Evaluating Genomic Selection in the First Two Cycles of a Winter Barley Breeding Program

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Agronomic and ecosystem benefits

- Increased yield
- Disease avoidance
- Weed suppression
- Water use efficiency
- Carbon sequestration
- Nutrient cycling
- Reduced soil erosion
- Potential relay-cropping system with soybean

Photos taken April 26, 2010

Genomic selection

- To initiate a breeding program for winter barley in the upper Midwest, we are using genomic selection
- Enables selection for any type of trait based on marker data alone
- So far, mostly simulation studies for rate of gain (empirical studies only on accuracy)

Genomic selection process:

1. Training population: Phenotypic and genotypic information
2. Estimate marker effects
3. Select candidates: Genotypic information only
4. Predict trait value (GEBVs)
5. Select parents
6. Make crosses
7. Generate new population
8. Re-train model

Meuwissen et al., 2001

Crossing

C0: 47 lines from OSU and UMN breeding programs
C1: 768 F3 lines (all facultative)
C1R: 100 lines chosen at random as control
C1GS: 100 lines chosen by genomic selection
C1PS: 100 lines chosen by phenotypic selection
C2: 768 F2 lines (all facultative)
C2R: 100 lines chosen at random as control
C2GS: 100 lines chosen by genomic selection

Hayes et al., 1993; von Zitzewitz et al., 2005
Selection

Genomic selection
- Training population – 148 breeding lines from Oregon State breeding program including some parental lines
  - Genotypic data: 3072 BOPA 1 and BOPA 2 SNP markers
  - Phenotypic data: evaluated for LTT in the field and controlled growth chamber tests as well as other traits in the field
- Selection candidates
  - Genotypic data: 384 BOPA SNPs; additional markers imputed for a total of 1333 SNPs

Genomic selections were based on an index trait combining genomic predictions for 5 traits:

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

Phenotypic selection
Visual selection for winter survival in the field

Advantage: uses all marker info
- In traditional marker-assisted selection, choice of markers is somewhat arbitrary
- Quantitative traits are affected by so many loci that it is inefficient to use MAS to pyramid desirable alleles

Advantage: reduces work and cost associated with phenotyping
- Winter hardiness is genetically complex—several large effect loci plus small effect loci
- Difficult to measure—some seasons will be too mild or too harsh to collect survival data
- With GS, only need to phenotype the training population
- Genotyping cost continually decreasing

Phenotypic Selection
Yield: $5/line (per rep per location)
Quality: $100/line

Genomic Selection
384 SNPs Veracode Assay: $17/line

Evaluating selected sets

C0 lines and 50 individuals from each selected set—C1R, C1GS, C1PS, C2R, C2GS—assessed in augmented design trials in 2014

<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>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>Spring (2 trials)</td>
<td></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>

Change in genotypic frequencies
- Shifts in marker genotypes linked to winter hardiness traits

Advantage: accelerates breeding cycle

Gain from selection

Winter Survival

index weight = +0.55

Gain from selection

Winter Survival

index weight = +0.55

Gain from selection

Winter Survival

index weight = +0.55

Gain from selection

Yield

index weight = -0.05

Gain from selection

Heading Date

index weight = +0.1

Gain from selection

FHB Severity

not part of Index
Influences on rate of gain

- Decreased accuracy over cycles of selection

\[ \text{Predictive ability} = \text{corr} (\text{Predicted, Phenotypic}) \]

\[ \text{Prediction accuracy} = \frac{\text{Predictive ability}}{\sqrt{H^2}} \]

<table>
<thead>
<tr>
<th>Winter survival</th>
<th>Yield</th>
<th>Heading date</th>
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</thead>
<tbody>
<tr>
<td>C1</td>
<td>0.34</td>
<td>1.03</td>
</tr>
<tr>
<td>C2</td>
<td>0.53</td>
<td>-0.59</td>
</tr>
</tbody>
</table>

Influences on rate of gain

- Decreased accuracy as alleles (and genotypes) move toward fixation

- Decreased accuracy as population variation (genetic variance) and therefore heritability decrease

Conclusions and future directions

- Large effect markers are selected for indirectly
- Genomic selection can improve traits under selection
  - May require more cycles but ability to perform multiple cycles of selection per year regardless of field conditions compensates
  - Decreased accuracy over cycles contributes to decreasing rates of gain
- Need data on further cycles of selection
  - do trends continue?
  - do other traits under selection show improvement?

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USDA-ARS
USDA-ARS
Competing with soybeans

2013 US barley production

Model training

Influences on rate of gain

- Decreased accuracy over cycles of selection