

Assessment of genetic variation and trait inter-relationship in QPM inbred lines in Vindhyan region of Eastern Uttar Pradesh

Ankit Phansal*, Shailesh Marker and Rajesh Aggarwal

Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj-211007, U. P., India.

Article history:

Received: 18 July, 2022

Revised: 29 Aug., 2022

Accepted: 14 Sept., 2022

Citation:

Phansal A., S. Marker and R. Aggarwal. 2022. Assessment of genetic variation and trait inter-relationship in QPM inbred lines in Vindhyan region of Eastern Uttar Pradesh. *Journal of Cereal Research* 14 (2): 183-188. <http://doi.org/10.25174/2582-2675/2022/131246>

*Corresponding author:

E-mail: ankitphansal11@gmail.com

© Society for Advancement of Wheat and Barley Research

Abstract

The present investigation was carried out to assess genetic variation and trait inter-relationship in QPM inbred lines in Vindhyan region of Eastern Uttar Pradesh for 18 characters during Rabi 2018-19. Analysis of variance showed significant differences for all the characters at 1 per cent level of significance, indicating that considerable genetic variability was present among different QPM inbred lines. The less difference between GCV and PCV revealed that there was a very low influence of environment on the expression of various characters. High heritability coupled with high genetic advance as per cent mean was depicted by for cob weight with sheath followed by cob weight without sheath and tassel length. Plant height followed by kernels per row, cob height, cob weight with sheath, tassel length, cobs per plant, cob weight without sheath and cob length showed positive significant correlation with grain yield and days to 50 per cent silking, followed by kernels per row, biological yield, harvest index, tassel length, cob length, anthesis-silking interval, cobs per plant and cob weight without sheath had shown the positive direct effect on grain yield per plant. Therefore, these characters may be used as selection indices for genetic improvement of QPM inbred lines.

Keywords: Genetic variation, Variability parameters, Correlation coefficient, Path analysis, QPM inbreds (*Zea mays* L.).

1. Introduction

Maize (*Zea mays* L.) or 'Queen of cereals' belongs to the family Graminae ($2n=2x=20$) and is an important staple food of many countries, particularly in the tropics and subtropics. It is the third most important cereal food crop of the world after Rice and Wheat (Poehlman, 2006). It can be grown throughout the year, due to the availability of thermo and photo insensitive varieties. Breeding for improved protein quality maize started in the mid-1960s with the discovery of mutants. The QPM has higher biological value, increased availability and better utilization of niacin, calcium, carbohydrate and carotene. Therefore, it is desirable to replace the present maize hybrids with QPM hybrids which are similar in

cultivation, grain yield, potentiality, and tolerance to biotic and abiotic stresses with that of normal maize hybrids.

Genotypic and phenotypic correlation coefficients tell us the association between and among two or more characters. A significant association proposes that such traits could be upgraded concurrently. However, such an improvement depends on phenotypic correlation, additive genetic variance and heritability (Hayes and Smith, 1955). A clear understanding of the association between yield and yield components is necessary for a successful crop improvement programme since grain yield is a complex character and is influenced by several genetic factors interacting with the environment. Correlation coefficient analysis reveals the



magnitude and direction of yield components, while path analysis identifies components that directly or indirectly influences yield. Both character association and path analysis help in formulating an effective breeding strategy to further develop productive inbreds in maize. Genetic correlation analysis is a handy technique that elaborates the degree of association among important quantitative traits (Malik *et al.*, 2005).

The estimates of path coefficient analysis are important for a better understanding of the crop. It gives specific measures of the direct and indirect effect of each component character under seed yield (Singh and Singh, 1974). The path analysis provides effective measures of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to the final product (Jakhar and Kumar, 2017). Coefficient measures the degree and strength of the relationship between the yield and other yield contributing characters which is helpful for the selection of desirable characters under a breeding programme (Falconer, 1989). The measurement correlation of coefficient between the characters is a matter of considerable importance in selection practices which help in the construction of selection indicates and also permit the prediction of correlated response (Lerner, 1985). Therefore, the present study of correlation and path coefficient analysis of various yield-related traits were conducted that would be a valuable aid in selecting and breeding for improved maize hybrids.

Keeping all these facts in view, the present study was planned to evaluate the QPM inbred lines for grain yield and its attributing traits, to assess the genetic variability among QPM inbred lines and to assess correlation and path analysis of yield and yield attributing traits.

2. Materials and methods

The present investigation was carried out at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini, Prayagraj, U.P. during Rabi 2018-19. The experimental materials comprising of 21 QPM inbred lines including 1 check were grown under RBD with 3 replications. The data were recorded on the 18 pre and post-harvest characters along with morphological characters of the lines i.e. Days to first silk emergence (50%), Days to first tassel emergence (50%), Anthesis-silking interval

(Days), Plant height (cm), Cob height (cm), Leaf area index, Tassel length (cm), Number of cobs per plant, Cob length (cm), Cob girth (cm), Cob weight with sheath (g), Cob weight without sheath (g), Number of kernel rows per cob, Number of kernels per row, Grain yield per plant (g), 100 kernel weight (g), Biological yield per plant (g), Harvest index (%). The observations were recorded on five randomly selected plants for all characters except for days to 50% silk emergence and days to 50% tassel emergence where the observation was recorded on a plot basis. The data recorded were subjected to the Analysis of Variance, Genetic Variability parameters, Heritability broad sense, Genetic Advance, Correlation Coefficient Analysis and Path Coefficient Analysis.

3. Results and discussion

The analysis of variance showed significant differences for all traits studied at a 1% level of significance except for anthesis-silking interval, leaf area index and the number of cobs per plant suggesting that the genotypes were genetically variant for each other and provide the scope for breeding. A perusal of mean values of yield and yield contributing characters revealed that QPM inbred line BHU-N4 X QPM-8 (38.09) followed by CML-161 X VL-1056 (35.98), YHPANTH-53 (35.39), BHU-B73-BC2 X BHU-N3 (34.00) were identified as top high yielding QPM inbreds in the present study.

A wide range of phenotypic (V_p) and genotypic variance (V_g) were observed in the experimental material for all the traits studied. The highest variability (V_g and V_p) were recorded for plant height followed by cob weight with sheath, cob weight without sheath, grain yield per plant, cob height, biological yield, days to 50% tasselling, days to 50% silking and harvest index. In the present investigation, it is depicted from Table 1, the values of Phenotypic variance (V_p) and phenotypic coefficient of variation (PCV) were higher than that of genotypic variance (V_g) and genotypic coefficient of variation (GCV) for all the traits studied which indicate that the apparent variation is not only due to genotype but also due to influence of environment. therefore, selection based on phenotype alone can be effective for the improvement of these traits. Similar findings for a genotypic and phenotypic variance were reported by Vashistha *et al.* (2013) and Kapoor and Batra (2015) and for GCV and PCV were reported by Reddy *et al.* (2012) and Hepziba *et al.* (2013).



Table 1. Genetic parameters for 18 quantitative traits of QPM inbred lines.

Characters	Vg	Vp	GCV	PCV	h ² (bs) %	GA	GA as % mean
Days to 50% Tasseling	43.49	49.77	5.84	6.25	87.38	12.70	11.24
Days to 50% silking	42.35	48.63	5.67	6.07	87.08	12.51	10.89
Anthesis-silking interval	0.17	0.53	21.97	38.66	32.29	0.49	25.72
Cob height	75.33	138.59	19.03	25.81	54.36	13.18	28.90
Plant height	495.08	557.17	16.37	17.37	88.86	43.21	31.79
Tassel length	7.73	8.62	9.16	9.68	89.63	5.42	17.87
Leaf area index	0.10	0.16	10.67	13.57	61.73	0.50	17.26
Cobs per plant	0.01	0.02	5.00	8.66	33.33	0.09	5.95
Cob Weight with sheath	425.00	432.19	26.20	26.42	98.34	42.11	53.51
Cob weight without sheath	390.55	426.98	30.04	31.41	91.47	38.94	59.18
Cob length	1.58	2.30	10.27	12.37	68.96	2.15	17.57
Cob girth	0.56	1.22	5.53	8.17	45.79	1.04	7.71
Kernels per row	5.12	7.45	24.37	29.40	68.72	3.86	41.62
Kernel rows per cob	1.39	2.19	8.66	10.86	63.58	1.94	14.22
100 kernel weight	6.5677	8.0891	10.98	12.19	81.19	4.76	20.39
Biological yield	69.7680	102.4791	20.38	24.71	68.08	14.20	34.65
Harvest index	28.052	32.891	6.76	7.32	85.29	10.08	12.86
Grain yield per plant	82.36	116.88	31.29	37.27	70.47	15.69	54.10

Johnson *et al.* (1955) suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression, without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability. High heritability alone is not enough to make sufficient improvement through selection in genetic advances generation. In the present study, high heritability (>60%) coupled with high genetic advance (>30%) was recorded for cob weight with sheath followed by cob weight without sheath, plant height, grain yield per plant, kernels per row and biological yield. Therefore, indicating a predominance of additive gene effects and the possibilities of effective selection can be conducted based on these traits for the crop improvement program.

High heritability (>60%) with moderate genetic advance (20-30%) was observed for 100 kernel weight. This trait is most probably controlled by both additive and non-additive gene action. This decrease in genetic advance is

due to the influence of the environment, hence this trait is less amendable for selection indicates that this character showed intermediate expression for both the additive and dominance gene effect. So, the improvement of this character is possible only through careful directional and restricted selection.

High heritability (>60%) with low genetic advance (10-20%) was observed for tassel length followed by days to 50% tasselling, days to 50% silking, harvest index, cob length, kernel rows per cob and leaf area index. This indicates that role of non-additive gene action in the inheritance of these characters, which revealed the importance of dominance and epistatic effects in the inheritance of these traits and selection would be less effective. Similar findings were reported by Kumar *et al.* (2014) and Mohan and Singh (2014).

The results for correlation coefficient analysis showed that the genotypic correlation coefficient was greater than the phenotypic correlation coefficient for all the traits indication a strong inherent association among these traits.



Grain yield per plant showed positive significant genotypic association with plant height (0.892**) followed by kernels per row (0.753**), cob height (0.615**), cob weight with sheath (0.314*), tassel length (0.311*), cobs per plant (0.299*), cob weight without sheath (0.291*) and cob length (0.275*). Grain yield per plant showed a positive significant phenotypic association with kernel per row (0.787**) followed by plant height (0.402**), cob weight without sheath (0.248*) and biological yield (0.273*). Grain yield per plant showed the positive non-significant phenotypic association with kernel rows per cob (0.224) followed by cob height (0.217), tassel length (0.207), harvest index (0.174), cob weight with sheath (0.169), anthesis-silking interval (0.097), 100 kernel weight (0.083), cob length (0.072), leaf area index (0.029) and cob girth (0.02). Similar findings were reported by Jadhav *et al.* (2014), Prasanna *et al.* (2015) and Bhiusal *et al.* (2017).

Days to 50% silking (11.00) followed by kernels per row (2.146), biological yield (1.969), harvest index (1.535), tassel length (1.359), cob length (1.320), anthesis-silking interval (1.185), cob per plant (0.385) and cob weight without sheath (0.383) had shown the positive direct effect on grain yield per plant at the genotypic level. While, days to 50% tasselling (-10.322) followed by plant height (-1.974), cob girth (-0.752), cob weight with sheath (-0.568),

kernel rows per cob (-0.488), 100 kernel weight (-0.436), cob height (-0.197) and leaf area index (-0.008) had shown the negative direct effect on grain yield per plant at the genotypic level. Similar findings were reported by Reddy *et al.* (2016) and Barua *et al.* (2017). Days to 50% silking (198.197) followed by kernels per row (1.052), 100 kernel weight (0.416), kernel rows per cob (0.363), biological yield (0.124), and cob weight with sheath (0.058), harvest index (0.052), leaf area index (0.045), cob girth (0.023) and tassel length (0.004) had shown the positive direct effect on grain yield per plant at the phenotypic level. While days to 50% tasselling (-200.513) followed by an anthesis-silking interval (-200.769), cob weight without sheath (-0.058), cob length (-0.026), cobs per plant (-0.01), cob height (-0.007), and plant height (-0.003) had shown the negative direct effect on grain yield per plant at the phenotypic level. These observations similarly reported by Lingaiah *et al.* (2014).

Traits like 50% silking, 100 kernel weight, kernels per row, kernel rows per cob, biological yield, harvest index, tassel length, cob length, anthesis-silking interval, cob weight with sheath, leaf area index, cob girth, cob per plant and cob weight without sheath show positive direct significant association. Therefore, these traits can be selected for the crop improvement program.

Table 2. Correlation coefficient between grain yield per plant and its components traits in QPM inbred lines at the genotypic and phenotypic level.

	Genotypic correlation coefficient		Phenotypic correlation coefficient
Plant height	0.807**	Kernels per row	0.787**
Kernels per row	0.753**	Plant height	0.402**
Cob height	0.615**	Biological yield	0.273*
Cob Weight with sheath	0.314*	Cob weight without sheath	0.248*
Tassel length	0.311*	Grain yield per plant	1
Cobs per plant	0.299*	Kernel rows per cob	0.224
Cob weight without sheath	0.291*	Cob height	0.217
Cob length	0.275*	Tassel length	0.207
Anthesis-silking interval	-0.249*	Harvest index	0.174
Grain yield per plant	1	Cob Weight with sheath	0.169
Cob girth	0.235	Anthesis-silking interval	0.097
Harvest index	0.235	100 kernel weight	0.083
Biological yield	0.231	Cob length	0.072
Kernel rows per cob	0.046	Leaf area index	0.029



Days to 50% Tasseling	0.021	Cob girth	0.02
Days to 50% silking	0.006	Days to 50% silking	-0.062
100 kernel weight	-0.093	Cobs per plant	-0.064
Leaf area index	-0.111	Days to 50% Tasseling	-0.072

Residual for genotypic and phenotypic levels are 0.02520 and 0.03787, while * and ** indicates significance at 5% and 1% level of significance respectively.

Table 3. Path coefficient between grain yield per plant and its components traits in QPM inbred lines at the genotypic and phenotypic level.

	Genotypic path coefficient		Phenotypic path coefficient
Days to 50% silking	11	Days to 50% silking	198.197
Kernels per row	2.146	Kernels per row	1.052
Biological yield	1.969	100 kernel weight	0.416
Harvest index	1.535	Kernel rows per cob	0.363
Tassel length	1.359	Biological yield	0.124
Cob length	1.32	Cob Weight with sheath	0.058
Anthesis-silking interval	1.185	Harvest index	0.052
Cobs per plant	0.385	Leaf area index	0.045
Cob weight without sheath	0.383	Cob girth	0.023
Leaf area index	-0.008	Tassel length	0.0043
Cob height	-0.197	Plant height	-0.0025
100 kernel weight	-0.436	Cob height	-0.0067
Kernel rows per cob	-0.488	Cob length	-0.026
Cob Weight with sheath	-0.568	Cob weight without sheath	-0.058
Cob girth	-0.752	Cobs per plant	-0.08
Plant height	-1.974	Anthesis-silking interval	-20.77
Days to 50% Tasseling	-10.322	Days to 50% Tasseling	-200.51

Residual for genotypic and phenotypic levels are 0.05907 and -0.00005 respectively.

Conclusion

It is concluded that considerable genetic variability was observed in different QPM inbred lines. The less difference between GCV and PCV revealed that there was a very low influence of environment on the expression of various characters. High heritability (>60%) coupled with genetic advance as per cent mean (>30%) was depicted for cob weight with sheath (98.34) followed by cob weight without sheath (91.47) and tassel length (89.63). Kernels per row, cob weight with sheath, tassel length, cobs per plant, cob weight without sheath and cob length showed a positive significant correlation and positive direct effect on grain yield. Therefore, these characters may be used as selection indices for genetic improvement of QPM inbred lines.

Author's contribution

Conceptualization of research (AP); Designing of the experiments (AP, SM and RA); Contribution of experimental materials (AP, SM and RA); Execution of field/lab experiments and data collection (AP, SM and RA); Analysis of data and interpretation (AP, SM and RA); Preparation of the manuscript (AP, SM and RA).

Declaration

The authors declare no conflict of interest.

4. References

1. Barua NS, VP Chaudhary and GN Hazarika. (2017). Genetic variability and correlation studies for morphological traits in maize (*Zea mays* L.)



- genotypes. *Indian Research Journal of Genetics and Biotechnology*, **9** (1): 38-48.
2. Bhiusal TN, GM Lal, S Marker and GJ Synrem. (2017). Genetic variability and traits association in maize (*Zea mays* L.) genotypes. *Annals of Plant and Soil Research*, **19** (1): 59-65.
 3. Falconer DS. (1989). Introduction to quantitative genetics. 3rd Ed. English Language Book Society, Longman.
 4. Hayes HK, RI Forrest and DC Smith. (1955). Methods of plant Breeding Correlation and regression in relation to plant breeding. McGraw-Hill Company Inc. 2nd Ed: 439-451.
 5. Hepziba SJ, K Geetha and SM Ibrahim. (2013). Evaluation of genetic diversity, variability, character association and path analysis in diverse inbreds of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **4** (1): 1067-1072.
 6. Jadhav RS and A Sarkar. (2014). Studies on Genotypic Variation and Character Association in Maize (*Z. mays* L.) Hybrids Grown Under Different Moisture Regimes in Terai Region of West Bengal. *Journal of Agricultural Science and Technology*, **1** (1): 20-24.
 7. Jakhar DS, R Singh and A Kumar. (2017). Studies on Path Coefficient Analysis in Maize (*Zea mays* L.) for Grain Yield and Its Attributes. *International Journal of Current Microbiology and Applied Sciences*, (6): 2851-2856.
 8. Johnson HW, HF Robinson and RE Comstock. (1955). Genotypic and phenotypic correlation in soybean and their implication in selection. *Journal of Agronomy*, 477-483.
 9. Kapoor R and C Batra (2015). Genetic variability and association studies in maize (*Zea mays* L.) for green fodder yield and quality traits. *Electronic Journal of Plant Breeding*, **6** (1): 233-240.
 10. Kumar GP, VN Reddy, SS Kumar and PV Rao. (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.
 11. Lerner, M. (1985). The genetic basis of selection. John Willey and Sons, New York, p122.
 12. Lingaiah N, GP Kumar and V Venkanna. (2014). Character Association and Path Analysis for Yield Contributing and Physiological Parameters for Grain Yield in Maize (*Zea mays* L.). *International Journal of Pure and Applied Bioscience*, **2** (1): 118-121.
 13. Malik HN, SI Malik, M Hussain, SUR Chughtai and HI Javed. (2005). Genetic correlation among various quantitative characters in maize (*Zea mays* L.) hybrids. *Journal of Agriculture and Social Science*, **1** (3): 262-265.
 14. Mohan L and Singh O. (2014). Studies of variability using morphological and quality traits in Quality Protein Maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **5** (3): 526- 530.
 15. Poehlman JM. (2006). Breeding Field Crops. 5th Edn. The AVI Publishing Company Incorporated, Westport, Connecticut.
 16. Prasanna SV, V. K. and DR Babu. (2015). Character association and path analysis of grain yield and yield components in Maize (*Zea mays* L.) *Electronic Journal of Plant Breeding*, **6** (2): 550- 554.
 17. Reddy VR and F Jabeen. (2016). Narrow sense heritability, correlation and path analysis in maize (*Zea mays* L.). *Sabrao Journal of Breeding and Genetics*, **48** (2): 120-126.
 18. Reddy VR, F Jabeen, MR Sudarshan and AS Rao. (2012). Studies on genetic variability heritability, correlation and path coefficient analysis in maize (*Zea mays* L.) over locations. *International Journal of Applied Biology and Pharmaceutical Technology*, **4** (1): 195-199.
 19. Singh, DD and D Singh. (1974). Correlation in Indian Colza *Brassica campestris* L., var. Sarsonprain. *Indian Journal of Agricultural Sciences*, **44** (3): 142-144.
 20. Vashistha A, NN Dixit, D Sharma, S K, S Marker (2013). Studies On heritability and genetic advance estimates in Maize genotypes. *Bioscience Discovery*, **4** (2): 165-168

