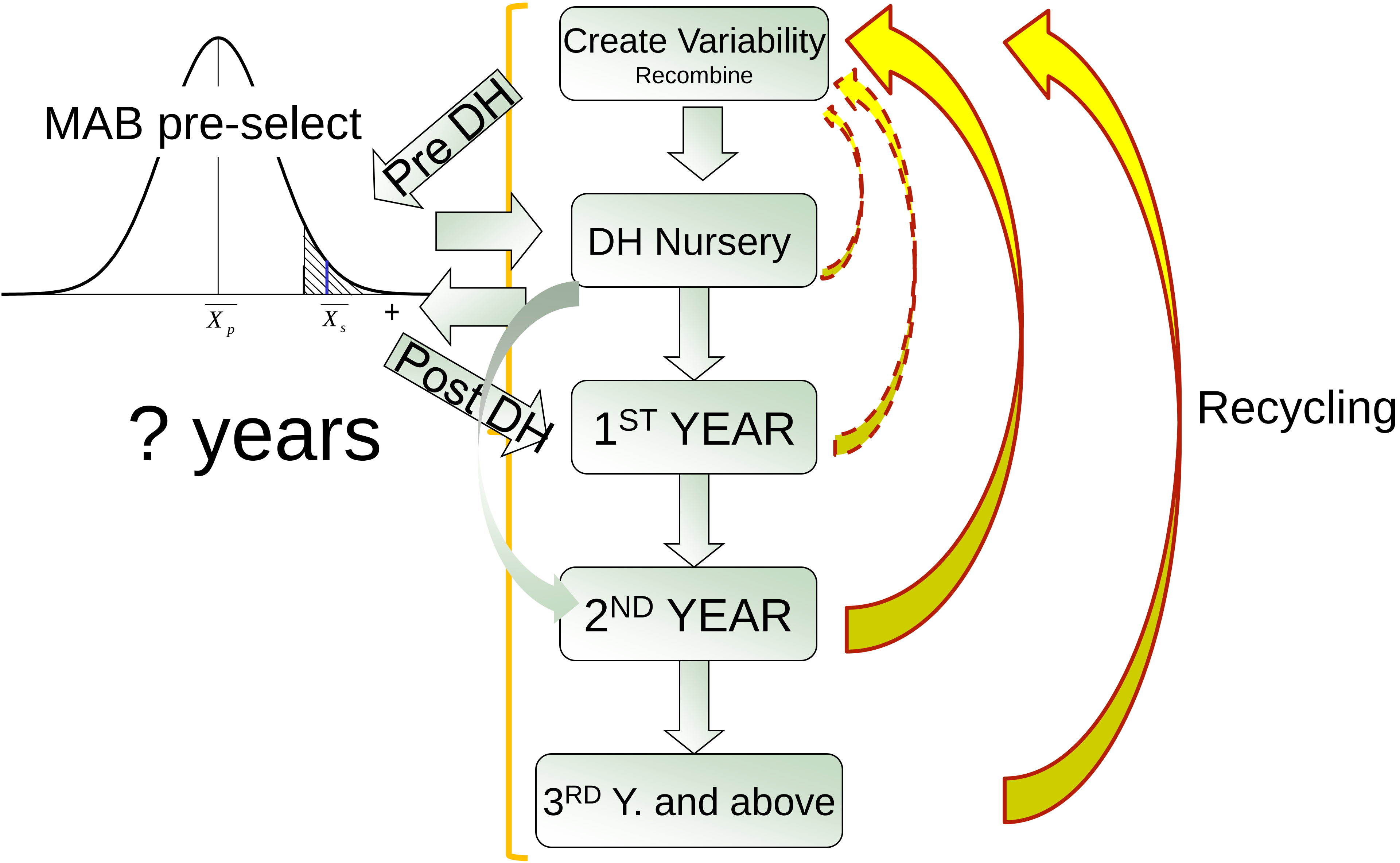
☐ GS= genomic selection: How much precision do we need?



High selection intensities in most plant breeding stages

α = 0.05 to 0.1

Breeding cycle



MAB pre-select

Pre DH

Post DH

? years

Create Variability
Recombine

DH Nursery

1ST YEAR

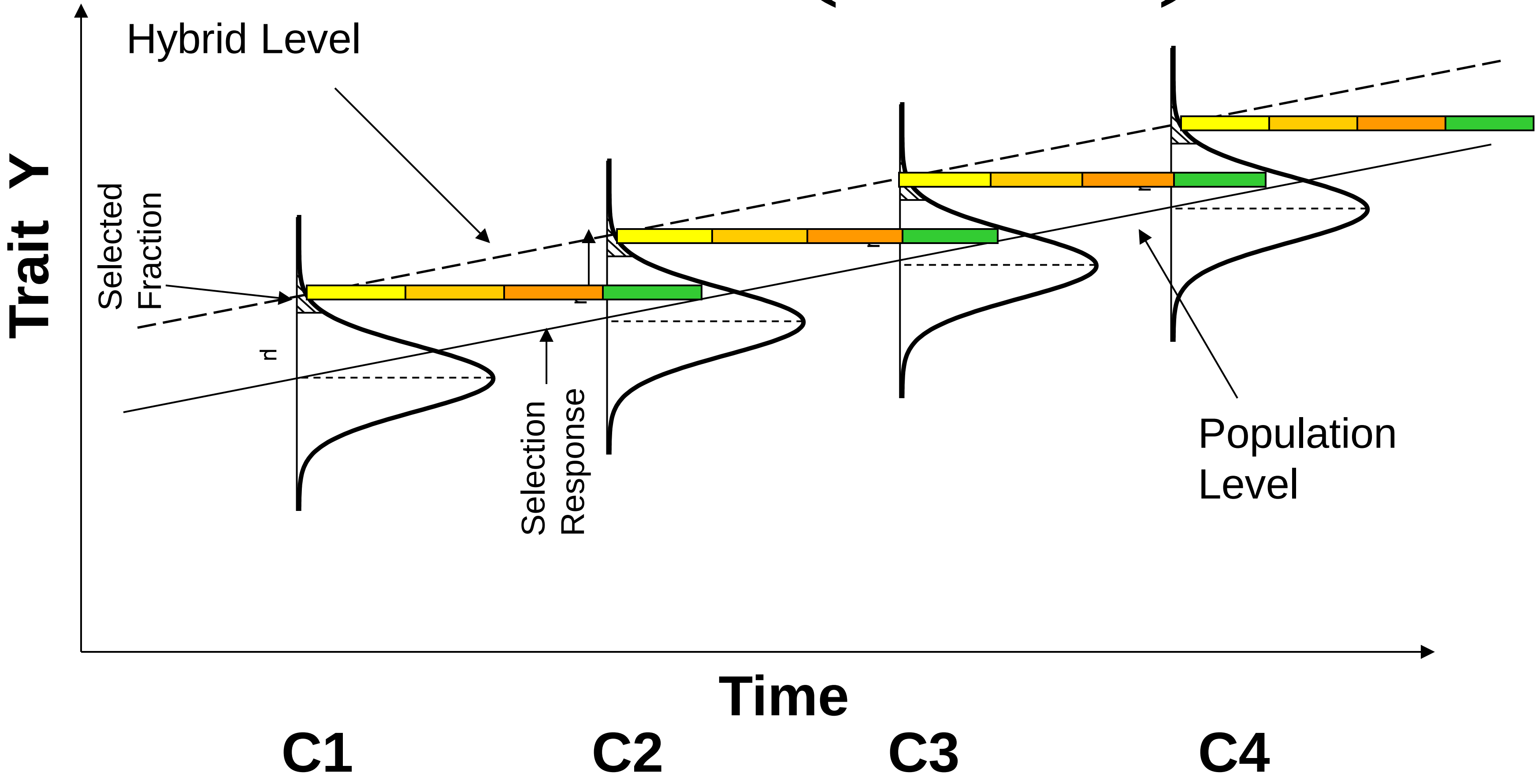
2ND YEAR

3RD Y. and above

Recycling

Germplasm improvement- Hybrid Development

$$G/Y = (h^2 i\sigma)/Y$$



Hybrid Level

Trait Y

Selected Fraction

Selection Response

Population Level

Time

C1

C2

C3

C4

Project with J. Morales and T. Rocheford; Purdue University unpublished

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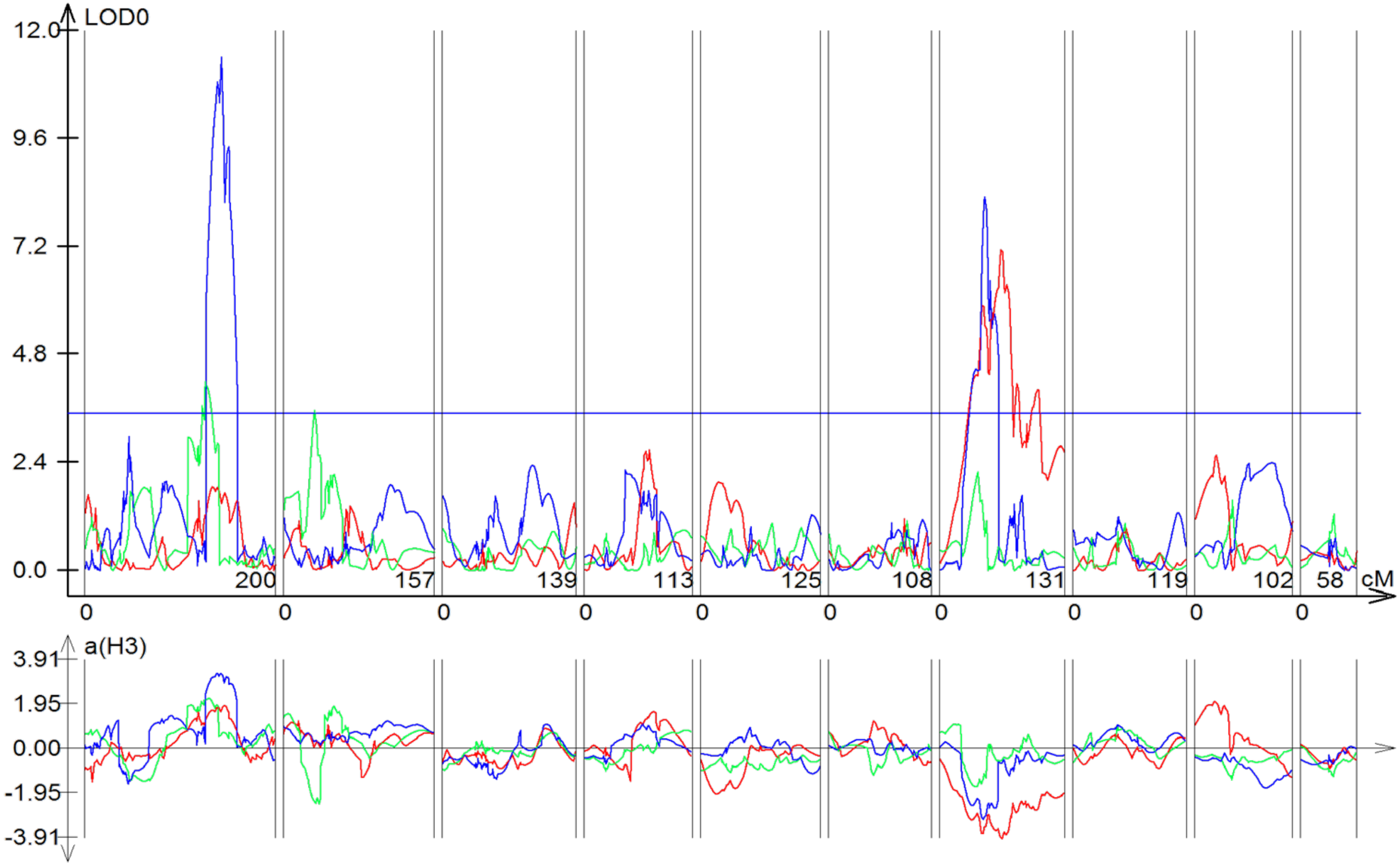
Solutions for the Growing World

QTL for Yield in $F_{2:3}$ Population of LH51xPHG35



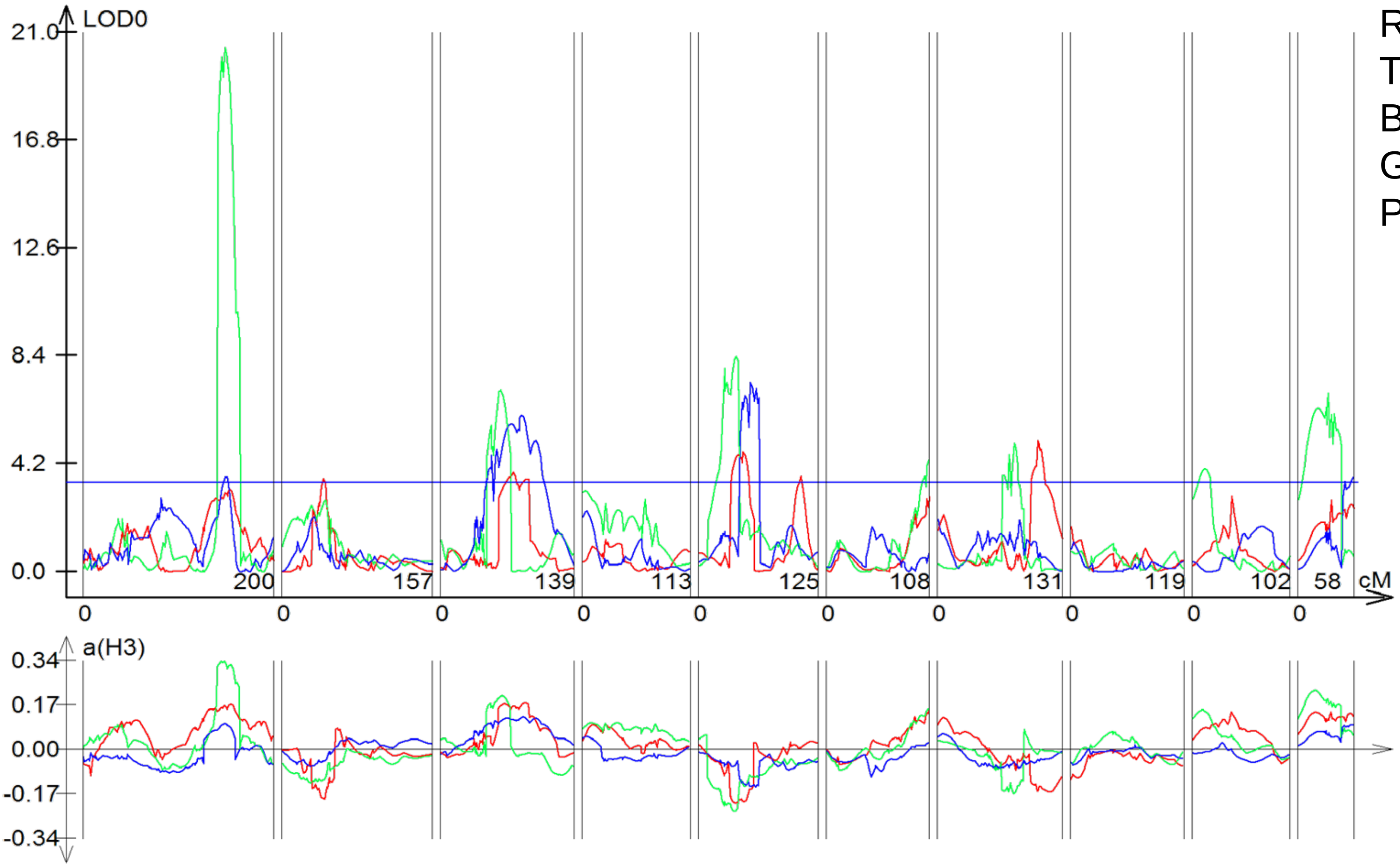
Red=DAS Tester
Blue = LH119
Green = PHG39

358 lines

407 polymorphic SNP markers from 1536 total

Figure 2-3. LOD profile (top) and additive effects (below) for yield in DAS (red), LH119 (blue), and PHG39 (green) testcrosses. Chromosomes are separated by vertical black lines. LOD threshold equal to p=0.05 is represented by a horizontal blue line.

QTL for Moisture in F2:3 Population



Red=DAS Tester
Blue = LH119
Green = PHG39

Figure 2-4. LOD profile (top) and additive effects (below) for moisture in DAS (red), LH119 (blue), and PHG39 (green) testcrosses. Chromosomes are separated by vertical black lines. LOD threshold equal to p=0.05 is represented by a horizontal blue line.

Significant QTL on Chromosome 1 in LH119 Testcross

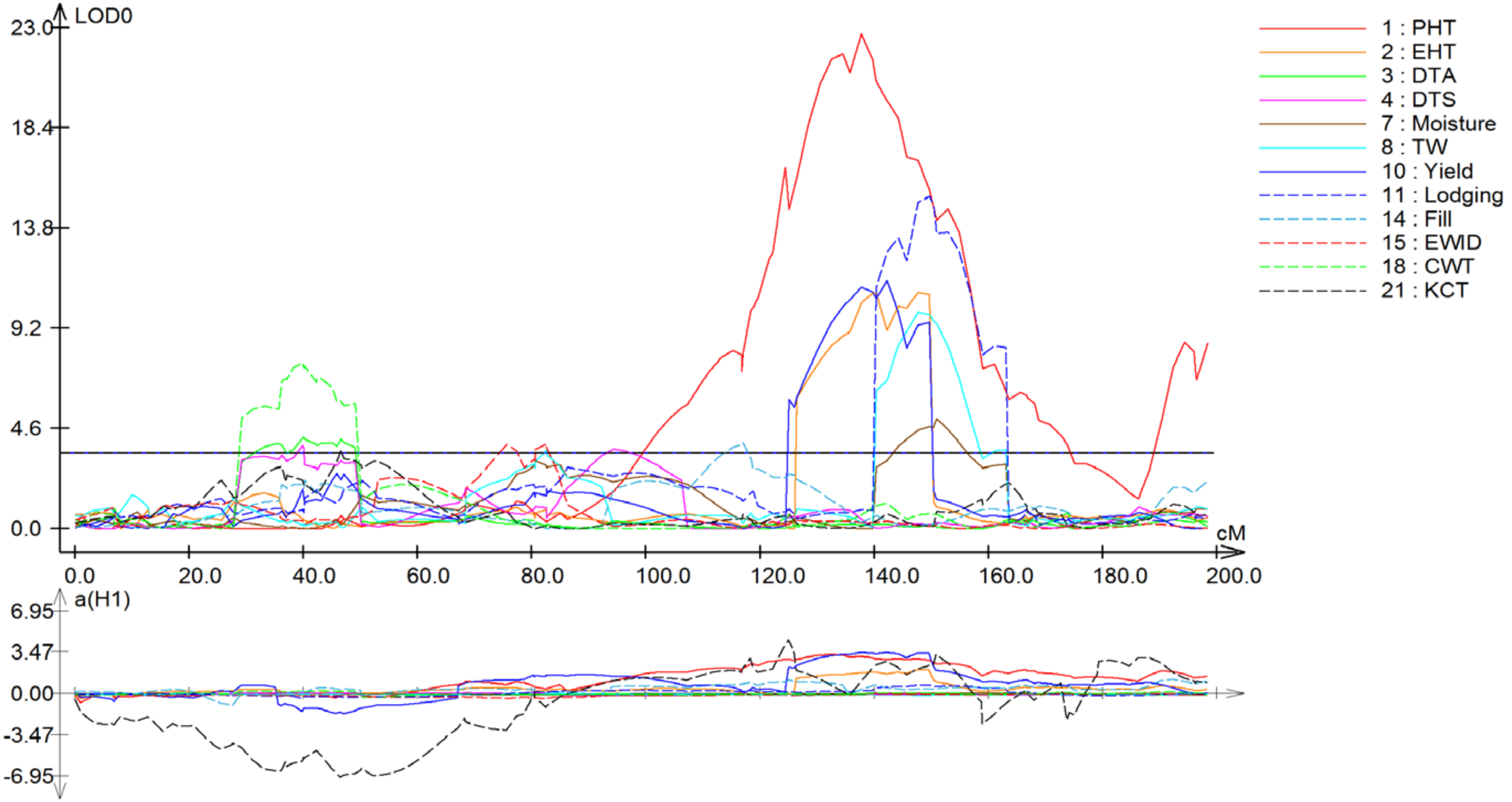
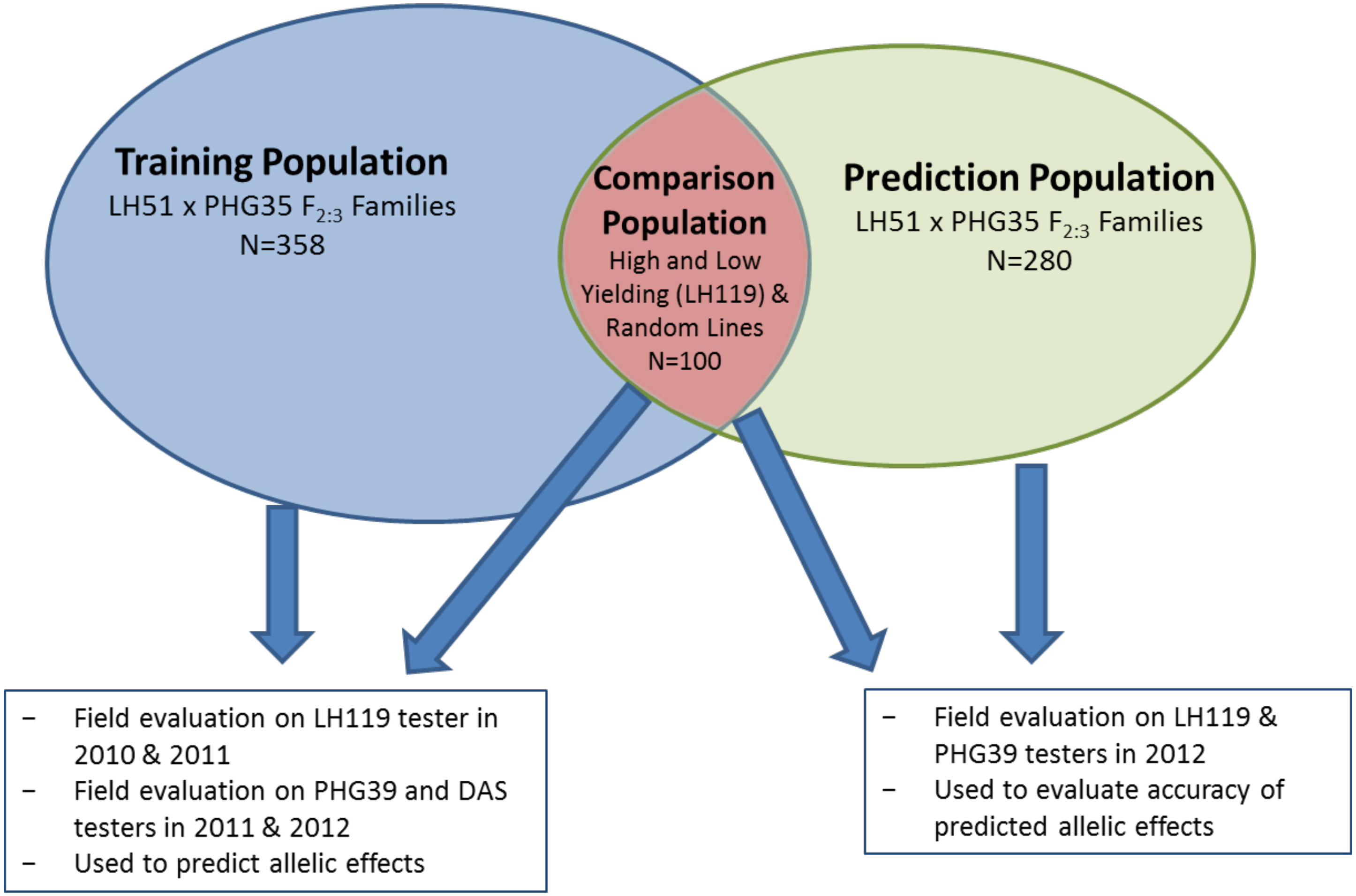


Figure 2-6. LOD profile (top) and additive effects (below) for traits with significant QTL on chromosome 1 in LH119 testcross. LOD threshold equal to p=0.05 is represented by a horizontal black line.

Experimental Design



Training Population
LH51 x PHG35 $F_{2:3}$ Families
N=358

Comparison Population
High and Low Yielding (LH119) & Random Lines
N=100

Prediction Population
LH51 x PHG35 $F_{2:3}$ Families
N=280

- Field evaluation on LH119 tester in 2010 & 2011
- Field evaluation on PHG39 and DAS testers in 2011 & 2012
- Used to predict allelic effects

- Field evaluation on LH119 & PHG39 testers in 2012
- Used to evaluate accuracy of predicted allelic effects

Training population tested in 7 environments using unreplicated design with replicated checks. Spatially corrected BLUPs were used to calculate predictions. Allelic effects of 284 markers were calculated

Validation of Genomic Selection Model

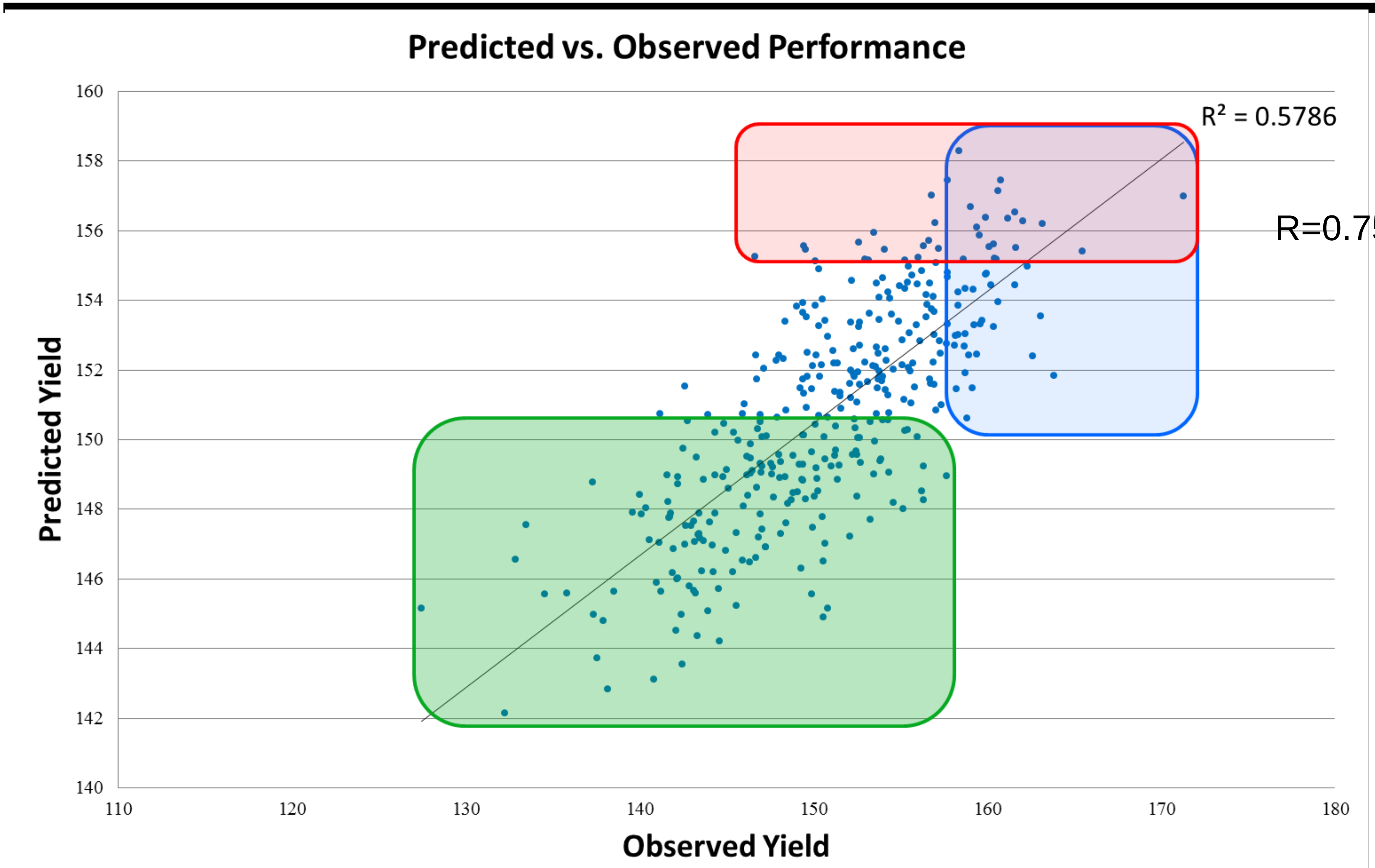
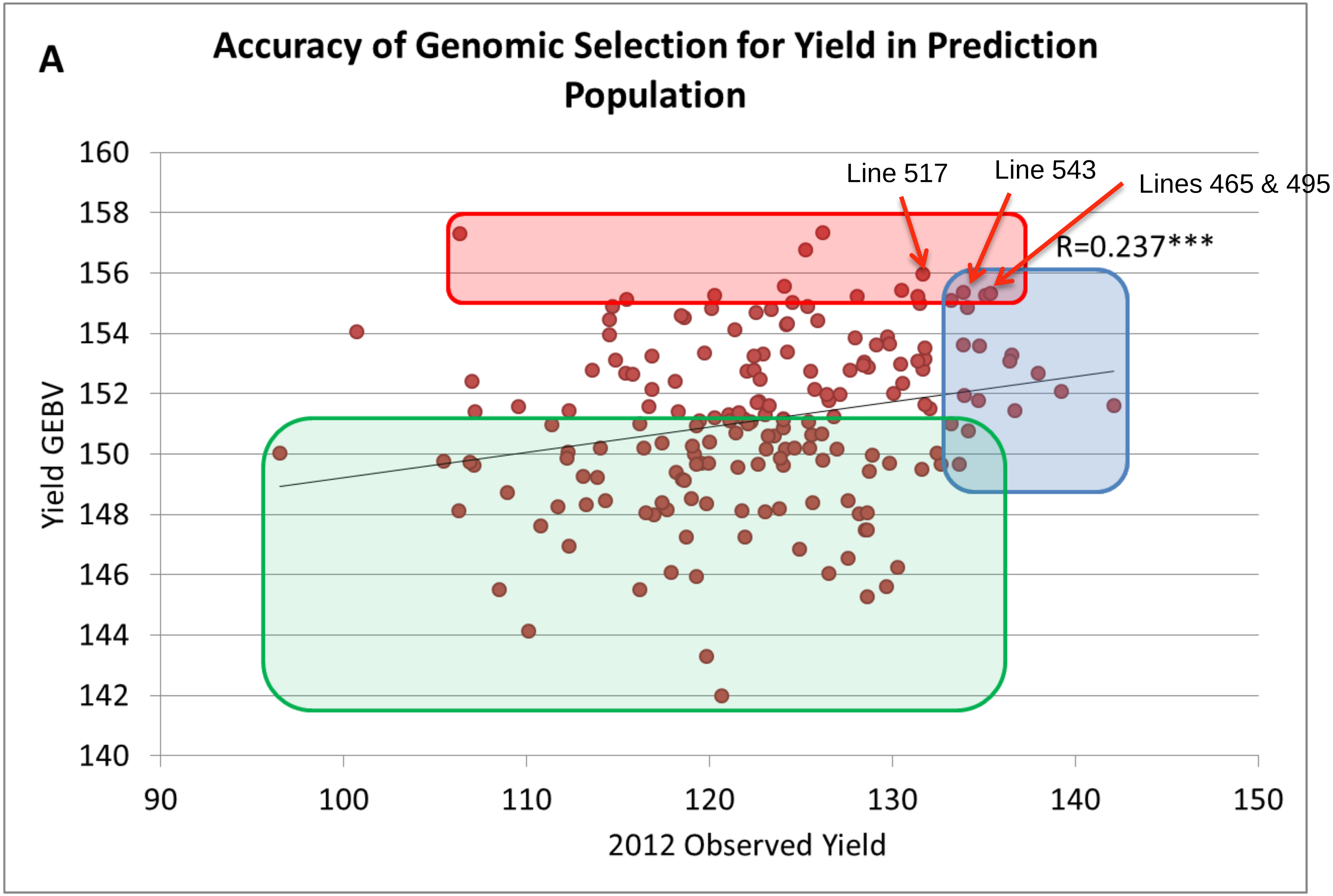


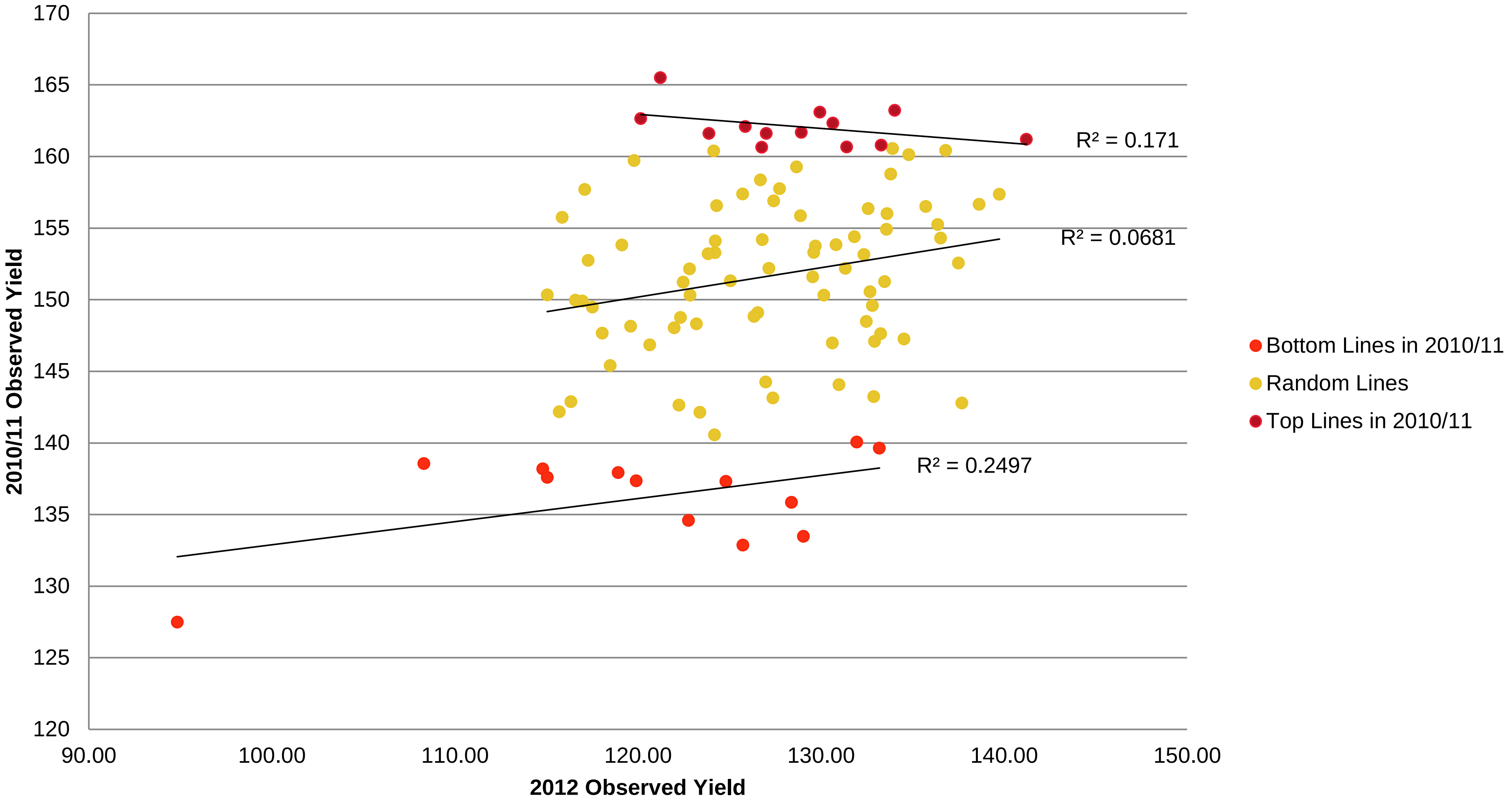
Figure 4-1. Cross-validation of Genomic Selection model. 358 $F_{2:3}$ families testcrossed to LH119 were evaluated for yield in 2010 and 2011 in 7 environments and BLUPs were calculated across environments (observed yield). BLUPs were used to estimate alleleic effects which were then used to estimate a genome estimated breeding value (GEBV) for the training population.

Accuracy of Predicting Untested Lines



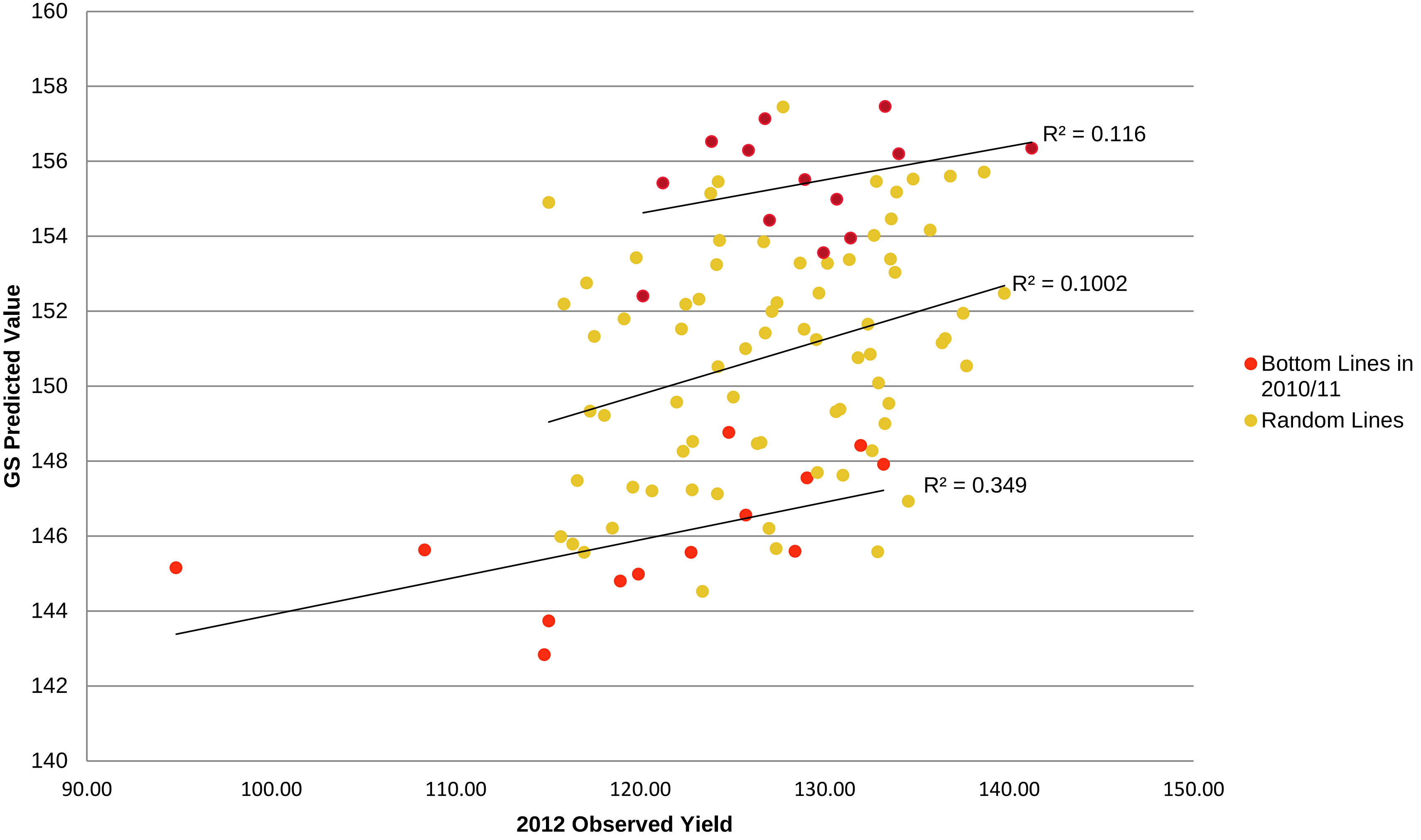
GEBV and 2012 yield data on 180 untested $F_{2:3}$ families were testcrossed to LH119. Arrows indicate families that were selected based on GEBVs and induced.

A. Accuracy of Yield Prediction Using 2010/2011 Yield Data



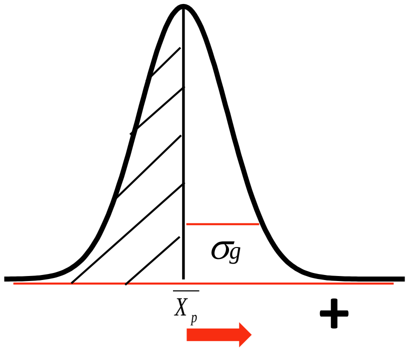
Comparison of 2010/2011 yield data and 2012 yield data in lines selected from the training population. 13 top, 13 bottom, and 76 random $F_{2:3}$ families from the training population were grown along side the untested (predicted) families and evaluated for yield. The correlation between 2010/2011 performance and 2012 performance is very similar to the correlation between predicted and observed performance in untested families.

B. Accuracy of 2012 Yield Predictions Using Genomic Selection



Comparison of GEBV and 2012 yield data in lines selected from the training population. 13 top, 13 bottom, and 76 random $F_{2:3}$ families from the training population were grown along side the untested (predicted) families and evaluated for yield.

Conclusion



- Genomic performance prediction can be better than phenotypic performance prediction based on previous year performance
- It might be easier to predict the lower performance distribution of our breeding populations through GS than the high
- Genomic selection in early breeding stages can improve efficiency of breeding programs as it might have a better potential to predict future performance, i.e. estimate true(er) breeding value than the phenotype for a given future year

Thank You