

Optimizing Resource Allocation in *Miscanthus* Breeding via Sparse Testing Designs for Genomic Prediction

Background/Objective

Phenotyping high-biomass perennial crops is laborious and the rate of genetic gain in conventional perennial crop breeding programs is typically low. Increasing biomass yield will increase profitability and environmental benefits, so it is a key target for breeding of *Miscanthus*, a C4 perennial grass with favorable characteristics for producing biomass as a feedstock for products and chemicals. The identification of well-adapted genotypes across a wide range of environmental conditions requires the establishment of multi-environment trials (METs). Sparse testing is a genomic prediction-based strategy that reduces the phenotyping costs in METs by selecting a subset of genotypes to evaluate in a subset of environments and predicting the performance of the unobserved genotype-environment combinations.

Approach

A *Miscanthus sacchariflorus* (MSA) population comprising 336 genotypes observed across three environments was analyzed implementing sparse testing designs. Three prediction models considering main effects (environments, genotypes, genomic) and interaction effects (genotype-by-environment; G×E interaction) were implemented for forecasting dry biomass yield (YDY), total culm (TCM), average internode length (AIL), and culm node number (CNN). Multiple calibration sets based on different compositions and sizes were considered to evaluate performance in terms of the predictive ability (PA) and the mean square error (MSE) for a fixed testing set size.

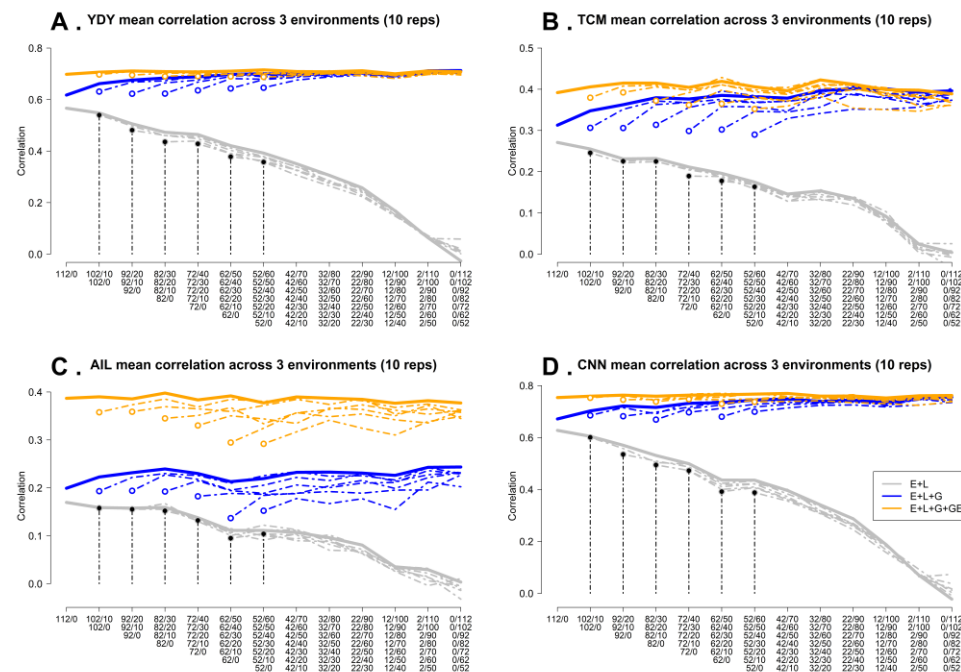
Results

The results showed that the model accounting for G×E interaction consistently presented the highest PA and the lowest MSE: for CNN (PA: ~0.77, MSE: ~0.5) and YDY (PA: ~0.70, MSE: ~1.3) while for TCM and AIL these ranged from ~0.28 to 0.41 and ~1.3 to 4.3, respectively. Overall, varying training sets and allocation strategies did not affect PA and MSE, with 52 non-overlapping and 0 overlapping genotypes per environment as the optimal cost-effective allocation framework.

Significance/Impacts

This study suggests that implementing sparse testing designs could significantly reduce phenotyping costs by fivefold, without compromising PA in breeding programs for perennial crops.

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Predictive ability for four traits in varying training sets and allocation designs.