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Research Article

Relationship between yield and its component traits for enhancing grain yield in single cross hybrids of maize (*Zea mays* L.)

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Abstract
Sixty single cross hybrids of maize synthesised through Line × Tester mating design along with their sixteen parental lines were evaluated for their performance in the experimental field. Genetic parameters *viz*., genotypic and phenotypic correlation and path coefficients were estimated to understand the association among yield and its attributes in enhancing the grain yield. The observed thirteen biometric traits differed significantly in all the genotypes. Correlation studies concluded that cob weight (r_g=0.994), the number of kernels per row (r_g=0.897), plant height (r_g=0.882), ear height (r_g=0.841), and hundred seed weight (r_g=0.830) were strongly and significantly correlated with grain yield. Path analysis showed that cob weight (0.887) and shelling percentage (0.150) had the highest direct effects over yield which emphasized their importance during selection for yield improvement. Developmental traits *viz*., days to 50% flowering and days to 50% silking negatively contributed to yield, and hence the selection for these traits could be restricted.

Key words
Correlation, association, path analysis, single cross hybrids, Maize

INTRODUCTION

Maize is regarded as "King of crops" and "Queen of cereals" due to its highest yielding potential. It holds a prominent position in the global economy owing to its multi-faceted uses as a dietary staple, feed, and industrial raw material. In the Indian context, it is the third most important food crop after rice and wheat. Currently, it is grown in 9.2 million hectares with an average production of 27.82 million tonnes and productivity hovered around 3.02 tonnes per hectare (FAOSTAT, 2018). It was anticipated that the maize demand will get doubled by the year 2050 in the developing economies due to its booming utility from diverse sectors (Rosegrant *et al*., 2009). In the light of above, there is an immense need to develop superior single cross hybrids that are intended to surpass the yield potential of present-day hybrids. On the other hand, grain yield is a complex quantitative trait governed by polygenes and greatly influenced by the environment (Grafius, 1956). It is the end product of many processes occurring throughout the plant's growth and development period (Cairns *et al*., 2012). Eventually, there exists inter-relation among yield and other morpho-agronomical traits which in turn, substantially impact breeding strategies (Zeeshan *et al*., 2013). Hence, while breeding for yield enhancement, it is imperative to practise selection targeting the simply inherited component traits rather than direct selection based on yield *per se*. Possibly, it demands the knowledge of nature and extent of mutual relationship which can be assessed by the association analysis.

Statistically, correlation is a simple measure that defines the strength of interdependency among the variables observed. In plant breeding perspective, causes of trait association may be attributed to the phenotype (or) genotype. Phenotypic correlation (r_p) is the observed association among the phenotypic values on account of the shared genetics and environmental deviations. Linkage and pleiotropy results in genotypic correlation (r_g) which describes the extent to which the traits are varying together at the genetic level. The positive and negative correlation between traits is genetically governed by the coupling phase and repulsion phase linkage respectively (Nadarajan, 2005). Considering the trait correlation in plant breeding broadens the scope for indirect and multi-trait selection consequently hastening the selection progress (Pavan *et al*., 2011). It also helps to eliminate the undesirable drag due to the shared antagonistic genetic effects.

The higher magnitude of correlation between two traits might be due to the influence of a third variable and thus, a simple correlation leads to misconception. Path analysis developed by Wright (1923) partitions the correlation coefficients into the measures of direct and indirect effects over the main variables. It is more informative than the correlation coefficient since it explains the accurate contribution of each independent trait on the dependent trait (Dewey and Lu, 1959). The present study therefore was, aimed to evaluate the correlation and path coefficients to formulate a suitable selection strategy for maize breeding programs.

MATERIALS AND METHODS

Ten elite maize inbreds *viz*., UMI1200, UMI1201, UMI 1205, UMI 1210, UMI 1220, UMI 1223, UMI 1230, N123, 52485 and 52021 were crossed with six Sorghum downy mildew resistant maize inbreds *viz*., RIL 18, RIL 64, RIL114, RIL114-1, RIL131, RIL131-1 in Line × Tester mating design. The synthesized sixty single cross hybrids along with the parents and checks (COH(M)6 and COH(M)8) were evaluated in Randomized block design with two replications at the experimental plot in the Department of Millets, Tamil Nadu Agricultural University, Coimbatore. Each entry was raised in two rows per replication with a spacing of 60cm×25cm. All the recommended agronomic and prophylactic plant protection measures were followed accordingly to maintain a healthy crop stand.

Five random plants per replication were tagged. The observations for the traits like plant height (cm.), ear height (cm.), cob length (cm.), cob girth (cm.), kernel rows per cob, the number of kernels per row, cob weight (g.), single plant yield (g.), hundred kernel weight (g.) were recorded. Days to 50% tasseling and days to 50% silking were recorded on a plot basis. The Analysis Of Variance (ANOVA) was performed with the replication mean values of all the genotypes (Panse and Sukhatme, 1964). The correlation coefficients were estimated as described by Singh and Chaudhary (1979). Path analysis was carried out using the genotypic and phenotypic correlation coefficients (Dewey and Lu, 1959). Data analysis was performed using IndoStat software (IndoStat Inc. Hyderabad, India). The significance of correlation coefficients was tested by

Table 1. Analysis of variance (ANOVA) for yield and the yield components in maize

Variation	Degrees of freedom	Days to 50% tasseling	Days to 50% Silking	Anthesis-siking Interval	Plant height	Cob placement height	Cob length	Cob girth	Kernel rows per cob	No. of kernels per row	Cob weight	Hundred seed weight	Shelling percent	Single plant yield
Replication	1	0.06	0.03	0.16	154.84	32.73	0.25	0.01	0.03	0.00	4.54	0.27	2.27	0.88
Genotypes	77	17.89**	20.02**	0.85**	2667.63**	788.39**	7.82**	4.20**	4.09**	85.38**	4822.00**	65.06**	88.03**	3376.18**
Error	77	0.06	0.05	0.06	66.69	24.75	0.19	0.09	0.03	0.26	7.60	0.21	1.60	5.75

Note: ** - Significant at 1% level

't' test with (n-2) degrees of freedom where 'n' represents the number of observations.

RESULTS AND DISCUSSION

Association analysis is a reliable measure to determine the vital associates from the non- vital ones. Analysis of variance revealed that the test genotypes differed significantly for all the thirteen biometric traits studied (**Table 1**). This signifies that there exists genetic variability among the genotypes for the evaluated traits. Although correlation may be phenotypic or genotypic in nature, only the latter leads to a correlated response. It is therefore of higher significance in breeding programs for ensuring an effective selection and hence, only the significant genotypic correlation and path coefficients are focussed and discussed here.

The genotypic correlation coefficients (r_g) were greater in magnitude than the phenotypic correlation coefficients (r_p) for all the traits except anthesis-silking interval. This implies that the genetic factors largely contributed to the trait association than the environment. Similar results were obtained by Kote *et al*. (2014). The strength of mutual dependency is classified as very weak ($r < 0.3$), weak ($0.3 < r < 0.5$), moderate ($0.5 < r < 0.7$) and strong ($r > 0.7$) based on the magnitude of correlation coefficients (Moore *et al*., 2015). The genotypic and phenotypic correlation coefficient matrix for the thirteen biometric traits is furnished in **table 2.**

From the results obtained, it is understood that the cob weight (r_g=0.9939) shared a highly significant, desirable, and strong association with grain yield. This is

in accordance with the results of Bocanski *et al.* (2009) and Soumya and Kamatar (2017). Highly significant strong inter-relation were exhibited by the number of kernels per row (r_g=0.897), plant height (r_g=0.882), ear height (r_g=0.841), hundred seed weight (r_g=0.830), cob length (r_g=0.773) and shelling percentage (r_g=0.772) over grain yield. These traits should be highly emphasized during selection to maximize the yield gain. The traits *viz*., cob girth (r_g=0.670) and kernel rows per cob (r_g=0.468) registered a moderately favourable significant

association with grain yield. Such positive significant dependency of yield could be substantiated with the observations of Begum *et al.* (2016) for cob length, cob girth and kernel rows per cob; Pandey *et al.* (2017) for cob length, plant height, the number of kernels per row, kernel rows per cob, hundred seed weight; Synrem *et al.* (2016) for cob length, kernel rows per cob, hundred seed weight, single plant yield; Reddy and Jabeen (2016) for plant height, ear height, cob girth, cob length, the number of kernels per row and hundred seed weight.

Table 2. Phenotypic and Genotypic correlation coefficients for yield and its attributing traits in maize

Characters		Days to 50% silking	Anthesis silking Interval	Plant height	Cob placement height	Cob length	Cob girth	Kernel rows per cob	Number of kernels per row	Cob weight	Hundred seed weight	Shelling percent	Single plant yield
Days to 50% tasseling	r_p	0.978**	0.150	-0.370**	-0.292*	-0.368**	-0.375**	-0.194	-0.529**	-0.428**	-0.302**	-0.313**	-0.424**
	r_g	0.981**	0.177	-0.380**	-0.301**	-0.380**	-0.385**	-0.196	-0.532**	-0.429**	-0.302**	-0.322**	-0.426**
Days to 50% silking	r_p	1.000	0.354**	-0.355**	-0.283*	-0.380**	-0.367**	-0.185	-0.490**	-0.385**	-0.268*	-0.298**	-0.384**
	r_g	1.000	0.367**	-0.361**	-0.290*	-0.391**	-0.377**	-0.187	-0.492**	-0.387**	-0.268*	-0.303**	-0.385**
Anthesis-silking interval	r_p		1.000	-0.024	-0.032	-0.149	-0.057	-0.009	0.052	0.091	0.083	-0.010	0.082
	r_g		1.000	-0.009	-0.025	-0.157	-0.062	-0.012	0.055	0.094	0.089	0.008	0.089
Plant height	r_p			1.000	0.916**	0.681**	0.631**	0.297**	0.715**	0.855**	0.832**	0.706**	0.859**
	r_g			1.000	0.947**	0.717**	0.653**	0.308**	0.738**	0.877**	0.851**	0.739**	0.882**
Cob placement height	r_p				1.000	0.678**	0.585**	0.273*	0.665**	0.809**	0.808**	0.709**	0.815**
	r_g				1.000	0.712**	0.607**	0.282*	0.690**	0.836**	0.833**	0.743**	0.841**
Cob length	r_p					1.000	0.389**	0.171	0.723**	0.765**	0.663**	0.512**	0.754**
	r_g					1.000	0.408**	0.180	0.742**	0.783**	0.683**	0.537**	0.774**
Cob girth	r_p						1.000	0.537**	0.540**	0.645**	0.553**	0.705**	0.657**
	r_g						1.000	0.549**	0.555**	0.656**	0.564**	0.740**	0.670**
Kernel rows per cob	r_p							1.000	0.414**	0.453**	0.078	0.361**	0.466**
	r_g							1.000	0.417**	0.456**	0.079	0.368**	0.4681**
Number of kernels per row	r_p								1.000	0.895**	0.608**	0.629**	0.894**
	r_g								1.000	0.899**	0.611**	0.640**	0.897**
Cob weight	r_p									1.000	0.824**	0.699**	0.992**
	r_g									1.000	0.827**	0.718**	0.994**
Hundred seed weight	r_p										1.000	0.705**	0.828**
	r_g										1.000	0.719**	0.830**
Shelling percent	r_p											1.000	0.763**
	r_g											1.000	0.773**

Note: * - Significant at 5% level; ** - Significant at 1% level; ' r_p' – Phenotypic correlation coefficient and ' r_g' – Genotypic correlation coefficient

The traits *viz*., days to 50% tasseling and days to 50% silking had a significant weak antagonistic association with grain yield. This indicates that delayed anthesis coupled with short grain filling period would drastically reduce the yield since the major stored assimilates are utilized for vegetative growth. It corroborated the results of Nataraj *et al*. (2014), Pavan *et al*. (2011), Reddy and Jabeen (2016), and Soumya and Kamatar (2017). Anthesis-silking interval showed a negligible non-significant association with yield. The results from *inter se* association among yield attributes showed that days to 50% tasseling and days to 50% silking were strongly and significantly correlated among

each other. Anthesis-silking interval showed a weak, positive and significant correlation with days to 50% silking and had non-significant relation with the rest of the traits. The findings for developmental traits were in accordance with Begum *et al*. (2016) and Nataraj *et al*. (2014). Cob weight is an important yield component and is strongly associated in the favourable direction with plant height, ear height, cob length, the number of kernels per row, shelling percentage, and test weight. The observed strong dependency of cob weight conformed with the observations of Bocanski *et al*. (2009) for all the above mentioned traits and Soumya and Kamatar (2017) for cob

length, cob girth, and the number of kernels per row. Plant height and cob placement height were strongly inter-related in a positive direction. Taller plants possess more photosynthetic leaves which accumulated high amount of dry matter and through stem-reserve mobilization at the kernel development stage enhances the yield (Sujiprihati *et al*., 2003). Meanwhile, cob placement height should be neither too high nor too low. Higher it is, the weight of the cob lodges the plant while the lower height impedes mechanized harvest. These results were supported by Soumya and Kamatar (2017), Nzuve *et al*. (2014) and Synrem *et al*. (2016). Furthermore, the plant height and cob placement height exerted a favourable, strong significant association with cob length, number of kernels per row, hundred seed weight and shelling percentage followed by a positive, significant, moderate association with cob girth and a weak association with kernel rows per cob. These results were perfectly in agreement with Nataraj *et al*. (2014).Similar association was observed by Reddy and Jabeen (2016) for plant height and cob weight with cob length, cob girth, and the number of kernels per row. Hundred seed weight shared a significant positive and moderate correlation among cob length, cob girth and the number of kernels per row. Similar results were recorded by Soumya and Kamatar (2017) for cob length and cob girth.

Moreover, there existed strong positive significant correlations of the number of kernels per row with cob length and plant height and, a moderate significant association of kernel rows per cob with cob girth, the number of kernels per row and cob placement height. Weak positive significant associations were exerted by cob girth on cob length and Number of kernels per

row on Kernel rows per cob. These associations could be corroborated with the results of Begum *et al*. (2016) and, Soumya and Kamatar (2017) for cob length with the number of kernels per row and cob girth with kernel rows per cob; Pandey *et al*. (2017) for the number of kernels per row with kernel rows per cob; Soumya and Kamatar (2017) for cob length with cob length and plant height; Bocanski *et al*. (2009) for cob placement height with the number of kernels per row.

The correlation coefficients cannot provide the relative contribution of explanatory variables over the main variable. Accordingly, decisions based on the above would be incongruous, unless the direct effect of the considered trait is high and influences the dependent variable in the same direction. Further studies by path analysis will provide the cause and effect relationship. The path diagram representing the direct and indirect effects was depicted in **fig.1**. The low phenotypic and genotypic residual effect of this study affirmed that all the observed traits are appropriate and explained the existing variation in the yield. The phenotypic and genotypic path coefficient matrixes for the thirteen biometric traits were given in **table 3 and 4** respectively.

All the observed biometric traits exhibited direct positive effects over yield except cob placement height, days to 50% silking, cob girth, and cob length. Cob weight (0.887) exhibited the highest direct positive effect followed by shelling percent (0.150), plant height (0.053), kernel rows per cob (0.029), the number of kernels per row (0.018) and hundred seed weight (0.012). Hence, the cob weight and shelling percent are the vital associates and should be given prime importance during selection. The highest

Table 3. The phenotypic direct and indirect effects of the component traits over yield

Characters	Days to 50% tasseling	Days to 50% silking	Anthesis silking Interval	Plant height	Cob placement height	Cob length	Cob girth	Kernel rows per cob	Number of kernels per row	Cob weight	Hundred seed weight	Shelling percent
Days to 50% tasseling	**-0.086**	-0.084	-0.013	0.032	0.025	0.032	0.032	0.017	0.046	0.037	0.026	0.027
Days to 50% silking	0.092	**0.094**	0.033	-0.033	-0.027	-0.036	-0.034	-0.017	-0.046	-0.036	-0.025	-0.028
Anthesis-silking interval	-0.004	-0.008	**-0.023**	0.000	0.000	0.004	0.001	0.000	-0.001	-0.002	-0.002	0.000
Plant height	-0.011	-0.010	-0.001	**0.028**	0.026	0.019	0.0179	0.008	0.020	0.024	0.024	0.020
Cob placement height	0.010	0.010	0.001	-0.032	**-0.035**	-0.024	-0.020	-0.010	-0.023	-0.028	-0.028	-0.025
Cob length	0.002	0.002	0.001	-0.004	-0.004	**-0.005**	-0.002	-0.001	-0.004	-0.004	-0.004	-0.003
Cob girth	0.020	0.020	0.003	-0.034	-0.031	-0.022	**-0.053**	-0.029	-0.029	-0.034	-0.029	-0.038
Kernel rows per cob	-0.006	-0.005	-0.000	0.008	0.008	0.005	0.015	**0.028**	0.012	0.013	0.002	0.010
No. of kernels per row	-0.010	-0.009	0.001	0.014	0.013	0.014	0.010	0.008	**0.019**	0.017	0.012	0.012
Cob weight	-0.379	-0.342	0.081	0.758	0.718	0.678	0.572	0.402	0.794	**0.887**	0.731	0.620
Hundred seed weight	-0.003	-0.003	0.000	0.008	0.008	0.006	0.005	0.000	0.006	0.008	**0.009**	0.007
Shelling percent	-0.050	-0.048	-0.002	0.113	0.113	0.082	0.113	0.058	0.101	0.112	0.112	**0.160**
Single plant yield	-0.424**	-0.384**	0.082	0.859**	0.815**	0.754**	0.657**	0.466**	0.894**	0.992**	0.828**	0.763**

Residual effect = 0.0685.   **Note**: ** - Significant at 1% level; Figures in bold size indicates the phenotypic direct effects of various traits over single plant yield.
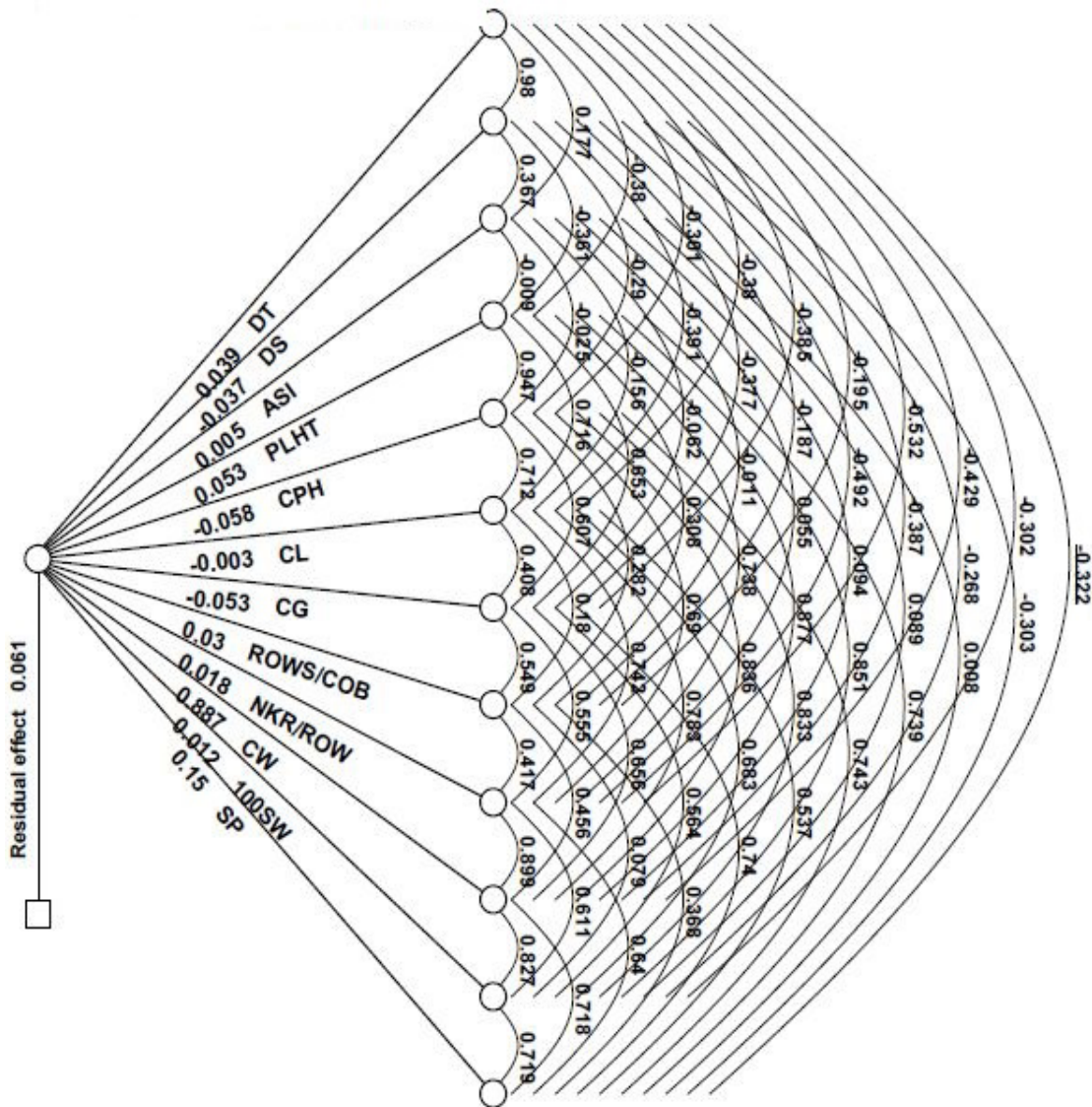
Fig. 1. Genotypic Path diagram for yield and its component traits in maize .

Where DT- Days to 50% tasseling, DS- Days to 50% silking, ASI- Anthesis-Silking Interval, PLHT- Plant height, CPH-Cob placement height, CL- Cob length, CG- Cob girth, ROWS/COB- kernel rows per cob, NKR/ROW-number of kernels per row, CW- Cob weight,100SW- hundred seed weight, SP-Shelling percentage.

positive indirect effects were exhibited by the trait number of kernels per row (0.798) followed by plant height (0.778), cob placement height (0.774) and shelling percent (0.733) and moreover, all these traits indirectly contributed to the grain yield *via* cob weight.

The genotypic and phenotypic effects of most of the traits were in the same direction except days to 50%tasseling, days to 50% silking, and anthesis-silking interval. Days to 50% tasseling and anthesis-silking interval had negative direct effects at phenotypic level and days to 50% silking had negative direct effects at genotypic level. Days to 50% tasselling and days to 50% silking indirectly decreased the

yield *via* cob weight. As stated earlier, delayed anthesis and silking at the expense of the length of grain filling period would reduce the cob weight and ultimately the grain yield. Hence, the selection index to be designed in such a way that the combination of traits should contribute for an enhanced grain yield.

The highest negative direct effect exerted by cob placement height (0.742) over yield suggests that its increment will decrease the yield. But it positively influenced the single plant yield *via* cob weight, shelling percent, and plant height. In maize, the leaves above the cob significantly contributes to the cob development through efficient

Table 4. The genotypic direct and indirect effects of the component traits over yield

Characters	Days to 50% tasseling	Days to 50% silking	Anthesis silking interval	Plant height	Cob placement height	Cob length	Cob girth	Kernel rows per cob	Number of kernels per row	Cob weight	Hundred seed weight	Shelling percent
Days to 50% tasseling	**0.039**	0.038	0.007	-0.015	-0.012	-0.015	-0.015	-0.008	-0.021	-0.017	-0.012	-0.013
Days to 50% silking	-0.036	**-0.037**	-0.014	0.013	0.012	0.014	0.014	0.007	0.018	0.014	0.020	0.011
Anthesis-silking interval	0.000	0.002	**0.005**	0.000	-0.000	-0.000	-0.000	0.000	0.000	0.000	0.000	0.000
Plant height	-0.020	-0.019	-0.000	**0.053**	0.050	0.038	0.035	0.016	0.039	0.047	0.045	0.039
Cob placement height	0.018	0.017	0.001	-0.055	**-0.058**	-0.041	-0.035	-0.016	-0.040	-0.049	-0.049	-0.043
Cob length	0.001	0.001	0.000	-0.002	-0.002	**-0.003**	-0.001	-0.000	-0.002	-0.002	-0.002	-0.002
Cob girth	0.020	0.020	0.003	-0.034	-0.032	-0.022	**-0.053**	-0.029	-0.029	-0.035	-0.030	-0.039
Kernel rows per cob	-0.006	-0.006	-0.000	0.009	0.008	0.005	0.016	**0.030**	0.012	0.014	0.002	0.011
No. of kernels per row	-0.010	-0.009	0.001	0.013	0.013	0.014	0.010	0.008	**0.018**	0.016	0.011	0.012
Cob weight	-0.381	-0.343	0.084	0.778	0.742	0.695	0.582	0.405	0.798	**0.887**	0.733	0.637
Hundred seed weight	-0.004	-0.003	0.001	0.010	0.010	0.008	0.007	0.000	0.007	0.010	**0.012**	0.008
Shelling percent	-0.049	-0.046	0.001	0.111	0.112	0.081	0.111	0.055	0.096	0.108	0.108	**0.150**
Single plant yield	-0.426**	-0.385**	0.089	0.882**	0.841**	0.774**	0.670**	0.468**	0.897**	0.994**	0.830**	0.773**

Residual effect = 0.0611.   **Note**: ** - Significant at 1% level; Figures in bold size indicates the genotypic direct effects of various traits over single plant yield.

reserve mobilization as the leaves beneath the ears mobilize their reserve to the roots (Subedi *et al.*, 2005). This indicates that a mere increase in cob placement height decreases the grain yield but its proportionate increment with plant height and cob weight, frequently enhances the yield. This holds equally true for cob length and cob girth since both indirectly enhances yield *via* cob weight and its attributes besides its negative direct effect. Except for developmental characters, these findings for direct and indirect effects were perfectly in agreement with Soumya and Kamatar (2017) for all the traits.

In summary, this study revealed the existence of genetic variability for all the traits.   Strong correlative traits conjoined with high direct effects in the desired direction over yield would be considered for the breeding process. Cob weight, shelling percentage, and plant height in one direction and the developmental traits in another direction would be employed to formulate a suitable selection index for indirect selection of grain yield. Among all, the cob weight is inherently associated with most of the yield attributes and the selection based on this directly leads to yield improvement. Plant height and cob placement height, cob weight, and the number of kernels per row showed high genotypic correlation and the favourable genes associated with these traits could be utilized for maize breeding programs. Moreover, simultaneous selection of these traits will increase the selection efficiency in the superior inbred line development subsequently increases the grain yield in the single cross hybrids of maize.

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