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Identification of a novel locus affecting soybean maturity

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The expansion of soybean cultivation has been challenged by long days and short growing seasons of far northern climates and cultivars are often limited to a narrow range of latitudes. In order to continue to meet the increasing demands of soybean worldwide, it is crucial to identify key genes regulating flowering and maturity to expand the area of cultivated regions into short season areas. Although several genes involved in early maturity have been identified and utilized for breeding programs, such as *E1* to *E10*, *Dt* and several *FT* genes, variations in maturity date are still observed for lines carrying identical alleles at these loci. As such, it is hypothesized that there remain other as yet unidentified genes that affect flowering and maturity date in soybean. The objective of this study was to identify novel loci and genes involved in early soybean maturity using genome-wide association (GWA) analyses. A population of 86 plant introduction (PI) lines in maturity groups 0 to 000 were phenotyped for days to flowering, maturity and pod filling at two sites for 2 years, genotyped using genotyping-by-sequencing and microarray approaches, and the data analyzed using GWA approaches to identify candidate loci and genes affecting each trait. Analyses identified several regions of interest including a region surrounding the *E1* gene for flowering and maturity, as well as a novel locus on chromosome 13 that had pleiotropic effects on several traits. The locus of chromosome 13 contained SNPs surrounding or within several orthologues of Arabidopsis flowering genes with one SNP causing an amino acid change within a gene exon and possibly causing protein tertiary structure changes, making this region particularly interesting for marker-assisted breeding. Overall, this study identified several candidate early maturity genes that can be utilized in breeding programs aimed at developing lines for expansion into far northern regions.