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Effect of the mutant Danbaekkong allele on soybean seed protein concentration, amino acid composition, and other seed quality and agronomic traits

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Soybean [*Glycine max* (L.) Merr.] is the world's leading source of vegetable oil and high quality protein meal. Increasing soybean protein concentration through selection while maintaining oil concentration and yield has been a constant goal for plant breeders, as there is a negative correlation between protein and oil and protein and yield. The objective of this study was to determine if marker assisted selection (MAS) for the Danbaekkong (Dan) protein allele influences agronomic and seed quality traits. A population of 24 F_{8:10} near isogenic lines (NILs) of soybean was created from a cross between G03-3101 and LD00-2817P. Of these 24 NILs, 12 were wild type (WT) and 12 were mutant Dan type. These NILs were grown in a replicated three location field trial across Tennessee. There were significant differences in protein and oil concentrations and yield between the two experimental groups ($p < 0.05$). The Dan experimental group had significantly more protein (414 g kg^{-1}) and less oil (206.9 g kg^{-1}) than the WT and check groups ($p < 0.05$). Additionally, the Dan experimental group was numerically the lowest for yield ranging from $2713\text{-}3183 \text{ kg ha}^{-1}$. This result supports previous findings and further solidifies the fact that protein and oil and protein and yield are negatively genetically correlated. Significant differences between Dan and WT experimental groups were observed for all amino acids tested as well ($p < 0.05$). It appears that protein concentrations of Dan NILs were raised with significant reductions in oil and yield.