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# Genome-wide identification of abiotic stress-regulated and novel microRNAs in mulberry leaf

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## Abstract

As the most important food plant for sericultural industry, mulberry trees have to suffer from a wide range of abiotic and biotic stresses, such as drought and high salinity. MicroRNAs (miRNAs) have been proved to play important roles in abiotic stresses regulation in many plants. However, there are selodm reports on the miRNAs expression profiles upon abiotic challenges in mulberry. In this study, three small RNA libraries from mulberry leaf tissue with or without drought or salt treatment were constructed and deep sequenced. Total of 48 conserved miRNAs (including miRNA\*) and 162 novel miRNAs were identified (processing precision value>0.1). A total of 270 and 1963 target genes were predicted for conserved miRNAs and novel miRNAs, respectively. 13 differentially expressed miRNAs were detected under drought or salt stresses by deep sequencing and qRT-PCR. 5' RLM-RACE validated *Morus 013341* to be the target gene of miR-395a. Our results provided initial clue to further study molecular mechanism on abiotic stresses regulation in mulberry.

**Key words:** mulberry; microRNAs; abiotic stresses; deep sequencing

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