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Genome-wide association study of seed protein, oil content and grain yield in *Glycine max* x *Glycine soja* populations

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Soybean [*Glycine max* (L.) Merr.] meal is used largely for livestock feed rations in developed countries, therefore soybean varieties with relatively high protein concentration are desirable to improve the crop value. However, over the last several decades there has been a reduction of protein concentration and improvement of oil content in soybeans varieties, mainly due to the selection of higher seed yield potential. Also, Given the narrow genetic base of the soybean, discovering useful traits in the exotic germplasm and extend the gene pool, may have enormous application to enhance genetic gain and the demand for yield increases. To dissect the genetic architecture of these agronomically important traits, a nested association panel comprising 464 RILs derived from three *Glycine max* x *Glycine soja* crosses was genotyped with the Illumina Infinium SoySNP6K BeadChip and phenotyped in four environments across Missouri. Williams 82 was used as a rubber parent and the *G. soja* were the PI464890B, PI458536 and PI522226. A genome-wide association study (GWAS) was conducted using the package NAM in R (Xavier et al., 2015). The Genome-wide association results identified 14 SNPs highly associated with protein and oil (13 on Chr 20 and 1 on Chr 15), 4 SNPs associated with protein and 7 associated with oil both located at Chr 20. A major seed protein QTL has been identified in the Chr 20 has a large additive effect and has consistently show the strongest association with protein in many soybean mapping populations (Chung et al., 2003; Bandillo et al., 2015). The GWAS results also detected 5 SNPs associated with grain yield in 4 different genomic regions (Chr 6, 11, 17 and 19), with an allelic effect ranging from -4.95 to 7.82 bu/acre.