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STUDY OF GENETIC PARAMETERS AND ASSOCIATION ANALYSIS AMONG MAIZE (*ZEA MAIZE L.*) GERMPLASMS

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ABSTRACT

The eighty eight maize germplasm collections were used in present study during *Kharif-2012* and *Rabi-2012-13*. The value of GCV and PCV both was found to be high for the character ear height from the ground 21.43 and 21.27. Heritability can be estimated in broad sense which ranges from 17.40% to 98.50% in of prop root, high heritability coupled with high genetic advance was found for traits like ear height from ground (98.50% and 43.48), ear weight (94.90% and 23.56) and stem girth (97.40% and 37.02). Grain yield per plant had positive and significant correlation ($p < 0.01$) with plant height ($rG = 0.510$, $rP = 0.503$), 1000-seed weight ($rG = 0.827$, $rP = 0.816$) ear girth ($rG = 0.705$, $rP = 0.770$), number of kernels per row ($rG = 0.739$, $rP = 0.684$), ear length ($rG = 0.749$, $rP = 0.711$), ear weight ($rG = 0.959$, $rP = 0.947$), cob diameter ($rG = 0.770$, $rP = .730$) and biological yield ($rG = 0.942$, $rP = 0.708$). In view of all desirable traits, the maize germplasm *i.e.* JLM 22, JLM 27, JLM 28, JLM 30, JLM 35, JLM 39, JLM 50 for *desi* maize and VL 101123, VL 1031, Bulk line 22, CML 429, CML 472, CML 470, HKI for QPM lines were identified and can be utilized for crop improvement

INTRODUCTION

The highly cross pollinated cereal and C_4 type plant like Maize (*Zea mays* L.) is one of the top three cereal crops grown and consumed throughout the world (Soni and Khanorkar, 2013) after rice and wheat (Rekha *et al.*, 2015) for human whereas feed for livestock. The cultivation of maize in an area of 8.49 m ha⁻¹ with a production of 21.28 mt. and productivity of 2507 kg per ha⁻¹ (Rao *et al.*, 2014) also used as an industrial raw material to produce various types of by-products (Ali *et al.*, 2015). Germplasm (land races) acquire huge potential and most valuable gene which can be successfully utilized for development of high yielding or trait specific of maize varieties *viz.* Biotic stresses, abiotic stresses, quality protein etc. Variability is one of the basic requirements for any successful breeding program in selecting genotypes with desirable characters (Gurjar *et al.*, 2015). Opportunity of achieving improvement in any crop plants depends on the existing of genotypic and phenotypic variability and heritability in base population (Idahosa *et al.*, 2010) and their estimation with genetic advance is more helpful for predicting the genetic gains under selection and crop improvement to evolve advanced cultivars (Johnson *et al.*, 1955). Partitioning of overall variance due to genetic and non genetic causes become necessary for effective breeding programme. The present study focused on resolving the extent of genetic variability across the maize germplasm lines with the objective for assessment of genotypic and phenotypic variability, heritability, genetic advance and correlation for yield and its attributing traits consequently identification of suitable donor *viz.* high protein, high yielding genotypes for utilization in maize improvement.

MATERIALS AND METHODS

The investigational possessions of eighty eight Maize germplasm lines were received from Department of Genetics and Plant breeding (62 *desi* genotypes, collected from various parts of Madhya Pradesh) and CIMMYT (26 QPM based lines) in present study.

The experiment was conducted at Seed Breeding Farm during *Kharif-2012* and *Rabi-2012-13*, Department of Plant Breeding and Genetics College of Agriculture JNKVV Jabalpur which is situated in 'Kymore Plateau and Satpura hills' agro-climatic zone of Madhya Pradesh at 23.910 North latitude, and 79.50 East longitudes, at an altitude of 411.78 meters above the mean sea level.

These germplasm were sown in ridges and furrows during the experimental period in a Randomized Complete Block Design in three replications. Each variety was sown in 3 rows of 4 m length adopting a spacing of 60 (cm) between rows and 20 (cm) between the plants. All the recommended agronomic package of practices was adopted during the entire crop growth period. In each replication, five random plants were selected for the following 17 biometrical observations were recorded *viz.*, plant height (cm), ear height from ground (cm), days to male flower initiation, days to female flower initiation, days to 50% male flowering, days to 50% female flowering, days to maturity, ear length (cm), number of rows/ear, 1000-grain weight

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(g), ear weight (g), stem girth (cm), ear girth (cm), biological yield per/plant (g), harvest index (%), number of prop roots, cob diameter and grain yield per plant. Pooled data were employed for assessment of genetic variability and yield associated study. Correlation was performed using the software "Statistical package for Agricultural Research (SPAR 1.0)

RESULTS AND DISCUSSION

Genetic assortment is a source of variation and long-term selection achieve through genetic improvement and promote rational use of genetic resources. Reflection of the level of genetic variability for each of the traits were employed by standard statistics including the extreme genotype mean values and means with their standard errors obtained on the basis of average data are summarized in Table (2). The various yield and its components were undertaken in this study with keeping the foregoing points (a) Assessment of genetic variability and quantitative traits in 88 maize genotypes (b) Assessment of variance components and (c) estimation of heritability in broad sense and genetic advance and correlation among the various traits in maize germplasm.

(Table 2)

Assessment of genetic variability and quantitative traits

Maize genotypes showed wide range of variability for most of the characters and all the traits exhibited broad spectrum of ranges between the maximum and minimum genotype mean values. For instance Plant height ranged from 149.43 to 232.83 with a mean of 174.14, days to maturity ranged from 107.8 to 126.11 with a mean of 101.02, ear weight ranged from 69.00 to 304.90 with a mean of 110.29, days to flower initiation male ranged from 77.33 to 94.00 with the mean of 66.45, days to flower initiation female ranged from 80.55 to 96.89 with the mean of 70.37, days to 50% male flower initiation ranged from 78.33 to 95.00 with the mean of 67.66, days to 50% female flower initiation ranged from 81.33 to 97.33 with the mean of 71.51, ear length ranged from 9.00 to 20.53 with the mean of 14.67, rows/ear ranged from 10.67 to 20.00 with the mean of 13.55, 1000 kernel weight ranged from 13.83 to 35.67 with the mean of 23.61, stem girth ranged from 4.33 to 10.56 with the mean of 6.321. Similarly the characters like grain yield per plant ranged from 345.67 to 800.89 with the mean of 456.06 biological yield per plant ranged from 127.73 to 675.33 with the mean of 241.50, harvest index ranged from 18.58 to 48.40 with the mean of 37.85. The maximum grain yield per hectare obtain was 800.89 kg ha⁻¹. Thus, it is possible to succeed in improving grain yield by direct selection. The result of analysis of variance on 17 quantitative characters for the genotypes is presented in Table -1. Mean square of all the characters studied, showed significant difference ($P < 0.05$) among the tested genotypes except for grain yield per plant indicating the presence of variability which can be exploited through selection. Genetic diversity showed no significant association with days to maturity, plant height and seed index (Soni and Khanorkar, 2013)

Assessment of variance components

The values of phenotypic coefficient of variation (PCV) ranged

from (3.04 %) in days to 50% male flower initiation to (21.43%) in ear height from ground whereas, genotypic coefficient of variation (GCV) ranged from (2.8%) in days to maturity to (28.27%) in ear height from ground. Similar results were also obtained by Abirami *et al.*, (2005) and Kumar *et al.*, 2014 for ear height in maize. The relative magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation is comparable which indicate very little effect of environment among the traits. The PCV and GCV values roughly more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium. Based on this delineation the value of PCV and GCV both was found to be high for the character ear height from the ground, the high GCV value of this character suggests that there is possibility of improving this trait through selection. Similarly Kumar *et al.*, (2014), Nzuve *et al.*, (2014) and Reddy *et al.*, (2016) also reported highest GCV and PCV for ear height. Hence, this character can be relied upon and simple selection can be practiced for further improvement. Whereas it was recorded to be low for days to male flower initiation, days to female flower initiation, days to 50% male and female flower initiation, days to maturity, no. of rows per ear and ear length and it was found to be moderate for rest of the traits under study such as grain yield per plant, harvest index, cob diameter, biological yield per plant and 1000 kernel weight. The difference between the PCV and GCV values was high for character such as prop root % and no. of rows per ear indicating the influence of environment on these characters. However, this difference was low for the characters like ear height from the ground, grain yield per plant, stem girth ear weight, cob diameter, biological yield per plant, harvest index, 1000 kernel weight, plant height, days to male and female flower initiation, days to 50% male and female flowering and days to maturity suggesting minimal influence of environment on the expression of these characters, thereby having the highest estimates of heritability. Similar result was found by Yucel *et al.*, (2006) for days to flowering, plant height and harvest indexed in Table (3).

Inference of heritability in broad sense and genetic advance

Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence knowledge about genetic advance coupled with heritability is most useful. Character exhibiting high heritability may not necessarily give high genetic advance. Johanson *et al.* (1955) showed high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. Estimates of heritability in broad sense ranged from (17.40%) in case of prop root to (98.50%) for ear height from ground. According to Singh (2001), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. Although, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical due to the masking effect of environment. Considering this benchmark, heritability estimate was high (>80%) for characters plant height 95.30 % stem girth 97.40 %, ear weight 94.40 %,

Table 1: Analysis of variance for yield and yield components in maize.

Source of variation	Degree of freedom	PH	EH	DFI(M)	DFI(F)	D50%M	D50%F	DM	EL	Rows/ear	1000GW	EW	SG	CD	GYPP	BY	HI	PR
Replication	2	43.5	1.5	5.44	16.25	7.06	12.94	5.63	0.29	0.17	10.7	43.75	0.16	0.17	0.00	77.75	298	0.53
Treatment	87	2292.00**	2507.95**	45.60**	43.08**	48.02**	44.19**	84.10**	17.68**	11.76**	100.72**	3954.36**	7.97**	1.05*	0.72	2797.34**	22452.59**	321.28**
Error	122	10.78	5.58	1.09	1.23	1.55	1.66	1.4	0.49	0.73	1.63	9.06	0.04	0.02	0.06	8.95	94.64	7.45
CV	-	1.88	2.64	1.57	1.57	1.83	1.8	1.17	4.74	6.3	5.4	2.72	2.98	3.82	14.53	3.43	4.02	7.12

*, ** Significance at 5% and 1% probability level, respectively

Table 2: Ranges, means and standard errors of means (SEM) for various quantitative traits of maize germplasms.

Source of variation	PH	EH	DFI(M)	DFI(F)	D50%M	D50%F	DM	EL	Rows/ear	1000GW	EW	SG	CD	BY	HI	PR	GYPP
Minimum	149.43	60.67	77.33	80.55	78.33	81.33	107.8	9.00	10.67	13.83	69.00	4.33	3.94	127.73	18.58	0.00	345.67
Maximum	232.83	151.67	94.00	96.89	95.00	97.33	126.11	20.53	20.00	35.67	304.90	10.56	3.99	675.33	48.40	2.00	800.89
Avg. value	174.14	89.43	66.45	70.37	67.76	71.51	101.02	14.67	13.55	23.61	110.29	6.321	3.89	241.50	37.85	1.66	456.06
SEM	1.90	1.36	0.60	0.64	0.72	0.74	0.68	0.40	0.49	0.74	1.74	0.11	0.09	5.62	1.58	0.14	1.73

Note: PH = Plant Height, EH = Ear Height from ground, DFI(M) = Days to male flower initiation, DFI(F) = Days to female flower initiation, D50%M = Days to 50% male flower initiation, D50%F = Days to 50% female flower initiation, DM = Days to maturities, EL = Ear Length, Rows/ear = No. of rows per ear, 1000GW = 1000 kernel weight, EW = Ear weight, SG = Stem Girth, CD = Cob Diameter, GYPP = Grain yield per plant, BY = Biological yield, HI = Harvest Index, PR = Prop roots.

cob diameter 87.70 %, days to maturity 85.20 % and grain yield per plant 84.30 %. Vashistha *et al.*, 2013 also reported the similar findings in his studies for high heritability in case of plant height, ear height and grain yield per plant. It was moderate (40 to 80%) for the remaining quantitative characters. Table (3)

Genetic advance under selection (GA) refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001). Estimates of GA for grain yield was 84.45 kg ha⁻¹ indicating that whenever we select the best, 5 % high yielding genotypes as parents, mean grain yield of progenies could be improved by 84.45 kg ha⁻¹. Like wise it will be for rest the traits. Maximum genetic advance as percentage of mean (GAM) was recorded for characters like ear height (43.48%), stem girth (37.02%). It was minimum for no. of rows per ear (3.91%) and (4.92%) for days to 50% female flower initiation. Similarly Bekele and Rao, (2014) also reported high genetic advance as percentage of mean for ear height.

Expected genetic advance as per cent of mean indicates the mode of gene action in the expression of a trait, which helps in choosing an appropriate breeding method. According to Johnson *et al.* (1955), high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The present study reveals high heritability coupled with high expected genetic advance as percent of mean was found for traits like ear height from ground, ear weight and stem girth.

The high heritability coupled with high genetic advance noticed for these traits indicate the role of additive gene action in controlling the traits while non additive gene played a major role in expression of traits (Dar *et al.*, 2015) hence pedigree method of breeding will be a rewarding one to improve the traits under investigation these finding were similar with the work Maruthi *et al.*, 2015. Therefore, these characters could be improved more easily than the other characters.

(Table 3)

Correlation

The correlation coefficient between grain yield and its components and inter correlation among the different yield attributes were estimated. In general the phenotypic correlation coefficient was high in magnitude than genotypic correlation coefficients suggesting the apparent association of two characters is not only due to genes but also due to favorable influence of environment. Grain yield had positive and significant correlation (p<0.01) with viz. with plant height (rG = 0.510, rP = 0.503), 1000-seed weight (rG = 0.827, rP = 0.816) ear girth (rG = 0.705, rP = 0.770), number of kernels per row (rG = 0.739, rP = 0.684), ear length (rG = 0.749, rP = 0.711), ear weight (rG = 0.959, rP = 0.947), cob diameter (rG = 0.770, rP = .730), and biological yield (rG = 0.942, rP = 0.708) recorded highly and positive significant correlation with grain yield per plant, which mean it is favorable to the breeder and can help in simultaneous improvement of both the characters. These observations are in consistent with the findings of others for ear girth (Pavan *et al.*, 2011), number of kernels per row (Sadek *et al.*, 2006), ear length (Choudhary

Table 3: Estimates of mean, coefficients of variability, broad sense heritability and genetic advance for 17 characters under study

Source of variation	PH	EH	DFI(M)	DFI(F)	D50%M	D50%F	DM	EL	Rows/ear	1000 GW	EW	SG	CD	GYP	BY	HI	PR
CVPCV	8.47	21.27	3.19	2.83	3.21	2.83	2.8	4.24	3.74	8.99	11.75	18.24	10.21	14.04	10.62	9.77	6.66
GCV	8.68	21.43	3.56	3.24	3.70	3.36	3.04	6.37	7.33	10.49	12.06	18.48	10.91	14.46	11.35	12.14	15.99
h ² bs%	95.30	98.50	80.50	76.50	75.30	71.20	85.20	44.40	26.20	73.50	94.90	97.40	87.70	84.30	67.40	64.70	17.40
GA	29.66	38.88	3.92	3.59	3.89	3.52	5.38	0.85	0.53	3.75	25.99	2.34	0.77	84.45	49.38	6.13	0.10
GAM	17.03	43.48	5.89	5.10	5.74	4.92	5.32	5.79	3.91	15.88	23.56	37.02	19.84	28.10	20.44	16.67	5.99

*Significant at probability level of 0.05 and **significant at probability level of 0.01, h²bs % is heritability in broad sense, GA = genetic advance, GAM = genetic advance as % of mean, CV = coefficient of variation (%); Note: PH = Plant Height, EH = Ear Height from ground, DFI(M) = Days to male flower initiation, DFI(F) = Days to female flower initiation, D50%M = Days to 50% male flower initiation, D50%F = Days to 50% female flower initiation, DM = Days to maturities, EL = Ear Length, Rows/ear = No. of rows per ear, 1000GW = 1000 kernel weight, EW = Ear weight, SG = Stem Girth, CD = Cob Diameter, GYP = Grain yield per plant BY = Biological yield, HI = Harvest Index, PR = Prop root.

Table 4: Estimation of Genotypic & Phenotypic correlation coefficient of yield and its components traits .

Character	CM	Plant Height	Ear Height from ground	Days to male flower initiation	Days to female flower initiation	Days to 50% male flower initiation	Days to 50% female flower initiation	Ear Length	Rows per ear	1000 grain weight	Ear weight	Stem Girth	Cob Diameter	Biological yield plant ⁻¹	Harvest Index	Proproots yield plant ⁻¹	
Plant Height	rG	1.000	0.745**	-0.751**	-0.766**	-0.756**	-0.776**	0.746**	0.722**	0.616**	0.587**	0.753**	0.692**	0.593**	0.438	-0.159	
Ear Height from ground	rP	1.000	1.000	-0.725**	-0.743**	-0.732**	-0.756**	0.706**	0.674**	0.603**	0.573*	0.737**	0.646**	0.513*	0.428	-0.145	
Days to male flower initiation	rG		1.000	-0.667**	-0.697**	-0.698**	-0.710**	0.657**	0.713**	0.610**	0.594**	0.683**	0.662**	0.631**	0.402	-0.156	
Days to female flower initiation	rP		1.000	-0.642**	-0.667**	-0.653**	-0.682**	0.613**	0.649**	0.594**	0.571*	0.650**	0.623**	0.593**	0.386	-0.135	
Days to 50% male flower initiation	rG		1.000	0.993**	0.999**	0.999**	0.988**	-0.845**	-0.846**	-0.781**	-0.785**	-0.879**	-0.772**	-0.685**	-0.673**	0.145	
Days to 50% female flower initiation	rP		1.000	0.992**	0.999**	0.999**	0.986**	-0.782**	-0.796**	-0.765**	-0.762**	-0.843**	-0.724**	-0.629**	-0.664**	0.137	
Days to maturity	rG		1.000	0.994**	0.999**	0.998**	0.919**	-0.802**	-0.817**	-0.788**	-0.778**	-0.873**	-0.756**	-0.665**	-0.663**	0.170	
Ear Length	rP		1.000	0.991**	0.944**	0.991**	0.944**	-0.855**	-0.856**	-0.791**	-0.794**	-0.893**	-0.789**	-0.689**	-0.688**	0.148	
No. of Rows per ear	rG		1.000	0.957**	0.957**	1.000	0.957**	-0.872**	-0.880**	-0.811**	-0.811**	-0.922**	-0.807**	-0.724**	-0.689**	0.205	
1000 kernel weight	rP		1.000	0.929**	0.929**	1.000	0.929**	-0.817**	-0.831**	-0.801**	-0.795**	-0.891**	-0.768**	-0.685**	-0.673**	0.189	
Ear weight	rG		1.000	0.858**	0.858**	1.000	0.858**	-0.814**	-0.896**	-0.814**	-0.835**	-0.909**	-0.838**	-0.733**	-0.699**	0.183	
Stem Girth	rP		1.000	0.805**	0.805**	1.000	0.805**	-0.820**	-0.820**	-0.801**	-0.820**	-0.882**	-0.800**	-0.695**	-0.681**	0.172	
Cob Diameter	rG		1.000	0.715**	0.715**	1.000	0.715**	0.700	0.804**	0.754**	0.750**	0.841**	0.770**	0.692**	0.661**	0.211	
Biological yield plant ⁻¹	rP		1.000	0.715**	0.715**	1.000	0.715**	0.700	0.715**	0.715**	0.785**	0.708**	0.644**	0.644**	0.618**	-0.164	
Harvest Index	rG		1.000	0.796**	0.796**	1.000	0.796**	0.784**	0.796**	0.796**	0.883**	0.832**	0.832**	0.737**	0.620**	-0.252	
Proproots	rP		1.000	0.752**	0.752**	1.000	0.752**	0.746**	0.752**	0.752**	0.818**	0.746**	0.746**	0.653**	0.576**	-0.216	
	rG		1.000	0.844**	0.844**	1.000	0.844**	0.847**	0.844**	0.844**	0.847**	0.765**	0.765**	0.724**	0.730**	-0.175	
	rP		1.000	0.832**	0.832**	1.000	0.832**	0.826**	0.832**	0.832**	0.735**	0.735**	0.735**	0.689**	0.716**	-0.170	
	rG		1.000	0.812**	0.812**	1.000	0.812**	0.812**	0.812**	0.812**	0.812**	0.744**	0.744**	0.740**	0.889**	-0.198	
	rP		1.000	0.792**	0.792**	1.000	0.792**	0.718**	0.792**	0.792**	1.000	1.000	0.718**	0.702**	0.875**	-0.155	
	rG		1.000	0.792**	0.792**	1.000	0.792**	0.718**	0.792**	0.792**	1.000	1.000	0.718**	0.702**	0.875**	-0.155	
	rP		1.000	0.465**	0.465**	1.000	0.465**	0.785**	0.465**	0.465**	0.465**	0.785**	0.733**	0.733**	0.650**	-0.156	
	rG		1.000	0.695**	0.695**	1.000	0.695**	1.000	0.695**	0.695**	0.695**	1.000	1.000	0.695**	0.540**	-0.085	
	rP		1.000	0.862**	0.862**	1.000	0.862**	0.862**	0.862**	0.862**	0.862**	0.862**	0.862**	0.862**	0.862**	0.862**	0.862**
	rG		1.000	0.942**	0.942**	1.000	0.942**	0.942**	0.942**	0.942**	0.942**	0.942**	0.942**	0.942**	0.942**	0.942**	0.942**
	rP		1.000	0.823**	0.823**	1.000	0.823**	0.823**	0.823**	0.823**	0.823**	0.823**	0.823**	0.823**	0.823**	0.823**	0.823**
	rG		1.000	0.934**	0.934**	1.000	0.934**	0.934**	0.934**	0.934**	0.934**	0.934**	0.934**	0.934**	0.934**	0.934**	0.934**
	rP		1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	rG		1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	rP		1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

and Chaudhary, 2002), plant height (Zahra Amini *et al.* 2013 and Aminu *et al.*, 2014) and ear height (Raghu *et al.* (2011) and Krupakar *et al.* 2013; Ram Reddy *et al.* (2012); Ravi *et al.* (2012); Khodadad *et al.*, 2013); Mahesh *et al.*, (2013); Sudika *et al.* (2015). Genotypes are identified by considering yield attributing traits and its desirable traits, comparing with the checks foremost of characters, the best genotype was identified *viz.*, JLM 22, JLM 27, JLM 28, JLM 30, JLM 35, JLM 39, JLM 50 for desi maize and VL 101123, VL 1031, Bulk line 22, CML 429, CML 472, CML 470, HKI for QPM lines which can be further utilized for crop improvement programme. The diverse characters and their correlation with other traits are existing in table-4.

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REFERENCES

- Abirami, S., Vanniarajan, C. and Armugachamy, S. 2005. Genetic variability Studies in maize (*Zea mays* L.) germplasm. *Plant Archives*, 5(1): 105-108.
- Ali, Q., Ahsan, M., Qasrani, S. A. and Ramzan, I. 2015. Genetic Variability and Correlation Analysis for Various Morpho-Physiological traits in Maize (*Zea mays* L.) for Green Fodder Yield. *American-Eurasian J. Agric. and Environ. Sci.* 15(7): 1298-1303.
- Aminu, D., Mohammed, F. K. and Gambo, F. M. 2014. Heritability and correlation coefficients analysis of maize (*Zea mays* L.) agronomic traits for drought tolerance in Savanna zones of Borno State, Nigeria. *Science J. Agricultural Research and Management*. pp. 1-4.
- Ansuman, V., Dixit, N. N., Dipika, Sharma, S. K. and Markers, S. 2013. Studies on heritability and genetic advance estimates in Maize genotypes. *Bioscience Discovery*. 4(2): 165-168.
- Bekele, A. and Rao, T. N. 2014. Estimates of heritability, genetic advance and correlation study for yield and its attributes in maize (*Zea mays* L.). *J. Plant Sciences*. 2(1): 1-4.
- Choudhary, A. K. and Chaudary, L. E. 2002. Genetic studies in some crosses of maize (*Zea mays* L.). *J. Research Bisra Agricultural University*. 14: 87-90.
- Dahal, D., Chetri, B., Ghosh, J. and Chowdhary, N. 2015. Impact of bio-accelerated and conventional farming system on growth and yield of maize under rainfed condition. *Green Farming*. 7(2): 332-336.
- Dar, Z. A., Lone, A. A., Alaie, B. A., Ali, G., Gazal, A. and Abidi, I. 2015. Estimation of combining ability involving quality protein maize (qpm) inbreds under temperate conditions. *The Bioscan*. (Supplement on Genetics and Plant Breeding). 10(2): 863-867.
- Gurjar, D., Shailesh, M. and Meghawal, D. R. 2015. Estimation of variability parameters for yield and its contributing traits in wheat (*Triticum aestivum* (L.) EM. THELL). *The Ecoscan*. (Special issue). 7: 119-123.
- Idahosa, D. O., Alika, J. E. and Omoregie, A. U. 2010. Genetic variability, heritability and expected genetic advance as indices for yield and yield components selection in Cowpea (*Vigna unguiculata* (L.) Walp. *Academia Arena*. 2(5): 22-26.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybeans. *Agron. J.* 47: 314-318.
- Khodadad, M., Mahdi, G. and Saeid, K. K. 2013. Using correlation and some genetics methods to study of morphological traits in corn (*Zea mays* L.) yield and yield components under drought stress condition. *International Research J. Applied and Basic Sciences*. 4(2): 252-259.
- Kumar, G. P., Reddy, V. N., Kumar, S. S. and Rao, P. V. 2014. Genetic Variability, Heritability and Genetic Advance Studies in Newly Developed Maize Genotypes (*Zea mays* L.). *Int. J. Pure App. Biosci.* 2 (1): 272-275.
- Mahesh, N., Wali, M. C., Gowda, M. V. C., Motangi, B. N. and Nagaratna, F. U. 2013. Correlation and path analysis of yield and kernel components in maize. *Karnataka J. Agricultural Sciences*. 26(2): 306-307.
- Maruthi, R. T. and Rani Jhansi, K. 2015 Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. *J. Appl. and Nat. Sci.* 7(1): 149-154.
- Nzuve, F., Githiri, S., Mukunya, D. M. and Gethi, J. 2014. Genetic variability and correlation studies of grain yield and related agronomic traits in maize. *J. Agricultural Science*. 6(9): 166-176.
- Pavan, R., Lohithaswa, H. C., Wali Mc, Prakash, G. and Shekara, B. G. 2011. Correlation and path analysis of grain yield and yield contributing traits in single cross hybrids of maize (*Zea mays* L.). *Electronic J. Plant Breeding*. 2(2): 253-257.
- Raghu, B., Suresh, J., Sudheer Kumar, S. and Saidaiah, P. 2011. Character association and path analysis in maize (*Zea mays* L.). *Madras Agricultural J.* 98(1-3): 7-9.
- Ram Reddy, V., Seshagiri Rao, A. and Sudarshan, M. R. 2012. Heritability and character association among grain yield and its components in maize (*Zea mays* L.). *J. Research ANGRAU*. 40(2): 45-49.
- Rao, P. V., Subbaiah, G. and veeraghavaiah, R. 2014. Agronomic response of Maize to plant population and nitrogen availability-A review. *International J. Plant, Animal and Environmental Sciences*. 4:107-117.
- Ravi, V. M., Chikkalingaiah and Shailaja, H. 2012. Correlation study for protein content, grain yield and yield contributing traits in quality protein maize (*Zea mays* L.). *Electronic J. Plant Breeding*. 3(1): 649-651.
- Reddy, R. V. and Jbeen, F. 2016. Narrow sense heritability, correlation and Path analysis in Maize (*Zea mays* L.). *SABRAO Journal of Breeding and Genetics*. 48(2): 120-126.
- Rekha, Mohankumar, H. D. and Netravati. 2015. Combining ability for grain yield and yield component traits in maize (*Zea mays* L.). *The Ecoscan*, Special Issue. 7: 341-347.
- Sadek, S. E., Ahmed, M. A. and El-ghaney, H. M. 2006. Correlation and path coefficient analysis in five parent inbred lines and their six white maize (*Zea mays* L.). *J. Applied Sciences Research*. 2(3): 159-167.
- Singh, B. D. 2001. Plant Breeding: Principles and methods. *Kalyani Publishers*, New Delhi. p. 896.
- Krupakar, A., Kumar, B. and Marker, S. 2013. Combining ability for yield and quality traits in single cross hybrids of maize (*Zea mays* L.). *The Bioscan*, (Supplement on Genetics & Plant Breeding) 8(4): 1347-1355,
- Soni, N. V. and Khanorkar, S. M. 2013. Association of genetic divergence with heterosis, combining ability and mean value for quantitative traits in popcorn (*zea mays* var. *everta*). *The Bioscan*, (Supplement on Genetics and Plant Breeding) 8(4): 1363-1367.
- Sudika I, Wayan, N. B., Arifin, N. S. and Andy, S. 2015. Estimation of genetics variance components from composite and hybrid maize (*Zea mays* L.) hybridization. *International J. Plant Research*. 5(5): 107-112.

Yucel, D. O., Anlarsal, A. E. and Yucel, C. 2006. Genetic variability, correlation and path analysis of yield and yield components in chickpea. *Turk. J. Agric.* **30**: 183-188.

Zahra, A., Mahmood, K. and Houshmand, S. 2013. Correlation and path coefficient analysis of seed yield related traits in maize. *International J. Agriculture and Crop Sciences.* **5(19)**: 2217-2220.

