INTISARI

Persilangan intraspesifik telah banyak dilakukan namun akan menghasilkan keragaman genetik populasi anakan yang tergolong rendah jika dibandingkan dengan hasil persilangan interspesifik. Mentimun (*Cucumis sativus* L.) memiliki sumber atau pusat gen (*gene pool*) yang sempit sehingga keragaman genetik hasil persilangan dalam spesies sangat kecil. Maka upaya peningkatan keragaman genetik mentimun dilakukan melalui persilangan intraspesifik dengan memilih tetua yang memiliki karakter agronomis dan distribusi geografik yang berbeda. Mentimun CS887 merupakan galur inbrida lokal dan telah dicoba untuk disilangkan dengan mentimun F1 hibrida Shira asli Jepang. Persilangan keduanya merupakan persilangan intraspesies menghasilkan F1 sebanyak 5 individu. Selain itu juga dilakukan *selfing* terhadap F1 hibrida Shira menghasilkan keturunan (S1) sebanyak 5 individu. Penelitian ini bertujuan untuk menilai keberhasilan persilangan tersebut berdasarkan nilai ragam genetik dan nilai kemiripan antara populasi tetua dengan anakan hasil persilangan maupun *selfing*. Penelitian dilakukan di Laboratorium Pemuliaan Tanaman, Departemen Budidaya Pertanian, Fakultas Pertanian, Universitas Gadjah Mada, Yogyakarta pada bulan September-November 2020. Analisis molekuler dilakukan menggunakan penanda SRAP dengan enam pasang kombinasi primer terpilih yaitu K1 (ME1-EM1), K7 (ME2-EM3), K10 (ME3-EM2), K11 (ME3-EM3), K14(ME4-EM2), K15(ME4-EM3). Nilai ragam genetik ditunjukkan oleh presentase lokus polimorfik, index shannon, serta keragaman antar dan dalam populasi. Hubungan kekerabatan antara tetua dan anakan hasil persilangan dan antara populasi F2 Shira dengan populasi hasil persilangan diketahui dengan analisis klustering serta analisis koordinat utama (PCoA). Nilai keragaman berdasarkan Indeks Shannon tergolong kecil hingga sedang yaitu berkisar antara 0-0,688, pada populasi F2 Shira rerata Indeks Shannon sebesar 0,378, populasi CS887 sebesar 0,212, dan pada populasi F1 hasil persilangan F1 hibrida Shira × CS887 sebesar 0,245. Nilai kemiripan berdasarkan koefisien kemiripan antar populasi tergolong hampir sama, namun populasi F1 hasil persilangan F1 hibrida Shira × CS887 memilki koefisien kemiripan yang paling besar terhadap F2 Shira yaitu sebesar 0,83, sedangkan F1 hasil persilangan F1 hibrida Shira × CS887 memilki koefisien kemiripan yang lebih kecil terhadap CS887 yaitu sebesar 0,76.

Kata kunci : *Cucumis sativus*, persilangan, *selfing*, populasi, SRAP

Analisis Genetik F1 Hasil Persilangan Mentimun (Cucumis sativus L.) 'Shira' dengan 'CS887' Berdasarkan Penanda SRAP
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ABSTRACT

Intraspecific crosses have been widely practiced but will result in a low genetic diversity of the progeny population when compared to interspecific crosses. Cucumber (*Cucumis sativus* L.) has a narrow gene pool so the genetic diversity resulting from crosses within the species is very small. Therefore, the efforts to increase the genetic diversity of cucumbers are carried out through intraspecific crossovers by selecting parents who have different agronomic characters and geographic distributions. The CS887 cucumber is a local inbred strain and has been attempted to be crossed with the original Japanese Shira F1 hybrid cucumber. The cross between the two is an intraspecies cross to produce F1 as many as 5 individuals. In addition, selfing was also carried out on the Shira F1 hybrid to produce offspring (S1) of 5 individuals. This study aims to assess the success of these crosses based on the value of genetic variance and the value of the similarity between the parent population and the offspring from crossing and selfing. The research was conducted at the Plant Breeding Laboratory, Department of Agricultural Cultivation, Faculty of Agriculture, Universitas Gadjah Mada, Yogyakarta in September-November 2020. Molecular analysis was carried out using SRAP markers with six pairs of selected primary combinations, namely K1 (ME1-EM1), K7 (ME2- EM3), K10 (ME3-EM2), K11 (ME3-EM3), K14 (ME4-EM2), K15 (ME4-EM3). The value of genetic variance is indicated by the percentage of polymorphic loci, Shannon index, and diversity between and within populations. The kinship relationship between the parents and offspring resulting from the cross and between the F2 Shira population and the population resulting from the cross was known by clustering analysis and main coordinate analysis (PCoA). The diversity value based on the Shannon Index is classified as small to moderate, ranging from 0 to 0,688, in the F2 Shira population the average Shannon Index is 0,378, the CS887 population is 0,212, and in the F1 population the result of crossing F1 hybrid Shira × CS887 is 0,245. The similarity value based on the similarity coefficient between populations is almost the same, but the F1 population resulting from the F1 hybrid Shira × CS887 crosses has the greatest similarity coefficient to F2 Shira, which is 0,83, while the F1 result of the Shira × CS887 hybrid F1 cross has a smaller coefficient of similarity to CS887 which is equal to 0,76.

Keyword : *Cucumis sativus*, crossing, *selfing*, population, SRAP