Kitti Boonlertnirun 2013: Genetic Distance and Heterotic Pattern among Single Cross Hybrids in Waxy Corn. Doctor of Philosophy (Plant Breeding), Major Field: Plant Breeding, Faculty of Agriculture at Kamphaeng Saen. Thesis Advisor: Associate Professor Choosak Jompuk, Dr.sc.nat. 85 pages.

Waxy corn is a traditional Asian vegetable, consumed as cooked green ears similar to that of sweet corn. A promising hybrid breeding program in Thailand has started, based on germplasm derived from old local landraces, but the genetic diversity and heterotic pattern must be better understood to efficiently plan and use the existing germplasm. The objectives of this study were to; (1) evaluate genetic distance among single cross hybrids of waxy corn in Thailand from different sources (2) investigate correlation among heterotic effects, combining ability and genetic diversity and (3) determine the relationship between phenotypic and genotypic groups investigated by molecular marker. The genetic distance and heterotic pattern were studied using direct diallel crosses of nine hybrids and evaluated in four environments. The result showed that inbreeding depression was high in green ear yield (38%) and marketable dehusk yield (53%), but low in ear length (9%) and ear width (5%). Heterosis of 36 double cross combinations ranged from -33 to 8% for marketable dehusk yield. Troyer's genetic diversity (TGD) estimated from the relationship between heterosis and inbreeding depression varied from 0.40 to 1.16. This indicates that waxy corn hybrids had a diverse genetic background with a good potential for improvement by breeding. The degree of relatedness did not agree with sources of the hybrids. Variation in GCA was significant in green ear yield, marketable dehusk yield and ear size, corresponding variation in SCA was significant for marketable dehusk yield and ear length. Based on cluster analysis of SCA for marketable dehusk yield matrix, two distinct clusters of heterotic pattern were identified for a targeted hybrid breeding. A very high positive correlation (r = 0.98**) was found between TGD and heterosis across four environments. The TGD also positively correlated with SCA (r = 0.63**). Unfortunately, There was no correlation between phenotypic and genotypic groups investigated by molecular marker.

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