International Journal of Advanced Biochemistry Research 2025; SP-9(12): 1666-1669

International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(12): 1666-1669
www.biochemjournal.com
Received: 17-09-2025
Accepted: 20-10-2025

Vaibhav G Gulhane
Department of Plant Breeding and Genetics, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India

Dr. Ashish Narayan
Department of Plant Breeding and Genetics, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India

Genetic variability, heritability and genetic advance studied in quality protein maize inbreds (*Zea mays* L.)

Vaibhav G Gulhane and Ashish Narayan

DOI: https://www.doi.org/10.33545/26174693.2025.v9.i12St.6782

Abstract

An experiment was conducted with thirty inbred lines of Quality Protein Maize to determining genetic variability, heritability and genetic advance for traits selection. Analysis of variance revealed highly significant differences among the genotypes for all the fifteen characters. From the variability studies, high magnitude of PCV and GCV were observed for traits like yield per plot followed by peduncle length, 100 kernel weight indicating that these traits could be used for yield improvement under maize breeding programme. In the present set of materials, high heritability with high genetic advance as *per cent* of mean was recorded for yield per plot, 100 kernel weight, peduncle length indicating effectiveness of selection due to preponderance of additive gene action for these traits and direct selection may be effective.

Keywords: PCV, GCV, heritability, genetic advance, QPM

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crop as it's contributed to food basket of world is maximum. Maize belongs to C_4 plant and physiologically efficient to use CO_2. Maize has great potential of higher grain yield. There are no other cereal's which has so much potentiality as the maize crop has and that is why it is called "Queen of Cereals" (Prassanna *et. al.* 2001) [12].

The scope of crop improvement is determined by the amount of heritable variation relative to that of non-heritable or environmental variation and by the natural and magnitude of genotype-environment interaction. Breeding methods are detected by the action, interaction and linkage relationship of gene conditioning continuous phenotypic variation of various metric traits. Both additive and non-additive components of genetic variance, along with their allied parameters are of use for plant breeders under different situation. Actually, the estimates of additive and non-additive variance provide a measure of how likely particular traits are being selected.

Greater the variability, more are the chances of getting desired types. Partitioning of the variability into heritable and non-heritable components helps in effectiveness of selection. High heritability with high genetic advance indicates additive gene action, where as high heritability with low variability and genetic advance suggest for non-additive gene action.

Thus the information on nature and relative magnitude of genetic components of variation (additive and non-additive) of character is essential for deciding an effective breeding programme for its genetic improvement. The information on character association for yield and its attributes in QPM is very much essential. The present experiment was conducted with thirty inbred lines of Quality Protein Maize for determining genetic variability, heritability and genetic advance for traits selection.

Materials and Methods

The experiment was conducted with thirty inbred lines derived from different maize populations at TCA, Dholi farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, during *kharif* 2012, within Randomized Block Design (RBD) with 3 replications. Each plot consisting of two rows of 4m length spaced at 60 cm row to row and 25 cm plant to plant, respectively. Brief description of the genotypes has been presented in (Table 1).

Corresponding Author:
Vaibhav G Gulhane
Department of Plant Breeding and Genetics, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India

The observation during present investigation were recorded on five competitive plants were randomly taken from each plot in each replication for recording data of the traits, namely, tessel length, plant height, ear height, leaves above ear, total number of leaves, ear length, peduncle length, ear diameter, number of kernel per row, number of kernel per ear, 100-kernel weight and ear weight. Traits, days to 50% silking, days to 50% tesseling and yield per plot were recorded on plot basis.

Genetic parameters GCV, PCV, heritability and GA were estimated by as described by Robinson *et al.* (1949) [13], Johnson *et al.* (1955) [7] and Sivsubramanian and Menon (1973) [14].

Table 1: List of the Materials and their Source

Sr. No.	QPM Inbreds	Source
1.	2007-1-CML-469	TCA, DHOLI
2.	2006-6-CML-471	TCA, DHOLI
3.	CML-196	TCA, DHOLI
4.	CML-163-7-2	TCA, DHOLI
5.	CML-169	TCA, DHOLI
6.	CML-165	TCA, DHOLI
7.	Dholi QPM-2009	TCA, DHOLI
8.	69-828 K CML-115	TCA, DHOLI
9.	POP-61-CL-QPM TEYF-S4-2-2-1-2-B-2-B-B	TCA, DHOLI
10.	POP-61-CL-QPM TEYF-S4-2-2-2-2-B-2-B-B	TCA, DHOLI
11.	POP-61-CL QPM TEYF-S4-2-2-2-2-B-1-B-B	TCA, DHOLI
12.	POOL-17 QPM-S6	TCA, DHOLI
13.	2006-6-CML-471	TCA, DHOLI
14.	DMR QPM-17-1	TCA, DHOLI
15.	DMR-QPM-03-119-2	TCA, DHOLI
16.	DMR-QPM-03-119-4	TCA, DHOLI
17.	DMR-QPM-03-107-1	TCA, DHOLI
18.	DMR-QPM-03-103-6	TCA, DHOLI
19.	DMR-QPM-03-103-7	TCA, DHOLI
20.	DMR-QPM-03-103-9	TCA, DHOLI
21.	DMR-QPM-03-103-10	TCA, DHOLI
22.	DMR-QPM-03-103-11	TCA, DHOLI
23.	DMR-QPM-03-103-12	TCA, DHOLI
24.	DMR-QPM-03-103-17	TCA, DHOLI
25.	DMR-QPM-03-115-#-10-3	TCA, DHOLI
26.	DMR-QPM-03-118-#-29-2	TCA, DHOLI
27.	CML-411	TCA, DHOLI
28.	DMRO-QPM-03-124	TCA, DHOLI
29.	DMR-QPM-S8-26	TCA, DHOLI
30.	CML-161	TCA, DHOLI

Results and Discussions

Analysis of variance

The analysis of variance presented in table 2. Revealed that mean square due to genotypes were highly significant for all the character under study which indicated that there were inherent genotypic differences among the genotypes. Character mean value, range and coefficient of variation has been presented in (Table 3) for all the fifteen characters. Considerable range of variation was observed for all the traits indicating scope for improvement in desired direction.

Genotypic and Phenotypic variance

The assessment of genotypic and phenotypic variance, GCV, PCV, heritability and genetic advance as *per cent* of mean in the material under study for the fifteen quantitative characters are presented in (Table 4). For all the fifteen characters phenotypic variance was higher than its corresponding genotypic variance. The difference in magnitude of phenotypic and genotypic variance among the above mentioned characters indicated that environment have played some role in the expression of characters.

High genotypic and phenotypic coefficient of variation were recorded for yield per plot (37.23, 39.30), peduncle length (23.63, 28.78), 100 kernel weight (23.34, 23.36), ear weight (21.23, 22.46), number of kernel per row (19.93, 20.87) and ear height (18.29, 20.00).

Characters having moderate genotypic and phenotypic coefficient of variability were tassel length (15.07, 16.19), plant height (14.97, 16.19) and ear length (12.81, 14.76). While some characters like leaves above ear (8.07, 15.64), number of kernel row per ear (7.85, 10.23), total number of leaves (9.14, 12.13) and ear diameter (9.84, 11.01) exhibited low genotypic coefficient with moderate phenotypic coefficient.

However, low genotypic and phenotypic coefficient of variability was recorded for days to 50% silking (7.79, 7.93) and days to 50% tasseling (7.81, 7.91).

Heritability and Genetic advance

The estimate of heritability in broad sense (Table 4) for most of the characters were recorded high as 100 kernel weight (97.54%) followed by the days to 50% tasseling (97.43%), days to 50% silking (94.54%), number of kernel per row (91.21%), peduncle length (90.96%), yield per plot (89.75%), ear weight (89.33%), tassel length (86.63%), plant height (85.52%), ear height (83.62%), ear diameter (79.91%), ear length (75.29). However, the moderate heritability estimates were recorded for number of kernel row per ear (58.84%), total number of leaves (56.81%) and low heritability estimate were recorded only by number of leaves above ear (26.66%).

Estimate of genetic advance as percent of mean ranged from 8.57 to 72.66. It was found high for yield per plot (72.66), 100 kernel weight (48.04), peduncle length (46.43), ear weight (41.34), number of kernel per row (39.22), ear height (34.46), plant height (28.52), tassel length (28.89), ear length (22.90), ear diameter (18.12). Moderate for days to 50% tasseling (15.89), days to 50% silking (15.78), total number of leaves (14.19), number of kernel row per ear (12.41) and lower for leaves above ear (8.57).

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

Sr. No.	Characters	Mean sum of square due to		
		Replication	**Replication**	**Replication**
1.	Days to 50% Silking	1.0111	55.91**	0.6433
2.	Days to 50% tasseling	0.0778	52.3559**	0.4571
3.	Plant Height	150.20	1227.71**	65.59
4.	Leaves above Ear	0.8361	0.9235**	0.4424
5.	Total no. Of leaves	0.2583	4.134**	0.8359
6.	Ear height	28.26	467.80**	28.6689
7.	Tassel length	0.2333	134.044**	6.558
8.	Ear length	0.1408	1.8745**	0.1848
9.	Peduncle length	1.104	47.3957**	1.5203
10.	Ear diameter	0.0163	0.8819**	0.0682
11.	Number of kernel row/ear	0.9590	3.1698**	0.5994
12.	Number of Kernel/row	1.5398	81.3439**	2.5316
13.	100 kernel weight	0.0254	52.5167**	0.0294
14.	Ear weight	27.5973	1363.67**	52.2377
15.	Yield per plot	0.0007	0.2784**	0.0102

**: Significant at 1% level of probability.

Table 3: Mean, range and coefficient of variation for various characters in quality protein maize (QPM).

Sr. No.	Characters	Mean	Range	C.V.
1.	Days to 50% silking	55.06±0.46	46.33-66.00	1.46
2.	Days to 50% Tasseling	53.21±0.39	45.33-61.00	1.27
3.	Plant height	131.43±4.68	86.17-161.67	6.16
4.	Leaves above ear	4.96±0.38	3.83-5.67	13.41
5.	Total number of leaves	11.47±0.53	9.00-13.33	7.97
6.	Ear height	66.12±3.09	45.00-89.67	8.10
7.	Tassel length	43.25±1.48	24.83-55.33	5.92
8.	Ear length	5.86±0.25	4.33-7.00	7.34
9.	Peduncle length	16.54±0.71	10.00-22.50	7.45
10.	Ear diameter	5.29±0.15	3.33-5.90	4.95
11.	Number of kernel row/ear	11.79±0.45	9.77-14.22	6.57
12.	Number of kernels/row	25.71±0.92	16.66-37.17	6.19
13.	100 kernel weight	17.92±0.10	9.97-26.53	0.96
14.	Ear weight	98.46±4.17	69.00-155.00	7.34
15.	Yield per plot	0.80±0.06	0.35-1.48	12.58

Table 4: Genetic Parameters, Heritability, Genetic advance and genetics advance as percent of mean of various characters in Quality Protein Maize in breads.

Sr. No.	Characters	σ^2_g	σ^2_p	GCV	PCV	h^2 (broad sense) %	GA as percent of mean	Genetic advance
1	Days to 50% silking	18.0222	19.0655	7.196	7.9309	94.54	15.7864	8.69
2	Days to 50% Tasseling	17.2996	17.7567	7.2166	7.9192	91.15	15.8935	8.46
3	Plant height	387.3742	452.9676	14.9748	16.193	85.52	28.5272	37.49
4	Leaves above ear	0.1603	0.6028	8.0714	15.64	26.66	8.5756	0.43
5	Total number of leaves	1.0995	1.9354	9.1446	12.1326	56.81	14.1985	1.63
6	Ear height	146.3784	175.0473	18.2975	20.0092	83.62	34.4682	22.79
7	Tassel length	42.4955	49.0535	15.0725	16.1938	86.63	28.8994	12.50
8	Ear length	0.5632	0.748	12.8117	14.7647	75.29	22.9011	1.34
9	Peduncle length	15.2918	16.8121	23.6377	28.7849	90.96	46.4399	7.68
10	Ear diameter	0.2712	0.3394	9.845	11.013	79.91	18.1299	0.96
11	Number of kernel row/ear	0.8568	1.4562	7.8542	10.2393	58.84	12.4108	1.46
12	Number of kernels/row	26.2707	28.8024	19.907	20.8756	90.21	39.2238	10.08
13	100 kernel weight	17.0958	17.5251	23.1429	23.9625	97.54	48.0462	8.61
14	Ear weight	437.1452	489.383	21.2344	22.4673	89.33	41.3424	40.71
15	Yield per plot	0.0894	0.0996	37.2339	39.3022	89.75	72.6655	0.58

Summary and Conclusion

Analysis of variance revealed significant differences among 30 genotypes of QPM for all the 15 characters under study. This indicated that there is ample scope for selection of promising genotypes for yield improvement.

From the variability studies, higher magnitude of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for yield per plot followed by peduncle length, 100 kernel weight, ear weight, number of kernel per row and ear height, indicating that these traits could be used for yield improvement under maize breeding programme.

In the present investigation, all the characters except leaves above ear had high value of heritability (In broad sense). High heritability coupled with high genetic advance as per cent of mean was recorded for yield per plot, 100 kernel weight, peduncle length, ear weight, number of kernel per row, ear height, plant height, tassel length, ear length and ear diameter indicating effectiveness of selection for the improvement of these traits and low heritability coupled with low genetic advance as percent of mean recorded for leaves above ear, which indicated the preponderance of additive gene action for these traits and direct selection may be effective for these traits.

References

1. Allard RW. Principles of plant breeding. London: John Wiley and Sons Inc.; 1960. p. 83-108.
2. Aminu D, Izge AU. Heritability and correlation estimates in maize (*Zea mays* L.) under drought conditions in Northern Guinea and Sudan savannas of Nigeria. World J Agric Sci. 2012;8(6):598-602.
3. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agron J. 1953;45:478-481.
4. Choudhuri A, Prodhan HS. Genetic variability and character association in baby corn. Environ Ecol. 2007;25(4):881-884.
5. Haddadi MH, Eesmaeilov M, Choukan R. Determination of genetic heritability for some agronomic traits in corn by diallel analysis. Int J Agric Crop Sci. 2013;5(15):1687-1693.
6. Hemavathy AT, Balaji K. Analysis of combining ability and heterotic groups of white grain quality protein maize (QPM) inbreds. Crop Res Hisar. 2008;36(1-3):224-234.
7. Johnson HW, Robinson HF, Comstock RF. Estimation of genetic and environmental variability of soybean. Agron J. 1955;47:341-318.
8. Murugan S, Padmanaban J, Manirajan S. Genetic variability and heritability studies in F_2 and F_3 generations of QPM and non-QPM maize crosses. Int J Plant Sci. 2010;5(1):290-293.
9. Nawar AA, El Absawy EA, El Shamarka SA, Ahmed MAE. Components of genetic variance and their interactions with years in one maize population. Ann Agric Sci. 2005;43(2):517-526.
10. Prakash O, Shanthi P, Satyanarayana E, Saikumar R. Studies on genetic variability exploitation for quality traits and agronomic characters in quality protein maize (QPM) germplasm (*Zea mays* L.). Ann Agric Res. 2006;27(2):147-153.
11. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 2nd ed. New Delhi: Indian Council of Agricultural Research; 1967.
12. Prasanna BM, Vasal SK, Kassahun B, Singh NN. Quality protein maize. Curr Sci. 2001;81(10):1308-1319.
13. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agron J. 1949;41(8):353-359.
14. Sivasubramanian S, Menon MR. Genotypic and phenotypic variability in rice. Madras Agric J. 1973;60(9-12):1093-1096.
15. Tengan KML, Obeng Antwi K, Akromah R. Genetic variances, heritability, and correlation studies on selected phenotypic traits in a backcross breeding program involving normal and opaque-2 maize. Agric Biol J N Am. 2012;3(7):287-291.
16. Turi NA, Shah SS, Ali S, Rahman H, Ali T, Sajjad M. Genetic variability for yield parameters in maize (*Zea mays* L.) genotypes. J Agric Biol Sci. 2007;2(4-5):1-3.
17. Kumar V, Singh PK, Gupta A. Studies of genetic diversity in quality protein maize (*Zea mays* L.) inbreds. Curr Adv Agric Sci. 2011;3(2):96-99.
18. Yusuf M. Genetic variability and correlation in single cross hybrids of quality protein maize (*Zea mays* L.). Afr J Food Agric Nutr Dev. 2010;10(2):2166-2175.