

Abstract

Piriformospora indica (*P. indica*), an endophytic root fungus, supports the growth and enhanced tolerance of plants to biotic and abiotic stresses. Several recent studies showed the significant role of small RNA (sRNA) molecules including microRNAs (miRNAs) in plant adaption to environmental stress, but little is known concerning the symbiosis-mediated salt stress tolerance regulated at miRNAs level. The overarching goal of this research is to elucidate the impact of miRNAs in regulating the *P. indica*-mediated salt tolerance in rice. Applying sRNA-seq analysis led to identify a set of 547 differentially abundant miRNAs in response to *P. indica* inoculation and salt stress. These included 206 rice-specific and 341 previously known miRNAs from other plant species. In silico analysis of miRNAs predictions of the differentially abundant miRNAs led to identifying of 193 putatively target genes, most of which were encoded either genes or transcription factors involved in nutrient uptake, sodium ion transporters, growth regulators or auxin responsive proteins. The rice-specific miRNAs were target with transcription factors involved in the import of potassium ions into the root cells, the export of sodium ions and plant growth and development. Interestingly, *P. indica* affected the differential abundance of miRNAs regulated genes and transcription factors linked to salt stress tolerance. Our data helps to understand the molecular basis of salt stress tolerance mediated by symbionts in plant and the potential impact of miRNAs for genetic improvement of rice varieties for tolerance to **salt** stress.

Key words: *Oryza sativa*, Endophytic Fungus, sRNA Sequencing, Illumina HiSeq.



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