

Plant Science

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Genome to phenome predictions, step 1: can temporal dynamics in biomass allocation increase the likelihood of the (projected) yield for different accessions of *Brassica rapa*?

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Fluctuating environmental conditions have always been shaping the praxes of agriculture management. Lately, the constant growth of world population and the aggravation of environmental change resulted in a ceaseless quest for new breeding methods, which allow for the highest crop yield despite the occurrence of hostile climate conditions. Since yield predictions are typically built on plant traits measured at organ-level and utilizing optimal conditions, forecasting crop production in a changing environment is highly challenging. The implementation of current process models with high-density data inputs from genomic and metabolomics analysis can augment the predictive power for unknown genotypes and environments. Utilizing high-throughput physiological and molecular screening, we expect to inform and test a pioneering Bayesian approach to predict final yield from physiological trait expression. The globally cultivated crop, *Brassica rapa*, represents an excellent species for this kind of exploration because it includes an extremely diverse array of morphological and physiological types. So far, we finely characterized life-history traits and morphological diversity in extreme *B. rapa*, grown under optimal environmental conditions. Specifically, different accessions of oilseed, cabbage, and turnip, along with two Wisconsin Fast Plants (Imb211 and FPsc) were utilized in the screening. Over a period of 12 weeks, we continuously examined the plants for height, inter nodal distance, and number of leaves; we also performed bi-weekly harvesting of above and below ground biomass, to assess Relative Water Content (RWC%) and Specific Leaf Area (SLA). Once a week, measurements of chlorophyll content, chlorophyll a fluorescence parameters, and gas exchange were taken, to complete the phenotyping of each accession. We correlated all measured traits to the final yield (measured as number of seeds) and analyzed how biomass allocation changes, during the life cycle of each accession, can help predicting final yield. Our results reflect the dramatic diversity among crop accessions within the same species and they are valuable to validate model simulations. Expansions of this analysis to environmental stress conditions, such as heat and drought, and the utilization of recombinant inbred lines (RILs) populations, will allow for reliable yield predictions in unknown genotypes and environments. This research may be the first step to help process modelers to fill the current gap between the genome and phenome under a changing climate.

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