STUDIES ON CHARACTER ASSOCIATION AND PATH-COEFFICIENT ANALYSIS FOR KERNEL YIELD AND ITS ATTRIBUTING TRAITS IN MAIZE (*Zea mays* L.)

ABSTRACT

Correlation coefficient measures the strength of the relationship between independent traits on the dependent trait like yield, that helps breeder in selection for yield enhancement. In this view, the present experiment was carried out to assess the correlation coefficient and path analysis using twelve quantitative traits. Eleven lines, four testers and their 44 crosses along with five checks were evaluated in simple lattice design during *rabi* 2021-22. Analysis of variance revealed significant differences among entries for all the characters under study, suggested the presence of substantial amount of genetic variability. Correlation studies specifies that plant height, ear placement height, ear length, ear girth, kernel rows per ear, number of kernels per row, 100-kernel weight exhibited significant positive association with kernel yield and among themselves at genotypic and phenotypic levels, signifying the importance of these traits during selection. Path analysis revealed that highest positive direct effects on kernel yield was exhibited by ear girth, number of kernels per row and days to 50% tasseling. As a result, the current study could aid in the reliable selection of parental lines based on these traits, as well as the development of high yielding varieties for future breeding programs.

Keywords: correlation, path analysis, phenotypic, genotypic, traits

1. INTRODUCTION

Zea mays is third most important cereal crop followed by rice and wheat (Singh, 2017). Maize has high productivity and vast genetic potentiality compared to any other cereal crops (Muraya *et al*., 2017). “At present grain yield of maize in India is much lower than world average. It is mainly due to the poor genetic composition of the cultivars, non-availability of good quality seed of varieties/hybrids with high yield potential and less acclimatization of exotic hybrids due to biotic and abiotic stresses. Therefore, evolution of improved cultivars/hybrids of maize is the need of the day” (Prasad & Shivani, 2017). “In India, it is cultivated over an area of 9.89 m ha with a production and productivity of 31.60 million tonnes and 3199 kg ha^{-1} respectively”. (www.indiaagristat.com, 2020 – 21).

Approximately 64% of India's total maize crop is utilised for chicken and dairy feed, piggery and fish meal, 16% used for human consumption, 19% for industrial starch and beverage, and 1% for seed. The urge for maize in Asia is steadily increasing, owing to rising per capita GDP and a growing demand for biofuel production (Falcon, 2008 & Dixon *et al*., 2008).

Yield is a complex quantitative trait, often referred to as 'super character' considerably affected by environment and various yield components. "Selection on the basis of grain yield character alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and reliable" (Muhammad *et al*., 2003). "The character association analysis simply measures the relation between yield and other traits. Correlation between various characters is of immense value as it indicates the degree to which various characters of a plant are associated with the economic productivity" (Ahsan *et al*., 2008). "The relationship among characters can be directly observed as phenotypic correlation, while genotypic correlation indicates the magnitude to which two traits are genetically related" (Pavlov *et al*., 2015). "Both genotypic and phenotypic correlations among and between pairs of agronomic traits provide scope for indirect selection in a crop improvement programs" (Muhammad & Muhammad, 2001).

"Path coefficient analysis has been extensively utilized in plant breeding to determine the essence of relationships between kernel yield (response variable) and its attributing characters (predictor variables), and to identify those components with significant effect on yield for potential use as selection criteria" (Mohammadi *et al*., 2003). "The utmost advantage of path analysis is that it permits the partitioning of the correlation coefficient into two components. One component being the path coefficient that measure the direct effect of a predictor variable upon its response variable; the second component being the indirect effect (s) of a predictor variable on the response variable through another predictor variable" (Dewey & Lu, 1959).

"Understanding of correlation between yield and its component traits is a basic and leading attempt to find out guidelines for selection of plants. Partitioning of total correlation into direct and indirect effects by path coefficient analysis helps to make the selection more effective" (Priya & Joel, 2009). In view of the above, studies were conducted to estimate direct and indirect effects of agronomic traits on maize grain yield by the application of the simple coefficient correlation and path coefficient analysis.

2. MATERIAL AND METHODS

Experimental material and experimental design

Eleven diverse inbred lines (VL171488-2, VL18828, VL19978-6, VL19705-8, VL19255, VL18142, CAL1733-13, VL175869-14, SBL19564-20, SNL19582-22, SNL19588-23) were crossed with four testers (BML6, BML7, LM13, LM14) in Line x Tester mating design (Kempthorne, 1957) during *rabi*, 2020-21. Geographically the site is located at 15^0 55' North latitude and 80^0 30' East longitude and an altitude of 5.49 m above Mean Sea Level (MSL). The resultant 44 hybrids along with parents and 5 checks were evaluated in simple lattice design with two replications at Agricultural College Farm, Bapatla, India. Each entry was sown in two rows of 3 m length having 60 x 20 cm spacing. All the recommended package of practices and need based plant protection measures were adopted throughout the crop growth period. The statistical analysis was performed for the mean data recorded on five randomly selected plants of each entry from each replication for traits like days to 50% tasseling, days to 50% silking, days to maturity, plant height (cm), ear placement height (cm), ear length (cm), ear girth (cm), kernel rows per ear, No. of kernels per row, 100-kernel weight (g), protein content (%) and kernel yield per plant (g).

Statistical analysis

The analysis of variance for the studied yield and yield component traits was done as per the standard statistical procedure given by Rao (2007) for simple lattice design. Correlation coefficients were determined as described by Falconer (1964). Path coefficient analysis was carried out by using the correlation coefficients to know the direct and indirect effects of the component characters on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). The statistical software used for analysis of datais Windostat Version 9.3 from Indostat Services.

2.1 Phenotypic Correlation

$$\text{Phenotypic coefficient of correlation } (r_p) = = \frac{Cov(x_i x_j)_p}{\left[V(x_i)_p . V(x_j)_p\right]^{1/2}}$$

2.2 Genotypic Correlation

$$\text{Genotypic coefficient of correlation } (r_g) = \frac{Cov(x_i x_j)_g}{\left[V(x_i)_g . V(x_j)_g\right]^{1/2}}$$

Where,

$Cov(x_i x_j)$ = covariance between i^{th} and j^{th} characters

$V(x_i)$ and $V(x_j)$ = variance of i^{th} and j^{th} characters, respectively

g- genotypic; p- phenotypic

2.3 Path Analysis

$$r_{1,y} = P_{1,y} + r_{1,2} P_{2,y} + r_{1,3} P_{3,y} + . . . + r_{1,k} P_{k,y}$$

$$r_{2,y} = P_{1,y} + r_{2,1} P_{2,y} + r_{2,3} P_{3,y} + . . . + r_{2,k} P_{k,y}$$

$$r_{k,y} = r_{k,1} P_{1,y} + r_{k,2} P_{2,y} + r_{k,3} P_{3,y} + . . . + r_{k,k} P_{k,y}$$

Where,

$r_{1,y}$ to $r_{k,y}$ = Correlation coefficients between independent characters

$r_{1,2}$ to $r_{k-1,k}$ = Correlation coefficients between all possible combinations of independent characters

$P_{1,y}$ to $P_{k,y}$ = Direct effects of characters 1 to k on character y

3. RESULTS AND DISCUSSION

3.1 ANOVA

The statistical procedure that separates the total variation into different components is known as analysis of variance. Variability in a crop species is of utmost importance as it provides the basis for effective selection. Analysis of variance for yield and yield component traits studied in the present investigation of 64 entries were furnished in Table 1. Analysis of variance revealed significant differences among entries for all the characters under study, indicating the presence of high degree of variability.

3.2 CORRELATION ANALYSIS

Kernel yield, a complex trait that which relies on several yield attributing traits. Hence, correlation was studied to assess the relationship among kernel yield and its attributes for enhancing the usefulness of selection (Reddy and Jabeen, 2016). Correlation coefficients among 64 entries for 12 studied traits were presented in Table 2. The magnitude of genotypic correlation coefficient was higher than phenotypic correlation coefficients.

The kernel yield per plant had highly significant and positive correlations both at genotypic and phenotypic levels with plant height (r_g = 0.473 and r_p = 0.458), ear placement height (r_g =0.441 and r_p = 0.356), ear length (r_g = 0.690 and r_p = 0.584), ear girth (r_g = 0.789 and r_p = 0.501), kernel rows per ear (r_g =0.409 and r_p = 0.243), number of kernels per row (r_g = 0.857 and r_p = 0.641) and 100-kernel weight (r_g =0.699 and r_p = 0.316). Whereas days to 50% tasseling (r_g = -0.751 and r_p = -0.455), days to 50% silking (r_g = -0.699 and r_p = -0.453) and days to maturity (r_g = -0.599 and r_p= -0.465) having significant negative associations both at genotypic and phenotypic levels and protein content (r_g = -0.397 and r_p = -0.102) was having genotypic negative significant and phenotypic negative non-significant association.

These results were in agreement with Krishna *et al*. (2021) and Jagadev *et al*. (2021) for plant height (cm), ear placement height (cm), ear girth (cm), kernel rows per ear, No. of kernels per row, Gazal *et al*.

(2018) for 100-kenel weight (g) and protein content (%); Damtie *et al*. (2021) and Aman *et al*. (2020) for ear length (cm). The traits days to 50% tasseling, days to 50% silking and days to maturity were having negative significant association with kernel yield these results were in accordance with Krishna *et al*. (2021)and Damtie *et al*. (2021).

3.3 PATH ANALYSIS

The genotypic correlation coefficients calculated for different pairs of characters were subjected to path coefficient analysis (Table 3) for partitioning these values into direct and indirect effects. The highest positive and direct effect was found for ear girth (G =0.988 and P =0.291) and No. of kernels per row (G =0.737 and P =0.429) which indicates that more ear girth followed by number of kernels per row may directly contributes for higher kernel yield. The negative and direct effects was found for days to maturity (G = -2.223 and P = -0.138) and protein content (G = -0.330 and P = -0.043) both at genotypic and phenotypic levels. (Fig 1 and Fig 2).These results were in conformity with Reddy and Jabeen (2016) for ear girth, Lakshmi *et al*. (2018) and Krishna *et al*. (2021) for No. of kernels per row and Krishna *et al*. (2021) for days to maturity and Mallikarjuna (2019) for protein content.

It is extremely difficult in plant breeding to have complete knowledge of all yield component traits. The residual effect quantifies the impact of other possible independent variables that were not included in the study on the dependent variable. In the present study residual effect observed was 0.42 at genotypic level which means the characters in the present study may contribute to more than 58% for kernel yield and 0.61 at phenotypic level indicating that more than 39% of the characters included in the present study may contribute for kernel yield.
Similar reports of having genotypic (0.330) and phenotypic path (0.554) residual effects were reported by Dar *et al*., 2015 and Amegbor *et al*., 2022 with residual effect of (0.280).

4. CONCLUSION

The study of character associations for kernel yield, yield components characters revealed consistent positive correlations for important yield attributing traits like plant height, ear placement height, ear length, ear girth, No. of kernels per ear, kernel rows per cob and 100 kernel weight and hence, these characters may be given importance in the selection of high yielding genotypes. Whereas protein content had recorded negative association with kernel yield. The characters like days to 50% tasseling, days to 50% silking and days to maturity are also negatively correlated with kernel yield and hence, these characters may be given importance in the development of early maturity genotypes. In general, the genotypic correlations are higher than phenotypic correlations and suggested that observed relationships among the characters were due to genetic factors. Therefore, simultaneous selection for yield and yield contributing traits may not be possible and balanced selection criteria should be followed while adopting simultaneous selection for yield along with protein content.

Path analysis revealed that ear girth and No. of kernels per row had true relationship by establishing significant positive association and positive direct effect on kernel yield per plant whereas days to 50% tasseling, days to 50% silking, days to maturity and protein content showed true relationship by establishing significant negative association and negative direct effect on kernel yield per plant. Considering the nature and magnitude of correlation along with direct and indirect effects, it can be inferred that simultaneous improvement of kernel yield per plant is possible through manifestation of days to 50% tasseling, days to 50% silking, days to maturity, ear girth, No. of kernels per row and protein content.

Table 1: ANOVA for kernel yield and its contributing traits in maize (*Zea mays* L.)

SOV	D.f	DFT	DFS	DM	PH	EPH	EL	EG	KRPE	NKPR	HKW	PC	KYPP
	Mean Sum of Squares												
Replications	1	0.07	0.78	0.37	3.16	2.70	6.35	0.67	0.75	2.55	0.59	0.37	225.74
Treatments (Unadj)	63	44.80*	40.64*	1.88*	741.47*	368.85*	9.10*	1.98*	2.21*	31.78*	42.37*	1.88*	795.89*
Blocks within replications (Adj.)	14	17.97*	10.33	1.34	155.44	57.56	2.53	0.38	0.61	17.47*	7.52	1.34	204.77
Intrablock Error	49	5.91	5.83	1.01	118.51	40.98	1.68	0.59	0.89	8.31	21.03	1.01	199.35
Total	127	68.77	57.58	4.61	1018.59	470.10	19.66	3.62	4.46	60.11	71.52	4.61	1425.76

****Significant at 1% level**

*** Significant at 5% level**

DFT-Days to 50% tasseling, DFT-Days to 50% silking, DM-Days to maturity, PH-Plant height (cm), EPH- Ear placement height (cm), EL- Ear length (cm), EG- Ear girth (cm), KRPE- Kernel rows per ear, NKPR- Number of kernels per row, KYPP- Kernel yield per plant (g), HKW- 100 kernel weight (g), PC- protein content (%)

Table 2: Genotypic and Phenotypic correlation coefficients between kernel yield and its contributing characters in maize (*Zea mays* L.)

character	r	DFT	DFS	DM	PH	EPH	EL	EG	KRPE	NKPR	HKW	PC	KYPP
DFT	r_g	1.000	0.999**	0.986**	-0.952**	-0.706**	-0.753**	-0.413**	-0.159	-0.584**	-0.594**	0.579**	-0.751**
	r_p	1.000	0.980**	0.902**	-0.682**	-0.576**	-0.356**	-0.310**	-0.144	-0.275**	-0.286**	0.059	-0.455**
DFS	r_g		1.000	0.993**	-0.938**	-0.686**	-0.731**	-0.403**	-0.143	-0.494**	-0.588**	0.515**	-0.699**
	r_p		1.000	0.887**	-0.687**	-0.566**	-0.369**	-0.305**	-0.138	-0.289**	-0.255**	0.066	-0.453**
DM	r_g			1.000	-0.901**	-0.671**	-0.607**	-0.330**	-0.303*	-0.579**	-0.588**	0.707**	-0.599**
	r_p			1.000	-0.672**	-0.528**	-0.322**	-0.245**	-0.204*	-0.310**	-0.274**	0.081	-0.465**
PH	r_g				1.000	0.688**	0.518**	0.149	-0.010	0.522**	0.521**	-0.666**	0.473**
	r_p				1.000	0.561**	0.368**	0.173	0.032	0.343**	0.210*	-0.143	0.458**
EPH	r_g					1.000	0.616**	0.222	0.001	0.449**	0.291*	-0.237	0.441**
	r_p					1.000	0.413**	0.160	-0.022	0.273**	0.177*	-0.083	0.356**
EL	r_g						1.000	0.395**	-0.161	0.756**	0.683**	-0.084	0.690**
	r_p						1.000	0.369**	0.009	0.647**	0.431**	0.047	0.584**
EG	r_g							1.000	0.472**	0.282*	0.420**	-0.219	0.789**
	r_p							1.000	0.488**	0.227**	0.244**	0.025	0.501**
KRPE	r_g								1.000	0.035	-0.213	-0.577**	0.409**
	r_p								1.000	0.084	0.0012	-0.133	0.243**
NKPR	r_g									1.000	0.405**	-0.265*	0.857**
	r_p									1.000	0.120	-0.058	0.641**
HKW	r_g										1.000	-0.253*	0.699**
	r_p										1.000	-0.124	0.316**
PC	r_g											1.000	-0.397**
	r_p											1.000	-0.102
GYPP	r_g												1.000
	r_p												1.000

** Significant at 1% level

* Significant at 5% level

r_g – Genotypic level

r_p – Phenotypic level

DFT = Days to 50% Tasseling

DFS = Days to 50% Silking

DM = Days to Maturity

PH = Plant Height (cm)

EPH = Ear Placement Height (cm)

EL = Ear Length (cm)

EG = Ear Girth (cm)

KRPE = Kernel Rows Ear^{-1}

NKPR = Number of Kernels Row^{-1}

KYPP=Kernel Yield per Plant(g)

HKW = 100 Kernel Weight

PC = Protein Content (%)

Table 3: Direct (diagonal) and indirect effects (above and below the diagonal) of different traits on kernel yield per plant at genotypic and phenotypic level in maize (*Zea mays* L.)

		DFT	DFS	DM	PH	EPH	EL	EG	KRPE	NKPR	HKW	PC	KYPP
DFT	**G**	**0.965**	-1.259	-2.191	1.003	0.368	0.416	-0.430	0.470	-0.430	0.528	-0.191	-0.751**
	P	**-0.079**	0.118	-0.125	-0.089	-0.011	-0.027	-0.090	-0.005	-0.118	-0.027	-0.003	-0.455**
DFS	**G**	2.526	**-0.986**	-2.206	0.653	0.027	0.074	-0.42	-0.02	-0.364	0.187	-0.17	-0.699**
	P	-0.077	**0.120**	-0.122	-0.090	-0.011	-0.028	-0.089	-0.005	-0.124	-0.024	-0.003	-0.453**
DM	**G**	2.318	-1.251	**-0.983**	0.317	0.027	0.061	-0.654	0.249	-0.327	0.187	-0.543	-0.599**
	P	-0.071	0.106	**-0.138**	-0.088	-0.010	-0.025	-0.071	-0.007	-0.133	-0.026	-0.004	-0.465**
PH	**G**	-2.538	1.182	2.002	**-0.696**	-0.027	-0.052	0.155	0.008	0.385	-0.165	0.220	0.473**
	P	0.054	-0.082	0.093	**0.131**	0.011	0.028	0.050	0.001	0.147	0.020	0.006	0.458**
EPH	**G**	-1.882	0.865	1.492	-0.479	**-0.040**	-0.062	0.232	-0.001	0.331	-0.092	0.078	0.441**
	P	0.045	-0.068	0.072	0.073	**0.019**	0.032	0.046	-0.001	0.117	0.017	0.004	0.356**
EL	**G**	-2.009	0.922	1.350	-0.361	-0.025	**-0.101**	0.412	0.133	0.557	-0.217	0.028	0.690**
	P	0.028	-0.044	0.045	0.048	0.008	**0.076**	0.107	0.000	0.278	0.041	-0.002	0.584**
EG	**G**	-1.101	0.508	0.733	-0.104	-0.009	-0.04	**0.988**	-0.388	0.262	-0.133	0.073	0.789**
	P	0.024	-0.037	0.034	0.023	0.003	0.028	**0.291**	0.016	0.098	0.023	-0.001	0.501**
KRPE	**G**	-0.423	0.180	0.673	0.007	0.000	0.016	0.493	**-0.821**	0.026	0.068	0.190	0.409**
	P	0.011	-0.017	0.028	0.004	0.000	0.001	0.142	**0.032**	0.036	0.000	0.006	0.243**
NKPR	**G**	-1.557	0.623	1.288	-0.363	-0.018	-0.076	0.294	-0.029	**0.737**	-0.129	0.087	0.857**
	P	0.022	-0.035	0.043	0.045	0.005	0.049	0.066	0.003	**0.429**	0.012	0.003	0.641**
HKW	**G**	-1.582	0.741	1.306	-0.363	-0.012	-0.069	0.437	0.175	0.299	**-0.318**	0.083	0.699**
	P	0.022	-0.031	0.038	0.027	0.003	0.033	0.071	0.000	0.052	**0.096**	0.005	0.316**
PC	**G**	1.544	-0.649	-1.572	0.464	0.009	0.008	-0.229	0.473	-0.195	0.080	**-0.330**	-0.397**
	P	-0.005	0.008	-0.011	-0.019	-0.002	0.004	0.007	-0.004	-0.025	-0.012	**-0.043**	-0.102

** Significant at 1% level
DFT = Days to 50% Tasseling
EPH = Ear Placement Height (cm)
NKPR = Number of Kernels Row^{-1}

* Significant at 5% level
DFS = Days to 50% Silking
EL = Ear Length (cm)
KYPP=Kernel Yield per Plant(g)

G – Genotypic level
DM = Days to Maturity
EG = Ear Girth (cm)
HKW = 100 Kernel Weight

P – Phenotypic level
PH = Plant Height (cm)
KRPE = Kernel Rows ear^{-1}
PC = Protein Content (%)

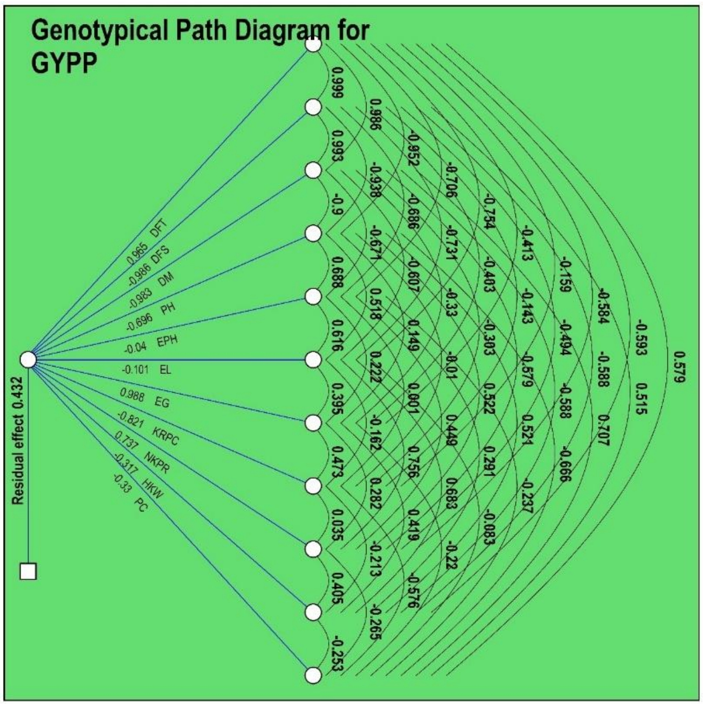

Fig 1: Genotypic path diagram showing direct and indirect effects of yield components on kernel yield in maize (*Zea mays* L.)

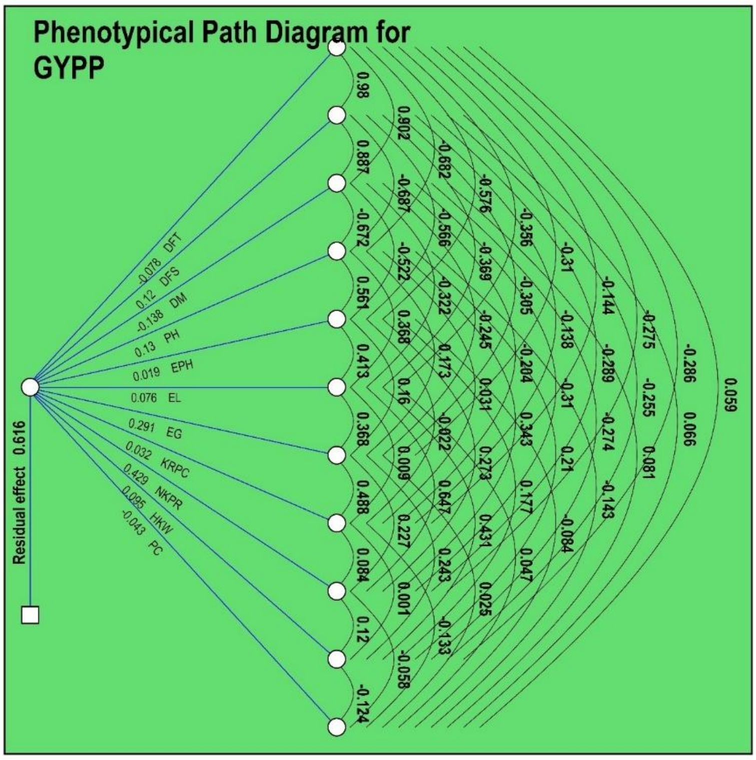

Fig 2: Phenotypic path diagram showing direct and indirect effects of yield components on kernel yield in maize (*Zea mays* L.)

Reference:

1. Ahsan, M., Hader, M. Z., Saleem, M. and Islam, M. Contribution of various leaf morpho-physiological parameters towards grain yield in maize. International Journal of Agricultural and Biology. 2008; 546-550.

2. Aman, J., Bantte, K., Alamerew, S and Sbhatu, D.B. 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;doi.org/10.1155/2020/9651537.

3. Amegbor, I.K., Van biljon, A., Shargie, N., Tarekegne, A and Labuschagne, M.T. 2022b. Heritability and associations among grain yield and quality traits in quality protein maize (QPM) and non-QPM hybrids. *Plants*. 11 (6): 713.

4. Damtie, Y., Assefa, G and Mulualem, T. Genetic variability, heritability, trait associations and path coefficient analysis of maize (*Zea mays* L.) inbred lines. *Journal of Current Opinion in Crop Science*. 2021; 2 (1): 86-94.

5. Dar, Z.A., Lone, A.A., Alaie, B.A., Ali, G., Gazal, A., Gulzar, S and Yousuf, N. Correlation studies in temperate maize (*Zea mays* L.) inbred lines. *Plant Archives*. 2015; 15 (2): 1191-1194.

6. Dewey, D. R and Lu, K. H. A correlation and path coefficient analysis of components of crestedwheat grass seed production. *Agronomy Journal*. 1959; 51:518

7. Dixon, J., Nalley, L and Hellin, J. Asian maize trade and value chains. In: Gulati, A., Dixon, J (Eds). Maize in Asia: changing markets and incentives, Academic Foundation, New Delhi. 2008; 457-460.

8. Falcon, W. P. The Asian maize economy in 2025. In: Gulati, A., Dixon, J (Eds). Maize in Asia: changing markets and incentives. Academic Foundation, New Delhi. 2008; 435-456.

9. Falconer, D.S. 1964. *An Introduction to Quantitative Genetics*. Oliver and Boyd, Edinburgh, London.

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

11. Jagadev, P.N., Kanungo, P and Lenka, D. Genetic variability, association and path coefficient studiesin quality protein maize inbreds. *The Pharma Innovation Journal*. 2021; 10 (12): 776-779.

12. Kempthorne, O. *An Introduction to Genetical Statistics*. John Willey and Sons Inc., New York. 1957; 323-331.

13. Krishna, B., Singh, B., Mandal, S.S., Rashmi, K. and Ranjan, T. Association and path coefficient analysis among grain yield and related traits in *kharif* maize (*Zea mays* L.). *The Pharma Innovation Journal*. 2021; 10 (7): 1062-1067.

14. Lakshmi, M.S., Jagadev, P.N., Das, S., Lenka, D., Swain, D and Tripathy, S.K. Genetic variability and association analysis of maize hybrids under excessive soil moisture condition. *Internantional Journal of Current Microbiology and Applied Science*. 2018; 7 (9): 2935-2941.

15. Mallikarjuna, S. Study of genetic diversity in elite inbred lines of (*Zea mays* L.). *M.Sc. Acharya N. G Ranga Agricultural University*, Guntur; 2019.

16. Ministry of Agriculture, Government of India. Indiastat. 2020-21. https://www.indiastat.com.

17. Mohammadi, S.A., Prasanna, B.M and Singh N.N. Sequential path model for determining interrelationships among grain yield and related characters in maize. *Crop Science*. 2003; 43:1690-1697.

18. Muhammad, B.A., Muhammad, R., Muhammad, S.T., Amer, H., Tariq, M and Muhammad, S.A. Character association and path coefficient analysis of grain yield and yield Components in maize. *Pakistan Journal of Biological Science*. 2003; 6 (2): 136-138.

19. Muhammad, Y and Muhammad, S. Correlation analysis of S1 families of maize for grain yield and its components. *International Journal of Agriculture and Biology*. 2001; 387-388.

20. Muraya, M.M., Chu, J., Zhao, Y., Junker, A., Klukas, C., Reif, J.C and Altmann, T. Genetic variation of growth dynamics in maize (*Zea mays* L.) revealed through automated non-invasive phenotyping. *Plant Journal*. 2017; 89:366–380.

21. Pavlov, J., Delic, N., Markovic, K., Crevar, M., Camdzija, and M. Stevanovic. Path analysis for morphological traits in maize (*Zea mays* L.). *Genetika*. 2015; 47 (1):295-301.

22. Prasad, B. and Shivani, D. Correlation and path analysis in maize (*zea mays* L.). *Journal of Genetics, Genomics and Plant Breeding*. 2017; 1 (2): 1-7.

23. Priya, A. A and Joel, A. J. Grain yield response of rice cultivars under upland condition. Electronic Journal of Plant Breeding. 2009; 1:6-11.

24. Rao, N.G. *Statistics for Agricultural Sciences*. BS Publications. Hyderabad. 2007; 262-267.

25. Reddy, V.R and Jabeen, F. Narrow sense heritability, correlation and path analysis. in maize (*Zea mays* L.). *SABRAO Journal of Breeding and Genetics*. 2016; 48 (2): 120-126.

26. Singh G. Genetic parameters and character association study for yield traits in maize (*Zea mays* L.). *Journal of Pharmacognosy and Phytochemistry*. 2017; 6:808–81.

27. Wright, S. Correlation and causation. *Journal of Agricultural Research*. 1921; 20: 557-585.