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High-resolution QTL mapping for fatty acid composition in soybean

*Bin Li* \*, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing, China

*Junming Sun*, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing, China

Soybean oil quality and stability are mainly determined by the fatty acid composition of the seed. The understanding of genetic networks for fatty acid biosynthesis and regulation in soybean seeds will facilitate the improvement of soybean oil quality. In this study, we genotyped 200 recombinant inbred lines (RIL) derived from a cross between cultivated soybean varieties Luheidou2 and Nanhuizao using specific-locus amplified fragment sequencing (SLAF-seq), and constructed a high-density genetic linkage map comprising 3,541 SNP markers. This map consists of 20 linkage groups and spans a genetic distance of 2,534.42 cM, with an average distance of 0.72 cM between adjacent markers. Inclusive composite interval mapping (ICIM) revealed 26 stable QTL for five fatty acids, explaining 0.4-37.0% of the phenotypic variance for individual fatty acids across environments. Of these QTL, nine stand for novel loci (*qLA1*, *qLNA2\_1*, *qPA4\_1*, *qLA4\_1*, *qPA6\_1*, *qSA12\_1*, *qPA16\_1*, *qOA18\_1*, and *qFA19\_1*). These stable QTL harbor three fatty acid biosynthesis genes (*GmFabG*, *GmACP*, and *GmFAD8*), and 66 genes encoding lipid-related transcription factors. These stable QTL and tightly linked SNP markers can be used for marker-assisted selection (MAS) in soybean breeding programs.