

Sago Palm Genome Size Estimation via Real-Time Quantitative PCR

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Abstract

Sago palm, *Metroxylon sagu* Rottb., is an underutilized indigenous food crop that can be found mainly in the South East Asia and Pacific regions. It is a main starch producer and socioeconomically important crop in the South East Asia region including Malaysia. The sago starch provides for considerable potential to food security in the places where it is grown. However, not many molecular works have been reported thus far. In the post genomic era, sago plant genome sequencing is very important for sustainable starch development in these regions. Therefore, determination of the genome size is prerequisite to full genome sequencing and assembly. Here we report on the use of real-time quantitative polymerase chain reaction (qPCR) in determining the genome size. For this work, we calculated the genome size, Γ (bp) of *M. sagu* based on qPCR-derived copy number of two single copy genes. *Pichia pastoris*, with a known genome size, was used as a control to estimate sago palm genome size. With this technique, the genome size of *M. sagu* was calculated to be 1.87 Gbp. This genome size information would be beneficial for subsequent molecular work including genome sequencing and analysis on this economically important crop plant.

Keywords: Genome size, *Metroxylon sagu*, real-time PCR, copy number, *Pichia pastoris*
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1. Introduction

Sago palm (*Metroxylon sagu* Rottb.) is a palm that is widely distributed in the South East Asia region. It is a starch-producing crop and economically important to the state of Sarawak in Malaysia. Sarawak has the largest acreage planted with sago palm and exports sago starch to countries such as Taiwan, Japan, Singapore and others, generating incomes of up to US\$10.8 million/year [1]. Despite its importance, little research in molecular biology has been completed on *M. sagu* molecular biology, and it has not been sequenced, because genome size is not known for this emerging crop. The genome size is a prerequisite in genome sequencing project where it is needed to calculate the number of clones needed to be generated in shotgun sequencing and library

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