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Genetic mapping and validation of the 7S α' and 11S A-type storage protein subunits in soybean [*Glycine max* (L.) Merr.]

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The storage protein globulins β-conglycinin (7S subunit) and glycinin (11S subunits) can affect the quantity and quality of proteins found in soybean seeds and account for more than 70% of total soybean protein. Manipulating the storage protein subunits to enhance soymeal nutrition and for desirable tofu manufacturing characteristics are two end-use quality goals in soybean breeding programs. To aid in developing soybean varieties with desired seed composition, an F_2 mapping population (n = 448) and an F_5 RIL population (n = 180) were created by crossing high protein cultivar 'Harovinton' with the breeding line SQ97-0263_3-1a, which lacks the 7S α', 11S A_1, 11S A_2, 11S A_3 and 11S A_4 subunits. Storage protein composition of each individual in the F_2 and F_5 populations were profiled using SDS-PAGE. Based on the presence/absence of the subunits, genomic DNA bulks were formed among the F_2 plants to identify genomic regions controlling the 7S α' and 11S protein subunits. By utilizing polymorphic SNPs between the bulks characterized with Illumina SoySNP50K iSelect BeadChips at targeted genomic regions, KASP assays were designed and used to map QTLs causing the loss of the subunits. Soybean storage protein QTLs were identified on Chromosome 3 (11S A_1), Chromosome 10 (7S α' and 11S A_4), and Chromosome 13 (11S A_3), which were validated in the F_5 RIL population. The results of this research could allow for the deployment of marker-assisted selection for desired storage protein subunits by screening breeding populations using the SNPs linked with the subunits of interest.