Prediction of wheat and barley phenology through integration of genomic prediction and a crop growth model

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Abstract: Wheat and barley phenology is a major determinant of adaptation to different environments. The productivity of wheat and barley can be maximised through phenology, so that flowering coincides with optimal environmental conditions (the optimal flowering period). Although many crop models have been parameterised to predict crop phenology, these models are reliant on estimation of model parameter values from phenology scores for a given variety obtained in multiple environment trials. Wheat and barley breeding and agronomy research would benefit from robust models that predict phenology based on genomic information (e.g., single nucleotide polymorphisms (SNPs)). Here, we present a framework that blends genomic prediction and a crop growth model to predict phenology for a given genotype across a range of environments, based on its genome.

Genome wide SNP (single nucleotide polymorphisms) data (Illumina 90K for wheat and Illumina XT 40K for barley) from 49 wheat and 25 barley cultivars were integrated into crop models in APSIM Next Generation (APSIM NG (Holzworth et al., 2018)) to predict traits associated with phenology such as the time of flag leaf emergence, heading and anthesis. Datasets collected from field experiments with up to 144 and 55 environments for wheat and barley, respectively (i.e., time of sowing and locations) were used to calibrate (train) and validate (test) the phenology model in APSIM NG (CGM) and the new integrated genomic prediction and crop growth model (GP-CGM). In GP-CGM, the model parameter values are estimated using semi one-step optimisations directly from genotypic information (i.e. SNP data) by constraining the model predictions to observed phenology. Leaving-one-out cross validation was used to test the model. The field trials covered sowing dates from January to September. The total number of observations were 4075 and 1402 for wheat and barley, respectively, for different growth stages (e.g., flag leaf stages, heading, flowering).

In GP-CGM, RMSE were 13.2 and 13.9 days for observed environments and genotypes, and 15.3 and 16.5 days for genotypes in unobserved environments for wheat and barley, respectively. The RMSE for new genotypes (UG) were 16.6 and 22.0 days for known environments (OEUG), and 17.8 and 22.1 days for unknown environments (UEUG) for wheat and barley, respectively. The new GP-CGM model can be used to explore the complexity of genotype by environment interactions and be combined with other crop models. Future studies will include other 'omics and phenotypic data from remote and proximal sensing for prediction. This allows breeders and agronomists to determine crop management decisions such as optimal sowing dates and select advanced genotypes adapted to different environments.

REFERENCES

Holzworth D, Huth NI, Fainges J, et al. 2018. APSIM Next Generation: overcoming challenges in modernising a farming systems model. Environmental Modelling & Software 103, 43–51.

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