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METHODOLOGY **Open Access**

Improved CTAB method for RNA extraction of thick waxy leaf tissues from sago palm (*Metroxylon sagu* Rottb.)

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Abstract

Background: There is a growing interest in transcriptomics studies parallel to the advancement of transcriptome databases and bioinformatics, which provided the opportunity to study responses to growths, stimuli and stresses. There is an increase in demand for excellent RNA extraction techniques. General RNA extraction protocols can be used in RNA extraction, but the quality and quantity vary in different types of tissues from different organisms. Hence, a specific RNA extraction method for each organism's tissue type is required to obtain the desired RNA quality and quantity.

Results: The improved CTAB RNA extraction method is superior to the PCI method and MRIP method for thick waxy leaves that were applied for mature sago palm (*Metroxylon sagu* Rottb.) leaf tissue and produce total RNA extract with good purity (OD 260/280 ≥ 1.8, OD 260/230 ≥ 2.0) and integrity (RIN ~ 7). RNA sequencing was conducted with the extracted samples and showed good assembly results (Q20 ≥ 97, Q30 ≥ 91%, assembly mean length ≥ 700 bp).

Conclusion: The improved CTAB RNA extraction method enables rapid, cost-effective, and relatively simple RNA extraction from waxy, fibrous and high-in-polyphenol sago palm (*M. sagu* Rottb.) leaf tissue with next-generation RNA sequencing recommended quality.

Keywords: *Metroxylon sagu*, RNA extraction, Transcriptomics, Improved CTAB method

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