

PHYLOGENETIC RELATIONSHIPS AMONG SEVERAL SALACCA SPECIES (*SALACCA* SPP.) USING RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD)

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ABSTRACT

Of 23 salacca species found in the world, 15 species are found in Indonesia. The high salacca diversity is caused by open pollination systems, frequent usage of seeds as planting material, and breeding practices. This research which was conducted at the Molecular Laboratory of the Indonesian Tropical Fruit Research Institute, aimed to determine the level of primer polymorphism and phylogenetic relationships among salacca species. Five species of salacca (10 accessions) and 9 progenies from their crossing were used as samples. Eleven Rapid Amplified Polymorphism DNA markers were utilized for molecular analysis. All primers were given ranges of 57.1-100% polymorphic level. The range of genetic similarity coefficients were 0.512 - 0.937. Observed accessions could be separated into four groups. The highest genetic similarity coefficient was determined between PH-K and PH-MJ accessions (0.937), meanwhile the lowest value was indicated on MW-AFN hybrid and *S. wallichiana* (0.512). For ensuring the efficiency in germplasm management, only accessions which showed high genetic similarities are chosen as representation of the group while eliminating others. On the contrary, accessions which showed low genetic similarity are used as crosses between parents to obtain wide genetic variability and high heterosis effects.

Keywords: *Salacca* spp., Phylogenetic relationship, RAPD