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 hardness
Winter hardness is a complex trait that 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 hardness QTL. These markers were included in the genotyping panel used on the lines from each cycle of selection.

<table>
<thead>
<tr>
<th>QTL</th>
<th>Chromosome, Marker</th>
<th>Favorable allele</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>PPD-H1</td>
<td>2H, 12_30872</td>
<td>AA</td>
<td>SNP-Causal polymorphism</td>
</tr>
<tr>
<td>VRNH2/4H</td>
<td>12_30889</td>
<td></td>
<td>INDEL-Polymorphism based on insertion/deletion of cluster 3 genes</td>
</tr>
<tr>
<td>VRNH1/SH</td>
<td>12_30883</td>
<td>AA</td>
<td>SNP-Significant for LTT (from Orange CAPN lines)</td>
</tr>
<tr>
<td>VRNH1/SH</td>
<td>11_11080</td>
<td>AA</td>
<td>SNP-Significant for LTT (from Orange CAPN lines)</td>
</tr>
<tr>
<td>FR-H2</td>
<td>12_30854</td>
<td>BB</td>
<td>SNP-Highly significant for LTT (from Zitzewitz et al. 2011)</td>
</tr>
<tr>
<td>FR-H2</td>
<td>12_31236</td>
<td>BB</td>
<td>SNP-Highly significant for LTT (from Zitzewitz et al. 2011)</td>
</tr>
<tr>
<td>VRNH1/SH</td>
<td>11_20126</td>
<td>BB</td>
<td>SNP-Highly significant for LTT (from Orange CAPN lines)</td>
</tr>
</tbody>
</table>

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 hardness genes or QTL.

Materials and methods

Training population
- 148 lines from Oregon State University breeding program
- Evaluated for LTT in 3 field trials and for 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 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.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Location</th>
<th>Planted</th>
</tr>
</thead>
<tbody>
<tr>
<td>Winter survival</td>
<td>St. Paul, MN</td>
<td>Fall</td>
</tr>
<tr>
<td></td>
<td>Lamberton, MN</td>
<td>Fall</td>
</tr>
<tr>
<td></td>
<td>Mead, NE</td>
<td>Fall</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Grain yield</td>
<td>Corvallis, OR</td>
<td>Fall</td>
</tr>
<tr>
<td></td>
<td>St. Paul, MN</td>
<td>Spring</td>
</tr>
<tr>
<td>Heading date</td>
<td>St. Paul, MN</td>
<td>Fall</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Spring (2 trials)</td>
</tr>
<tr>
<td>FHB severity</td>
<td>St. Paul, MN</td>
<td>Spring</td>
</tr>
<tr>
<td></td>
<td>Crookston, MN</td>
<td>Spring</td>
</tr>
</tbody>
</table>

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 in an equal number of crosses (i.e., parental lines have different contributions to cycle 1 overall).
- Winter survival increased significantly from C1R to C2G8 (Fig 2).
- The mean value of the C2G8 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 hardness 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 hardness 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<0.05).

Figure 3. Changes in frequency of AA genotype from Cycle 1 to Cycle 2 for 384 loci used to calculate genomic predictions. Seven makers known to be linked to winter hardness 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 hardness or other traits under selection.

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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