Maize Journal (April 2025) 14(1): 69-81

RESEARCH PAPER

Genetic variability and character association for floral, yield and it's components in maize (*Zea mays* L.) inbred lines

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Abstract The present study was conducted to determine the nature and magnitude of genetic variability and character association for floral, yield and it's component traits of maize inbred lines. The experiment was conducted during *rabi,* 2022-23 at Agricultural Research Station, Peddapuram, Andhra Pradesh. A set comprising of 112 maize inbred lines was evaluated using alpha lattice design with two replications. The analysis of variance (ANOVA) for 18 metric traits revealed existence of ample genetic variation in these inbred lines. The result showed the existence of high heritability along with high genetic advance, higher phenotypic and genotypic coefficient of variation for anthesis-silking interval, number of kernels per row, 100-kernel weight, ear yield per plant and kernel yield per plant indicating the predominance of additive gene action. Hence, direct phenotypic selection using these traits may be useful for improvement in maize. Yield attributing characters; plant height, tassel size, ear height, ear position, ear girth, kernel rows per ear, number of kernels per row, shelling percentage, 100-kernel weight, ear yield per plant may be given due importance in selection of inbred lines as these characters recorded consistent positive correlation with kernel yield per plant. The path analysis also confirmed the effectiveness of indirect selection based on traits like plant height, tassel size, tassel extrusion, number of kernels per row, 100-kernel weight and ear yield per plant in enhancing kernel yield with the present genetic material indicating that the characters included in the present study clearly explained the direct and indirect effects to some extent on the dependent variable.

Keywords: Maize • Variability • Inbred • Correlation • Path analysis

Introduction

Maize (*Zea mays* L.), the 'Queen of Cereals' is one of the major cereals cultivated throughout the world after rice and wheat. It belongs to the tribe Maydeae of family, Poaceae. The plant is native to South America. *Zea mays* is the only species in cultivation from the genus *Zea* which has chromosome number; 2n=20. Maize is known as the poor man's nutricereal as it's grain is having an extensive nutritional value *i.e.*, rich in various vitamins, proteins and carbohydrates. It provides food, feed, fodder, fuel and serves as raw material for several industry products *viz*., starch, oil, protein, alcoholic beverages, food sweeteners, cosmetics and biofuel.

Maize is widely cultivated throughout the world. In India, maize is the third most important cereal crop after rice and wheat and it occupies an area of 10.04 mha with a production of 33.62 mt and average productivity of 3349 kg ha^{-1} (agricoop.nic.in, 2024). In Andhra Pradesh, it is cultivated in an area of 0.34 mha with a production of 2.05 mt and average productivity of 5990 kg ha^{-1} (Agricultural Statistics at Glance, AP, 2023-24).

Genetic variability is pre-requisite and important tool of any breeding programme. It provides not only the basis of selection but also some valuable information regarding selection of diverse parents for hybridization programme. Knowledge of these genetic parameters is essential for

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Received: 18 November 2024/ Accepted: 24 March 2025

successful breeding in maize. The genetic variability contained in the breeding material employed in the program is critical for a successful plant breeding program (Khan *et al*., 2017). The effectiveness with which genotypic variability can be exploited by selection is determined by the heritability of individual trait and genetic advance. Heritability is utilized to determine the genetic advance *i.e*., degree of gain in characteristics achieved under specific selection pressure. As a result, genetic progress is a critical selection attribute that supports the breeder in a selection procedure (Shukla *et al*., 2004). Information on the interrelationships between quantitatively inherited plant features and their direct and indirect consequences on grain production is critical for successful breeding programmes (Khan *et al*., 2006). Precise information on the genetic parameters such as coefficient of variation, heritability, genetic advance and the influence of environment on the expression of yield and yield components, helps the breeder in the selection of diverse parents for the exploitation of heterosis (Singh *et al.,* 2020).

Yield is a complex quantitative trait that is greatly influenced by the environment. As a result, genotype selection based on yield alone is ineffective. The direction and degree of relationship between yield and it's contributing components determines the efficiency of breeding effort. Thus, by examining the relative influence of different characters on yield and with each other, the correlation analysis assists in determining the character or combination of characters that could be useful as an indicator of high yield. As a result, knowledge of the correlation coefficients between grain yield and its components is critical for yield enhancement. Path analysis is a standardized partial regression coefficient that divides the total correlation coefficient into direct and indirect effects, as well as measuring the direct and indirect contributions of each independent variable on to the dependent variable. The knowledge gained through correlation and path coefficient analyses can be utilized to establish selection criteria for improving grain yield. Hence, the present study was planned to determine the estimates of genetic variability and association for yield components in the used set of maize inbred lines.

Materials and methods

The experimental material used in the present study comprising of 112 maize inbred lines, evaluated during

Table 1. List of maize inbred lines studied during *rabi* 2022-23 at Agricultural Research Station, Peddapuram

Entry	Pedigree	Source of the material
1	PL 22424	ARS, Peddapuram
2	PL 22429	ARS, Peddapuram
3	PL 22394	ARS, Peddapuram
4	PL 22396	ARS, Peddapuram
5	PL 22436	ARS, Peddapuram
6	PL 22444	ARS, Peddapuram
7	PL 22440	ARS, Peddapuram
8	PL 22389	ARS, Peddapuram
9	PL 22408	ARS, Peddapuram
10	PL 22426	ARS, Peddapuram
11	PL 22449	ARS, Peddapuram
12	PL 22445	ARS, Peddapuram
13	PL 22422	ARS, Peddapuram
14	PL 22428	ARS, Peddapuram
15	PL 22431	ARS, Peddapuram
16	PL 22434	ARS, Peddapuram
17	PL 22401	ARS, Peddapuram
18	PL 22427	ARS, Peddapuram
19	PL 22421	ARS, Peddapuram
20	PL 22407	ARS, Peddapuram
21	PL 22390	ARS, Peddapuram
22	PL 22392	ARS, Peddapuram
23	PL 22397	ARS, Peddapuram
24	PL 22448	ARS, Peddapuram
25	PL 22399	ARS, Peddapuram
26	PL 22393	ARS, Peddapuram
27	PL 22417	ARS, Peddapuram
28	PL 22432	ARS, Peddapuram
29	PL 22404	ARS, Peddapuram
30	PL 22416	ARS, Peddapuram
31	PL 22402	ARS, Peddapuram
32	PI394	ARS, Peddapuram
33	PI 395	ARS, Peddapuram
34	PI 1	ARS, Peddapuram
35	PI 397	ARS, Peddapuram
36	PI 398	ARS, Peddapuram
37	PI 399	ARS, Peddapuram
38	PI 400	ARS, Peddapuram
39	PI 401	ARS, Peddapuram
40	PI 402	ARS, Peddapuram
41	PI 403	ARS, Peddapuram
42	PI 404	ARS, Peddapuram

Table 1 contd....

Entry	Pedigree	Source of the material
43	PI 405	ARS, Peddapuram
44	PL 22435	ARS, Peddapuram
45	PL 22398	ARS, Peddapuram
46	PL 22395	ARS, Peddapuram
47	PL 22414	ARS, Peddapuram
48	PL 22413	ARS, Peddapuram
49	PL 22425	ARS, Peddapuram
50	PL 22420	ARS, Peddapuram
51	PL 22400	ARS, Peddapuram
52	PL 22406	ARS, Peddapuram
53	PL 22433	ARS, Peddapuram
54	PL 22443	ARS, Peddapuram
55	PL 22419	ARS, Peddapuram
56	PL 22418	ARS, Peddapuram
57	PL 22391	ARS, Peddapuram
58	PL 22412	ARS, Peddapuram
59	PL 22415	ARS, Peddapuram
60	PL 22405	ARS, Peddapuram
61	PL 22423	ARS, Peddapuram
62	PL 22439	ARS, Peddapuram
63	PL 22409	ARS, Peddapuram
64	PL 22441	ARS, Peddapuram
65	PL 22411	ARS, Peddapuram
66	PL 22437	ARS, Peddapuram
67	PL 22430	ARS, Peddapuram
68	PL 22450	ARS, Peddapuram
69	PL 22442	ARS, Peddapuram
70	PL 22447	ARS, Peddapuram
71	PL 22410	ARS, Peddapuram
72	PL 22446	ARS, Peddapuram
73	PL 22403	ARS, Peddapuram
74	PL 22438	ARS, Peddapuram
75	PI 406	ARS, Peddapuram
76	PI 407	ARS, Peddapuram
77	PI 408	ARS, Peddapuram
78	PI 409	ARS, Peddapuram
79	PI 410	ARS, Peddapuram
80	PI 411	ARS, Peddapuram
81	PI 412	ARS, Peddapuram
82	PI 413	ARS, Peddapuram
83	PI 414	ARS, Peddapuram
84	PI 415	ARS, Peddapuram
85	PI 416	ARS, Peddapuram

Table 1 contd....

Entry	Pedigree	Source of the material
86	PI UK	ARS, Peddapuram
87	PI 417	ARS, Peddapuram
88	PI 418	ARS, Peddapuram
89	PI 419	ARS, Peddapuram
90	PI 420	ARS, Peddapuram
91	PI 421	ARS, Peddapuram
92	PI 422	ARS, Peddapuram
93	PI 423	ARS, Peddapuram
94	PI 424	ARS, Peddapuram
95	PI 425	ARS, Peddapuram
96	PI 426	ARS, Peddapuram
97	PI 427	ARS, Peddapuram
98	PI 428	ARS, Peddapuram
99	CML72	CIMMYT
100	UMI1200	TNAU, Coimbatore
101	CML425	CIMMYT
102	CML451	CIMMYT
103	CML474	CIMMYT
104	CML581	CIMMYT
105	CML582	CIMMYT
106	CL02450	CIMMYT
107	LM13	PAU, Ludhiana
108	LM14	PAU, Ludhiana
109	BML6	PJTSAU, Hyderabad
110	BML7	PJTSAU, Hyderabad
111	BML45	PJTSAU, Hyderabad
112	CAL1812	CIMMYT

rabi, 2022-23 using alpha lattice design at Agricultural Research Station, Peddapuram, Andhra Pradesh which is located at a latitude of 17º.07' N, longitude of 82º.14' E and altitude of 46.26 meters above mean sea level (MSL) and soil texture is sandy loam. The whole experimental area was divided into two replications. Each replication consisted of 28 blocks. In each block, 4 inbred lines were allocated and each inbred line was planted in two rows each of 4 meter in length with spacing of 60 cm between rows and 20 cm between plants within row. The recommended package of practices and need based plant protection measures were adopted throughout the crop growth period to raise a good crop. Observations on various floral and yield parameters were recorded on five plants selected at random from each entry in each replication *viz*., days to 50% silking, days to 50% tasseling based on plot, anthesis-silking interval, plant height, tassel height, tassel extrusion, tassel size, ear height, ear position, ear diameter (cm), ear length (cm), days to maturity, number of kernel rows per ear, number of kernels per row, 1000-grain weight, ear yield per plant, grain yield per plant (kg) and shelling percentage. Ear position was measured with the ratio of ear height /plant height. Analysis of variance was carried out as suggested by Panse and Sukhatme (1978). GCV and PCV were carried out as suggested by Burton (1952) and Singh and Choudhary (1979). Heritability (BS) and genetic advance were estimated by using formula suggested by Burton and De-Vane (1953) and Lush (1949).

Results and discussion

Analysis of variance

The statistical technique known as analysis of variance divides the total variation into its component parts. It is crucial that a crop species exhibits variability which creates the framework for efficient selection. Table 2 provides the results of the analysis of variance for the 112 inbred lines for floral traits, yield and it's component traits. For all the characters, the analysis of variance revealed significant variations among the inbred lines, indicating the presence of enough genetic variability for exploitation. In the present study, the genotypic coefficient of variation for all the characters was less than phenotypic coefficient of variation indicating larger influence of environment in the expression of a trait, meaning that environmental factors have a greater impact on the observed variation than genetic factors alone.

Genotypic and phenotypic coefficients of variation

The maximum coefficient of genotypic and phenotypic variation was recorded in the Anthesis-silking interval (47.23 and 71.57%), kernel yield per plant (28.35 and 36.14%) and ear yield per plant (27.55 and 39.45%) It indicates that there was greater variation among the inbred lines studied for these traits while high PCV and moderate GCV respectively, were detected in the ear height (28.85 and 19.81%), ear position (24.90 and 10.84%) and 100-kernel weight (22.12 and 18.89%) (Table 3 and Figure 1).

In the present study, moderate PCV and GCV respectively, were observed in number of kernels per

Table 2. Analysis of variance for 18 characters under study in maize (*Zea mays* L.)

	df	Mean sum of squares							
		Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Plant height (cm)	Tassel height (cm)	Tassel extrusion	Tassel size	Ear height (cm)	Ear position
Replications	1	2.571	4.018	0	3689	100.45	0.00446	2.3616	2958	0.02587
Treatments	111	14.935**	15.754**	2.634**	930**	24.39**	0.164*	0.495*	516.5**	0.0123*
Blocks within replication	26	3.155	2.942	1.38	511	10.96	0.083	0.169	195.4	0.084
Residuals	85	2.687	3.065	0.930	455	10.07	0.11	0.467	182.5	0.008

	df	Ear length (cm)	Ear girth (cm)	Days to maturity	Kernel rows per ear	No. of kernels per row	Shelling percentage	100 kernel weight (g)	Ear yield per plant (g)	Kernel yield per plant (g)
Replications	1	0	0.0015	42.87	0.677	0.896	1054.8	3.25	1228	265.1
Treatments	111	7.746*	1.765**	58.11*	3.534**	24.739**	213.9*	63.25**	1731.1**	1263.4**
Blocks within replication	26	5.471	0.729	34.03	1.775	13.907	163.8	13.75	343.9	429.4
Residuals	85	5.304	0.5485	43.73	1.111	6.549	209.2	8.69	433.7	437.9

DF: Degrees of freedom; Where * and ** significant at 5% and 1% level of significance respectively

Table 3. Estimates of genetic parameters for 18 characters under study in maize (*Zea mays* L.)

Genetic Parameters	Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Plant height (cm)	Tassel height (cm)	Tassel extrusion	Tassel size	Ear height (cm)	Ear position
GCV %	3.77	3.75	47.23	9.61	8.41	3.57	6.23	19.81	10.84
PCV %	4.56	4.56	71.57	16.73	13.18	7.50	20.47	28.85	24.90
Heritability (Broad Sense) %	68.50	67.70	43.50	33.00	40.70	22.70	9.30	47.10	19.00
Genetic Advance	4.20	4.27	1.22	17.99	3.49	0.17	0.13	18.20	0.04
Genetic Advance as % of Mean	6.43	6.36	64.21	11.38	11.05	3.51	3.90	28.02	9.73
General Mean	65.35	67.21	1.89	158.03	31.60	2.32	1.93	64.94	0.41
Minimum	58.50	60.50	0.00	110.00	23.00	1.87	1.58	32.50	0.25
Maximum	73.00	75.00	6.50	202.50	43.50	2.35	2.35	102.50	0.81

Table 3 contd...

Genetic Parameters	Ear length (cm)	Ear girth (cm)	Days to maturity	Kernel rows per ear	Number of kernels per row	Shelling percentage	100 kernel weight (g)	Ear yield per plant (g)	Kernel yield per plant (g)
GCV %	11.87	6.35	2.37	8.31	12.46	1.27	18.89	28.35	27.55
PCV %	16.09	8.99	5.80	12.06	17.63	9.40	22.12	36.14	39.45
Heritability (Broad Sense) %	54.50	49.90	16.70	47.50	50.00	1.80	72.90	61.50	48.80
Genetic Advance	2.02	1.12	2.43	1.51	4.18	0.29	9.08	41.49	29.29
Genetic Advance as % of Mean	18.05	9.24	2.00	11.80	18.15	0.35	33.23	45.80	39.64
General Mean	11.19	12.07	121.64	12.82	23.04	82.92	26.91	90.59	77.90
Minimum	7.00	10.17	86.50	10.15	15.50	52.35	17.40	28.35	42.50
Maximum	15.67	16.42	130.00	15.65	34.70	89.32	35.85	245.65	199.50

PCV: Phenotypic coefficient of variation GCV: Genotypic coefficient of variation

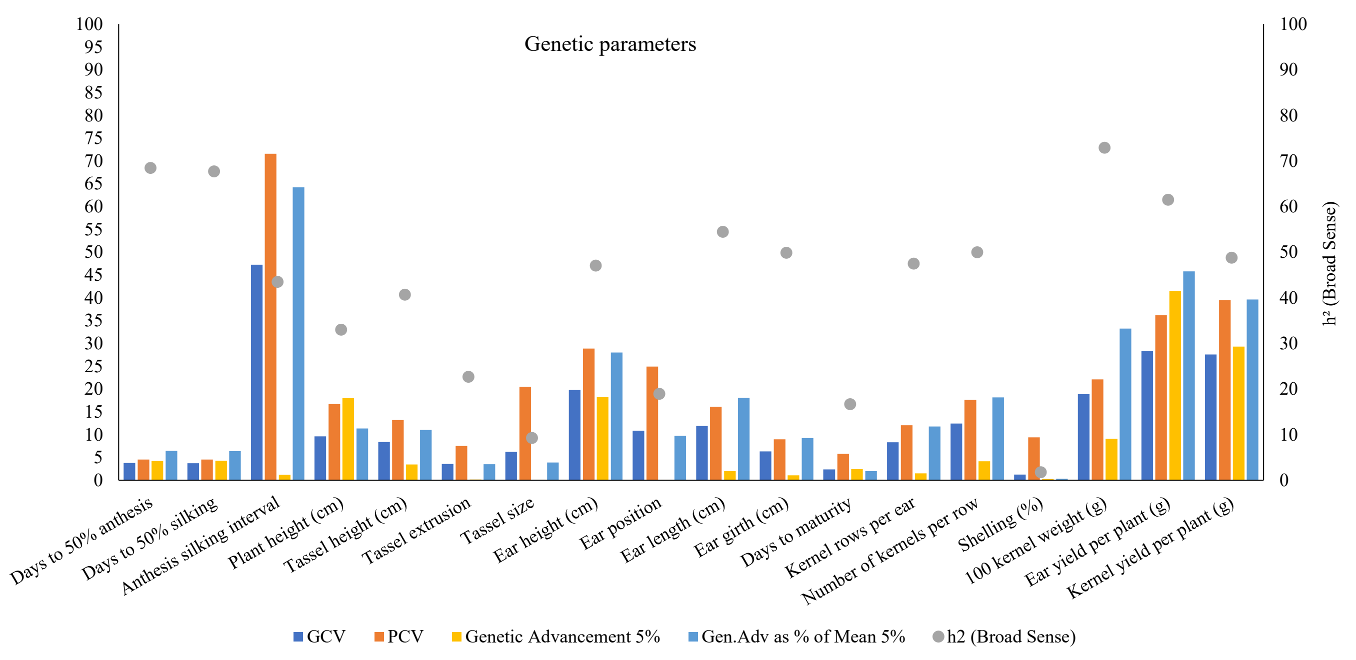

Figure 1. Pattern of GCV, PCV, Genetic advance as percent of mean and heritability for various traits in 112 inbred lines of maize (*Zea mays* L.)

row (12.46 and 17.63%) and ear length (11.87 and 16.09%). The smallest PCV and GCV respectively, were found in ear girth (6.35 and 8.99%), kernel rows per ear (8.31 and 12.06%), days to 50% anthesis (3.77 and 4.56%), days to 50% silking (3.75 and 4.56%), tassel extrusion (3.57 and 7.50%), days to maturity (2.37 and 5.80%) and shelling percentage (1.27 and 9.40%). It indicates that there was less variation among the inbred lines for these trait. The difference between PCV and GCV values was high indicating the greater role of environmental factors on the expression of this trait.

The high PCV and low GCV were found in tassel size (6.23 and 20.47%) while moderate PCV and low GCV were detected in the plant height (9.61 and 16.73%) and tassel height (8.41 and13.18 %).

Heritability and genetic advance

Anthesis-silking interval, 100 kernel weight, ear yield per plant, showed high heritability (68.50%), (72.90%), (61.50%) combined with high genetic advance as a percentage of the mean (64.21%), (33.23%), (45.80%), respectively. It indicates the preponderance of additive gene effects and the use of simple selection for the improvement of these traits. Similar results were also reported by Veeravishnu *et al*. (2023) for days to 50% anthesis, ear yield per plant and 100-kernel weight whereas Nataraj *et al.* (2014) and Simran *et al.* (2022) for days to 50% silking (Table 3).

Plant height, tassel height, kernel rows per ear, number of kernels per row exhibited moderate heritability (33.00%), (40.70%), (47.50%), (50.00%) and moderate genetic advance as a per cent of mean (11.38%), (11.05%), (11.80%), (18.15%), respectively. It indicating the involvement of both additive and non-additive gene effects in their inheritance. Similar kinds of results were reported by Simran *et al.* (2022) and Veeravishnu *et al.* (2023) for number of kernels per row and kernel yield per plant.

Tassel extrusion, Tassel size, ear position, days to maturity showed low heritability (22.70), (9.30), (19.00%), (16.70%), (16.70%) and low genetic advance as a per cent of mean (3.51%), (3.90%), (9.73%), (9.73%), (2.00%), respectively. It indicates the major influence of non-additive gene effects in its inheritance. Similar results were also reported by Sravanti *et al.* (2017) and Lemi *et al.* (2022) for days to maturity.

Correlation analysis

When a plant breeder aims to integrate high yield potential, understanding the correlation between yield and it's component traits becomes crucial. Correlation studies offer valuable insights into the extent and direction of the associations between the traits. The character associations for kernel yield and yield components displayed similar trends in both phenotypic and genotypic correlations. Genotypic correlation values were generally higher than phenotypic correlation values indicating less environmental influence on these traits (Table 4; Figure 2 and 3).

In the present study, significant positive phenotypic and large genotypic association of plant height (r_p=0.392**, r_g=0.381**), tassel size (r_p=0.177*, r_g=0.170*), ear height (r_p=0.359**, r_g=0.345**), ear position (r_p=0.136*, r_g=131*), ear length (r_p=0.472**, r_g=0.468**), ear girth (r_p=0.439**, r_g=0.438**), kernel rows per ear (r_p=0.145*, r_g=0.143*), number of kernels per row (r_p=0.442**, r_g=0.442**), shelling percentage (r_p=0.239**, r_g=0.210*), 100-kernel weight (r_p=0.414**, r_g=0.415**) and ear yield per plant (r_p=0.851**, r_g=0.851**) were observed with kernel yield per plant. Hence, these traits can be utilized in indirect selection to improve the yield per plant. These results are in accordance with reports of Emmanuel *et al.* (2023) for days to plant height and ear height; Sayed *et al.* (2022) for ear length; Bal Krishna *et al.* (2021) for ear girth, 100-kernels weight, kernel rows per ear and the number of kernels per row.

On contrary, significant negative association of days to 50% silking (r_p= -0.188*, r_g= -0.186*) with kernel yield per plant was observed indicating that increase in number of days to silking leads to linear decrease in kernel yield per plant. These results are in accordance with the reports of Raghu *et al.* (2011) for days to 50% silking.

From the correlation studies it can be concluded that the dependent variable kernel yield per plant had significant positive correlation with the independent variables viz., plant height, tassel size, ear height, ear position, ear girth, kernel rows per ear, number of kernels per row, shelling percentage, 100-kernel weight and ear yield per plant. Traits like tassel height, tassel extrusion and days to maturity had positive non-significant correlation with kernel yield per plant. Whereas the traits, days to 50% anthesis, days to 50% silking and anthesis silking interval showed negative correlation with yield. So, it can be inferred that simultaneous selection for yield traits may not be possible hence, balanced selection criteria should be followed depending on the objective in the plant breeding programmes.

Path coefficient analysis

Path coefficient analysis is a valuable tool for dissecting correlation coefficients into direct and indirect effects of different yield component traits on kernel yield. It provides valuable insights into the specific factors contributing to the observed correlations and allows for a comprehensive examination of the forces influencing these relationships. Additionally, it helps to determine the relative importance of each causal factor in influencing kernel yield. The path coefficient analysis for various yield component traits on kernel yield was conducted using phenotypic and genotypic correlations (Table 5) and (Figure 4 and 5).

Ear yield per plant showed a positive direct effect (P=0.8001, G=0.8311) and a positive significant correlation (r_p=0.851**, r_g=0.851**) with kernel yield per plant. This trait also exhibited positive indirect effects *via* plant height (P=0.3502, G=0.3495), tassel height (P=0.0275, G=0.0186), tassel extrusion (P=0.1121, G=0.1169), tassel size (P=0.1611, G=0.1564), ear height (P=0.3310, G=0.3253), ear position (P=0.1346, G=0.1324), ear length (P=0.4235, G=0.4343), ear girth (P=0.4194, G=0.4347), kernel rows per ear (P=0.1769, G=0.1811), number of kernels per row (P=0.4046, G=0.4201) and 100-kernel weight (P=0.3740, G=0.3886).

Thus, this trait showed a positive direct effect and a positive significant association with kernel yield per plant. Hence, selection based on this trait would be effective in increasing the kernel yield. Similar kind of positive direct effect of ear yield per plant on kernel yield per plant was found by Rajasekhar *et al.* (2022).

Thus, in the present investigation, path analysis revealed that plant height, tassel size, ear height, ear position, ear length, ear girth, kernel rows per ear, number of kernels per row showed true relationship with kernel yield per plant by establishing high significant positive associations and positive direct effects. Hence, these traits are to be considered during selection of inbred lines for improving the dependent variable *i.e.*, kernel yield per plant.

In plant breeding, it is difficult to have all component traits of yield as there is residual effect which permits precise explanation about the pattern of interaction of even other possible components. Residual effects measure the role of the possible independent variables which are not included in the study. In this study, the residual effect was 0.396 and 0.405 at phenotypic and genotypic

Table 4. Correlation coefficients for kernel yield per plant and its component traits in inbred lines of maize (Zea *mays* L.)

		DFA	DFS	DSA	PH (cm)	TH (cm)	TE	TS	EH (cm)	EP	EL (cm)	EG (cm)	DM	KRPE	NKPR	SP	HKW (g)	EYP (g)	KYP (g)
DFA	r_p	1.0000	0.901**	-0.1258	-0.0050	0.145*	0.0012	-0.0790	0.0055	0.0043	0.0917	-0.0980	0.377**	0.0615	0.0675	-0.1307	-0.135*	-0.157*	-0.1175
	r_g	1.0000	0.901**	-0.1257	-0.0105	0.137*	0.0017	-0.0834	-0.0015	0.0005	0.0892	-0.0978	0.374**	0.0602	0.0680	-0.135*	-0.134*	-0.154*	-0.1160
DFS	r_p		1.0000	0.304**	-0.0244	0.1286	-0.0295	-0.0495	0.0105	0.0424	0.0206	-0.0693	0.447**	0.0825	0.0261	-0.1206	-0.196*	-0.213*	-0.188*
	r_g		1.0000	0.304**	-0.0308	0.1199	-0.0289	-0.0554	0.0019	0.0375	0.0178	-0.0692	0.443**	0.0808	0.0268	-0.1282	-0.195*	-0.209*	-0.186*
ASI	r_p			1.0000	-0.0571	-0.0412	-0.0626	0.0659	-0.0063	0.0736	-0.168*	0.0543	0.192*	0.0458	-0.1096	0.0139	-0.143*	-0.141*	-0.1132
	r_g			1.0000	-0.0565	-0.0407	-0.0626	0.0651	-0.0062	0.0732	-0.168*	0.0543	0.191*	0.0458	-0.1096	0.0130	-0.143*	-0.141*	-0.1131
PH (cm)	r_p				1.0000	-0.0289	0.181*	0.0401	0.700**	0.0525	0.415**	0.140*	0.0572	-0.0800	0.258**	0.0915	0.367**	0.438**	0.392**
	r_g				1.0000	-0.0038	0.177*	0.0615	0.708**	0.0677	0.419**	0.138*	0.0659	-0.0738	0.252**	0.139*	0.360**	0.421**	0.381**
TH (cm)	r_p					1.0000	-0.231**	0.200*	-0.0446	-0.0295	0.0650	0.0444	0.0520	0.215*	0.166*	-0.0451	-0.195*	0.0343	0.0310
	r_g					1.0000	-0.230**	0.219**	-0.0127	-0.0121	0.0740	0.0434	0.0612	0.218*	0.162*	0.0151	-0.196*	0.0223	0.0248
TE	r_p						1.0000	-0.1275	0.169*	0.1010	0.158*	0.0858	-0.0405	0.1244	0.174*	-0.0058	0.0698	0.140*	0.1267
	r_g						1.0000	-0.1279	0.163*	0.0991	0.157*	0.0858	-0.0412	0.1239	0.174*	-0.0098	0.0700	0.141*	0.1271
TS	r_p							1.0000	0.0503	-0.0084	0.0817	0.1132	-0.0650	0.0296	0.1062	-0.0126	0.0768	0.201*	0.177*
	r_g							1.0000	0.0768	0.0072	0.0898	0.1116	-0.0551	0.0343	0.1028	0.0404	0.0730	0.188*	0.170*
EH (cm)	r_p								1.0000	0.696**	0.337**	0.188*	0.0647	-0.0307	0.301**	0.0743	0.288**	0.414**	0.359**
	r_g								1.0000	0.700**	0.342**	0.184*	0.0752	-0.0235	0.292**	0.136*	0.279**	0.391**	0.345**
EP	r_p									1.0000	0.1096	0.136*	0.0563	0.0425	0.202*	0.0147	0.0408	0.168*	0.136*
	r_p									1.0000	0.1153	0.135*	0.0624	0.0459	0.199*	0.0514	0.0384	0.159*	0.131*
EL (cm)	r_g										1.0000	0.236**	-0.0023	0.0246	0.739**	-0.0052	0.239**	0.529**	0.472**
	r_p										1.0000	0.235**	0.0016	0.0267	0.737**	0.0173	0.238**	0.523**	0.468**
EG(cm)	r_g											1.0000	0.0340	0.448**	0.319**	-0.1189	0.222**	0.524**	0.439**
	r_p											1.0000	0.0338	0.448**	0.319**	-0.1120	0.222**	0.523**	0.438**
DM	r_g												1.0000	-0.0343	-0.0001	0.143*	-0.1173	-0.0079	0.0263
	r_p												1.0000	-0.0321	-0.0010	0.155*	-0.1183	-0.0123	0.0240
KRPE	r_g													1.0000	0.203*	-0.150*	-0.221**	0.221**	0.145*
	r_p													1.0000	0.202*	-0.1275	-0.222**	0.218*	0.143*
NKPR	r_g														1.0000	0.0347	0.0341	0.506**	0.442**
	r_p														1.0000	0.0268	0.0344	0.506**	0.442**
SP	r_g															1.0000	-0.0613	-0.0075	0.239**
	r_p															1.0000	-0.0643	-0.0325	0.210*
HKW (g)	r_g																1.0000	0.468**	0.414**
	r_p																1.0000	0.468**	0.415**
EYP (g)	r_g																	1.0000	0.851**
	r_p																	1.0000	0.851**

DFA- Days to 50% anthesis, DFS-Days to 50% silking, ASI-Anthesis silking interval, PH-Plant height, TH-Tassel height, TE-Tassel extrusion, TS-Tassel size, EH-Ear height, EP-Ear position, EL-Ear length, EG-Ear girth, DM-Days to maturity, KRPE-Kernel rows per ear, NKPR-Number of kernels per row, SP-Shelling percentage, HKW-100-kernel weight, EYP-Ear yield per plant.

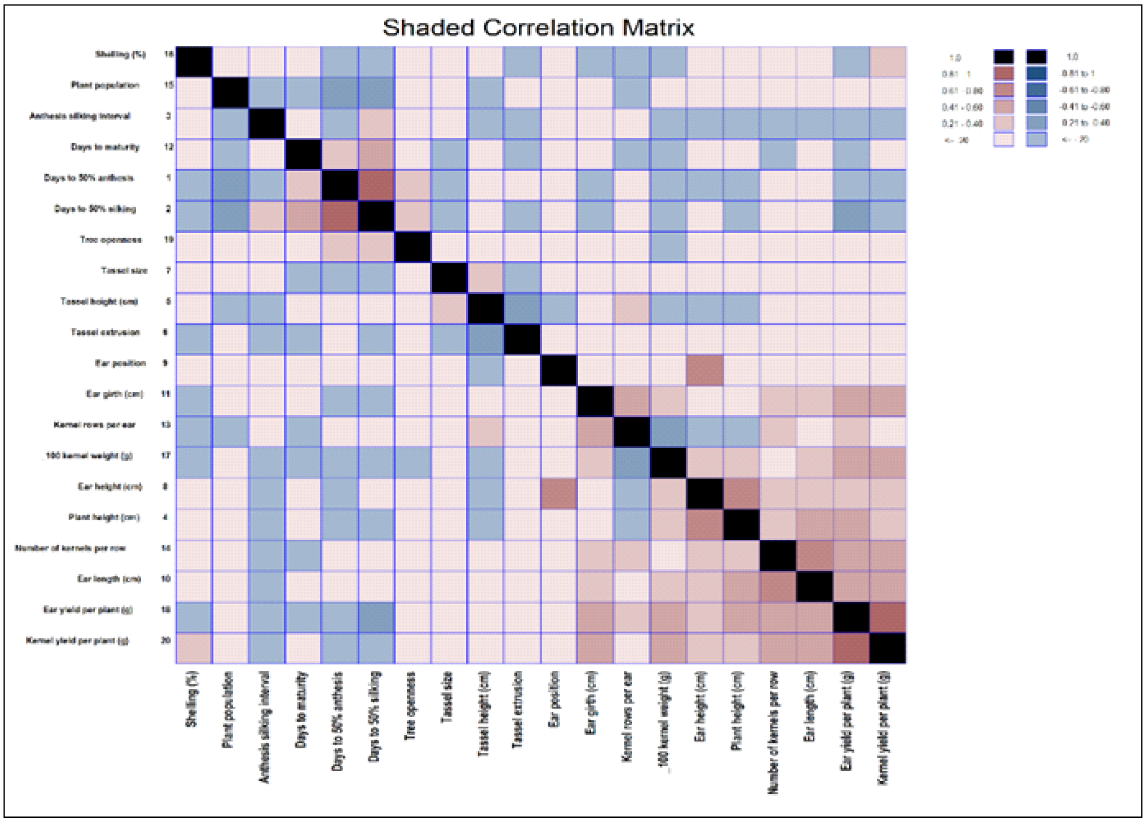

Figure 2. Genotypic shaded correlation matrix for all the characters studied in maize (*Zea mays* L.) inbred lines

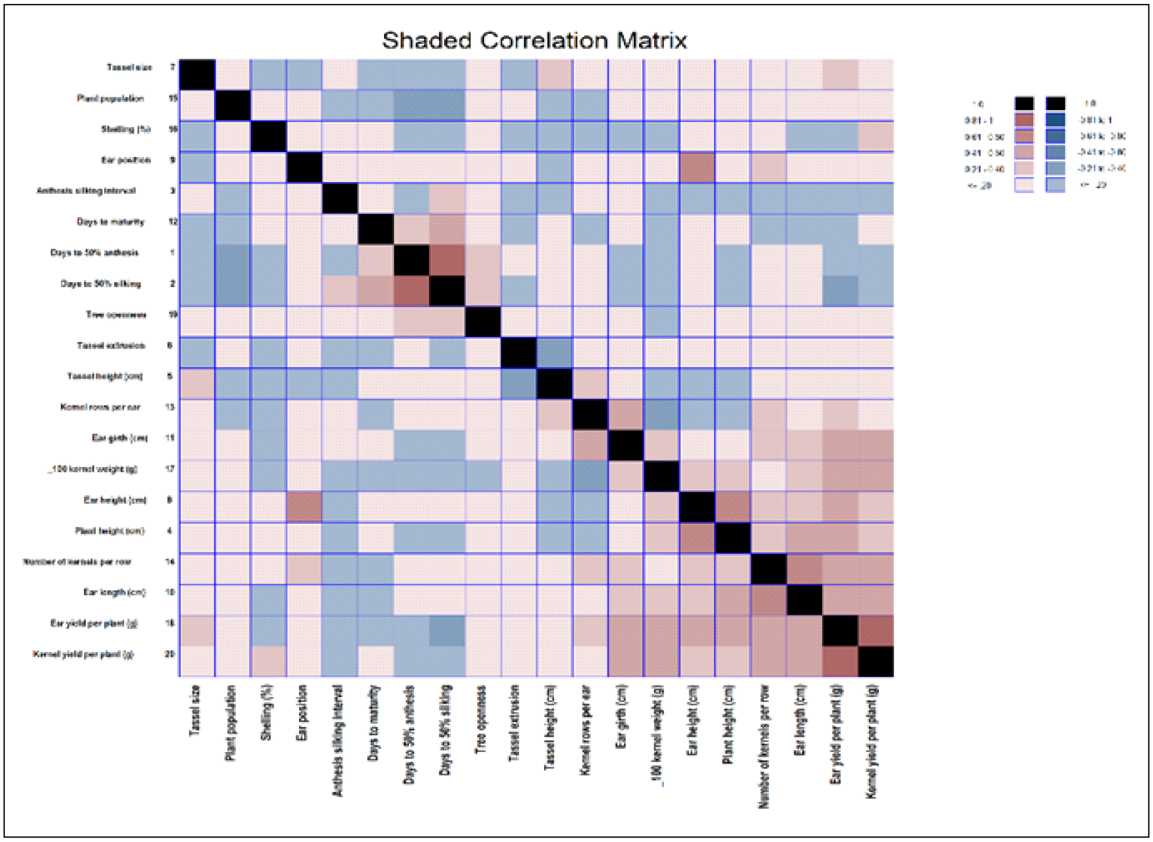

Figure 3. Phenotypic shaded correlation matrix for all the characters studied in maize (*Zea mays* L.) inbred lines

Table 5. Estimates of direct and indirect effects on kernel yield per in maize (*Zea mays* L.)

		DFA	DFS	DSA	PH	TH	TE	TS	EH	EP	EL	EG	DM	KRPE	NKPR	SP	HKW	EYP	KYP
DFA	P	**2.0425**	1.8398	-0.2569	-0.0103	0.2965	0.0025	-0.1613	0.0112	0.0088	0.1873	-0.2002	0.7709	0.1257	0.1379	-0.2669	-0.2754	-0.3208	-0.1175
	G	**1.9679**	1.7729	-0.2474	-0.0206	0.2704	0.0033	-0.1641	-0.0030	0.0009	0.1756	-0.1925	0.7364	0.1185	0.1338	-0.2654	-0.2637	-0.3030	-0.1160
DFS	P	-1.8947	**-2.1034**	-0.6392	0.0514	-0.2706	0.0621	0.1042	-0.0221	-0.0891	-0.0433	0.1458	-0.9407	-0.1734	-0.0550	0.2537	0.4130	0.4473	-0.188*
	G	-1.8199	**-2.0201**	-0.6133	0.0623	-0.2421	0.0585	0.1118	-0.0039	-0.0757	-0.0360	0.1397	-0.8953	-0.1632	-0.0541	0.2590	0.3944	0.4217	-0.186*
ASI	P	-0.1132	0.2735	**0.8999**	-0.0514	-0.0371	-0.0564	0.0593	-0.0057	0.0663	-0.1513	0.0488	0.1724	0.0412	-0.0986	0.0125	-0.1289	-0.1268	-0.1132
	G	-0.1090	0.2633	**0.8673**	-0.0490	-0.0353	-0.0543	0.0565	-0.0054	0.0635	-0.1456	0.0471	0.1658	0.0397	-0.0950	0.0113	-0.1243	-0.1219	-0.1131
PH	P	0.0000	-0.0002	-0.0004	**0.0075**	-0.0002	0.0014	0.0003	0.0052	0.0004	0.0031	0.0010	0.0004	-0.0006	0.0019	0.0007	0.0027	0.0033	0.392**
	G	-0.0001	-0.0003	-0.0005	**0.0084**	0.0000	0.0015	0.0005	0.0059	0.0006	0.0035	0.0012	0.0006	-0.0006	0.0021	0.0012	0.0030	0.0035	0.381**
TH	P	0.0036	0.0032	-0.0010	-0.0007	**0.0245**	-0.0057	0.0049	-0.0011	-0.0007	0.0016	0.0011	0.0013	0.0053	0.0041	-0.0011	-0.0048	0.0008	0.0310
	G	0.0014	0.0012	-0.0004	0.0000	**0.0101**	-0.0023	0.0022	-0.0001	-0.0001	0.0007	0.0004	0.0006	0.0022	0.0016	0.0002	-0.0020	0.0002	0.0248
TE	P	0.0000	-0.0001	-0.0001	0.0004	-0.0005	**0.0023**	-0.0003	0.0004	0.0002	0.0004	0.0002	-0.0001	0.0003	0.0004	0.0000	0.0002	0.0003	0.1267
	G	0.0000	0.0000	0.0000	0.0000	0.0000	**0.0002**	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1271
TS	P	-0.0003	-0.0002	0.0003	0.0002	0.0009	-0.0006	**0.0044**	0.0002	0.0000	0.0004	0.0005	-0.0003	0.0001	0.0005	-0.0001	0.0003	0.0009	0.177*
	G	0.0007	0.0004	-0.0005	-0.0005	-0.0017	0.0010	**-0.0079**	-0.0006	-0.0001	-0.0007	-0.0009	0.0004	-0.0003	-0.0008	-0.0003	-0.0006	-0.0015	0.170*
EH	P	-0.0001	-0.0002	0.0001	-0.0131	0.0008	-0.0032	-0.0009	**-0.0188**	-0.0131	-0.0063	-0.0035	-0.0012	0.0006	-0.0057	-0.0014	-0.0054	-0.0078	0.359**
	G	0.0001	-0.0001	0.0003	-0.0308	0.0006	-0.0071	-0.0033	**-0.0436**	-0.0305	-0.0149	-0.0080	-0.0033	0.0010	-0.0127	-0.0059	-0.0122	-0.0171	0.345**
EP	P	0.0001	0.0006	0.0010	0.0007	-0.0004	0.0014	-0.0001	0.0093	**0.0134**	0.0015	0.0018	0.0008	0.0006	0.0027	0.0002	0.0005	0.0023	0.136*
	G	0.0000	0.0006	0.0012	0.0011	-0.0002	0.0017	0.0001	0.0118	**0.0169**	0.0019	0.0023	0.0011	0.0008	0.0034	0.0009	0.0006	0.0027	0.131*
EL	P	0.0031	0.0007	-0.0057	0.0140	0.0022	0.0053	0.0027	0.0113	0.0037	**0.0336**	0.0079	-0.0001	0.0008	0.0248	-0.0002	0.0080	0.0178	0.472**
	G	0.0011	0.0002	-0.0021	0.0052	0.0009	0.0019	0.0011	0.0042	0.0014	**0.0124**	0.0029	0.0000	0.0003	0.0091	0.0002	0.0029	0.0065	0.468**
EG	P	-0.0042	-0.0029	0.0023	0.0060	0.0019	0.0036	0.0048	0.0080	0.0057	0.0100	**0.0424**	0.0014	0.0190	0.0135	-0.0050	0.0094	0.0222	0.439**
	G	-0.0036	-0.0025	0.0020	0.0051	0.0016	0.0032	0.0041	0.0068	0.0049	0.0086	**0.0367**	0.0012	0.0165	0.0117	-0.0041	0.0081	0.0192	0.438**
DM	P	-0.0036	-0.0043	-0.0018	-0.0005	-0.0005	0.0004	0.0006	-0.0006	-0.0005	0.0000	-0.0003	**0.0096**	0.0003	0.0000	-0.0014	0.0011	0.0001	0.0263
	G	-0.0050	-0.0059	-0.0026	-0.0009	-0.0008	0.0005	0.0007	-0.0010	-0.0008	0.0000	-0.0005	**-0.0134**	0.0004	0.0000	-0.0021	0.0016	0.0002	0.0240
KRPE	P	-0.0004	-0.0005	-0.0003	0.0005	-0.0014	-0.0008	-0.0002	0.0002	-0.0003	-0.0002	-0.0030	0.0002	**-0.0066**	-0.0013	0.0010	0.0015	-0.0015	0.145*
	G	-0.0012	-0.0016	-0.0009	0.0015	-0.0043	-0.0024	-0.0007	0.0005	-0.0009	-0.0005	-0.0088	0.0006	**-0.0197**	-0.0040	0.0025	0.0044	-0.0043	0.143*
NKPR	P	0.0001	0.0000	-0.0002	0.0004	0.0003	0.0003	0.0002	0.0005	0.0003	0.0013	0.0005	0.0000	0.0003	**0.0017**	0.0001	0.0001	0.0009	0.442**
	G	0.0012	0.0005	-0.0020	0.0046	0.0030	0.0032	0.0019	0.0053	0.0036	0.0135	0.0058	0.0000	0.0037	**0.0183**	0.0005	0.0006	0.0092	0.442**
SP	P	-0.0339	-0.0313	0.0036	0.0237	-0.0117	-0.0015	-0.0033	0.0193	0.0038	-0.0013	-0.0308	0.0370	-0.0388	0.0090	**0.2594**	-0.0159	-0.0020	0.239**
	G	-0.0332	-0.0315	0.0032	0.0341	0.0037	-0.0024	0.0099	0.0335	0.0126	0.0043	-0.0276	0.0382	-0.0314	0.0066	**0.2460**	-0.0158	-0.0080	0.210*
HKW	P	-0.0054	-0.0079	-0.0058	0.0148	-0.0078	0.0028	0.0031	0.0116	0.0016	0.0096	0.0089	-0.0047	-0.0089	0.0014	-0.0025	**0.0402**	0.0188	0.414**
	G	-0.0048	-0.0070	-0.0052	0.0129	-0.0070	0.0025	0.0026	0.0100	0.0014	0.0086	0.0080	-0.0043	-0.0080	0.0012	-0.0023	**0.0360**	0.0168	0.415**
EYP	P	-0.1257	-0.1701	-0.1127	0.3502	0.0275	0.1121	0.1611	0.3310	0.1346	0.4235	0.4194	-0.0063	0.1769	0.4046	-0.0060	0.3740	**0.8001**	0.851**
	G	-0.1280	-0.1735	-0.1168	0.3495	0.0186	0.1169	0.1564	0.3253	0.1324	0.4343	0.4347	-0.0102	0.1811	0.4201	-0.0270	0.3886	**0.8311**	0.851**

Diagonal effects-Direct effects, off-diagonal values-indirect effects * Significant at 5% level ** Significant at 1% level

DFA- Days to 50% anthesis, DFS-Days to 50% silking, ASI-Anthesis silking interval, PH-Plant height(cm), TH-Tassel height(cm), TE-Tassel extrusion, TS-Tassel size, EH-Ear height, EP-Ear position, EL-Ear length(cm), EG-Ear girth(cm), DM-Days to maturity, KRPE-Kernel rows per ear, NKPR-Number of kernels per row, SP-Shelling percentage, HKW-100-kernel weight(g), EYP-Ear yield per plant (g).

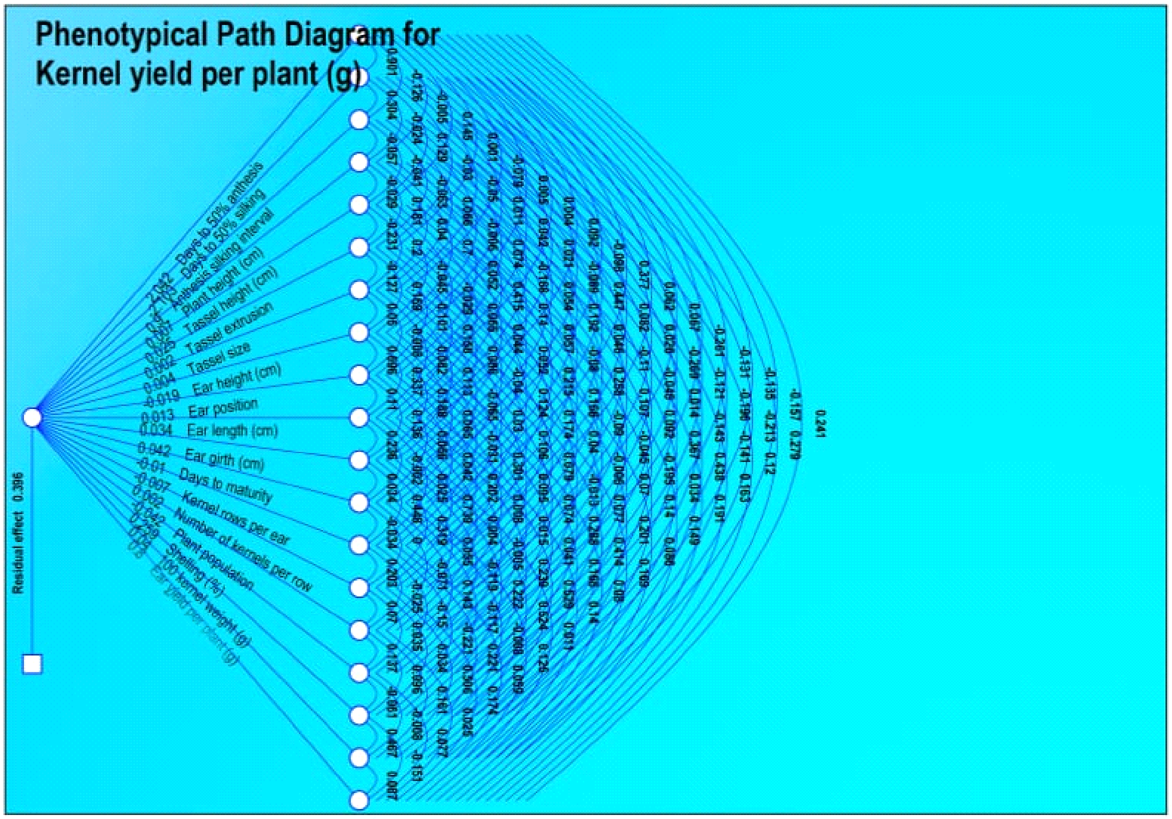

Figure 4. Phenotypic path diagram showing direct and indirect effects of yield components on kernel yield per plant in inbred lines of maize (*Zea mays* L.)

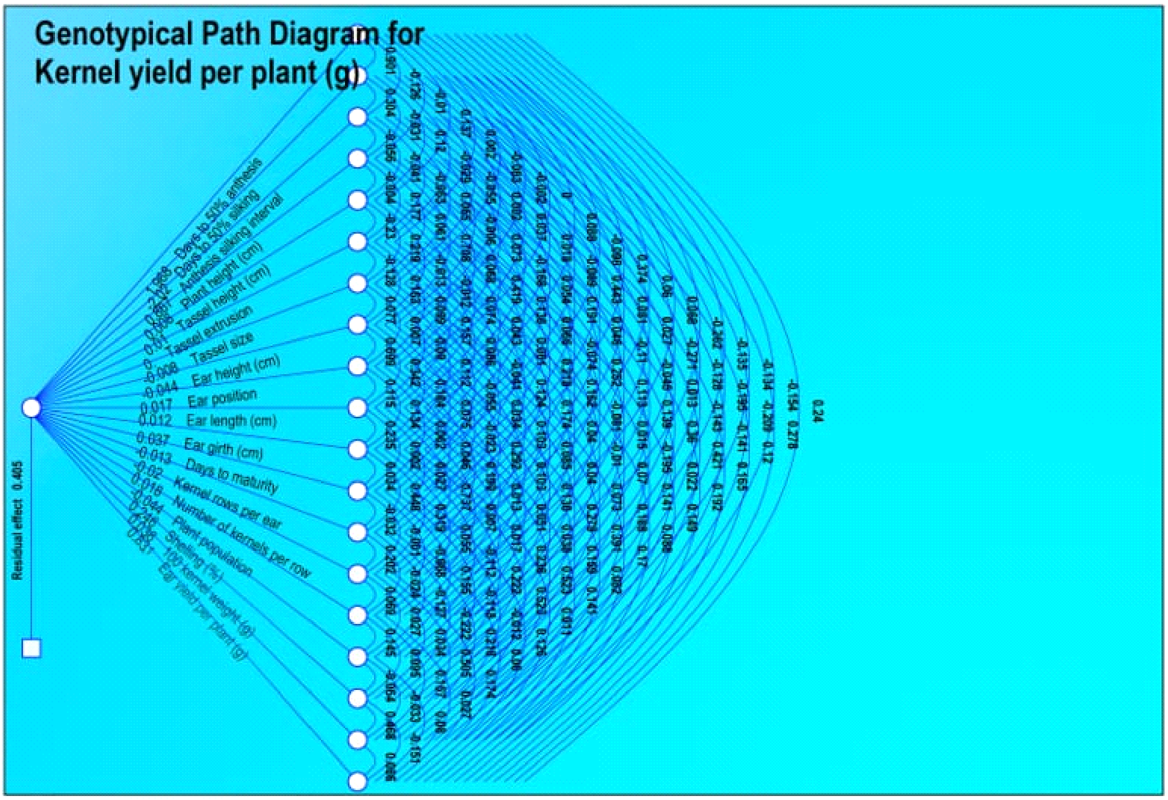

Figure 5. Genotypic path diagram showing direct and indirect effects of yield components on kernel yield per plant in inbred lines of maize (*Zea mays* L.)

levels, respectively, indicating that the characters included clearly explained the direct and indirect effects to some extent on the dependent variable, but not completely.

Conclusion

Upon examining the genetic variability parameters, it was noticed from the results that traits like anthesis silking interval, ear length, ear height, 100-kernel weight, kernel yield per plant, ear yield per plant, and number of kernels per row are important in selection programs aiming for maize yield improvement. These traits exhibit high genotypic and phenotypic coefficients of variation indicating that these characters are under genetic control and have high potential for selection along with high and moderate heritability and high genetic advance as percentage of mean (genetic gain) present for these traits indicated that additive gene action played a dominant role in their inheritance suggesting these traits as promising targets for improvement through selection driven by additive genetic factors.

Traits such as plant height, tassel size, ear height, ear position, ear girth, kernel rows per ear, number of kernels per row, shelling percentage, 100-kernel weight, ear yield per plant were significantly and positively associated with kernel yield per plant, underscoring their importance as traits of selection for yield improvement in the present breeding material. So, it can be inferred that simultaneous selection for yield traits may not be possible hence, balanced selection criteria should be followed depending on the objective.

Traits like days to 50% anthesis, anthesis-silking interval, plant height, tassel height, tassel extrusion, tassel size, ear position, ear length, ear girth, number of kernels per row, shelling percentage, 100-kernel weight and ear yield per plant had positive direct effects on kernel yield. Hence these traits were considered as important yield attributes and could be utilized as selection criteria for genetic improvement of kernel yield in the present breeding material.

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