Genetic Diversity and Relationship of *Alpinia galanga* (L.) Willd. in Indonesia Using SRAP Markers for Genetic Conservation Strategy

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ABSTRACT

Genetic diversity and relationship analysis among *Alpinia galanga* (L.) Willd. populations in Indonesia was carried out using Sequence Related Amplified Polymorphism (SRAP) markers. A total of 120 individuals from 28 populations were screened using eight primer combinations, which resulted 75 polymorphic fragments. The dendrogram, distance matrix, and similarity coefficients were constructed using the Popgene (version 3.2) software package. The feature provided by the software package also applied to estimate the total genetic diversity (H_T), within-population diversity (H_S), genetic differentiation (G_{ST}), and gene flow (N_M). Total Nei's genetic diversity (h) among 28 populations ranged from 0.0000 to 0.1268 while Shanon's information index (I) ranged from 0.0000 to 0.1920. The genetic diversity of galangal in this study showed a fairly low level with random clustering among populations. Based on the results, we recommend a genetic conservation strategy for the species sustainability.

Key words: Alpinia galanga, genetic conservation, genetic diversity, greater galangal, , SRAP marker