



RESEARCH PAPER

Assessment of genetic variability and trait association for yield and its components in bi-parental early segregating generation of maize

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Abstract : The present investigation was carried out to understand the co-efficients of variation, heritability, genetic advance, correlation co-efficient and path analysis in F_2 population of maize. The study comprised of 303 F_2 progeny plants, parents and F_1 of the cross, CM 111 \times DHKN 509 evaluated under un-replicated trial during *Rabi* 2020-21. The observations were recorded for ten traits viz., days to tasseling, days to silking, anthesis-silking interval, plant height, ear height, ear girth, number of kernels per row, pith weight, shelling per cent and grain yield per plant in all the F_2 progeny plants and ten plants each from parents and F_1 and noticed wide variation among the traits studied in the F_2 population. The extent of phenotypic and co-efficient of variation was higher than genotypic co-efficient of variation for all the traits studied. High PCV and GCV was recorded for anthesis-silking interval, number of kernels per row, pith weight and grain yield per plant. High heritability coupled with high genetic advance over mean were observed for anthesis-silking interval, number of kernels per row, pith weight and grain yield per plant suggesting that these traits are governed by additive gene action and can be improved through simple selection. Positive and significant association with grain yield was recorded with number of kernels per row, pith weight, cob girth and shelling per cent. Days to tasseling and anthesis-silking interval exhibited highest direct positive effect on grain yield per plant followed by pith weight and shelling per cent indicating the effectiveness of direct selection, whereas direct negative effects were recorded by days to silking and ear height indicating the effectiveness of indirect selection.

Key Words : Maize, GCV, PCV, Heritability, Genetic advance, Correlation, Path analysis

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INTRODUCTION

Maize (*Zea mays* L.) is the world's third most important cereal food crop, known as the "Queen of Cereals" due to its high genetic yield potential. It has a

prominent position in the global economy due to its numerous applications, including staple food in many African countries, poultry and cattle feed, and industrial raw material for the production of starch, dextrose, sugar,

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syrup, adhesive paper, plastic and so on (Omprakash *et al.*, 2017; Tippannavar *et al.*, 2019 and Reddy *et al.*, 2021). It is grown on 197.0 million ha of land worldwide (Suresh *et al.*, 2021), with a total production of 1265.09 million tonnes and an average productivity of 5.75 t/ha (FAOSTAT, 2020). India ranks fourth in terms of total area and seventh in terms of total maize production. It is currently grown on 9.72 million ha, with an average production of 28.64 million tonnes and a productivity of around 2.94 tonnes per hectare (DACNET, 2020). Maize is grown on 1.4 million ha in Karnataka, with average production and productivity of 3.96 million tonnes and 2.83 tonnes/ha, respectively. In a developing country like India, the rapidly increasing population may outnumber cereal grain production. As a result of its high yield potential and numerous human benefits, the demand for maize grain production is increasing. As a result, breeders are focusing on increasing maize grain yield.

The increasing plant disease and pest outbreaks leading larger crop yield losses threatening the food security of the world. The important diseases such as downy mildew in sorghum (Sharma *et al.*, 2010), dry root rot in chickpea (Talekar *et al.*, 2017 and 2021), phyllody in chickpea (Balol *et al.*, 2021), leaf spots in groundnut (Kolekar *et al.*, 2016), wilt in pigeonpea (Saxena *et al.*, 2012), necrosis disease in sunflower (Sundaresha *et al.*, 2012) and bud blight caused by groundnut bud necrosis virus (Balol and Patil, 2014), Turicum leaf blight in maize (Hooda *et al.*, 2017), *etc.* are contributing for the yield loss. Genetic variability for resistance to different diseases and yield components is important in determining grain yield variation among genotypes. Grain yield variation is the interaction of and environmental factors. In maize, only when there is a significant amount of variability in the parental population, which is calculated using the variability parameters, phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV), can elite genotypes be selected (GCV). Thus, in order for selection to be effective, we must consider highly variable characters with a high level of heritability (Robinson *et al.*, 1949). Furthermore, the type of gene action involved in governing the trait can be assessed using traits with high heritability combined with genetic advance and simple selection can be used for these traits (Johnson *et al.*, 1955). Knowledge of the interaction between grain yield and its component traits is required for success in any selection process that involves calculating correlation co-

efficients and path co-efficients. As a result, a thorough understanding of the interaction between grain yield and its components can greatly improve the crop improvement program's effectiveness (Wright, 1921). With this context in mind, the current study sought to assess the genetic variability of ten traits, their correlation and the direct and indirect effects of the traits on grain yield in a biparental F_2 maize population.

MATERIAL AND METHODS

The current study was carried out at the Agricultural Research Station in Mugad during *Rabi* 2020-21 and the experimental material included 303 F_2 individuals of the cross combination, CM 111 DHKN 509, their parental lines, and F_1 . The experimental site is located in the northern transitional tract of Karnataka at 150.15' N latitude and 740.40' E longitude, at an elevation of 697m above mean sea level, with an annual rainfall of 1017.0 mm. The genetic material was evaluated in an un-replicated fashion with a spacing of 60 × 20 cm while complying to all of the recommended practices. To calculate genotypic variance of the F_2 population, the parents and F_1 were evaluated to determine the effect of environment in uniform lines using the following formulae (Globerson *et al.*, 1987), Environmental variance = $(V_{pp1} + V_{pp2} + V_{pF1})/3$

Genotypic variance of F_2 population = Phenotypic variance of F_2 population - Environmental variance

where,

V_{pp1} = Phenotypic variance in parent 1

V_{pp2} = Phenotypic variance in parent 2

V_{pF1} = Phenotypic variance in parent F_1

Days to tasseling, days to silking, anthesis-silking interval, plant height (cm), ear height (cm), ear girth (cm), number of kernels per row, pith weight (g), shelling per cent and grain yield per plant (g) were observed for 303 F_2 progeny plants, as well as ten plants each from two parental lines and F_1 . The MS-EXCEL and R programmes were used to analyze the data.

RESULTS AND DISCUSSION

The investigation of variability and genetic progress in germplasm will aid in determining the genotype's true potential. Genetic parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance as a percent of mean provide a clear picture of the extent of variability

present in a plant population, as well as a relative measure of the efficiency of genotype selection based on phenotype in a highly variable population. The F₂ population of the cross, DHKN 509 × CM 111, exhibited large variation for all traits studied (Table 1 Fig. 1) and the Phenotypic Co-efficient of Variation (PCV) was greater than the Genotypic Coefficient of Variation (GCV) for all traits studied in the F₂ population, representing the effect of environment. PCV and GCV

estimates for anthesis-silking interval (69.14 % and 65.48 %, respectively) were high, followed by pith weight (37.25 % and 36.21 %), grain yield per plant (37.07 % and 33.12 %), and number of kernels per row (26.44 % and 22.76 %), indicating a greater scope for selection to improve these traits. These results are in accordance with Beulah *et al.* (2018) for anthesis-silking interval and grain yield per plant, Chandana (2018) for grain yield per plant and number of kernels per row and Prakash *et*

Table 1 : Estimates of variability, heritability and genetic advance as per cent of mean for grain yield and its attributes in F₂ population of CM 111 × DHKN 509

	DTT	DTS	ASI	PH	EH	EG	NKR	PW	SP	GYP
MEAN	69.96	72.60	2.64	213.15	132.00	4.26	17.91	17.17	77.71	61.16
MIN	64.00	65.00	-4.00	135.00	84.00	3.00	4.00	5.80	66.15	27.50
MAX	79.00	80.00	6.00	255.00	178.00	5.20	37.00	46.80	90.05	178.50
PCV (%)	3.55	4.26	69.14	10.44	14.69	9.92	26.44	37.25	6.30	37.07
GCV (%)	3.33	4.07	65.48	9.52	13.60	9.26	22.76	36.21	6.05	33.12
h ² _{bs} (%)	88.02	91.23	90.51	83.32	86.07	87.67	74.91	95.21	92.63	80.54
GAM (%)	6.45	7.99	127.73	17.88	25.96	17.81	40.37	72.52	11.97	60.96

DTT = Days to tasseling
 EH = Ear height
 SP = Shelling percent
 PCV (%) = Phenotypic co-efficient of variance
 h²_{bs} (%) = Heritability in broad sense

DTS = Days to silking
 EG = Ear girth
 GYP = Grain yield per plant

ASI = Anthesis-silking interval
 NKR = No. of kernels per row
 MIN = Minimum value
 GCV (%) = Genotypic co-efficient of variance
 GAM = Genetic advance as per cent of mean

PH = Plant height
 PW = Pith weight
 MAX = Maximum value

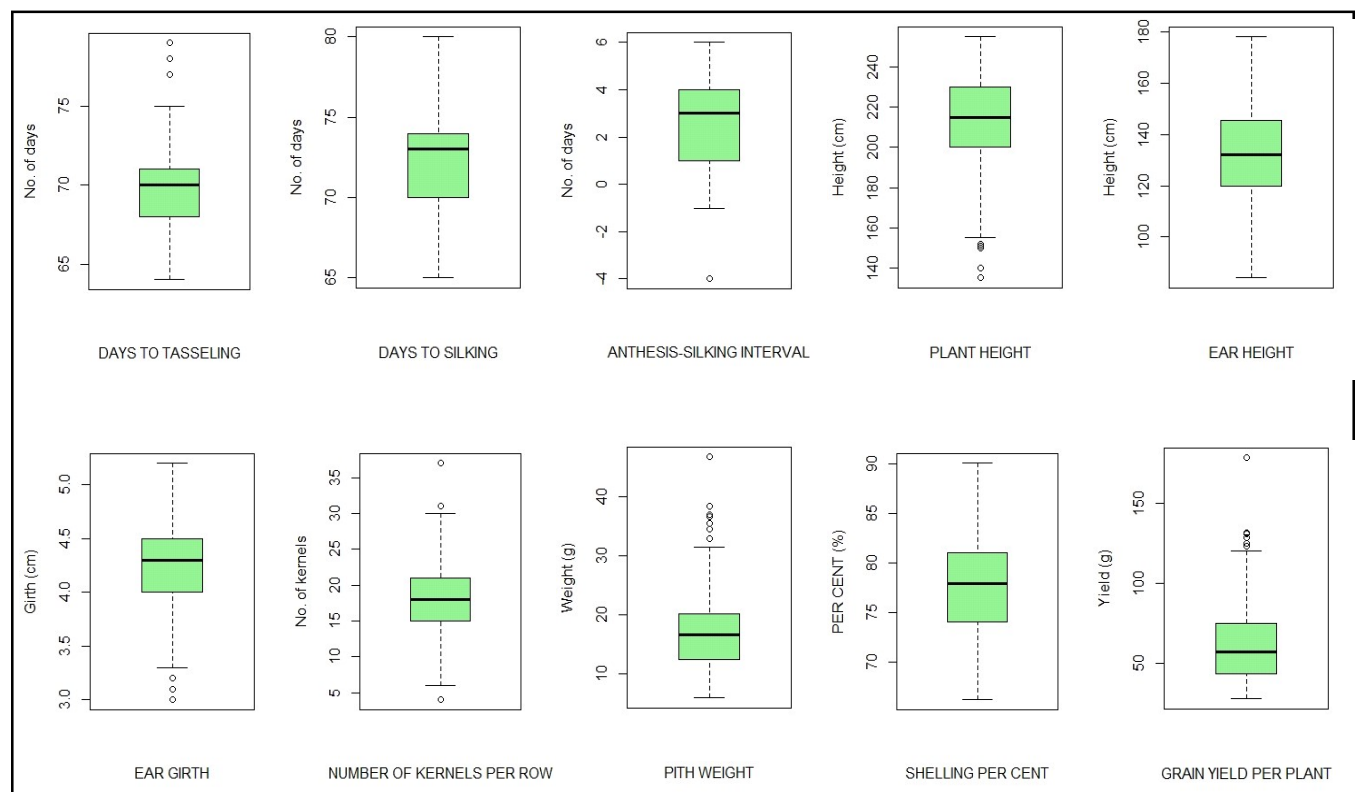


Fig. 1 : Boxplots showing variation in yield and its component traits in F₂ population of CM 111 × DHKN 509

al. (2019) for anthesis-silking interval, number of kernels per row and grain yield per plant. However, moderate PCV and GCV was recorded for ear height (14.69 % and 13.60 %) only which was in accordance with that of Patil *et al.* (2016). Plant height had a moderate PCV (10.44%) but a low GCV (9.52%). Furthermore, low PCV and GCV were found for ear girth (9.92% and 9.26%), shelling per cent (6.30% and 6.05%), days to silking (4.26% and 4.07%) and days to tasseling (3.55% and 3.33%), indicating that rigorous selection should be used to select superior genotypes. Similar results of low PCV and GCV for days to tasseling and days to silking were observed by Begum *et al.* (2016), Reddy and Jabeen (2016), Beulah *et al.* (2018), Pandey *et al.* (2017), Chethan and Nataraja (2020) and Tasfaye *et al.* (2021), and for shelling per cent by Prakash *et al.* (2019).

Traits with a high heritability can be easily fixed through simple selection, resulting in a rapid response. All of the traits studied were found to have a high heritability. Heritability was very high for pith weight (95.21%), followed by shelling percentage (92.63%), days to silking (91.23%) and anthesis-silking interval (90.51%) where heritability was over 90% and ranged to 74.91 per cent for number of kernels per row. The results were in accordance with Jawaharlal *et al.* (2011), Hussain and Hassan (2014), Begum *et al.* (2016), Synrem *et al.* (2016), Pandey *et al.* (2017), Prakash *et al.* (2019) and Neelima *et al.* (2020).

Genetic advance is defined as an improvement in a selected individual's performance over the initial population. Estimates of genetic advance aid in understanding the type of gene action involved in the expression of polygenic traits. Anthesis-silking interval

(127.73%) had the highest genetic advance as a percentage of mean (GAM), followed by pith weight (72.52 %), grain yield per plant (60.96 %), number of kernels per row (40.37 %), and ear height (25.96 percent), indicating that these traits are controlled by additive gene action and thus, selection can be practiced. All of these traits yielded similar results according to Chandana (2018). According to Pandey *et al.* (2017) and Chandana, moderate GAM was recorded for plant height (17.88%), followed by ear girth (17.81%) and shelling per cent (11.97 %) (2018). However, low GAM was observed for days to silking (7.99%) and days to tasseling (6.45 %). These findings were in parallel with the experiments of Pandey *et al.* (2017), Begum *et al.* (2016), Beulah *et al.* (2018), Chandana (2018), Neelima *et al.* (2020) and Tasfaye *et al.* (2021).

High heritability with high genetic advance as a percentage of mean was observed for anthesis-silking interval, followed by pith weight, ear height, grain yield per plant, and number of kernels per row, implying that selection could be effective for desired genetic improvement for these traits under the control of additive gene action. This was consistent with Jawaharlal *et al.* (2011), Reddy *et al.* (2012), Nataraj *et al.* (2014) and Chandana *et al.* (2014) for ear height, grain yield per plant and number of kernels per row (2018).

The effectiveness of any breeding programme is heavily reliant on understanding the relationships between the traits being studied. Grain yield, being a complex and quantitatively inherited character, should be improved through indirect selection of characters that contribute to yield. This is possible with the help of association studies. The character association studies revealed that

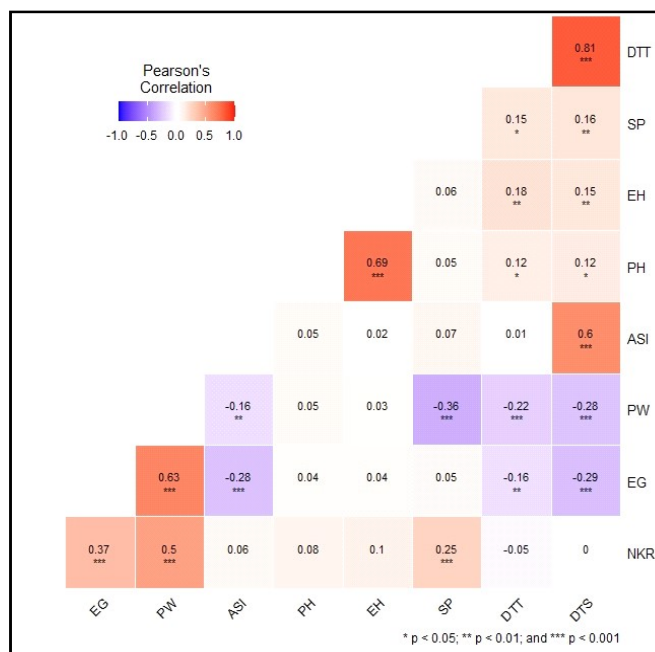
Table 2 : Path co-efficient analysis of nine characters on grain yield per plant in F₂ population of CM 111 × DHKN 509

	DTT	DTS	ASI	PH	EH	EG	NKR	PW	SP	Phenotypic correlation with grain yield per plant
DTT	1.2447	-1.2702	0.0090	0.0006	-0.0013	-0.0154	-0.0066	-0.1715	0.0906	-0.12*
DTS	1.0082	-1.5681	0.5398	0.0006	-0.0011	-0.0279	0.0001	-0.2182	0.0967	-0.17**
ASI	0.0124	-0.9409	0.8997	0.0003	-0.0001	-0.0270	0.0079	-0.1247	0.0423	-0.13*
PH	0.1494	-0.1882	0.0450	0.0051	-0.0048	0.0039	0.0106	0.0390	0.0302	0.09
EH	0.2240	-0.2352	0.0180	0.0035	-0.0070	0.0039	0.0132	0.0234	0.0362	0.08
EG	-0.1991	0.4547	-0.2519	0.0002	-0.0003	0.0963	0.0489	0.4910	0.0302	0.67**
NKR	-0.0622	0.0001	0.0540	0.0004	-0.0007	0.0356	0.1322	0.3897	0.1510	0.70**
PW	-0.2738	0.4391	-0.1440	0.0003	-0.0002	0.0606	0.0661	0.7794	-0.2175	0.71**
SP	0.1867	-0.2509	0.0630	0.0003	-0.0004	0.0048	0.0330	-0.2806	0.6041	0.36**

Note: * and ** indicate significance of values at P=0.05 and 0.01, respectively
Residual effect=0.0719627

grain yield per plant had a highly significant and positive relationship with pith weight (0.71), followed by number of kernels per row (0.70), ear girth (0.67) and shelling percentage (0.36), implying that selecting for these traits could improve maize yield (Fig. 2). Such kind of association were reported by Reddy *et al.* (2012), Pandey *et al.* (2017), Rajwade *et al.* (2018), Prakash *et al.* (2019), Chaurasia *et al.* (2020), Verma *et al.* (2020) and Yahaya *et al.* (2021). Plant and ear height had no significant relationship with grain yield per plant. Days to tasseling (-0.12), days to silking (-0.17) and anthesis to silking interval (-0.13) all had a negative and significant association with grain yield per plant, implying that these traits can be used to identify early maturing genotypes. These results are in accordance with the studies of Reddy and Jabeen (2016), Pandey *et al.* (2017), Prakash *et al.* (2019), Verma *et al.* (2020) and Chaurasia *et al.* (2020).

effect on grain yield per plant, followed by anthesis-silking interval (0.8997), pith weight (0.7794), shelling percentage (0.6041), number of kernels per row (0.1322), ear girth (0.0963) and plant height (0.0051). As a result, these traits, such as days to tasseling, anthesis-silking interval, pith weight, shelling percentage and number of kernels per row, should be prioritized when developing a breeding programme. Similar results were reported by Reddy *et al.* (2012), Reddy and Jabeen (2016) and Jakhar *et al.* (2017). Although the direct effects of ear girth and number of kernels per row are relatively low, these traits have indirectly contributed significantly through pith weight and shelling percentage, resulting in a stronger association between these two characters and grain yield. As a result, emphasising these traits when developing maize selection strategies would be beneficial. Days to tasseling (-0.12) and anthesis-silking interval (-0.13) also had a negative association with grain yield, but it had a positive direct effect due to the negative indirect effects of the other traits. Furthermore, the days to silking had the greatest negative direct effect (-0.7065), followed by ear height (-0.0632). These findings were in parallel with the experiments of Reddy *et al.* (2012), Kumar *et al.* (2017) and Hosamani *et al.* (2018).



DTT = Days to tasseling
 ASI = Anthesis-silking interval
 EH = Ear height
 NKR = No. of kernels per row
 SP = Shelling percent
 DTS = Days to silking
 PH = Plant height
 CG = Ear girth
 PW = Pith weight
 GYP = Grain yield per plant

Fig. 2 : Correlation co-efficients among grain yield and its attributes in F₂ population of CM 111 x DHKN 509

We can assess the relative contribution of each causal factor to yield by partitioning correlation co-efficients into components of direct and indirect effects. The path co-efficient analysis (Table 2) revealed that days to tasseling (1.2447) had the greatest positive direct

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