

Genomic Selection Workshop Report

NCSU, Raleigh, NC

7 - 9 September, 2016

Participants

University of Arkansas (1)
University of Georgia (2)
University of Kentucky (3)
Louisiana State University (2)
Ohio State University (1)
North Carolina State University (3)
Michigan State University (3)
University of Illinois (1)
Virginia Tech (2)
Purdue University (2)
USDA-ARS, NCSU (5)
USDA-ARS, Cornell (1)

Summary

A major aim of the workshop was to provide tools for application of markers in breeding programs, with an emphasis on genome wide marker data. Additional goals were to provide a forum for the public breeding programs to discuss approaches to MAS and genomic selection and to identify ways that the genotyping lab and the T3 database could facilitate the use of markers in wheat breeding. Workshop design allowed for hands on analysis of a soft winter wheat data set. Day 1 topics ranged from SNP calling using the recently released IWGSC whole genome assembly and imputation of missing data to analyses of unbalanced phenotypic data. Day 2 topics focused on genomic prediction with and without the addition of information from allele specific markers. Strategies for selection of individuals in the training set and prediction of the best cross combinations were also covered. Target traits for GS discussed by breeders included yield, test weight, end-use quality, and resistance to Fusarium head blight. GS for other traits was seen as possible as long as data were available to train models. Most indicated that they use marker data for major genes that are segregating in their respective germplasm (ie. *Rht*, *Vrn*, *Lr*, *Fhb1*) when planning crosses and would continue to do so. Determination of superior cross combinations was a topic of considerable interest and discussion as breeders felt that this is an area of large effect on efficiency. Having phenotypic and genotypic information for entries in the eastern winter wheat collaborative nurseries in the T3 database was identified as an important goal as the combination of phenotypes, genome-wide markers, and alleles at causal loci could be used by breeders to evaluate the potential usefulness of new parents. The genotypic data can also aid in determination of the best lines for inclusion in the training sets to predict performance of progeny.