VARIASI DAN ANALISIS FENETIK AKSESI SAWI TANAH (*Cardamine hirsuta* L.) DI PULAU JAWA BERDASARKAN KARAKTER MORFOLOGIS DAN MOLEKULER MENGGUNAKAN *INTER-SIMPLE SEQUENCE REPEAT*

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INTISARI

Cardamine hirsuta L. merupakan species yang berpotensi menjadi organisme model tumbuhan berbunga dan objek studi evolusi morfologis melalui studi komparatif dengan *Arabidopsis thaliana* (L.) Heynh. Sebagai tumbuhan potensial yang dapat ditemukan di Pulau Jawa, pengumpulan data taksonomik diperlukan. Penelitian ini bertujuan untuk menentukan variasi fenotipik dan genotipik *C. hirsuta* berdasarkan karakter morfologis dan molekuler dengan penanda ISSR, serta menganalisis hubungan kekerabatan fenetik *C. hirsuta* di Pulau Jawa. Metode yang digunakan adalah eksplorasi, koleksi data tumbuhan dan lingkungan, serta karakterisasi karakter morfologis dan molekuler. Data morfologis dianalisis secara deskriptif dan numerik. Konstruksi dendrogram menggunakan rumus *Percent Similarity* dengan metode UPGMA. Analisis komponen utama dengan membentuk diagram *scatter plot* tipe *Euclidean biplots*. Data molekuler dianalisis secara numerik dengan teknik DNA fingerprinting menggunakan tujuh penanda ISSR, meliputi persentase polimorfisme dan PIC. Konstruksi dendrogram menggunakan rumus *Jaccard's Coefficient* dengan metode UPGMA, dan PIC menggunakan persamaan dominan marker. Hasil penelitian menunjukkan bahwa variasi morfologis paling banyak ditemukan pada organ daun dan bunga berupa ukuran, warna, dan perilaku organ yang merupakan karakter plastis. Pada dendrogram berdasarkan karakter morfologis terbentuk 4 subklaster pada similaritas 95%. Karakter molekuler berdasarkan visualisasi hasil amplifikasi menghasilkan 54 pita dengan rata-rata persentase polimorfisme 58,70%, dan rata-rata nilai PIC adalah 0,33. Pada dendrogram berdasarkan karakter molekuler terbentuk 4 subklaster pada similaritas 92%. Variasi berdasarkan karakter morfologis dan molekuler memisahkan *C. hirsuta* menjadi 4 subklaster berdasarkan lokasi yaitu Cibodas, Kaliurang, Dataran Tinggi Dieng, dan Senduro yang tergolong ekotipe-plastodeme. Variasi rendah pada *C. hirsuta* karena termasuk tumbuhan *self-compatible* yang menghasikan bunga *cleistogamous* dengan sistem *autonomous self-pollinating*.

Kata kunci: analisis fenetik, ekotipe, ISSR, variasi fenotipik, variasi genotipik

VARIATION AND PHENETIC ANALYSIS OF HAIRY BITTERCRESS (*Cardamine hirsuta* L.) ACCESSION IN JAVA BASED ON MORPHOLOGICAL AND MOLECULAR CHARACTERS USING INTER-SIMPLE SEQUENCE REPEAT

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ABSTRACT

Cardamine hirsuta L. is a species that has the potential to become a model organism for flowering plants and the object of morphological evolution studies through comparative studies with *Arabidopsis tha*liana (L.) Heynh. As a potential plant that can be found in Java, taxonomic data collection is needed. This study aims to determine the phenotypic and genotypic variations of *C. hirsuta* based on morphological and molecular characters with ISSR markers, and analyze the phenotypic relationship of *C. hirsuta* in Java. The methods used are exploration, plant and environmental data collection, and characterization of morphological and molecular characters. Morphological data were analyzed descriptively and numerically. The dendrogram construction uses the Percent Similarity formula with the UPGMA method. Principal component analysis by forming a scatter plot diagram of the Euclidean biplot type. Molecular data were analyzed numerically by DNA fingerprinting technique using seven ISSR markers, including the percentage of polymorphism and PIC. The dendrogram construction uses the Jaccard's Coefficient formula with the UPGMA method, and the PIC uses the dominant marker equation. The results showed that the most morphological variations were found in the leaf and flower organs in the form of size, color, and organ attitude, which were plastic characters. In the dendrogram based on morphological characters, 4 sub-clusters were formed at 95% similarity. Molecular characters based on visualization of the amplification results produced 54 bands with an average polymorphism proportion of 58.70%, and an average PIC value of 0.33. In the dendrogram based on the molecular character, 4 sub-clusters were formed at 92% similarity. Variations based on morphological and molecular characters separated *C. hirsuta* into 4 sub-clusters based on location, namely Cibodas, Kaliurang, Dieng Plateau, and Senduro, which were classified as plastodeme-ecotypes. *C. hirsuta* has low variation because it is a self-compatible plant with cleistogamous flowers and an autonomous self-pollinating system.

Keywords: phenetic analysis, ecotype, ISSR, phenotypic variation, genotypic variation