

**PENDUGAAN KERAGAMAN GENETIK DAN KEMAJUAN SELEKSI  
BEBERAPA GALUR JAGUNG MANIS (*Zea mays var. Saccharata* Sturt)  
GENERASI S-2**

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**ABSTRAK**

Jagung manis (*Zea mays var. saccharata* Sturt) merupakan salah satu sayuran yang banyak diminati oleh masyarakat Indonesia. Seleksi tanaman merupakan salah satu tahapan yang penting dilakukan dalam pemuliaan tanaman untuk memperbaiki karakter tanaman. Tujuan dari penelitian ini adalah untuk mengetahui keragaman genetik, nilai duga heritabilitas, kemajuan seleksi dan calon tetua dari galur jagung manis generasi S-2. Penelitian ini dilaksanakan di Kebun Percobaan Fakultas Pertanian UPN "Veteran" Yogyakarta pada bulan Maret sampai dengan Juni 2021. Rancangan percobaan yang digunakan adalah Rancangan Acak Kelompok Lengkap (RAKL). Perlakuan yang digunakan 9 galur jagung manis generasi S-2 meliputi CMP-2A/51, CMP-3/63, CMP-5/49, CMP-6/7, CMP-8/1, CMP-9B/56, TMR-1/20, TLT-2/43, dan SBO-2/25. Data dianalisis dengan menggunakan sidik ragam taraf 5 %. Apabila dalam analisis ragam terdapat peubah yang berbeda nyata maka dilakukan uji lanjut Scott Knott. Data juga dianalisis dengan menggunakan pendugaan keragaman genetik, heritabilitas dan kemajuan seleksi. Hasil Penelitian menunjukkan nilai koefisien keragaman genetik tinggi pada parameter tinggi letak tongkol dan bobot tongkol tanpa kelobot. Nilai heritabilitas tinggi pada tinggi tanaman, jumlah daun, umur berbunga jantan, umur berbunga betina, tinggi letak tongkol, bobot tongkol tanpa kelobot, diameter tongkol, panjang tongkol, dan jumlah baris biji. Nilai kemajuan genetik harapan tinggi pada parameter tinggi tanaman, tinggi letak tongkol dan bobot tongkol tanpa kelobot. Galur yang berpotensi dapat dijadikan calon tetua adalah CMP 9B/56 dan CMP 2A/51.

**Kata Kunci : Jagung Manis, Keragaman Genetik, Heritabilitas, Kemajuan Seleksi**

**ESTIMATION OF GENETIC VARIAN  
AND PROGRESS OF SELECTION OF SOME SWEET CORNS (*Zea mays*  
*var. saccharata* Sturt) S-2 GENERATION**

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**ABSTRACT**

Sweet corn (*Zea mays var. saccharata* Sturt) is one of the most popular vegetables in Indonesia. Plant selection is one of the important stages in plant breeding to improve plant character. The purpose of this study was to determine genetic diversity, heritability predictability, selection progress and prospective parents of the S-2 generation sweet corn. This research was conducted at the Experimental Garden of the Faculty of Agriculture, UPN "Veteran" Yogyakarta from March to June 2021. The experimental design used was a Randomized Completely Block Design (RCBD). The treatments used were 9 sweet corn strains of the S-2 generation including CMP-2A/51, CMP-3/63, CMP-5/49, CMP-6/7, CMP-8/1, CMP-9B/56, TMR-1/20, TLT-2/43, and SBO-2/25. The data were analyzed using the variance level of 5%. If in the analysis of variance there are variables that are significantly different, Scott Knott's further test is carried out. Data were also analyzed using estimates of genetic varian, heritability and selection progress. The results showed that the value of the coefficient of genetic varian was high on the parameters of the height of the cob location and weight without corn husk. High heritability values were plant height, number of leaves, age of male flowering, age of female flowering, the height of cob location, weight without corn husk, diameter of ear, length of ear, and number of rows of seeds. The value of genetic progress was high on the parameters of plant height, cob height and weight without corn husk. The line that has the potential to be used as a candidate for parentage is CMP 9B/56 and CMP 2A/51.

Keywords: Sweet Corn, Genetic Varian, Heritability, Selection Progress