Genomic selection in perennial ryegrass: pilot study with small, advanced breeding populations

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- Two multi-parent populations (n=238 total)
- Spaced plants at one site, over two years
- Herbage dry weight (DW) and days to heading (DTH)
- Genotyping-by-sequencing
  - UNEAK (3k SNPs)
  - TASSEL (11k SNPs)
- GEBV
  - Random Forest (RF)
  - Ridge regression BLUP (RR-BLUP)
  - Accuracy by 10-fold cross validation
Moderate GS accuracy achievable in small populations with relatively low marker number

Superior prediction accuracy for DTH compared with herbage DW

RF model gave better predictive accuracy for DW

Minimal influence of marker number on predictive accuracy
Improved accuracy with a combined population dataset

Accuracy using data combined from two populations > models for individual populations

Composite population approach to genomic selection feasible

Current: larger (n>1100), composite training set

- HS families to provide phenotype/breeding value
- Yield potential in sown rows, multiple environments