An Empirical Evaluation of Genomic Selection in Perennial Ryegrass (*Lolium perenne* L.)

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There is concern in New Zealand regards the rate of genetic gain in pasture species compared to that realised in dairy animals and crop species such as maize. Genomic selection (GS) is expected to improve the rate and efficiency of genetic gain in breeding programs by reducing generation interval and improving prediction accuracy for some traits. GS uses genome-wide molecular marker data to predict genomic estimated breeding values (GEBVs) for prospective selection candidates.

Both theoretical and empirical means of evaluating GS have been reported in a number of economically valued plant and animal species. However, there are few reports of GS in forage grass and legume species. Here we report an empirical approach investigating the potential of GS, relying on small population size and moderate marker density. We generated 3100 markers using a genotyping-by-sequencing (GBS) data stream processed through the UNEAK informatics pipeline in the absence of a reference genome. These marker data were analysed in conjunction with existing phenotypic datasets from two perennial ryegrass commercial breeding populations (n = 120 and 92, respectively), constituting part of a larger GS training population.

Our specific goal was to assess differences in predictive accuracy among GS statistical models (ridge regression-BLUP, RR-BLUP; Random Forest, RF) applied to data for contrasting traits (seasonal and annual herbage production of single plants; flowering time), using a repeated ten-fold cross-validation approach across both constituent populations. Prediction accuracies varied among traits and models. RR-BLUP was most effective for flowering time, with prediction accuracy of 0.61 (compared with 0.56 by RF) while RF was superior for herbage production measures with prediction accuracy for mean annual herbage production of 0.44 by RF, compared with 0.23 by RR-BLUP.

The combination of affordable, high-throughput genotyping and GS prediction methods has generated marker-based prediction that shows promise for increasing the rate of genetic gain in perennial ryegrass. To optimise results, other GS statistical models (e.g. G-BLUP, Bayesian, Reproducing Kernel Hilbert Space etc.) are being explored. The acquisition of field-derived phenotypic data with high accuracy from relevant training populations, of appropriate size and composition, remains the primary constraint in terms of using GS. We outline further research planned to guide, develop and implement GS for improvement of trait indices in a farm and pasture-relevant context for perennial ryegrass and white clover (*Trifolium repens* L.).