

High Density Graphic Genotypes of Near Isogenic Lines Revealed Genomic Regions Controlling Peanut Nodulation

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Peanut (*Arachis hypogaea* L.) nitrogen fixation efficiency and rhizobia infection process for symbiosis are very different from many other legume crops. Further understanding the genetic control of peanut symbiosis and nodulation mechanisms would facilitate improvement of biological N fixation efficiency and yield of peanut. To identify the genomic regions controlling peanut nodulation, we genotyped two pairs of near isogenic sister inbred lines (NISILs) with one nodulating line and the other non-nodulating line through calling SNPs from data generated by RNA-seq, genotype by sequencing (GBS), exome-seq, and SNP array assay. Large number of SNPs between the two pairs of NISILs allowed us to compare their dense graphic genotypes to identify the genomic regions controlling peanut nodulation. The results provide a useful reference for further fine-mapping the genes controlling peanut nodulation, which will facilitate developing strategies to improve peanut nitrogen fixation efficiency and yield.