

## Expressed sequence tags (ESTs) from young leaves of *Metroxylon sagu*

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**Abstract** Sago palm, or *Metroxylon sagu*, is a hardy and versatile plant that is able to tolerate many stresses, biotic and abiotic, during its growth. It is one of the plants that are able to grow in waterlogged area where others could not. Apart from that sago palm is also a source of starch, contributes economically to the people and an important export for the state of Sarawak. Despite the importance of sago palm especially in the production of starch and its ability to withstand stresses, so far, not many molecular studies have been reported on sago palm. To study the characters in sago palm, transcriptome analysis was conducted where it would give a better understanding of the plant development through gene expression. Here, we report the construction of a cDNA library and preliminary expressed sequence tags analysis from the young leaves of sago palm. A total of 434 clones were sequenced with inserts ranging from 1,000 to 3,000 bps with primary and amplified titers of  $8 \times 10^5$  and  $1.0 \times 10^9$  pfu/ml, respectively. Clustering of these sequences resulted in a set of 372 tentative unigenes comprising 340 singletons and 32 contigs. The database was also annotated with BLAST2GO which showed that majority of the transcripts were involved in primary metabolism and stress tolerance.

**Keywords** EST · cDNA · Sequencing · *Metroxylon sagu* · Sago palm

### Introduction

Sago palm (*Metroxylon sagu* Rottb.) is a monocotyledonous plant belonging to the order Arecales, family Palmae, and subfamily Calamoideae. This plant grows well at temperature of 25 °C and above together with 70% humidity. The plant can be found around South East Asia and diffused from its native to other places due to human activity (Yen 1995). It is an important agricultural crop for the state of Sarawak, Malaysia, and having the largest growing area in the state. Sarawak is also one of the world's biggest exporter of sago starch, exporting 44,700 tonnes of sago starch in 2007 to Japan, Taiwan, Singapore and other countries, procuring incomes of between US\$3.4 million to US\$10.8 million (DOA, Sarawak). Starch, accumulated in the pith of sago palm, is the major product of sago palm. It has been reported that the production of starch from sago palm is four times higher than starch derived from rice (*Oryza sativa*) (Lal 2003). Another advantage of sago palm is in its ability to grow in swamp or waterlogged area in the South East Asia and surrounding (Singhal et al. 2008), and acidic peat soil with high concentration of metals such as aluminum, iron, and manganese, to which most crops are unable to thrive (Yen 1995). Despite its adaptability towards harsh conditions and the economic importance of sago palm, reports on molecular work for this plant is very few.

An expressed sequence tag (EST) library was constructed to gain a better understanding of the molecular mechanism and gene expression during sago palm development and its ability to withstand the various stresses. The cDNA library created contained the expression pattern of a selected tissue is an effective tool for research of gene expression. The ESTs generated from specific tissues represents the presence of active mRNAs in the selected tissue

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