Original Research Article

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

ABSTRACT

An investigation was carried out to study the correlation and path coefficient analysis at Agricultural College Farm, Bapatla during *rabi* 2021-22 for kernel yield and its contributing traits. The experimental material consists of 44 hybrids, 15 parents and 5 checks *viz.,* P3396, DKC8171, P3546, DKC9120 and PAC751 which were raised in simple lattice design with two replications. Analysis of variance revealed significant differences among entries for all the characters under study, indicating the presence of high degree of variability. 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), 100-kernel weight (r_g =0.699 and r_p =0.316). The positive and direct effect was found for ear girth (G =1.043 and P =0.291) and No. of kernels per row (G =0.737 and P =0.429). 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.

Keywords: correlation, path analysis, maize

1. INTRODUCTION

Along with rice and wheat, maize (Zea mays L.) is one of the world's three most significant cereal crops. Maize is known as the "Queen of Cereals" around the world because it has the highest genetic production potential of all cereals (Kumari *et al.* 2016). It is the only cultivated species in the Maydeae tribe of the Poaceae family with greater economic value, and it plays a critical role in global food and nutritional security. Being a C4 plant, it is physiologically more efficient, yields more grain, and adapts to a wider range of environments. Maize is expected to overtake rice as the world's most important grain by 2030, owing to rising demand for dairy and meat products in developing countries and declining rice production in China and India (Salvi *et al*., 2007).

Yield is a complex quantitative trait, often referred to as ‘super character’ considerably affected by environment and various yield components. Therefore, selection of genotypes based on yield is not effective. A thorough understanding of the interaction of characters among themselves had been of great use in plant breeding.

The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. However, if the correlation is mainly due to the indirect effect of the character through other component traits, the breeder has to select for the particular character through which the indirect effect is expected to improve yield. Thus, correlation coefficients are also useful if an indirect selection of a secondary trait is to be used for improving the primary trait of interest (Muhammad & Muhammad, 2001).

Path coefficient analysis has been widely used in crop breeding to determine the nature of relationships between grain yield (response variable) and its contributing components (predictor variables), and to identify those components with significant effect on yield for potential use as selection criteria (Mohammadi *et al*., 2003). The major 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).

2. MATERIAL AND METHODS

Experimental material and experimental design

3. RESULTS AND DISCUSSION

Kernel yield is a complex trait and is dependent on several contributing traits.

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, 2021-22. The resultant 44 hybrids along with parents and 5 checks were evaluated at Agricultural College Farm, Bapatla, Guntur, India. Each entry was sown in two rows of 3 m length having 60 x 20 cm spacing. 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-kenel 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 Singh and Chaudhary (1979). The statistical software used for analysis of data is R software and INDOSTAT 9.1.

Hence, correlation was studied to know the relationship among kernel yield and its contributing traits for enhancing the usefulness of selection (Reddy and Jabeen, 2016).

The statistical procedure that seperates 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.

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), 100-kernel weight (r_g =0.699 and r_p =0.316) were presented in Table 2. 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*. (2021) 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).

The genotypic correlation coefficients calculated for different pairs of characters were subjected to path coefficient analysis for partitioning these values into direct and indirect effects. The positive and direct effect was found for ear girth (G =1.043 and P =0.291) and No. of kernels per row (G =0.737 and P =0.429). 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 and were pesented in Table 3; Fig 1 and Fig 2.

In plant breeding, it is very difficult to have complete knowledge on all component traits of yield. Residual effect measures the role of other possible independent variables which are 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 residual effect was 0.61 at phenotypic level indicating that more than 39% of the characters included in the present study may contribute for kernel yield.

These results were in conformity with Reddy and Jabeen (2016) for ear girth, No. of kernels per row and Krishna *et al*. (2021) for days to maturity.

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.

REFERENCES

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

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

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

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

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

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

Kumari, R., Singh, A.K and Sharma, V.K. 2016. Heterosis and genetic divergence correlation studies for yield and its related traits in maize (*Zea mays* L.). *The Bioscan*. 11 (3): 1849-1854.

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

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

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

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

Salvi, S., Sponza, G and Morgante, M. 2007. Conserved noncoding genomic sequences associated with a flowering-time quantitative trait locus in maize. *Proceedings of the National Academy of Sciences of the United States of America.* 104: 11376- 11381.

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**	**2.666**	-1.259	-2.191	0.663	0.028	0.076	-0.430	0.130	-0.430	0.188	-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**	2.664	**-1.260**	-2.206	0.653	0.027	0.074	-0.420	0.117	-0.364	0.187	-0.170	-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**	2.628	-1.251	**-2.223**	0.627	0.027	0.061	-0.344	0.249	-0.327	0.187	-0.233	-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	-0.040	**1.043**	-0.388	0.208	-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)

* Significant at 5% level
DFS = Days to 50% Silking
EL = Ear Length (cm)

G – Genotypic level
DM = Days to Maturity
EG = Ear Girth (cm)

P – Phenotypic level
PH = Plant Height (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 (%)

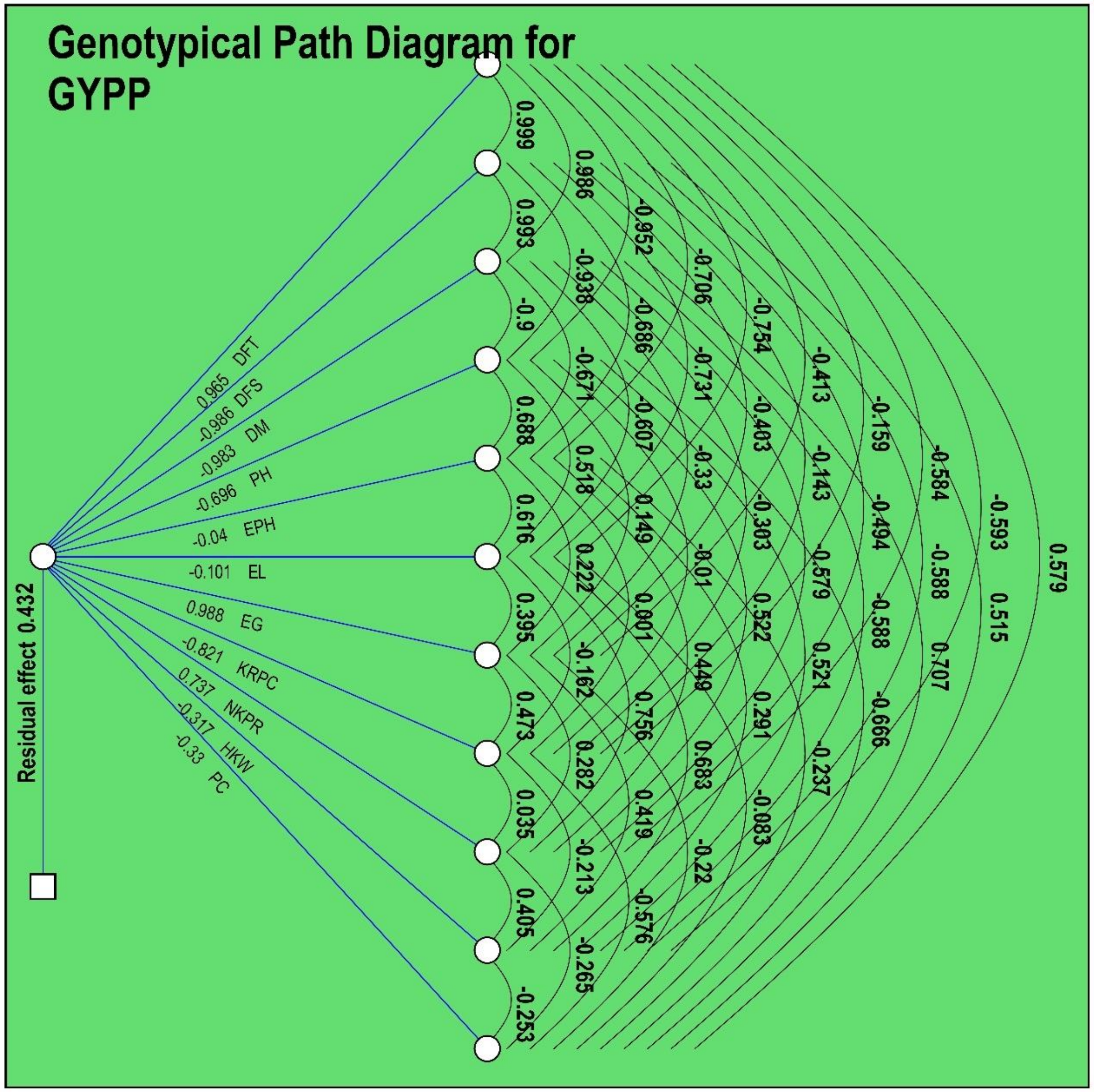

Fig 1: Genotypic path diagram showing direct and indirect effects of yield components on kernel yield in maize (*Zea mays* L.)

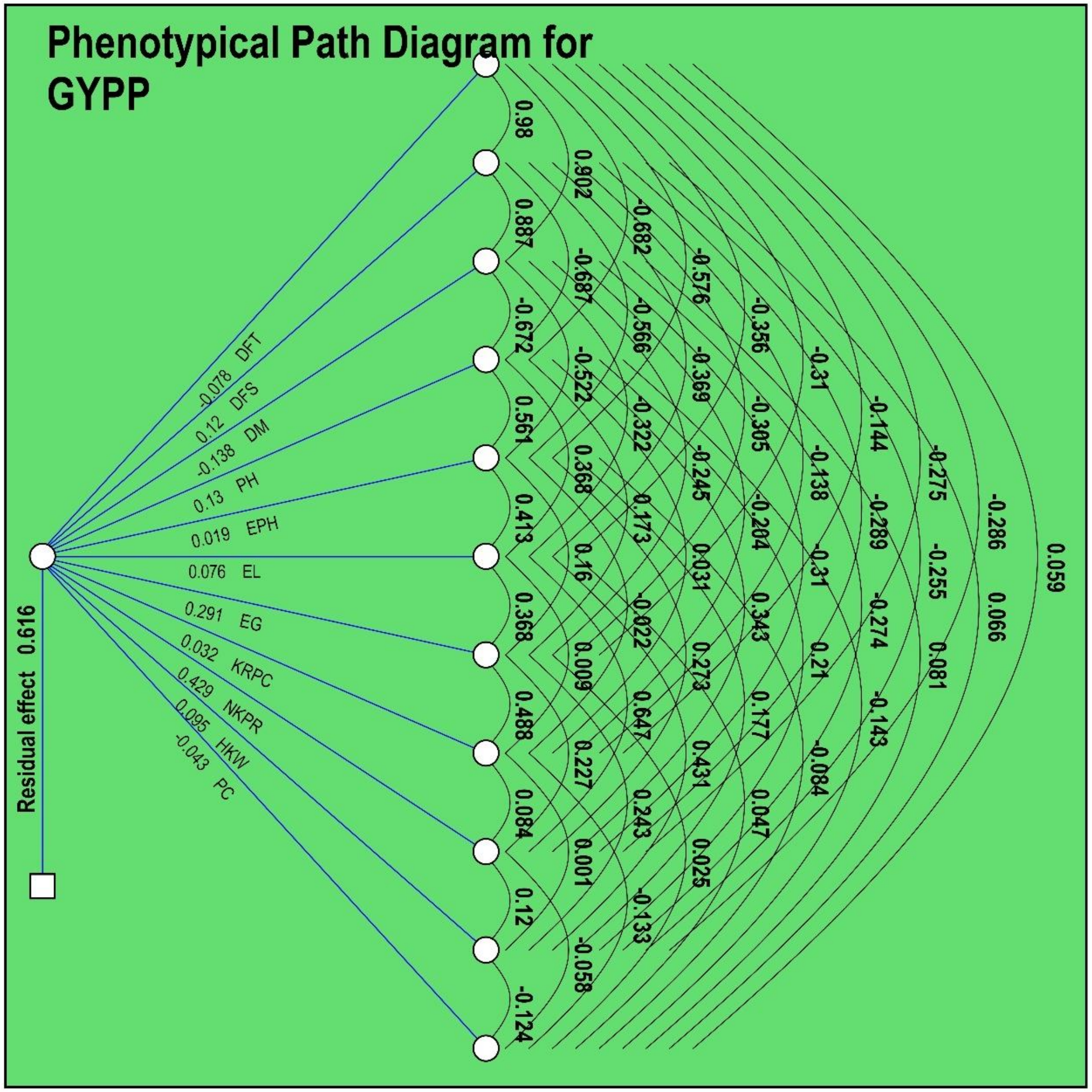

Fig 2: Phenotypic path diagram showing direct and indirect effects of yield components on kernel yield in maize (*Zea mays* L.)