

Identification of gene transcripts contributing to trunking and non-trunking sago palm (*Metroxylon sagu* Rottb.)

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Identification of gene transcripts contributing to trunking and non-trunking sago palm (*Metroxylon sagu* Rottb.)

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Abstract: Sago palm (*Metroxylon sagu* Rottb.) is an economically valuable crop and cultivated widely in Sarawak, Malaysia, for its storage starch. Under certain conditions, such as deep peat areas, some sago palms do not develop well and become stunted, described as non-trunking sago palms. Morphologically, this type of sago palm is abnormal, leading to wastage of various resources and affecting starch production. The research objective was to understand the molecular process that affects non-trunking and starch synthesis in sago palm. Representational Difference Analysis was performed to identify the differences between trunking and non-trunking sago palm transcriptome. This subtractive hybridisation technique detects the differences in gene expression. After three rounds of hybridisation, the differentiated RDA products were cloned and 24 DNA sequences obtained were compared with the sequences in the NCBI database. Results showed that the differentiated genes in response to the non-trunking sago palm have similarities to genes implicated in plant growth, cell metabolism, and salt or osmotic stress. Some of these genes are related to growth, development and signaling involving neutralising the imbalance in plant stress. The information obtained through this work could be used to develop a database on related genes and enzymes contributing to trunking and non-trunking sago palm.

