

## **Host Gene Expression and Epigenetic Regulation in Peanut (*Arachis hypogaea*) in Response to Rhizobial Early Infection**

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Peanut (*Arachis hypogaea*) establishes symbiosis with rhizobia through an intercellular infection pathway called “crack entry”, which is relatively primitive compared to the well-studied “root hair” entry in model legume and many other legume crop species. Understanding the “crack entry” mechanism will facilitate nitrogen fixation efficiency improvement in peanut and the symbiosis engineering in cereal crops. In this study, we profiled the transcriptome of a pair of recombinant inbred lines, a nodulating line, E6 and non-nodulating line, E7 at 2 hour-post-inoculation (hpi) and 12 hpi. Differentially expressed genes, long noncoding RNAs (lncRNAs) and micro RNAs (miRNAs) related to early rhizobia infection were identified. The regulatory network between mRNA, lncRNA and miRNA provided an insight into the plant genetic response to symbiotic bacteria. We further profiled the epigenomes of E6 at 2 hpi and 12 hpi through whole genome bisulfite sequencing. Differentially methylated loci and regions near or on the differentially expressed genes were identified. The integrated analysis of transcriptome and methylation profiles allow us to understand the gene expression and epigenetic regulation controlling peanut response to symbiotic infection at early stage. Our study provided a set of crucial peanut genes involved in crack entry for further functional characterization.