

Characterisation of new cultivars in national variety trials using genomic prediction and crop growth model

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Abstract: Optimising flowering to align with the optimal flowering window in a target environment plays a critical role in maximising crop productivity. Well timed flowering reduces exposure to abiotic stresses such as frost, heat, and terminal drought, thereby maximising yield and economic returns (Zheng *et al.*, 2012; Flohr *et al.*, 2017; Lilley *et al.*, 2019). Crop growth models (CGMs) have been widely applied to predict flowering time and yield by capturing the interactions between genotype, environment, and management (G×E×M), and to identify optimal flowering periods across diverse environments (Zheng *et al.*, 2012; Flohr *et al.*, 2017; Lilley *et al.*, 2019). To remain relevant CGMs must be able to simulate currently grown cultivars. Characterisation of new cultivars in these models requires extensive multi-environment trials to obtain field observations across contrasting conditions. This process requires significant time and resources, which limits the effective use of crop models for evaluating new cultivars.

In this study, we characterised new cultivars of wheat, barley, and canola in the National Variety Trials (NVT) by integrating genomic prediction with the CGM (e.g. APSIM). Whole-genome information, represented by single nucleotide polymorphisms (SNPs), was used to estimate genotypic parameters of the APSIM model via genomic prediction methods (Zheng *et al.*, 2022). These predicted parameters were then applied to simulate phenological traits such as flowering time across Australian grain belt. Model validation using independent field experiments demonstrated that the integrated framework was able to explain more than 50% of the variation in flowering time using genomic information alone in new or untested environments. While this level of accuracy may not be sufficient for direct deployment in practice, additional sparse observations from NVT sites significantly improved prediction accuracy and reliability.

The framework was further applied to assess optimum flowering periods under changing climate and to explore the extent of genotypic variation for adaptation. This provides a pathway to identify cultivars with improved resilience and productivity for future climates.

Our results highlight the potential of integrating genomic prediction and CGMs as a cost-effective and scalable approach for rapid characterisation of new cultivars. This approach reduces reliance on extensive multi-environment trials, shortens the time required to release improved cultivars, and provides breeders and farmers with robust tools to predict crop phenology and make better-informed management decisions.

Keywords: Multiple Environment Trial, Breeding, Genomics, Enviromics

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