

A Regional Approach to Genomic Selection for Scab Resistance

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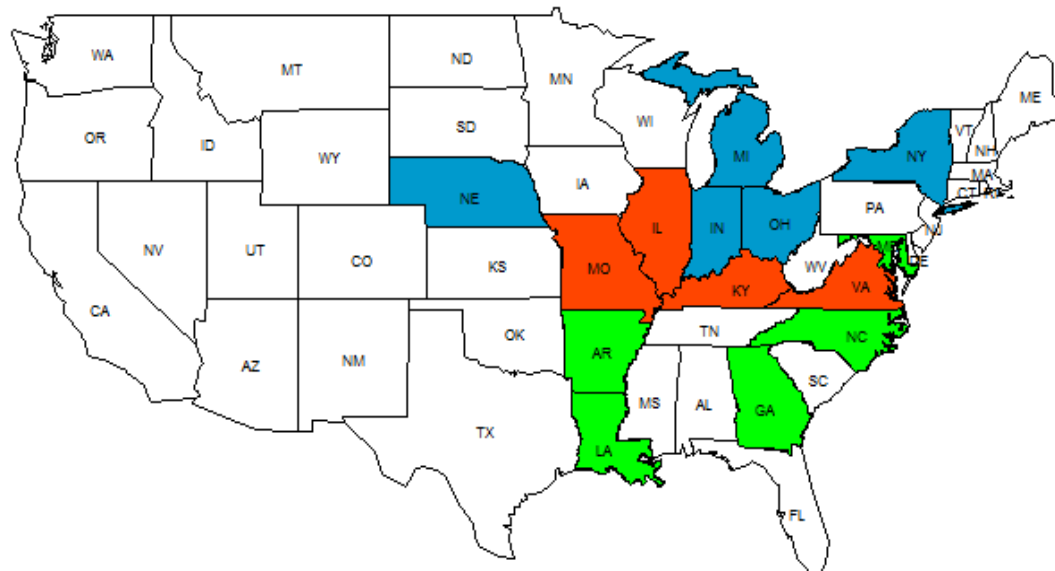
US Wheat & Barley Scab Forum



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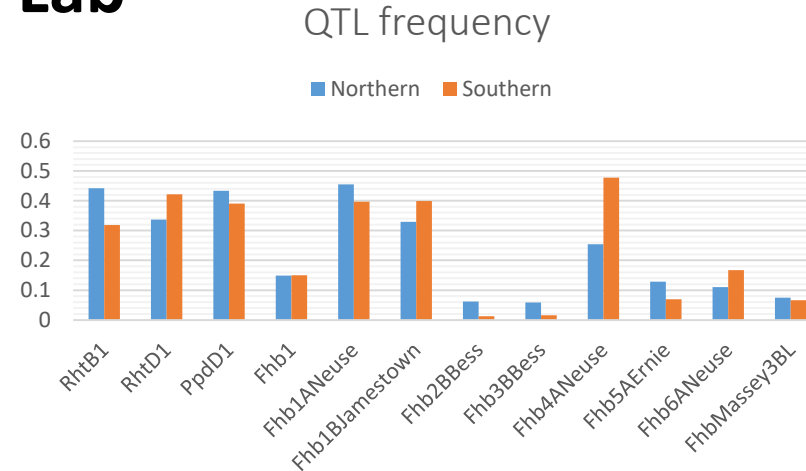
Cooperative Scab Nurseries

- Eastern Cooperative Nurseries:
 - **Northern Uniform Scab Nursery** (Blue, Red)
 - **Preliminary Northern Uniform Scab Nursery** (Blue, Red)
 - **Southern Uniform Scab Nursery** (Green, Red)
 - Public and private breeding effort
 - Facilitate germplasm exchange
 - Identify new sources of Scab resistance

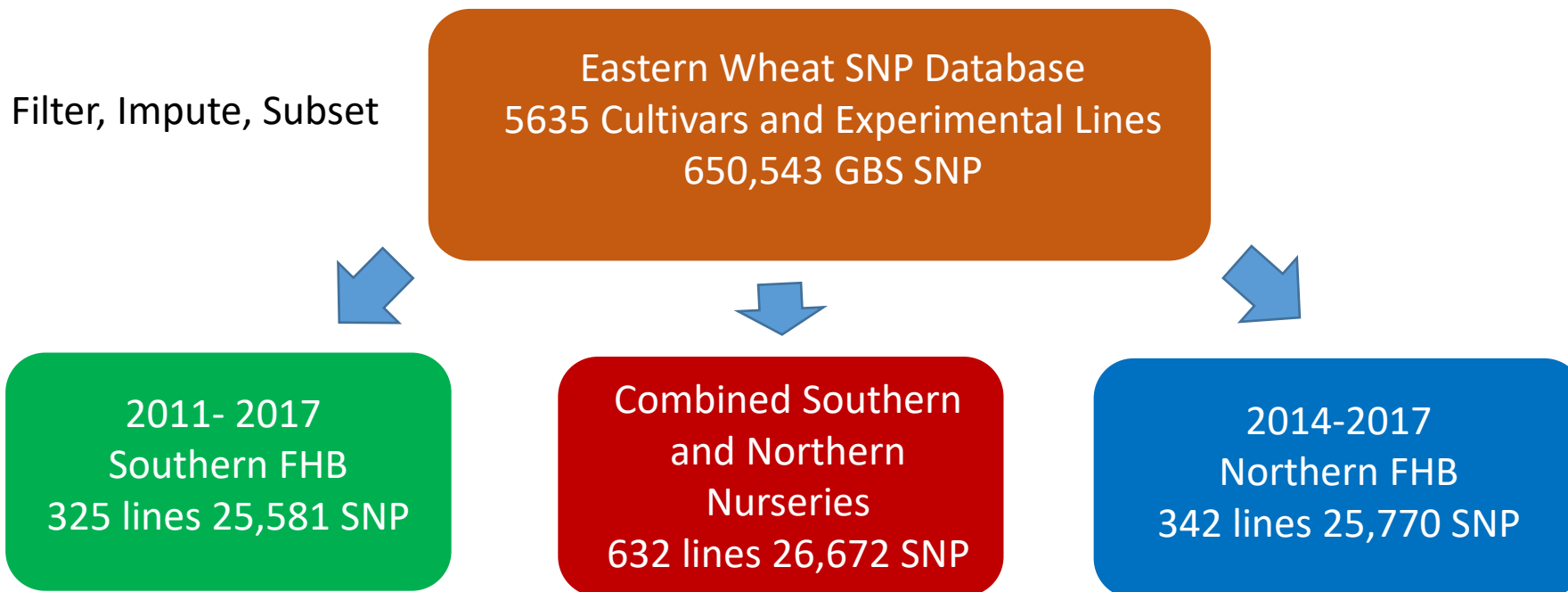


Eastern Regional Genotyping Lab

- Assay samples with trait related markers
- Evaluated FHB nurseries since 2008
- Added markers for QTL from SRWW cultivars
- Genome-wide marker data



Genome-Wide Marker Data



Phenotypic Summary Regional Nurseries

- Linear mixed model for phenotypic data analysis:

$$y = \mu + E + G + \varepsilon$$

- μ = Overall mean
- E = Effect of Environment



| | Severity (%) | | | FDK (%) | | | DON (ppm) | | |
|-------------|--------------|-------|----------|---------|-------|----------|-----------|-------|----------|
| Nursery | North | South | Combined | North | South | Combined | North | South | Combined |
| No. Env | 68 | 68 | 136 | 42 | 49 | 91 | 32 | 35 | 67 |
| No. Records | 3536 | 3735 | 7271 | 2208 | 2696 | 4904 | 1696 | 1903 | 3599 |
| Mean | 30.3 | 30.8 | 30.56 | 29.4 | 30.1 | 29.1 | 8.73 | 10.1 | 9.5 |
| H2 | 0.26 | 0.3 | 0.29 | 0.2 | 0.33 | 0.27 | 0.31 | 0.38 | 0.37 |

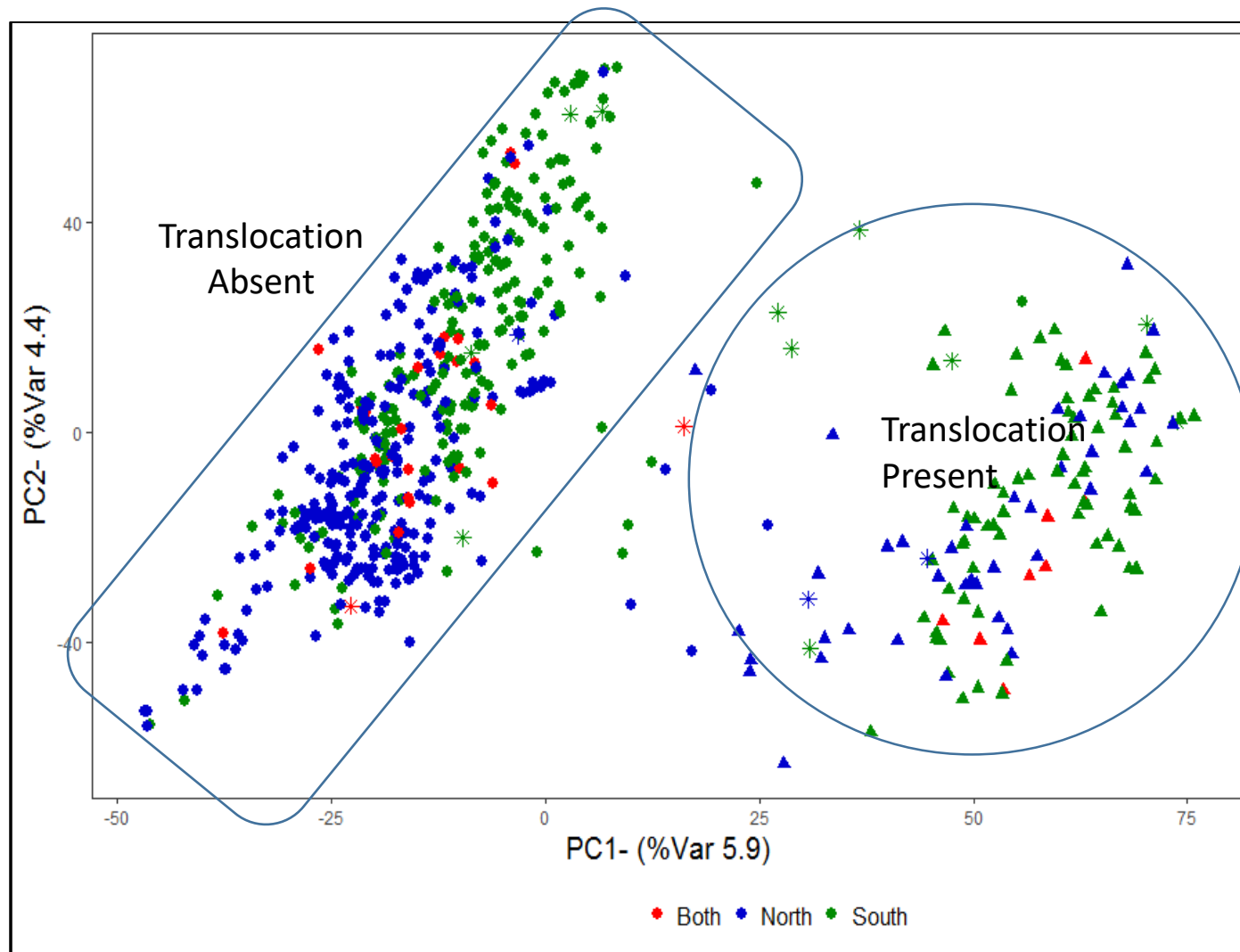
- Genotype/Variety was fixed and the other effects random
- BLUE: Overall mean plus the genotypic effect was used in the genomic selection model

Association Mapping



- **Materials and method**
 - **Plant Material:**
 - NUWWSN- PNUWWSN 2014-2017 (342 genotypes)
 - SUWWSN 2011-17 (325 genotypes)
 - Combined regional nurseries (625 genotypes)
 - **Mixed Model: (Q + K)** (Yu et al., 2006)
 - $y = X\beta + Qv + Zu + e$
 - Software for AM: GAPIT R Package

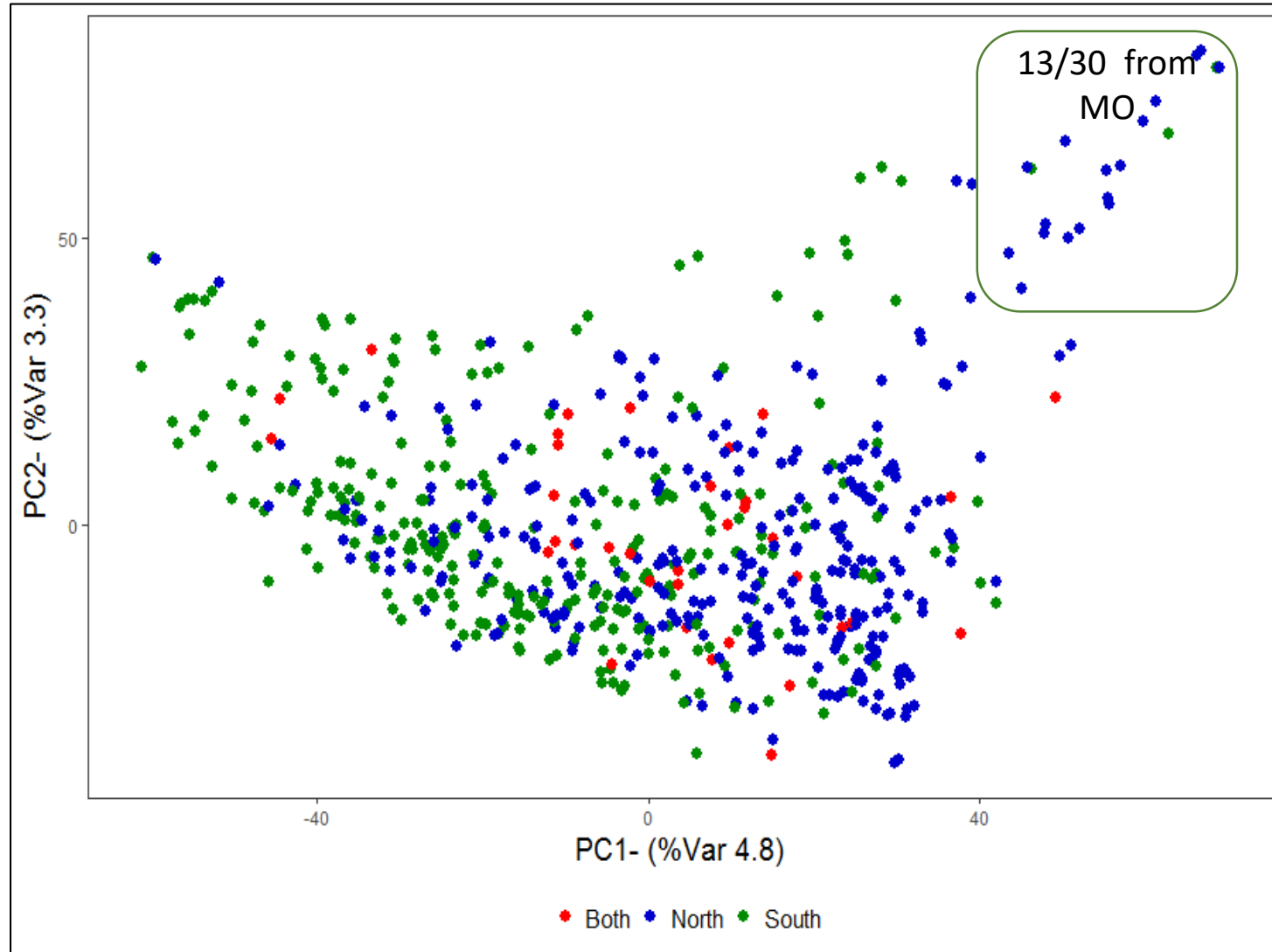
Population Structure in the Regional Nurseries



The translocation 2BS:2GS·2GL:2BL from *Triticum timopheevii* was the main driver of subpopulation differentiation identified from PCA.

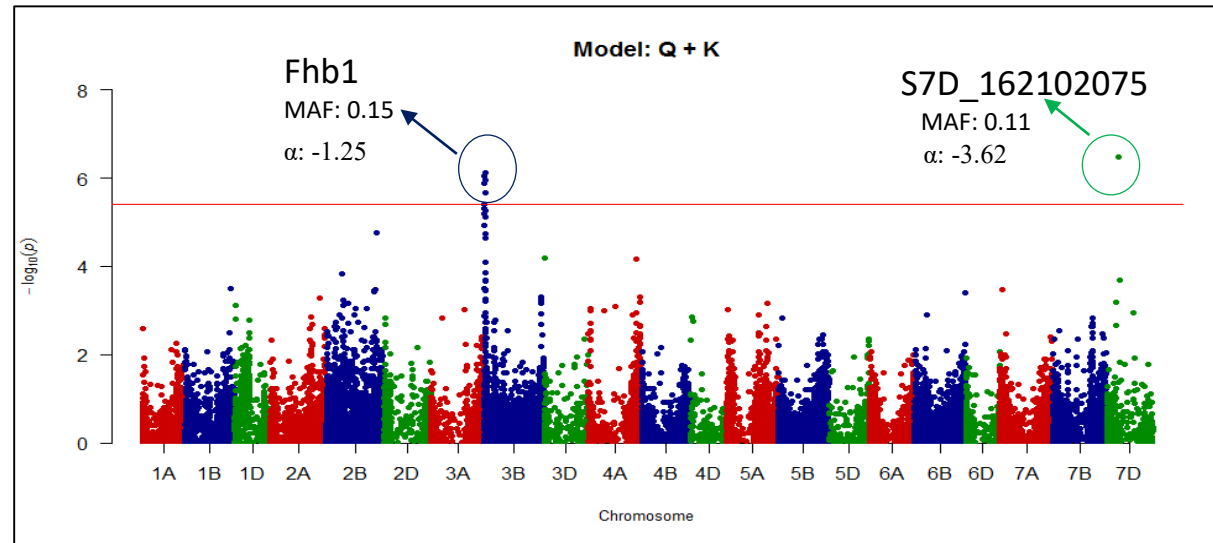
Population Structure in the Regional Nurseries

Principal component analysis after remove chromosome 2B

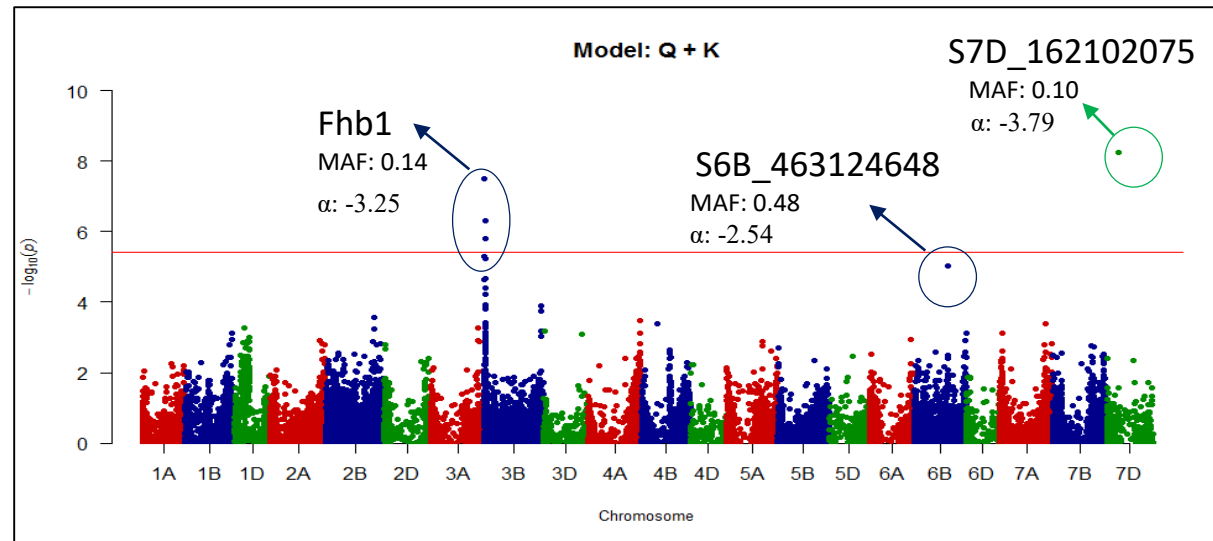


Association mapping Severity

North

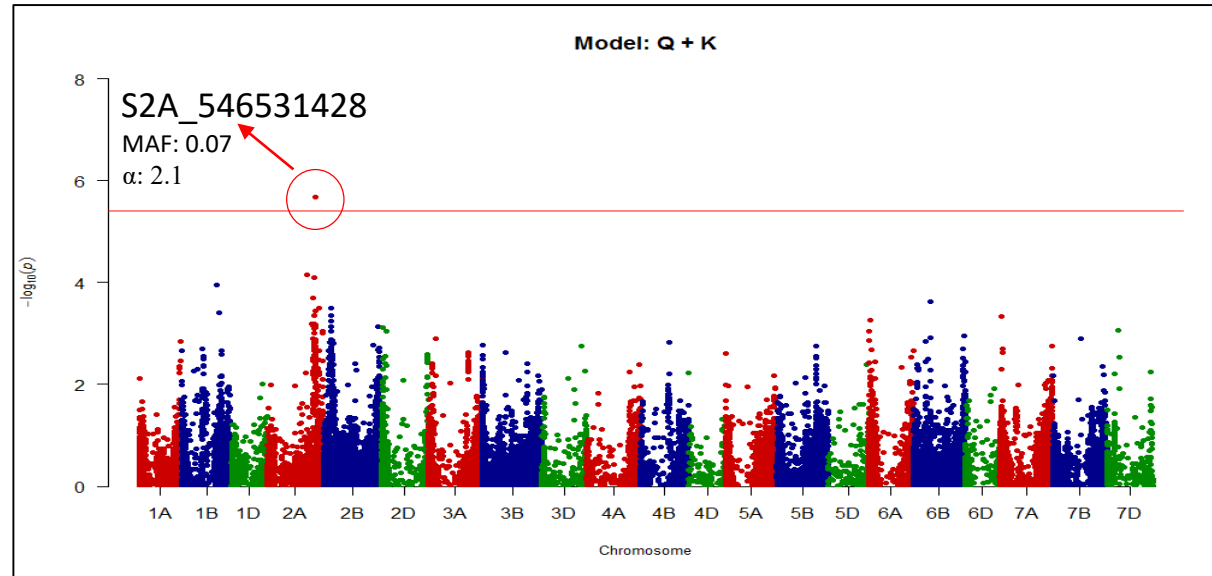


Combined

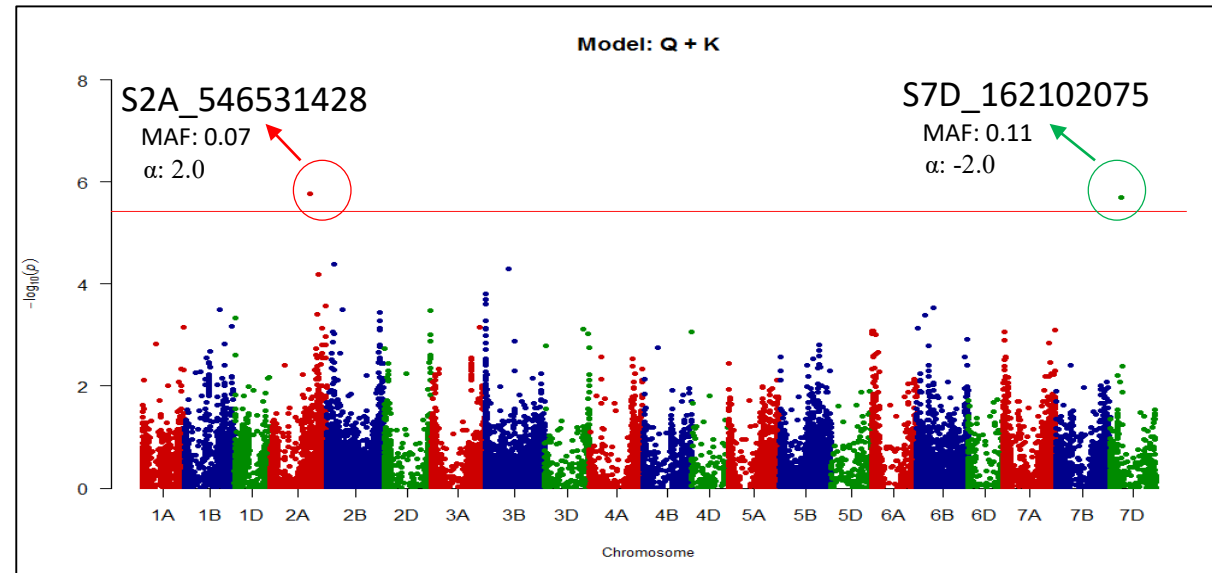


Association mapping DON

South

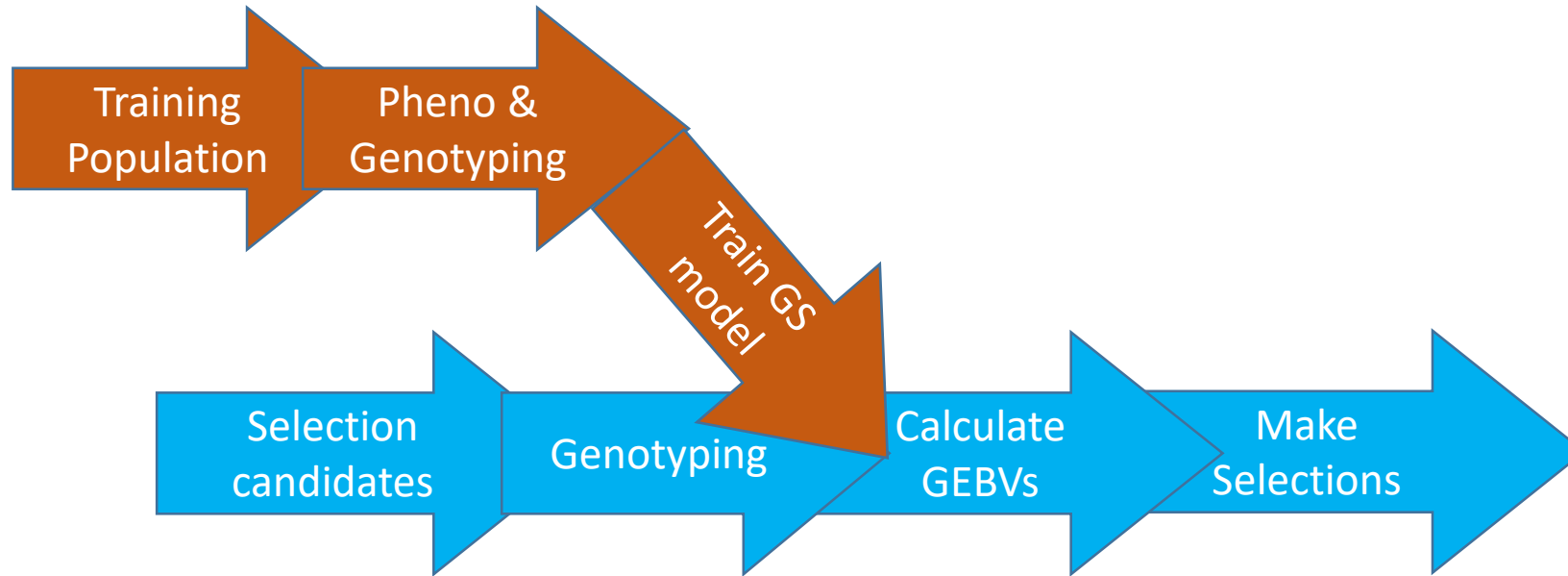


Combined



Genomic selection

- Plant breeding tool that uses statistical modeling to predict how a genotype will perform, without field-testing
- How does GS work?

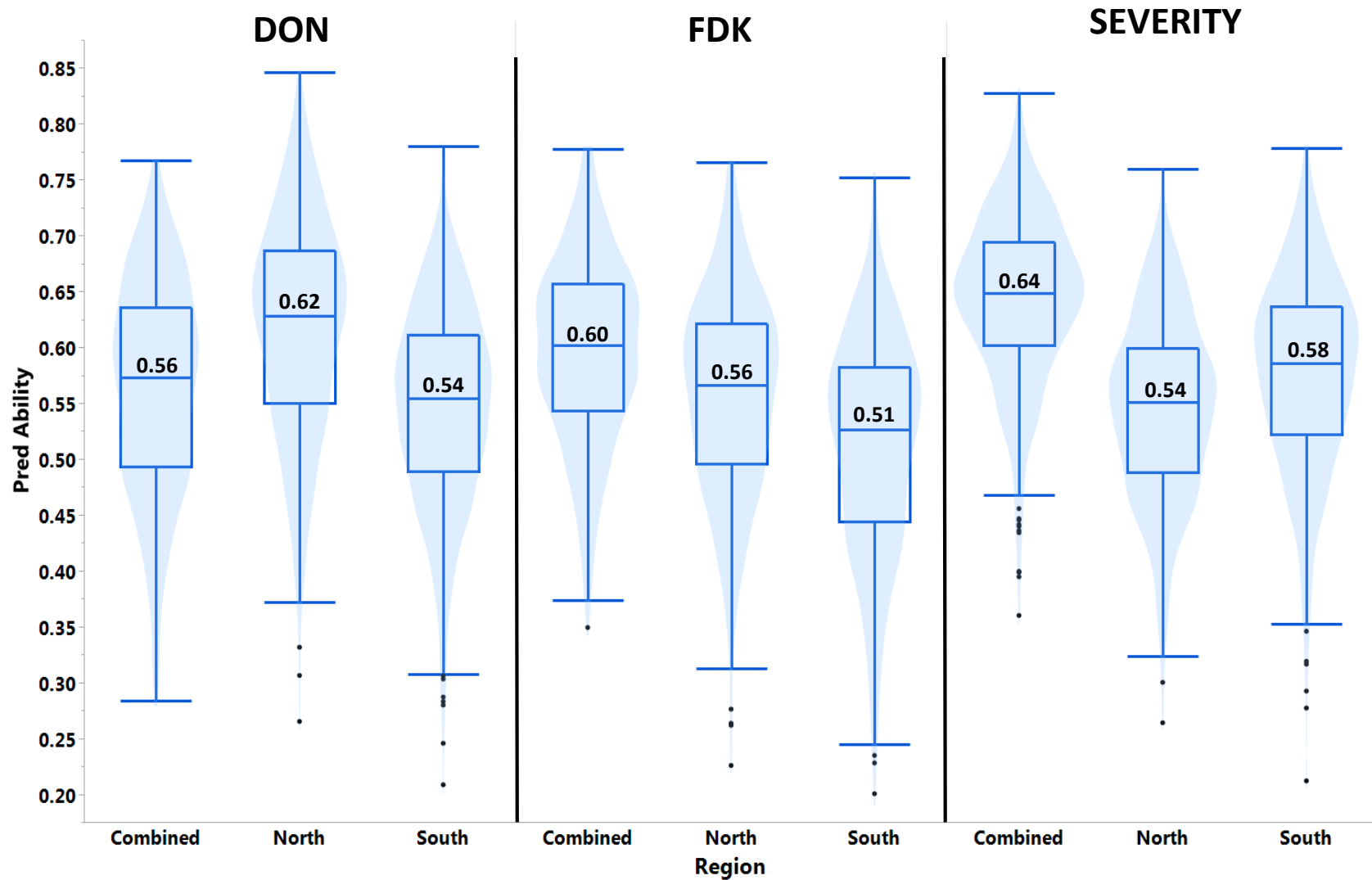


Adapted from Heffner, et al. 2009. Genomic selection for crop improvement. *Crop Science*, 49: 1-12.

- Prediction model to integrate Phenotypic and Genotypic Data (RR-BLUP)

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$$

Prediction Ability FHB Uniform Scab Nurseries

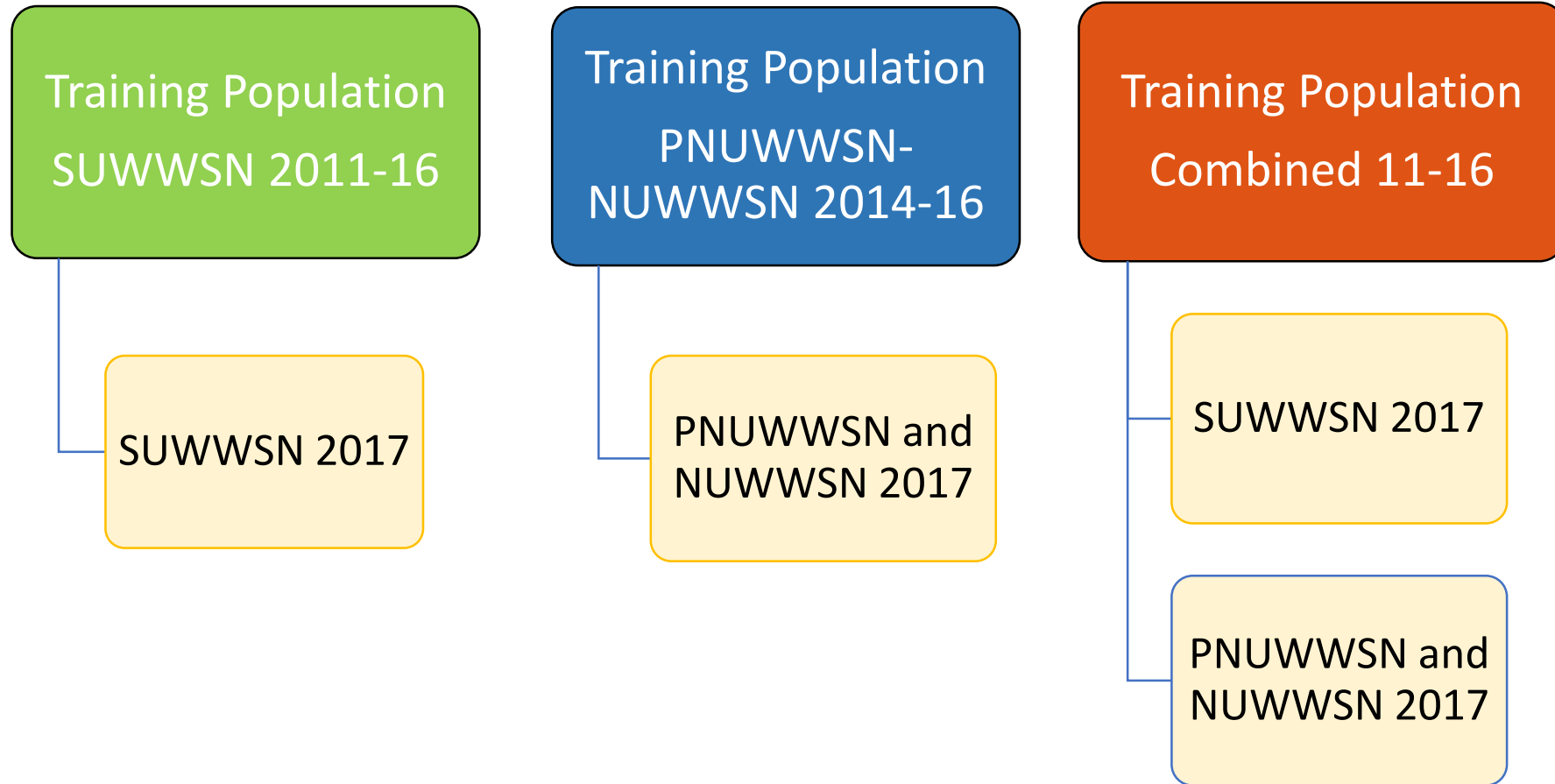


10 Fold Cross Validation- 500 cycles

Pred Ability: $\rho(\text{GEBV}/\text{BLUE})$

Prediction of independent sets

Comparison of predictions within and between regional Scab nurseries

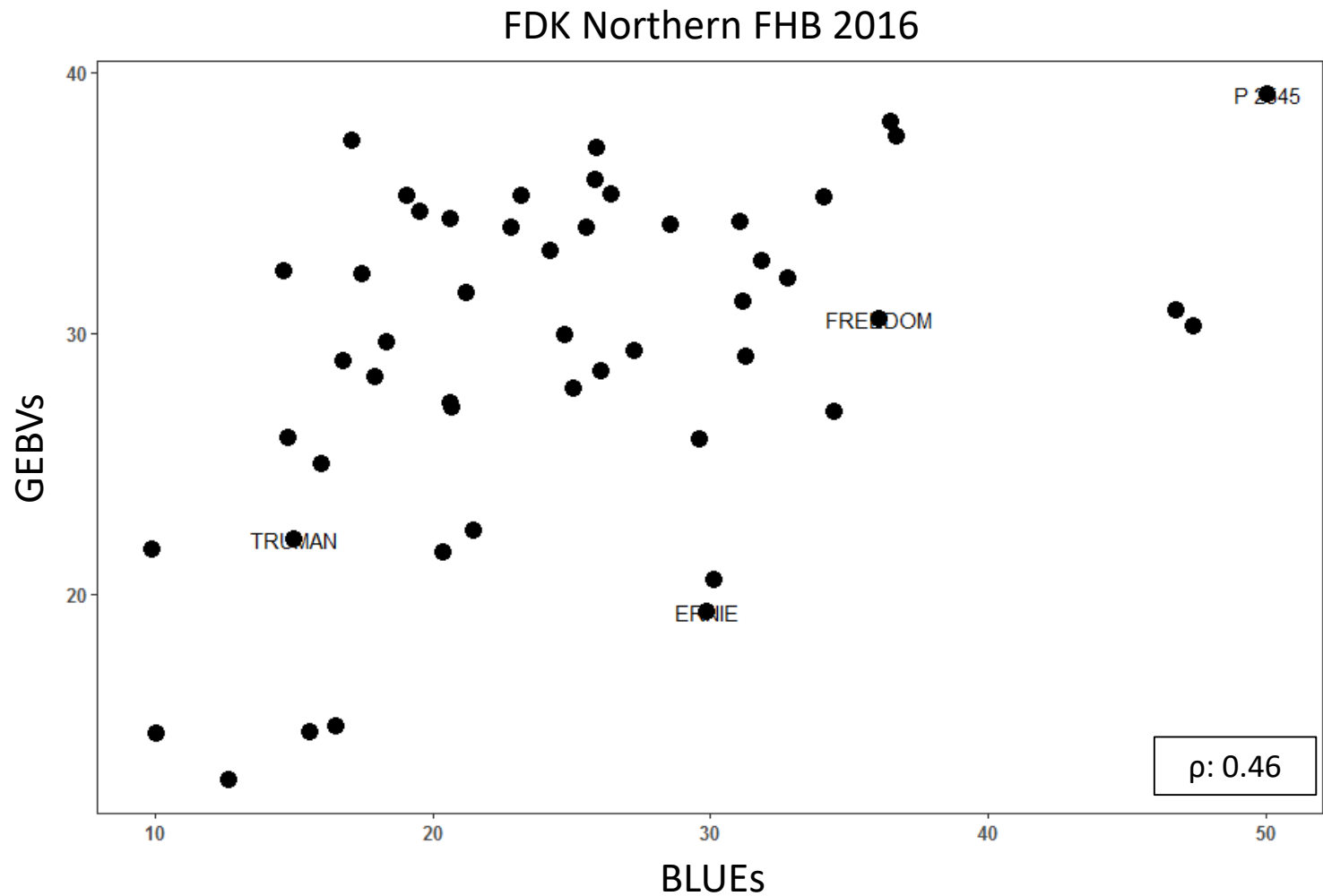


The procedure was repeated to predict 1 year at a time for year 2014-15-16-17

FHB Prediction by Combining Scab Nurseries



BLUEs vs GEBVs

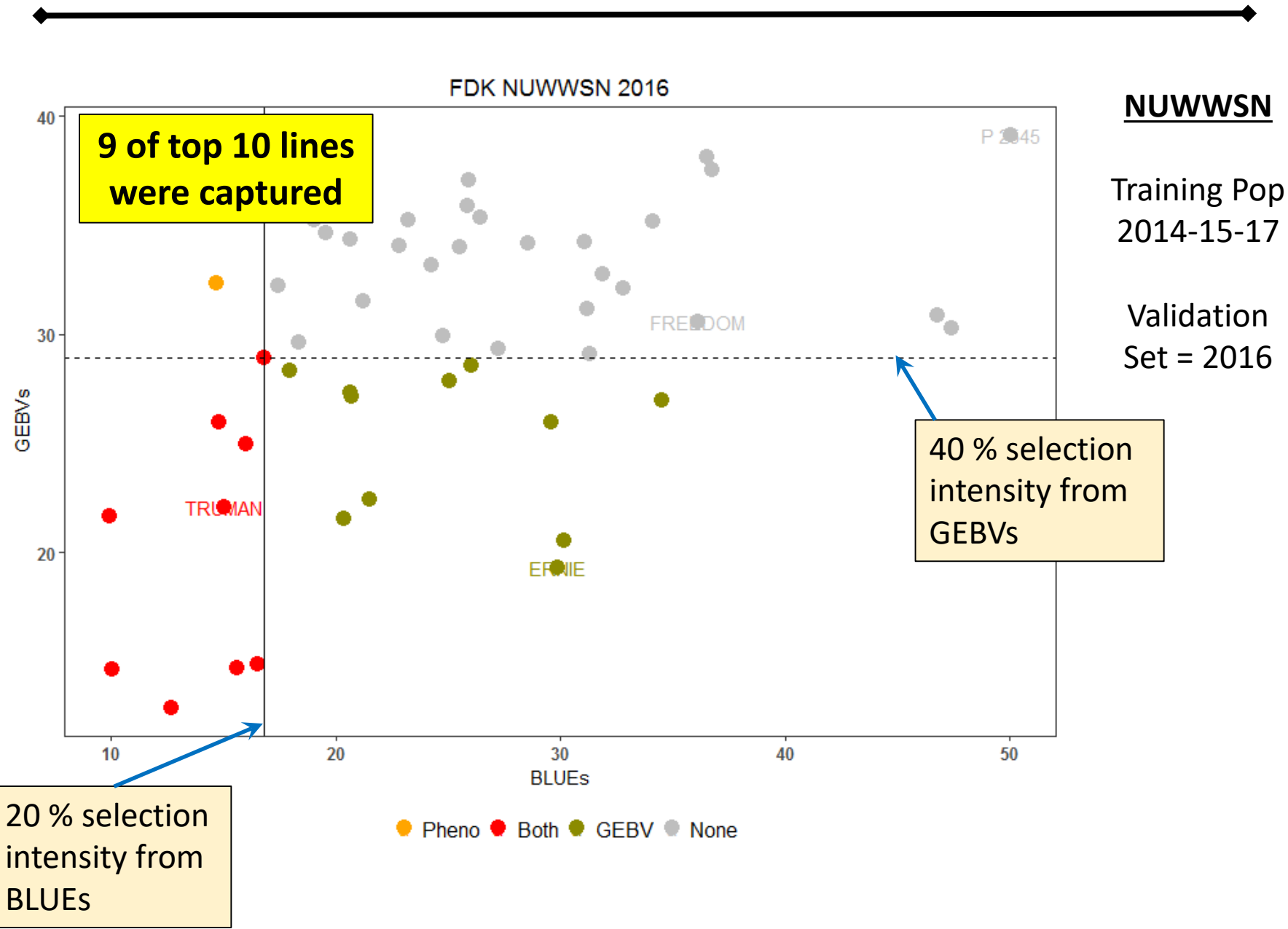


NUWWSN

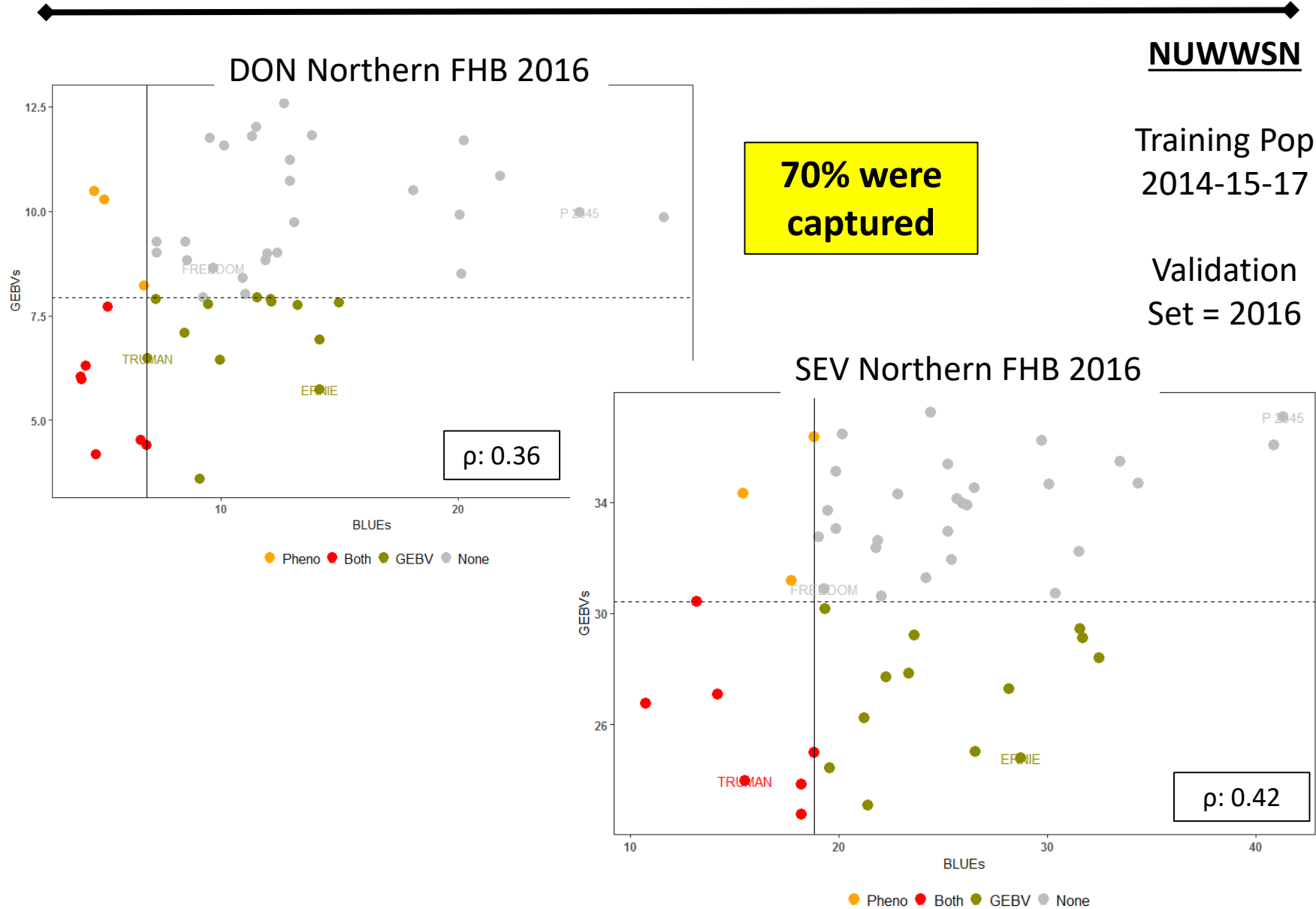
Training Pop
2014-15-17

Validation
Set = 2016

BLUEs vs GEBVs

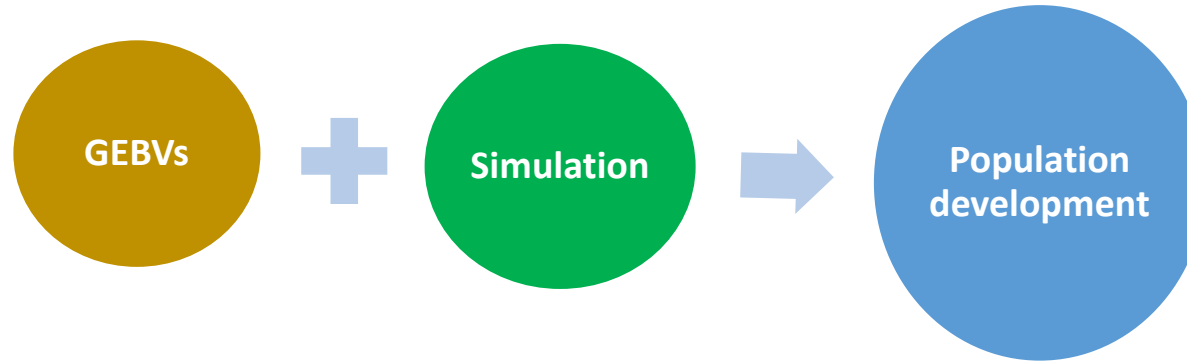


BLUEs vs GEBVs



Parental Selection for Fhb resistance

Genomic approach (PopVar):



- TP SUWWSN 2011-16
- Set: SUWWSN 2017
- # Parents: 50
- Possible crosses: 1035
- 5000 markers
- PopSeq linkage map

| Parent 1 | Parent 2 | SEV | | | | FDK | | | | DON | | | |
|-----------------|---------------|------|-------------|-------------|----------------|------|-------------|-------------|----------------|------|------------|------------|----------------|
| | | Rank | Pop μ | G Var | μ best 10% | Rank | Pop μ | G Var | μ best 10% | Rank | Pop μ | G Var | μ best 10% |
| NC13-20076 | VA13W-38 | 1 | 17.2 | 11.6 | 11.3 | 2 | 15.9 | 8.5 | 10.8 | 173 | 5.8 | 1.9 | 3.3 |
| BESS | NC13-20076 | 2 | 20.3 | 17.3 | 13.1 | 1 | 15.9 | 9.7 | 10.5 | 112 | 6.0 | 2.9 | 3.0 |
| NC13-20076 | VA07MAS1-7047 | 3 | 19.0 | 11.5 | 13.1 | 7 | 16.9 | 7.5 | 12.2 | 236 | 5.9 | 1.7 | 3.7 |
| BESS | VA13W-38 | 4 | 19.4 | 11.6 | 13.5 | 3 | 16.8 | 10.7 | 11.0 | 155 | 6.4 | 3.1 | 3.3 |
| LES15-5369 | VA13W-38 | 5 | 20.5 | 13.0 | 14.2 | 71 | 21.5 | 10.3 | 15.8 | 187 | 6.4 | 3.1 | 3.4 |
| NC13-20076 | NC14-23373 | 6 | 21.4 | 16.1 | 14.5 | 14 | 17.4 | 6.3 | 13.0 | 99 | 5.3 | 1.9 | 2.9 |
| GA09163-16ES19 | VA13W-38 | 7 | 21.7 | 17.0 | 14.6 | 163 | 24.2 | 12.4 | 18.1 | 813 | 10.1 | 3.0 | 7.1 |
| NC13-20076 | NC14-23372 | 8 | 21.5 | 15.0 | 14.8 | 25 | 18.0 | 6.3 | 13.6 | 92 | 5.1 | 1.7 | 2.8 |
| ERNIE | NC13-20076 | 9 | 22.7 | 20.0 | 15.0 | 10 | 18.3 | 9.8 | 12.9 | 169 | 6.4 | 3.2 | 3.3 |
| LW08049C-74-2-5 | VA13W-38 | 10 | 20.1 | 8.5 | 15.0 | 19 | 18.1 | 8.0 | 13.2 | 35 | 4.8 | 2.4 | 2.1 |
| Mean | | | 33.8 | 15.3 | 27.1 | | 29.1 | 11.7 | 23.2 | | 8.8 | 4.0 | 5.4 |

Concluding Remarks



- Association Mapping:
 - Identified regions known to harbor Scab resistance genes (Fhb1)
 - New candidate regions to further study
- Genomic Selection:
 - Mean model predictive ability
 - **Severity: 0.61**
 - **FDK: 0.56**
 - **DON: 0.59**
 - Incidence: 0.45
 - Index: 0.56
 - ISK: 0.59
- Parental Selection:
 - Complementary genomic tool to incorporate in population development

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Questions