

# Evaluation of genomic selection in the context of initiating a winter barley breeding program



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## Introduction

To respond quickly to climate, disease, and market changes, plant breeders must implement new selection methods to release improved varieties more quickly. Genomic selection (GS), a relatively new method for selection in plants, is faster than phenotypic selection because lines can be evaluated in earlier generations and at multiple times per year. While spring barley has been produced in Minnesota for over a century, winter barley is envisioned as a new valuable crop that could be part of a double cropping system with soybeans.

## Winter hardiness

Winter hardiness is a complex trait which comprises low temperature tolerance (LTT), photoperiod sensitivity (PPD), and vernalization sensitivity (VRN) (Hayes et al. 1993). In barley, several markers known to be linked to QTL for these traits are available (Table 1).

**Table 1. Markers linked to winter hardiness QTL.** These markers were included in the genotyping panel used on the lines from each cycle of selection.

| QTL         | Chromosome, Marker | Favorable allele | Description  |
|-------------|--------------------|------------------|--|
| PPD-H1      | 2H, 12_30872       | AA               | SNP-Causal polymorphism  |
| VRN-H2      | 4H, 12_30889       | Missing data     | INDEL-Polymorphism based on insertion/deletion of cluster of 3 genes                     |
| VRNH1/FR-H1 | 5H, 12_30883       | AA               | INDEL-Polymorphism based on insertion/deletion of region on the first intron of the gene |
| VRNH1/FR-H1 | 5H, 11_11080       | AA               | SNP-Significant for LTT in a AM paper about Oregon CAPIV lines (unpublished)             |
| FR-H2       | 5H, 12_30854       | BB               | SNP-Highly significant for LTT (von Zitzewitz et al. 2011)                               |
| FR-H2       | 5H, 12_31236       | BB               | SNP-Highly significant for LTT (von Zitzewitz et al. 2011)                               |
| VRN-H3      | 7H, 11_20126       | BB               | SNP-Highly significant in a AM paper about Oregon CAPIV lines (unpublished)              |

## Objectives

1. Assess GS for rate of gain from selection
2. Determine the change in genotype frequencies in each cycle of selection for markers linked to known winter hardiness genes or QTL

## Materials and methods

### Training population

- 148 lines from Oregon State University breeding program
- Evaluated for LTT in 3 field trials and 1 controlled environment test
- Evaluated for yield, height, heading date, malt extract, Fusarium head blight (FHB) severity, and stripe rust severity in field experiments
- Genotyped with 3,072 BOPA 1 and BOPA 2 SNP markers

### Selection scheme

- Lines selected as described in Figure 1
- Phenotypic selections were based on visual selection for winter survival in the field
- Genomic predictions were made for using a reproducing kernel Hilbert space model
- Genomic selections were based on an index trait combining those predictions:

$$y = 0.1 \text{ grain yield} - 0.1 \text{ plant height} - 0.05 \text{ heading date} + 0.2 \text{ malt extract} + 0.55 \text{ LTT}$$

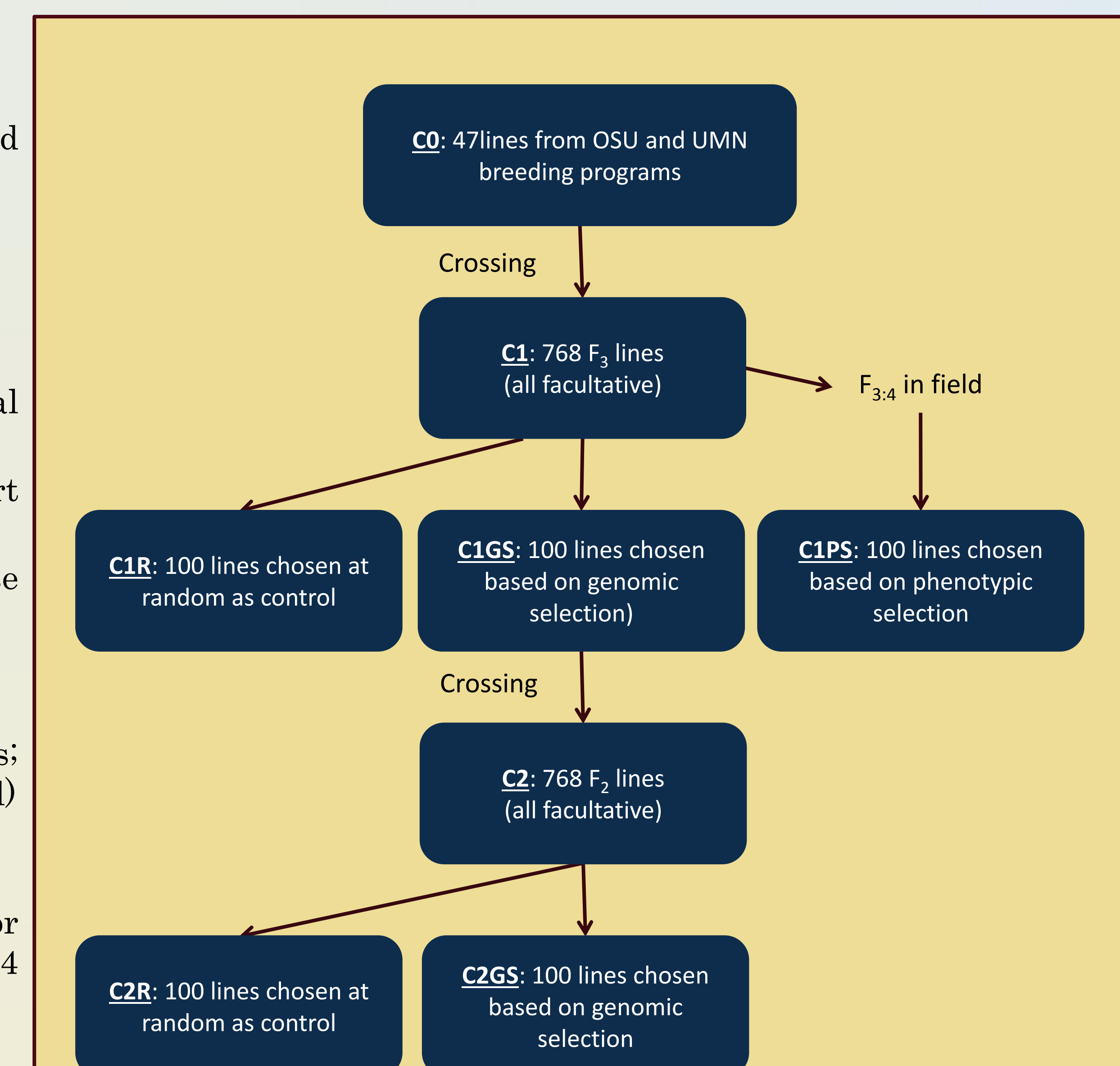
- C0 lines were genotyped with 3,072 BOPA 1 and BOPA 2 SNP markers; C1 and C2 lines were genotyped with 384 markers (LTT VeraCode panel)

### Phenotypic data collection

- C0 lines and 50 individuals from each selected set were assessed for winter survival, grain yield, heading date, and FHB severity in 2014 (Table 2)

**Table 2. Phenotypic data collection.** Data for winter survival, grain yield, FHB severity, and heading date were collected in 2 or 3 locations depending on the trait.

| Trait           | Location      | Planted           |
|-----------------|---------------|-------------------|
| Winter survival | St. Paul, MN  | Fall              |
|                 | Lamberton, MN | Fall              |
|                 | Mead, NE      | Fall              |
| Grain yield     | Corvallis, OR | Fall              |
|                 | St. Paul, MN  | Spring            |
| Heading date    | St. Paul, MN  | Fall              |
|                 |               | Spring (2 trials) |
| FHB severity    | St. Paul, MN  | Spring            |
|                 | Crookston, MN | Spring            |



**Figure 1. Selection scheme.** Initial population consisted of 47 lines which were crossed to create 768 progeny. From these, 100 lines were selected at random (R), 100 were selected based on GS, and 100 were selected based on phenotypic selection (PS). The 100 lines chosen based on genomic selection were crossed to generate another 768 progeny, and from these 100 lines were chosen at random and 100 were chosen based on genomic selection.

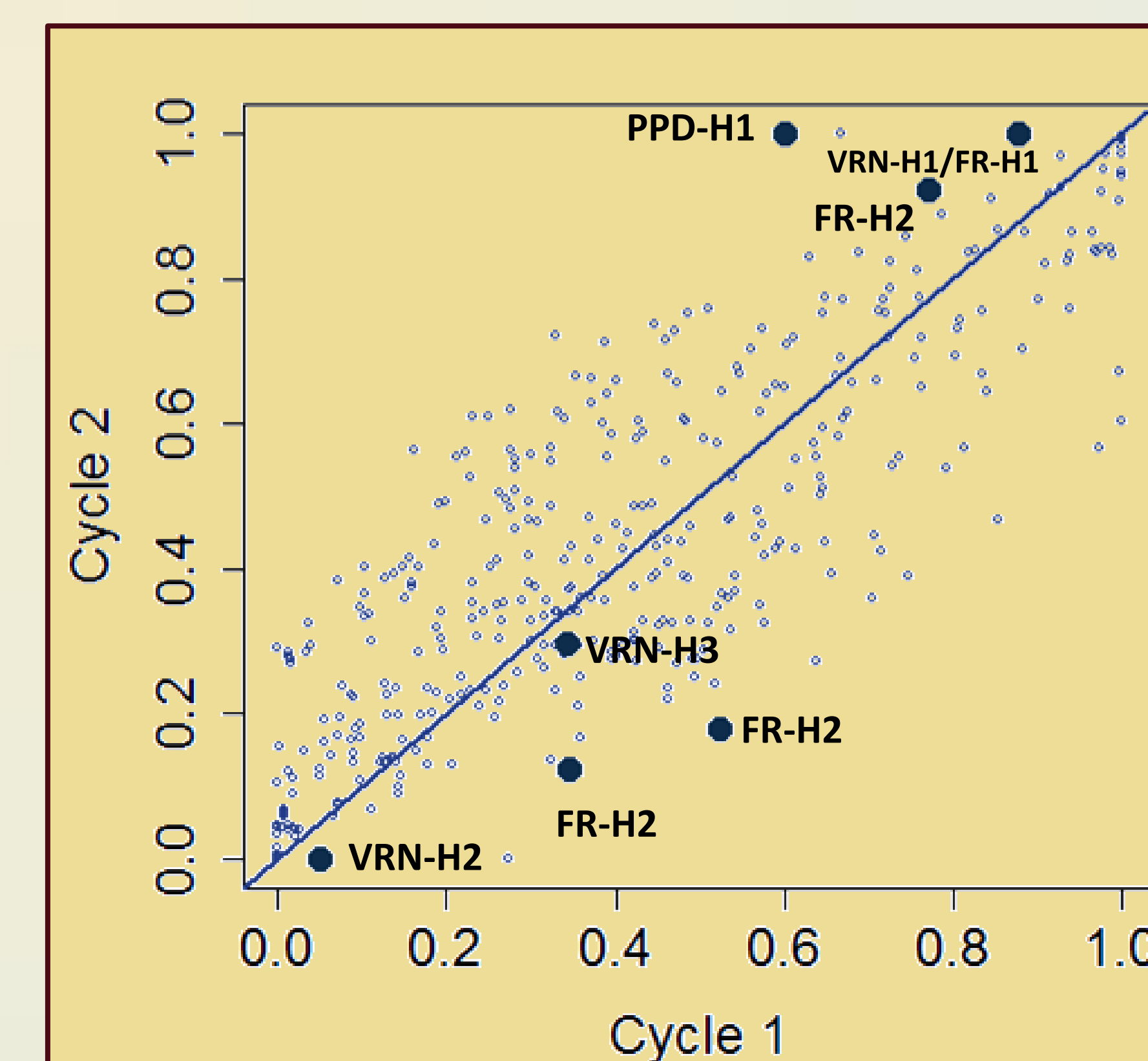
## Results and Discussion

### Objective 1 (Gain from selection)

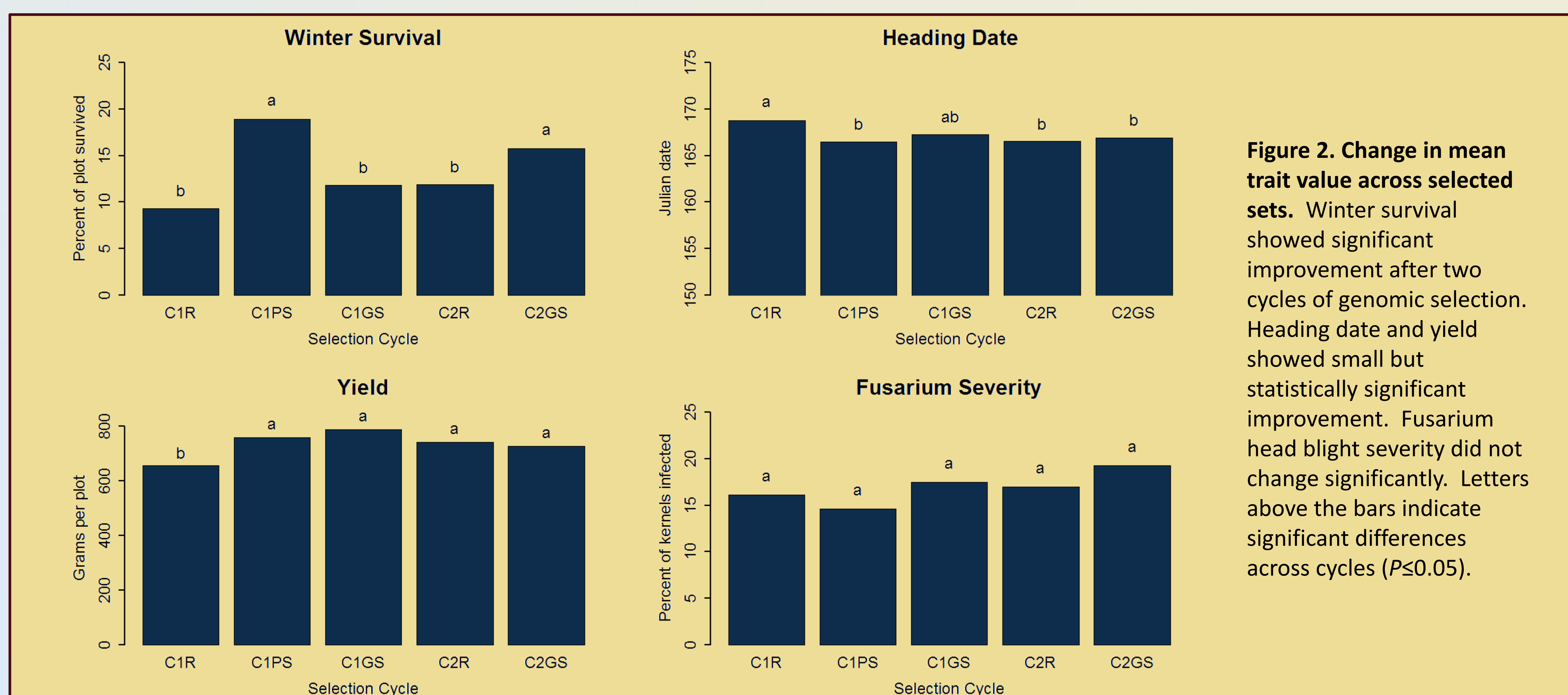
- C1R is a better representation of the parental set (C0) values because each parent line was not used in an equal number of crosses (i.e. parental lines have different contributions to cycle1 overall)..
- Winter survival increased significantly from C1R to C2GS (Fig 2).
- The mean value of the C2GS selected set is not significantly different from C1PS (Fig 2) indicating that two cycles of genomic selection resulted in a net gain equal to the gain from one cycle of phenotypic selection.
- Considering that 3 cycles of GS can be completed per year, that genomic selection can be conducted in earlier generations, and that phenotypic selection was conducted in an unusually favorable year, genomic selection is a better breeding method for this trait.
- Yield and heading date, which had low weights in the selection index, showed small but statistically significant improvements (Fig 2).
- FHB severity, which was not under selection, did not change significantly across cycles (Fig 2).

### Objective 2 (Change in allele frequencies)

- Genotype frequency of seven loci known to be linked to genes or QTL for winter hardiness moved toward fixation (Fig 3).
- All of these loci moved in the expected direction (i.e. toward the favorable allele) (Table 1, Fig 3).
- Other markers also moved toward fixation (Fig 3) and warrant further investigation to determine whether they affect winter hardiness or other traits under selection.



**Figure 3. Changes in frequency of AA genotype from Cycle 1 to Cycle 2 for 384 loci used to calculate genomic predictions.** Seven markers known to be linked to winter hardiness genes or QTL (larger dark blue circles) were included in the genotyping panel. These markers tended to move in the expected direction toward fixation by Cycle 2. Other markers also moved toward fixation and warrant more investigation to determine whether they affect winter hardiness or other traits under selection.



**Figure 2. Change in mean trait value across selected sets.** Winter survival showed significant improvement after two cycles of genomic selection. Heading date and yield showed small but statistically significant improvement. Fusarium head blight severity did not change significantly. Letters above the bars indicate significant differences across cycles ( $P \leq 0.05$ ).

## Conclusions

- Genomic selection can improve traits under selection. Although it may require more cycles of selection that phenotypic selection would, the ability to perform multiple cycles of selection per year regardless of field conditions compensates for this.
- Marker allele frequency changes demonstrate that large effect markers are being selected for indirectly.
- Data on further cycles of selection are needed to determine whether these trends continue and whether other traits under selection show improvement.

## References

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2. von Zitzewitz, J., A. Cuesta-Marcos, F. Condon, A.J. Castro, S. Chao, A. Corey, T. Filichkin, S.P. Fisk, L. Gutierrez, K. Haggard, I. Karsai, G.J. Muehlbauer, K.P. Smith, O. Veisz, and P.M. Hayes. 2011. The genetics of winter hardiness in barley: Perspectives from genome-wide association mapping. *The Plant Genome* 4:76-91.

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