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Genetic analysis of sucrose concentration in soybean using genotyping by sequencing  
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Soybean (*Glycine max* L. Merr) is the largest oilseed crop in the world, which is grown for its high oil and protein concentration in the seed. Understanding the genetic control of seed compositional traits is required for further advancement of soybean breeding. Sucrose concentration is becoming an increasingly important trait for the production of soy products. The objectives of this study are to identify qualitative trait loci (QTL) for sucrose concentration, and to determine the effect of genotype and environment on varying sucrose levels. A genomic panel consisting of 141 diverse genotypes including modern and historical cultivars, ancestral and breeding lines was grown in two locations, St. Pauls and Woodstock, ON, Canada, in 2015 and 2016, to determine the range and variation in sucrose concentration available for the enhancement of food-grade cultivars. Preliminary results from the 2015 field trials showed significant variation in sucrose concentration across the genotypes in the panel in each location. The minimum, maximum and average values of sucrose in St. Pauls were 5.1734, 8.867 and 7.38425, whereas in Woodstock they were 4.8865, 8.5785 and 6.7589, respectively. Radial smoothing was implemented to look at the variation in sucrose concentration. Association mapping (AM) will be performed using genotyping-by-sequencing (GBS) data in TASSEL and GAPIT to identify new or validate current sucrose QTL. SNPs were called using Fast-GBS. Phenotypic data from both 2015 and 2016 traits will be used for the AM of sucrose concentration, which will be presented. Improved understanding of the genes responsible for this trait will allow for manipulation of sucrose concentration when developing future soybean cultivars.