



GENETIC VARIABILITY, HERITABILITY AND CORRELATION STUDIES IN HALF SIB RECURRENT FAMILIES OF CIMMYT MAIZE POPULATION CZP-132011

Amir Sohail¹, Hidayatur Rahman¹, Quaid Hussain¹, Fazal Hadi², Ubaid Ullah¹, Waleed Khan¹, Muhammad Ayoub Khan¹, Muhammad Asad², Zarghoona Yousafzai², Sidra Sami² and Salah Uddin²

¹Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Khyber Pakhtunkhwa, Pakistan

²Department of Botany, University of Peshawar, Pakistan

E-Mail: amirsohail@aup.edu.pk

ABSTRACT

Recurrent selection is a vital selection method for improving the traits of interest in maize crop. This research was carried out to estimate genetic variability, heritability, index of variation and genotypic and phenotypic correlations among half sib recurrent families for various traits. Sixty four half sib recurrent families were evaluated in 8×8 lattice square design with two replications at Cereal Crops Research Institute CCRI, Pirsabak during 2017. Results showed highly significant differences among the half sib families for all the studied traits. High heritability ($h^2 > 0.60$) were recorded for all traits except plant height and ear height which exhibited moderate heritability. High index of variation ($I.V > 1$) was observed for all traits. After completion of one cycle of recurrent selection in half sib families, the percent gain cycle⁻¹ was recorded negative for physio-morphic traits, while for grain yield the percent gain cycle⁻¹ was positive. All physiological traits showed non significant negative genotypic and phenotypic correlation with grain yield except days to 50% silking. The magnitude of genotypic correlations were higher than phenotypic correlations for studied traits, which means that selection for these traits will improve grain yield. The study also observed that correlations as well as heritability were suitable as models for yield improvement and selection for best families. Traits that had higher heritability and positive correlation with grain yield may be considered as important traits in selection programme aiming to maize yield improvement and the breeder may consider these traits as main selection criteria.

Keywords: maize; half sib families; recurrent selection; genetic variability; heritability; index of variation; correlation.

INTRODUCTION

Maize (*Zea mays* L.) is the third leading cereal crop across the world after wheat and rice. It is a short day crop with monoecious nature of flower. It is highly cross pollinated and does not survive in wild form. It is grown twice in year i.e. in spring and summer due to its short cropping duration (Kaleemullah *et al.* 2013). Maize is mostly grown on tropical subtropical and temperate regions of the world. It is consumed as food, feed as well as a fodder. In Pakistan, maize is third most important cereal crop after wheat and rice, and is consumed as parched, baked, boiled, roasted and as popcorn. In flour form, it is used for making breads and as thickening agent in many foods. Ethanol is another good product of maize, which is used as biomass fuel. (Noor *et al.* 2013a). Maize occupies an important space in Pakistan's cropping system. In Pakistan it was grown on an area of 1168.5 thousand hectares with the production of 4944.5 thousand tons and yield of about 44317 kg hectare⁻¹. In Khyber Pakhtunkhwa the cultivated area is 470.9 thousand hectares with a total production of 914.8 thousand tons and average yield of about 1943 kg hectare⁻¹ (MINFAL. 2016).

Maize is a crop with high grain yield potential and productivity. Development of improved maize variety with high yield potential is seen as possibility to enhance productivity. For development of improved maize variety, maize breeders use numerous methods of selection particularly, ear to row selection, mass selection, full sib and half sib recurrent selection etc. Every breeding method

mainly focuses on improvement of yield and its associated characters. Improvement from selection in any recurrent selection method is the predictable changes in their allelic frequencies and extent of genetic variance in a breeding population (Mahmood *et al.*, 2004). It is well observed that recurrent selection has two main aims: first, to enhance the frequency of favorable alleles which will give rise to improvement of overall population performance and second is to keep population with a sustainable rate of genetic variability for continued selection and progress in subsequent generations (Sumathi, 2005).

Half sib refers to the individual having one parent in common. Half sib family selection is a type of recurrent selection which is used for intra population improvement. In maize, improvement in grain yield is always of greater importance and used most frequently to improve maize populations for the traits of interest. Previous studies have shown that 2-4% increase in maize grain yield could be expected per cycle depending upon the method used for selection in a specific population (Dona *et al.* 2012). About 3.9% increases in grain yield cycle⁻¹ have been reported after seven cycles of selection by Lamkey (1992). Heritability is defined as the proportion of genetic variation to the total phenotypic variation of a trait in a particular population. Genetic variability is the key concept to broaden the gene pool of important characters for extensive breeding programs (Ahmad *et al.* 2011). Only genetic variability cannot give success to crop but to ensure how much heritable is the character is the most important thing. Heritability is playing an important role in



prediction of a character response and hence guides to select characters having high heritability to get quick result of progress. Genotypic and phenotypic correlation is important in determining the extent to which the traits are correlated (Bekele *et al.*, 2014). Keeping in view the above mentioned facts, this experiment was designed with objective to study genetic variability, heritability and correlation studies in half sib recurrently selected families of CIMMYT maize population CZP-132011 for various traits.

MATERIALS AND METHODS

The experiment was layout at Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera during 2017. This experiment was performed in two seasons; during first season (spring) selected half sibs were planted in ear to row. Selection in these families was done for desirable traits. The selected families were intermated through controlled hand pollination using bulk pollination method. During second season (summer) a set of those selected families along with base population were planted in 8×8 lattice design with two replications. Row length was 5m, row to row distance was 75cm and plant to plant distance was 25 cm. Based on visual observation, at least 15% selection was followed at harvest as to start new version of recurrent selection cycle. After completion of one cycle of recurrent selection in half sib families, data were noted on days to tasseling, anthesis and silking, anthesis silking interval, plant height, ear height and grain yield.

Statistical analysis

Data recorded on each trait was subjected to analysis of variance (ANOVA) appropriate for 8×8 square lattice design as suggested by Milles *et al.*, (1980) using Mstat-C (1991) statistical package.

ANOVA

SOV	Df	MS	Expected MS
Replications (r)	r-1	-	-
Blocks (k)	k-1	-	-
Half sib families (HS)	HS-1	M ₂	σ ² E + rσ ² G
Error	(k-1)(rk-k-1)	M ₁	σ ² E

Variances and heritability estimate were calculated as:

$$M_1 (\text{Error mean squares}) = \sigma^2 E$$

$$M_2 (\text{HS mean squares}) = \sigma^2 E + r\sigma^2 G$$

$$\text{Genotypic variance } (\sigma^2 G) = M_2 - M_1/r$$

$$\text{Phenotypic variance } (\sigma^2 P) = \sigma^2 E + r\sigma^2 G / r$$

Heritability (b.s) for each traits were calculated according to Allard (1960) as:

$$h^2 (\text{b.s}) = \sigma^2 G / \sigma^2 P$$

Genotypic and environmental coefficient of variation was calculated according to Johnson *et al.* (1955):

$$GCV = \sigma G/y \times 100$$

$$ECV = \sigma E/y \times 100$$

Index of variation (I.V), measure the relative variability as:

$$I.V = GCV / ECV$$

Genotypic and phenotypic correlation coefficients were computed according to Singh and Chaudhary (1979) using META-R software.

$$\text{Genotypic correlation coefficient } (r_{Gxy}) = \frac{\sigma G_{xy}}{\sqrt{\sigma^2 G_x \cdot \sigma^2 G_y}}$$

$$\text{Phenotypic correlation coefficient } (r_{pxy}) = \frac{\sigma P_{xy}}{\sqrt{\sigma^2 P_x \cdot \sigma^2 P_y}}$$

RESULTS

Days to 50% tasseling

Mean squares showed significant ($P \leq 0.01$) differences among the half sib families of CIMMYT maize population CZP-132011 for days to 50% tasseling in C₁ (Table-1). For days to 50% tasseling, genetic, environmental and phenotypic variances were 3.68, 0.93 and 4.61, respectively. High heritability value (0.80) was noted for the mentioned trait (Table-2). Genotypic and environmental coefficient of variation for days to 50% tasseling was 3.81% and 1.92%, respectively with an index of variation of 1.99. (Table-3). Days to 50% tasseling revealed highly significant and positive correlation with anthesis ($r_G = 0.73^{**}$ and $r_P = 0.68^{**}$) and silking ($r_G = 0.73^{**}$ and $r_P = 0.68^{**}$) at both genotypic and phenotypic levels. Similarly days to 50% tasseling showed significant genotypic association with plant height ($r_G = 0.26^*$) and ear height ($r_G = -0.24^*$). However, days to 50% tasseling revealed non significant correlation with the remaining traits at both levels (Table-4).

Days to 50% anthesis

Differences among half sib families were significant ($P \leq 0.01$) for days to 50% anthesis in C₁ (Table-1). For days to 50% anthesis, genetic, environmental and phenotypic variances were 3.09, 0.66 and 3.75, respectively. High value of heritability (0.82) was recorded for days to 50% anthesis (Table-2). Genotypic and environmental coefficient of variation for days to 50% anthesis was 3.33% and 1.54%, respectively with an index of variation of 2.16. (Table-3). Days to 50% anthesis showed highly significant and positive genotypic and phenotypic association with anthesis silking interval ($r_G = 0.92^{**}$ and $r_P = 0.92^{**}$). Similarly days to 50% anthesis exhibited highly significant and positive genotypic correlation with anthesis silking interval ($r_G = 0.92^{**}$), However it showed non significant association with remaining studied traits (Table-4).



Days to 50% silking

Mean squares showed significant ($P \leq 0.01$) differences among the half sib families of CIMMYT Mize population CZP-132011 for days to 50% silking in C_1 (Table-1). For days to 50% anthesis the genetic, environmental and phenotypic variances were 3.13, 0.57 and 3.70 respectively, which lead to high heritability value (0.85) for the said trait (Table-2). Genotypic and environmental coefficient of variation for anthesis silking interval was 3.28% and 1.40%, respectively with an index of variation of 2.34. (Table-3). Days to 50% anthesis showed significant and positive association with tasseling ($r_G = 0.73^{**}$ and $r_P = 0.68^{**}$) and 50% anthesis ($r_G = 0.92^{**}$ and $r_P = 0.92^{**}$) both at genotypic and phenotypic levels. Days to 50% anthesis showed non-significant correlation with the remaining traits at both levels (Table-4).

Anthesis silking interval (ASI)

Significant ($P \leq 0.01$) differences were observed among the half sib families for anthesis silking interval in C_1 (Table-1). Genetic, environmental and phenotypic variances were 0.50, 0.17 and 0.67 respectively for anthesis silking interval. High heritability value (0.75) was noted for the said trait (Table 2). Genotypic and environmental coefficient of variation for anthesis silking interval was 58.40% and 34.14%, respectively with an index of variation of 1.71. (Table-3). Anthesis silking interval exhibited significant and positive association with silking at both genotypic and phenotypic levels ($r_G = 0.21^{**}$ and $r_P = 0.22^*$), while with remaining traits it had non significant genotypic and phenotypic correlations (Table-4).

Plant height (cm)

Mean square exhibited significant ($P \leq 0.01$) differences among the half sib families for plant height in C_1 (Table-1). Genetic, environmental and phenotypic variances for plant height were 8.32, 6.81 and 15.13, respectively. Moderate heritability value (0.55) was noted for plant height (Table-2). Genotypic and environmental coefficient of variation for ear height was 1.79% and 1.62%, respectively and index of variation for the mentioned trait was 1.11 (Table 3). Ear height exhibited significant and positive genotypic correlation with tasseling ($r_G = -0.26^{**}$) and ear height ($r_G = -0.310^{**}$), while ear height had non significant genotypic and phenotypic correlation with remaining traits (Table 4).

Ear height (cm)

Analysis revealed significant difference ($P \leq 0.01$) among the half sib families for ear height in C_1 (Table-1). For ear height the genetic, environmental and phenotypic variances were 14.08, 11.67 and 25.75 respectively. Moderate heritability value of 0.55 was noted for ear height (Table-2). Genotypic and environmental coefficient of variation for ear height was 5.22% and 4.75%, respectively with an index of variation of 1.10 (Table-3). Ear height showed significant and negative genotypic association with days to 50% tasseling ($r_G = -0.24^*$), while significantly and positively correlated with ear height at

genotypic levels ($r_G = 0.34^{**}$). However, ear height showed non significant correlation with rest of the traits at both levels (Table-4).

Grain yield (kg ha⁻¹)

Significant ($P \leq 0.01$) differences were noted among the half sib families for grain yield in C_1 (Table 1). Genetic, environmental and phenotypic variances for grain yield were 39716.87, 21196.52 and 60913.38 respectively. High heritability value of 0.65 was noted for grain yield (Table-2). Genotypic and environmental coefficient of variation for grain yield was 6.62% and 4.39%, respectively with an index of variation of 1.37 (Table-3). Grain yield was non significantly and negatively correlated with tasseling, anthesis and anthesis silking interval at both levels, However, it was non-significantly but positively correlated with days to 50% silking and ear height at both levels (Table 4).

DISCUSSIONS

Flowering traits

Data pertaining to physiological traits revealed highly significant differences among the half sib families of CIMMYT maize population CZP-132011 for days to tasseling, anthesis, silking and anthesis silking interval. Noor *et al.* (2013b) observed significant difference in half sib families of maize Variety Pahari for physiological traits. Similarly Barros *et al.* 2010 also reported significant differences in maize landraces/populations for physiological traits. However, Khan (2017) reported significant differences in full sib families of different maize varieties for flowering traits. High heritability values for flowering traits indicates that these traits are under genetic control with comparatively less environmental influence. High index of variation of maturity traits shows the presence of greater genetic variability. Ogunniyan *et al.* 2014 reported 100% heritability and high index of variation for days to tasseling, anthesis and silking. Positive genotypic and phenotypic association were noted among flowering traits. All the flowering traits revealed negative genetic and phenotypic association with grain yield except days to silking which exhibited positive association with grain yield at both levels. Ahmad *et al.* (2012) and Ullah *et al.* (2013) observed negative phenotypic correlation between grain yield and maturity traits, while Taimur *et al.* (2011) reported positive genotypic and phenotypic association with grain yield.

Plant and ear height

Plant and ear height are an important agronomic traits which perform an important role in lodging and ultimately affect the final grain yield. Maize breeders should give preference to plant and ear height in order to prevent lodging. Mean squares showed significant ($P \leq 0.01$) differences among the half sib families for plant and ear height in C_1 . Our consequences are in line with Khalil *et al.* (2010) who also observed significant differences among S_1 lines of Azam maize population for



plant and ear height. Intermediate heritability values were noted for plant and ear height. Ishaq et al. (2014) also noted moderate heritability in maize hybrids for plant and ear height. High index of variation was noted for plant and ear height showing high genetic variability and selection possibility. Peterniani *et al.*, (2004) also noted high index of variation for plant and ear height in a maize composite. Plant height had negative genotypic correlation with anthesis silking interval, and grain yield while positive genotypic correlation with remaining traits. Plant height was phenotypically positive correlated with remaining traits. Ear height was genotypically correlated with days to tasseling, anthesis and silking but negative in nature, whereas positive genetic correlation was observed with the remaining traits. Barua *et al.* (2017) and Nzube *et al.* (2014) also noted negative genotypic and positive phenotypic correlation of plant height with grain yield, while ear height had positive genotypic and phenotypic correlation with grain yield.

Grain yield

Grain yield is a complex trait, which is the product of several yield attributing traits. Mean squares exhibited highly significant differences among the half sib recurrent families for grain yield. After completion of one cycle of recurrent selection the gain cycle⁻¹ was 4.17%. Our results are in line with Ribeiro et al. (2016) who also noted significant difference in UENF-14 popcorn population using recurrent selection procedure for grain yield. Similarly Weyhrich *et al.* (2012) also reported significant differences in BS-11 maize population. High heritability (0.65) of grain yield indicates that the said trait is considerably under genetic control. Durrishahwar et al. (2008) and Barua *et al.* (2017) also noted high value of heritability for grain yield. High index of variation (1.37) noted for the said trait, reflects the presence of genetic variability and chances for further selection. Andrade *et al.* (2008) also reported $I.V > 1$ for grain yield in maize population, ESALQ-PB1. Grain yield had negative genotypic and phenotypic relationship with tasseling, anthesis, anthesis silking interval and plant height, while positively correlated with days to silking, ear height, ears plant⁻¹, ear length, grain rows ear⁻¹, grains row⁻¹ and 1000 grain weight at both levels. Kaleemullah *et al.* (2013) and Singh *et al.* (2017) noted positive genotypic and phenotypic correlation of grain yield with silking.

CONCLUSIONS AND RECOMIDATION

Mean squares revealed highly significant differences for all the studied traits. High values of heritability and index of variation indicated the existence of sufficient amount of genetic variability among the half sib families for further improvement and potential for recurrent selection. Here we noted for first time that maize population CZP-132011 have sufficient genetic variability and a remarkable improvement through recurrent selection, which may give rise the opportunity of desirable traits selection. CZP-132011 can be used as base population for derivation of inbred lines and have the

potential for further improvement in yield and yield attributes.

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**Table-1.** Mean squares and coefficient of variation of various traits and grain yield in half sib recurrent families.

Trait	Mean	Squares	Coefficient of variation (%)
	Families (df=64)	Error (df=49)	
Days to tasseling	8.30**	0.93	1.92
Days to anthesis	6.84**	0.66	1.54
Days to silking	6.83**	0.57	1.40
Anthesis silking interval	1.17**	0.17	33.14
Plant height	23.46**	6.81	1.62
Ear height	39.83**	11.67	4.75
Grain yield	100630.25**	21196.52	4.39

**= Significant and highly significant at 1% level of probability.

Table-2. Estimation of genetic, environmental and phenotypic variances (σ^2_G , σ^2_E and σ^2_P) and broad sense heritability (h^2 (b.s)) of various traits in half sib recurrent families.

Trait	σ^2_G	σ^2_E	σ^2_P	h^2 (b.s)
Days to tasseling	3.68	0.93	4.61	0.80
Days to anthesis	3.09	0.66	3.75	0.82
Days to silking	3.13	0.57	3.70	0.85
Anthesis silking interval	0.50	0.17	0.67	0.75
Plant height	8.32	6.81	15.13	0.55
Ear height	14.08	11.67	25.75	0.55
Grain yield	39716.87	21196.52	60913.38	0.65

Table-3. Genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV) and index of variation (I.V) for various traits in half sib recurrent families.

Trait	GCV (%)	ECV (%)	I.V
Days to tasseling	3.81	1.92	1.99
Days to anthesis	3.33	1.54	2.16
Days to silking	3.28	1.40	2.34
Anthesis silking interval	58.40	34.14	1.71
Plant height	1.79	1.62	1.11
Ear height	5.22	4.75	1.10
Grain yield	6.02	4.39	1.37



Table-4. Coefficient of genetic correlation (below the diagonal) and phenotypic correlation (above the diagonal) among various traits in half sib families of C₁.

Traits	Days to tasseling	Days to anthesis	Days to silking	Anthesis silking interval	Plant height	Plant height	Grain yield
Days to tasseling	1	0.68**	0.68**	0.08	0.15	0.07	-0.17
Days to anthesis	0.73**	1	0.92**	-0.12	0.08	0.06	-0.10
Days to silking	0.73**	0.92**	1	0.22*	0.09	0.08	0.01
Anthesis silking interval	0.09	-0.10	0.21*	1	0.02	0.05	-0.03
Plant height	0.26*	0.07	0.06	-0.07	1	0.14	0.01
Ear height	-0.24*	-0.04	-0.01	0.07	0.34**	1	0.14
Grain yield	-0.19	-0.07	0.01	-0.07	-0.04	0.19	1

*, **= significant at 1 and 5% probability level.