Genomic selection of wheat - First experiences

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Abstract

Genomic selection (GS) was first successfully applied in animal breeding and has since become the predominate way of breeding cattle. GS identifies individuals that have superior genetic breeding values based on their marker profiles and holds promise to reduce breeding cycles in order to improve gain per year. Only recently GS found its way into plant breeding and just a few studies are available that report on the use of GS in real plant breeding situations. Here we present our first experiences when applying this new paradigm in a breeder's current breeding scheme.

A total of four GS models, which predict breeding values for yield, protein-yield, *Fusarium graminearum* resistance and rust resistance were developed based on a training population of about 700 elite winter wheat lines. The lines were genotyped using the DArT-Seq genotyping platform and the marker information co-analysed together with several thousand phenotypic records that were collected over several years and locations. The phenotypes were adjusted for linear trends per environment using linear mixed models. We treated the phenotypes as random effects in the mixed model equations thus estimating the best linear unbiased prediction per line. To assess the influence of non-additive (e.g. epistatic) effects a series of different statistical models were implemented and their relative performance evaluated. The accuracy of a specific model was estimated as the correlation between the observed phenotypes and the predicted phenotypes. We used 10-fold stratified cross-validation as well as a test set of 167 lines for which initial phenotypes were available.

The accuracy of the model predictions generated by cross-validation agrees well with published literature. For the additive effects model it ranged from 0.46 for protein-yield to 0.66 for yield, which is high: In other studies accuracies above roughly 0.3 led to an increased relative efficiency compared to traditional breeding efforts.

When comparing different statistical models we used a reduced training set of 585 lines and compared models that were commonly used in literature. The models, which differ in computation time as well as their ability to account for gene interactions or epistatic effects.

We found that the simple additive model rr-BLUP is well-suited in terms of computational speed as well as accuracy (0.51). Bayesian models achieve the same accuracy as the rr-BLUP model, whereas support vector machines lag behind. Random forest, a statistical model that can account for non-additive effects, achieved the highest accuracy of 0.57 but at the cost of computation time.

To estimate the relative efficiency of one selection cycle of GS compared to one selection cycle of traditional breeding, we selected 70 lines based on their genetic estimated breeding values and 70 lines that have been selected in traditional breeding programs from the pool of 800 lines. Furthermore, we chose 25 lines randomly to assess the gain from either selection method. The results of this comparison are due for summer 2015.

References

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