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Genetic Diversity of Corn Hybrids from Different Sources in Thailand as Verified by Their Heterotic Pattern and Inbreeding Depression

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ABSTRACT

Growing a single cross or single crosses of genetically related inbreds in a large area has proved to be vulnerable to biological and physical hazards and lead to crop disaster when such genetic background became susceptible to ever changing environment. The purpose of this study was to measure genetic diversity of twelve commercial hybrids in Thailand. The genetic diversity was estimated by the formula : GD = 1 – [(H-C)/(H-S)], where GD, H, C and S stand for genetic diversity, average performance of the two hybrids, hybrid by hybrid cross, and average of the self-hybrids, respectively. The method assumes that heterosis is caused by cummulated effect of dominance and absence of epistasis. Theoretically, Two closely related hybrids with a GD of 0.25 should have one common inbred and other two inbreds are genetically related. Two hybrids with one inbred in common and the other two unrelated inbreds have the expected GD of 0.5. Two slightly related hybrids with a GD of 0.75 should have one related inbred and other two distinct inbreds. Two unrelated hybrids have an expected GD of 1.0. The estimation of genetic diversity of 12 commercial hybrids indicated that pairs of hybrids from the same company such as CP 999 x CP 888 (GD=0.25) and Pioneer 3013 x Pioneer 3012 (GD=0.26) each has closely related inbreds on both sides of the pedigree. Other three pairs of hybrids, Cargill 922 x Cargill 919 (GD=0.51), Pacific 700 x Pacific 328 (GD=0.57) and Uni. 98 x Uni-H 9728 (GD=0.67) each should have one inbred in common. The hybrids from different companies have GD in the range of 0.37–0.98 such as CP 999 x Cargill 919 (GD=0.37), SW 3853 x Pioneer 3013 (GD=0.75), Pacific 700 x Cargill 922 (GD=0.97), G5445A x Pioneer 3013 (GD=0.96), Uni-H 9728 x Cargill 919 (GD=0.96) and Cargill 922 x Uni. 98 (GD=0.98). The results showed that, the hybrids in Thai market still had considerable genetic diversity with noticeably exchanged of genetic background.

Key words : heterosis, inbreeding, genetic diversity, corn hybrid

INTRODUCTION

Single cross hybrids have been very popular among corn growers. The single cross not only gave higher yield but also possesssed other good agronomic traits especially uniformity. Private seed companies as well as public research centers have released new hybrids into the market every year. Several hybrids look very similar in general appearances which may be due to usage of few elite

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germplasm that adapted to Thai environment. This was a very common practice for all breeding programs and eventually led to genetic vulnerability and disease disaster e.g. *Phytophthora infestans* in tomato, Victoria leaf blight (*Helminthosporium victoria*) in oat and southern corn leaf blight (*H. maydis*, T type) in corn. While single cross is very popular because of its uniformity, growing the same hybrid or similar hybrids in vast area had proved to be harzardous.

Most of inbred lines derived from well adapted germplasm either from narrow genetic base synthetic populations or well adapted single crosses. Most plant breeders tended to use the best germplasm in the area which led to similarity of inbreds of different breeding programs which inturn ended up with similar hybrids in the market (Hallauer *et al*., 1988)

Assessment of genetic similarity can be done directly by DNA analysis (Smith *et al*., 1990) or indirectly by pedigree information to assess the relatedness of lines. The latter method normally use in self-pollinated crops such as wheat, oat, barley, soybean, peanut, etc. Accuracy of pedigree is the key for precision of assessment. Using pedigree information to assess the relative of corn inbred lines is of limited because only few generations can be traced back and some inbred lines were derived from open-pollinated population. However, Smith *et al*. (1990 and 1992) found that there was high correlation (r > 0.85) between molecular marker and pedigree method. Moreover, Messmer *et al*. (1993) showed that there was also high correlation between pedigree method and RFLP method.

Troyer *et al*. (1988) used the positive association between genetic diversity and heterosis to assess the diversity or relatedness of parent lines of hybrids. The same principle can be used when parents are single crosses in stead of inbred lines.

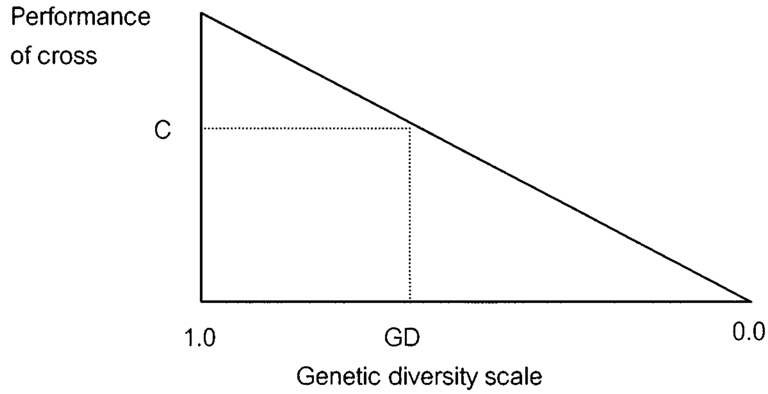
This study followed the method used by Troyer *et al*. (1988) to assess the diversity or relatedness of leading commercial hybrids available in the Thai market.

MATERIALS AND METHODS

Twelve leading commercial single cross hybrids, namely, SW 3853 from The National Corn and Sorghum Research Center and another eleven hybrids from private companies, Cargill 919, Cargill 922, CP 888, CP 999, G 5445A, Pacific 328, Pacific 700, Pioneer 3012, Pioneer 3013, Uni-H 9728 and Uni. 98 were used in this study. Crosses were made in all possible pairs of twelve hybrids (diallel), excluded the reciprocal crosses. Hence, sixty-six double crosses, 10 ears of each were obtained. Simultaneously, 10 ears of each single cross were selfed and seeds were harvested seperately for further testing.

Seeds of single crosses, double crosses and self-seeds were planted in August, 1997 at The National Corn and Sorghum Research Center, Nakhon Ratchasima province. Statistical design was randomized complete block, 5 replications, two 5-meter rows per plot with plant spacing 75 cm between rows and 25 cm between plants within row. Basal fertilizer 15-15-15 was applied at the rate of 50 kg/rai before planting. Atrazine mixed with Pendimethalin, a pre-emergence herbicide was used at the rate of 640 g/rai and 640 ml/rai, respectively. After 2 weeks, plants were thinned to 1 plant/hill or population size of 8,533 plants/rai. At 4th week, 50 kg/rai of ammonium sulfate was topdressed. Grain yield was measured from the average of 5 replications at 15 % seed moisture content.

Assessment of genetic diversity was followed that of Troyer *et al*. (1998)



GD = 1-[(H-C)/(H-S)]

When GD = Genetic diversity

H = Average of hybrids (counterpart single crosses)

C = Value of hybrid x hybrid cross (double cross)

S = Average of self-hybrid (counterpart hybrids)

Figure 1 Algebraic formula for determining genetic diversity with geometric interpretation for use with yield data.

RESULTS AND DISCUSSIONS

Twelve single crosses yielded 694.30-1,205.06 kg/rai and average yield was 929.71 kg/rai while 12 S_1's yielded 242.26 - 599.03 kg/rai and gave the average yield only 398.30 kg/rai (Table 1). The 66 double crosses derived from diallel cross of 12 single crosses yielded 468.87 - 979.50 kg/rai with the average of 751.17 kg/rai (Table 2). Genetic diversity index of each pair of single crosses was presented in Table 3.

Theoretically, identical hybrids have genetic diversity equal to 0, therefore, GD = 0 because (H-C) = (H-S) or crossing between identical hybrids is the same as selfing. When GD = 0.25 indicates that both hybrids have 1 common parent and another 2 inbred lines are 50% genetically related. GD = 0.5 means both hybrids have 1 common parent and another 2 inbred lines are genetically unrelated. GD = 0.75 means both hybrids have 2 genetically unrelated parents and another 2 inbred lines are 50% related. Two unrelated hybrids derived from 4 genetically distinct inbreds have GD equal to 1. However, genetic diversity indices have value ranging from 0-1 which depend upon the percentage of relatedness of the 4 parents involve in both

Table 1 Yields (kg/rai) of selfing (S_1) and 12 single crosses.

	Uni.9728	Uni.98	Pi.3012	Pi.3013	Ca.919	Ca.922	Pac.328	Pac.700	CP 888	CP 999	G5445A	SW3853
Selfing (S_1)	516.35	417.84	314.69	443.78	376.34	272.36	303.07	370.86	242.26	344.78	578.31	599.03
Sigle cross	813.37	877.50	968.04	815.90	1003.55	694.30	897.25	838.95	886.29	1103.16	1046.72	1205.06

Mean (self) = 398.30 kg/rai Mean (hybrid) = 929.71 kg/rai

CV. (self) = 16.94 % CV. (hybrid) = 15.16 %

Table 2 The average yields (kg/rai) of 66 double crosses.

	Uni.98	Pi.3012	Pi.3013	Ca.919	Ca.922	Pac.328	Pac.700	CP 888	CP 999	G5445A	SW3853	x̄
Uni.9728	726.40	690.54	691.64	898.69	648.69	646.48	793.17	740.34	724.39	904.15	849.97	755.86
Uni.98		730.48	715.11	757.00	777.23	649.73	825.03	671.37	704.08	909.44	979.50	767.67
Pi.3012			510.30	645.83	665.88	613.97	733.03	634.13	673.23	891.13	944.91	703.03
Pi.3013				896.47	693.02	600.28	772.65	676.44	701.06	912.58	886.29	732.34
Ca.919					590.63	728.84	822.71	589.90	615.42	908.49	916.68	760.96
Ca.922						729.52	755.10	669.59	635.23	852.39	796.15	710.31
Pac. 328							642.18	587.43	586.00	660.25	918.24	669.32
Pac. 700								711.77	820.18	861.29	893.90	784.63
CP 888									468.87	802.33	873.74	675.08
CP 999										826.45	900.56	695.95
G5445A											929.03	859.77
SW 3853												898.99
Mean												751.17

CV. = 16.91%

Table 3 Genetic diversity indices of 12 commercial single crosses in Thailand.

	Uni.98	Pi.3012	Pi.3013	Ca.919	Ca.922	Pac.328	Pac.700	CP888	CP999	G5445A	SW3853	x̄
Uni.9728	0.67	0.57	0.62	0.96	0.69	0.52	0.89	0.75	0.55	0.91	0.63	0.71
Uni.98		0.65	0.68	0.66	0.98	0.55	0.93	0.62	0.53	0.89	0.88	0.73
Pi.3012			0.26	0.47	0.69	0.49	0.70	0.55	0.49	0.79	0.78	0.58
Pi.3013				0.97	0.84	0.47	0.87	0.66	0.54	0.96	0.75	0.69
Ca.919					0.51	0.64	0.82	0.44	0.37	0.79	0.70	0.67
Ca.922						0.87	0.97	0.77	0.55	0.96	0.70	0.78
Pac.328							0.57	0.51	0.39	0.41	0.78	0.56
Pac. 700								0.73	0.75	0.83	0.76	0.80
CP888									0.25	0.70	0.72	0.61
CP999										0.59	0.63	0.51
G5445A											0.63	0.77
SW3853												0.72
Mean												0.68

hybrids. The genetic diversity index works under the assumption that heterosis is a cumulative effect of dominant genes and absence of epistasis.

The genetic diversity index of each pair of hybrids ranged from 0.25-0.98 and average of 0.68. GD of hybrids from the same company ranged from 0.25-0.67 indicated that each pair of hybrids had 1 common parent with different degree of relatedness of another 2 inbred lines, e.g. CP 999 x CP 888 (GD = 0.25), Pioneer 3012 x Pioneer 3013 (GD=0.26), Cargill 622 x Cargill 919 (GD = 0.51), Pacific 100 x Pacific 328 (GD=0.57), and Uni.98 x Uni-H 9728 (GD = 0.67).

Genetic diversity indices of hybrids from different companies ranged from 0.37-0.98 indicated that some of hybrids from different sources were derived from very diverse parents, e.g. SW 3853 x Pioneer 3013 (GD=0.75), Pacific 700 x Cargill 922 (GD=0.97), G5445A x Pioneer 3013 (GD=0.96) Cargill 919 x Uni-H 9728 (GD=0.96) and Cargill 922 x Uni. 98 (GD=0.98) However, 2 pairs of hybrids from different sources showed relatively high degree of relatedness of parents, e.g. CP 999 x Cargill 919 (GD = 0.37) and CP 999 x Pacific 328 (GD = 0.39). In general, hybrids which possessed a high degree of relatedness with other hybrids were old hybrids which had been released more than 5 years, e.g. CP 999, Pacific. 328, Pioneer 3012 and CP 888. Their average GD were 0.51, 0.56, 0.58 and 0.61, respectively. The rest of hybrids had average GD ranged from 0.67-0.80. Although, majority of hybrids in the Thai market still had high genetic diversity but there was a tendency of moving toward high degree of relatedness.

CONCLUSION

Practically, genetic diversity can be estimated from heterosis of cross but the figure shows only a relative comparison not relationship of involved parents. However, heterosis can be used to set up heterotic groups of germplasm sources. From this study, genetic diversity indices of selected hybrids ranged from 0.25-0.98 with average of 0.68. Hybrids of the same source showed very high degree of relatedness while hybrids from different sources had more diverse parents with tendency toward high degree of relatedness.

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