Identification of Cassava MicroRNAs under Abiotic Stress

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Abstract

MicroRNAs (miRNAs) are small non-coding endogenous RNA molecules that regulate gene expression in plants and animals. miRNAs play a key role in multiple biological processes including stem cell differentiation, organ development, signaling, and response to biotic and abiotic stresses. Cassava (Manihot esculenta Crantz), one of the most important crops in tropical regions of the world, is tolerant to drought and other adverse conditions, making it a desirable model for understanding post-transcriptional control in plants in the light of climate change. Most miRNAs discovered in cassava were predicted using bioinformatics alone or through sequencing of plants challenged by biotic stress. Here, we use deep-sequencing and a combination of bioinformatics methods to identify potential cassava miRNAs expressed in plants under drought conditions, and to predict their target genes. We also explore the expression of miRNAs in drought-induced post-transcriptional regulation in cassava and other plants.

Introduction

Deep sequencing of smallRNAs

Validation of cassava miRNAs related to stress response using qRT-PCR

Results and Discussion

Deep sequencing of cassava miRNAs:

Validation by qRT-PCR of cassava miRNAs related to stress response

Conclusions

Acknowledgements

References

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