Genetic Diversities of Sago Palm Forest in South Sorong, West Papua, Indonesia Based on RAPD Markers

Abstract

Sago palm commodities have the highest ability resulting carbohydrates than others commodity. The potential of sago palm resulting starch can reach 200-220 kg tree\(^{-1}\) (Jong, 2014). Ecological conditions of sago palm stand in Indonesia are divided into three groups: Sago palm forest, sago palm semi cultivation and sago palm cultivation. Information of plant genetic diversities and genetic relationship is very important to be used for germ plasm collection and conservation. This study aimed to evaluate the genetic diversity of forest stands of sago in South Sorong. The sample population used is located in Tarof village, Tambani village, Bedari village, and Tawangire village. Fragments amplification PCR products were separated on 1.7% agarose gel, fixation in Ethidium Bromide, and visualized by using digital camera. Polymorphisms of RAPD amplification fragments by using ten RAPD primers and performed in the PCR tools were resulted low polymorphic fragments. Generally, forest stands of sago palm in South Sorong almost the same based on RAPD markers.
Dry starch production of sago palm in Maluku reach 345 kg tree\(^{-1}\) (Bintoro, 1999). According to our experience, one trunk of sago palm can be resulting 500 kg dry starch. Ecological conditions of sago palm stand in Indonesia are divided into three conditions: sago palm forest, sago palm semi cultivated and sago palm cultivated. Estimation 1.25 million hectares of sago forest and 148,000 hectares of sago palm plantations (semi cultivated and cultivated) located in Indonesia. Papua Province and West Papua province of Indonesia is estimated that there are 1.2 million hectares of sago palm forest and 14,000 hectares of sago palm plantations (Flach, 1997). The genetic diversities of sago palm forest are interesting to study because it is important to determine a strategy to maintain and preserve germplasm of sago palm. Based on morphological Characteristics of sago palm in the forest stand are almost similarities overal huge areas.

Materials and Methods

1. Sample Collection
   Sample populations of sago palm used in this study were collected in the large stand of sago palm forest. Sample populations are divided into four locations, namely Tarof, Tambani, Bedare, and Tawangire which coordinate 132°26'7.598"E and 2°10'26.833"S; 132°36'34.528"E and 2°11'59.744"S; 132°17'15.705"E and 2°3'14.187"S; and 132°17'19.219"E and 1°58'29.447"S respectively.

2. DNA extraction
   Isolation and extraction of total genomic DNA from dried sago palm leaf samples were conducted using procedures as described in Genomic DNA mini Kit Plant Protocol from Geneaid. The total DNA were stored in -20°C in freezer until ready for using.

3. PCR Amplification
   10 RAPD primers were used in this study. The PCR reagents were mixed in a 25 µl volume containing 10 ng genomic DNA, 2.0 µl of 10 mM primer, 5 µl KAPA 2G Buffer A, 0.5 µl dNTPs (10 mM), 1.0 U KAPA2G Robust HotStart DNA polymerase, and ddH\(_2\)O. Amplification was performed in a programmable Thermal Cycler (BioRad) for an initial denaturation at 95°C for 10 min, 45 cycles denaturation at 93°C for 1 min, annealing at 42°C, extension at 72°C for 2 min, final extension at 72°C for 7 min, and holding at 4°C. The Amplified DNA fragments were resolved in 1.7% agarose gel, electrophoresis at 200 V using 1 x TAE buffer, standard molecular weight marker using a 100 bpDNA ladder (Invitrogen), staining with ethidiumbromide (1 µl/l) for 30 min, visualization and documentation by using camera Casio digital. The PCR reaction was repeated more than one times per sample for each primer to ensure the reproducibility of the amplified bands. Faint bands were not considered for scoring and calculation.

Results and Discussion

Polymorphism of RAPD Markers
   Amplification fragments by using ten RAPD primers and performed in the PCR mesin were resulted low polymorphic fragments and many monomorphic band. This indicated that sago palm forest in South Sorong, Indonesia is low diversities. An example of amplification pattern for molecular characterization generated by RAPD markers is shown in Figure 2.

1  2  3  4  5  M  6  7  8  9
CONCLUSIONS

1. Genetic diversity of sago palm forest in South Sorong, Indonesia was observed low differentiation

2. Clustering analyses show that the coefficient of genetic distance above 0.5 of sago palm population are divided into two groups

3. Sago palm populations in the location of Tarof, Tambani, dan Bedare, are almost the same, but different from sago palm population in the locatin of Tawangire

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