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Comparing prediction accuracy of genomic and phenotypic selection in winter wheat

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Introduction

In early yield trial generations, selection decisions are often based on results from a single year and several locations. However, due to G x E interaction and variation in yearly conditions, phenotypic results from single years are only partly representative of any future years.

As genomic selection (GS) models are trained on data from several years, we hypothesize that GS models produce more stable predictions across years than pure phenotypic testing.

Objective

To test our hypothesis, we compared three different selection scenarios for grain yield in the first year of multi-location yield trials (YT1) of our breeding program:

A. **Phenotypic selection** based on only the results from the yield trails (YT1).

B. **Genomic selection** based on only GS predictions, without any previous observations of the test lines included in the training model.

C. **Genomic selection with updated model after harvest** based on GS predictions after updating the model with results from the yield trials (YT1).

To assess, the efficiency of selection, we correlated the predictions from the different scenarios with the mean yield of the two following years (YT2 and YT3, including only selected lines), representing the best available estimate of performance in other years than the selection year.

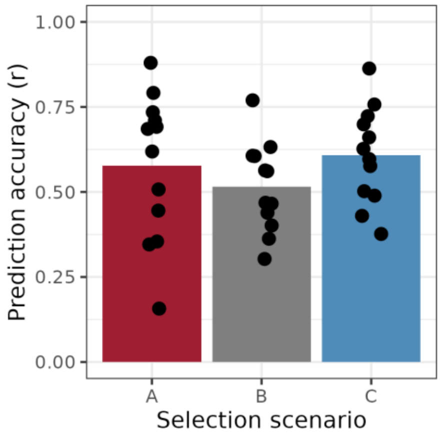

Figure 2: Average prediction accuracy over all years. Each point represents one testing year of YT1.

Results and Discussion

- Over all years, predictions based on only phenotypic observations are slightly better than prediction from genomic selection (r=0.58 vs r=0.51, Figure 2). However, yield trials are much more costly and only a limited number of lines can be assessed .
- Although slightly better, phenotypic prediction shows to be less stable across years than genomic selection as indicated by the greater spread of the prediction accuracies in Figure 2. In some years, the prediction accuracy of phenotypic selection was very low (e.g. 2019 and 2021, Figure 1). In these years, genomic selection would have been more precise.
- The selection scenario C, where the genomic selection models was updated with phenotypic observations, showed best prediction accuracies across all years.

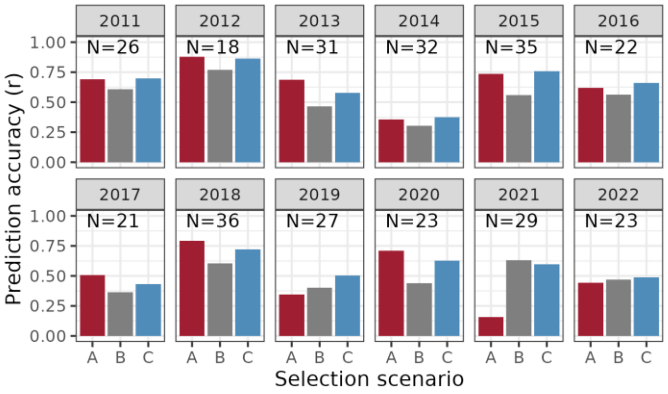

Figure 1: Prediction accuracies of the selection scenarios (A, B, C) for the different YT1 years. N: number of lines.

Material and Methods

Data were taken from the winter wheat breeding program of Agroscope and DSP. Yield trials are performed as lattice designs with 25 or 36 entries over three generations (YT1 ca. 250 lines, YT2 ca. 75 lines, YT3 ca. 30 lines). Trials are conducted in 4 to 5 locations across Switzerland with 2 (YT1 and YT2) to 3 (YT3) replications.

Lines were genotyped with the 25k SGS - TraitGenetics SNP array.

Means over replicates were first calculated per lattice within each location and year. Subsequently, means were calculated across locations (and years) with a mixed model with genotype and lattice as random effect.

Genomic selection models were performed as GBLUP with the rrBLUP package in R. YT data from the breeding program were used as training data and consisted of about 1600 to 1800 lines, depending on YT1 year and prediction scenario.

DSP
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