Int.J.Curr.Microbiol.App.Sci (2022) *11*(01): 368-374

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 11 Number 01 (2022)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2022.1101.044

Genotypic and Phenotypic Correlation Coefficient Study to Identify Best Yield and Yield Attributing Trait for Selection in Maize (*Zea mays* L.)

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Keywords

Genotypic correlation, Phenotypic correlation, Maize

Article Info

Received:
12 December 2021
Accepted:
04 January 2022
Available Online:
10 January 2022

ABSTRACT

Selection based on perseperformance may not prove effective because yield is a complex trait, whereas selection based on its component character would prove more effective. In this study, plant height, ear height, number of kernels per row, number of kernels per ear, shelling percentage and test weight all had significant and positive associations with grain yield per plant at genotypic and phenotypic levels. General results of correlation studies suggested that grain yield per plant had positive and significant correlation with plant height, ear height, number of kernels per ear, number of kernels per row, ear weight, shelling percent and test weight. While days to 50 per cent tasseling and days to 50 per cent silking established negative but nonsignificant association in at both genotypic and phenotypic levels.

Introduction

The crop maize (*Zea mays* L.) belongs to the tribe Maydeae of the grass family Poaceae with chromosome number 2n=20 and 2.36 Gb genome size. Since the crop has high yield potential, it is called “Queen of Cereals”. Maize is the only cereal crop that is grown over diverse seasons and different ecologies leading to the existence of diverse landraces in several countries worldwide (Rebourg *et al.*, 2003). Maize plant is monoecious where male and female flowers are present on separate inflorescences in the same plant. Male inflorescences called tassel are located at the top, which consists of a central spike and 10-50 lateral branches. Each spikelet of a tassel contains two florets and each floret has three anthers. Pollen grains produced by anthers are very small, barely visible to the naked eye, light in weight and are easily flown out by wind. Female inflorescences known as silk, cob or ear, arises at midway on the main stalk. Ear arises from axillary buds having two florets at the time of initiation, but only the upper one is developed. Each functional floret of an ear produces an ovary with elongated style called silk, covered with hairs (trichomes) (Matsuoka *et al.*, 2002; Hofmann *et al.*, 2014).

Maize contributes nearly 9 per cent to national food basket and more than 400billion to the agricultural GDP at current price. Besides it generates employment to over 650 million-man days at the farm and downstream agricultural and industrial sectors. On the basis of per cent dry matter, maize grain contains protein (9-10%),oil(4%), carbohydrate (71-72%), crude fiber (2.3%), albuminoids (10.4%) and ash(1.4%) and sufficient quantities of carotenoids and other vitamins. It is an adequate source of essential amino acids. For monogastric animals, including humans, maize protein is deficient in lysine and tryptophan and many poultry diets, it is inadequate in sulphur containing amino acids *viz.*, methionine and cysteine.

Primary objective of most maize breeding programme is development of well adopted high yielding cultivars. Efficiency of selection based on component traits depends on the degree of association between yield and component traits. Correlation and path coefficient studies between yield and yield components themselves is a pre-requisite to plan a meaningful breeding programme. Several workers have attempted to determine association between the characters on which the selections for high yields can be made and they emphasized the utility of the estimates of genetic components in the response of predicting quantitative characters for selection as well as the correlated response of various traits to grain yield.

Materials and Methods

The present investigation on genotypic and phenotypic correlation study was carried out at the department of genetics and plant breeding, B. A. College of agriculture, Anand Agricultural University, Anand, Gujarat (Fig 1). The experimental material for present investigation was comprised of 51 genotypes of maize (*Zea mays* L.).

The name and source of genotypes included in the present investigation are listed in Table 2.1. The crop was raised in the Randomized complete block design with two replications with 60 x 30 cm spacing.

Observations recorded

Observations were recorded on five randomly selected competitive plants of each genotype in each replication for various characters like days to 50% tasseling and silking, plant height, ear height (cm), ears per plant, ear length (cm), ear girth (cm), ear weight (g), number of kernel rows per ear, number of kernels per row, number of kernels per ear, shelling percentage (%), test weight (g), grain yield per plant (g), protein content (%), total soluble sugar (%), β- carotene (ppm), lysine and tryptophan profiling.

Statistical Analysis

The form of analysis used for estimating covariance components between different pairs of observation was the same as that for analysis of variance, except that the sum of squares and mean squares which were replaced by sum of products and mean products, respectively. The following estimates of covariances were worked out as reviewed by Singh and Choudhary (1985).

$\sigma_{pipj} = \sigma_{gigj} + \sigma_{eiej}$

Where,

σ_{pipj} = Phenotypic covariance between ith and jth character

σ_{gigj} = Genotypic covariance between ith and jth character

σ_{eiej} = Environmental covariance between ith and jth character

The estimates of covariance and variance were utilized in computing genotypic and phenotypic correlation coefficients.

Genotypic correlation coefficient (r_{gigj})

The genotypic correlation is chiefly caused by pleiotropy and linkage action of genes and r_{gigj} was estimated as suggested by Hazel (1943) using variability v0.1.0 package (Popat *et al.*, 2020) through RStudio (RStudio team, 2020).

$$r_{gigj} = \frac{\sigma_{gigj}}{\sqrt{\sigma^2_{gi} \times \sigma^2_{gj}}}$$

Where,

r_{gigj} = Genotypic correlation coefficient between ith and jth character

σ_{gi} = Genotypic variance of ith character

σ_{gj} = Genotypic variance of jth character

σ_{gigj} = Genotypic covariance between ith and jth characters

Phenotypic correlation coefficient (r_{pipj})

The genetic and environmental causes of correlation combined together gives phenotypic correlation coefficient (r_{pipj}) and was estimated with the help of following formula.

$$r_{pipj} = \frac{\sigma_{pipj}}{\sqrt{\sigma_{pi} \times \sigma_{pj}}}$$

Where,

r_{pipj} = Phenotypic correlation coefficient between ith and jth character,

σ_{pi} and σ_{pj} = Phenotypic variances of ith and jth character, respectively.

σ_{pipj} = Phenotypic covariance between ith and jth character.

The genotypic and phenotypic correlation coefficients were worked out for all possible pairs and were tested against standardized tabulated values of r with (g-2) and (rg-2) degree of freedom at 0.05 and 0.01 levels of probabilities for genotypic and phenotypic correlation, respectively (Fisher and Yates, 1963).

Results and Discussion

Prior to any breeding programme, it is imperative to obtain information regarding inter-relationship of yield and contributing characters, as it facilitates the quicker assessment of high yielding genotypes in selection programmes. The prime genetic cause of correlation is pleiotropy, though linkage is a cause of transit correlations particularly in a population derived from crosses between divergent strains.

Enhanced repression of genes controlling different traits manifest correlation, while enhanced expression of one or more reveal negative correlation.

Genotypic and phenotypic correlation coefficient values were given into table 3.1. Grain yield per plant exhibited significant and positive association with plant height, ear height, number of kernels per row, number of kernels per ear, shelling percentage and test weight at genotypic and phenotypic levels. Ear weight established positive and significant association with grain yield at both the levels.

Table.1 List of maize genotypes and their source

Sr. No.	Genotypes	Source
1	I-07-14-1-2	AAU, Godhra
2	I-07-28-3-2	AAU, Godhra
3	I-07-29-1-3	AAU, Godhra
4	I-07-66-1-2	AAU, Godhra
5	I-07-66-2-3	AAU, Godhra
6	I-07-66-3-2	AAU, Godhra
7	I-07-66-4-1	AAU, Godhra
8	I-07-56-4-3	AAU, Godhra
9	I-077-59-5	AAU, Godhra
10	I-07-60-4-3	AAU, Godhra
11	I-07-65-44-4	AAU, Godhra
12	I-07-6-4-4	AAU, Godhra
13	I-07-6-4-5	AAU, Godhra
14	I-07-9-5	AAU, Godhra
15	I-07-13-1-3	AAU, Godhra
16	IL-14-28	AAU, Godhra
17	IL-14-48	AAU, Godhra
18	IL-14-60	AAU, Godhra
19	IL-17-28	AAU, Godhra
20	IL-17-32	AAU, Godhra
21	IL-17-34	AAU, Godhra
22	IL-17-44	AAU, Godhra
23	GYL-10	AAU, Godhra
24	PFSR5-3-5	AAU, Godhra
25	IL-15-39	AAU, Godhra
26	IL-15-11	AAU, Godhra
27	IGI-1101	AAU, Godhra
28	IGI-1103	AAU, Godhra
29	GYL-2	AAU, Godhra
30	CML-307	AAU, Godhra
31	IGI-1102	AAU, Godhra
32	IGI-1104	AAU, Godhra
33	LTP-1-1	AAU, Godhra
34	LM-B-2	AAU, Godhra
35	LM-5	AAU, Godhra
36	H07R-1-3	AAU, Godhra
37	GWQPM-5-3	AAU, Godhra
38	GWQPM-11	AAU, Godhra
39	GWQPM-17-2	AAU, Godhra
40	GWQPM-22-5	AAU, Godhra
41	GWQPM-26-1	AAU, Godhra
42	GWQPM-26-3	AAU, Godhra
43	GWQPM-40-3	AAU, Godhra
44	GWQPM-40-5	AAU, Godhra
45	GWQPM-46-2	AAU, Godhra
46	GWQPM-47-1	AAU, Godhra
47	GWQPM-55-2	AAU, Godhra
48	GWQPM-67-2	AAU, Godhra
49	GWQPM-68-4	AAU, Godhra
50	I-07-54-3-2	AAU, Godhra
51	I-07-7-3-2	AAU, Godhra

Table.2 Genotypic and phenotypic correlation coefficients among different characters in maize (E_1: Anand)

		TA	**SI**	**PH**	**EH**	**EPP**	**EL**	**KPR**	**EG**	**KRP**	**NKE**	**EW**	**SH**	**TW**	**Pro**	**TSS**	**LYS**	**TRP**	**Car**	**GY**
TA	rg	1.00	0.98**	-0.09	0.05	0.28*	-0.05	0.00	0.48**	0.51**	0.16	-0.12	-0.33*	-0.53**	-0.49**	-0.11	-0.35*	-0.39**	0.24	-0.24
	rp	1.00	0.97**	-0.08	0.04	0.18	-0.07	0.00	0.27**	0.24*	0.11	-0.09	-0.28**	-0.28**	-0.44**	-0.11	-0.32**	-0.35**	0.22*	-0.18
SI	rg		1.00	-0.10	0.05	0.32*	-0.07	-0.02	0.51**	0.55**	0.16	-0.11	-0.33*	-0.51**	-0.52**	-0.11	-0.38**	-0.40**	0.28*	-0.21
	rp		1.00	-0.09	0.04	0.21*	-0.08	-0.01	0.28**	0.26**	0.11	-0.08	-0.28**	-0.27**	-0.46**	-0.11	-0.33**	-0.36**	0.26**	-0.15
PH	rg			1.00	0.82**	0.14	0.47**	0.55**	0.12	0.15	0.50**	0.60**	0.08	0.40**	0.15	-0.02	0.37**	0.31*	-0.22	0.50**
	rp			1.00	0.82**	0.08	0.37**	0.43**	0.09	0.09	0.38**	0.51**	0.06	0.25**	0.15	-0.02	0.33**	0.29**	-0.20*	0.34**
EH	rg				1.00	0.06	0.41**	0.44**	0.19	0.07	0.40**	0.40**	0.01	0.31*	0.27*	-0.11	0.29*	0.28*	-0.25	0.36**
	rp				1.00	0.01	0.34**	0.38**	0.15	0.07	0.33**	0.36**	0.01	0.22*	0.23*	-0.10	0.27**	0.27**	-0.23*	0.27**
EPP	rg					1.00	-0.02	0.04	0.28*	0.11	0.03	0.24	0.14	0.01	-0.07	0.27*	-0.20	-0.13	0.48**	0.00
	rp					1.00	0.04	0.08	0.03	-0.09	0.03	0.09	0.10	-0.04	-0.04	0.19	-0.15	-0.09	0.31**	0.02
EL	rg						1.00	0.64**	0.10	-0.07	0.54**	0.61**	0.00	0.05	0.18	-0.08	0.30*	0.22	-0.24	0.59**
	rp						1.00	0.63**	0.06	0.05	0.55**	0.52**	-0.01	0.04	0.12	-0.06	0.25**	0.19	-0.20*	0.51**
KPR	rg							1.00	0.13	0.25	0.94**	0.56**	0.03	0.14	0.22	-0.07	0.26	0.21	0.03	0.89**
	rp							1.00	0.00	0.12	0.87**	0.49**	0.02	0.10	0.16	-0.04	0.23*	0.19	0.04	0.70**
EG	rg								1.00	0.67**	0.33*	-0.07	-0.23	-0.41**	-0.32*	-0.14	-0.23	-0.30*	-0.07	0.03
	rp								1.00	0.75**	0.36**	0.10	-0.17	-0.20*	-0.20*	-0.11	-0.16	-0.21*	-0.07	0.19*
KRP	rg									1.00	0.53**	-0.20	-0.17	-0.32*	-0.53**	-0.26	-0.30*	-0.39**	0.24	0.25
	rp									1.00	0.567**	0.09	-0.11	-0.08	-0.26**	-0.17	-0.16	-0.22*	0.12	0.38**
NKE	rg										1.00	0.42**	-0.01	0.01	-0.01	-0.13	0.11	0.04	0.10	0.86**
	rp										1.00	0.44**	-0.02	0.05	-0.01	-0.10	0.10	0.03	0.09	0.76**
EW	rg											1.00	-0.08	0.25	0.02	0.00	0.21	0.11	-0.10	0.39**
	rp											1.00	-0.07	0.24*	0.02	0.00	0.19*	0.10	-0.09	0.40**
SH	rg												1.00	0.45**	0.12	-0.07	-0.02	0.06	0.13	0.29*
	rp												1.00	0.34**	0.10	-0.07	-0.02	0.06	0.13	0.22*
TW	rg													1.00	0.07	0.13	0.24	0.24	-0.12	0.37**
	rp													1.00	0.02	0.07	0.18	0.17	-0.09	0.30**
Pro	rg														1.00	0.05	0.26	0.47**	-0.17	0.19
	rp														1.00	0.05	0.24*	0.45**	-0.16	0.12
TSS	rg															1.00	0.16	0.21	0.04	-0.08
	rp															1.00	0.16	0.20*	0.04	-0.05
LYS	rg																1.00	0.86**	-0.30*	0.26
	rp																1.00	0.86**	-0.30**	0.18
TRP	rg																	1.00	-0.32*	0.33*
	rp																	1.00	-0.32**	0.24*
Car	rg																		1.00	-0.08
	rp																		1.00	-0.05
GY	rg																			1.00
	rp																			1.00

*, ** Significant at 5% and 1% levels, respectively

Fig.1 Experimental location (B. A. College of Agriculture, AAU, Anand)

Tryptophan showed positive and significant correlation at both the levels while ear girth showed positive and significant correlation with grain yield at phenotypic level. Bello *et al.,* (2010) recorded significant correlation of grain yield in maize with days to 50 per cent tasseling and 50 per cent silking, ear height, number of kernels per plant and plant height. Similar results were also recorded by Selvaraj and Pothiraj, (2011); Munawar *et al.,* (2013) and Gazal *et al.,* (2018).

Overall results of correlation studies revealed that grain yield per plant had positive and significant correlation with plant height, ear height, number of kernels per ear, number of kernels per row, ear weight, shelling percent and test weight. While days to 50 per cent tasseling and days to 50 per cent silking established negative but nonsignificant association in at both genotypic and phenotypic levels. Hence, Similar results were reported by Selvaraj and Pothiraj, (2011); Munawar *et al.,* (2013) and Aman *et al.,* (2020). Observable association among different characters is confirmed through phenotypic correlation, whereas true association could be known through genotypic correlation only, which eliminates environmental influence. Genotypic correlation permits prediction of correlated response and evaluation of relative influence of one character on other. Genotypic correlation in particular is helpful in construction of selection indices. Simultaneous improvement of grain yield and its attributing trait is possible and provide broad range to select breeding methodology for improving yield and yield contributing traits but it was not possible for days to 50 per cent tasseling and days to 50 per cent silking with grain yield which suggested that the breeding methodology has to be suitably framed for improving the earliness in maize.

References

Aman, J., Bantte, K., Alamerew, S., & Sbhatu, D. B. (2020). Correlation and path coefficient analysis of yield and yield components of quality protein maize (*Zea mays* L.) hybrids at Jimma, western Ethiopia. *International Journal of Agronomy*, 2020, 1-7.

Bello, O. B., Abdulmaliq, S. Y., Afolabi, M. S., & Ige, S. A. (2010). Correlation and path coefficient analysis of yield and agronomic characters among open pollinated maize varieties and their F_1 hybrids in a diallel cross. *African Journal of Biotechnology*, 9(18), 2633-2639.

Fisher, R. A., & Yates, F. (1963). *Statistical tables for biological, agricultural and medical research (6th ed.).* Oliver and Boyd, Edinburgh.

Gazal, A., Dar, Z. A., Lone, A. A., Yousuf, N., & Gulzar, S. (2018). Studies on maize yield under drought using correlation and path coefficient analysis. *International Journal of Current Microbiology and Applied Sciences*, 7(1), 516-521.

Hazel, L. (1943). The genetic bases for constructions of selection indices. *Genetics*, 28, 476-490.

Hofmann, F., Otto, M., & Wosniok, W. (2014). Maize pollen deposition in relation to distance from the nearest pollen source under common cultivation-results of 10 years of monitoring (2001 to 2010). *Environmental Sciences Europe*, 26(1), 1-14.

Matsuoka, Y., Vigouroux, Y., Goodman, M. M., Sanchez, J., Buckler, E., & Doebley, J. (2002). A single domestication for maize shown by multilocus microsatellite genotyping. *Proceedings of the National Academy of Sciences*, 99(9), 6080-6084.

Munawar, M., Shahbaz, M., Hammad, G., & Yasir, M. (2013). Correlation and path analysis of grain yield components in exotic maize (*Zea mays* L.) hybrids. *International Journal of Sciences: Basic and Applied Research*, 12(1), 22-27.

Popat, R., Patel, R. & Parmar, D. (2020). variability: Genetic Variability Analysis for Plant Breeding Research. R package version 0.1.0. CRAN Repository

Rebourg, C., Chastanet, M., Gouesnard, B., Welcker, C., Dubreuil, P., & Charcosset, A. (2003). Maize introduction into Europe: the history reviewed in the light of molecular data. *Theoretical and Applied Genetics*, 106(5), 895-903.

RStudio Team. (2015). *RStudio: Integrated Development Environment for R*. Boston, MA. Retrieved from http://www.rstudio.com/

Selvaraj, C. I., & Pothiraj, N. (2011). Interrelationship and path-coefficient studies for qualitative traits, grain yield and other yield attributes among maize (*Zea mays* L.). *International Journal of Plant Breeding and Genetics*, 5(3), 209-223.

Singh, R. K., & Choudhary, B. D. (1985). *Biometrical methods in quantitative genetics analysis (3rd ed.).* Kalyani publishers, New Delhi.

How to cite this article:

Rumit Patel, Dipak A. Patel, Dinesh J. Parmar and Praful Sondarava. 2022. Genotypic and Phenotypic Correlation Coefficient Study to Identify Best Yield and Yield Attributing Trait for Selection in Maize (*Zea mays* L.). *Int.J.Curr.Microbiol.App.Sci.* 11(01): 368-374.
doi: https://doi.org/10.20546/ijcmas.2022.1101.044