



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.03
TPI 2018; 7(11): 307-312
© 2018 TPI
www.thepharmajournal.com
Received: 05-09-2018
Accepted: 10-10-2018

Nida Yousuf
DARS, Budgam SKUAST-
Jammu & Kashmir, India

Habib M
DARS, Budgam SKUAST-
Jammu & Kashmir, India

Dar ZA
DARS, Budgam SKUAST-
Jammu & Kashmir, India

Lone AA
DARS, Budgam SKUAST-
Jammu & Kashmir, India

Shazia Gulzar
DARS, Budgam SKUAST-
Jammu & Kashmir, India

Assessment of genetic variance components in single cross hybrids of maize (*Zea mays* L.) using line x tester analysis

Nida Yousuf, Habib M, Dar ZA, Lone AA and Shazia Gulzar

Abstract

The study comprised of twenty four F_1 's generated by crossing eight genetically diverse lines with three testers as per procedure suggested by Kempthorne (1957). The parents along with their F_1 's were evaluated in a randomized complete block design with two replications at two locations for yield and yield contributing traits. Highly significant differences were found among lines and line \times testers for all the traits both in individual as well as pooled analysis confirming that the material selected for crossing was diverse. The estimates of components of genetic variance revealed that dominance component played a predominant role for traits viz., plant height, kernel rows cob^{-1} , grain depth, 100-grain weight, shelling percentage, grain yield $plant^{-1}$ and protein content whereas additive component played a great role in rest of the traits in individual as well as in pooled analysis. The degree of dominance was greater than unity (over dominance range) for most of the traits that included plant height, kernel rows cob^{-1} , grain depth, 100-grain depth, shelling percentage, grain yield $plant^{-1}$ and protein content indicating that the present study of materials was diverse and contained contrasting alleles in most of the cases in dispersion phase, which on combination through hybridization increased heterozygosity. So, in the present set of experimental material greater contribution of non-additive gene action suggested exploitation of the gene action through heterosis breeding.

Keywords: *Zea mays* L., genetic components of variance, heterosis and line x tester

Introduction

Maize (*Zea mays* L., $2n=20$) is the leading cereal worldwide, originated in Central America and Mexico but because of its wide adaptability and higher productivity potential, it is grown over a wide range of environments around the world. It belongs to the tribe *Maydeae*, of the grass family, *Poaceae*. *Zea mays* is the only cultivated species in the genus *Zea* with chromosome number $2n=20$. Because of high production potential and wider adaptability of maize, it is acknowledged as queen of cereals. At global level maize is cultivated over an area of 177.4 million hectares with an annual production of about 960.2 million tonnes and average productivity of 5.5 tonnes ha^{-1} (Anonymous, 2013-14) [1]. In the State Jammu and Kashmir, maize is second most important crop after rice and is a staple food of some tribal areas such as Gujar and Bakarwall (nomadic race). At State level maize is cultivated over an area of 0.30 million hectares with an annual production of 0.46 million tonnes and an average productivity of 1.49 tonnes ha^{-1} (Anonymous, 2014-15a) [2]. In Kashmir Division maize production is 0.15 million tonnes from an area of 0.1 million ha area with an average yield of 1.2 tonnes ha^{-1} (Anonymous, 2012 b) [3]. Low grain yield in the valley can be attributed to a number of constraints which primarily includes predominance of local land races/ open pollinated varieties, non-availability of vital inputs and scattered and small land holdings. All these constraints have limited the horizontal improvement of maize production in the valley. The only resource available is to effect vertical improvement in terms of developing the maize hybrids that demonstrate high yielding ability. This emphasizes 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.

Materials and Methods

The basic material for the present investigation comprised of eight diverse maize inbred lines viz., KDM-2104, KDM-2107, KDM-2111, KDM-2113, KDM-2117, KDM-2121, KDM-2122 and KDM-2123 and three testers viz., SM C-4, KDM-914A, and KDM-343A.

Correspondence

Dar ZA
DARS, Budgam SKUAST-
Jammu & Kashmir, India

Twenty four crosses were obtained from the set of parents using the methodology of line × tester mating design as suggested by Kempthorne (1957) [1]. During rabi 2012-13 at Winter Nursery Centre, Hyderabad. Twenty four crosses along with their parents were evaluated at two locations during *Kharif* 2013 in a complete randomized block design with two replications at both the locations. The experimental plot comprised of two rows each of 4 metre length with a planting geometry of 75 × 20 cm. All the recommended agronomic practices were followed to raise a good crop. Observations on various traits viz., plant height (cm), ear height (cm), grain depth, number of kernel rows ear-1, number of kernels row-1, shelling percentage (%), 100-grain weight (g), prolificacy index, grain yield plant-1(g) and protein content (%) were recorded on five randomly selected competitive plants except for maturity traits (days to 50 per cent tasseling and days to 50 per cent silking) where data were recorded on plot basis. Estimation of genetic variance components was carried out according to model as suggested by Kempthorne (1957) [1]. 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 1. Perusal of the results revealed significant differences among parents (lines), crosses and line × testers for all traits under study, indicating that the material selected was diverse for all the traits under study. Similar results were reported by Jamshidian *et al.* (2013) [10]. For the traits viz., days to 50 per cent tasseling, days to 50 per cent silking, grain depth, 100-grain weight, ear yield, plant height, ear height, number of grains ear⁻¹ and number of grains row⁻¹ and protein content. It was also found that mean squares due to lines were larger when compared to testers for all the traits indicating greater diversity among lines. The crosses × environment interaction was significant for plant height, ear height, kernels row⁻¹, 100-grain weight and grain yield plant⁻¹. Similar results were reported by Beck *et al.* (1990) [6]. For traits like yield, plant height but not ear height.

Table 1: Analysis of variance for different characters in maize (*Zea mays* L.)

Source of variation	d.f.	Days to 50% tasseling			Days to 50% silking			Plant height (cm)		
		E ₁	E ₂	Pooled	E ₁	E ₂	Pooled	E ₁	E ₂	Pooled
Environments	1	-	-	1327.593**	-	-	1335.041**	-	-	50592.360**
Replications	1	0.750	0.520	0.010	1.190	0.187	0.375	29.230	8.130	17.543
Replications × environments	1	-	-	1.260	-	-	1.500	-	-	0.339
Crosses	23	14.170**	17.020**	30.640**	13.716**	15.368**	28.521**	842.523**	552.938**	1368.560**
Lines	7	37.645*	54.395**	91.166*	42.583**	56.33**	98.375**	1657.252*	1087.777*	2702.331*
Testers	2	13.797	18.258	31.343	14.30	15.497	28.690	292.645	328.120	618.567
Line × tester	14	11.002**	11.062**	21.642**	9.297**	9.452**	18.458*	513.714**	317.636**	808.817**
Crosses × environments	23	-	-	0.550	-	-	0.563	-	-	26.901**
Lines × environments	7	-	-	0.712	-	-	1.113*	-	-	42.697
Testers × environments	2	-	-	0.875	-	-	0.541	-	-	2.198
Lines × Testers × environments	14	-	-	0.874*	-	-	1.2300*	-	-	22.532**
Error										
Individual	23	0.315	0.477	-	0.296	0.752	-	7.267	1.973	-
Pooled	46	-	-	0.396	-	-	0.524	-	-	4.620
Environments	1	-	-	18869.237**	-	-	0.001	-	-	1.181**
Replications	1	13.130	3.560	8.230	0.000	0.007	0.002	0.024	0.056	0.077
Replications × environments	1	-	-	4.725	-	-	0.005	-	-	0.003
Crosses	23	447.267**	320.170**	735.382**	0.021**	0.017**	0.037**	3.637**	3.306**	6.911**
Lines	7	760.246*	604.393**	1338.545*	0.043*	0.043**	0.086**	12.000*	11.678*	23.501*
Testers	2	651.965	654.008*	1305.800	0.023	0.010	0.030	0.186	0.057	0.203
Line × tester	14	261.534**	130.367**	352.312**	0.009**	0.005	0.013**	4.137**	4.008**	8.116**
Crosses × environments	23	-	-	32.055**	-	-	0.001	-	-	0.032
Lines × environments	7	-	-	26.094	-	-	0.001	-	-	0.037
Testers × environments	2	-	-	0.173	-	-	0.002	-	-	0.040
Lines × Testers × environments	14	-	-	39.589**	-	-	0.004	-	-	0.112**
Error										
Individual	23	3.229	0.894	-	0.001	0.005	-	0.019	0.049	-
Pooled	46	-	-	2.061	-	-	0.003	-	-	0.034
Environments	1	-	-	149.675**	-	-	0.002**	-	-	9.519**
Replications	1	0.980	1.121	2.100	0.001	0.001	0.002	0.285	1.011	0.968
Replications × environments	1	-	-	0.974	-	-	0.004	-	-	0.457
Crosses	23	50.913**	42.487**	92.341**	0.018**	0.017**	0.035**	21.438**	22.255**	43.047**
Lines	7	102.667*	86.234*	190.000*	0.034*	0.030*	0.064*	78.000**	86.000**	164.001**
Testers	2	11.538**	11.676**	23.20**	0.022**	0.024**	0.044**	9.874	15.193	24.679
Line × tester	14	35.100**	30.120**	65.000**	0.011**	0.010**	0.021**	19.451**	19.962**	38.776**
Crosses × environments	23	-	-	1.059**	-	-	0.001	-	-	0.646**
Lines × environments	7	-	-	1.426	-	-	0.001	-	-	0.736
Testers × environments	2	-	-	0.009	-	-	0.001	-	-	0.388
Lines × Testers × environments	14	-	-	1.026**	-	-	0.006**	-	-	0.638**
Error										
Individual	23	0.239	0.305	-	0.001	0.001	-	0.234	0.263	-
Pooled	46	-	-	0.272	-	-	0.001	-	-	0.248

Environments	1	-	-	1.680*	-	-	309.350**	-	-	0.181**
Replications	1	0.091	1.032	0.860	24.500	29.281	26.001	0.008	0.013	0.021
Replications × environments	1	-	-	0.255	-	-	3.884	-	-	0.0003
Crosses	23	27.793**	28.975**	56.440**	2085.257**	2026.510**	4083.823**	0.455**	0.377**	0.789**
Lines	7	49.550*	58.001*	109.000*	4501.000*	5012.000*	9102.700*	1.101*	1.02*	1.966*
Testers	2	49.322	43.801	93.014	52.381	141.548	181.286	0.141	0.124	0.262
Line × tester	14	17.050**	20.047**	36.782**	1509.000**	1801.781	3169.133**	0.370**	0.343**	0.670**
Crosses × environments	23	-	-	0.332	-	-	27.945**	-	-	0.043
Lines × environments	7	-	-	0.428	-	-	77.530**	-	-	0.052
Testers × environments	2	-	-	0.109	-	-	12.649	-	-	0.003
Lines × Testers × environments	14	-	-	0.315	-	-	19.675**	-	-	0.044*
Error										
Individual	23	0.125	0.363	-	6.021	-	-	0.021	0.013	-
Pooled	46	-	-	0.244	-	-	6.666	-	-	0.017

*, ** Significant at 5 and 1 percent levels, respectively

The estimates of GCA and SCA variances were compared to assess the relative importance of the genetic variance components. For most of the traits viz., plant height, kernel rows cob⁻¹, kernels row⁻¹, grain depth, 100-grain weight, shelling percentage, grain yield plant⁻¹ and protein content, σ^2 D values were observed to be much higher than σ^2 A, indicating that non additive gene action played a major role in the expression of these traits (Table 2). However, σ^2 A values observed to be greater than σ^2 D for traits that included days to 50 per cent tasseling, days to 50 per cent silking, ear height and prolificacy indicating that additive gene action played a predominant role in the expression of these traits in both environments and pooled analysis. Vasal *et al.* (1992) [17]. And Joshi *et al.* (1998) [11]. Reported that non-additive gene effects played a predominant role in the inheritance of kernels row⁻¹, 100-grain weight, grain yield hectare⁻¹ which were in line with above findings. However, they observed that for days to 50 per cent silking, non-additive gene action was more important than additive gene action which was contrary to the above results. Alam *et al.* (2008) [4]. Highlighted the role of non-additive gene action in the control of plant height, which was in line with above results whereas for days to 50 per cent tasseling, days to 50 per cent silking and ear height, contrary results were obtained. However, they observed almost equal importance of additive and non-additive gene action for days to 50 per cent maturity. Shanthi *et al.* (2010) [16]. Carried out genetic analysis in maize and reported that protein content to be controlled by non-additive gene action, since SCA variance was greater than GCA variance Abadi *et al.* (2011) [5d]. Reported that additive type of gene action played a major role in ear height, days to 50 per cent anthesis, days to 50 per cent silking and prolificacy which supported the above findings. Pavan *et al.* (2011) [14]. Reported non-additive gene action to be more important for the expression of grain yield hectare⁻¹, 100-grain weight, grain yield plant⁻¹, kernel rows ear⁻¹, kernels row⁻¹ and shelling percentage. The average degree of dominance was greater than unity (over dominance range) for most of the traits that included plant height, kernel rows cob⁻¹, grain depth, 100-grain depth, shelling percentage, grain yield plant⁻¹ and protein content, indicating that the present study of materials was diverse and contained contrasting alleles in most of the cases in dispersion

phase, which on combination through hybridization increased heterozygosity. This again points to the evidence that non additive gene action had a predominant role in the expression of these traits. So, in the present set of experimental material greater contribution of non-additive gene action suggested exploitation of the gene action through heterosis breeding. If heterosis is due over-dominance, it is not fixable rendering the development of hybrid cultivars indispensable. However, Eberhart (1977) [8]. Pointed out that in the statistical genetic studies the complete dominance may be much more important than over-dominance in improvement of maize hybrids. The expression of over-dominance for most of the traits in F₁ generation might not be real order of dominance at genetic level because combination of positive and negative genes in complementary type of gene interaction and/or correlated gene distribution might seriously inflate the degree of dominance and convert a mere partial dominance in to perceptible over-dominance (Hayman, 1954) [9]. The average degree of dominance in the range of over-dominance results from repulsion phase linkage which are in real sense partially or completely dominant range. On the other hand, the average degree of dominance was less than unity (partial dominance range) for the remaining traits viz., days to 50 per cent tasseling, days to 50 per cent silking, ear height and prolificacy in individual and pooled analysis.

The narrow sense heritability was in moderate range for most of the traits. The results of the present investigation revealed that additive genetic variance is important for exhibiting high heritability. Low narrow sense heritability estimates for most of the traits indicated in the present investigation, the material selected were showing non additive type of gene action and isolation of high yielding inbred 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 generations.

Moderate estimates of heritability in maize has been reported by several workers for plant height, kernel row ear⁻¹, 100-grain weight (Viola *et al.*, 2003) [18]. Grain yield (Noor *et al.*, 2010) [13]. Contrarily high estimates of heritability for yield and its component traits, plant height have been reported by several workers (Bekele and Rao, 2014 and Rajesh *et al.*, 2013) [15].

Table 2: Estimates of genetic components of variance, degree of dominance, genetic advance and heritability for different traits in maize (*Zea mays* L.)

Components of variance	Days to 50% tasselling			Days to 50% Silking			Plant height (cm)		
	E ₁	E ₂	Pooled	E ₁	E ₂	Pooled	E ₁	E ₂	Pooled
σ ² lines	2.239* ±1.263	2.960* ±1.57	2.581* ±1.391	2.310* ±1.250	2.430* ±1.338	2.351* ±1.251	275.041* ±133.589	181.035* ±87.4894	224.81* ±108.810
σ ² lines × environments	-	-	0.060 ±0.060	-	-	0.092 ±0.091	-	-	6.340 ±3.611
σ ² testers	2.330 ±1.681	-3.368* ±2.415	2.840 ±2.030	2.632* ±1.893	3.464* ±2.498	3.061 ±2.181	17.852 ±17.208	20.409 ±16.110	19.181 ±16.330
σ ² testers × environments	-	-	0.030 ±0.041	-	-	0.012 ±0.021	-	-	-0.151 ±0.510
σ ² gca	2.305* ±1.270	3.257** ±1.809	2.760* ±1.520	2.544** ±1.418	3.182** ±1.853	2.860* ±1.620	87.994* ±38.546	64.216** ±26.5822	75.261** ±31.961
σ ² gca × environments	-	-	0.040 ±0.010	-	-	0.022 ±0.031	-	-	1.621 ±1.051
σ ² sca (lines × testers)	5.319** ±1.945	5.284** ±1.955	5.310** ±1.910	4.422** ±1.643	4.271** ±1.671	4.480** ±1.631	253.353** ±90.812	158.035* ±56.150	201.041** ±71.511
σ ² sca × environments (L × T × E)	-	-	0.010 ±0.080	-	-	-0.121 ±0.072	-	-	8.950* ±4.011
σ ² E	0.181	0.246	0.090	0.226	0.455	0.131	3.503	0.786	1.151
σ ² A	4.610	6.515	5.531	5.089	6.364	5.720	175.989	128.433	150.531
σ ² D	5.319	5.284	5.311	4.422	4.271	4.480	253.353	158.035	201.050
Degree of dominance	1.074	0.900	0.971	0.932	0.819	0.880	1.199	1.109	1.150
Heritability (N.S.) %	45.59	54.084	50.120	52.263	57.386	55.710	40.658	44.711	41.241
Genetic advance (5%)	2.986	3.867	3.430	3.359	3.936	3.680	17.425	15.610	16.231
Mean	68.670	75.65	72.160	72.810	79.850	76.330	170.210	128.280	149.240
σ ² lines	126.287** ±61.687	100.575** ±48.103	111.370** ±53.620	0.007** ±0.003	0.006** ±0.003	0.002 ±0.001	0.600* ±0.374	0.463* ±0.324	0.530* ±0.350
σ ² lines × environments	-	-	4.000 ±3.101	-	-	-0.002 ±0.001	-	-	0.011 ±0.011
σ ² testers	40.590* ±29.386	40.816* ±29.0465	40.740 ±29.120	0.001 ±0.001	0.001 ±0.002	0.002 ±0.001	0.010 ±0.092	0.002 ±0.088	0.010 ±0.100
σ ² testers × environments	-	-	-0.120 ±0.870	-	-	0.002 ±0.001	-	-	0.010 ±0.010
σ ² gca	63.962** ±27.199	57.114* ±24.866	60.000** ±25.73	0.002** ±0.001	0.002* ±0.001	0.002 ±0.001	0.171** ±0.122	0.127** ±0.109	0.151** ±0.120
σ ² gca × environments	-	-	1.012 ±1.062	-	-	-0.001 ±0.002	-	-	0.010 ±0.010
σ ² sca (lines × testers)	129.505** ±46.233	64.711** ±23.046	87.560** ±31.330	0.003** ±0.002	0.002 ±0.001	0.002* ±0.001	2.057** ±0.731	1.978** ±0.708	2.02** ±0.72
σ ² sca × environments (L × T × E)	-	-	18.760** ±7.000	-	-	-0.001 ±0.001	-	-	-0.011 ±0.010
σ ² E	1.262	0.473	0.510	0.001	0.002	0.001	0.012	0.025	0.011
σ ² A	127.924	114.228	120.001	0.006	0.004	0.010	0.342	0.253	0.292
σ ² D	129.505	64.711	87.560	0.004	0.001	0.002	2.057	1.978	2.021
Degree of dominance	1.006	0.753	0.851	0.815	0.382	0.710	2.452	2.793	2.601
Heritability (N.S.) %	49.450	63.668	52.440	55.414	61.581	70.810	14.187	11.231	12.810
Genetic advance (5%)	16.384	17.567	16.340	0.116	0.104	0.120	0.454	0.347	0.402
Mean	99.610	74.021	86.820	1.061	1.051	1.050	14.400	14.160	14.200
σ ² lines	10.151** ±5.683	7.747** ±4.532	8.870** ±5.040	0.004 ±0.002	0.004 ±0.002	0.004 ±0.002	4.719** ±2.530	4.765** ±2.554	4.711** ±2.501
σ ² lines × environments	-	-	0.190 ±0.120	-	-	0.002 ±0.001	-	-	0.080 ±0.070
σ ² testers	0.703 ±1.245	0.699 ±1.113	0.720 ±1.170	0.002 ±0.001	0.002 ±0.001	0.001 ±0.001	0.590 ±0.615	0.933 ±0.803	0.763 ±0.69
σ ² testers × environments	-	-	-0.020 ±0.020	-	-	0.001 ±0.001	-	-	0.012 ±0.021
σ ² gca	3.279** ±1.795	2.621** ±1.477	2.940** ±1.620	0.003** ±0.001	0.002** ±0.001	0.002* ±0.001	1.715* ±0.821	1.978* ±0.909	1.841* ±0.850
σ ² gca × environments	-	-	0.041 ±0.040	-	-	0.002 ±0.001	-	-	0.031 ±0.021
σ ² sca (lines × testers)	25.549** ±9.085	22.079** ±7.892	23.680** ±8.390	0.006** ±0.002	0.006** ±0.002	0.006* ±0.001	9.515** ±3.438	9.848** ±3.529	9.630** ±3.421
σ ² sca × environments	-	-	0.371 ±0.180	-	-	0.001 ±0.001	-	-	0.191 ±0.110

environments (L × T × E)									
σ^2E	0.146	0.243	0.061	0.001	0.001	0.001	0.210	0.133	0.061
σ^2A	6.559	5.243	5.880	0.005	0.005	0.01	3.432	3.956	3.681
σ^2D	25.549	22.079	23.680	0.006	0.006	0.006	9.515	9.848	9.631
Degree of dominance	1.973	2.052	2.010	1.436	1.430	1.434	1.665	1.577	1.611
Heritability (N.S.) %	20.336	19.019	19.550	47.777	46.887	47.00	26.081	28.385	27.020
Genetic advance (5%)	2.379	2.057	2.210	0.103	0.101	0.102	1.948	2.183	2.050
Mean	29.700	26.950	28.320	0.631	0.6210	0.621	28.790	28.260	28.320
σ^2 lines	7.162* ±3.534	7.043* ±3.549	7.090* ±3.520	462.241** ±248.873	387.080** ±222.316	418.460** ±232.621	0.116* ±0.060	0.084* ±0.045	0.091* ±0.050
σ^2 lines × environments	-	-	0.030 ±0.040	-	-	11.811 ±6.090	-	-	0.010 ±0.010
σ^2 testers	3.073 ±2.212	2.717 ±1.986	2.891 ±2.091	2.986 ±44.901	8.5206 ±47.818	5.451 ±46.203	0.008 ±0.010	0.007 ±0.009	0.010 ±0.010
σ^2 testers × environments	-	-	-0.011 ±0.011	-	-	0.370 ±0.570	-	-	-0.010 ±0.011
σ^2 gca	4.188** ±1.875	3.897* ±1.738	4.040** ±1.800	128.237** ±75.321	111.764** ±69.895	118.090** ±71.800	0.037* ±0.018	0.027* ±0.014	0.030* ±0.010
σ^2 gca × environments	-	-	0.010 ±0.010	-	-	3.490* ±1.710	-	-	0.011 ±0.010
σ^2 sca (lines × testers)	8.448** ±3.014	9.857** 3.544	9.130** ±3.250	1012.330** ±358.727	1069.989** ±379.220	1040.611** ±368.500	0.177** ±0.065	0.164** ±0.060	0.161* ±0.060
σ^2 sca × environments (L × T × E)	-	-	0.030 ±0.06	-	-	-0.660 ±1.160	-	-	0.010 ±0.011
σ^2E	0.076	0.166	0.060	2.304	2.609	1.660	0.008	0.007	0.001
σ^2A	8.377	7.793	8.080	256.474	223.528	236.180	0.074	0.055	0.060
σ^2D	8.448	9.857	9.130	1012.331	1069.989	1040.610	0.177	0.164	0.160
Degree of dominance	1.004	1.124	1.060	1.986	2.187	2.090	1.539	1.719	1.590
Heritability (N.S.) %	49.561	43.741	46.670	20.177	17.246	18.380	28.755	24.469	25.880
Genetic advance (5%)	4.197	3.803	4.000	14.819	12.790	13.570	0.302	0.240	0.260
Mean	80.330	80.080	80.210	110.110	107.370	108.740	7.740	7.600	7.670

*,** Significant at 5 and 1 percent levels, respectively

Conclusion

As the degree of dominance was greater than unity for most of the traits indicating that the present study of materials was diverse and contained contrasting alleles in most of the cases in dispersion phase. Thus, the estimates of the genetic component variances are important because they allow the choice of efficient breeding methodologies with the resources available and constitute the raw material by breeders to develop superior genotypes.

References

- Anonymous. Food and Agricultural Organization year book of the United Nations Rome, Italy, 2013-14. <http://faostat.fao.org/faostat/servlet/xteServlet3>
- Anonymous. Directors Review. Indian Institute of Maize Research, New Dehli, 2014-15a.
- Anonymous. Directorate of Maize Research, Annual report of directorate of Maize Research, New Delhi, 2012b.
- Alam AKMM, Ahmed S, Begum M, Sultan MK. Heterosis and combining ability for grain yield and its contributing characters in maize. Bangladesh Journal of Agricultural Research. 2008; 33(3):375-379.
- Abadi JM, Khorasani SK, Sar BS, Movafeg S, Golbashi M. Estimation of combining ability and gene effects in forage maize (*Zea mays* L.) using line × tester crosses. Journal of Plant Physiology and Breeding. 2011; 1(1):57-67
- Beck DL, Vasal SK, Crossa J. H. Heterosis and combining ability of CIMMYT,s tropical early and intermediate maturity maize (*Zea mays* L.) germplasm. Maydica. 1990; 35:279-285.
- Bekele A, Rao TN. Estimates of heritability, genetic advance and correlation study for yield and it's attributes in maize (*Zea mays* L.) Journal of Plant Sciences. 2014; 2(1):1-4.
- Eberhart SA. Quantitative genetics and practical corn breeding. In: Proceedings of International Conference on Quantitative Genetics (Eds. E. Pollack, Kempthorne and T.B. Baily, Jr.). IOWA State University Press, 1977, 491-502.
- Hayman BI. The analysis of variance of diallel crosses. Biometrics. 1954; 10:235-244
- Jamshidian P, Golparvar AR, Naderi MR, Darkhal H. Phenotypic correlations and path analysis between ear yield and other associated characters in corn hybrids (*Zea mays* L.). International Journal of Farming and Allied Sciences. 2013; 2(S):1273-1276.
- Joshi VN, Pandiya NK, Dubey RB. Heterosis and combining ability for quality and yield in early maturing single cross hybrids of maize (*Zea Mays* L.). Indian Journal of Genetics. 1998; 58(4):519-524.
- Kempthorne O. An Introduction to Genetic Statistics. John Wiley and Sons, Inc. New York, USA, 1957, 468-473.
- Noor M, Rahman H, Iqbal DM, Shah SMA, Ihteramullah.

- Evaluation of maize half sib families for maturity and grain yield attributes. *Sarhad Journal of Agriculture*. 2010; 26(9):545-549
14. Pavan R, Lohithaswa HC, Prakash G, Wali MC, Shekara BG. Combining ability analysis of newer inbred lines derived from national yellow pool for grain yield and other quantitative traits in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*. 2011; 2(3):310-319
 15. Rajesh V, Kumar SS, Reddy VN, Sankar AS. Studies on genetic variability, heritability and genetic advance estimates in newly developed maize genotypes (*Zea mays* L.). *International Journal of Applied Biology and Pharmaceutical Technology*. 2013; 4(4):242-245.
 16. Shanthi P, Babu GS, Satyanarayana E, Kumar RS. Combining ability and stability studies for grain yield and quality parameters in QPM (*Zea mays* L.) inbred line crosses. *Indian Journal of Genetics*. 2010; 70(1):22-29.
 17. Vasal SK, Srinivasan G, Gunzalez CF, Hang GC, Crossa J. Heterosis and combining ability of CIMMYT tropical × subtropical maize germplasm. *Crop Science*. 1992; 32:1483-1489.
 18. Viola G, Ganesh M, Reddy SS, Kumar CVS. Study on heritability and genetic advances in elite baby corn (*Zea mays* L.) lines. *Progressive agriculture*. 2003; 3(2):127-128.