



# Identification of Regulatory Networks of MicroRNAs and Their Targets in Response to *Colletotrichum gloeosporioides* in Tea Plant (*Camellia sinensis* L.)

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Anthraxnose disease is caused by *Colletotrichum gloeosporioides*, and is common in leaves of the tea plant (*Camellia sinensis*). MicroRNAs (miRNAs) have been known as key modulators of gene expression in response to environmental stresses, disease resistance, defense responses, and plant immunity. However, the role of miRNAs in responses to *C. gloeosporioides* remains unexplored in tea plant. Therefore, in the present study, six miRNA sequencing data sets and two degradome data sets were generated from *C. gloeosporioides*-inoculated and control tea leaves. A total of 485 conserved and 761 novel miRNAs were identified. Of those, 239 known and 369 novel miRNAs exhibited significantly differential expression under *C. gloeosporioides* stress. One thousand one hundred thirty-four and 596 mRNAs were identified as targets of 389 conserved and 299 novel miRNAs by degradome analysis, respectively. Based on degradome analysis, most of the predicted targets are negatively correlated with their corresponding conserved and novel miRNAs. The expression levels of 12 miRNAs and their targets were validated by quantitative real-time PCR. A negative correlation between expression profiles of five miRNAs (PC-5p-80764\_22, csn-miR160c, csn-miR828a, csn-miR164a, and csn-miR169e) and their targets (WRKY, ARF, MYB75, NAC, and NFY transcription factor) was observed. The predicted targets of five interesting miRNAs were further validated through 5'RLM-RACE. Furthermore, Gene Ontology and metabolism pathway analysis revealed that most of the target genes were involved in the regulation of auxin pathway, ROS scavenging pathway, salicylic acid mediated pathway, receptor kinases, and transcription factors for plant growth and development as well as stress responses in tea plant against *C. gloeosporioides* stress. This study enriches the resources of stress-responsive miRNAs and their targets in *C. sinensis* and thus provides novel insights into the miRNA-mediated regulatory mechanisms, which could contribute to the enhanced susceptibility of *C. gloeosporioides* in tea plant.

**Keywords:** *Colletotrichum gloeosporioides*, *Camellia sinensis*, microRNA, regulatory network, degradome