

## Research Article

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# Estimation of genetic variability, heritability, index of variation and correlation in the half sib families of CIMMYT maize population CZP-132011

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### Abstract

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. Data were noted on ears plant<sup>-1</sup>, ear length, ear diameter, grain rows ear<sup>-1</sup>, grains row<sup>-1</sup>, 1000 grain weight and grain yield. Analysis of variance showed highly significant differences among the half sib families for all the studied traits. High heritability ( $h^2 > 0.60$ ) was recorded for all traits except 1000 grain weight which exhibited moderate heritability (0.54). High index of variation ( $I.V > 1$ ) was observed for all traits. Grain yield showed significant and positive genotypic correlation with ears plant<sup>-1</sup> ( $r_G = 0.46^{**}$ ), ear length ( $r_G = 0.50^{**}$ ), grain rows ear<sup>-1</sup> ( $r_G = 0.24^*$ ), grains row<sup>-1</sup> ( $r_G = 0.34^{**}$ ) and 1000 grain ( $r_G = 0.39^{**}$ ). On other hand grain yield exhibited highly significant and positive phenotypic correlation with ear length ( $r_P = 0.33^{**}$ ). Present research indicates the presence of significant genetic variability in CIMMYT maize population CZP-132011. Substantial variability exists in half sib recurrent families for yield attributes, indicating that there is an opportunity for improvement via selection. The magnitude of genotypic correlations were higher than phenotypic correlations for yield attributes, 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:** Correlation; Half sib families; Heritability; Index of variation; Maize (*Zea mays* L.)

## 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 [1]. It 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 [2]. Maize occupies an important space in Pakistan's cropping system. In Pakistan it is grown on an area of 1168.5 thousand hectares with production of 4944.5 thousand tons and yield of about 44317 kg hectare<sup>-1</sup>. 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<sup>-1</sup> [3]. 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, full sib and half sib recurrent selection, mass 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 expected changes in their allelic frequencies and magnitude of genetic variance in a breeding population [4]. 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 [5].

Half sib refers to the individuals 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 [6]. About 3.9% increases in grain yield cycle<sup>-1</sup> have been reported after seven cycles of selection by [7].

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 [8]. 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 [9]. 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 maize population CZP-132011 for yield attributes.

## 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 inter-mated 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

**Table 1. ANOVA**

SOV	Df	MS	Expected MS
Replications (r)	r-1	-	-
Blocks (k)	k-1	-	-
Half sib families (HS)	HS-1	M <sub>2</sub>	σ <sup>2</sup> E + rσ <sup>2</sup> G
Error	(k-1)(rk-k-1)	M <sub>1</sub>	σ <sup>2</sup> 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 [12] as:

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

Genotypic and environmental coefficient of variation was calculated according to [13]:

$$\text{GCV} = \sigma G / y \times 100$$

$$\text{ECV} = \sigma E / y \times 100$$

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

$$\text{I.V} = \text{GCV} / \text{ECV}$$

Genotypic and phenotypic correlation coefficients were computed according to [14] using software [15].

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

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

## Results

### Ears plant<sup>-1</sup>

Mean square revealed significant difference (P≤0.01) among half sib families for ears plant<sup>-1</sup> in C<sub>1</sub> (Table 2). High heritability value (0.73) was noted for the said trait. For ears

cycle. After completion of one cycle of recurrent selection in half sib families, data were noted on ears plant<sup>-1</sup>, ear length, ear diameter, grain rows ear<sup>-1</sup>, grains row<sup>-1</sup>, 1000 grain weight and grain yield.

### Statistical analysis

Data recorded on each trait was subjected to analysis of variance (ANOVA) (Table 1) appropriate for 8×8 square lattice design as suggested by [10], using statistical package [11].

plant<sup>-1</sup>, the genetic, environmental and phenotypic variances were 0.02, 0.01 and 0.03, respectively (Table 3). Genotypic and environmental coefficient of variation for ears plant<sup>-1</sup> were 12.34% and 7.53% with an index of variation of 1.64 (Table 4). Ears plant<sup>-1</sup> exhibited significant (P≤0.01) and positive correlation with grain row ear<sup>-1</sup> (r<sub>G</sub> = 0.38\*\*) and grain yield (r<sub>G</sub> = 0.46\*\*) at genotypic level only, while ears plant<sup>-1</sup> showed non-significant correlation with remaining traits (Table 5).

### Ear length (cm)

Mean square revealed significant difference (P≤0.01) among half sib families for ears length in C<sub>1</sub> (Table 2). High heritability value (0.74) was recorded for the mentioned trait. For ears length, the genetic, environmental and phenotypic variances were 1.25, 0.44 and 1.69, respectively (Table 3). Genotypic and environmental coefficient of variation for ears length were 7.23% and 4.29% with an index of variation of 1.69 (Table 4). Ear length exhibited significant (P≤0.01) and positive correlation with 1000 grain weight (r<sub>G</sub> = 0.28\*) and grain yield (r<sub>G</sub> = 0.50\*\*) at genotypic level only. However ear length showed significant and negative correlation

with grain rows ear<sup>-1</sup> ( $r_G = -0.23^*$ ), while with remaining traits it showed non-significant correlation (Table 5).

### Ear diameter (cm)

Mean square revealed significant difference ( $P \leq 0.01$ ) among half sib families for ears diameter in C<sub>1</sub> (Table 2). High heritability value (0.76) was noted for ear diameter. For ears diameter, genetic, environmental and

phenotypic variances were 0.07, 0.02 and 0.09, respectively (Table 3). Genotypic and environmental coefficient of variation for ears diameter were 11.81% and 6.72% with an index of variation of 1.76 (Table 4). Ear diameter revealed non-significant correlation with all the studied traits at both genotypic and phenotypic level (Table 5).

**Table 2. Mean squares and coefficient of variation of half sib recurrent families of maize population CZP-132011 for yield attributes**

Trait	Mean Families (df=64)	Squares Error (df=49)	Coefficient of variation (%)
Ear plant <sup>-1</sup>	0.05**	0.01	7.53
Ear length	2.94**	0.44	4.29
Ear diameter	0.16**	0.02	6.72
Grain rows ear <sup>-1</sup>	2.17**	0.26	3.60
Grains row <sup>-1</sup>	13.78**	1.67	7.87
1000 grain weight	840.24**	250.13	6.08
Grain yield	100630.25**	21196.52	4.39

\*\* = significant at 1% level of probability

**Table 3. Estimation of genetic variance ( $\sigma^2_G$ ), environmental variance ( $\sigma^2_E$ ), phenotypic variance ( $\sigma^2_P$ ) and broad sense heritability ( $h^2$  (b.s)) of yield attributes**

Trait	$\sigma^2_G$	$\sigma^2_E$	$\sigma^2_P$	$h^2$ (b.s)
Ears plant <sup>-1</sup>	0.02	0.01	0.03	0.73
Ear length	1.25	0.44	1.69	0.74
Ear diameter	0.07	0.02	0.09	0.76
Grain rows ear <sup>-1</sup>	0.95	0.26	1.21	0.79
Grains row <sup>-1</sup>	6.05	1.67	7.73	0.78
1000 grain weight	295.06	250.13	545.18	0.54
Grain yield	39716.87	21196.52	60913.38	0.65

### Grain rows cob<sup>-1</sup>

Mean square revealed significant difference ( $P \leq 0.01$ ) among half sib families for kernel rows cob<sup>-1</sup> in C<sub>1</sub> (Table 2). High heritability value (0.79) was noted for kernel rows cob<sup>-1</sup>. The genetic, environmental and phenotypic variances for kernel rows cob<sup>-1</sup> were 0.95, 0.26 and 1.21 respectively (Table 3). Genotypic and environmental coefficient of variation for kernel rows cob<sup>-1</sup> were 6.93%

and 3.60% with an index of variation of 1.93 (Table 4). Grain rows cob<sup>-1</sup> exhibited significant and positive genotypic correlation with ear plant<sup>-1</sup> ( $r_G = 0.38^{**}$ ), 1000 grain weight ( $r_G = 0.23^*$ ) and grain yield ( $r_G = 0.24^*$ ), while significant and negative phenotypic correlation was observed with ear length ( $r_P = -0.33^{**}$ ). Grain rows cob<sup>-1</sup> showed non-significant association with remaining traits at both levels (Table 5).

**Table 4. Genetic coefficient of variation (GCV), environmental coefficient of variation (ECV) and index of variation (I.V) of yield attributes**

Parameter	GCV (%)	ECV (%)	I.H
Ears plant <sup>-1</sup>	12.34	7.53	1.64
Ear length	7.23	4.29	1.69
Ear diameter	11.81	6.72	1.76
Grain rows ear <sup>-1</sup>	6.93	3.60	1.93
Grains row <sup>-1</sup>	14.98	7.87	1.90
1000 grain weight	6.60	6.08	1.09
Grain yield	6.02	4.39	1.37

**Table 5. Coefficient of genotypic correlation (below the diagonal) and phenotypic correlation (above the diagonal) among yield attributes in half sib recurrent families**

Traits	Ears plant <sup>-1</sup>	Ear length	Ear diameter	Grain rows ear <sup>-1</sup>	Grains rows	1000 grain weight	Grain yield
Ears plant <sup>-1</sup>	1	0.10	-0.03	0.02	0.14	-0.01	0.20
Ear length	0.21	1	0.17	-0.23*	0.06	0.16	0.33**
Ear diameter	0.21	0.22	1	-0.08	-0.08	-0.09	-0.02
Grain rows ear <sup>-1</sup>	0.38**	-0.14	0.06	1	0.01	0.16	0.10
Grains rows	0.11	0.03	0.01	0.09	1	-0.29*	0.15
1000 grain weight	0.16	0.28*	-0.02	0.23*	-0.28*	1	0.20
Grain yield	0.46**	0.50**	-0.02	0.24*	0.34**	0.39**	1

\*,\*\* = significant at 5 and 1% level of probability

### Grains row<sup>-1</sup>

Mean square revealed significant difference ( $P \leq 0.01$ ) among half sib families for Grains row<sup>-1</sup> in C<sub>1</sub> (Table 2). High heritability value (0.78) was recorded for the mentioned trait. For grains row<sup>-1</sup> the genetic, environmental and phenotypic variances were 6.05, 1.67 and 7.73 respectively (Table 3). Genotypic and environmental coefficient of variation for grains row<sup>-1</sup> were 14.98% and 7.87% with an index of variation of 1.90 (Table 4). Grains row<sup>-1</sup> exhibited significant and negative correlation with anthesis silking interval ( $r_G = 0.30^{**}$  and  $r_P = -0.23^*$ ) at both level. Significant and negative genotypic correlation was noted with 1000 grain weight ( $r_G = -0.28^*$ ). Significant ( $P \leq 0.01$ ) and positive correlation was noted with grain yield ( $r_G = 0.34^{**}$ ) at genotypic level only. However grains row<sup>-1</sup> had non-significant correlation

with remaining studied traits at both levels (Table 5).

### 1000 grain weight (g)

Mean square revealed significant difference ( $P \leq 0.01$ ) among half sib families for 1000 grain weight in C<sub>1</sub> (Table 2). Moderate heritability value (0.54) was noted for 1000 grain weight. For 1000 grain weight, the genetic, environmental and phenotypic variances were 295.06, 250.13 and 545.18, respectively (Table 3). Genotypic and environmental coefficient of variation for 1000 grain weight were 6.60% and 6.08% with an index of variation of 1.09 (Table 4). Hundred grain weight exhibited significant and positive genotypic correlation with ear length ( $r_G = 0.28^*$ ), grain rows ear<sup>-1</sup> ( $r_G = 0.23^*$ ) and grain yield ( $r_G = 0.39^{**}$ ), while significant and negative genotypic correlation was observed with grains row<sup>-1</sup>

( $r_G = -0.28^*$ ). The mentioned trait showed significant ant negative phenotypic correlation was grains row<sup>-1</sup> ( $r_P = -0.29^*$ ). With the remaining traits 1000 grain weight revealed non-significant correlations at both genotypic and phenotypic levels (Table 5).

#### **Grain yield (kg ha<sup>-1</sup>)**

Mean square revealed significant ( $P \leq 0.01$ ) difference among the half sib families for grain yield in C<sub>1</sub> (Table 2). High heritability value (0.65) was noted for grain yield. For grain yield, the genetic, environmental and phenotypic variances were 39716.87, 21196.52 and 60913.38 respectively (Table 3). Genotypic and environmental coefficient of variation for Grain yield was 6.62% and 4.39% with an index of variation of 1.37 (Table 4). Grain yield had significant genotypic correlation with ear plant<sup>-1</sup> ( $r_G = -0.46^{**}$ ), ear length ( $r_G = 0.50^{**}$ ), grain row ear<sup>-1</sup> ( $r_G = -0.24^*$ ), grains row<sup>-1</sup> ( $r_G = 0.34^{**}$ ) and 1000 grain weight ( $r_G = 0.39^*$ ). Grain yield exhibited significant and positive phenotypic correlation with ear length ( $r_G = 0.33^{**}$ ). The mentioned trait showed non-significant genotypic and phenotypic correlations with the remaining traits (Table 5).

#### **Discussion**

##### **Ears plant<sup>-1</sup>**

Ears plant<sup>-1</sup> along ear length, ear diameter and 1000 grain weight contributes to grain yield. Data concerning ears plant<sup>-1</sup> expressed highly significant differences among half sib families of CIMMYT maize population CZP-132011 for ears plant<sup>-1</sup> in C<sub>1</sub>. The current findings are in line with [16], who also observed significant differences among the half sib families of maize Varsity Pahari for plant and ear height. Maximum heritability value was observed in cycle one for ears plant<sup>-1</sup>. High heritability for ears plant<sup>-1</sup> has also noted [17]. High index of variation for ears plant<sup>-1</sup> revealed presence of genetic variability and selection possibilities. Correlation analysis showed positive genotypic correlation with all the traits except ear height. Ears plant<sup>-1</sup> was

positive phenotypically correlated with all traits except plant height, ear height, ear diameter and 1000 grain weight. Positive genotypic and phenotypic correlation between ears plant<sup>-1</sup> and grain yield was also noted [18].

##### **Ear length and ear diameter**

Like other yield components ear length and ear diameter also contribute to final grain yield. Mean squares revealed highly significant differences among half sib recurrent families for ear length and ear diameter. Significant differences in modified full sib families for ear length and ear diameter has been reported [19]. While [20] noted significant difference in IG-1 and IG-2 maize populations for ear length and ear diameter. [3, 21] also got high heritability for ear length and ear diameter. High index of variation revealed the presence of genetic variability and possibilities of selection. Both the traits exhibited negative genotypic and phenotypic correlation with physiological traits. Similarly the mentioned traits were positively correlated with 1000 grain weight at both levels. Ear length had highly significant and positive genotypic and phenotypic correlated with grain yield, while ear diameter showed negative correlation with grain yield at both genotypic and phenotypic levels. [21] also noted negative correlation between ear diameter and grain yield, while [22] reported positive correlation of grain yield with ear length and ear diameter at both genotypic and phenotypic levels.

##### **Grains row ear<sup>-1</sup> and grains row<sup>-1</sup>**

Grains row ear<sup>-1</sup>, grains row<sup>-1</sup>, ear length, ear diameter and 1000 grain weight adds to ultimate grain weight. Statistical results showed highly significant differences among half sib families in cycle one for grains row ear<sup>-1</sup> and grains row<sup>-1</sup>. Our results for the mentioned are in line with [6] who also noted significant differences in two recombination cycles. High heritability values for grains row ear<sup>-1</sup> (0.79) and grains row<sup>-1</sup> (0.78) indicates that these traits was less under environmental

influence. High value of  $I.V > 1$  indicates the possibility of selection. Maximum heritability, selection differential, expected response and index of variation were also noted for grains row  $\text{ear}^{-1}$  and grains row $^{-1}$  by [23]. Similarly these traits were positively correlated with grain yield both at genotypic and phenotypic levels. Positive correlation was noted between grain yield and grains row  $\text{ear}^{-1}$  both at genotypic and phenotypic levels by [24].

#### **1000 grain weight**

Grain weight contribute directly to final grain yield. Grain with large grain size have high grain yield. Data regarding 1000 grain weight exhibited significant differences among the recurrent half sib families for 1000 grain weight. After one cycle of recurrent selection the percent gain cycle $^{-1}$  was 5.87%. Improvement in percent gain cycle $^{-1}$  for 1000 grain weight was also reported by [25]. Moderate heritability and index of variation reflects that there is environmental influence on 1000 grain weight. Low and moderate index of variation reduce the possibilities of genetic variability and chances of selection [26]. 1000 grain weight was positive genotypic and phenotypic correlated with days to 50% anthesis, silking, plant and ear height, ears plant $^{-1}$ , ear length, grain rows  $\text{ear}^{-1}$  and grain yield, while negative correlated with tasseling, anthesis silking interval, ear diameter and grains row $^{-1}$  at genotypic level. However 1000 grain weight was positive phenotypically correlated with all traits except days to tasseling, silking, anthesis silking interval and ear diameter. Positive correlation between 1000 grain weight and ears plant $^{-1}$ , ear length and grain yield also observed by [27].

#### **Grain yield**

Yield is a complex trait which is the interaction of several yield attributing traits. Mean squares showed significant ( $P \leq 0.01$ ) differences among the half sib recurrent families for grain yield. After one cycle of recurrent selection the percent gain cycle $^{-1}$  was

4.17%. Our results are in line with [28], who also noted significant difference in UENF-14 popcorn population using recurrent selection procedure for grain yield. Similarly [29] also noted significant differences in BS-11 maize population. [30] also got high heritability (0.90) for grain yield. High index of variation (1.37) was noted for the said trait reflects the presence of genetic variability and chances of selection. [31] also reported  $I.V > 1$  for grain yield in maize population, ESALQ-PB1. Grain yield was negative genotypic and phenotypically correlated with tasseling, anthesis, anthesis silking interval, ear diameter and plant height, while positive correlated with days to silking, ear height, ears plant $^{-1}$ , ear length, grain rows  $\text{ear}^{-1}$ , grains row $^{-1}$  and 1000 grain weight at both levels. Positive phenotypic association of grain yield with ear length, kernel rows  $\text{ear}^{-1}$  and kernel weight was also noted by [32].

#### **Conclusion**

Analysis of variance revealed highly significant differences for all studied traits. High values of heritability ( $h^2 > 0.60$ ) and index of variation ( $I.H > 1$ ) indicate the existence of sufficient amount of genetic variability among the half sib families and the potential for further improvement using 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 raise the opportunity of selection desirable traits. The maize population CZP-132011 can be used as base population for derivation inbred lines and have the potential for further improvement in yield and yield attributes.

#### **Authors' contributions**

Conceived and designed the experiments: H Rahman & MY Khan, Performed the experiments: A Sohail, Analyzed the data: A Sohail, Contributed reagents/ materials/ analysis tools: T Burni, SMA Shah, R Naz & Manzoor, Wrote the paper: A Sohail.

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