High-density Graphical Genotype Maps of Recombinant Inbred Lines Reveal Genomic Regions Controlling Peanut Nodulation.

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Cultivated peanut (*Arachis hypogaea* L.) forms a symbiotic relationship with rhizobia for biological nitrogen fixation. Rhizobia enter peanut roots through an intercellular crack entry, which is different from model legumes and remains understudied. To reveal the genetic mechanisms and genomic regions controlling peanut nodulation, several next generation sequencing (NGS) methods including RNA-sequencing, target enrichment sequencing (TES), genotyping by sequencing (GBS), and the 48K Axiom *Arachis2* SNP array were applied to genotype two pairs of sister recombinant inbred lines (RILs) with each pair containing a nodulating (Nod+) and non-nodulating (Nod-) line, and their Nod+ parental lines. The overall genotyping revealed a total of 219 (between one pair of RILs) and 1,072 (between the other pair of RILs) homozygous single nucleotide polymorphisms (SNPs), which were mostly located on five chromosomes. High-density graphical genotype maps of the sister RILs were constructed, which showed the candidate genomic regions controlling nodulation. A total of 229 differentially expressed genes (DEGs) upon infection of rhizobia and 55 orthologs of nodulation-related genes located within these genomic regions were identified as candidate genes for further genetic mapping. The results from this study not only provide a reference for application of different NGS methods for peanut genotyping, but also provide important genetic resources to narrow down the genomic regions and discover the genes controlling peanut nodulation, which will lay the foundation for understanding the genetic control of peanut nodulation and improving nitrogen fixation efficiency in peanut.