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Association mapping of agronomic traits in soybean and molecular dissection of contribution from *Tokachi nagaha* to its derived cultivars

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The founder parents have played important roles in soybean cultivars released in China. It is important to identify the key genome regions in the founder parents and to elucidate their genetic contribution to derived cultivars. In this study, The SNPs underlying soybean yield and quality related traits were identified using *Tokachi nagaha* and its 137 derived cultivars as materials, and the genetic contribution of *Tokachi nagaha* were analyzed. The results are as following: The general stability of *Tokachi nagaha* was bad because the D_i of nine traits were higher. Principal component analysis indicated that *Tokachi nagaha* had more number of pods per plant, number of seeds per plant (SN) and seed weight per plant (PSW); and cluster analysis showed that *Tokachi nagaha* had made larger genetic contribution to its derived in PN, SN and PSW. 87 SNPs with significant signal were detected, and some markers were located in or close to the QTL reported by linkage analysis previously. Eleven SNPs were located in the genes; Eighteen SNPs could be detected in two environments simultaneously; 10 SNPs were co-associated with two or more different traits, and the QTL/gene underlying those SNPs maybe pleiotropic or tightly linked to each other. *Tokachi nagaha* contained the largest number of favorable alleles, 37 and 34, in two planting-density environments, respectively. Of the 23 SNPs associated with number of branch per plant, *Tokachi nagaha* contained 22 positive effective alleles, and the frequency of which were 4.38%~16.79% in derived cultivars. Of the 19 yield related SNPs, *Tokachi nagaha* contained 15 positive effective alleles, and the frequency of the most of which were more than 57% in derived cultivars. A large number of yield-related favorable alleles in *Tokachi nagaha* with high frequency in derived elite cultivars have made *Tokachi nagaha* a founder parent.