

Genetic Dissection of Yield and Yield Contributing Traits Employing Descriptive Statistics and Character Association Analysis in Doubled Haploid Population of Maize (*Zea mays* L.)

Noor E. Mujassim¹, H.C. Lohithaswa^{2*}, Kalmeshwer Gouda Patil³, A. Mohan Rao⁴,
Sunil Kumar Biradar⁵, Nataraj N. Karaba⁶ and N. Mallikarjuna⁷

¹Ph.D. Scholar, Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru (Karnataka), India.

²Principal Scientist (Plant Breeding) and Scheme Head,
AICRP on Pigeonpea, ZARS, UAS, GKVK, Bengaluru (Karnataka), India.

³Pipeline Breeder, Bayer Crop Science Pvt. Ltd., India,
Kallinayakanahalli, Gauribidanur (T) Chikkaballapur (D) (Karnataka), India.

⁴Professor, Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru (Karnataka), India.

⁵Genetic Discovery Lead, Bayer Crop Science Pvt. Ltd., India,
Kallinayakanahalli, Gauribidanur (T), Chikkaballapur (D) (Karnataka), India.

⁶Professor, Department of Crop Physiology, UAS, GKVK, Bengaluru (Karnataka), India.

⁷Maize Pathologist, AICRP on Maize, ZARS, Mandya (Karnataka), India.

(Corresponding author: H.C. Lohithaswa*)

(Received: 25 June 2023; Revised: 26 July 2023; Accepted: 26 August 2023; Published: 15 September 2023)

(Published by Research Trend)

ABSTRACT: The present study was performed to understand the distribution pattern for seven yield related traits through the estimation of descriptive statistics and to perform correlation coefficient and path analysis in 273 doubled haploid lines developed from the cross PL#08× PL#15 in maize. Analysis of variance revealed mean squares attributable among and between the DHs and the checks were significant for all the traits. These results suggested significant differences among the maize doubled haploid lines. All the quantitative traits exhibited kurtosis value of less than three indicating platykurtic distribution of these traits are platykurtic. It indicated that genetic control of these traits was influenced by many genes, with the majority of them displaying complementary epistasis with increasing effects. Correlation studies revealed that Kernel weight per cob had a significant positive correlation with cob length, cob girth, kernel rows per cob ($p < 0.001$) followed by plant height ($p < 0.01$), and ear height ($p < 0.05$). It indicated that kernel weight per cob can be increased by giving importance to these traits while formulating selection criteria in yield improvement programme.

Keywords: Maize, Doubled haploids, Correlation, Complementary epistasis, Platykurtic distribution.

INTRODUCTION

Maize (*Zea mays* L.) is an important food crop having wider adaptability under different agro-climatic conditions. It is the third most important cereal crop in India after rice and wheat due to its highest genetic yield potential among cereals. It belongs to the tribe *Maydeae* and the family *Poaceae*. Currently, nearly 1147.7 million MT of maize is being produced together by over 170 countries from an area of 193.7 million ha with average productivity of 5.75 t/ha (FAOSTAT, 2020). As a rapid generation advancement tool, doubled haploid (DH) has decreased the time needed to create maize inbreds from six to seven selfing generations to just two generations. The DHs offer several advantages over other mapping populations as they allow the genes of recombinant gametes to be fixed directly as complete homozygous lines and phenotyping with greater precision is possible compared to families in early segregating generations (F3 or F4) (Yan *et al.*, 2017). Among the most statistical tools, skewness and kurtosis are more powerful which help us to understand relative mean performance, nature of distribution of traits and Mujassim *et al.*,

for characterizing the nature of epistasis. Fasoulas (1981) considered that departure from normal distribution is an indication of the presence of unfavorable genes that a breeder has to remove during the selection procedure. Yield is a complex trait and is influenced by several component traits and we need to identify those characters that contribute to improvement of kernel yield. Correlation studies provide knowledge of association among different characters and kernel yield (Greveniotis *et al.*, 2017). Information on association of characters, direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process. Correlation and path analysis establish the extent of association between yield and its components and also bring out relative importance of their direct and indirect effects, thus giving an understanding of their association with kernel yield (Babu *et al.*, 2012). Ultimately, this could help the breeder to design the selection strategies to improve kernel yield. In the light of the above scenario, the present investigation was carried out with the objective of estimating population

parameters and character association in maize doubled haploid population for yield improvement.

MATERIAL AND METHODS

A. Basic Genetic Material and Development of Doubled Haploid Population

The basic genetic material consisted of 273 maize doubled haploid lines developed from the cross PL#08×PL#15 along with parental inbreds. The inbred line (PL#08) was crossed with PL#15 during *kharif* 2020 and F₁ was selfed to obtain F₂ plants. These F₂ plants were crossed with male haploid inducer inbred. The dominant grain purple colour marker gene (R1-nj marker) was employed to separate haploid kernels without pigmentation on embryo, and those with pigmentation as regular diploids. The haploid kernels thus separated were placed in the paper towels for germination (Chaikam *et al.*, 2018). When the coleoptiles were about 2-cm long the tip was cut-off and submerged in colchicine solution with Dimethyl Sulphoxide (DMSO). The seedlings were washed under tap water, and planted in biodegradable ellepots filled with peat pellets. These pots were kept in the shade house till three-leaf stage, and then transplanted in the DH nursery net house and selfed to obtain doubled haploids (DH₁). This process resulted in 273 doubled haploid lines from F₂ plants of the cross PL#08×PL#15.

B. Field Layout

The 273 maize inbred lines and their respective parents as checks were evaluated in the augmented design (Federer, 1961) and checks were repeated after every 20th row of test entries. All the entries were planted in rows spaced 0.60 m apart with an intra-row spacing of 0.20 m at the Mega Breeding Station, Bayer Crop Science Pvt. Ltd., Kallinayakanahalli, Gauribidanur (T), Chikkaballapur District with 13.464013°N, 77.519178° E during, 2021 *kharif*. The observations were recorded

on five plants in all 273 doubled haploid lines for plant height (PH), ear height (EH), cob girth (CG), cob length (CL), number of kernel rows per cob (KRC), kernel weight per cob (KWC) and test weight (TW).

C. Statistical Analysis

The mean of five plants was used to perform the analysis of variance as per augmented design. Descriptive statistics were employed to study the distribution pattern of DH lines with respect to quantitative traits and analysed using R software. Skewness was worked out by using Agostino test and kurtosis, that of fourth-degree statistics by using Anskombi test. Correlation and path analysis were performed by using corrplot package in R software. Three types of kurtosis recognised based on the values which depends on the distribution curve.

If kurtosis value = 3 = Normal curve = Mesokurtic

If kurtosis value > 3 = leaping curve = Leptokurtic

If kurtosis value < 3 = Flat curve = Platykurtic

Similarly, the lack of symmetry *i.e.*, skewness was recognised based on the coefficient of skewness values which ranged from -3 to +3. The type of distribution based on the skewness values are as follows.

If skewness value is zero = symmetrical distribution

If skewness value is negative = negatively skewed distribution

If skewness value is positive = positively skewed distribution

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among doubled haploid lines for all the traits (Table 1). Similarly, a significant mean square due to doubled haploid lines *vs* checks was also observed. These results suggested the existence of wide variability among the maize doubled haploid lines for all the traits under study.

Table 1: Analysis of variance for seven quantitative traits in 273 maize doubled haploid lines derived from the cross PL#08×PL#15.

Source	df	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob girth (cm)	Number of kernel rows/ cob	Kernel weight/ cob (g)	Test weight (g)
Blocks	13	162.8 ^{ns}	50.53 ^{ns}	2.1 ^{ns}	0.26 ^{ns}	7.36 ^{ns}	172 ^{ns}	4.72 ^{ns}
Checks	2	3257.14 ^{**}	1326.27 ^{**}	38.21 ^{**}	36.20 [*]	43.76 ^{ns}	934.26 [*]	1862.45 ^{**}
Doubled haploids	27	452.6 ^{**}	152.43 ^{**}	17.48 [*]	24.56 ^{**}	68.97 [*]	1247.40 ^{**}	21.46 ^{**}
Doubled haploids vs checks	27	421.20 ^{**}	136.5 ^{**}	27.40 ^{**}	26.04 [*]	50.10 ^{ns}	1082.24 ^{**}	24.76 ^{**}
Error	26	61.63	36.34	5.42	0.29	4.75	186.06	7.05

ns-non-significant; *, **significant at $P < 0.05$, $P < 0.01$

A. Box and Whisker Plots

Box plot is the way to represent range of numerical data of several traits by constructing box and whisker plots (Tukey, 1977). It is expected to provide information about a sample's range, median, and skewness of the distribution (Kumar *et al.*, 2019). It can also identify and plot extreme cases within the sample. The distribution properties of seven quantitative parameters estimated in doubled haploid population are presented

in box plots (Fig. 1) depicting the degree of dispersion in the population. Bold lines within boxes indicate median value and box limits indicate interquartile range (*i.e.*, 50% of values lie within the box) and whiskers indicate highest and lowest excluding outliers or extremes. In our data set, among seven traits, only number of kernel rows per cob, cob girth and kernel weight per cob showed very few outliers as indicated by the points outside the whisker.

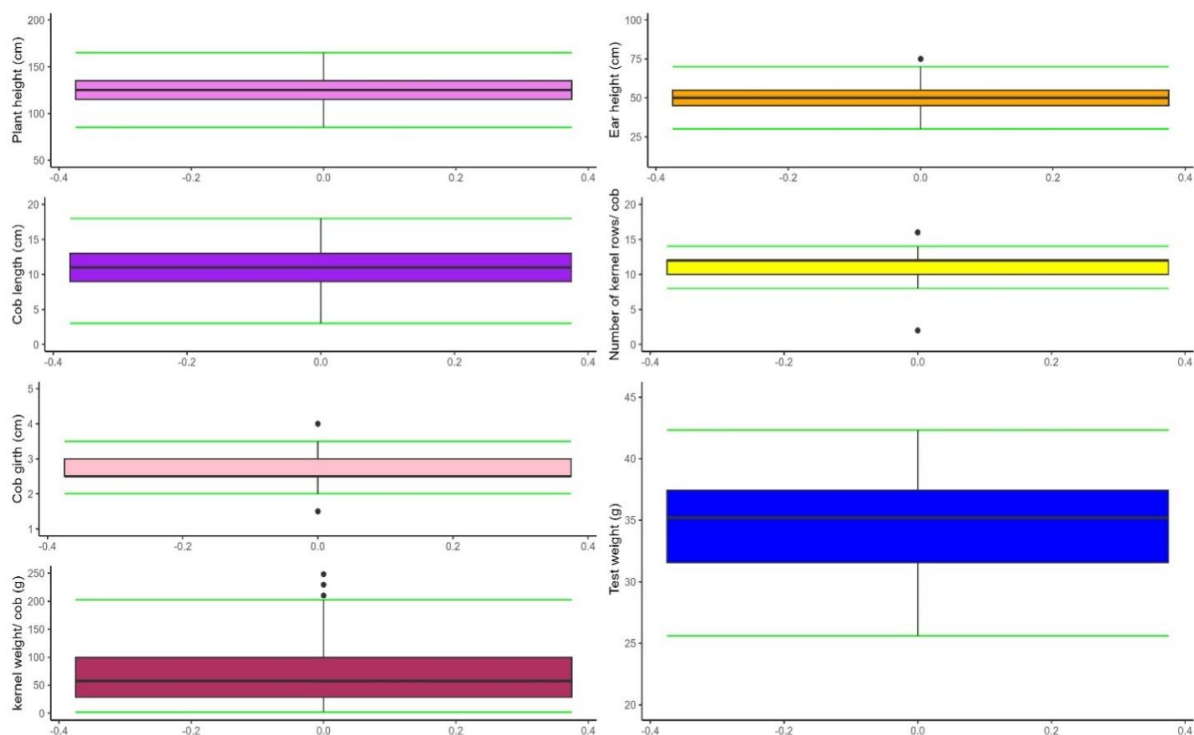


Fig. 1. Box plot depicting the distribution properties of seven quantitative traits in maize doubled haploid population.

B. Test for Skewness and Kurtosis

The results of phenotypic statistics which includes mean, skewness, kurtosis, minimum, maximum, and variance are shown in Table 2. The genetic expectation of coefficient of skewness for the distribution of DH lines for plant height, ear height, cob girth, number of kernel rows/ cob and kernel weight/ cob were positively skewed (Table 2). Positive skewness indicated the involvement of complementary gene interactions predominantly in the same direction (Snape and Riggs 1975).

Similarly, all the quantitative traits exhibited platykurtic distribution (<3.0). It indicated the involvement of many genes, with the majority of them displaying complementary epistasis with increasing effects (Table 2). From these statistical values, it was concluded that the seven quantitative traits were controlled by many genes. Whereas, platykurtic and negatively skewed distribution recorded for cob length and test weight revealed large number of genes displaying duplicate dominant epistasis. Sumathi *et al.* (2018) also reported positive skewness for cob diameter, 100 grain weight and grain yield per plant in maize.

Table 2: Descriptive statistics on seven quantitative traits in maize doubled haploid lines derived from the cross PL#08× PL#15.

Traits	Mean	Range	Min	Max	Std. Error	Skewness	Kurtosis	Variance	Coefficient of Variation (CV)
Plant height (cm)	125.95	80	85	165	0.96	0.25	0.15	253.12	12.65
Ear height (cm)	50.18	40	30	70	0.52	0.27	-0.45	75.6	14.38
Cob girth (cm)	2.6	2.5	2	3.5	0.02	0.18	0.66	0.18	11
Cob length (cm)	11.01	15	3	18	0.15	-0.08	-0.15	6.46	17.5
Number of kernel rows per cob	11.19	6	8	14	0.1	0.07	0.63	2.78	14.93
Kernel weight per cob (g)	67.1	95.56	5.7	202.3	1.2	0.81	0.04	342.51	12.5
Test weight (g)	34.62	16.73	25.6	42.33	0.22	-0.17	-0.6	16.76	10.72

C. Correlation and Path Studies for Yield and Yield Component Traits in Doubled Haploid Population

Selection based on the correlation studies gives an idea about magnitude and direction of association between yield and its attributes. Phenotypic correlations between kernel weight per cob and yield components *viz.*, plant height; ear height, cob girth, cob length, number of kernel rows per cob, kernel weight per cob and test weight were computed for doubled haploid population and the results are presented in Fig. 2 & 3. The trait kernel weight per cob had a significant positive correlation with cob length, cob girth, kernel rows per

cob ($p < 0.001$) followed by plant height ($p < 0.01$), and ear height ($p < 0.05$). It indicated that kernel weight per cob can be increased through improvement in characters that showed positive and significant association. Similar results were reported earlier in maize by several workers on association of different characters *viz.*, for the association of kernel yield with plant height (Raghu *et al.*, 2011; Zarei *et al.*, 2012), ear height (Raghu *et al.*, 2011; Munawar *et al.*, 2013), number of kernel rows per cob (Sofi and Rather 2007) and 100 grain weight (Raghu *et al.*, 2011; Nataraj *et al.*, 2014; Zarei *et al.*, 2012).

A precise information on relevance of the indirect and direct impact of each component trait on the desired trait cannot be obtained from simple correlation data. However, path coefficient analysis will provide this information as it splits the correlation coefficient into measures of direct and indirect effects, helping to perceive information on interrelationships among traits and their effects on kernel weight per cob (Table 3).

The path coefficient analysis revealed that the cob length (0.42) exhibited the largest direct effect on kernel weight per cob followed by plant height (0.19), test weight (0.18), cob girth (0.17), kernel rows per cob (0.16) and ear height (0.033). These results are in conformity with the findings of Kumar *et al.* (2006); Raghu *et al.* (2011); Devi and Mohammed (2001); Nataraj *et al.* (2014) in maize.

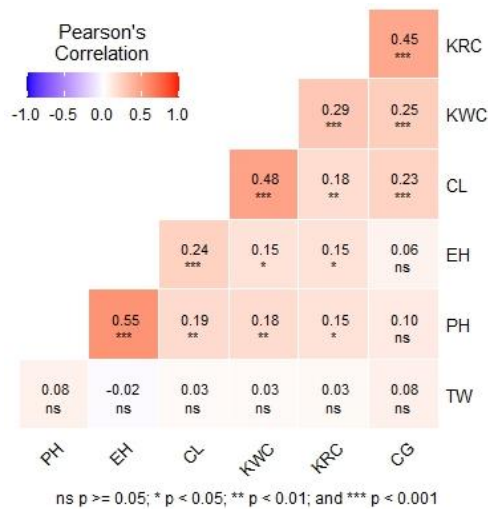
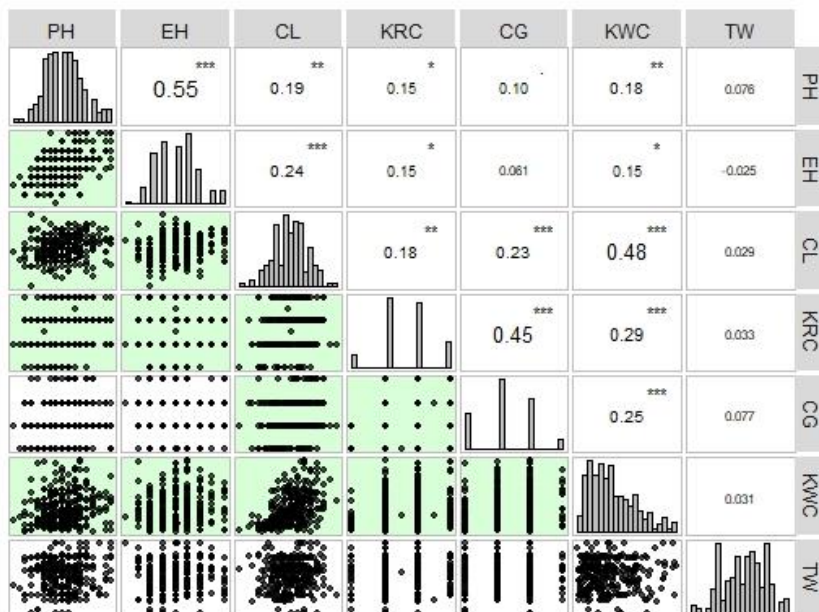


Fig. 2. Pearson correlations among seven morphological traits in doubled haploid population in maize (*Zea mays* L.)



Note: PH = plant height (cm); EH = ear height (cm); CG = cob girth (cm); CL= cob length (cm); KRC= number of kernel rows per cob; KWC = kernel weight per cob (g); TW = test weight(g)

Fig. 3. Scatter plot with correlation values of seven quantitative traits in doubled haploid population in maize (*Zea mays* L.).

Table 3: Estimates of direct and indirect effects of characters on kernel weight per cob in doubled haploid population derived from the cross PL#08× PL#15.

	PH	EH	CL	CG	KRC	TW
PH	0.19011	-0.01830	0.08067	0.00753	0.02487	0.0137
EH	0.04960	0.03324	0.09902	0.00447	0.02569	0.0445
CL	0.01725	-0.00781	0.42138	0.01667	0.03045	0.00520
CG	0.00925	-0.00202	0.09578	0.17337	0.07633	0.00139
KRC	0.01323	-0.00504	0.07576	0.03306	0.16939	0.0066
TW	0.00684	0.00082	0.01216	0.00565	0.00566	0.180

Bold values are direct effects; Residual effect = 0.28

Note: PH = plant height (cm); EH = ear height (cm); CG = cob girth (cm); CL= cob length (cm); KRC= number of kernel rows per cob; KWC = kernel weight per cob (g); TW = test weight (g)

CONCLUSIONS

All the quantitative traits exhibited platykurtic distribution (< 3.0) which indicated the involvement of many genes, with the majority of them displaying complementary epistasis with increasing effects. Kernel weight per cob had a significant positive correlation with cob length, cob girth, kernel rows per cob followed by plant height and ear height. It indicated that kernel weight per cob can be increased through improvement in characters that showed positive and significant association.

Acknowledgement. The authors acknowledge financial assistance from Prime Minister's Fellowship for Doctoral Research, SERB- CII and industry partner Bayer Crop Science Pvt. Ltd.

Conflict of Interest. None.

REFERENCES

- Babu, V. R., Shreya, K., Dangi, K. S., Usharani, G. and Shankar, A. S. (2012). Correlation and path analysis studies in popular rice hybrids of India. *International Journal of Scientific and Research Publications*, 2(3), 1-5.
- Chaikam, V., Nair, S. K., Martinez, L., Lopez, L. A., Utz, H. F., Melchinger, A. E. and Prasanna, B. M. (2018). Marker-Assisted breeding of improved maternal haploid inducers in maize for the tropical/ subtropical regions. *Front. Plant Sci.*, 9, 1527.
- Devi, I. S. and Mohammed, S. (2001). Character association and path coefficient analysis of grain yield and yield components in double crosses of maize. *Crop Research Hisar*, 21, 355-359.
- FAOSTAT (2020). Statistical database of the food and agriculture organization of the United Nations. <https://www.fao.org/faostat>.
- Fasoulas, A. C. (1981). Principles and methods of plant breeding. *Arist. Univ. Thessaloniki*, 147.
- Greveniotis, V., Sioki, E. and Ipsilandis, C. G. (2017). Frequency distribution analysis of a maize population. *cereal. res. Commun.*, 45(4), 687-698.
- Kumar, S., Shahi, J. P., Singh, J. and Singh, S. P. (2006). Correlation and path analysis in early generation inbreds of maize (*Zea mays L.*). *Crop Improvement*, 33(2), 156-160.
- Kumar, R., Mishra, T. K. and Pradhan, B. (2019). Studies on frequency distribution, skewness and kurtosis in F₁m₁ mutant populations of sesame. *Int. J. Curr. Microbiol. App. Sci.*, 8(4), 1755-1760.
- Munawar, M., Shahbaz, M., Hammad, G. and Yasir, M. (2013). Correlation and path analysis of grain yield components in exotic maize (*Zea Mays L.*) Hybrids. *Int. J. Sci. Basic Appl. Res.*, 12(1), 22-27.
- Nataraj, V., Shahi, J. P. and Agarwal, V. (2014). Correlation and path analysis in certain Inbred genotypes of maize (*Zea Mays L.*) at Varanasi. *Int. J. Innov. Res.*, 3(1): 14-17
- Raghu, B., Suresh, J., Kumar, S. S. and Saidaiah, P. (2011). Character association and path analysis in maize (*Zea mays L.*). *Madras Agric. J.*, 98, 7-9.
- Snape, J. W. and Riggs, T. J. (1975). Genetical consequences of single seed descent in the breeding self-pollinated crops. *Heredity*, 35, 211-219.
- Sofi, P. and Rather, A. G. (2007). Studies on genetic variability, correlation and path analysis in maize (*Zea mays L.*). *Maize Genetic Cooperation Newsletter*, 81, 26-27.
- Sumathi, K., Natesan, S. and Ganesan, K. N. (2018). Studies on skewness and kurtosis of sorghum downy mildew resistant BC₃F₃ progenies in maize. *Int. J. Curr. Microbiol. App. Sci.*, 7(6), 3834-3838.
- Tukey, J. W. (1977). Exploratory data analysis. Addison-Wesley Pub Co, 26, 163-182.
- Yan, G., Liu, H., Wang, H., Lu, Z., Wang, Y., Mullan, D., Hamblin, J. and Liu, C. (2017). Accelerated generation of selfed pure line plants for gene identification and crop breeding. *Front. Plant Sci.*, 8, 1786.
- Zarei, B., Kahrizi, D., Aboughadaresh, A. P. and Sadeghi, F. (2012). Correlation and path coefficient analysis for determining interrelationships among grain yield and related characters in corn hybrids. *Int. J. Agric. Crop Sci.*, 4(20), 1519-152.

How to cite this article: Noor E. Mujjassim, H.C. Lohithaswa, Kalmeshwer Gouda Patil, A. Mohan Rao, Sunil Kumar Biradar, Nataraj N. Karaba and N. Mallikarjuna (2023). Genetic Dissection of Yield and Yield Contributing Traits Employing Descriptive Statistics and Character Association Analysis in Doubled Haploid Population of Maize (*Zea mays L.*). *Biological Forum – An International Journal*, 15(9): 374-378.