

Keragaman dan Hubungan Kekerabatan Pepaya Gunung (*Vasconcellea pubescens*, A.DC.) di Dataran Tinggi Dieng berdasarkan Penanda Morfologis dan Sekuen *Internal Transcribed Spacer*

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Intisari

Pepaya Gunung (*Vasconcellea pubescens* A.DC.) atau disebut Carica di daerah Dieng merupakan tumbuhan yang berasal dari Pegunungan Andes. Pepaya Gunung tumbuh dengan baik di daerah beriklim subtropis dan daerah dengan ketinggian 1400-2400 meter di atas permukaan laut (dpl) seperti di dataran tinggi Dieng, Jawa Tengah. Studi mengenai keragaman dan kekerabatan genetik Pepaya Gunung yang berada di dataran tinggi Dieng masih terbatas. Tujuan penelitian adalah untuk mengetahui keragaman dan hubungan kekerabatan Pepaya Gunung yang berada di dataran tinggi Dieng berdasarkan penanda morfologis dan molekuler ITS rDNA. Penelitian ini dilakukan di Dataran tinggi Dieng Banjarnegara dan Wonosobo, Jawa Tengah. Sebanyak 41 penanda morfologis digunakan untuk mengkaji hubungan kekerabatan fenetik dan penanda molekuler sekuen daerah *Internal Transcribed Spacer* (ITS)-rDNA digunakan untuk analisis hubungan kekerabatan filogenetik. Analisis data fenetik dilakukan berdasarkan metode UPGMA (*Unweighted Pairgroup Method with Arithmetic Average*) menggunakan MVSP versi 3.1A. Analisis data filogenetik berdasarkan sekuen daerah ITS-rDNA dan pembentukan pohon filogenetik menggunakan metode *Maximum Likelihood* (ML) dalam MEGA 11. Variasi genetik dianalisis menggunakan program DnaSP 6.12.03. Pohon fenetik berdasarkan penanda morfologis menunjukkan dua kelompok yang terpisah berdasarkan karakter distribusi seks, panjang tangkai bunga dan kerapatan bunga. Nilai indeks Shannon's (H') menunjukkan keragaman fenetik sedang dengan nilai rerata sebesar 2,514. Pohon filogenetik 14 sekuen ITS-rDNA Pepaya Gunung menunjukkan adanya 3 cabang utama. Variasi genetik pada Pepaya Gunung menunjukkan keragaman yang tinggi dengan nilai keragaman haplotype (H_d) sebesar 1.000 ± 0.027 dan nilai keragaman nukleotida (π) yang tinggi sebesar 0.09674 ± 0.00978 .

Kata kunci: *carica*, dataran tinggi, fenogram, filogram.

Species Diversity and Relationships of Mountain Papaya (*Vasconcellea pubescens* A.DC.) in Dieng Plateau based on Morphological and Internal Transcribed Spacer Sequence Markers

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Abstract

Mountain papaya (*Vasconcellea pubescens* A.DC.) or called Carica in Dieng region is a plant native to the Andes Mountains. Mountain papaya grows well in subtropical climates and areas with an altitude of 1400–2400 meters above sea level (asl), such as in the Dieng Plateau, Central Java. Studies on the diversity and genetic relationships of Mountain Papaya in the Dieng Plateau are still limited. The purpose of this study was to determine the diversity and relationship of Mountain Papaya in the Dieng Plateau based on morphological and molecular markers of ITS rDNA. This research was conducted in the Dieng Plateau, Banjarnegara, and Wonosobo, Central Java. A total of 41 morphological markers were used to study the phenetic relationship, and molecular markers of the Internal Transcribed Spacer (ITS)-rDNA region sequence were used for the analysis of phylogenetic relationships. The phenetic data analysis was performed based on the UPGMA (*Unweighted Pairgroup Method with Arithmetic Average*) method using MVSP version 3.1A. Analysis of phylogenetic data based on ITS-rDNA regional sequences and the formation of phylogenetic trees using the Maximum Likelihood (ML) method in MEGA 11. Genetic variation was analyzed using the DnaSP 6.12.03 program. The phenetic tree based on morphological markers showed two separate groups based on sex distribution, flower stalk length, and flower density. The Shannon's (H') index value indicates moderate phenetic diversity with a mean value of 2.514. The phylogenetic tree of 14 ITS-rDNA sequences of mountain papaya shows three main branches. Genetic variation in mountain papaya showed high diversity, with haplotype diversity (H_d) values of 1.000 ± 0.027 and high nucleotide diversity (π) values of 0.09674 ± 0.00978 .

Key words: *carica*, *plateau*, *phenogram*, *phylogram*.