

Abstract

A Decade of Tropical Sweet Corn Breeding Using Conventional and Molecular Approaches in Malaysia [†]

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Abstract: To increase self-sufficiency in sweet corn production in Malaysia, a long-term breeding study was conducted to develop merit inbred lines using conventional and molecular techniques toward production of superior local hybrid varieties. A germplasm consisting of 18 tropical source populations was established and used for inbred line development. Forty tropical inbred lines were developed through continuous self-pollination and selection. Agronomic performance of these newly developed inbred lines was evaluated in replicated blocks in two locations. Significant variations in agronomic performance indicated presence of high genetic diversity among the inbred lines for potential utilization towards hybrid production. In addition, the level of genetic homozygosity for each inbred line and genetic similarities among the inbred lines were estimated through amplification of 100 microsatellite loci. The 40 inbred lines were clustered into five main heterotic groups based on their agronomic and molecular characteristics. Eleven inbred lines were selected to conduct two sets of half-diallel cross (5×5 and 6×6), resulting a total of 25 single-cross hybrids. Greater estimates of GCA mean squares than SCA mean squares showed relatively more important effect of additive gene action in controlling yield and yield components in the hybrids. Genetic distances among the parental lines were used to predict hybrid performance, showing significant positive associations between genetic similarities and SCA estimates. Among the 25 hybrids produced, five hybrids exhibited high and competitive yield performance in comparison to those from the commercial imported hybrids and can be released as new hybrids in Malaysia after evaluation in large scale multi-locational trials.

Keywords: sweet corn; inbred line; molecular breeding.

Author Contributions: G.S. devised the project and supervised the experiments. P.K. performed the experiments, collected morphological and molecular data and analyzed those data using various statistical genetic models. P.K. and G.S. interpreted and discussed the results of this work and prepared the manuscript. All authors have read and agreed to the published version of the manuscript.

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