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GENETIC RELATIONSHIP OF SWEET POTATO (*Ipomea batatas*)

ACCESSIONS FROM MALAYSIA AND INDONESIA

USING RAPD MARKERS

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ABSTRACT

Genetic relationship among sweet potato accessions collected from Malaysia and Indonesia was analysed using molecular marker. The aim of this study was to characterise and provide scientific evaluation on preservation and utilisation of germplasm resources. Ninety-two accessions of sweet potato originally from Malaysia and Indonesia were characterized. In total, 212 polymorphic fragments (98.86%) out of 214 total fragments generated from five primers. The

range of fragment size is between 117–3035 bp, each primer produced an average of 20 fragments. These results indicated that the level of polymorphism among all sweet potato were extremely high. The Jaccard's similarity values ranged from 0.08 to 0.69 and this showing high level of genetic variability among the accessions. The cluster analysis separated Malaysian and Indonesian accessions into different groups with a number of additional clusters. Some of the Malaysian and Indonesian accessions were clustered based on their geographic source. The results suggest that very large genetic variation exists and this germplasm collection is a valuable genetic resource. All of this information could be useful in the germplasm management and hybridisation programs.

Key words: Ultrasonic spray-drying, antioxidative activities, microencapsulated powder (MPP)