

KERAGAMAN GENETIK JAMBU METE (*Anacardium occidentale* L.) DI SULAWESI BERDASARKAN KARAKTER MORFOLOGIS DAN MOLEKULER

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INTISARI

Jambu mete (*Anacardium occidentale* L.) merupakan tanaman tropis yang berasal dari Amerika kemudian menyebar ke Afrika dan Asia hingga Indonesia. Pulau Sulawesi merupakan salah satu sentra produksi jambu mete di Indonesia. Salah satu masalah dalam pengembangan produksi jambu mete di Indonesia adalah penggunaan bahan tanaman unggul, oleh karena itu penelitian bertujuan untuk melakukan eksplorasi dan identifikasi keragaman serta kekerabatan Jambu mete di Pulau Sulawesi. Metode yang digunakan adalah identifikasi karakter morfologis dan molekuler dengan *Inter Simple Sequence Repeat* (ISSR). Data morfologis dianalisis secara fenetik dengan metode *Unweighted Pair Group Method* (UPGMA) pada program *Multi-Variate Statistical Package* (MVSP). Data alel polimorfik dari ISSR dianalisis dengan *Principal coordinate analysis* (PCoA) menggunakan program GenAEx ver. 6.5. Hasil penelitian menunjukkan keragaman genetik jambu mete di Pulau Sulawesi berdasarkan karakter morfologis pada level sedang sedangkan berdasarkan karakter molekuler ISSR tergolong rendah berdasarkan indeks keragaman Nei dengan rata-rata heterozigositas harapan Nei (H_e) 0,046, indeks Shannon (I) 0,068, dan persentase lokus polimorfik 12,06%. Hubungan kekerabatan jambu mete di Pulau Sulawesi berdasarkan karakter morfologis menunjukkan bahwa 39 aksesori terbagi menjadi dua klaster utama dengan koefisien similaritas 72-88%. Hubungan kekerabatan jambu mete di Pulau Sulawesi berdasarkan karakter molekuler ISSR membagi 40 aksesori menjadi dua klaster dengan indeks similaritas Jaccard 74,4-96,1%. Studi ini meningkatkan pemahaman tentang keragaman genetik pada tanaman jambu mete di Indonesia dan membangun dasar ilmiah bagi kebijakan konservasi serta pengembangan kultivar unggul di masa mendatang.

Kata kunci : Jambu mete, keragaman, morfologis, molekuler

GENETIC DIVERSITY OF CASHEW (*Anacardium occidentale* L.) IN SULAWESI ISLAND BASED ON MORPHOLOGICAL AND MOLECULAR CHARACTERS

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ABSTRACT

The cashew (*Anacardium occidentale* L.) is a tropical plant originating from the Americas, which subsequently spread to Africa and Asia, including Indonesia. Sulawesi Island is one of the central production areas for cashew in Indonesia. A primary issue in enhancing cashew production in Indonesia is the utilization of superior planting materials; therefore, this research aims to conduct an exploration and identification of the diversity and genetic relationships of cashew on Sulawesi Island. The methods employed involved morphological and molecular characterization using Inter-Simple Sequence Repeat (ISSR). Morphological data were analyzed phenetically using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) in the Multi-Variate Statistical Package (MVSP) program. Polymorphic allele data from ISSR were analyzed using Principal Coordinate Analysis (PCoA) with the GenALEx ver. 6.5 program. The results of the study indicate that the genetic diversity of cashew nuts on Sulawesi Island is categorized as moderate based on morphological characters, while based on ISSR molecular characters, it is categorized as low based on the Nei diversity index with an average Nei expected heterozygosity (H_e) of 0.046, Shannon index (I) of 0.068, and a percentage of polymorphic loci of 12.06%. The genetic relationships based on morphological characteristics showed that 39 accessions were divided into two main clusters, with a similarity coefficient ranging from 72% to 88%. Meanwhile, the genetic relationships based on ISSR molecular markers divided 40 accessions into two clusters, with a Jaccard similarity index ranging from 74.4% to 96.1%. This study enhances the understanding of genetic diversity in cashew plants in Indonesia and provides a scientific basis for future conservation policies and the development of superior cultivars.

Keywords: Cashew, diversity, morphological, molecula