

Genetic variability and Selection Parameters for yield and its contributing characters in Quality Protein Maize (*Zea mays* L.)

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ABSTRACT: Ten QPM inbred lines and their all-possible cross combinations excluding their reciprocals (10 parents + 45 F₁s) were evaluated in a randomized block design with three replications during Rabi 2020-2021 at Student's Instructional Farm, C. S. Azad University of Agriculture and Technology- 208002, Kanpur, U.P. to get the extent of variability and related parameters to select effectively for grain yield and quality characters. It is a big challenge for researchers to get high grain yield with high protein. The data was recorded on sixteen characters viz., days to tasseling, days to silking, Days to maturity, Plant height (cm), Cob length (cm), Cob diameter (cm), Number of grain rows per cob, Number of grains per row, Cob yield per plant(g), Grain yield per plant (g), Shelling %, 100 kernel weight (g), Protein content (%), Lysine content (%), Tryptophan content (%), Seed vigour index. The result showed higher estimated values for Phenotypic Coefficient of Variability (PCV) of all the sixteen characters as compared to their corresponding Genotypic Coefficient of Variability (GCV). Highest values of PCV and GCV were noted for Lysine content (%) followed by Cob diameter (cm), Cob length (cm), Number of grain rows per cob and Protein content (%) based on F₁ while it was lowest for Days to maturity and Plant Height (cm). Difference between the PCV and GCV for Number of grain rows per cob and Plant Height (cm) were found higher indicating these two characters more influenced by environment, while low value of difference for remaining characters showed stability of the characters. High heritability in broad sense was observed for all the characters. High genetic advance % over mean was found for Lysine content (%) and Cob diameter (cm) while moderate for Cob length (cm), Number of grain rows per cob, Cob yield per plant(g), Shelling %, Protein content (%) and Seed vigour index and low for Days to tasseling, Days to silking, Days to maturity, Plant height (cm), Number of grains per row, Grain yield per plant (g), 100 kernel weight (g) and Tryptophan content (%). An advancement of 24.19% in Lysine content (%) followed by 20.69% in Cob diameter (cm) per cycle of selection at K=2.06. Both additive genes and non-additive genes were found effective for all the characters whereas Cob diameter (cm) and Lysine content (%) were under the control of non-additive genes. Simple selection based on progeny performance may be helpful for improving grain yield per plant.

Keywords: Quality Protein Maize, *Zea mays*, genetic variability, heritability, genetic advance, selection parameters.

INTRODUCTION

Maize (*Zea mays* L.) is the third most important cereal crop next to rice and wheat and has the highest production potential among cereals. It plays very important role in human and animal nutrition in many developed and developing countries worldwide. Due to high content of carbohydrate, fats, proteins, some of the vitamins and minerals maize established as a "poor man's nutri-cereal". Several million people particularly in the developing countries derive their protein and calorie requirements from maize. It is diploid species with chromosome number $2n = 20$. *Tripsacum* (Gamma

grass) $2n = 18$ and Teosinte, $2n = 36$ are two close relatives. The native place of corn is believed to be America from where it was introduced in South East Asia by Portuguese traders in 16th century.

At global level maize accounts for 15 per cent of proteins and 20 per cent of calories in food diet. The global production of maize was recorded 1151.78 MT, the productivity 5.73 MT per hectare with area of 200.96 mha during 2022 (USDA, 2022). India contributes around 2.35 per cent of global maize production from 9.89 mha area (DAES, 2022) and 31.65 MT production with 3199 kg per hectare productivity. Unfortunately, the nutritional profile of

normal maize is quite poor, as it is deficient in some essential amino acids such as lysine and tryptophan and relatively high proportion of prolamins in maize storage protein which are essentially devoid of lysine and tryptophan. The reason concerning with this fact that lysine, tryptophan and threonine are the limiting amino acids in human beings and in non-ruminants as well.

The present study is based on sixteen quantitative characters measured on ten germplasm lines with two checks. Information on the variability was measured by estimating the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance for individual quantitative character and through equilibrium distance over the characters. In addition, the present study will also helpful in identification of high yielding genotypes with better quality (Prasanna *et al.*, 2001). In crop improvement only the genetic components of variation are important because this is the only component which transmit to the next generation. Heritability is the ratio of genotypic variance (V_g) to the phenotypic variance

(V_p). Heritability is an important parameter in the selection process as it determines the response to selection. Heritability is used by plant breeders to enhance the precision of single field trial and/or series of trials (Allard, 1962). Study of the estimates of heritability with genetic advance is more meaningful and reliable than considering the parameters individually.

MATERIALS AND METHODS

Ten genetically diverse inbred lines were crossed in all possible combinations excluding reciprocal during *Rabi* 2019-20 at Student's Instructional Farm, C. S. Azad University of Agriculture and Technology- 208002, Kanpur, U.P. Basic material consisting of ten morphological diverse genotypes *viz.*, HKI-193-1, HKI-163, CML-141, CML-157, CML-150, VQL-3, VQL-30, VQL-1, VQL-8 and VQL-12. The salient features of these parental lines are given in Table 1.

Table 1: Details of genotypes/varieties.

Sr. No.	Line	National Identity	Source	Kernel color	Kernel Texture	Maturity	Other Specific Characters	Centre
1.	HKI 193-1	IC 470149	CML193	Y	F	L	Green leaves, erect tassel branches, sparse tassel, strong plant, yellow grains	Karnal
2.	HKI 163	IC 470150	CML 163	Y	SD	L	Dark green leaves, good GCA, productive	Karnal
3.	CML 141	—	Pop 62	W	F	M	Green plant, tall, sparse and green tassel	DMR
4.	CML 157	—	Pop 62	W	F	L	Green plant, tall, sparse and green tassel	DMR
5.	CML 150	—	P 24QPM	W	D	L	Green plant, tall, sparse and green tassel	DMR
6.	VQL-3	IC 568701	(CM145 × CML 170) BC3P1bbb##-⊗b	Y	F	E	Early, orange, flint, high tryptophan (0.83%)	VPKAS, Almora
7.	VQL 30	IC 569176	(V360 × CML 109) BC2P1-bb##-⊗b	Y	F	E	Leaves drooping, Dense tassel and orange grain, high tryptophan (0.71%)	VPKAS, Almora
8.	VQL-1	IC 542343	(CM212 × CML 180)	Y	F	M	Medium, semi-flint, yellow with cap grains, high tryptophan Early, orange, flint, high tryptophan (0.71%)	VPKAS, Almora
9.	VQL 8	IC 568703	(CM145×CML173)	Y	F	M	Leaves straight, sparse tassel and yellow grain, Medium, orange, flint, high tryptophan (>094%)	VPKAS, Almora
10.	VQL 12	IC 568706	(V25×CML184)	Y	F	M	Straight tassel branches and dense tassel, Early, orange, flint,high tryptophan (0.75%)	VPKAS, Almora

The lines were sown in a randomized complete block design (RCBD) with three replications where each entry sown in one row of five-meter length with row to row and plant to plant distances as 60 cm and 25 cm,

respectively at Student's Instructional Farm, C. S. Azad University of Agriculture and Technology, Kanpur during *Rabi* 2020-21. All the recommended agronomical practices were adopted to raise the crop.

For sixteen characters *viz.* Days to tasseling, Days to silking, Days to maturity, Plant height (cm), Cob length (cm), Cob diameter (cm), Number of grain rows per cob, Number of grains per row, Cob yield per plant(g), Grain yield per plant (g), Shelling %, 100 kernel weight (g), Protein content (%), Lysine content (%), Tryptophan content (%), Seed vigour index observations were recorded from the five randomly selected plants from each genotype. "Azad Uttam a composite and DKC-7074 a hybrid" maize variety of this region were used as 'check varieties' in this experiment.

Estimation of coefficient of variability: The computation of genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) was done by the formula given by Burton and de Vane (1953).

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Or } \frac{\sigma_g}{\bar{X}} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Or } \frac{\sigma_p}{\bar{X}} \times 100$$

Heritability: Heritability (h^2) in broad sense was computed following the formula given by Johnson *et al.* (1955).

$$h^2_{bs} (\%) = Vg/Vp \times 100$$

where,

h^2 = Heritability in broad sense

Vg = Genotypic variance

Vp = Phenotypic variance

Genetic advance: The calculation of the estimates of genetic advance was done according to the formula given by Robinson *et al.* (1949).

$$\text{Genetic Advance} = (\sigma_{ph}) \times (K) \times (h^2_{bs})$$

Genetic advance in per cent of mean of the character

$$G.A. (\%) = \frac{\sigma_{ph} \times K \times h^2}{\bar{X}} \times 100$$

Where,

G.A. = Genetic advance estimate

K = Selection differential at 5% selection intensity ($K = 2.06$)

h^2 = Coefficient of heritability in broad sense.

σ_{ph} = Phenotypic standard deviation.

\bar{X} = Mean value of the concerned character

RESULT AND DISCUSSION

A. Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) for all the sixteen characters was given in Table 2. Parents and F_1 's showed highly significant differences for all the characters. The comparison of parent's vs F_1 generation indicated highly significant differences for all the sixteen characters. These results indicated the plenty of variability among the genotypes studied and this would respond positively to selection. Several researchers like Kumar *et al.* (2014); Rojaria *et al.* (2023) revealed that

the mean sum of squares due to genotypes showed significant differences for all the twelve characters studied *viz.* grain yield per plant, plant height, ear height, number of kernels per row and 100-kernel weight and also Kandel *et al.* (2018) studied analysis of variance which revealed significant differences for ten characters studied among the genotypes.

B. Mean and Range

In Table 3 range and mean values of parents and F_1 's for all the sixteen characters is presented. Mean value for days to tasseling reported 95.32 ranged from 88.31 to 106 for Days to silking 98.34 ranged from 92.33 to 108 while for Days to maturity it ranged from 138 to 155.33 with the mean of 144.61 and the range of 153.60 to 185 found for Plant height (cm) having mean of 170.18. The average Cob length (cm) was 15.42 with the minimum 13 and maximum 18. Cob diameter (cm) ranged from 8.15 to 12.40 with the mean value of 10.26. The average number of grain rows per cob found 13.40 ranged from 11.33 to 15.60 while Number of grains per row have the range 22.93 to 26.60 with the average value 24.61 and mean Cob yield per plant(g) found 127.49 having the values from 111.99 to 146.01. The average 87.95 grain yield per plant (g) ranged from 82 to 98. Mean shelling % found 69.20 with the range of 60.44 to 77.68 while the average of 100 kernel weight (g) found 23.84 with the minimum and maximum values 22 and 26 respectively. Protein content (%) ranged from 9 to 12 with the mean value 12 and the average lysine content (%) 3.08 ranged from 2.26 to 3.91 while tryptophan content (%) ranged from 0.63 to 0.78 with the mean value of 0.67. Seed vigour index ranged from 1868.18 to 2447.03 with the average value of 2199.51. Lal and Singh (2014) reported high range of variation for almost all the characters.

C. Coefficients of variation

In Table 4 the estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are presented. It is observed from the table that phenotypic coefficient of variation (PCV) was invariably greater than the corresponding genotypic coefficient of variation (GCV) revealed the influence of environment on the expression of all the traits.

Deshmukh *et al.* (1986) classified the PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above) values. Considering this classification, moderate GCV was found for two characters *viz.*, lysine content (%) (12.04) and cob diameter (cm) (10.29) while remaining characters have the low values of genotypic coefficient of variation.

Moderate PCV was found for two characters *viz.*, lysine content (%) (12.34) and cob diameter (cm) (10.54) while remaining characters have the low values of genotypic coefficient of variation.

The result observed were in accordance with the findings of Bartaula *et al.* (2019) reported for 100 kernel weight (g).

D. Heritability and genetic advance

Heritability (h^2_{bs}), genetic advance (GA) and genetic advance as percent of mean (GAM) estimates for

characters under study are indicated in Table 4. The genotypic coefficient of variation (GCV) along with estimates of heritability provides reliable estimates of genetic advance to be expected through phenotypic selection (Burton and DeVane 1953). Classification of heritability values as high (>60%), moderate (30-60%) and values less than 30% low was done by Robinson *et al.* (1949).

High heritability in broad sense was observed for all the characters. High genetic advance % over mean was found for Lysine content (%) and Cob diameter (cm) while moderate for Cob length (cm), Number of grain

rows per cob, Cob yield per plant(g), Shelling %, Protein content (%) and Seed vigour index and low for Days to tasseling, Days to silking, Days to maturity, Plant height (cm), Number of grains per row, Grain yield per plant (g), 100 kernel weight (g) and Tryptophan content (%). An advancement of 24.19% in Lysine content (%) followed by 20.69% in Cob diameter (cm) per cycle of selection at K=2.06.

High heritability coupled with high genetic advance were observed for two characters *viz.*, Lysine content (%) followed by Cob diameter (cm). Phansal *et al.* (2022) reported the similar results related to cob.

Table 2: ANOVA for grain yield and its components in QPM.

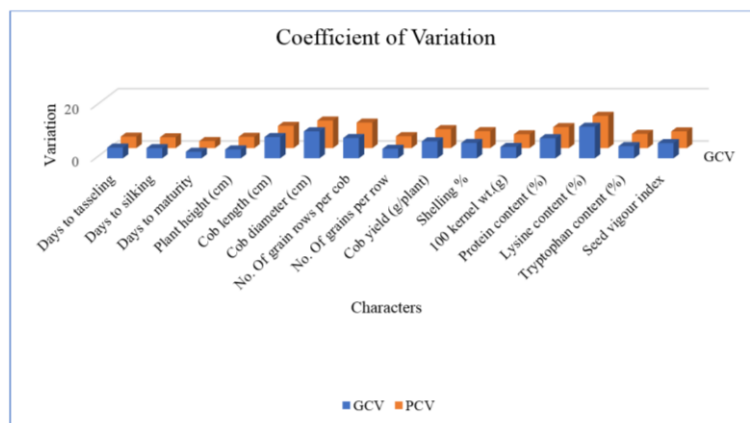
Source of variation	df	Days to tasseling	Days to silking	Days to maturity	Plant height (cm)	Cob length (cm)	Cob diameter (cm)	No. of grain rows per cob	No. Of grains per row	Cob yield (g/plant)	Shelling %	100 kernel wt.(g)	Protein content (%)	Lysine content (%)	Tryptophan content (%)	Seed vigour index	Grain yield (g/plant)
Rep	2	1.93	3.12	3.57	26.20	0.06	0.12	7.10	0.04	8.79	3.99	0.36	0.06	0.01	0.00	13294.09	2.70
Parents	9	16.95**	18.42**	28.35**	74.93**	5.59**	3.29**	2.63**	5.50**	39.63**	10.22**	3.55**	2.58**	0.241**	0.0043**	96353.16**	25.61**
F ₁	44	47.75**	45.77**	41.17**	120.25**	4.85**	3.39**	3.86**	2.86**	221.16**	53.06**	3.74**	2.07**	0.420**	0.0033**	52337.06**	62.02**
P vs F ₁	1	539.05**	528.87**	15.15**	226.10**	16.55**	1.45**	6.70**	210.81**	15956.72**	505.16**	75.96**	5.13**	3.423**	0.0037**	158208.93**	11892.12**
ERROR	108	2.28	1.92	3.01	19.07	0.15	0.06	0.59	0.42	14.37	3.25	0.47	0.07	0.01	0.00	3141.84	6.38

Table3: Mean and range of parents and F₁s for sixteen characters based on ten parents diallel in QPM.

Characters	General mean		Range			
	Parents	F ₁ 's	Parents		F ₁ s	
			Minimum	Maximum	Minimum	Maximum
Days to tasseling	100.01	95.32	96.82	104.76	88.31	106.00
Days to silking	102.98	98.34	101.00	108.00	92.33	108.00
Days to maturity	145.40	144.61	142.67	152.33	138.00	155.33
Plant height (cm)	167.14	170.18	158.60	173.20	153.60	185.00
Cob length (cm)	14.60	15.42	13.00	17.00	13.00	18.00
Cob diameter (cm)	10.01	10.26	9.00	12.00	8.15	12.40
No. Of grain rows per cob	12.87	13.40	11.80	14.30	11.33	15.60
No. Of grains per row	21.68	24.61	19.86	24.07	22.93	26.60
Cob yield (g/plant)	101.99	127.49	95.48	107.25	111.99	146.01
Shelling %	64.66	69.20	62.00	68.12	60.44	77.68
100 kernel wt.(g)	22.08	23.84	21.00	24.00	22.00	26.00
Protein content (%)	11.12	10.66	9.53	12.55	9.00	12.00
Lysine content (%)	3.46	3.08	3.02	3.98	2.26	3.91
Tryptophan content (%)	0.663	0.67	0.617	0.732	0.63	0.78
Seed vigour index	2279.78	2199.51	2059.49	2596.10	1868.18	2447.03
Grain yield (g/plant)	65.94	87.95	61.28	70.69	82.00	98.00

Table 4: Estimates of components of genetic variability for yield and its components in QPM.

Characters	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to tasseling	15.15	17.45	86.79	7.47	7.84	4.08	4.38
Days to silking	14.61	16.56	88.20	7.39	7.52	3.89	4.14
Days to maturity	13.00	15.16	85.76	6.88	4.76	2.49	2.69
Plant height (cm)	33.08	54.09	61.16	9.26	5.44	3.38	4.32
Cob length (cm)	1.57	1.71	91.48	2.47	15.99	8.12	8.49
Cob diameter (cm)	1.11	1.17	95.29	2.12	20.69	10.29	10.54
No. of grain rows per cob	1.08	1.71	62.95	1.69	12.65	7.74	9.75
No. Of grains per row	0.80	1.26	63.45	1.47	5.96	3.64	4.56
Cob yield (g/plant)	68.01	85.15	79.87	15.18	11.91	6.47	7.24
Shelling %	16.48	20.10	82.00	7.57	10.94	5.87	6.48
100 kernel wt.(g)	1.07	1.60	66.91	1.74	7.31	4.34	5.30
Protein content (%)	0.67	0.74	90.81	1.60	15.05	7.67	8.04
Lysine content (%)	0.14	0.14	95.20	0.75	24.19	12.04	12.34
Tryptophan content (%)	0.00	0.00	72.88	0.05	8.15	4.63	5.43
Seed vigour index	16319.65	19695.71	82.86	239.55	10.89	5.81	6.38
Grain yield (g/plant)	18.19	25.63	70.97	7.40	8.42	4.85	5.76



Graph 1: Graphical representation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

CONCLUSIONS

The present study generally indicated that there was plenty of genetic variability among the genotypes. Thus, there is vast opportunity in the improvement of protein, lysine and tryptophan content in these quality protein maize genotypes. Therefore, the results and information generated from current study need to be used by interested plant breeders. Since the experiment was carried out at one location and in one season, it is advisable to continue over several years and locations with this study for the improvement of normal maize to QPM.

Studies revealed that the lysine content (%) followed by Cob diameter (cm) with high heritability and high genetic advance followed by Cob length (cm), Number of grain rows per cob, Cob yield per plant(g), Shelling %, Protein content (%) and Seed vigour index and low for Days to tasseling, Days to silking, Days to maturity, Plant height (cm), Number of grains per row, Grain yield per plant (g), 100 kernel weight (g) and Tryptophan content (%) were the major yield attributing characters coupled with moderate genetic advance, so emphasis should be given for these characters at the time of simple selection.

FUTURE SCOPE

Through the studies of genetic variability and direct selection parameters the desirable genotypes for the improvement of yield and its contributing traits can be identified. The higher extent of genetic variability has found among the material used and it can be used further for the improvement of quality protein maize by making improved varieties for doubling the production of QPM in the upcoming years.

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Conflict of interest. None.

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