Maize Journal (October 2022) 11(2): 101-108

RESEARCH PAPER

Heritability and genetic variance for grain yield and its component characters in single cross hybrids of maize (*Zea mays* L.)

Shazia Gulzar[1] · **Z. A. Dar**[2] · **Ajaz A. Lone**[3] · **M. A. Ahangar**[4] · **M. A. Khan**[5] · **Nida Yousuf**[6] · **Gazala Gulzar**[7] · **Nusrat ul Islam**[1]

Abstract: Estimates of genetic variability and heritability in selection of desirable characters could assist the plant breeder in ascertaining criteria to be used for the breeding programmes. Twelve inbred lines and 66 F_1s generated by crossing these twelve genetically diverse parents in a half diallel mating design were evaluated at the two agricultural research stations of Kashmir in 2018 cropping season to estimate genetic variability, and heritability for, grain yield and its component characters. The estimates related to genetic components of variance revealed that estimates of additive component (D) significant for all the traits except for ear height and cob length, whereas the two measures of dominance component (H_1 and H_2) were significant for all the traits. This suggested the involvement of both these components in the inheritance of these traits, however greater magnitude of dominance component than its corresponding additive component of variance demonstrated greater role of dominance component in the inheritance of traits studied. Estimation of h^2 was significant and positive for all characters. The estimate of h^2/H_2 was less than unity for days to maturity, number of ear plant^{-1} and protein percentage indicating greater proportion of recessive group of genes for these two traits and for rest of traits h^2/H_2 was more than unity indicating greater proportion of dominance group of gene. The genetic ratio KD/KR was greater than unity for all characters under study except for plant height, ear height, cob length and kernel rows cob^{-1} where it was less than unity. The narrow sense heritability was high for days to maturity and protein percentage and low for rest of traits in the present study which indicate that additive genetic variance for these traits was relatively less pronounced than non-additive and more ever suggested importance of dominance component.

Keywords: Heritability · Diallel · Grain Yield · Dominance

Introduction

Maize (*Zea mays* L.) belongs to the tribe *Maydeae*, of the grass family, *Poaceae*. *Zea mays* is the only cultivated species in the genus Zea with chromosome number 2n=20. It contributes nearly 9 per cent to the National food basket, 5 per cent to the world dietary energy supply and more than 100 billion to the agricultural GDP at current prices (Malhotra, 2017). Globally maize is cultivated over an area of 197 million hectare with a production of 1137 million metric tonnes and productivity of 5.85 tonnes per hectare (FAOSTAT, 2022). In In India, maize is cultivated on 10.2 million hectare with a production of 27.8 million metric tonnes and productivity of 2.97 tonnes per hectare (DACNET, 2022). Textile, foundry, corn starch, corn syrup, corn oil dextrose, corn flakes, gluten, grain cake, lactic acid and acetone are

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✉ Shazia Gulzar: shaziashameem@yahoo.com

[1]Division of Genetics and Plant Breeding, FOA-Wadora, SKUAST-K, J&K, India

[2]Dry land (Karewa) Agriculture Research Station, Budgam, SKUAST-K, J&K, India

[3]High Mountain Arid Agriculture Research Institute, SKUAST-K, Leh, J&K, India

[4]Mountain Crop Research Station, Larnoo, J&K, India

[5]Division of GPB, FoA Wadura, J&K, India

[5]Division of Genetics & Plant Breeding, PAU, Ludhiana, Punjab, India

[6]Division of Plant Pathology, Shalimar, SKUAST-K, J&K, India

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Received: 15 June 2022/ Accepted: 13 September 2022

among main products of maize. It is the third most important cereal in India after wheat and rice. The major maize growing states are Uttar Pradesh, Bihar, Rajasthan, Madhya Pradesh, Punjab, Andhra Pradesh, Himachal Pradesh, West Bengal, Karnataka and Jammu and Kashmir. Heritability is an important property of quantitative traits because it is a measure of the relationship between phenotypic values and breeding values (Falconer, 1981). A successful breeding programme not only depends on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection (Najeeb, 2009 and Wang, 2011). Genetic variability for agronomic characters therefore is a key component of breeding programmes for broadening the gene pool of crops (Ahmad 2011). Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects (Kashiani, 2010 and Laghari, 2010). The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Falconer, 1996). Diallel analysis provides good information on the genetic identity of genotypes especially on dominance-recessive relations and some other genetic interactions. Diallel crosses have been used in genetic research to determinate the inheritance of a trait among a set of genotypes and to identify superior parents for hybrid or cultivar development (Yan and Kang, 2003). The importance of estimation of the genetic component variances that have been found to be a useful tool for selection of parents which when used meticulously in a hybridization programme is likely to yield successful results. Thus present study was conducted to assess genetic variability and heritability for grain yield and its component characters in twelve maize inbred lines to provide necessary information that could be useful in maize improvement programmes aimed at improving grain yield.

Materials and methods

The experimental material for the present study comprised of 12 genetically diverse inbred lines/parents developed and maintained at Dryland Agriculture Research Station, Budgam, Jammu & Kashmir were crossed in January at experimental farm of Winter Nursery Centre, ICAR-Indian Institute of Maize Research, Hyderabad, Telangana in half-diallel mating design to generate sixty-six F_1s cross combinations. Detailed description of the germplasm is presented in Table 1.

The cross progenies were developed through controlled hand pollination at WNC, Hyderabad during *rabi* 2018. The 66 progenies so developed were evaluated along with their parents (12 inbred lines) and one check

Table 1. Description of maize inbred lines under evaluation

S.No.	Inbred line	Colour	Pedigree	
1.	KDM-340A	Yellow	(DMR) PRO-349 (Trial No. = 71 of 2001)	Hyderabad
2.	KDM-895A	Yellow	DMR (Z. T. No. = 102 of 2003)	Pantnagar
3.	KDM-914A	Yellow	(AH-1139) DMR (Trial No. = 63 of 2000)	Delhi
4.	KDM-445A	Yellow	SSFX-9919 (Trial No. = 71 of 2001) DMR	New Delhi
5.	KDM-916A	Yellow	DMR (Tr. No. = 68) 2001 Hyd. 00RIBK114	Hyderabad
6.	KDM-926B	Yellow	Tr. No. = 62B of (Navjot) 2001 (DMR)	Ludhiana
7.	KDM-362A	Yellow	DMR (Trial No. = 69 of 2001, E. No. = 6520)	New Delhi
8.	KDM-439	Yellow	DMR (Tr. No. = 71 of 2001) E. No. = 6127	Hyderabad
9.	KDM-969	Yellow	FH-3209 (Z. Trial 102 of 2002 DMR)	Almora
10.	KDM-1095	Yellow	Tr. No. = 47A of 2002 from WNC	Hyderabad
11.	KDM-1156	Yellow	Pop-446C1F2-110-1 x Pop-445C1F2	
12.	V-351	Yellow	Shakti (So) SN25≠CCBf≠ x -1-F-4≠ x b	Almora

*KDM: Karewa Dryland Maize

i.e., SMH-2 at two diverse locations of Kashmir valley i.e., Dryland Agricultural Research Station (DARS), Old Airport, Budgam (E_1) and Experimental Farm of the Division of Plant Breeding and Genetics, SKUAST-K, Shalimar Srinagar (E_2) during *kharif* 2019. The material was evaluated separately in a complete randomized block design using two replications over two environments. The standard check was randomized along with F_1's while as parents were randomized separately. Each genotype was represented by single row of five meters. The intra and inter row spacing was maintained at 20 and 60 cm respectively. Two seeds were planted per hill and later thinned to one seedling per hill at 4 leaf stage. One row of non-experimental material was planted on either side of each replication as border row to avoid the border effect. Recommended package of practices were adopted to raise a good crop. Data was recorded on yield and different yield contributing traits viz., days to tasseling, days to silking, days to maturity, plant height, ear height, number of ears per plant, cob length, cob diameter, kernel rows per plant, kernels per row, hundred grain weight, yield per plot, shelling percentage and protein content. The narrow sense heritability as low (10-30), medium (30-60) and high (>60) was estimated for all the traits.

Statistical analysis

The specific combining ability effect of ij^th and ji^th (reciprocal) cross was calculated as:

$S_{ij}= (X_{ij}./l) – [(X_{i}.. + X_{ii}. + X_{j}.. + X_{jj}.)/(P + 2) 1] + 2_{X...}/ (P+1)\ (P+2)\ 1$

$S_{ji}= (X_{ji}./l) – [(X_{j}.. + X_{jj}. + X_{i}.. + X_{ii}.)/(P +2)/l] + 2_{X}.../ (P+1)\ (P+2)\ 1$

Where, P = number pf parents, l = number of environments, $X_{i}..$ = total of arrays of i^th parents over environments, $X_{ii.}$= mean value of i^th parents over environments, X… = grand total of P (P +1)/2 progenies and P is parental value over environments, $X_{ij}.$ = progeny mean value in diallel table (crosses) over environments, $X_{j}..$= total of arrays of j^th parents over environments, and $X_{jj}.$= mean value of j^th parents over environments.

Heritability was estimated in both single and pooled over environments as per the procedure presented by Burton and Dewane (1953); Johnson *et al*. (1955) and Hanson *et al*. (1956).

Using Hayman's (1954a) least square estimates, the following genetic components of variations in F_1 were calculated:

1) $D = 4\ \Sigma uvd^2$ = components of variation due to additive effect of genes arising from differences between a pair of corresponding homozygotes.

   If u = v = 0.5 then $D = d^2$. Where, u = proportion of positive genes in the parents, v = proportion of negative genes in the parents, d = additive effect, and u + v = 1
2) $H_1 = \Sigma\ uvh^2$= component of variation due to dominance effect of genes arising from the departure of heterozygotes from the mean of the corresponding pair of homozygotes.
3) $H_2 = H_1\ [1 – (u-v)^2] = 16\ \Sigma\ u^2 v^2 h^2$ = proportion of dominance variance due to positive (u) and negative (v) effects of genes.
4) h^2 = net dominance effect (algebraic sum over all loci in heterozygous phase in all crosses)
5) Fr = Proportion of dominant and recessive alleles of genes in j^th parent
6) F = relative frequency of dominant and recessive alleles in parents
7) The average degree of dominance was calculated as positive square root of ratio between components of variation due to dominance effects of the genes to component of variation due to additive effects of genes i.e.

$$\text{Degree of dominance (a)} \left[\frac{H_1}{D}\right]^{1/2}$$

Where, H= dominance component of variance, and D= additive component of dominance.

The proportion of positive and negative alleles at loci exhibiting dominance was calculated by formulae: $UV = H_2/4H_1$

The ratio has maximum value of 0.25 signifying thereby that there is symmetrical distribution of positive and negative alleles. The value less than 0.25 indicates that positive and negative alleles are not in equal proportion in parents. The prevalence of dominant and recessive genes was calculated by ratio:

$$\frac{(4\ DH_1)^{½} + F}{(4\ DH_1)^{½} - F} = \frac{KD}{KR}$$

Where, positive and negative sign of F indicated dominant and recessive genes respectively. If the ratio was 1 dominant and recessive genes in parents were indicated to be in equal proportion. If it was less than 1, it indicated an excess of recessive genes and if it was more than 1, it indicated an excess of dominant genes.

In addition, estimation of genetic variance components was also carried out according to model as suggested by Kempthorne (1957) using statistical software package Windostat version 9.1.

Results and discussion

Analysis of variance for the traits under study in pooled analysis is presented in Table 2. The Table revealed highly significant mean sum of squares for the parents under study for all the traits thus indicating significant difference amongst the maize lines for all the traits. Mean sum of squares due to hybrids showed significant differences among replications for all the traits except cob length and shelling percentage, suggesting that the spectrum of genetic variability created after hybridization in the present material was significantly different from mean of parents. This was in conformation of the results reported by Choudhary *et al.* (2000). Parents vs hybrids was also highly significant in both environments and pooled analysis indicating presence of heterosis. Highly significant differences due to environment were observed in parents as well as hybrids for all the traits studied. This confirmed that each of target locations were unique and desired.

The estimates of components of genetic variance and their corresponding standard errors were estimated for fourteen traits in E_1, E_2 and pooled analysis. Results for pooled analysis are presented in Table 3. The proportional values of these components of genetic variances together with estimates of average degree of dominance and heritability in narrow sense are given in Table 4.

The genetic components of variance and other components like D, H_1, H_2, h^2, F are important to obtain sound genetic information about the materials used for generating new variability. The estimates related to genetic components of variance revealed that estimates of additive component (D) significant for all the traits except for ear height and cob length, whereas the two measures of dominance component (H_1 and H_2) were significant for all the traits. This suggested the involvement of both

Table 2. Analysis of variance for different characters in maize (*Zea mays* L.)

Source of variation	d.f	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear plant^{-1}	Cob length (cm)	Cob diameter (cm)	Kernel rows Cob^{-1}	Kernels row^{-1}	100-grains weight (g)	Grain yield (q/ha)	Shelling (%)	Protein (%)
Environments	1	119.388*	70.885*	195.926**	846.782**	257.388**	0.206**	148.767*	1.712**	6.321*	205.157**	9.131**	600.013*	81.027**	0.693*
Block within Environments	2	4.888	9.263	265.862**	948.314**	251.234**	0.120*	52.044	0.094	8.321**	41.978**	15.951**	95.929**	4.344	0.419
Treatments	77	60.617**	82.240**	304.418**	2715.526**	1729.368**	0.138**	188.584**	4.902**	15.457**	116.533**	41.971**	1507.108**	72.096**	2.359**
Parents	11	121.538**	24.188	507.475**	669.748*	328.203**	0.047	4.629	0.128**	9.455**	36.112**	19.194**	158.385**	23.464	3.375**
Hybrids	65	125.748**	112.950**	337.522**	1214.972**	833.108**	0.209**	88.325	0.571**	10.254**	57.082**	12.625**	360.722**	12.042	1.848**
Parents vs. Hybrids	1	192.002**	274.640**	318.986**	12055.100**	77599.100**	0.850**	5648.934**	338.904**	669.688**	4865.507**	2200.029**	90858.200**	3630.545**	24.418**
Treatment x Environments	77	24.037	26.956	474.978**	631.730*	488.602*	0.564**	75.990	0.489	8.879**	22.592**	6.375*	60.805*	23.600	1.399**
Parent x Environments.	11	124.811**	136.748**	470.839**	946.794**	306.339*	0.574**	155.380*	0.320**	7.242*	54.460**	30.961**	128.869**	139.387**	2.074**
Hybrids x Environments.	65	81.500**	65.950*	463.279**	985.806**	284.041*	0.358**	87.266	0.518**	9.408**	15.238**	2.152	33.735	3.935	0.082
Parent x Hybrids x Environments	1	380.457**	444.640**	380.928*	1251.091**	369.966**	0.322**	109.771	0.423**	21.483**	150.091**	20.433**	301.679**	28.205	2.608**
Error	154	23.050	25.471	78.388	273.892	121.000	0.054	71.347	0.058	3.048	6.510	3.260	28.468	18.674	0.287
Total	311	25.361	27.685	83.964	868.365	544.655	0.077	91.294	1.369	6.795	38.406	13.623	400.178	32.972	0.831

*,** significant at 5 and 1 per cent level, respectively

Table 3. Estimates of components of genetic variation for maturity, morphological and yield attributing traits in Maize (*Zea mays* L.)

Components	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear plant^{-1}	Cob length (cm)	Cob diameter (cm)	Kernel rows cob^{-1}	Kernels row^{-1}	100-grains weight (g)	Grain yield (q/ha)	Shelling (%)	Protein (%)
$\hat{D}$	2.814* ±0.932	3.023** ±1.122	22.169** ±2.816	22.411** ±5.006	4.0132 ±88.250	0.037* ±0.016	26.976 ±50.458	0.165* ±0.074	2.202* ±0.828	6.399* ±3.120	3.720** ±1.378	31.311* ±13.200	2.437* ±1.266	0.836* ±0.062
$\hat{F}$	3.859 ±2.113	4.686 ±2.544	5.825 ±6.384	14.104 ±215.326	16.894 ±200.013	0.013 ±0.036	44.140 ±114.359	0.110 ±0.168	0.111 ±1.877	2.660 ±9.338	4.664 ±3.124	7.098 ±36.716	2.335 ±2.870	0.473 ±0.367
$\hat{H}_1$	14.273** ±1.865	16.572** ±2.245	34.106** ±5.634	1609.550** ±190.064	1067.780** ±176.547	0.137** ±0.031	86.9836** ±10.942	2.983** ±0.148	11.188** ±1.656	76.842** ±8.243	23.621** ±2.758	810.345** ±32.408	28.291** ±2.533	2.333** ±0.324
$\hat{H}_2$	12.181** ±1.551	14.065** ±1.868	23.124** ±4.687	1532.470** ±158.100	988.210** ±146.857	0.092* ±0.026	98.741** ±8.967	2.876** ±0.123	10.746** ±1.378	75.157** ±6.856	21.272** ±2.294	790.650** ±26.958	26.218** ±2.107	1.535* ±0.269
$\hat{h}^2$	43.745** ±1.037	55.816** ±1.249	15.524** ±3.134	7377.981** ±105.707	4717.457** ±98.190	0.050* ±0.017	363.600** ±56.141	21.765** ±0.082	39.326** ±0.921	300.778** ±4.584	127.162** ±1.534	5817.051** ±18.024	169.110** ±1.408	0.928** ±0.180
$\hat{E}$	1.130** ±0.258	1.284* ±0.311	1.675 ±1.781	67.942* ±26.350	41.330 ±24.476	0.019** ±0.004	28.358* ±13.994	0.019 ±0.020	1.082** ±0.229	1.489 ±1.142	0.716 ±0.382	9.978* ±4.493	0.643 ±0.351	0.017 ±0.044

*,** Significant at 5 and 1 per cent levels, respectively

$\hat{D}$ = additive component of variance; $\hat{F}$ = covariance of additive and dominance effects; $\hat{H}_1$ = Variance due to dominance effect of genes arising from the departure of heterozygotes from the mean of the corresponding pair of homozygotes; $\hat{H}_2$ = proportion of dominance variance due to positive (u) and negative (v) effects of genes; $\hat{h}^2$ = Estimate of heritability in broad sense; $\hat{E}$ = environmental component of variance

these components in the inheritance of these traits, however greater magnitude of dominance component than its corresponding additive component of variance demonstrated greater role of dominance component in the inheritance of traits studied, which was also found while estimating variance arising due to dominance deviation through combining ability analysis by Griffing (1956a, b) approach. The distribution of alleles in the parents revealed that positive and negative alleles at these loci are not in equal proportion in parents since H_1 exceeds H_2 and dominance gene action resulted mainly from positive gene action. Similar results have been reported by Rakesh *et al.* (2005) and Lata *et al.* (2006).

Estimation of h^2 was significant and positive for all characters revealing that net dominance effect over all the loci in heterozygote was significantly more and exhibited the positive direction of dominance. The value of F estimate was positive and non significant for all traits under study thus revealing contribution of more recessive alleles towards dominance deviation. The study of proportions of various genetic components of variance revealed that the proportion of $(H_2/4H_1)$ was less than 0.25 for all the traits under study indicating asymmetrical gene distribution in the parents. The estimate of h^2/H_2 was less than unity for days to maturity, number of ear plant^{-1} and protein percentage indicating greater proportion of recessive group of genes for these two traits and for rest of traits h^2/H_2 was more than unity indicating greater proportion of dominance group of gene. The genetic ratio KD/KR which gives the proportion of dominant and recessive alleles in the parent was greater than unity for all characters under study except for plant height, ear height, cob length and kernel rows cob^{-1} where it was less than unity. This suggested that barring these characters there was higher proportion of dominant alleles in the parents for all the characters. The study of proportion of average degree of dominance measured form genetic components of variance $(H_1/D)^{0.5}$ was more than unity thus revealing over dominance range for all traits under study. Similar results have been reported by Kumar and Gupta (2004); Rakesh (2005) and Lata *et al.* (2006).

This dominance was due to high heterozygosity in F_1 indicating that parents selected were diverse and from different source population. However, the discrepancy in the degree of dominance estimated from genetic components resulted mostly from G x E interaction or

Table 4. Proportion of genetic components of variation for yield attributing traits in Maize *(Zea mays* L.)

Compo-nents	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear plant^{-1}	Cob length (cm)	Cob diameter (cm)	Kernel rows cob^{-1}	Kernels row^{-1}	100-grains weight (g)	Grain yield (q/ha)	Shelling (%)	Protein (%)
$[\frac{\hat{H}_1}{\hat{D}}]^{½}$	1.902	2.537	1.034	4.826	8.606	1.530	2.719	5.413	4.059	2.726	2.059	4.152	3.902	1.376
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.164	0.162	0.136	0.191	0.185	0.138	0.252	0.193	0.191	0.196	0.180	0.195	0.184	0.132
$(\frac{KD}{KR})$	1.748	1.859	2.263	0.863	0.854	2.426	0.666	1.026	0.854	1.500	1.324	1.434	1.159	2.577
$\frac{\hat{h}^2}{\hat{H}_2}$	2.494	2.761	0.551	3.852	3.819	0.383	3.824	6.063	2.882	3.024	4.782	5.878	5.135	0.487
Heritability (n.s)	0.092	0.069	0.758	0.148	0.275	0.075	0.064	0.032	0.054	0.102	0.084	0.076	0.063	0.134
B	0.470	0.325	0.266	0.072	0.088	0.265	0.082	0.365	0.247	0.119	0.272	0.514	0.227	-0.144
	±0.505	±0.392	±0.232	±0.214	±0.374	±0.227	±0.145	±0.658	±0.460	±0.231	±0.425	±0.688	±0.483	±0.196
b-0/SE(b)	-1.031	-0.989	-1.212	-0.736	-1.374	-1.092	-1.122	-3.682	-1.786	-0.774	-1.593	-4.270	-2.313	-0.985
b-1/S.E (b)	1.445	2.114	1.478	6.816	10.913	4.529	34.124	42.947	4.105	4.754	3.103	2.371	-2.006	-0.723
t^2	0.069	0.431	0.594	13.984	42.394	0.498	10.702	9.881	6.142	5.853	2.438	2.699	4.139	3.944

$[\frac{\hat{H}_1}{\hat{D}}]^{½}$ = average degree of dominance; $\frac{\hat{H}_2}{4\hat{H}_1}$ = proportion of genes with positive and negative effects

$(\frac{KD}{KR})$ = The proportion of dominant and recessive alleles; $\frac{\hat{h}^2}{\hat{H}_2}$ = approximation of groups of genes exhibiting dominance

Table 5. Mean performance of traits

Characters	Mean
Days to tasseling	78.257
Days to silking	81.938
Cob length (cm)	19.68
Plant height (cm)	155.061
Ear height	74.55
Days to maturity	147.855
Cob diameter (cm)	4.567
No. of kernel rows/cob	14.623
Ear plant^{-1}	1.229
No. of kernels/row	21.849
100 grain weight	20.674
Grain yield/plant (g)	511.077
Shelling percentage	79.089
Protein content (%)	7.994

from sampling error, which subsequently had an influence on the estimation of dominance components. Over dominance in most cases may result from a particular combination of positive and negative genes or complementary type of gene action due to correlated gene distribution, which may seriously inflate mean degree of dominance and convert partial dominance into apparent over dominance (Hayman, 1954a; Comstock and Robinson, 1952).

Success of breeder in changing the characters of population depends upon the degree of correspondence between genotype and phenotypic values. This degree when measures in terms of heritability in narrow sense has been used as a direct selection parameter to improve the efficiency of the process. The variation in the estimates of heritability usually arises because of the choice of reference population, plot size, planting density, number of replications and method of estimation. Thus the comparison of estimates obtained by different workers must be treated with caution (Robinson, 1963).

The narrow sense heritability was high for days to maturity and protein percentage and low for rest of traits in the present study. The results are compatible with those of genetic analysis which indicate that additive genetic variance for these traits was relatively less pronounced than non-additive and more ever suggested importance of dominance component. The result also inferred that though these characters are amenable for improvement through selection but these characters would be influenced much by the environment. Low narrow sense heritability estimates for most traits indicated that in the present set of materials, the genes were showing non additive gene action and isolation of high yielding inbreeds would not be feasible unless the non allelic interactions and / or linkage are not dissipated through a selection procedure, which can slow down the rate of homozygosity in the segregating generation.

Conclusion

From the study it can be concluded that there is prevalence of greater magnitude of non-additive genetic component of variance relative to additive component individuals. Therefore, for these traits hybridization followed by selection is expected to result in some promising hybrids and thus favors the hybrid production. Wide range of variability existed in the maize inbreeds under study as indicated by the magnitude of their variability parameters implying considerable scope for maize improvement through phenotypic selection and development of transgressive segregates in the population. High estimates of heritability are useful in predicting the resultant effect of selecting the best individuals.

References

Ahmad, S. Q., Khan, S., Ghaffar, M., & Ahmad, F. (2011). Genetic diversity analysis for yield and other parameters in maize (*Zea mays* L.) genotypes. *Asian Journal of Agricultural Sciences*, **3**(5): 385-388.

Burton, G. W. & Devane, D. E. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. *Agronomy Journal*, **45**(10): 478-481.

Burton, G. W. & Devane, I. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal,* **45**: 478-481.

Choudary, A. K., Choudary, L. B. & Sharma, K. C. (2000). Combining ability estimates of early generation inbred lines derived from two populations. *Indian Journal of Genetics and Plant Breeding,* **60**(11): 55-61.

Comstock, H. E. & Robinson, H. F. (1952). Estimation of average degree of dominance of genes. In: *Heterosis* (Eds. Gowen, J.). Iowa State College Press Ames, Iowa. pp 25-36.

DACNET (2022). https://eands.dacnet.nic.in

Falconer, D. C. (1981). An introduction to quantitative genetics. 2nd Edn., Longman, New York, USA., pp 67-68.

Falconer, D. S. & Mackay, T. F. C. (1996). Introduction to quantitative genetics. 4th ed. Benjamin Cummings, England, pp 245-247.

FAOSTAT (2022). FAOSTAT. *http://www.fao.org/faostat Google Scholar*

Griffing, B. (1956a). A generalised treatment of the use of diallel crosses in quantitative inheritance. *Heredity*, **10**(1): 31-50.

Griffing, B. (1956b). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences,* **9**: 463-493.

Griffing, B. R. U. C. E. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences*, **9**(4): 463-493.

Hanson, C. H., Robinson, H. F. & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agronomy Journal,* **47**: 268-272.

Hayman, B. I. (1954a). The theory and analysis of diallel crosses. *Genetics,* **39**: 789-809.

Johnson, H. W., Robinson, H. F. & Comstock, R. E. (1955). Estimation of genetic and environmental variability in Soyabean. *Agronomy Journal,* **46**: 314-318.

Kashiani, P., Saleh, G., Abdullah, N. A. P. & Abdullah, S. N. (2010). Variation and genetic studies on selected sweet corn inbred lines. *Asian journal of Crop Science,* **2**(2); 78-84.

Kempthorne, O. (1957). An introduction to genetic statistics. John Wiley and Sons, Inc. New York, USA, 468473.

Kumar, P. & Gupta, S. C. (2004). Genetic analysis in maize (*Zea mays* L.). *Journal of Research Birsa Agricultural University*, **16**(1): 113-117.

Laghari, K. A., Sial, M. A., Afzal Arain, M. A., Mirbahar, A. A., Pirzada, A. J., Dahot, M. U. & Mangrio, S. M. (2010). Heritability studies of yield and yield associated traits in bread wheat. *Pakistan Journal of Botany,* **42**(1): 111-115.

Lata, S., Kanta, G., Sharma, J. K. & Dev, J. (2006). Components of variation, combining ability and heterosis studies for yield and its related traits in maize (*Zea mays* L.). *Crop Improvement,* **33**(2): 151-155.

Malhotra, S. K. (2017). Diversification in utilization of maize and production. In: *Proceedings of Gyan Manthan Conference: Perspective of Maize Production and Value Chain. A Compendium,* pp 49-57.

Najeeb, S., Rather, A. G., Parray, G. A., Sheikh, F. A. & Razvi, S. M. (2009). Studies on genetic variability, genotypic correlation and path coefficient analysis in maize under high altitude temperate ecology of Kashmir. *Maize Genetics Cooperation Newsletter,* **83**: 1-8.

Rakesh, K., Singh, M., Narwal, M. S. & Sudhir, S. (2005). Gene effects for grain yield and its attributes in maize (*Zea mays* L.). *National Journal of Plant Improvement,* **7**(2): 105-107.

Robinson, P. (1963). Heritability: A Second Look. In: *Genetics and Plant Breeding* (Eds. Hanson, W. D. & Robinson, W. F.). NAS-NRC Statistical Publication 982, Washington, pp 258-267.

Rosegrant, M. W., Leach, N. & Gerpacio, R. V. (1999). Alternative future for world cereal and meat consumption. Summer meeting of the Nutrition Society. 1999; Guildford, UK. 29 June-2 July 1998. *Proceedings of the Nutrition Society,* **58**: 219-234.

Wang, X., Chang, J., Qin, G., Zhang, S., Cheng, X. & Li, C. (2011). Analysis on yield components of elite maize variety Xundan 20 with super high yield potential. *African Journal of Agricultural Research,* **6**(24): 5490-5495.

Yan, W. & Kang, M. S. (2002). *GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists*. CRC press.

Yan, W. & Kang, M. S. (2003). GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticist and Agronomists. CRS Press, Boca Raton, FL., pp 207-228.