

Natural Mutations in Peanut Genomes Involved in Nodulation.

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Understanding the genetic and molecular mechanisms of peanut nodulation will not only reveal novel insights into nodule organogenesis, but also will provide the bases for improving peanut nitrogen fixation efficiency. Through map-based cloning and QTL-seq approach, we discovered a pair of homoeologous gene of transcription factor controlling nodulation in peanut and exhibiting non-Mendelian and Mendelian inheritance, respectively. Overexpression and complement test of this pair of genes validated their function in governing peanut nodulation. This pair of homoeologous gene were complementary to each other. The expression patterns of genes upstream or downstream of these genes during nodule organogenesis in peanut were different from that in model legumes, implying a different regulation mechanism of nodulation in peanut. Genotyping peanut mini core collection indicated that much more loss of function mutations on the gene copy on B sub-genome (13%) than on the copy on A sub-genome (4%) exist in the natural germplasm. To date, this is the first report of identification and cloning of a nodulation gene in the symbiosis signaling pathway in polyploidy legume crops. Our findings provided implications and insights into the evolution of homoeologous genes between sub-genomes in allopolyploid species.