

## **Abstract**

Phenomic experiments are carried out in large-scale plant phenotyping facilities that acquire a large number of pictures of hundreds of plants simultaneously. With the aid of automated image processing, the data are converted into genotype-feature matrices that cover many consecutive days of development. Here, we explore the possibility of predicting the biomass of the fully grown plant from early developmental stage image-derived features. We performed phenomic experiments on 195 inbred and 382 hybrid maize varieties and followed their progress from 16 days after sowing (DAS) to 48 DAS with 129 image-derived features. By applying sparse regression methods, we show that 73% of the variance in hybrid fresh weight of fully-grown plants is explained by about 20 features at the three-leaf-stage or earlier. Dry weight prediction explained over 90% of the variance. When phenomic features of parental inbred lines were used as predictors of hybrid biomass, the proportion of variance explained was 42 and 45%, for fresh weight and dry weight models consisting of 35 and 36 features, respectively. These models were very robust, showing only a small amount of variation in performance over the time scale of the experiment. We also examined mid-parent heterosis in phenomic features. Feature heterosis displayed a large degree of variance which resulted in prediction performance that was less robust than models of either parental or hybrid predictors. Our results show that phenomic prediction is a viable alternative to genomic and metabolic prediction of hybrid performance. In particular, the utility of early-stage parental lines is very encouraging.