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Identification of 14 candidate loci associated with symbiotic nitrogen fixation in soybean through genome-wide analyses

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Symbiotic nitrogen fixation (SNF) complex supply biological nitrogen for crops to enhance yields without disturbing the ecosystem that leads to sustainability. Understanding of this complex biological process is critical for addressing the triple challenges of food security, environmental degradation and climate change. Here we report the most comprehensive genome-wide association study (GWAS) of SNF in soybean, the most important legume worldwide. We identified 14 QTL regions encompassing 31 putative SNF-related genes including 16 candidate genes with no prior known role in SNF. In a line with a large deletion (164 kb) of the QTL region containing a strong candidate gene (CASTOR), we observed the loss of SNF. Another QTL region harbored the NFR5a gene known to play an important role in the very first steps of symbiosis. One wild-type and two mutant alleles of this gene each exhibited a distinct phenotype, with one mutation causing a severe decrease in SNF activity and yield while the second mutation partially compensated for these decreases. Structural analysis of NFRa protein structure offered a possible mechanism for this loss of function and partial compensation. This study provides fundamental insights of SNF with a comprehensive catalogue of SNF-related candidate genes that will accelerate future efforts aimed at sustainable agriculture.