M-143

Assessment of genetic diversity and historical genomic changes between two public soybean breeding programs at the University of Guelph

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Istvan Rajcan, Department of Plant Agriculture, University of Guelph, Ontario, Canada To understand diversity within soybean breeding germplasm in Ontario, Canada, a 296 line panel named University of Guelph Germplasm Panel (UGGP) from two U. of Guelph soybean breeding programs was studied. The University of Guelph's Ridgetown campus breeding program (maturity group II) located in Ridgetown, Ontario contributed 34 released cultivars and 31 experimental lines. The Guelph campus breeding program (maturity groups 00, 0 and I) contributed 63 released cultivars and 76 experimental lines. The remaining genotypes were chosen to represent the pedigrees of the Guelph campus breeding program to understand and study selection signatures and historical trends in Ontario-adapted soybeans. Release dates for UGGP varieties ranged from 1907 to 2016. The UGGP was field tested in 2015 and 2016 at two locations per breeding program in Ontario, Canada, to assess phenotypic diversity across the UGGP and perform genome-wide association studies (GWAS) for traits of interest. Phenotypic data highlighted differing breeding objectives and regional adaptation between the breeding programs. UGGP lines were sequenced using genotyping-by-sequencing (GBS) and called using Fast-GBS resulting in 40,307 genome-wide single nucleotide polymorphisms (SNPs), with approximately 1 SNP per 23 kb. Linkage disequilibrium (LD) analysis of the UGGP lines indicated long regions of high LD within UGGP lines. Principal component and cluster analyses revealed overlap between germplasm from both breeding programs and the historical germplasm. Understanding the genetic landscape of breeding germplasm within a breeding program and the associated phenotypes can help breeders to make informed decisions for targeted crosses to guide future breeding efforts.