

# Inbreeding Effects in Two Subpopulations of a Maize Variety

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## ABSTRACT

Inbreeding effects were studied in a maize variety, Cupurico × Flint Compuesto, which had undergone full-sib family selection for four cycles. After yield evaluation in the fourth cycle, 16 full-sib families were selected for this study. Eight of the highest yielding families were designated as "selected" subpopulation and eight other families which yielded around the population mean as "non-selected" subpopulation. Four levels of inbreeding, 0.250, 0.125, 0.062 and 0.031, were obtained by using full-sib family per se, intermating of 2, 4 and 8 full-sib families, respectively. In order to increase enough seeds for testing, random mating within each entry was made. This resulted in closer genetic relationship and the inbreeding coefficient of each entry became 0.2749, 0.1492, 0.0854 and 0.0511, respectively.

Two evaluation trials were conducted, one in 1975 and another in 1976. The combined analyses showed that most of the differences between the inbreeding level of 0.2749 and the others were highly significant for grain yield, plant height, ear height, downy mildew percentage, and days to silking. The differences among other lower levels of inbreeding were not significant for all traits. The results suggested that the use of a single full-sib family in forming a new population resulted in inbreeding depression and therefore, more than two families should be used in intermating.

Maize breeding program of Kasetsart University has emphasized its effort in developing corn varieties through population improvement. Recurrent selections such as  $S_1$  selection, full-sib and half-sib family selection (5) are often used in increasing favorable genes in the improved population. The breeding procedure involves the extraction of families, progeny testing, and recombining by intermating among the selected families. Expected gain from selection depends partly on number of lines recombined to form a new population (1). More improvement is expected when less number of lines involved in the recombination. However, the population derived from less number of lines may result in inbreeding depression. Sing, *et al.* (6) studied inbreeding effects resulted from 6 different levels of inbreeding in Jarvis Golden Prolific and Indian Chief varieties. They found that the inbreeding depression increased as the inbreeding levels increased in grain yield, plant height, ear height, days to silk, and number of

ears. Other investigators such as Cornelious and Dudley (2) and Stringfield (7) found similar results. Therefore, the proper number of selected families involved in forming the improved variety is of interest among maize breeders in order to avoid inbreeding depression. Information on this is quite limited at present.

The objectives of this investigation were: To study inbreeding depression resulted from 4 levels of inbreeding : 0.0511, 0.0854, 0.1492 and 0.2749. To find a guide line in determining how many families should be selected in forming new improved variety.

## Materials and Methods.

A maize variety, Cupurico × Flint Compuesto, which had undergone full-sib family selection for 4 cycles was used in this study. After progeny testing in the fourth cycle, 16 full-sib families were selected for this investigation. Eight of the highest yielding families were

designated as "selected" subpopulation and the symbols  $S_1, S_2, S_3, \dots, S_8$ , were used to represent each family. Another group consisted of 8 families with grain yield around the mean and were designated as "non-selected" subpopulation. The symbols  $R_1, R_2, R_3, \dots, R_8$ , were used to represent each family in this group.

Since each of full-sib family was derived from 2 parents, its coefficient of inbreeding was 0.250. In order to obtain the materials with the coefficient of inbreedings 0.125, 0.062 and 0.031, the intermatings of 2, 4 and 8 families, respectively, were made in each subpopulation. In order to increase enough seeds for testing, random mating within each entry was made. The coefficient of inbreeding became 0.2749, 0.1492, 0.0854 and 0.0511, for each full-sib family, 2, 4 and 8 families recombined, respectively (Table 1).

These 30 entries were evaluated against their base population (parent) for 2 seasons at Farm Suwan. Randomized complete block design with 4 replications was used in both 1975 late rainy season and 1976 early season. Grain yield and other agronomic characters were recorded and analysed.

### Results and Discussion

Mean performance of entries with different inbreeding levels are shown in Table 2. With increasing the inbreeding level from 0.0511 to 0.2749, grain yield of entries in both subpopulations S and R decreased. The differences among entries with different inbreeding levels in subpopulation S was significant and that in subpopulation R was highly significant (Table 3).

**Table 1.** Symbols used for entries with different inbreeding levels.

Symbols	Coefficient of inbreeding	Entry structure
$S_1 - S_8$	0.2749	families in selected subpopulation.
$S_9 - S_{12}$	0.1492	entries derived from intermating of 2 families
$S_{13} - S_{14}$	0.0854	entries derived from intermating of 4 families
$S_{15}$	0.0511	entries derived from intermating of 8 families
$R_1 - R_8$	0.2749	families in non-selected subpopulation.
$R_9 - R_{12}$	0.1492	entries derived from intermating of 2 families
$R_{13} - R_{14}$	0.0854	entries derived from intermating of 4 families
$R_{15}$	0.0511	entries derived from intermating of 8 families
P	0.00	base population (parent)

**Table 2.** Mean performance of entries with different inbreeding levels.

Inbreeding level	Days to silking	Plant height (cm.)	Ear height (cm.)	Grain yield (kg/ha.)
Subpopulation S				
0.2749	70.95	183	95	3080
0.1492	70.13	194	100	3830
0.0854	71.63	191	98	4000
0.0511	69.88	190	101	4196
Subpopulation R				
0.2749	71.50	174	88	2845
0.1492	69.41	185	93	3562
0.0854	70.34	185	94	3897
0.0511	71.00	174	90	3639
parent	71.25	197	1051	3995

Data averaged from 2 seasons.

Source of variation	df.	Mean square				Percent downy mildew
		Days to silking	Plant height	Ear height	Grain yield	
Environments	1	53,926.00	103,039.24	19,594.27	2,261,600.27	246.22
Replications/Environments	6	11.29	611.52	380.06	827,743.27	375.
Treatments	30	5.03	679.08**	376.38**	2,325,970.97*	
subpopulations vs. parent	1	2.24	1,688.80**	898.84**	3,188,790.51	
subpopulation S vs. subpopulation R	1	6.34	4,758.56**	2,741.86**	3,678,901.98	
within subpopulation S	14					
Inbreeding levels	3	7.57	958.64**	262.46	7,519,802.36*	
S <sub>1</sub> -S <sub>8</sub> vs. S <sub>9</sub> -S <sub>15</sub>	1	22.29**	2,731.69**	733.59**	21,596,646.83**	
S <sub>9</sub> -S <sub>12</sub> vs. S <sub>13</sub> -S <sub>15</sub>	1	0.10	138.70	26.48	758,313.45	
Treatments × Environments in S <sub>9</sub> -S <sub>15</sub>	6	1.31	213.99	58.46	2,285,457.77	
S <sub>13</sub> -S <sub>14</sub> vs. S <sub>15</sub>	1	0.33	5.54	27.30	204,446.80	
Treatments × Environments in S <sub>13</sub> -S <sub>15</sub>	2	1.79	532.59	182.43	3,219,970.40	
among 0.2739	7	4.18	75.62	147.80	1,208,474.24	
among 0.1492	3	1.08	276.49	257.04	489,351.97	
among 0.0854	1	0.25	294.98	197.40	18,806.23	
Treatments × Environments in S						
subpopulation	14	2.32	165.17	82.98	1,945,846.64	
within subpopulation R	14					
Inbreeding levels	3	10.41	1,151.38**	248.01*	7,148,459.88**	
R <sub>1</sub> -R <sub>8</sub> vs. R <sub>9</sub> -R <sub>15</sub>	1	30.13**	2,710.93**	625.49**	20,242,393.17**	
R <sub>9</sub> -R <sub>12</sub> vs. R <sub>13</sub> -R <sub>15</sub>	1	0.33	201.85	1.03	849,556.55	
Treatments × Environments in R <sub>9</sub> -R <sub>15</sub>	6	1.62	177.19	116.74	426,843.89	
R <sub>13</sub> -R <sub>14</sub> vs. R <sub>15</sub>	1	0.75	541.36	117.50	353,429.90*	
Treatments × Environments in R <sub>13</sub> -R <sub>15</sub>	2	0.50	40.28	12.08	16,886.03	
among 0.2749	7	5.28	691.96**	573.21**	1,093,613.25*	
among 0.1492	3	5.53	351.11	116.53	391,942.82	
among 0.0854	1	2.25	44.22	6.13	145,546.94	
Treatments × Environments in R						
subpopulation	14	3.19	190.30	68.55	369,616.29	
Treatments × Environments remainder	2	4.88	111.81	48.27	1,271,957.74	
Treatments × Environments	30	2.87**	173.35*	73.93	1,165,346.55**	
Pooled error	180	1.37	106.77	56.32	552,139.36	
Total	247					

\*, \*\* Significant at the 5 and 1% levels of probability, respectively.

**Table 4.** Comparison of inbreeding depression per 1 percent of homozygosity between S and R subpopulations.

Characters	Subpopulation	
	S	R
Downy mildew, %	- 0.0999	- 0.0561
Days to silking	+ 0.0278	+ 0.0389
Plant height, cm	- 0.5053	- 0.6017
Ear height, cm	- 0.2960	- 0.3691
Lodging, %	+ 0.1392	- 0.1017
Ear rot, %	+ 0.0724	+ 0.0980
Grain yield, kg/hectare	-44.7784	-46.4104

Entries with coefficient of inbreeding 0.2749 were highly significant different from the others, however, no difference was found among other lower levels of inbreeding. Other characters showed more or less the same trend.

Results from this investigation indicated that inbreeding depression tends to increase with increasing the inbreeding level. This is in agreement with the results reported by several workers (2,6). The rates of inbreeding depression are reported in Table 4. The changes in grain yield per 1 percent homozygosity was -44.7784 and -46.4104 kg/ha in subpopulation R and subpopulation S, respectively. The changes in other characters are also shown in the same Table. The changes found in these characters per 1 percent homozygosity are similar to those reported by Hallauer and Sears (4).

The small degree of inbreeding depression could be attributed to the small differences of inbreeding level among entries under studied. The inbreeding levels of 0.0511, 0.0854, 0.1492 and 0.2749 are too small comparing to those of 0.0625, 0.125, 0.1875, 0.2500, 0.3750 and 0.5625 studied by Sing *et al.* (6). Moreover, inbreeding depression tends to occur less in the advanced cycles of selection (3). This may also be the case since this maize variety had undergone full-sib family selection for 4 cycles.

The significant difference was found only between the entries with the inbreeding level of 0.2749 and the others. This tends to suggest

that recombination can be made using at least 2 full-sib families. However, with less number of families recombined may result in inbreeding depression in the more advanced generations. Appropriate number of families used may be 8 or 10. More investigation in this respect should be carried out in the future.

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