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Genetic association analysis and genomic prediction of soluble carbohydrates in soybean seeds

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Soybean [*Glycine max* (L.) Merr.] seed contains approximate 35% of soluble sugar components, including sucrose, raffinose, and stachyose. Among these, sucrose is easy to digest and a desirable trait for taste and flavor. In contrast, raffinose and stachyose are difficult to digest by monogastric animals and act as anti-nutritional factors; thus, reducing raffinose and stachyose biosynthesis is considered as a key quality trait goal in soy food and feed industries. Soybean germplasm with low stachyose content was identified and employed in soybean breeding; however, more efforts need to be made to improve carbohydrate components. The objective of this study was to discover new sources of carbohydrates with desirable combinations of these three soluble sugar components in an effort to identify and characterize genomic regions or genes controlling these traits. The evaluations of exotic soybean germplasm identified many plant introductions with elevated sucrose (>8.0%) and reduced raffinose and stachyose (<2.5%). Linkage genetic analysis conducted in a bi-parental mapping population detected and mapped major quantitative trait loci for high sucrose and low stachyose. Genome-wide association mapping of a diverse germplasm panel using a whole-genome sequence-based DNA marker data set identified several single nucleotide polymorphism (SNP) loci significantly associated with high sucrose and low stachyose phenotypes in new sources. Genomic prediction using the diverse germplasm panel as a training population was subsequently performed to identify new soybean germplasm with desirable sugar components. The significant SNP loci and new accessions are valuable resources, facilitating the improvement of soluble carbohydrates in soybean seeds.