TRANSCRIPTOME ANALYSIS AND GENE MINING OF BROOMRAPE IN SUNFLOWER-BROOMRAPE PATHOSYSTEM

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ABSTRACT

Orobanche cumana (sunflower broomrape), a weedy root parasite, mainly attack sunflower and entirely attract water and nutrition from the host. Broomrape causes severe yield losses of sunflower worldwide, but it is difficult to control by traditional practices because of its complex life cycle. In order to elucidate the molecular mechanism of interaction between sunflower and broomrape, some genes about infestation are being uncovered in broomrape by our RNA-seq analysis. In this study, two sunflower varieties (resistant/sensitive sandaomei strain) were selected and inoculated with broomrape respectively. During the interaction between sunflower and broomrape, broomrape nodule was sampled and transcriptome sequencing was performed. We finally deployed the Deseq2 assay to screen differentialy expressed genes (DEGs) from the broomrape that inoculating in sunflower resistant cultivars and sensitive cultivars respectively. A total of 868 DEGs were obtained, including 437 up-regulated genes and 431 down-regulated genes. The GO enrichment analysis showed that DEGs were mainly enriched in the sucrose/starch metabolic process, cell wall and protein serine/threonine kinase activity. The process of sugar metabolism can affect the osmotic pressure of sunflower broomrape, causing the variation of water content and nutrition in the broomrape derived from host. The enzymes that catalyze sucrose into reducing sugars are located at the cellulose synthesising tissues, mainly in the cell wall. The study of the genes about sucrose/starch metabolic process can provide the detail that how to the enzyme promote the broomrape infesting sunflower, and provide insight into exploiting effective measures to control the weedy parasite.

Key words: Broomrape, Sunflower, Transcriptome analysis, Gene mining, Pathosystem