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Genetic mapping of a phosphorus tolerance QTL in a soybean NAM population

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Phosphorus (P) is an essential nutrient for plant growth and development. Soybean in particular has a high demand for P, so low soil P can put major constraints on soybean yields. Fertilizer often is used to alleviate low-P stress, but it is expensive and not available to many farmers in developing countries who operate on soils depleted of P. Given the current global concerns regarding food security and depleting natural resources, it is important to identify germplasm with P-efficiency and understand the genetics of its stress tolerance. The objective of this study was to detect quantitative trait loci (QTL) that impact P-efficiency. Parents of a soybean Nested Association Mapping (NAM) population were screened for tolerance to P starvation. A family with 140 recombinant inbred lines (RILs) that showed the greatest difference in tolerance between its parents was selected and evaluated for low P tolerance in greenhouse tests. Based on a genetic linkage map spanning 1763 cM and containing 4312 markers over 20 chromosomes, a low-P tolerance QTL for shoot dry weight was identified on chromosome 15. A new population of RILs segregating for this QTL was developed to further study the genetics of the trait.