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Research Article

Exploring genetic variability and association in QPM maize (*Zea mays*) inbred lines

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Abstract

Variability and association studies help to assess the variation among the genotypes and interactions between grain yield and its component traits for enhancing the usefulness of selection. In view of this, the present experiment was conducted at Maize research farm TCA, Dholi, DRPCAU, Pusa, Samastipur, Bihar using 25 inbred lines of maize for various traits to determine the extent of variability and association between these lines for different characteristics. Traits including plant height, ear height, ear length, ear girth, number of kernels per row, harvest index, tryptophan content and lysine content, exhibited high heritability and genetic advance as percentage of the mean. Grain yield showed significant positive associations with ear length, ear girth, number of kernel rows per ear, number of kernels per row and harvest index while it exhibited negative association with plant height, ear height, days to 75% brown husk, protein, lysine, and tryptophan content. Furthermore, certain traits, such as ear length, ear girth, number of kernel rows per ear, number of kernels per row, harvest index, days to 50% silking, and ear height, had a direct positive effect on grain yield. Therefore, selecting these traits directly would be desirable for future hybridization endeavors.

Keywords: Association, QPM maize, Direct & indirect effects, PCV, GCV

INTRODUCTION

Maize (*Zea mays* L.) belongs to the grass family (Graminae), tribe Maydeae, and has somatic chromosome number 20 (2n = 2x 20). The crop is distinguished by an efficient CO_2 concentrating and assimilating pathway known as the C4 pathway, which is aided by a unique type of leaf make up known as Kranz anatomy. The glutamic acid and leucine content of maize protein is high. Lysine and tryptophan are the limiting amino acids in maize since prolamine forms the major primary storage protein in the crop. Zein, which accounts for 50-60% of the storage protein, is made by the collection of hydrophobic proteins that do not contain tryptophan and lysine. As a result, alteration of protein quality for better nutritional worth was seen as a laudable aim. The finding of a recessive opaque 2 mutant in maize that resulted in increased concentrations of lysine and tryptophan in endosperm protein sparked this effort (Mertz *et al*., 1964). Later, CIMMYT breeders were successful in combining the nutritional strength of opaque 2 with endosperm modifiers, resulting in the new maize cultivars known as “Quality Protein Maize” (QPM). The finding of this mutant and its modifier, was extraordinary, and it sparked the idea

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for developing Quality Protein Maize (QPM) varieties. Quality protein maize (QPM) populations with strong agronomic traits, high yield potential, and superior lysine content are now available, same as conventional maize (Ortega *et al*., 1983). Knowledge on genetic variability and association among traits would help in priotising the traits to be included in QPM breeding program and to this end the research was carried out.

MATERIALS AND METHODS

The experiment was done to evaluate 25 inbred lines of maize for various traits to calculate the extent of variability and association between these lines for different traits. The experiment was carried out during *rabi,* 2021 in a randomized block design with three replications. Each entries were sown in a plot of 6 m^2 size at Maize research farm TCA, Dholi, DRPCAU, Pusa, Samastipur, Bihar.

The characters *viz.,* Days to 50 percent tasseling, Days to 50 percent silking, Days to 75 percent brown husk, No. of kernel rows ear^{-1}, No. of kernels row^{-1}, Plant height (cm), Ear height (cm), Ear length (cm), Ear girth (cm), Lysine content (%), Tryptophan content (%), Protein content (%), 100 grain weight (gm), Harvest index (%), Grain yield (kg/ha) were observed.

Analysis of Variance (ANOVA) was carried out as proposed by Panse and Sukhatme (1967), genetic variability analysis as per the formulas given by Burton and De vane (1953), association analysis as per the formula proposed by Al-Jibouri *et al* (1958) along with Panse and Sukhatme (1967) and path analysis as per Deway and Lu (1959) method. All the statistical analyses were done in “INDOSTAT” software

RESULTS AND DISCUSSION

Analysis of Variance: The 25 genotypes of maize showed substantial variation for all the investigated traits, as revealed by the ANOVA (**Table 1**). The variation observed could be due to the diverse source of material along with environmental influence on the traits plant height, ear height, days to 50% tasseling, days to 50% silking, days to 75% brown husk, ear length, ear girth, no. of kernel rows ear^{-1}, no. of kernels row^{-1}, protein content, tryptophan content, lysine content, 100 grain weight, grain yield. The presence of variability in the current experiment demonstrated the possibility of selecting based on these characters.

Variability: Phenotypic variance for almost all the 15 characters was slightly higher than the genotypic variance, indicating that there was less influence of environment on the expression of most of the characters. For every trait, GCV was lower than PCV. The highest GCV and PCV were noted in ear length (cm) followed by harvest index (%). Ear height (cm), had moderate GCV but high PCV. The characters with moderate GCV values were plant height (cm), no. of kernels per row, 100-grain weight (gm), no. of kernel rows per ear and ear girth (cm). Lowest GCV was recorded for grain yield (kg/ha), tryptophan content (%), lysine content (%), protein content (%), days to 50% tasseling, days to 50% silking, days to 75% brown husk and lowest PCV was recorded for grain yield (kg/ha), tryptophan content (%), lysine content (%), protein content (%), days to 50% tasseling, days to 50 % silking, days to 75% brown husk. Similar findings were reported by Magar *et al* (2021), Khan *et al* (2021), Tesfaye *et al* (2021), Gokulkrishnan *et al* (2021), Kanna *et al* (2021).

Table 1 Analysis of variance of variance for 15 characters in QPM inbred lines

S.No.	Source of variation Characters	Mean sum of squares		
		Replication (df=2)	Treatment (df=24)	Error (df=48)
I	Plant height (cm)	64.36	1453.11**	64.11
II	Ear height (cm)	2.65	440.21**	22.26
III	Days to 50% tasseling	14.56	30.17**	8.26
IV	Days to 50% silking	13.77	32.80**	8.20
V	Days to 75% brown husk	10.17	18.34**	5.03
VI	Ear length (cm)	2.13	26.02**	1.84
VII	Ear girth (cm)	0.38	4.79**	0.36
VIII	No. of kernel rows per ear	0.76	8.79**	2.55
IX	No. of kernels per row	9.05	49.36**	3.99
X	Tryptophan content (%)	0.008	0.01**	0.002
XI	Lysine content (%)	0.07	0.23**	0.02
XII	Protein content (%)	0.17	0.80**	0.17
XII	100 grain test weight(gm)	7.58	32.98**	7.21
XIV	Harvest index (%)	2.89	250.52**	19.21
XV	Grain yield (kg/ha)	119800.00	256659.26**	37609.78

Note: * and ** indicate significance at 5% level and 1% levels, respectively.

Table 2. Mean, range, and coefficient of variation for 15 characters in QPM inbred lines

S.No.	Character	Mean	S.E	Range		C.V
				Min	Max	
1	Plant height (cm)	131.33	4.62	92.2	186.0	6.09
2	Ear height (cm)	63.11	2.72	43.63	95.6	7.48
3	Days to 50% tasseling	118.16	1.66	112.0	127.6	2.43
4	Days to 50% silking	121.53	1.65	114.0	131.0	2.36
5	Days to 75% brown husk	146.74	1.29	139.6	150.0	1.53
6	Ear length (cm)	13.76	0.78	8.4	19.4	9.88
7	Ear girth (cm)	10.83	0.34	9.3	14.0	5.56
8	No.of kernel rows per ear	12.64	0.92	8.6	15.9	12.65
9	No.of kernels per row	27.19	1.15	19.7	32.6	7.35
10	Protein content (%)	9.36	0.23	8.40	10.5	4.43
11	Tryptophan content (%)	0.84	0.02	0.7	1.0	4.80
12	Lysine content (%)	3.35	0.08	2.9	4.1	4.63
13	100 grain test weight (gm)	24.35	1.55	17.06	31.33	11.03
14	Harvest index (%)	43.06	2.53	26.3	57.0	10.18
15	Grain yield (kg/ha)	2882.5	111.9	2344.3	3323.3	6.73

In present investigation, high heritability was recorded for plant height, ear height, ear length, ear girth, harvest index, no. of kernels row^{-1}, lysine content, grain yield, tryptophan content, protein content,100 grain weight, days for 50% silking, days for 50% tasseling, days for 75% brown husk, no. of kernel rows ear^{-1}. For plant height, ear height, ear length, ear girth, number of kernels per row, and harvest index strong heritability and high genetic advance as percentage of mean were observed. The variation could be primarily due to additive gene effect and hence selection based on these traits could yield desirable results. Tryptophan and lysine content along with grain yield showed high heritability but low GAM. This could be due to environmental factors, indicating that selection for these traits might not be beneficial. Similar findings were reported by Rai *et al* (2021), Regm*i et al* (2022), Tefera *et al* (2022)

Table 3. Genetic parameters, heritability and genetic advance as per cent of mean of various characters in QPM inbred lines

S.No.	Characters	σ^2_g	σ^2_p	GCV	PCV	Heritability (broad sense) (%)	GA as % of mean
1	Plant height (cm)	462.99	527.10	16.38	17.48	87.8	31.63
2	Ear height (cm)	139.31	161.57	18.70	20.14	86.2	35.77
3	Days to 50% tasseling	7.30	15.56	2.28	3.33	46.9	3.22
4	Days to 50% silking	8.20	16.40	2.35	3.33	50.0	3.43
5	Days to 75% brown husk	4.43	9.47	1.43	2.09	46.8	2.02
6	Ear length (cm)	8.06	9.90	20.62	22.87	81.3	38.31
7	Ear girth (cm)	1.47	1.84	11.22	12.52	80.3	20.72
8	No.of kernel rows per ear	2.08	4.63	11.41	17.03	44.9	15.75
9	No.of kernels per row	15.12	19.12	14.30	16.07	79.1	26.20
10	Protein content (%)	0.21	0.38	4.92	6.61	55.3	7.54
11	Tryptophan content (%)	0.005	0.007	8.05	9.92	65.8	13.44
12	Lysine content (%)	0.07	0.09	7.88	9.13	74.4	13.99
13	100 grain test weight (gm)	8.58	15.8	12.03	16.32	54.3	18.27
14	Harvest index	77.10	96.31	20.38	22.78	80.1	37.58
15	Grain yield	73016.49	110626.3	9.37	11.53	66.0	15.68

Table 4. Degree and direction of association between 15 characters at genotypic level

Characters	PH	EH	DTT	DTS	DBH	EL	EG	KR/E	K/R	PC	LC	TC	100 GW	HI	GY
PH	1	0.9867	-0.3125	-0.2904	-0.3232	0.0133	0.2110	-0.2538	-0.0042	-0.1198	-0.0886	-0.0599	0.3141	0.0603	-0.0019
EH		1	-0.3333	-0.3105	-0.3519	-0.0029	0.2053	-0.1939	-0.0832	-0.0964	-0.0580	-0.0157	0.2512	-0.0238	-0.0142
DTT			1	0.9972	0.8555	0.1983	-0.1434	-0.0818	0.0857	-0.1287	-0.0596	0.0625	0.5966	0.0893	0.1768
DTS				1	0.8578	0.1805	-0.1845	-0.1399	0.0809	-0.1392	-0.0796	0.0422	0.5529	0.0459	0.1546
DBH					1	0.3617	-0.3497	-0.3752	0.2486	-0.0777	-0.1652	0.0396	0.5168	-0.0646	-0.0211
EL						1	0.1576	0.1908	-0.0993	-0.1729	-0.5737	-0.5697	-0.1191	-0.2011	0.4121
EG							1	0.0030	-0.0599	0.3289	0.0073	0.0250	-0.0772	-0.0759	0.2691
KR/E								1	-0.0041	-0.3311	-0.0342	-0.1372	-0.6073	-0.0127	0.3738
K/R									1	-0.0489	0.2177	0.3149	0.4804	0.4257	0.4201
PC										1	0.3001	0.2428	0.0435	-0.3580	-0.2886
LC											1	0.9849	0.0489	0.0138	-0.1903
TC												1	0.1009	-0.1585	-0.2765
100 GW													1	0.5130	0.1235
HI														1	0.5341
GY															1

PH = Plant height (cm), EH=Ear height (cm), DTT = Days to 50 percent tasseling, DTS = Days to 50 percent silking, DBH = Days to 75 percent brown husk, EL = Ear length (cm), EG = Ear girth (cm), KR/E = No. of kernel rows per ear, K/R = No. of kernels per row, PC = Protein content (%), LC = Lysine content (%), TC = Tryptophan content (%), 100 GW = 100 grain weight (gm), HI = Harvest index (%), GY = Grain yield (kg/ha)

Association studies: Yield is a most complex trait governed by the influence of a number of interrelated quantitative features. Selection based just on yield may not be successful because it is greatly impacted by environmental variations. Therefore, consideration may be given to the selection of yield components that affect yield directly or indirectly but are less affected by the environment.

Grain yield showed a significant positive relation with characters like the length of the ear, girth of the ear, kernel rows ear^{-1}, no. of kernels row^{-1}, harvest index. However, it showed a significant negative association with protein content, tryptophan content. Similar findings were reported by Chaurasia *et al.* (2020) for association of ear length, ear girth, no. of kernels per row with yield, Singh *et al*. (2020) reported for ear length with yield, Anusha *et al* (2021) for ear length, ear girth, no. of kernel rows per ear, no of kernels per row with yield, Amegbor *et al*. (2022) for ear length with yield, Yadesa *et al* (2022) for ear diameter with yield, Raju *et al* (2023) for ear length, ear girth, no. of kernels per row, no. of kernel rows per ear with yield. Hence selection of these characters could simultaneously improve grain yield

Path coefficient analysis was conducted to examine the direct and indirect relationship between quantitative traits and grain yield. The method described by Dewey and Lu (1959) was used to separate the correlation coefficients into direct and indirect effects. In general, component traits that showing positive association with yield also had a positive direct effect on yield and traits that are showing negative association with yield also had a negative direct effect on yield. Similarly traits such as days to 50% silking, ear length, ear girth, no. of kernel rows/ear, no. of kernels/row, 100 grain weight and harvest index showing positive association with yield also had a positive direct effect on yield and the traits such as plant height, days to 75% brown husk, lysine content, tryptophan content are showing negative association with yield and also had a negative direct effect on yield. Hence the direct selection of the characters which are showing positive association along with positive direct effect may be beneficial for grain yield in contrast the characters which are showing negative association and negative direct effect may not be selected. In contrast Ear height had positive direct effect with yield but its association with yield was negative which was due to the indirect negative effects of plant height, days to 50% silking, ear length, no. of kernel rows/ear, no. of kernels/row, protein content, harvest index., days to 50% tasseling had negative direct effect with grain yield but its association with yield was positive which was due to the indirect positive effects of height of the plant, days to 50% silking, length of the ear, no. of kernels/row, lysine content, tryptophan content, 100g grain test weight, harvest index, protein content had positive direct effect on grain yield but its association with yield is negative which was due to the indirect negative effect ear height, days

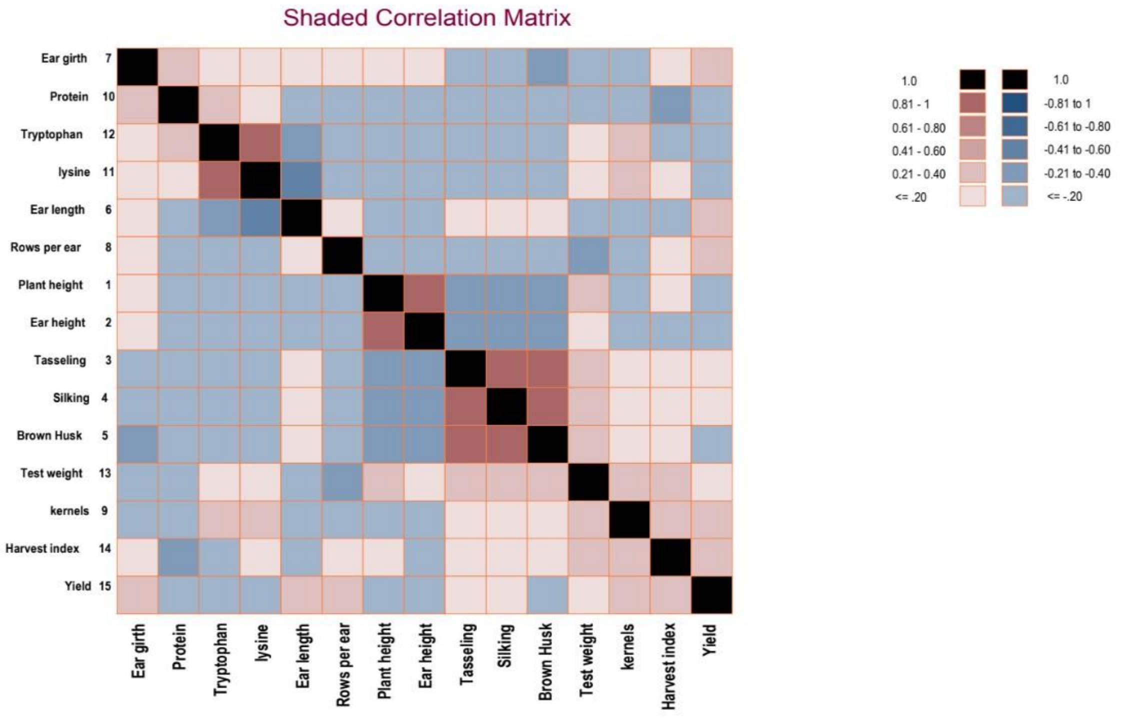

Fig. 1. Correlation between 15 characters of QPM Maize inbred lines

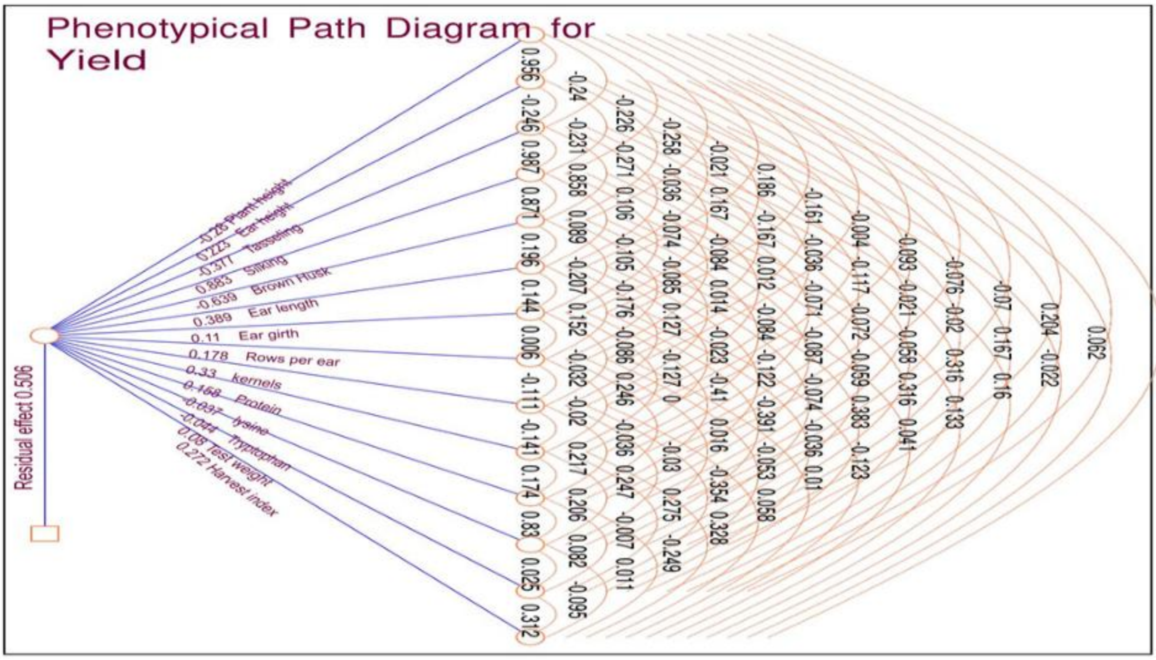

Fig. 2. Phenotypic Path for fifteen yield attributing characters in QPM inbred line

Table 5. Phenotypic Path coefficient analysis for fifteen yield attributing characters in QPM inbred lines

Characters	PH	EH	DTT	DTS	DBH	EL	EG	KR/E	K/R	PC	LC	TC	100 GW	HI
PH	**-0.2805**	-0.2682	0.0674	0.0635	0.0725	0.0058	-0.0521	0.0452	0.0011	0.0262	0.0214	0.0197	-0.0573	-0.0173
EH	0.2132	**0.2229**	-0.0548	-0.0516	-0.0605	-0.0081	0.0373	-0.0373	-0.0080	-0.0261	-0.0047	-0.0045	0.0373	-0.0048
DTT	0.0907	0.0928	**-0.3774**	-0.3725	-0.3238	-0.0400	0.0280	0.0318	-0.0044	0.0269	0.0272	0.0219	-0.1194	-0.0606
DTS	-0.1997	-0.2043	0.8712	**0.8827**	0.7686	0.0789	-0.0931	-0.0749	0.0127	-0.0741	-0.0764	-0.0521	0.2790	-0.1175
DBH	0.1651	0.1735	-0.5485	-0.5567	**-0.6393**	-0.1254	0.1323	0.1128	-0.0182	0.0147	0.0780	0.0474	-0.2446	-0.0264
EL	-0.0080	-0.0142	0.0413	0.0348	0.0764	**0.3894**	0.0560	0.0590	-0.0335	-0.0494	-0.1598	-0.1524	-0.0140	-0.0478
EG	0.0204	0.0183	-0.0081	-0.0116	-0.0227	0.0158	**0.1095**	0.0006	-0.0035	0.0269	0.0000	0.0018	-0.0058	0.0011
KR/E	-0.0287	-0.0298	-0.0150	-0.0151	-0.0314	0.0270	0.0010	**0.1781**	-0.0198	-0.0036	-0.0064	-0.0053	-0.0630	0.0103
K/R	-0.0013	-0.0118	0.0038	0.0047	0.0419	-0.0283	-0.0104	-0.0366	**0.3297**	-0.0464	0.0716	0.0816	0.0907	0.1080
PC	-0.0148	-0.0185	-0.0113	-0.0133	-0.0036	-0.0201	0.0388	-0.0032	-0.0222	**0.1580**	0.0275	0.0326	-0.0011	-0.0394
LC	0.0028	0.0008	0.0027	0.0032	0.0045	0.0152	0.0000	0.0013	-0.0080	-0.0064	**-0.0370**	-0.0307	-0.0030	-0.0004
TC	0.0031	0.0009	0.0025	0.0026	0.0032	0.0171	-0.0007	0.0013	-0.0108	-0.0090	-0.0363	**-0.0438**	-0.0011	0.0041
100 GW	0.0164	0.0134	0.0253	0.0253	0.0306	-0.0029	-0.0043	-0.0283	0.0220	-0.0006	0.0066	0.0020	**0.0801**	0.0250
HI	0.0167	-0.0059	0.0436	0.0362	0.0112	-0.0334	0.0027	0.0157	0.0890	-0.0678	0.0030	-0.0257	0.0847	**0.2718**
GY	-0.0047	-0.0302	0.0427	0.0323	-0.0723	0.2909**	0.2450*	0.2656*	0.2656*	-0.0307	-0.0853	-0.1074	0.0625	0.3410**

Residual value = 0.50; * and ** indicate significance at 5% level and 1% levels, respectively.

PH = Plant height (cm), EH=Ear height (cm), DTT = Days to 50 percent tasseling, DTS = Days to 50 percent silking, DBH = Days to 75 percent brown husk, EL = Ear length (cm), EG = Ear girth (cm), KR/E = No. of kernel rows per ear, K/R = No. of kernels per row, PC = Protein content (%), LC = Lysine content (%), TC = Tryptophan content (%), 100 GW = 100 grain weight (gm), HI = Harvest index (%), GY = Grain yield (kg/ha) for 50% silking, length of the ear, no.of kernel rows/ear, no. of kernels/row, lysine content, tryptophan content, 100 grain test weight, harvest index. Singh *et al* (2022) have reported that ear height, ear length had direct positive effect on grain yield, Priyanto *et al* (2023) have reported that ear diameter, no. of kernels per row had direct positive effects on grain yield and Praveena *et al* (2022) have reported that no. of kernels per row, ear length had direct positive effects on yield.

Thus in the experiment, genetic variability studies indicated high GCV and PCV, h^2 and GA as percent of for ear length which is due to additive gene action showing the significance of these traits in evaluation and selection for future hybridization programme. Correlation studies showed that length of the ear (cm), girth of the ear (cm), no. of kernel rows ear^{-1}, no. of kernels row^{-1}, harvest index exhibited significant positive relation towards grain yield (kg/ha). Path analysis showed that days for 50% silking, length of the ear, ear girth, no. of kernel rows ear^{-1}, no. of kernels row^{-1}, protein content and harvest index are most important characters accounting for cause and effect relationship on yield. As a result, it would be more effective to select plants based on these characteristics in order to improve yields.

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