

## VARIASI GENETIK DAN HUBUNGAN KEKERABATAN SAMBILOTO (*Andrographis paniculata* (Burm.f.) Wall. ex Nees.) DI INDONESIA BERDASARKAN PENANDA MOLEKULER ISSR DAN RAPD

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### INTISARI

Sambiloto (*Andrographis paniculata* (Burm.f.) Wall. ex Nees.) merupakan tumbuhan yang banyak dimanfaatkan oleh sebagian besar penduduk Indonesia dan mampu tumbuh secara baik di Indonesia seperti di Pulau Jawa, Sumatera, Sulawesi, Nusa Tenggara, dan Papua. Tujuan penelitian ini adalah untuk menganalisis variasi genetik dan hubungan kekerabatan sambiloto dari lima aksesori yang mewakili pulau-pulau di Indonesia secara molekuler. Tumbuhan sambiloto dianalisis variasi genetik dan hubungan kekerabatan fenetiknya dengan penanda molekuler ISSR dan RAPD. Hasil amplifikasi dua belas primer ISSR dan RAPD dianalisis dengan Microsoft Excel, MVSP, Corel Draw, dan genA1Ex. Karakter pita amplifikasi ISSR dan RAPD diberikan skor, dikonversi ke dalam matriks biner, dan dihitung persentase polimorfisme serta PIC dari setiap primernya. Hasil skoring juga digunakan untuk menghitung variasi genetik dengan melihat nilai *expected heterozygosity*, *Shannon's Information Index*, *unbiased expected heterozygosity*, dan AMOVA. Dendrogram hubungan kekerabatan fenetik dikonstruksi menggunakan metode Pengklasteran UPGMA dengan *Jaccard's Coefficient*. Penanda ISSR menghasilkan rata-rata persentase polimorfisme yang lebih tinggi dari penanda RAPD yaitu 60,37%, sedangkan penanda RAPD menghasilkan nilai rata-rata 59,52%. Nilai PIC setiap primer berkisar antara 0,22 hingga 0,49. Data variasi genetik dan AMOVA menunjukkan variasi genetik sambiloto dari lokasi aksesori yang sama masih relatif rendah tetapi variasi genetik antar pulau relatif lebih tinggi.

Kata kunci: Variasi genetik, *Andrographis paniculata*, ISSR, dan RAPD

**GENETIC DIVERSITY AND RELATIONSHIP OF SAMBILOTO  
(*Andrographis paniculata* (Burm.f.) Wall. ex Nees.) IN INDONESIA BASED ON  
ISSR AND RAPD MARKERS**

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**ABSTRACT**

Sambiloto (*Andrographis paniculata* (Burm.f.) Wall. Ex Nees.) is widely used by most Indonesians. It is able to grow well in five major islands in Indonesia such as Java, Sumatra, Sulawesi, Nusa Tenggara, and Papua. The purposes of this study were to analyze genetic diversity and the relationship of the sambiloto from five different locations representing islands in Indonesia using a molecular approach. The genetic diversity and relationship of sambiloto's accessions were analyzed using ISSR and RAPD markers. The results of amplification using 12 primers of ISSR and RAPD were analyzed using Microsoft Excel, MVSP, and genAlEx. The ISSR and RAPD bands were converted and scored into binary matrix. The percentage of polymorphism and PIC of each primer were calculated. The scoring results were used to calculate the genetic diversity via expected heterozygosity values, the Shannon's Information Index, unbiased expected heterozygosity, and AMOVA. The dendrogram was constructed using the UPGMA clustering method with the Jaccard's coefficient. ISSR marker produced an average percentage of polymorphisms which was 60.37%, while RAPD marker produced an average value of 59.52%. PIC value for each primer was ranging from 0.22 to 0.49. Genetic diversity and AMOVA data showed that genetic variation of sambiloto from the same location was still relatively low but genetic variation between islands was relatively higher.

Keywords: Genetic diversity, *Andrographis paniculata*, ISSR, and RAPD