

BM-09

Genomics-assisted breeding overview

*Aaron Lorenz*, Department of Agronomy and Plant Genetics, University of Minnesota, Minnesota, USA

Relatively inexpensive and rapid whole-genome genotyping has dramatically altered the way in which breeding programs use molecular marker data for mining genetic variation and making selections. At the time of the last World Soybean Research Conference held in 2013, genomic selection was just catching on in soybean and several other crops and the research focus in the public sphere was mostly on assessment of prediction accuracy and economic feasibility. In the short time since, genomic prediction and selection has blossomed into nearly a sub-discipline of its own, capturing an enormous amount of attention from both private and public plant breeders. Extensive research has been conducted on new statistical models, prediction of genotype-by-environment interaction, design of training populations, resource allocation for phenotyping, marker imputation, and more. In addition, many publicly available genome-wide genotype and whole-genome sequence datasets have been created and made available since 2013. This presentation will summarize the current status of genomic prediction in soybean breeding, and discuss limitations and promising opportunities.