B-217

maxPedigree©: An interactive and user-friendly pedigree and trait visualization software Benjamin B. Stewart-Brown*, Institute of Plant Breeding, Genetics, & Genomics, University of Georgia, Georgia, USA

Jeffrey D. Boehm Jr, Institute of Plant Breeding, Genetics, & Genomics, University of Georgia, Georgia, USA

Ankit Joshi, Department of Computer Sciences, University of Georgia, Georgia, USA Krzysztof J. Kochut, Department of Computer Sciences, University of Georgia, Georgia, USA

Zenglu Li, Institute of Plant Breeding, Genetics, & Genomics, University of Georgia, Georgia, USA

The narrow genetic base among U.S. soybean cultivars is a limitation to the current rate of yield improvement. Empowering soybean breeders with the ability to easily access the pedigrees and traits of existing and historical cultivars/breeding lines for both parental and progeny selection will help improve the rate of genetic gain by increasing genetic diversity in breeding populations. Additionally, plant breeding programs often have great difficulty in properly managing pedigree information due to pedigree complexity and the feasibility of maintaining a centralized resource where this information is easily inputted and effectively visualized. To assist breeders in making parental selections and tracking breeding materials within their breeding programs, we have developed maxPedigree[©], a program for managing pedigree and trait data for cultivars and breeding lines. maxPedigree[©] was developed using JavaScript and MySQL, an open-source relational database system, which can store data on a local computer or network server. The maxPedigree[©] interface is connected to the MySQL database and is able to pull pedigree and trait information for visualization by breeders. The current version of maxPedigree[©] features: (1) an interactive searchbased cultivar-pedigree database that will allow breeders to look up and visualize pedigree tree information; (2) phenotypic data for descriptors and agronomic traits; and (3) exportation of customizable data tables with desired lines and trait data. Future features will include: (1) colored trait tracing through pedigree trees; (2) storing of genotypic data for haplotype calling and population structure/diversity analyses; and (3) integration of established tools for genome-wide association study (GWAS) and genomic selection (GS) applications. For the first time, soybean breeders will have access to this trove of information in one convenient, user-friendly platform. The program for this assistive plant breeding tool, once established, could also be applied to other crops such as maize, cotton, peanut, and wheat.