Abstract

Helopeltis theivora or the tea mosquito bug (TMB) is reportedly one of the most devastating pests of tea plant (*Camellia sinensis*) causing threat to the beverage crop. This study revealed a significant alternation of tea plant's biochemistry in terms of phenolics and flavonoids content, and increase in antioxidative enzymatic activities in response to TMB herbivory. Long non-coding RNAs (lncRNAs) constitute a group of endogenous RNAs that play gene regulatory roles in eukaryotes. In the present study, 9502 lncRNAs were identified from healthy and TMB-infested *C. sinensis* tissues using high-throughput RNA sequencing data, out of which 80 lncRNAs got differentially expressed in response to TMB infestation. Determination of genes that could act as potential targets of lncRNAs revealed that the identified lncRNAs could possibly target as many as 5804 genes. Differential gene expression (DGE) analysis led to the identification of 3665 differentially expressed genes (DEGs), of which, expression of 1767 genes got upregulated and 1898 genes got downregulated during tea plant's response to TMB. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis of DEGs and lncRNA-target genes have shown that TMB infestation might have triggered transcriptomic reprogramming leading to altered primary and secondary metabolism in *C. sinensis*. Identification of TMB-responsive circRNAs (another class of non-coding RNA) in tea plant revealed differential expression of 34 circRNAs during TMB feeding. These circRNAs are found to be associated with biological pathways like "tryptophan metabolism", "biosynthesis of secondary metabolites", "porphyrin metabolism", "nucleocytoplasmic transport", "N-glycan biosynthesis" etc. LncRNAs and circRNAs can act as competing endogenous RNAs (ceRNAs) to bind with common microRNA (miRNA) response elements (MREs) involving a competition between mRNAs, lncRNAs and circRNAs. Assessment of this "sponging" activity of lncRNAs and circRNAs led to the construction of the ceRNA network consisting of 5 lncRNAs, 17 circRNAs, 33 mRNAs competing against each other to bind with 37 miRNAs. The expression of 6 DEGs and 5 differentially expressed lncRNAs (DELs) have been validated by qRT-PCR.