Entry No. 8RGS-0086

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetics of Abiotic interactions: Stress tolerance and Mitigation
Endorsement email	:
Genetics of Abiotic interactions Stress tolerance and Mitigation Keyword 1	: Drought
Genetics of Abiotic interactions Stress tolerance and Mitigation Keyword 2	: heat
Genetics of Abiotic interactions Stress tolerance and Mitigation Keyword 3	:
Title of Entry	: Utilizing random regression models for genomic prediction of a longitudinal trait derived from high-throughput phenotyping platforms
Presenting author	: Gota Morota
Presenting author email	: morota@unl.edu
Co author 1	: Malachy Campbell
Co author 2	: Harkamal Walia
Affiliation presenting author	: University of Nebraska–Lincoln
Affiliation 1	: University of Nebraska–Lincoln
Affiliation 2	: University of Nebraska–Lincoln
Select only one type of presentation	: 15 minute oral presentation
Abstract	: The accessibility of high-throughput phenotyping platforms in both the greenhouse and field, as well as the relatively low cost of unmanned aerial vehicles, have provided research groups with an effective means to characterize large populations throughout the growing season. These longitudinal phenotypes can provide important insight into development and responses to the environment. Despite the growing use of these new phenotyping approaches in plant breeding, the use of genomic prediction models for longitudinal phenotypes is limited in major crop species. The objective of this study is to demonstrate the utility of random regression (RR) models using Legendre polynomials for genomic prediction of shoot growth trajectories in rice (Oryza sativa). An estimate of shoot biomass, projected shoot area (PSA), was recored over a period of 20 days for a panel of 357 diverse rice accessions using an image-based greenhouse phenotyping platform. A RR that included a fixed second-order Legendre polynomial, random second-order Legendre polynomials for additive genetic and environmental effects, and heterogeneous residual variances was used to model PSA trajectories. The utility of the RR approach over a single time point (TP) where PSA is fit at each time point independently is shown through four prediction scenarios. In the first scenario, the RR and TP approaches were used to predict PSA for a set of lines lacking phenotypic data. The RR approach showed a 11.6% increase in prediction accuracy over the TP

approach. Much of this improvement could be attributed to the greater additive genetic variance capture by the RR approach. The remaining scenarios focused forecasting future phenotypes using a subset of early time points for known lines with phenotypic data, as well new lines lacking phenotypic data. In all cases, PSA could be predicted with high accuracy (0.79 to 0.89 and 0.55 to 0.58 for known and unknown lines, respectively). This study provides the first application of RR models for genomic prediction of a longitudinal trait in rice, and demonstrates that RR models can be effectively used to improve the accuracy of genomic prediction for complex traits.

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