

Morphology and RAPD (Random Amplification of Polymorphic DNA) Based Classification of genetic Variability of Java Salacca (*Salacca zalacca* Gaertner. Voss)

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Abstrak

The research aimed to role out the genetic variability and the classification of Java Salacca based on its morphological and molecular characters and to find out the genetic relationship among salacca cultivars that can be selected as parental material for breeding program. The salacca from Manonjaya (West Java), Banjarnegara, Bejalen, Lawu and Saratan (Central Java), Super Pondoh, Black Pondoh, Gading, Kembangarum, Madu and Manggala (Sleman-Yogyakarta) and Suwaru (East Java) were used in our study. Morphological characters and classification analysis by RAPD method with six random primers (OPA-11, OPA-16, OPA-17, OPA-18, OPX-15, OPX-17) were used as classification variable. The genetic variability among cultivars of Java Salacca was presented by the similarity matrixes and dendogram. Based on the morphological classification, the twelve salacca cultivars was divided at four clusters: 1) Manonjaya, Manggala, Suwaru and Kembangarum, 2) Super Pondoh and Black Pondoh, 3) Banjarnegara, Saratan and Bejalen, 4) gading, Madu and Lawu. Based on the molecular-RAPD method, the twelve salacca cultivars was also divided into four clusters but difference member of cultivars: 1) Super Pondoh, Banjarnegara, Black Pondoh, gading, Kembangarum and Suwaru, 2) Bejalen, Saratan and Lawu, 3) madu and Manggala, and 4) Manonjaya. Based on the two classification system used in the study I found the close relationship of Saratan Salacca and Bejalen Salacca from Central Java origin also Super Pondoh Salacca and Black Pondoh Salacca from Sleman-Yogyakarta origin.