

Integrating crop physiology and modelling with genetic improvement

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The potential to add significant value to the revolution in plant breeding associated with genomic technologies is a new frontier for crop physiology and modelling. Yield advance by genetic improvement continues to require prediction of phenotype based on genotype. Recently, molecular breeding strategies using genome wide prediction and genomic selection approaches have developed rapidly. However, their applicability to complex traits, such as crop yield, remains constrained by gene-gene and gene-environment interactions, which restrict the predictive power of associations of genomic regions with phenotypic responses. Here it is argued that crop ecophysiology and functional whole plant modelling can provide an effective link between molecular and organism scales and enhance molecular breeding by adding value to genetic prediction approaches. Crop physiology and modelling provide opportunities to improve breeding efficiency by either dissecting complex traits to more amenable targets for genetic prediction, or by trait evaluation via phenotypic prediction in target production regions to help prioritise effort and assess breeding strategies (Fig. 1). But this requires a transdisciplinary approach that integrates physiology and modelling into quantitative genetic improvement systems, rather than a model-based focus on ‘genotypic coefficients’ and ‘ideotypes’.

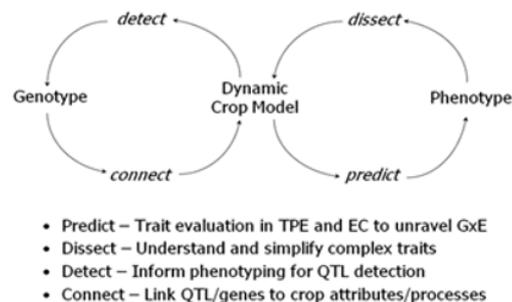


Figure 1. Schematic of transdisciplinary approach to breeding systems highlighting integration and roles of physiology and modelling with genetics (after Messina et al., (2009) and Hammer et al., (2014)).

A dynamic physiological framework that facilitates dissection and modelling of complex traits can inform phenotyping methods for marker/gene detection and underpin prediction of likely phenotypic consequences of trait and genetic variation in target environments. This will require models where capturing biological understanding in a crop growth and development context is as important as the predictive capability of the model – the right answer for the right reason. Models with more robust biological underpinning and the ability to link parameters with the genetic architecture of adaptive traits in a stable manner will come to the fore (Hammer et al., 2010; Boote et al., 2016). Specific examples focussed on drought adaptation (Borrell et al., 2014) are presented here to highlight these concepts.

The putative role of crop modelling as a support technology in plant breeding has been tested intensively over the past decade or two. Crop modelling, utilised in an appropriate manner, has emerged from this process as a useful contributing component of comprehensive plant breeding programs (Messina et al., 2011; Cooper et al., 2014; Hammer et al., 2016). Further advance in the effective application of crop modelling in breeding will undoubtedly occur. As the technology of genomic prediction gains impetus, so will the awareness of the significant value-adding role crop modelling can play in adding biological knowledge to these advanced statistical methods (e.g. Technow et al., 2015). This advance will require attention to underpinning biology in crop models while limiting their complexity, as they strive to make more effective connections between genotype and phenotype than could otherwise occur. The importance of the modelling adage “the right answer for the right reason” and Einstein’s remark of “as simple as possible but no simpler”, will become evident!

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