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## Character association studies for grain yield and its component traits in maize (*Zea mays* L.) inbreds

S Veera Vishnu, I Sudhir Kumar, K Vinay Teja, Pushpalatha G and K Krishnam Raju

### Abstract

Therefore, the experiment was conducted during *Rabi*, 2022 at College Farm, M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha, India to estimate the character association in 51 inbred lines and one check tested in randomized block design with three replications. The objective was to determine the phenotypic and genotypic relationships between traits and to evaluate the direct and indirect effects of attributes on grain yield in maize. In order to increase the effectiveness of the selection, character association studies will be helpful in determining the relationship between the yield and its components. In light of this, 51 inbred and one check of maize was employed in the current study's investigation of the correlation coefficient and path analysis using 16 quantitative and qualitative criteria. According to correlation studies, there is a positive non-significant correlation between the number of ears per plant, plant height, and days to maturity at both the genotypic and phenotypic levels and the grain yield per plant, as well as a positive significant correlation between the ear height, ear length, number of kernel rows per ear, number of kernels per row, and 100 kernel weight. Therefore, choosing any one of these traits will enhance the other characters as well as raise the production of grain yield per plant. The number of kernels per row, 100 kernel weight, and number of rows per ear were found to have the strongest positive direct effects on grain yield per plant, and their correlations with grain yield plant-1 were also considerably favourable. As a result, the current research may help in the development of high yielding varieties and the reliable selection of parental lines based on the aforementioned characteristics.

**Keywords:** *Rabi* maize, agro-morphometric traits, correlation and path analysis

### Introduction

Maize (*Zea mays* L.) is a member of the sub-family Panicoideae of the family Poaceae and tribe Maydeae. It is believed to be the native of Central America and Mexico and is evolved from teosinte (*Zea mexicana*). Maize, known as queen of cereals, globally occupies 1<sup>st</sup> rank in productivity among cereals with 5.82 t/ha followed by 4.66 t/ha of rice and 3.55 t/ha of wheat. Maize, being a C4 plant, is physiologically more efficient with higher per day productivity. It has wider adaptation over different environmental conditions and cultivated from latitude 58° N to 40° S, from mean sea level to higher than 3000 m altitude and in areas receiving 250 mm to 5000 mm yearly rainfall (Downswell *et al.*, 1996) [6].

As per FAOSTAT (2020) [9] the worldwide maize is grown in 193.7 million hectares with a total production of 1147.7 million metric tons and average productivity of 5.75 t/ha. Worldwide maize is grown in over 170 countries. The United States, China and Brazil accounted for about 62% of global maize production (2020). In India it is grown in an area of 9.9 m ha with a production of 31.51mt and a productivity of 3.07 t/ha (FAOSTAT, 2020) [9]. In India Madhya Pradesh and Karnataka states (15% each) have the major maize area followed by Maharashtra (10%), Rajasthan (9%), Uttar Pradesh (8%) and others. Karnataka has the highest maize production followed by Madhya Pradesh, Bihar and others. Andhra Pradesh has the highest productivity because of some highly productive districts like Krishna, West Godavari etc.

The rapidly increasing demand of maize is driven by increase in demand for direct human consumption as a staple food crop (Ghimire *et al.*, 2007) [10] and for livestock feed (Pandey *et al.*, 2007) [19]. Maize starch can be hydrolyzed and enzymatically treated to produce syrups, particularly high fructose corn syrup sweetener that upon fermentation and distillation produces grain alcohol (Doebley, 2004) [7]. In Odisha around seven major cluster districts contributed 74% of the total production, of which Nabarangpur district alone contributed 30%

share in total production. Adoption of high yielding varieties in 89% of total land area contributed 93.3% of the total production. Almost 92% of the total maize is produced in *Kharif* season alone (APICOL 2020) [26].

The complicated characteristic of maize grain yield is regulated by a variety of variables. The selection of acceptable genotypes should take into account grain yield as well as other yield characteristics that affect grain yield. To create viable genotypes with high yield, it is essential to understand the correlations between many features, especially grain yield. Determine the relative strength of each independent variable's influence on a dependent variable, such as grain yield, using the correlation analysis. Understanding these interactions between grain production and the traits that contribute to it can greatly improve breeding programmes through the use of appropriate selection indices (Mohammadia *et al.*, 2003) [17]. In 52 inbreds and one check of maize for 16 characters, the aim of this study was to assess the degree of association between grain yield and yield attributes.

**Materials and Methods**

The experiment was conducted to estimate the genetic variability in 52 inbred lines that are tested in randomized block design with three replications at CUTM Farm, M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha during *Rabi*, 2022. The farm is located between 18°48' to 19°39' North latitude and 83°48' to 84°08' East Longitude. The climatic condition of Gajapati district varies between 16° to 40°C and receives a rainfall of 1403.30 mm. The sand loam texture soil with pH of 6.5 units and soil consist good organic carbon and nitrogen.

Fifty-two genotypes of maize were sown in Randomized Block design (RBD) with three replications. Each genotype was sown in three rows of three-meter length each with a spacing of 60cm between the rows and 25cm within the row. Recommended package of practices and need based plant protection measures were followed to raise a healthy crop.

**Data Collection**

Observations were recorded on five randomly selected plants in each treatment and in each replication. The plants were selected from the middle of the row excluding the border plants were subjected to record the observations for fourteen quantitative traits *viz.*, days to 50% tasseling, days to 50% silking, anthesis-silking interval (ASI), days to maturity, plant height (cm), ear height (cm), number of ears per plant, ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, shelling percentage (%), 100 kernel weight (g) and grain yield per plant (g) followed by two qualitative traits *viz.*, protein content (%) is estimated through the Lowry's method and oil content (%) is estimated through the Soxhlet apparatus method.

**Statistical Analysis**

The data from the 16 quantitative and quality traits were analyzed in 'RStudio (4.1.2)' using various packages. Correlation Coefficient analysis and Path Coefficient analysis were done using the 'Character association' package with level of significance 5%. Using the approach recommended by Panse and Sukhatme, (1985) [21] the phenotypic (rp) and genotypic (rg) correlation coefficients for various traits were determined. As suggested by Dewey and Lu (1959) [5] and developed by Wright, the first step in establishing a cause-and-effect relationship is to partition the genotypic and phenotypic correlation coefficient into direct and indirect effects.

**Genotypic correlation coefficient**

Genotypic correlation between traits x and y:

$$R_{xy}(g) = \sigma^2(xy) / \sqrt{\sigma^2_g(x) \times \sigma^2_g(y)}$$

**Phenotypic correlation coefficient**

Phenotypic correlation between traits x and y:

$$R_{xy}(p) = \sigma^2_p(xy) / \sqrt{\sigma^2_p(x) \times \sigma^2_p(y)}$$

Where,

$\sigma^2_g(x y)$  = genotypic covariance between traits x and y,  
 $\sigma^2_p(x y)$  = phenotypic covariance between traits x and y

**Results and Discussion**

Correlation coefficients can be used to analyse how qualities are related to one another (both phenotypic and genotypic). In general, the association between qualities is attributed to hereditary and environmental causes. Genetic correlations are caused by genetic factors and provide information about the degree of additive relationship between two traits, which is important for efficient selection, whereas phenotypic correlations are caused by both environmental and genetic factors and can be identified by measuring the phenotype (Bocanski *et al.*, 2009) [3]. Due of the two characters' tight ties, a significant positive correlation between them demonstrates that they can both be developed simultaneously in a selection programme (Hayes *et al.*, 1955; Eleweanya *et al.*, 2015) [12, 8].

In the current study, sixteen characters were examined for correlation coefficients at the genotypic and phenotypic levels (Tables 1 and 2). The genotypic correlation coefficient was larger than the corresponding phenotypic correlation coefficient for sixteen of the character pairs. Both genotypic and phenotypic correlation coefficients were significant in the majority of character associations, and for the majority of the characters, the genotypic correlation coefficients were larger than the phenotypic correlation coefficients, with a few exceptions. This demonstrates that the overall expression of the inbred is not greatly influenced by the environment.

**Table 1:** Phenotypic correlation analysis of the morphological and maturity parameters to the grain yield per plant in 52 maize genotypes.

	DT	DS	ASI	DM	PH	EH	NEP	EL	EG	KRPE	KPR	SP	100KW	PC	OC	GYP
DT	1	0.6188***	-0.0458	-0.0707	-0.1436	-	-0.0542	0.0745	0.1096	-0.1428	0.0787	-	-0.1294	-0.0039	-0.0008	-0.1295
DS		1	0.5122**	0.1848*	-0.0867	-	-0.1858*	-0.1411	0.1623*	-0.1865*	-0.0601	-0.0589	-	0.0427	-0.1535	-0.3459 **
ASI			1	-	-0.0090	-	-	-0.3744**	0.0230	-0.1219	-0.2599**	0.1149	-0.3230**	0.0470	-0.2398**	-0.4445 **
DM				1	0.1350	-	0.0749	-0.0412	-0.0490	0.0745	0.0144	-0.1565	-0.0996	-0.0049	-0.1190	0.0716

							0.1093													
PH					1		0.0126	0.1660*	-0.0008	0.1076	0.0206	0.0301	0.0591	-0.0771	0.2053*	0.1196	0.0539			
EH						1		-0.0111	0.1927*	-0.1135	-0.1961*	0.2000*	0.1229*	-0.2891***	-0.0856	0.1768*	0.2920 **			
NEP							1		0.2968***	0.1834*	-0.0840	0.0404	-0.0775	0.0040	0.0948	0.0781	0.0910			
EL								1		0.1080	-0.0015	0.5546***	-0.1541	0.1835*	0.1105	0.1492	0.4092 **			
EG									1			0.2513**	0.1200	0.1664*	-0.1167	0.2130*	0.0616	-0.1827 *		
KRPE										1			-0.0393	-0.1404	-0.2512***	-0.0783	0.2789**	0.2365 **		
KPR											1			-0.0404	0.0189	0.0858	0.0830	0.4646 **		
SP												1			-0.0004	0.1347*	0.0391	-0.0521		
100 KW													1			0.2079*	0.0277	0.4115 **		
PC														1			-0.269***	-0.1878 *		
OC															1			0.1677 *		
GYP																			1	

\* Significant at 5 percent level ( $p \leq 0.05$ ) \*\* Significant at 1 percent level ( $p \leq 0.01$ ) \*\*\* Significant at 0.1 percent level ( $p \leq 0.001$ )

DT: Days to 50% tasseling; DS: Days to 50% silking; ASI: Anthesis-silking interval; DM: Days to maturity; PH: Plant height; EH: Ear height; NEP: Number of ears per plant; EL: Ear length; EG: Ear girth; KRPE: Number of kernel rows per ear; KPR: Number of kernels per row; SP: Shelling percentage; 100KW: 100 kernel weight; PC: Protein content; OC: Oil content; GYP: Grain yield per plant

**Table 2:** Genotypic correlation analysis of the morphological and maturity parameters to the grain yield per plant in 52 maize genotypes.

	DT	DS	ASI	DM	PH	EH	NEP	EL	EG	KRPE	KPR	SP	100KW	PC	OC	GYP
DT	1	0.9186**	-0.0578	-0.1241	-0.2546	-0.0240	-0.0689	0.1896	0.2078	-0.232	0.2017	-0.2838 *	-0.1809	0.0314	0.0166	-0.1473
DS		1	0.6139 **	-0.2158	-0.2406	-0.1330	-0.2480	-0.1354	0.1538*	-0.2717	-0.0522	-0.3669**	-0.3723 **	0.0434	-0.1426	-0.4475**
ASI			1	-0.2173	-0.0046	-0.1183	-0.2843 *	-0.4333**	0.0289	-0.1309	-0.3049 *	-0.2121	-0.3538 *	0.0553	-0.2555	-0.4881**
DM				1	0.3114 *	-0.1066	0.1118	-0.0715	0.0093	0.1081	0.0244	0.1414	-0.1323	0.0507	-0.1675	0.1123
PH					1	0.046	0.2637 **	-0.075	0.1839	-0.0731	0.0581	-0.2838 *	-0.1388	0.374 **	-0.1295	0.0737
EH						1	-0.0499	0.2755 *	-0.1463	-0.2321	0.3115 *	0.339 *	0.3657 **	-0.1654	0.1970 *	0.3034 *
NEP							1	0.4261 **	0.2581 **	-0.1133	0.0766	0.207	-0.0154	0.1121	-0.0762	0.1023
EL								1	0.1549	-0.0256	0.7619**	-0.0453	0.2661 *	0.1358	0.1786	0.5337 **
EG									1	-0.3326 *	0.1976	-0.2052	-0.1445	0.1746 *	0.0792	-0.2161*
KRPE										1	-0.0665	0.2462	-0.2992 *	-0.0734	0.3167 *	0.2983 *
KPR											1	-0.1625	0.021	0.1258	0.1112	0.5957 **
SP												1	0.0541	0.2357*	0.0874	-0.1331
100KW													1	-0.2315	0.0424	0.5081 **
PC														1	-0.3317 *	-0.2082 *
OC															1	0.2083 *
GYP																1

\* Significant at 5 percent level ( $p \leq 0.05$ ) \*\* Significant at 1 percent level ( $p \leq 0.01$ )

DT: Days to 50% tasseling; DS: Days to 50% silking; ASI: Anthesis-silking interval; DM: Days to maturity; PH: Plant height; EH: Ear height; NEP: Number of ears per plant; EL: Ear length; EG: Ear girth; KRPE: Number of kernel rows per ear; KPR: Number of kernels per row; SP: Shelling percentage; 100KW: 100 kernel weight; PC: Protein content; OC: Oil content; GYP: Grain yield per plant

Significant differences were observed among the 52 inbreds for all the 16 characters studied. The grain yield per plant manifested a positively significant correlation with ear height (0.2920 P, 0.3034 G), ear length (0.4092 P, 0.5337 G), number of kernel rows per ear (0.2365 P, 0.2983 G), number of kernels per row (0.4646 P, 0.5957 G), 100 kernel weight (0.4115 P, 0.5081 G) and oil content (0.1677 P, 0.2083 G) at both genotypic and phenotypic level while, realizing a positively non-significant correlation with the number of ears per plant (0.0910 P, 0.1023 G), plant height (0.0539 P, 0.0737 G) and days to maturity (0.0716 P, 0.1123 G) at both genotypic and phenotypic level. Further grain yield per plant displayed a negatively significant correlation with days to 50% silking (-0.3459 P, -0.4475 G), anthesis-silking Interval (-0.4445 P, -0.4881 G), and protein content (-0.1878 P, -0.2082 G) while, realizing a negatively non-significant correlation with days to 50% tasseling (-0.1295 P, -0.1473 G) and shelling percentage (-0.0521 P, -0.1331 G) at both genotypic and phenotypic level. The significant correlation indicates that there is a strong association between various traits and grain yield per plant.

A positive correlation between desirable characters is favourable to the plant breeder because it helps in the simultaneous improvement of both characters (Premlatha and

Kalamani, 2009) [22]. Sandeep *et al.* (2017) [25] reported similar findings wherein ear height (0.2920 P, 0.3034 G), ear length (0.4092 P, 0.5337 G), number of kernel rows per ear (0.2365 P, 0.2983 G), number of kernels per row (0.4646 P, 0.5957 G), and 100 kernel weight (0.4115 P, 0.5081 G) showed a positive significant correlation with grain yield per plant at both genotypic and phenotypic level. Likewise the above findings are in good agreement with the observations of Chaurasia *et al.* (2020) [4] wherein days to 50% silking (-0.3459 P, -0.4475 G) and anthesis-silking interval (ASI) (-0.4445 P, -0.4881 G) recorded a negatively significant correlation with grain yield per plant at both genotypic and phenotypic level. Similarly Saleem *et al.* (2008) [24] reported significant negative correlation between grain yield per plant and protein content ((-0.1878 P, -0.2082 G) at both genotypic and phenotypic level. Munawar *et al.* (2013) [18] showed that the grain yield per plant had a significant negative correlation with ear girth (-0.1827 P, -0.2161 G) at both phenotypic and genotypic level. In concurrence with the above findings Khan and Mahmud, (2021) [14] reported that the grain yield per plant had a positive non-significant correlation with plant height (0.0539 P, 0.0737 G) and days to maturity (0.0716 P, 0.1123 G) while maintaining negative non-significant correlation with days to 50% tasseling (-0.1295 P, -0.1473 G) at both

genotypic and phenotypic level. Bhiusal *et al.* (2017) [2] reported positive non-significant correlation between grain yield per plant and number of ears per plant (0.0910 P, 0.1023 G).

### Path coefficient analysis

The partitioning of the genotypic correlation coefficients into direct and indirect effects through path coefficient analysis are presented in Table 3. Path coefficient analysis at genotypic level revealed that number of kernels per row (2.3069) exerted the highest positive direct effect on grain yield per plant followed by 100 kernel weight (1.5349), number of ears per plant (1.0736), number of kernel rows per ear (0.8609), protein content (0.4454), oil content (0.3541), anthesis-silking interval (0.3825), ear height (0.1206), days to 50% tasseling (0.0680), ear girth (0.0402) and plant height (0.0290). Further, days to 50% silking (-0.0720), days to maturity (-0.2676), ear length (-2.2969) and shelling percentage (-0.9362) recorded

negative direct effect on grain yield per plant. Reddy *et al.* (2012) [23] reported that ear height (0.1206), number of kernel rows per ear (0.8609), number of kernels per row (2.3069), 100-kernel weight (1.5349), days to 50% tasseling (0.0680) and plant height (0.0290) had a positive direct effect while, days to 50% silking (-0.0720) had a negative direct effect on grain yield per plant. Grace *et al.* (2018) [11] reported that ear girth (0.0402) had a positive direct effect and days to maturity (-0.2676) had a negative direct effect on grain yield per plant. Kumar *et al.* (2018) [1, 15] reported positive direct effect of protein content (0.4454) and anthesis-silking interval (0.3825) on grain yield per plant. Pandey *et al.* (2017) [20] reported negative direct effect of ear length (-2.2969) on grain yield per plant. Likewise similar results were reported earlier by Aparna *et al.* (2018) [1] wherein number of ears per plant (1.0736) had a positive direct effect and shelling percentage (-0.9362) had a negative direct effect on grain yield per plant.

**Table 3:** Direct and indirect path coefficients (genotypic) of yield components on grain yield per plant in 52 maize genotypes.

	DT	DS	ASI	DM	PH	EH	NEP	EL	EG	KRPE	KPR	SP	100KW	PC	OC
DT	0.0680	0.0625	-0.0039	-0.0084	-0.0173	-0.0016	-0.0047	0.0129	0.0141	-0.0158	0.0137	-0.0250	-0.0123	0.0021	0.0011
DS	-0.0661	-0.0720	-0.0442	0.0155	0.0173	0.0096	0.0179	0.0097	-0.0111	0.0196	0.0038	0.0153	0.0268	-0.0031	0.0103
ASI	-0.0221	0.2348	0.3825	-0.0831	-0.0018	-0.0452	-0.1088	-0.1658	0.0110	-0.0501	-0.1166	0.0541	-0.1353	0.0211	-0.0977
DM	0.0332	0.0577	0.0581	-0.2676	-0.0833	0.0285	-0.0299	0.0191	-0.0025	-0.0289	-0.0065	0.0760	0.0534	-0.0136	0.0448
PH	-0.0074	-0.0070	-0.0001	0.0090	0.0290	0.0013	0.0076	-0.0022	0.0053	-0.0021	0.0017	0.0098	-0.0040	0.0108	-0.0038
EH	-0.0029	-0.0160	-0.0143	-0.0129	0.0055	0.1206	-0.0060	0.0332	-0.0176	-0.0280	0.0376	0.0250	0.0441	-0.0199	0.0238
NEP	-0.0740	-0.2663	-0.3052	0.1201	0.2831	-0.0535	1.0736	0.4574	0.2771	-0.1216	0.0822	-0.0486	-0.0166	0.1204	-0.0818
EL	-0.4356	0.3110	0.9953	0.1641	0.1723	-0.6329	-0.9786	-2.2969	-0.3558	0.0587	-1.7500	-0.4714	-0.6111	-0.3120	-0.4103
EG	0.0084	0.0062	0.0012	0.0004	0.0074	-0.0059	0.0104	0.0062	0.0402	-0.0134	0.0079	0.0099	-0.0058	0.0070	-0.0032
KRPE	-0.1997	-0.2339	-0.1127	0.0930	-0.0629	-0.1998	-0.0975	-0.0220	-0.2863	0.8609	-0.0572	-0.1399	-0.2576	-0.0632	-0.2727
KPR	0.4653	-0.1204	-0.7034	0.0563	0.1340	0.7186	0.1767	1.7577	0.4558	-0.1534	2.3069	0.1362	0.0484	0.2901	-0.2564
SP	0.3435	0.1986	-0.1324	0.2657	-0.3174	-0.1938	0.0424	0.1921	-0.2305	0.1522	-0.0553	-0.9362	-0.0507	-0.2260	-0.0819
100KW	-0.2777	-0.5714	-0.5430	-0.2031	-0.2131	0.5613	-0.0237	0.4084	-0.2218	-0.4593	0.0322	0.0831	1.5349	-0.3554	0.0651
PC	0.0140	0.0193	0.0246	0.0226	0.1666	-0.0736	0.0499	0.0605	0.0778	-0.0327	0.0560	0.1050	-0.1031	0.4454	-0.1477
OC	0.0059	-0.0505	-0.0905	-0.0593	-0.0458	0.0698	-0.0270	0.0632	0.0280	0.1122	0.0394	0.0310	0.0150	-0.1174	0.3541
GYP	-0.1473	-0.4475**	-0.4881**	0.1123	0.0737	0.3034**	0.1023	0.5337**	-0.2161*	0.2983**	0.5957**	-0.1331	0.5081**	-0.2082*	0.2083*
Partial R <sup>2</sup>	-0.0100	0.0322	-0.1867	-0.0301	0.0021	0.0366	0.1099	-1.2259	-0.0087	0.2568	1.3741	0.1246	0.7799	-0.0927	0.0738

Residual effect = 0.2359

DT: Days to 50% tasseling; DS: Days to 50% silking; ASI: Anthesis-silking interval; DM: Days to maturity; PH: Plant height; EH: Ear height; NEP: Number of ears per plant; EL: Ear length; EG: Ear girth; KRPE: Number of kernel rows per ear; KPR: Number of kernels per row; SP: Shelling percentage; 100KW: 100 kernel weight; PC: Protein content; OC: Oil content; GYP: Grain yield per plant

The partitioning of the phenotypic correlation coefficients into direct and indirect effects through path coefficient analysis are presented in Table 4. Path coefficient analysis at phenotypic level and revealed that number of kernels per row (0.3933) exerted the positive direct effect on grain yield per plant followed by 100 kernel weight (0.3647) and number of kernel rows per ear (0.3392), ear height (0.1320), ear length (0.0796), plant height (0.0648), shelling percentage (0.0583), number of ears per plant (0.0579) and days to maturity (0.0548). Further, days to 50% tasseling (-0.0311), days to 50% silking (-0.0100), anthesis-silking interval (-0.1214), ear girth (-0.0811), protein content (-0.1331) and oil content (-0.0499) recorded negative direct effect on grain yield per plant. Reddy *et al.* (2012) [23] reported that ear height (0.1320), plant height (0.0648), days to maturity (0.0548), ear length (0.0796), number of kernels per row (0.3933) and 100-kernel weight (0.3647) had a positive direct effect while, days to 50% silking (-0.0100) had a negative direct effect on grain yield per plant. Chaurasia *et al.* (2020) [4] reported that

number of kernel rows per ear (0.3392) had a positive direct effect and days to 50% tasseling (-0.0311) and anthesis-silking interval (-0.1214) had a negative direct effect on grain yield per plant. Hussain *et al.* (2020) [13] reported that number of ears per plant (0.0579) had a positive direct effect and ear girth (-0.0811) had a negative direct effect on grain yield per plant. Mahesh *et al.* (2014) [16] reported that protein content (-0.1331) and oil content (-0.0499) has negative direct effect on grain yield per plant.

Path coefficient analysis revealed a high positive direct contribution of number of kernels per row, 100 kernel weight and kernel rows per ear to the grain yield per plant and their correlations with grain yield per plant were also significantly positive. Therefore direct selection based on these morphological traits (number of kernels per row, 100 kernel weight and number of kernel rows per ear) would be more effective in simultaneous improvement of grain yield per plant in maize breeding programs.

**Table 4:** Direct and indirect path coefficients (phenotypic) of yield components on grain yield per plant in 52 maize genotypes.

	DT	DS	ASI	DM	PH	EH	NEP	EL	EG	KRPE	KPR	SP	100KW	PC	OC
DT	-0.0311	-0.0193	0.0014	0.0022	0.0045	0.0011	0.0017	-0.0023	-0.0034	0.0044	-0.0025	0.0053	0.0040	0.0001	0.0000
DS	-0.0062	-0.0100	-0.0051	0.0018	0.0009	0.0004	0.0019	0.0014	-0.0016	0.0019	0.0006	0.0006	0.0030	-0.0004	0.0015
ASI	0.0056	-0.0622	-0.1214	0.0213	0.0011	0.0124	0.0318	0.0455	-0.0028	0.0148	0.0316	-0.0140	0.0392	-0.0057	0.0291
DM	-0.0039	-0.0101	-0.0096	0.0548	0.0074	-0.0060	0.0041	-0.0023	-0.0027	0.0041	0.0008	-0.0086	-0.0055	-0.0003	-0.0065
PH	-0.0093	-0.0056	-0.0006	0.0087	0.0648	0.0008	0.0108	-0.0001	0.0070	0.0013	0.0019	0.0038	-0.0050	0.0133	-0.0077
EH	-0.0045	-0.0057	-0.0134	-0.0144	0.0017	0.1320	-0.0015	0.0254	-0.0150	-0.0259	0.0264	0.0162	0.0382	-0.0113	0.0233
NEP	-0.0031	-0.0108	-0.0151	0.0043	0.0096	-0.0006	0.0579	0.0172	0.0106	-0.0049	0.0023	-0.0045	0.0002	0.0055	-0.0045
EL	0.0059	-0.0112	-0.0298	-0.0033	-0.0001	0.0153	0.0236	0.0796	0.0086	-0.0001	0.0442	-0.0123	0.0146	0.0088	0.0119
EG	-0.0089	-0.0132	-0.0019	0.0040	-0.0087	0.0092	-0.0149	-0.0088	-0.0811	0.0204	-0.0097	-0.0135	0.0095	-0.0173	-0.0050
KRPE	-0.0484	-0.0633	-0.0414	0.0253	0.0070	-0.0665	-0.0285	-0.0005	-0.0853	0.3392	-0.0133	-0.0476	-0.0852	-0.0266	0.0946
KPR	0.0310	-0.0236	-0.1022	0.0057	0.0118	0.0787	0.0159	0.2182	0.0470	-0.0154	0.3933	-0.0159	0.0074	0.0337	0.0326
SP	-0.0099	-0.0034	0.0067	-0.0091	0.0034	0.0072	-0.0045	-0.0090	0.0097	-0.0082	-0.0024	0.0583	0.0000	0.0079	0.0023
100KW	-0.0472	-0.1095	-0.1178	-0.0363	-0.0281	0.1054	0.0015	0.0669	-0.0426	-0.0916	0.0069	-0.0002	0.3647	-0.0758	0.0101
PC	0.0005	-0.0057	-0.0063	0.0007	-0.0273	0.0114	-0.0126	-0.0147	-0.0284	0.0104	-0.0214	-0.0179	0.0277	-0.1331	0.0358
OC	0.0000	0.0077	0.0120	0.0059	0.0060	-0.0088	0.0039	-0.0074	-0.0031	-0.0139	-0.0041	-0.0019	0.0014	0.0134	-0.0499
GYP	-0.1295	-0.3459**	-0.4445**	0.0716	0.0539	0.2920**	0.0910	0.4092**	-0.1827*	0.2365**	0.4646**	-0.0521	0.4115**	-0.1878*	0.1687*
Partial R <sup>2</sup>	0.0040	0.0035	0.0540	0.0039	0.0035	0.0386	0.0053	0.0326	0.0148	0.0802	0.1828	-0.0030	0.1501	0.0250	-0.0084

Residual effect= 0.6428

DT: Days to 50% tasseling; DS: Days to 50% silking; ASI: Anthesis-silking interval; DM: Days to maturity; PH: Plant height; EH: Ear height; NEP: Number of ears per plant; EL: Ear length; EG: Ear girth; KRPE: Number of kernel rows per ear; KPR: Number of kernels per row; SP: Shelling percentage; 100KW: 100 kernel weight; PC: Protein content; OC: Oil content; GYP: Grain yield per plant

## Conclusion

The most essential characters accounting for cause and effect relationships on grain yield are number of kernels per row, 100 kernel weight and kernel rows per ear, according to the results of both correlation and path analysis. As a result, these features have been identified as key yield contributors, and greater attention may be placed on selecting these traits to improve grain yield. As a result, these features should be prioritized when developing selection criteria for increasing grain yield.

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