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Morphological Characters and Genetic Varibility Analysis of Inbreds of QPM Maize (*Zea mays* L.)

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Abstract

With the aim to assess the extent of genetic variability, heritability, genetic advance for yield and kernel quality traits in twenty five diverse QPM (Quality Protein Maize) inbred lines, the crop was raised at Research Farm, Tirhut College of Agriculture, DRPCAU, Pusa, Samastipur (Bihar) during *kharif* 2020.The trail were set up in randomized block design with three replications having plot size of 6 square meter. Analysis of variance revealed significant differences for 11 characters studied among the genotypes. The characters studied were viz. Days to 75% tasseling, Days to 75% silking, Days to 75% brown husk, Plant height (cm), Ear height (cm), Ear length (cm), Ear girth (cm),Tassel length (cm), Number of kernel rows per ear, Number of kernels per row and Grain yield (Kg/ha). Genetic variability parameter showed that phenotypic coffecient of variation (PCV) was higher than the respective genotypic coefficient of variation (GCV). High magnitude of GCV and PCV was observed for Grain yield (kg/ha) indicating the importance of these traits in evaluation and selection of inbred lines for yield improvement under maize breeding programme. Data recorded for heritability showed that High heritability accompanied with high genetic advance as percent of mean was recorded for ear length, plant height, ear height and grain yield indicating effectiveness of selection due to preponderance of additive gene action and breeder may consider these traits as main selection criteria.

Key words : *QPM, genetic variability, heritability and genetic advance percentage of mean*

Introduction

Maize is one of the most important cereal crop in the world after rice and wheat. Apart from its pivotal role in world's economy and trade as a food, feed and industrial input it is widely explored as a model cropfor various genetic studies (1). QPM caters to the need of billions of people worldwide for proteins and calories requirement, particularly, in Africa, South America and Asia. It is cultivated in a wider range of environments than wheat and rice because of its greater adaptability (2). It is grown at latitudes varying from the equator to slightly north and south of latitude 500, at meter elevation from sea level to over 3000 meters above sea level under heavy rain-fed and semi-arid conditions, and cold and very hot climates.

Maize is a low cost and rich repository of carbohydrates, fats, proteins, vitamins and minerals and therefore it is also called 'poor man's nutricereal' (3). Protein from cereals including normal maize, have poor nutritional value because of reduced content of essential amino-acids such as lysine and tryptophan leading to harmful consequences such as growth retardation, protein energy malnutrition, anemia, pellagra, free radical damage etc. Normal maize varieties are deficient to two essential amino acids, lysine and tryptophan (4). Maize mutants for high lysine and tryptophan have been reported in several studies.

The lysine and tryptophan content in normal maize varieties is less than a half of the recommended rate for human nutrition. This problem has been addressed through research breakthroughs at CIMMYT in the late 1990's that lead to the development of quality protein maize (QPM) that content twice the amount of lysine and tryptophan.

Genetic improvements in traits of economic importance, along with maintaining sufficient amount of variability are always the desired objectives in maize breeding programs. Genetic variability is the primary need for sound plant breeding approach for realizing higher economic yield because selection and its success would depend on the availability of wider genetic variability.

Therefore, an assessment of genetic variability is a pre-requisite for basic step in breeding and essential for genetic improvement of any character.

It is well known that high heritability estimates coupled with high genetic advance provide a great scope for making efficient selection among the different existing lines. A relative comparison of heritability and expected genetic advance gives an idea about the nature of gene action. Genetic advance as per cent of mean gives performance of genotypes due to selection of superior genotypes. Information on the genetic parameters such as coefficient of variation, heritability, genetic advance and the influence of environment on the expression of

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Table-1 : List of the Materials and their Source.

S. No.	Inbred lines	Abbreviation	Source
1.	[CL-G2501*CML170]-B-2-2-2-B-1-1-BBB-#	CLG-2501-170	AICRP, Dholi, Centre
2.	CML161*165-18-2-1-2-BBB-#	CML61*65-18	AICRP, Dholi, Centre
3.	CML161*165-50-1-3-B*4-#	CML61*65-50	AICRP, Dholi, Centre
4.	(CML161*165)-F2-21-3-1-B*5-#	CML61*65-21	AICRP, Dholi, Centre
5.	(CML176*CLG2501)-B-55-1-5-2-BBB-#	CML*CLG-55	AICRP, Dholi, Centre
6.	(CML165*CL-02843)-B-12-2-4-B-3-BBB-#	CML*CL02843-12	AICRP, Dholi, Centre
7.	(CLQ-6601*CL-02843)-B-23-2-1-B-1-BBB-#	CLQ*CL-23	AICRP, Dholi, Centre
8.	(CLQ-6601*CL-02843)-B-26-1-1-BB-1-B*6-#	CLQ*CL-26	AICRP, Dholi, Centre
9.	P70C0-BBB-6-B*6-#	P70C0-6	AICRP, Dholi, Centre
10.	CLQ-RCYQ28-B-3-B*6-#	CLQ-RCYQ-28	AICRP, Dholi, Centre
11.	CLQ-RCYQ41-BB-2-B*6-#	CLQ-RCYQ-41	AICRP, Dholi, Centre
12.	CLQ-RCYQ035-B*11-#	CLQ-RCYQ-035	AICRP, Dholi, Centre
13.	CLQ-RCYQ12-B-1-B*6-#	CLQ-RCYQ-12	AICRP, Dholi, Centre
14.	CML161*165-3-2-3-B*4-#-B1	CML61*65-B*4	AICRP, Dholi, Centre
15.	G34QC24-BBB-16-B*8-#-B	G34QC-BB-16	AICRP, Dholi, Centre
16.	POO117C8(TEYFQPM)-B-117-B*10	POO-TEYFQM	AICRP, Dholi, Centre
17.	CML161*165-16-2-1-B*10	CML61*65-16	AICRP, Dholi, Centre
18.	G33QMH103-3-1-5-1-B*14	G33QMH-103	AICRP, Dholi, Centre
19.	(CML176*CLG2501)-B-55-1-2-B*4	CML76*CLG-B*4	AICRP, Dholi, Centre
20.	CLQRCYQ44-B*4-1-#-B	CLQ-RCYQ-44	AICRP, Dholi, Centre
21.	CML161-1-B*8-#-B	CML61-B*8	AICRP, Dholi, Centre
22.	CML451Q-B*8	CML451-B*8	AICRP, Dholi, Centre
23.	CML165-B*9-#	CML65-B*9	AICRP, Dholi, Centre
24.	CML193-B*6-#	CML93-B*6	AICRP, Dholi, Centre
25.	(CML161*CLQ-RCYQ31)-B-22-2-B*5	CML61*CLQ-B*5	AICRP, Dholi, Centre

yield and yield components will help the breeder to evolve suitable cultivars within short time. Therefore, Keeping this back ground in view, the present study was undertaken to analyze the variance, genetic variability, heritability, genetic gain among 25 elite genotypes of maize.

Materials and Methods

The present investigation was carried out at the Research Farm, Tirhut College of Agriculture, DRPCAU, Pusa, Samastipur (Bihar) during *kharif* 2020. The breeder seed of twenty five genotypes of high quality protein maize were obtained from AICRP, Dholi (Table-1). Twenty five diverse genotypes were raised in randomized block design with three replications having plot size of 1.5 x 4.0 = 6 $m^{2.}$ Each plot consisting of two rows of 4m length spaced at 75 cm row to row and 20 cm plant to plant, respectively. All the recommended package of practices were applied to raise a good and healthy crop. The data were recorded on five randomly selected plant samples from each replication for different quantitative characters, *viz.* plant height, Ear height, Days to 75 % tasseling, Days to 75% silking, Days to 75 % Brown husk, Tassel length, Cob length, Cob diameter, No. of kernel rows per ear, No. of kernels per row, and Grain yield (kg/ha). Out of the 11 quantitative characters, days to 75% tasseling, days to 75% silking and days to 75% brown husk were recorded on plot basis. Rest of the traits was recorded on the basis of five randomly chosen plants at appropriate stage.The data recorded on different characters were statistically analyzed using software WINDOSTAT version 7.0 developed by Indostat Services Ltd., Hyderabad, India. The analysis of variance for Randomized Block Design was carried out on the basis of the model described by (5) for individual characters. To estimate the extant of magnitude of variation among examined traits.

Results and Discussion

Success of a breeding programme largely depends on the extent of genetic variability present in the material, greater the diversity in the material better the chances for evolving promising and desired types. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. The genotypic components being the heritable part of the total variability, its magnitude for yield and related characters influence the selection strategies to be adopted by the breeders. Morphological markers differ among species, genus and varieties of plants. It is the easiest and quickest way to identify or detect the variation in morphological traits for improvement. However, these traits are largely affected by

Table-2 : Analysis of variance for eleven characters in QPM inbred lines.

S. No.	Source of Variation	Mean sum of squares		
	Characters	Replication (df=2)	Treatment (df=24)	Error (df=48)
1.	Plant Height (cm)	130.54	808.73**	111.14
2.	Ear Height (cm)	22.48	316.72**	25.5
3.	Days to 75 % tasseling	51.25	29.98**	5.98
4.	Days to 75 % silking	44.01	25.22**	3.99
5.	Days to 75 % Brown husk	7.41	9.05**	3.98
6.	Tassel length (cm)	0.68	18.65**	5.06
7.	Ear length (cm)	4.79	16.25**	1.18
8.	Ear girth (cm)	4.40	3.60**	1.02
9.	No. of kernel rows per ear	1.51	3.56**	2.90
10.	No. of kernels per row	12.77	26.48**	8.02
11.	Grain yield (kg/ha)	106247.10	794520.29**	82309.70

** Significant at P = 0.01

Table-3 : Mean, range and coefficient of variation for various characters in QPM inbred lines.

S.No.	Character	Mean	S.E	Range		C.V.
				Min	Max	
1.	Plant Height (cm)	120.59 ± 6.08	6.08	93.33	145.16	8.74
2.	Ear Height (cm)	55.17 ± 2.91	2.91	32.50	77.50	9.15
3.	Days to 75 % Tasseling	56.17 ± 1.28	1.28	49.33	60.66	3.97
4.	Days to 75 % Silking	59.33 ± 1.15	1.15	53.66	63.66	3.36
5.	Days to 75 % Brown Husk	93.77 ± 1.15	1.15	90.00	97.00	2.12
6.	Tassel length (cm)	28.82 ± 1.29	1.29	24.03	32.53	7.80
7.	Ear length (cm)	17.25 ± 0.62	0.62	13.43	22.58	6.29
8.	Ear girth (cm)	12.71 ± 0.58	0.58	11.23	15.78	7.96
9.	No. of kernel rows/ear	13.60 ± 0.98	0.98	12.00	16.23	12.50
10.	No. of kernels /row	29.29 ± 1.63	1.63	24.16	35.66	9.67
11.	Grain yield (kg/ha)	2105.38 ± 165.63	165.63	1211.75	3081.55	13.62

environmental variations until and unless these are studied minutely over locations and variable environmental conditions *viz.,* temperature and climate.

Analysis of variance : The analysis of variance for the design of an experiment (Table-2) indicated the existence of significant variability among the 25 genotypes of maize for all the characters under study. The presence of large amount of variability is due to diverse source of the material as well as environmental influence, which pre-dominantly governed the phenotype. The variability was highly significant for grain yield (kg/ha) followed by plant height, ear height, days to 75 % tasseling, No. of kernels per row, days to 75 % silking, tassel length, ear length. Existence of these significant differences amongst the inbred lines indicated the presence of considerable phenotypic and genotypic differences and thus, the presence of variability in present investigation indicated the ample scope of selection for these traits. It is apparent that differences among the inbred lines were observed due to differences in the genes carried by different genotypes and interaction of different gene combinations possessed by different inbred lines with the environment to which the genotypes were exposed. The difference in magnitude of phenotypic and genotypic variance among all eleven characters indicated that environment have played some role in the expression of characters. These results are in accordance with the results of (6,7,8).

Mean performance : A perusal of the data on mean values of twenty five maize inbred lines (Table-3) indicated Mean performance of different inbredlines revealed that the best inbred line for grain yield (Kg/ha) was CLQ-RCYQ-28. It was highest yielder having superior in ear length, ear girth and having moderate no. of kernel rows per ear followed by CML65-B*9 and the inbred line CML61-65-18 showed lowest in grain yield among all inbred lines. The best inbred lines for anthesis- silk interval showed early in days to 75% tasseling and silking were CML-373 (55.67, 58.67) whereas the inbred line WNC DMR 11 R 4776 (60.33, 64.00) showed very late anthesis-silk interval among all inbred lines. The best inbred line for early in days to 75% brown husk was CLQ*CL-23 and inbred line CML93-B*6 (97.00) was late in days to 75% brown husk among all other inbred lines. The best inbred line for dwarf in plant height was CML61*65-50 and inbred CLG2501-170 was tallest among inbred lines. The best inbred lines for significantly lower ear height was

Table-4 : Mean performance of twenty five QPM inbreds for eleven characters.

Character Genotype	Plant Height (cm)	Ear Height (cm)	Day to 75 % Tasseling	Day to 75 % silking	Day to 75 % Brown husk	Tassel length (cm)	Ear length (cm)	Ear girth (cm)	No. of kernel rows/Ear	No. of kernels/ Row	Grain yield (kg/ha)
1	145.16	57.83	51.33	55.00	90.33	27.15	19.51	13.36	13.00	32.00	2509.17
2	144.16	55.66	58.00	60.66	94.33	28.73	18.98	14.75	12.33	31.33	2378.97
3	93.33	32.50	55.66	59.33	93.33	28.66	13.78	11.33	12.00	24.16	1211.75
4	141.83	59.60	54.33	58.00	93.33	31.36	16.01	12.85	12.66	29.83	1868.93
5	112.83	55.16	60.66	63.33	95.66	29.78	16.41	12.30	13.33	27.83	1584.68
6	97.83	50.26	56.00	60.33	94.66	32.53	18.51	12.23	12.50	24.56	1426.25
7	124.16	55.90	49.33	53.66	90.00	30.38	18.23	13.33	14.23	33.16	2944.07
8	118.66	56.66	59.33	61.00	94.00	32.26	16.20	11.23	13.56	30.66	2130.84
9	113.66	48.33	53.33	56.33	92.33	29.26	16.15	11.96	14.43	33.00	2834.82
10	118.53	52.26	58.00	61.66	94.33	27.48	22.58	15.78	13.06	27.33	3081.55
11	116.83	53.83	53.66	57.33	93.33	32.21	18.18	12.41	13.76	28.50	1754.90
12	97.16	48.00	54.66	56.66	93.66	24.13	17.38	12.85	12.53	35.66	2431.90
13	122.10	53.33	52.66	56.00	91.66	24.03	13.43	11.26	13.06	28.16	1534.50
14	108.33	42.26	59.66	63.00	94.33	29.05	15.55	12.40	15.43	25.00	2229.94
15	100.50	43.40	55.33	58.33	93.00	29.21	14.15	12.20	13.56	26.83	1568.00
16	122.66	50.16	57.33	59.33	94.33	25.43	18.36	11.90	16.23	25.50	2298.06
17	143.26	68.56	59.66	62.33	95.66	32.13	16.25	14.15	14.00	26.83	1609.39
18	97.90	50.03	58.00	61.66	94.66	28.13	14.16	12.70	14.20	29.66	1829.91
19	115.10	48.50	53.33	56.66	93.00	28.76	19.18	11.96	13.56	27.50	1658.31
20	136.73	75.60	60.33	63.66	95.33	29.30	16.78	14.16	12.86	29.66	1927.13
21	111.00	58.66	54.33	57.33	93.00	26.31	16.88	12.86	13.36	30.66	2123.70
22	139.03	77.50	52.33	56.00	91.33	29.61	20.60	12.38	16.00	29.50	2347.11
23	119.16	49.76	58.66	62.00	96.00	30.93	21.43	13.25	14.40	33.33	2988.23
24	141.00	68.36	60.33	62.66	97.00	28.98	16.06	12.51	12.53	31.50	2326.78
25	133.83	67.10	58.00	61.00	95.66	24.61	16.63	11.76	13.53	30.16	2035.6400
Mean	120.59	55.17	56.17	59.33	93.77	28.82	17.25	12.71	13.60	29.29	2105.38
SEm (±)	6.08	2.91	1.28	1.15	1.15	1.29	0.62	0.58	0.98	1.63	165.63
CD 5 %	17.30	8.28	3.66	3.27	3.27	3.69	1.78	1.66	1.71	4.65	470.99

1	CLG-2501-170	6	CML*CL02843-12	11	CLQ-RCYQ-41	16	POO-TEYFQM	21	CML61-B*8
2	CML61*65-18	7	CLQ*CL-23	12	CLQ-RCYQ-035	17	CML61*65-16	22	CML451-B*8
3	CML61*65-50	8	CLQ*CL-26	13	CLQ-RCYQ-12	18	G33QMH-103	23	CML65-B*9
4	CML61*65-21	9	P70C0-6	14	CML61*65-B*4	19	CML76*CLG-B*4	24	CML93-B*6
5	CML*CLG-55	10	CLQ-RCYQ-28	15	G34QC-BB-16	20	CLQ-RCYQ-44	25	CML61*CLQ-B*5

cml61*65-18 and inbred line CML451-B*8 showed higher ear height among rest of inbred lines. The best inbred line for maximum ear length was CLQ-RCYQ-28 and inbred line CLQ-RCYQ-12 showed minimum in ear length among all other inbred lines. The best inbred line for maximum in ear girth was CLQ-RCYQ-28(15.78 cm) and inbred line CLQ-CL-26 showed minimum ear girth among the inbred lines. The best inbred line for maximum in number of kernel rows per ear were POO TEYFQM followed by CML451-B*8, CML61*65-B*4 and the inbred line CML61*65-50 showed minimum number of kernel rows per ear among all inbred lines. The best inbred lines for maximum number of kernels per row was CLG-2501-170 followed by CML61*65-18 and inbred line CML61*65-50 showed minimum number of kernels per row among all the inbreds.

Genetic variability for yield and component traits : Environment has great influence on many quantitative and qualitative traits of plants. This influence showed heritable and non-heritable variation, which can be estimated by the parameters like genotypic coefficient of variation (GCV), heritability and genetic gain. Mean standard error, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic gain as percentage of mean were given in table-4. For all the eleven characters phenotypic variance

Table-5 : Genetic parameters, heritability and genetic advance as per cent of mean of various characters in QPM inbred lines.

S. No.	Characters	^{2}g	^{2}p	GCV	PCV	h^{2} (Broad sense) %	GA as % of Mean
1.	Plant Height (cm)	232.53	343.67	12.64	15.37	68	21.42
2.	Ear Height (cm)	97.08	122.57	17.86	20.07	79	32.74
3.	Days to 75 % Tasseling	8.33	13.31	5.84	6.49	63	8.37
4.	Days to 75 % Silking	7.08	11.06	4.48	5.61	64	7.38
5.	Days to 75 % Brown Husk	1.69	5.67	1.39	2.54	30	1.55
6.	Tassel length (cm)	4.53	9.59	7.38	10.75	47	10.44
7.	Ear length(cm)	5.02	6.20	12.99	14.43	81	24.07
8.	Ear girth (cm)	0.86	1.88	7.28	10.79	45	10.11
9.	No. of kernel rows/Ear	0.22	3.12	3.45	12.97	07	1.89
10.	No. of kernels /row	6.15	14.18	8.46	12.85	43	11.48
11.	Grain yield (kg/ha)	237403.5	319713.2	23.14	26.86	74	41.08

was higher than its corresponding genotypic variance. This may be due to non-genetic factor which played some role in manifestation of these characters. High genotypic coefficient of variation and high phenotypic coefficient of variation were recorded for grain yield (kg/ha) indicating the importance of these traits in development and selection of inbred lines. Characters having moderate genotypic coefficient of variability was recorded for ear height (cm),ear length (cm) ,plant height (cm) and moderate phenotypic coefficient of variation were recorded for plant height (cm), ear height (cm), number of kernel rows per ear and number of kernels per rows ,ear length (cm), tassel length (cm), ear girth (cm). The present findings are in accordance with the earlier findings of (6,7,9,10,11) in maize.

Heritability and genetic advance : Heritability and genetic advance were regarded as important selection parameters. Genetic variation along with heritability estimates would give a better idea about the efficiency of selection. Heritability measures transmission of hereditary values from parent to their offspring. It is most important factor that determines the genetic improvement or response to selection. The estimates of heritability help the plant breeder in selection of elite characters from diverse genetic populations. The higher value of the heritability estimates are advantageous where improvement is sought through phenotypic selection. Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. High heritability was recorded for ear length, ear height, grain yield (kg/ha), Plant height, 75 % silking and 75 % tasseling (Table-5). Characters having moderate heritability were recorded for days to 75% brown husk, tassel length, ear girth and No. of kernels per row. However, low heritability was recorded for number of kernel rows per ear. Similar findings were recorded by (6,12,13,14) in maize. High heritability accompanied with low genetic advance as percent of mean was observed for days to 75% tasseling and days to 75% silking indicated that most likely heritability is due to non-additive gene action and the high heritability was being exhibited due to favourable influence of environment rather than genotypes and selection for these traits may not be rewarding. Similar finding were recorded for these characters in maize by (14). Low heritability coupled with low genetic advance was recorded for Number of kernel rows per ear and days to 75% brown husk indicates that the character is highly influenced by environmental effects and selection would be ineffective. Similar results were obtained by (9) in maize.

References

1. Ambhure, R.G.,Patil, K.H. and Mahajan, R.C. (2020). Combining ability analysis for yield and yield components in single cross hybrids of Maize (*Zea mays). Frontiers in Crop Improvement,* Vol. 8(1): 45-48.
2. Koutsika-Sotiriou M. (1999). Hybrid seed production in maize.*In* Basra, A.S. (2ed) Heterosis and Hybrid Seed Production in Agronomic Crops, Food Products.
3. Prasanna B.M., Vasal S.K., Kassahun B. and Singh N.N. (2001). Quality protein maize. *Current Scencei,* 81: 1308-1319.
4. Azevedo R.A., Lea P.J., Damerval C., Landry J., Bellato C.M., Meinhardt L.W., Le Guilloux M., Delhaye S., Varisi V.A., Gaziola S.A., Gratao P.L. and Toro A.A. (2004). Regulation of lysine metabolism and endosperm protein synthesis by the opaque-5 and opaque-7 maize mutations.*J. Agric. Food Chem.,* 52: 4865-4871.
5. Panse V.G. and Sukhatme P.V. (1967).Statistical methods of Agricultural Research Works.*III edition, ICAR,* New Deihi. PP.146.
6. Om Prakash, Shanthi P., Satyanarayana E. and Saikumar R. (2006). Studies on genetic variability exploitation for quality traits and agronomic characters on quality protein maize (QPM) germplasm (*Zea mays* L.).*Annals of Agricultural Research,* 27(2): 147-153.
7. Umar U.U., Abdulrahman M.D. and Abdullahi S. (2016). Assessment of genetic variability of maize inbred lines and their hybrids under normal and drought conditions. *Nigeria Agricultural Journal,* 46(2): 82-88.

8. Beulah G., Marker S. and Rajasekhar D. (2018). Assessment of quantitative genetic variability and character association in maize (*Zea mays* L.), *Journal of Pharmacognosy and Phytochemistry,* 7(1): 2813-2816.
9. Murugan S., Padmanaban J. and Manirajan S. (2010). Genetic variability and heritability studies in F2 and F3 generations of QPM and Non-QPM maize crosses. *International Journal of Plant Sciences, Muzaffarnagar,* 5(1): 290-293.
10. Sharma R., Maloo S.R. and Joshi A. (2014). Genetic variability analysis in diverse maize genotypes (*Zea mays* L.). *Electronic Journal of Plant Breeding,* 5(3): 545-551.
11. Arunkumar B., Gangapp E., Ramesh S., Savithramma D.L. and Nagaraju N. (2020). Study of genetic variability and its organization in Maize (*Zea mays)* inbred lines. *Frontiers in Crop Improvement*, 8(2): 97-100.
12. Aboyi I.K., Ojo A.A., Kalu B.A. and Adeyemo M.O. (2004). Genetic variability, heritability and genetic advance in progenies of extra-early and early maize (*Zea mays* L.) populations. *Journal of Sustainable Agricultural and Enviroment,* 6(2): 179-184.
13. Vashistha A., Dixit N.N., Sharma S.K. and Marker S. (2013) Studies on heritability and genetic advance estimate in maize genotypes.*Bioscience Discovery,* 4(2): 165-168.
14. Kumar P.G., Reddy N.V., Kumar Sudheer and Rao V.P. (2014). Genetic variability, heritability and genetic advance studies in newly developed maize genotypes (*Zea mays* L.). *International Journal of pure and applied Bioscience,* 2(1): 272-275.