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Multi-scale modeling of sunflower crop responses to genetic and environment variations.

Gosseau Florie¹ (florie.gosseau@inra.fr), Bonnafous Fanny¹, Pegot-Espagnet Prune¹, Mangin Brigitte¹, Langlade Nicolas¹, Casadebaig Pierre²

¹ UMR LIPM, INRA, Castanet-Tolosan, France; ² UMR AGIR, INRA, Castanet-Tolosan, France

Current research in genomics and ecophysiology strive to improve gene-to-phenotype predictions beyond methods based solely on genetic information such as whole genome prediction (WGP). Predictive approaches coupling quantitative genetics and crop modeling are designed, either with an emphasis on ecophysiology or on statistics, according to the modeling scale of traits: from molecular to crop level (Bustos-Korts et al., 2016). Gene-to-phenotype predictions are generally carried to predict the breeding values from genome-wide information using statistical models. The difficulty with this method lies in the prediction of non-additive gene effect and gene-by-environment interactions. Crop simulation models, by representing dynamic responses of crop and soil processes to the environment, are successfully used to predict phenotypic plasticity for agronomical traits (Chenu et al., 2017). Therefore, coupling quantitative genetics and process-based modeling should improve the accuracy of breeding value prediction, with different options depending on the phenotypic distance, as illustrated by Hammer et al. (2016).

This study aims to predict the performance of a panel of sunflower hybrids in different farming environments, and therefore to identify the most promising genotypes and key physiological traits controlling yield stability and adaptation to future climatic scenarios. Our multiscale modeling strategy proceeded in two steps: (1) building whole genome prediction models to predict a set of component traits as a function of allelic combination of genotypes and (2) predicting the hybrid yield as a function of component traits, environmental variables and management practices using a crop simulation model (Casadebaig et al., 2016). We evaluated the accuracy of this multiscale model on a multi-environmental network (13 environments) where the training population was phenotyped and on independent trials with non-observed genotypes and environments (9 environments).

Over these 22 environments, we found that the overall accuracy of our multi-scale model was worse than the accuracy of a single genomic prediction model fitted for crop yield. The WGP model showed a good accuracy on the training environments and on the test environments including hybrids selected for their yield range. However, the multiscale model showed a better accuracy than the WGP model in 4 out of 9 test environments, specifically when tested hybrids were not selected for their extreme yield levels.

Overall, we identified new bottlenecks related to the design of combined crop and genetic models, such as the definition of component traits articulating genomic and ecophysiological models and the environment(s) used to train the genomic models.

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