17 June 2016

**Improving Genomic Selection Prediction Accuracies for Switchgrass Breeding**

Accounting for linkage disequilibrium improves accuracy of genomic prediction in switchgrass.

**The Science**

This study assessed the possibility of producing reliable predictions for genomic selection using a small sample size of two different switchgrass populations genotyped by exome sequencing and tested in two different locations for three important agronomic traits: biomass yield, plant height, and heading date (flowering time). We assessed various prediction procedures, differing by prediction model and also by type of marker-data transformation.

**The Impact**

Results here suggest that marker-data transformations and, more generally, the account of linkage disequilibrium among markers, offer valuable opportunities for improving prediction procedures in genomic selection. High prediction accuracies, especially with particular traits at particular locations, should motivate implementation of genomic selection breeding programs in switchgrass that will help to accelerate the progress needed to reach bioenergy crop yield goals.

**Summary**

Switchgrass is a relatively high-yielding and environmentally sustainable biomass crop, but further genetic gains in biomass yield must be achieved to make it an economically viable bioenergy feedstock. Genomic selection is an attractive technology for generating rapid genetic gains in switchgrass and meeting the goals of a substantial displacement of petroleum use with biofuels in the near future. In this study, we empirically assessed prediction procedures for genomic selection in two different populations of switchgrass, genotyped by exome capture sequencing and tested in two locations in the United States for three agronomic traits: dry matter yield, plant height and heading date. We evaluated prediction procedures that varied not only by learning schemes and prediction models, but also by the way the data was preprocessed to account for redundancy in marker information. A highly significant gain in prediction accuracy was achieved by transforming the marker data through a marker correlation matrix. Our results suggest that marker-data transformations and, more generally, the account of linkage disequilibrium among markers, offer valuable opportunities for improving prediction procedures in genomic selection.

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**Funding**This work was funded by the DOE Great Lakes Bioenergy Research Center (DOE BER Office of Science DE-FC02-07ER64494), the DOE Joint Genome Institute (DOE Office of Science under Contract No. DE-AC02-05CH11231), the USDA Agriculture and Food Research Institute (USDA National Institute of Food and Agriculture Competitive Grant No. 2011-68005-30411), USDA-Agricultural Research Service Congressionally allocated funds, and the University of Wisconsin Agricultural Research Stations.

**Publications**

Ramstein, G. P. *et al.* “Accuracy of genomic prediction in switchgrass (*Panicum virgatum* L.) improved by accounting for linkage disequilibrium**.”** *G3* **6**, 1049-1062 (2016) [DOI: 10.1534/g3.115.024950].

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[Yes or No]