



INTISARI

Crassulaceae merupakan salah satu famili tanaman sukulen yang banyak diminati sebagai tanaman hias dan berpotensi untuk menghasilkan spesies dengan variasi yang unik. Penelitian ini bertujuan untuk menentukan keragaman genetik dan hubungan kekerabatan antar dua puluh tiga spesies famili Crassulaceae menggunakan penanda molekuler SRAP. Analisis dilakukan pada bulan Desember 2024-Juni 2025 di Laboratorium Genetika dan pemuliaan Tanaman, Departemen Budidaya Pertanian, Fakultas Pertanian, Universitas Gadjah Mada, Yogyakarta. Sebanyak 23 spesies famili Crassulaceae yang masing-masing diwakili oleh 3 tanaman, dianalisis menggunakan kombinasi lima primer SRAP terpilih, yaitu ME2-EM4, ME2-EM9, ME2-EM10, ME3-EM2, dan ME4-EM2. Data yang diperoleh dianalisis menggunakan perangkat lunak GenAlEx 6.5 dan NTSYS 2.10. Parameter yang dianalisis meliputi persentase lokus polimorfik (PLP), jumlah alel yang diamati (N_a), jumlah alel yang efektif (N_e), indeks Shannon (I), heterozigositas harapan (H_e), jarak genetik, dendogram DICE *similarity* UPGMA, PcoA, dan AMOVA. Hasil analisis menunjukkan adanya perbedaan yang signifikan, antar spesies memiliki keragaman genetik sebesar 85% dan keragaman genetik dalam spesies sebesar 15%. Hubungan kekerabatan terdekat dimiliki spesies E5 dan E6, serta hubungan kekerabatan terjauh dimiliki oleh spesies S6 dan K4.

Kata kunci: molekuler, SRAP, Crassulaceae, keragaman, genetik.



ABSTRACT

Crassulaceae is a family of succulent plants that is much sought after as an ornamental plant and has the potential to produce species with unique variations. This study aims to determine the genetic diversity and kinship relationships among twenty-three species of the Crassulaceae family using SRAP molecular markers. The analysis was conducted from December 2024 to June 2025 at the Genetics and Plant Breeding Laboratory, Department of Agricultural Cultivation, Faculty of Agriculture, Gadjah Mada University, Yogyakarta. A total of 23 species of the Crassulaceae family, each represented by 3 plants, were analyzed using a combination of five selected SRAP primers, namely ME2-EM4, ME2-EM9, ME2-EM10, ME3-EM2, and ME4-EM2. The data obtained were analyzed using GenAlEx 6.5 and NTSYS 2.10 software. The parameters analyzed the polymorphic locus percentage (PLP), observed alleles (N_a), effective alleles (N_e), Shannon index (I), expected heterozygosity (H_e), genetic distance, DICE similarity UPGMA dendogram, PcoA, and AMOVA. The analysis results showed significant differences between species with a genetic diversity of 85% and a genetic diversity within species of 15%. The closest kinship relationship was found between species E5 and E6, and the most distant kinship relationship was found between species S6 and K4.

Keywords: molecular, SRAP, Crassulaceae, diversity, genetic.