

INTISARI

Bunga telang (*Clitoria ternatea*) menarik banyak minat karena banyak bermanfaat. Penelitian bunga telang telah banyak dilakukan khususnya di bidang farmasi sedangkan terkait bidang pertanian masih sedikit. Analisis keragaman genetik plasma nutfah bunga telang perlu dilakukan untuk perancangan program pemuliaan. Penelitian bertujuan untuk mendapatkan keragaman genetik dan kekerabatan sepuluh aksesori bunga telang berdasarkan penanda ISSR (*Inter Simple Sequence Repeats*) dan ISAP (*Inter-SINE Amplified Polymorphism*). Penelitian dilakukan pada bulan September 2021-Maret 2022. Tanaman ditanam di Kebun Tridharma Banguntapan Fakultas Pertanian UGM. Ekstraksi dan isolasi DNA dari sampel daun, PCR, elektroforesis, dan analisis data dilakukan di Laboratorium Genetika dan Pemuliaan Tanaman, Fakultas Pertanian, Universitas Gadjah Mada, Yogyakarta. Penelitian ini menggunakan 4 primer ISSR yaitu (CT)9G, UBC 887, UBC 889, P4 dan 5 kombinasi primer ISAP yaitu K1 (SolS-IIIaF + SolS-IVR), K2 (CsSINE1-01 + CsSINE1-02), K3 (CsSINE1-02 + CsSINE1-03), K4 (CsSINE1-01 + CsSINE1-03), K5 (CmLINE1-ISAP 1 + CmLINE1-ISAP 2). Sepuluh aksesori bunga telang menunjukkan keragaman genetik fenotipe (warna bunga, jumlah kelopak bunga) dan genotipe. Marka ISSR dan ISAP dari sepuluh aksesori menghasilkan polimorfisme masing masing sebesar 65,7% dan 43,4%. Aksesori BS2-UDb2 berhubungan jauh dengan nilai kemiripan 61,8%. Pada penanda ISAP, nilai kemiripan terendah yaitu 76,1% pada aksesori BD2-BMS1. Pada marka ISSR keragaman genetik antar dan dalam populasi sebesar 55% dan 45% sedangkan pada marka ISAP keragaman genetik antar dan dalam populasi berturut turut sebesar 40% dan 60%.

Kata kunci: *Clitoria ternatea*, polimorfisme, ISSR, ISAP

ABSTRACT

Butterfly pea (*Clitoria ternatea*) attracts an interest because of its many benefits. The research on the butterfly pea in the pharmaceutical sector have been conducted, while there is merely related to agriculture even plant breeding. Genetic diversity analysis of butterfly pea germplasm was needed for designing breeding programs. The aim of the study was to obtain genetic diversity of ten accessions of butterfly pea based on ISSR (Inter Simple Sequence Repeats) and ISAP (Inter-SINE Amplified Polymorphism) markers. The research was conducted in September 2021-March 2022. Extraction and isolation of DNA from leaf samples, PCR, electrophoresis, and data analysis were carried out at the Laboratory of Genetics and Plant Breeding, Faculty of Agriculture, Gadjah Mada University, Yogyakarta. Four ISSR primers (CT)9G, UBC 887, UBC 889, P4 and five ISAP primer combinations namely K1 (SolS-IIIaF + SolS-IVR), K2 (CsSINE1-01 + CsSINE1-02), K3 (CsSINE1-02 + CsSINE1-03), K4 (CsSINE1-01 + CsSINE1-03), K5 (CmLINE1-ISAP 1 + CmLINE1-ISAP 2) were used. Ten accessions of butterfly pea showed genetic diversity of phenotype (flower color, number of petals) and genetics. ISSR and ISAP markers applied in ten accessions produced 65.7% and 43.4% polymorphisms, respectively. Accession BS2-UDb2 significantly correlated with a similarity value of 61.8%. In the ISAP marker, the lowest similarity value was 76.1% in the BD2-BMS1 accession. In the ISSR markers, the genetic diversity among and within the population was 55% and 45%, while on the ISAP markers the genetic diversity among and within the population was 40% and 60%, respectively.

Keywords: *Clitoria ternatea*, polymorphism, ISSR, ISAP