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Assessment of the genetic variations of sago palm *Metroxylon sagu* in three regions of Sarawak, Malaysia using amplified fragment length polymorphism (AFLP) marker

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Abstract

Background: Sago palm (*Metroxylon sagu*) is an important staple crop in the rural area of Sarawak, Malaysia. The palms grow well in the rough, swampy peat, from low flooded areas to uplands and acidic to neutral soils. Among the starch-producing crops, this palm is the most productive and promising, where it can store a significant amount of carbohydrate in the trunk. Due to the lack of molecular study of sago palm, the work described here aimed to develop molecular markers for identifying *M. sagu* and accessing the genetic variations of sago palm in different locations of Sarawak.

Results: Amplified fragment length polymorphism was employed to determine the genetic variations of sago palm between fifteen populations collected from three different locations: Mukah, Pusa and Samarahan. Based on 35,016 polymorphic fragments generated from 32 primer combinations, polymorphic information content (PIC), marker index (MI) and resolving power (RP) averaged 0.269, 0.005157 and 51.52039 per primer combination, respectively, were obtained, signifying the effectiveness and accuracy of the AFLP marker. Mukah showed higher diversity ($I = 0.428$, $H = 0.232$), while Pusa showed the lowest ($I = 0.367$, $H = 0.240$). The average value of the Shannon information index was 0.404. AMOVA showed 99% of the variation was found within the population. The Mantel test was performed with 9999 permutations. A significantly positive correlation ($r = 0.220$, $p = 0.010$) was observed between the genetic divergence of the population (Nei genetic distance) with the geographical distance.

Conclusions: Our study considered AFLP is as an effective and reliable method to assess the genetic variations and the identification of *M. sagu*.

Keywords: AFLP, DNA fingerprinting, Genetic diversity, Genetic variation, *M. sagu*

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