

## EVALUATION OF MATURITY AND ITS CORRELATED TRAITS IN AN UNADAPTED F<sub>2</sub> MAIZE POPULATION

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### ABSTRACT

*This study was conducted to understand the mode of inheritance of maturity in an adapted by unadapted F<sub>2</sub> maize population and to identify the best progeny of introgressed population to be used for single cross hybrid development. Thermal indices (growing degree days or heat units or thermal time), calculated from minimum and maximum temperatures, and a base temperature were used to measure the maturity of maize progenies. Two hundred and eleven (211) S<sub>1</sub> families developed from a cross between an adapted Corn Belt maize inbred line (B73) and an unadapted maize population and their testcrosses were evaluated in two planting dates and two locations in 1995. Maturity was quantitatively inherited as transgressive segregation for all the traits observed, and few factors were responsible for the expression of maturity in maize. Earliness was dominant to lateness. Maturity measured in thermal units was better than calendar days. Based on the performance of the test crosses up to ten S<sub>1</sub> lines could be selected for the development of single cross hybrids that could produce more grain than the check hybrids*

### INTRODUCTION

In maize, maturity is measured in calendar days, days from planting to anthesis, days from planting to silk emergence, days from planting to physiological maturity and percent moisture of the kernel. Thermal indices, such as, growing degree days, thermal units or thermal time have also been used (Gilmore and Rogers, 1958). The accurate prediction of time to maturity is important for the efficient exchange of genetic materials among environments (Koester *et al.*, 1993 and Bonhomme *et al.*, 1994).

Most studies on the inheritance of maturity have been on the basis of days to anthesis or silking. Maize is a qualitative short-day plant as it is sensitive to day length changes in temperate re-

gions. However, many cultivars are known to show no delay in flowering time under all types of day length. These cultivars are referred to as day length insensitive or are day neutral. Earlier maturity in maize tends to be dominant to lateness in the temperate areas and has relatively high heritability on individual plant and progeny bases (Hallauer, 1990). Giesbrecht (1960a; 1960b) has indicated that two to multiple genes were involved, while the data of Hallauer (1965) suggested that up to three factors governed days to silking in a cross between an early and a late variety, and that additive gene action was of major importance. Using molecular marker technology, Koester *et al.* (1993) and Berke and Rochefield (1995) identified QTLs controlling days to flowering and two of its correlated traits (plant

height and total leaf number) in two near isogenic lines.

When exotic germplasm was used to improve an adapted maize population, Crossa and Gardiner (1987) reported that the cross with 50% of adapted germplasm yielded significantly less than those from the purely adapted and backcross with 75% adapted germplasm. Both the adapted and backcross populations were early maturing and yielded similarly, suggesting that major genes for lack of adaptation were acting in the cross population. Elite hybrids were also improved by the introgression of favorable alleles not already present in the hybrid (Fabrizius and Openshaw, 1994; Mejaya and Lambert, 1992). For populations, Brun and Dudley (1987) observed that those with 25% of flint germplasm was the most suitable for developing high-yielding hybrids with good standability.

The objectives of this study were to understand the mode of inheritance of maturity in an adapted by unadapted  $F_2$  maize population and to identify the best progeny of introgressed population to be used for single cross hybrid development.

## MATERIALS AND METHODS

The materials used for the study included two popular Corn belt inbred lines, B73 and Mo17, and an unadapted CIMMYT population, MBI-TA86MRB CHILO. The CIMMYT population obtained from Dr. Mimh, an entomologist at CIMMYT has been described as having general borer resistance. The history further traced back to the University of Missouri where the initial crosses were done by crossing Mexican maize with Corn belt germplasm. Initial observations in Nebraska, and later in Florida nurseries, clearly demonstrated that some photoperiod responses existed in the CIMMYT population. In 1990, full-sib families were formed within each population, and in 1992, were observed under hot and dry conditions in Lincoln, Nebraska. During the same season, the families were ad-

vanced to  $S_1$  families. After observation of the  $S_1$  families, a single plant, designated 2042, was selected and crossed to B73. A single (B73 x 2042)  $F_1$  plant was self-pollinated in 1993 main season to produce  $F_2$  seed. During the winter of 1993 the  $F_2$ s were self-pollinated to obtain  $S_1$  families in Florida, USA. During the summer of 1994, 211 of the  $S_1$  families were grown at Lincoln, Nebraska for observation. In addition to the observation nursery, test crosses were developed in isolation using Mo17 as the pollen donor. The  $S_1$  families were planted at Havelock on May 16 and June 13, 1995 for the first and second sowing, respectively. The season was characterized by dry spells, so the trials were irrigated when necessary. During the same season, the test crosses were evaluated at Havelock and Shelton.

An incomplete block design was used. For each trial, the initial subdivision of the experimental field was into two replications, then into incomplete field blocks with each entry appearing with a different group of entries in each of the two incomplete blocks in which it occurred (Schutz and Cockerham, 1966). Thus, no two incomplete blocks were the same. There were 27 incomplete blocks, each comprised 8 entries. The total number of entries per trial was 216, including 5 check entries. For each trial, the blocks were randomized within each replication, and the entries within each incomplete block were also randomized. One row plots each 5 m in length and 0.8 m between rows was used for the  $S_1$  lines. Two rows per plot were used for the yield evaluation. At Shelton (350 km NW of Lincoln), the row length was increased from 5 m to 6 m. Seedling establishment of the  $S_1$  lines was good in both trials. To maintain normal plant growth during high temperatures and drought, supplemental irrigation was applied. Data were taken for the number of leaves produced at tasseling, days from planting to fifty percent pollen shed, days from planting until fifty percent of the plants produced silk, plant and ear heights. A thermal time for estimating the days from plant-

ing to anthesis was calculated using, maximum and minimum air temperatures and a base temperature of 10°C. The yield trials at both Have-lock and Shelton were machine harvested and the grain moisture determined electronically in the field. The grain yield in Mg/ha was adjusted to 15% moisture. Grain yield was not recorded for the S<sub>1</sub> families

The data from each individual planting date for the S<sub>1</sub> families and individual location for the testcrosses were analyzed separately. The data for the planting dates or locations were then combined and analyzed in order to estimate the genotype by environment interaction effects using the following model,

$$y_{ijkm} = \mu + l_m + r_{i(m)} + b_{ijm} + g_{ijk} + g_{ijkm} + e_{ijkm}$$

where  $y_{ijkm}$  is the observation of the  $k^{\text{th}}$  entry in the  $j^{\text{th}}$  block of  $i^{\text{th}}$  replicate in environment  $m$ ,  $\mu$  is the mean of the observations,  $l_m$  is the effect of  $m^{\text{th}}$  environment,  $r_{i(m)}$  is the effect of replications within environment,  $b_{ijm}$  is the effect of blocks within replications within environment,  $g_{ijk}$  is the effect of entries,  $g_{ijkm}$  is the entries by environment interaction and  $e_{ijkm}$  is the random error. All the effects are assumed random, independent and normally distributed with zero means and variances due to each effect. The entries were partitioned into S<sub>1</sub> families, check entries and their contrast.

## RESULTS AND DISCUSSION

The unadapted Mexican population used in this study contained Corn Belt germplasm and had undergone partial selection for adaptation to the Corn Belt of the USA (initial crosses were made to B73 which is a popular Corn Belt inbred line). Hence, any character not favorable to maize adaptation in the USA was selected against. Mean squares for the analysis of variance across planting dates are presented in Table 1. There were significant differences ( $p < 0.01$ ) between the sowing dates for the maturity traits (days to pollen shed, days to silk extrusion, days from plant-

ing to anthesis and thermal indices) and total number of leaves at tasseling. Planting dates did not significantly affect ear and plant heights. Significant differences ( $p < 0.05$ ) were observed among the S<sub>1</sub> lines for all the traits observed. There were significant differences also among the check entries, and between the S<sub>1</sub> lines and the check entries. S<sub>1</sub> families X planting dates interaction effect was highly significant ( $p < 0.01$ ) for days to silking and days to 50% pollen shed, thermal time, ear height and total number of leaves but not significant for plant height. Check entry X planting date interaction effect was not significant for any of the traits measured. Unlike the S<sub>1</sub> lines, the check inbred lines were adapted to the conditions prevailing in Nebraska, and grown within the recommended time range in that environment, these lines showed similar performance. The contrast, S<sub>1</sub> lines versus check entries X planting date interactions, was also not significant for any of the traits. The means and ranges of the traits for the families and values for the traits of the two parents (B73 and 2042) are presented in Table 2. The S<sub>1</sub> families showed a considerable range for each trait. They exceeded the parental means for days to pollen shed, days to 50% silk extrusion, ear and plant heights, indicating that there was transgressive segregation for the maturity and its correlated characters. Therefore, segregation distortions obtained could be due to the partial selection in the unadapted population. Transgressive segregation, was attributed to additive gene action resulting from combinations of alleles conferring the character from both parents. The mean number of days from planting to 50% silking (silk extrusion) and from planting to 50% pollen shed (anthesis) were 77 and 76 for the first planting date, and 64 and 63 for the second planting, respectively. The range or period within which the plants flowered for the two sowing dates were 13 and 15 days for the first and second planting dates, respectively. The difference between the date of sowing of the trials (May 16 and June 13) was 28 days, but the dif-

ference between their mean flowering dates was 10 days. The anthesis-silking interval (ASI) for the first planting was zero, while that of the second planting was two. The delayed planting resulted in delayed silking which could account for lower grain production (Ribaut *et al.*, 1996) due to reduced pollen production as well as poor stigma reception. It took longer for the earlier sowing plants to flower. This suggests that the genotypes had some factor that caused them to tend to flower about the same time irrespective of time of planting. The factor was thought to be photoperiodic effect. The mean thermal indices were 1021 and 935 °C days for the first and second sowing, respectively. The ranges for the two sowings were 230 and 251, respectively. The difference between the sowings for 50% pollen shed was 13 days and that for thermal index was 86 °C days. A delay of 13 days in flowering can adversely affect the development of maize. From the formula used to estimate thermal indices in this research, 86 °C days is insignificant. Therefore, thermal indices used for measuring maturity might be better than calendar days in temperate environments.

Heritability ( $h^2$ ) is the proportion of the total phenotypic variation expressed among genotypes that can be attributed to genetic differences among them. The genotypic variance could not be partitioned into additive and dominance variance. Therefore, the heritability of a trait was estimated as the ratio between the genotypic variance and the total phenotypic variance. The broad sense heritability estimates for the maturity characters obtained were between 0.50 and 0.70 (Table 4). This range is within the limits of previous studies compiled by Hallauer and Miranda (1988). From the heritability estimates there was still a lot of chance for manipulating the families to develop superior inbred lines based on the maturity traits and the correlated ones, except the number of leaves at flowering. The heritability for number of leaves was 0.33. The low figure suggests that not much could be

done to improve the number of leaves. It also confirms why inbred lines usually have fewer leaves than hybrids developed from them. Very high genetic correlation coefficients (Table 3) were obtained for the maturity characters. This was expected as effects due to pleiotropy are removed during estimation of the values. The correlation coefficient for plant and ear heights was also high. The genetic correlation coefficient between the number of days to anthesis and plant height was similar to those compiled by Hallauer and Miranda (1988) from previous experiments. Selection for earliness using any of the correlated traits would be effective. The correlation between the traits of  $S_1$  families and those of their testcrosses were generally low, but significant ( $p < 0.01$ ) for plant height, number of leaves and maturity characters. There was a negative correlation between  $S_1$  family total number of leaves at flowering and testcross grain yield. This implied that those families with fewer number of leaves at flowering combined well with Mo17 to produce superior hybrids.

Testcrosses were more vigorous, taller, had wider stalk diameters, were more uniform and earlier in maturity. This expression of vigour was due to heterosis or hybrid vigour. The genetic basis of heterosis has been reviewed by Hallauer and Miranda (1988) as physiological stimulation and dominant favorable growth factors. Inbreeding leads to the expression of recessive deleterious genes that weaken, if they do not kill, the offsprings. So when such offsprings are mated to individuals of different heterotic groups, the recessive deleterious genes are instantly rendered ineffective, hence the progeny from such a cross becomes vigorous.

Location did not affect ( $p > 0.05$ ) the mean height of the test crosses (266.81 cm for Havelock and 269.81 cm for Shelton). However, in Havelock, the plants produced wider stalk diameters so there was less lodging at this location as compared to those at Shelton. These differ-

Table 1: Mean squares for six traits of 211 S<sub>1</sub> lines and five checks evaluated at two planting dates in 1995.

Source	degrees of freedom	days to silk extrusion	days to anthesis	thermal index (°Cdays)	ear height (cm)	plant height (cm)	leaf number per plant
Pdate	1	40303.01***	39772.36***	1580753.73***	125.28	57.56	134.58***
Rep(pdate)	2	23.99*	37.45***	12727.73***	239.17	869.34**	24.01
Block(rep pdate)	104	2.03	1.71***	573.99***	95.03***	161.31*	1.06
Entry	215	14.42***	14.89***	4997.85***	650.75***	869.62***	4.74***
Sline	210	11.86***	12.42***	4199.17***	513.81***	732.30***	3.40***
Check	4	77.62***	71.50***	23584.60***	3722.03***	3202.90***	25.78***
Sline vs check	1	117.53***	114.54***	36856.77***	10410.82***	17609.10***	136.17***
Entry * Pdate	215	2.16**	2.01***	601.00**	83.29**	151.39	1.26**
Sline*Pdate	210	1.94***	1.70***	516.50**	74.59**	124.30	1.23**
Check*Pdate	4	0.94	1.28	229.22	32.67	90.38	0.73
Sline vs Check*Pdate	1	0.17	0.80	132.56	7.83	126.60	1.75
Error	316	1.34	1.04	356.40	50.98	116.04	0.89
CV		1.64	1.47	1.93	5.79	5.20	4.25
Means		70.40	69.50	976.59	115.74	206.98	22.24

\*, \*\*, \*\*\* Denote significance at 0.05, 0.01, 0.001 probability levels respectively. Also, pdate denotes planting date/sowing.

**Table 2: Means and Ranges of B73, 2042 and 211 S<sub>1</sub> lines for six Quantitative Traits Observed Across Planting Dates**

	Days to Silking	Days to Anthesis	Thermal Index	Ear Height	Plant Height	Leaf Number Per Plant
B73	67.50	67.00	931.09	93.75	177.55	19.75
2042	75.00	73.75	1053.17	124.50	196.00	23.50
S <sub>1</sub> lines	70.46 ± 0.25	69.56 ± 0.25	977.65 ± 2.01	116.35 ± 0.49	207.80 ± 0.62	22.31 ± 0.05
Ranges	57.00 - 85.00	55.00 - 84.00	791.01 - 1155.57	58.00 - 170.00	130.00 - 257.00	16.00 - 26.00

**Table 3: Phenotypic correlation coefficients (upper figures) and genetic correlation coefficients (lower figures) for 211 S<sub>1</sub> lines evaluated in two planting dates**

TRAITS	Days to Anthesis	Thermal Index	Ear Height	Plant height	No of leaves
Days to silking	0.987***	0.8593***	0.0777*	0.0704*	0.3626***
	0.8943	0.8957	0.4312	0.3899	0.6486
Days to anthesis		0.8987***	0.1028**	0.0818*	0.3763***
		0.9083	0.5377	0.3814	0.7391
Thermal index			0.2662***	0.1985***	0.4787***
			0.5261	0.3728	0.7071
Ear height				0.7411***	0.4133***
				0.8320	0.0995
Plant height					0.3629***

\*, \*\*, \*\*\*, denote significance at 0.05, 0.01, 0.001 probability levels, respectively.

**Table 4: Variance components and broad sense heritability estimates for some traits of S<sub>1</sub> lines**

TRAIT	$\sigma^2_g$	$\sigma^2_{ge}$	$\sigma^2_e$	$\sigma^2_p$	$h^2$
Days to silk extrusion	2.46	0.31	1.29	4.06	0.61
Days to anthesis	2.67	0.34	1.02	4.03	0.66
Thermal index	916.86	83.54	346.48	1346.88	0.68 ± 0.37
Ear height	109.50	11.38	51.78	172.66	0.63 ± 0.04
Plant height	150.39	4.97	114.85	270.21	0.56 ± 0.05
Number of leaves	0.54	0.17	0.91	1.62	0.33

**Table 5: Means of traits of S<sub>1</sub> families, testcrosses and hybrid checks across environments**

Trait	S <sub>1</sub>	Test crosses	Hybrid checks
Days to silk Extrusion	70.49 ± 2.43	74.28 ± 0.18	72.95 ± 1.39
Days to anthesis	69.51 ± 2.39	73.36 ± 0.18	72.30 ± 1.35
Thermal index	976.70 ± 33.65	-	-
Ear height	115.70 ± 4.00	150.41 ± 0.47	131.00 ± 3.71
Plant height	207.00 ± 7.15	268.47 ± 0.42	261.80 ± 2.98
Number of leaves	22.24 ± 0.77	-	-
Grain yield	-	6.92 ± 0.10	7.25 ± 0.92
Grain moisture	-	14.45 ± 0.05	13.38 ± 0.31

ences in plant size was attributed to more appropriate maize growing environment observed at Havelock. Testcross entries X location interaction was significant ( $p < 0.01$ ) only for grain yield and percent moisture at harvest. The male parent was Mo17 so the test crosses were 50% similar in genome composition. The other variable portion having come from each  $S_1$  family. Therefore, it is likely that the significant ( $p < 0.05$ ) differences detected for the grain yield and percent grain moisture at harvest could be due to the alleles from the  $S_1$  families. The check hybrids X location interaction was significant ( $p < 0.01$ ) for days to 50% silk extrusion, days to pollen shed and ear height. The check hybrids were commercial hybrids that were bred for adaptation to different parts of the USA. The significant interaction between the check entries and the environments showed that the hybrids responded differently in the two environments. Even though, the contrast between the check hybrids and testcrosses was not significant ( $p < 0.05$ ), the mean grain yield of the check hybrids was 7.25 Mg/ha whereas that of the testcrosses was 6.92 Mg/ha (Table 5). Up to ten testcrosses produced more grain than any of the check hybrids. The presence of transgression for the maturity traits (days to flowering and thermal indices) suggested that the expression of maturity is controlled by several factors. Based on the performance of the test crosses and the heritability of the maturity and its correlated traits, single cross hybrids developed from inbred lines from the  $S_1$  families will be superior to the check hybrids used in this study.

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