



Category: Plant Genomics

Identification and characterization of salt-responsive novel miRNAs and their targets in *O. sativa*

Shaifaly Parmar

Institute of Life Sciences, Bhubaneswar, INDIA

Abstract

Salinity is an inevitable environmental constraint leading to devastated crop productivity. Rice, being a glycophyte, is highly susceptible to salt stress specifically during early vegetative and late reproductive stages. To cope up, the plant has evolved a considerable degree of developmental plasticity so that the potential stress impacts are minimized. One such mechanism is driven by a class of endogenously expressed small RNAs, miRNAs, which have emerged as ubiquitous post-transcriptional gene regulatory molecules. Sequenced genome coupled with high throughput sequencing significantly advances our ability to unravel miRNA-guided stress tolerance mechanisms. Computational analysis revealed hundreds of miRNAs and their potential targets in different plant conditions. A total of eight conserved, and nine novel miRNAs were tested for their expression profiles in non-stressed and stressed conditions. All of these were found to be differentially expressing in different tissues and varied concentrations. Their presence was also checked in a distant wild relative (*O. coarctata*) and a halophyte (*S. maritima*). Targets of respective novel miRNAs were identified and the credibility was duly checked. Target prediction revealed several proteins directly or indirectly involved in imparting salt tolerance to the plant. Our study demonstrates genotype-specific miRNA regulation under salinity stress and evidence for their role in mediating expression of target genes for abiotic stress response. It can also be contemplated in developing transgenic crop cultivar which has increased salt stress tolerance.

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