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Identification of meta-QTLs associated with protein and oil contents and compositions in soybean [*Glycine max* (L.) Merr.] seed

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The seed protein and oil concentrations as well as specific amino acid and fatty acid profiles impact the use and value of the seed in feed applications. Thus, variation for and genetic control of these traits have been widely studied in soybean. Although numerous studies have identified quantitative trait loci (QTLs) associated with seed composition traits, validation of the QTLs has rarely been carried out. From over 80 studies, information, including genetic location and additive effects, for each QTL for seed contents of protein and oil, as well as amino acid and fatty acid compositions was collected. We conducted a meta-QTL analysis using this genetic information which described 175 QTLs for protein, 205 QTLs for oil, 156 QTLs for amino acids, and 113 QTLs for fatty acids. A total of 55 meta-QTL for seed composition were detected on 6 out of 20 chromosomes. Meta-analysis reduced the confidence interval of meta-QTLs relative to the projected QTLs by a wide margin, with the projected QTLs which contributed to meta-QTLs spanning an average of 21.77 cM and meta-QTLs spanning an average of only 3.88 cM. The combined meta-analysis of QTLs from correlated traits and the incorporation of QTL identified at a less stringent threshold acted to further identify and narrow meta-QTL. The meta-QTLs encompassed a total of 7,412 positional candidate genes with each meta-QTL encompassing an average of 135 positional candidate genes. The mechanisms by which these positional candidate genes might contribute to protein and oil biosynthesis and accumulation were postulated. We expect the data presented here will provide meaningful information to further soybean breeding programs and basic functional analyses.