

**P0194**
Expression Profiling of miRNAs and Their Target Genes Under Salt Stress in the Halophyte Smooth Cordgrass (*Spartina alterniflora* Loisel)

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Room:

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MicroRNAs (family of small noncoding RNAs, ~18-22 nt) are known to play an important role in posttranscriptional gene regulation by degrading target mRNAs through cleavage and/or inhibiting translation. In the present study, expression analysis of a selected set of miRNAs and their targets of a salt marsh monocot halophyte smooth cordgrass (*Spartina alterniflora* Loisel) was investigated. Our microarray analysis showed significant up-regulation of Sal-miR397a and Sal-miR528 under salt stress compared to control. The (s)qRT-PCR results provided detail expression kinetics of these microRNAs under salt stress. In leaf tissue, Sal-miR397a showed an up-regulation of its expression at 6h and 24 h of salt stress while at 12h and 72h the expression level was too low to be detected. But, in the root, it was up-regulated at all the time points except at 72h. On the other hand, Sal-miR528, maintained its basal expression at high level under salt stress in leaf, whereas in the root, it showed up-regulation at all the time points except at 12 h. In addition, several microRNAs including a few putative novel ones with high read counts (from deep sequencing) also showed differential up/down-regulation in leaf and root tissues under salinity. Similarly, expression analysis of target genes of Sal-miR397 (Os01g44330) and Sal-miR528 (Os08g04310) and other selected miRNAs showed temporal and spatial variation in up/down-regulation of their transcript accumulation under salt stress. Understanding the gene regulation mechanism(s) at the miRNA level would broaden our fundamental understanding of the biology of the salt stress tolerance of the halophyte.

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