

Intisari

Pembentukan galur tomat unggul dilakukan dengan cara persilangan ganda (*double cross*) dalam rangka peningkatan keragaman genetik. Marka molekuler dapat digunakan untuk mengidentifikasi keragaman antar galur tomat berdasarkan jarak genetik tanpa pengaruh lingkungan. Penelitian ini bertujuan untuk mengetahui keragaman genetik dan hubungan kekerabatan antara sepuluh galur F3 tanaman tomat terhadap tetua F1 Servo dan tetua F1 Betavila menggunakan marka SRAP (*Sequence Related Amplified Polymorphism*). Penelitian ini dilaksanakan pada bulan Februari hingga April 2023 di Laboratorium Genetika dan Pemuliaan Tanaman, Fakultas Pertanian, Universitas Gadjah Mada dengan menggunakan 12 galur tomat dengan 5 sampel per galur. Sampel daun tomat diambil lahan di Dusun Bumirejo, Wonosobo. Marka SRAP yang digunakan terdiri dari 10 kombinasi primer terseleksi, yaitu K1 (ME 5 × EM 5), K5 (ME 9 × EM 9), K7 (ME 5 × EM 6), K8 (ME 5 × EM 7), K10 (ME 5 × EM 9), K11 (ME 5 × EM 10), K12 (ME 6 × EM 5), K13 (ME 6 × EM 7), K15 (ME 6 × EM 9), K16 (ME 6 × EM 10). Analisis data menggunakan *software* NTSYS 2.02 dan GenAlEx 6.503. Hasil penelitian menunjukkan bahwa nilai heterozigositas harapan (H_e) dalam populasi tomat sebesar 0,115 sehingga dikategorikan keragaman rendah. Nilai AMOVA menunjukkan keragaman antar populasi tomat sebesar 46 % dan keragaman dalam populasi tomat sebesar 54 %. Analisis kekerabatan menunjukkan bahwa BV II – 7 – 5 dan BV II – 13 – 1 lebih dekat pada tetua F1 Servo, sedangkan BV II – 5 – 7, BV – 9 – 11, BV I – 9 – 1, BV I – 2 – 8, BV III – 6 – 2, BV III – 6 – 1, BV III – 6 – 1, dan BV II – 5 – 2 lebih dekat pada tetua F1 Betavila.

Kata kunci : *Solanum lycopersicum*, *double cross*, galur, SRAP.

Abstract

Superior tomato lines were developed through double-cross in order to increase genetic diversity. Molecular markers can identify the tomato lines diversity based on genetic distance without considering environmental factors. This study aimed to determine the genetic diversity and relationship between ten F3 lines of tomato with their parental lines, F1 Servo and F1 Betavila, using SRAP (Sequence Related Amplified Polymorphism) markers. This research was conducted from February to April 2023 at the Genetics and Plant Breeding Laboratory, Faculty of Agriculture, Gadjah Mada University using 12 tomato lines with 5 samples for each lines. Samples of tomato leaves were taken from a farmland in Bumirejo Hamlet, Wonosobo. The SRAP markers used in this research are consisted of 10 combinations of selected primer, there are K1 (ME 5 × EM 5), K5 (ME 9 × EM 9), K7 (ME 5 × EM 6), K8 (ME 5 × EM 7), K10 (ME 5 × EM 9), K11 (ME 5 × EM 10), K12 (ME 6 × EM 5), K13 (ME 6 × EM 7), K15 (ME 6 × EM 9), K16 (ME 6 × EM 10). The data was analyzed using NTSYS 2.02 and GenAlEx 6.503 software. The result shows that the value of expected heterozygosity in tomato population is 0.115 and classified as low diversity. The AMOVA value indicates that the genetic diversity between tomato populations is 46% and the genetic diversity within tomato populations is 54%. The genetic relationship analysis shows that BV II – 7 – 5 and BV II – 13 – 1 are closer to F1 Servo parents, while BV II – 5 – 7, BV – 9 – 11, BV I – 9 – 1, BV I – 2 – 8, BV III – 6 – 2, BV III – 6 – 1, BV III – 6 – 1, and BV II – 5 – 2 are closer to Betavila F1 parents.

Keyword : *Solanum lycopersicum*, double cross, lines, SRAP.