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

S. Devasree¹, K. N. Ganesan²*, R. Ravikesavan¹, N. Senthil³ and V. Paranidharan⁴

¹Department of Millets, 
²Department of Genetics and Plant Breeding, Centre for Plant Breeding and Genetics, 
³Department of Plant Molecular Biology and Bioinformatics, Centre for Plant Molecular Biology and Biotechnology, 
⁴Department of Plant Pathology, Centre for Plant Protection Studies, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India 
*E-Mail:knganesan71@gmail.com

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 interrelation 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.
Relationship between yield and its component traits

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, UMI1205, UMI1210, UMI1220, UMI1223, UMI1230, N123, 52485 and 52021 were crossed with six Sorghum downy mildew resistant maize inbreds viz., RIL 18, RIL 64, RIL 114, RIL 114-1, RIL 131, 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

### 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.

### 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-silking 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**             | 86.03**            | 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.

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 \((r=0.9939)\) shared a highly significant, desirable, and strong association with grain yield. This is

https://doi.org/10.37992/2020.1103.131
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_s=0.897), plant height (r_s=0.882), ear height (r_s=0.841), hundred seed weight (r_s=0.830), cob length (r_s=0.773) and shelling percentage (r_s=0.772) over grain yield. These traits should be highly emphasized during selection to maximize the yield gain. The traits viz., cob girth (r_s=0.670) and kernel rows per cob (r_s=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 | Shelling percent | Hundred Shelling weight | Single plant yield |
|---------------------|---------------------|----------------------------|--------------|----------------------|------------|-----------|---------------------|--------------------------|------------|------------------|------------------------|---------------------|
| Days to 50% silking | r_p 0.978**         | 0.150                      | -0.370**     | -0.292*              | -0.368**   | -0.375**  | -0.194             | -0.519**                 | -0.428**   | -0.302**         | -0.313**               | -0.424**             |
| Tasseling           | r_p 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**                    | -0.283*      | -0.380**             | -0.367**   | -0.185    | -0.490**          | -0.385**                 | -0.268**   | -0.298**         | -0.384**               |                     |
| Anthesis-silking interval | r_p 1.000 | 0.367**                    | -0.290*      | -0.391**             | -0.377**   | -0.187    | -0.492**          | -0.378**                 | -0.268**   | -0.303**         | -0.385**               |                     |
| Plant height        | r_p 1.000           | 0.916**                    | 0.681**      | 0.631**              | 0.297**    | 0.715**   | 0.855**            | 0.832**                  | 0.706**    | 0.859**          | 0.859**                |                     |
| Cob placement height| r_p 1.000           | 0.947**                    | 0.717**      | 0.653**              | 0.308**    | 0.738**   | 0.877**            | 0.851**                  | 0.739**    | 0.882**          | 0.882**                |                     |
| Cob length          | r_p 1.000           | 0.712**                    | 0.607**      | 0.282*               | 0.690**    | 0.836**   | 0.833**            | 0.743**                  | 0.841**    | 0.815**          | 0.815**                |                     |
| Cob girth           | r_p 1.000           | 0.408**                    | 0.180        | 0.742**              | 0.783**    | 0.683**   | 0.537**            | 0.774**                  | 0.540**    | 0.645**          | 0.555**                | 0.657**              |
| Kernel rows per cob | r_p 1.000           | 0.537**                    | 0.540**      | 0.645**              | 0.555**    | 0.656**   | 0.564**            | 0.740**                  | 0.670**    | 0.670**          |                        |                     |
| Number of kernels per row | r_p 1.000 | 0.414**                    | 0.453**      | 0.078                | 0.361**    | 0.466**  | 0.079              | 0.368**                  | 0.468**    | 0.084**          | 0.084**                |                     |
| Cob weight          | r_p 1.000           | 0.895**                    | 0.608**      | 0.629**              | 0.694**    | 0.897**   | 0.640**            | 0.897**                  | 0.992**    | 0.992**          | 0.992**                |                     |
| Hundred seed weight | r_p 1.000           | 0.824**                    | 0.699**      | 0.629**              | 0.694**    | 0.897**   | 0.640**            | 0.897**                  | 0.992**    | 0.992**          | 0.992**                |                     |
| Shelling percent    | r_p 1.000           | 0.705**                    | 0.828**      | 0.719**              | 0.832**    | 0.832**   | 0.832**            | 0.832**                  | 0.832**    | 0.832**          | 0.832**                |                     |

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 weight.
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 matrices 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 cob | 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 | 0.17 | 0.046 | 0.037 | 0.26 | 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 | 0.043 | 0.020 | 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. ** - Significant at 1% level; Figures in bold size indicates the phenotypic direct effects of various traits over single plant yield.

https://doi.org/10.37992/2020.1103.131
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 |
|----------------------------------|-----------------------|---------------------|---------------------------|--------------|----------------------|------------|-----------|---------------------|---------------------------|------------|--------------------|---------------------|
|                                  | 0.039                 | 0.038               | 0.007                     | -0.015       | -0.012               | -0.15      | -0.015    | -0.008              | -0.021                    | -0.017     | -0.012             | -0.013               |
| Days to 50% tasseling            |                       |                     |                           |              |                      |            |           |                     |                           |            |                    |                     |
| 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               | 0.016                     | 0.011      | 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     | 0.065               | 0.096                     | 0.108      | 0.108              | 0.150               |
| Single plant yield               | -0.428**              | -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. ** - Significant at 1% level; Figures in bold size indicates the genotypic direct effects of various traits over single plant yield.

In summary, this study revealed the existence of genetic variability for all the traits. Strong correlative traits conjointed 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 cob 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.

REFERENCES

Begum, S. Ahmed, A. Omy, S. H. Rohman, M. M. and Amiruzzaman, M. 2016. Genetic variability, character association and path analysis in maize (Zea mays L.), Bangladesh J. Agr. Res., 41:173-182. [Cross Ref]

Boćanski, J. Srećkov, Z. and Nastasić, A. 2009. Genetic and phenotypic relationship between grain yield and components of grain yield of maize (Zea mays L.). Genetika, 41(2):145-154. [Cross Ref]

Cairns, J. E. Sonder, K. Zaidi, P. H. Verhulst, N. Mahuku, G. Babu, R. and Rashid, Z. 2012. Maize production in a changing climate: impacts, adaptation, and mitigation strategies. In: Adv agron., Academic Press, p. 1-58. [Cross Ref]

Dewey, D. R. and Lu, K. 1959. A Correlation and Path-Coefficient analysis of components of crested Wheatgrass seed production. Agron. J., 51(9):515-518. [Cross Ref]

Food and Agricultural Organization. 2018. http://www.fao.org/faostat/

Grafius, J. E. 1956. Components of yield in Oats: A Geometrical Interpretation. Agron. J., 48(9): 419-423. [Cross Ref]

Kote, U. B. Kumar, P. V. Ahamed, M. L. Rani, Y. A. Rao, V. S. and Adilakshmi, D. 2014. Correlation and path analyses in maize (Zea mays L.). Electron. J. Plant Breed, 5(3):538-544.

Moore, D. S. Notz, W. I. and Fligner, M. A. 2015. The basic practice of statistics. Macmillan Higher Education.

Nadarajan, N. 2005. Quantitative genetics and biometrical techniques in plant breeding. Kalyani publishers. New Delhi.

Nataraj, V. Shahi, P. J. and Agarwal, V. 2014. Correlation and path analysis in certain inbred genotypes of maize (Zea Mays L.) at Varanasi. Intl. J. Inno. Res. & Dev., 3(1):14-17.

https://doi.org/10.37992/2020.1103.131
Nzuve, F. Githiri, S. Mukunya, D. M. and Gethi, J. 2014. Genetic variability and correlation studies of grain yield and related agronomic traits in maize. *J. Agric. Sci.*, 6(9):166-176. [Cross Ref]

Pandey, Y. Vyas, R. P. Kumar, J. Singh, L. Singh, H. C. and Yadav, P. C. 2017. Heritability, Correlation and Path coefficient analysis for determining inter-relationships among grain yield and related characters in maize (*Zea mays L.*). *Internat. J. of Pure Appl. Biosci.*, 5(2):596-603. [Cross Ref]

Panse, V. G. and Sukhatme, P. V. 1964. Statistical methods for agricultural research workers. ICAR, New Delhi, 381.

Pavan, R. Lohithaswa, H. C. Wali, M. C. Prakash, G. and Shekara, B. G. 2011. Correlation and path coefficient analysis of grain yield and yield contributing traits in single cross hybrids of maize (*Zea mays L.*). *Electron. J. Plant Breed.*, 2(2):253-257.

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

Rosegrant, M. R. Ringler, C. Sulser, T. B. Ewing, M. Palazzo, A. Zhu, T. and Batka, M. 2009. Agriculture and food security under global change: Prospects for 2025/2050. *International Food Policy Research Institute, Washington, DC*, 145-178.

Singh, R. K. and Chaudhary, B. K. 1979. Biometrical methods in quantitative genetic analysis., Kalyani Publishers, New Delhi.

Soumya, H. and Kamatar, M. 2017. Correlation and path analysis for yield and yield components in single cross maize hybrids (*Zea mays L.*). *J. Agric. Sci.*, 30(2):153-156.

Subedi, K. D. and Ma, B. L. 2005. Ear position, leaf area, and contribution of individual leaves to grain yield in conventional and leafy maize hybrids. *Crop science.*, 45(6):2246-2257. [Cross Ref]

Sujiprihati, S. Saleh, G. B. and Ali, E. S. 2003. Heritability, performance and correlation studies on single cross hybrids of tropical maize. *Asian J. Plant Sci.*, 2(1):51-57. [Cross Ref]

Synrem, G. J. Marker, S. Bhusal, T. and Kumar, L. N. 2016. Correlation and path coefficient analysis in maize genotypes. *Annals of Plant and Soil Research.*, 18(3): 232-240.

Zeeshan, M. Ahsan, M. Arshad, W. Ali, S. Hussain, M. and Khan, M. I. 2013. Estimate of correlated responses for some polygenic parameters in yellow maize (*Zea mays L.*) hybrids. *Int. J. Curr. Adv. Res.*, 1(5):24-29.