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Identification of quantitative trait loci underlying protein and amino acid composition in soybean seeds

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Soybean (*Glycine max* (L.) Merrill) is a predominant source of plant-based dietary protein that provides all amino acids essential for proper human and livestock nutrition. Soy protein is equivalent to dairy protein in nutrient value and quality, while containing no cholesterol. Western society has increasingly embraced soy as a more healthful substitute for meat and dairy products. The nutritional value of soy-food products can be amplified by increasing the protein content and modifying the amino acid profile of soybean seeds. Protein content is a complex trait that is negatively associated with yield, which discourages the production of high-protein soybean cultivars through classical phenotypic selections. Quantitative trait loci (QTL) can be used to expedite the improvement of protein content, while mitigating yield loss. The objective of this study is to identify QTL associated with seed protein content and amino acid composition. Two recombinant inbred line (RIL) populations derived from crosses between one very-high protein (49%, dry basis) line, AC X790P, and two high-protein (41-42%, dry basis) elite soybean cultivars, S18-R6 (designated as Population 1) and S23-T5 (designated as Population 2). Population 1 and Population 2 yielded 192 and 195 RILs for QTL mapping, respectively. The RILs were evaluated for yield, seed protein content, and amino acid composition at three locations for two years, comprising five environments. The populations were genotyped using genotyping-by-sequencing to identify single nucleotide polymorphism (SNP) markers. The identification of QTL associated with elevated seed protein and modified amino acid profiles would be of immense value to the development of new high-yielding soybean cultivars with improved nutritional value using marker-assisted selection.