Genomic Selection to Increase the Rate of Genetic Gain of Intermediate Wheatgrass (Thinopyrum intermedium)
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Introduction
Intermediate Wheatgrass (IWG) is a promising perennial species that is being domesticated as a grain and biomass crop. Initial breeding work began at the Rodale Institute, Kutztown, PA, in the 1980’s. In 2002, The Land Institute, Salina, KS, began breeding IWG using selections made by the Rodale Institute [1]. Early and contemporary work has been encouraging, with seed yield increasing 77% over two cycles of selection, and seed mass increasing 23% [1]. While these gains have been important, if the current rate of gains holds, it is estimated that it would take between 24 and 110 years of breeding to reach the yield and seed size of annual wheat [1]. There are numerous challenges to breeding IWG including:

- Large genome size 12.6 Gb
- Allohexaploid (2n = 6x = 42)
- Outcrossing and heterozygous

As a perennial, breeding IWG is a time intensive process, with a typical breeding cycle length of two years (Figure 1).

Materials and Methods
Cycle 6 of The Land Institute IWG breeding program formed the training population, genotyping-by-sequencing (GBS) was used for marker discovery and genotyping. The population included:

- 3,658 genets in a single replicate row-column design.
- Genets were phenotyped for 46 traits over two years.

Seed yield, spike fertility, seed mass, ..., stem strength.

For each trait, 1,880-2,400 observations were recorded.

- 2,974 plants genotyped using GBS.

Using the available data, best linear unbiased predictors (BLUPs) were calculated for each trait. Heritability ($h^2$) was calculated using the genomic marker matrix. Cross-validation proceeded by leaving entire parents out of the training set, to prevent bias of close relatives predicting performance, and several GS models were tested to identify the best performing models.

Results and Discussion
Heritability across all traits ranged from 0.28-0.67, and the cross-validation prediction accuracy was high for all traits ranging from 0.45-0.93 (Table 1). Across multiple GS models, the prediction values among genets were quite stable, with the Gaussian Kernel and rrBLUP having the most variation in prediction. Even with this variation, for any individual trait the minimum correlation between these two models was $r^2 > 0.94$ (Figure 3).

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$</th>
<th>$r^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Free Threshing 2016</td>
<td>0.61</td>
<td>0.45</td>
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<tr>
<td>Free Threshing 2017</td>
<td>0.50</td>
<td>0.91</td>
</tr>
<tr>
<td>Spike yield in grams</td>
<td>0.36</td>
<td>0.89</td>
</tr>
<tr>
<td>Milligrams per seed</td>
<td>0.58</td>
<td>0.86</td>
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<tr>
<td>Plant height 2016</td>
<td>0.63</td>
<td>0.80</td>
</tr>
</tbody>
</table>

*Further work is investigating the discrepancy between 2016 and 2017 model predictions.

References