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Transcriptome profiling of stress responsive noncoding RNAs and their target genes

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Plant transcriptome profiling has provided a tool for understanding the mechanisms by which plants respond to stress conditions. Analysis of genome-wide transcriptome will provides a useful dataset of drought responsive non-coding RNAs and their candidate target genes that may be involved in drought stress responses. Here RNA-seq analyses of leaves from drought stressed rice plants were performed, producing differential expression profiles of non-coding RNAs. We found that the transcript levels of 66 miRNAs changed significantly in response to drought conditions and that they were negatively correlated with putative target genes during the treatments. The negative correlations were further validated by qRT-PCR using total RNAs from both drought-treated leaves and various tissues at different developmental stages. The drought responsive miRNA/target pairs were confirmed by the presence of decay intermediates generated by miRNA-guided cleavages in Parallel Analysis of RNA Ends (PARE) libraries. We observed that the precursor miR171f produced two different mature miRNAs, miR171f-5p and miR171f-3p with 4 candidate target genes, the former of which was responsive to drought conditions. We found that the expression levels of the miR171f precursor negatively correlated with those of one candidate target gene but not with the others, suggesting that miR171f-5p was drought-responsive with Os03g0828701-00 being a likely target. Pre-miRNA expression profiling indicated that miR171f is involved in the progression of rice root development and growth, as well as the response to drought stress. Ninety-eight lncRNAs were also identified, together with their corresponding antisense transcripts, some of which were responsive to drought conditions.

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