

Integrating multi-scale phenotypic information into prediction models for genotype by environment interaction by a synthesis of statistical-genetic and physiological models

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New phenotyping techniques at multiple scales of biological organisation will allow biologists to monitor plant growth and development at high temporal and spatial resolutions. Now that technical problems on how to record such types of phenotypic information increasingly are solved, a greater challenge presents itself in how to make use of this information. A major question in plant biology and genetics concerns understanding and predicting genotype by environment interactions (GxE), which includes questions on adaptation, stability and resilience. In plant breeding and genetics, for the prediction of target traits like yield (say fitness) across environmental ranges in the face of GxE two main approaches are followed. The most common approach uses statistical genetic models in which a target phenotypic trait (yield) is predicted from a linear function that has as inputs DNA polymorphisms and low resolution environmental characterizations (quantitative and qualitative). As an alternative, crop growth models can be used, where the inputs typically contain multiple physiological parameters and component traits together with detailed and high resolution environmental information. New types of phenotypic information require a reconsideration of traditional quantitative methodology to predict and understand GxE in target phenotypes. A synthesis of statistical genetic and crop growth modelling approaches can be shown to produce improved accuracy for the prediction of GxE. We will describe the outlines of a modelling framework and give illustrations in maize and wheat.