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**SD Rathod**

PG Student, Mahatma Phule  
Krishi Vidyapeeth, Rahuri,  
Maharashtra, India

**GC Shinde**

Assistant Professor, Dept. of  
Agricultural Botany, Mahatma  
Phule Krishi Vidyapeeth,  
Rahuri, Maharashtra, India

**SD Shinde**

SRA, Dept. of Agricultural  
Statistics, Mahatma Phule  
Krishi Vidyapeeth, Rahuri,  
Maharashtra, India

## Genetic variability and path coefficient analysis studies in forage maize genotypes (*Zea mays* L.)

SD Rathod, GC Shinde and SD Shinde

**Abstract**

In present investigation fifty four genotypes of maize were evaluated at research farm of AICRP on Forage Crops and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri during *rabi* 2018-19 in a Randomized Block Design with two replications. The observations were recorded on yield and yield contributing traits *viz.*, days to 50% tasseling, days to silking, plant height (cm), number of leaves/tiller, number of internodes/tiller, leaf length (cm), leaf breadth (cm), L/S ratio, stem girth (cm), green forage yield (kg/plant), dry matter percentage and crude protein percentage. The analysis of data revealed the significant difference among the genotypes for all the characters. Phenotypic coefficient of variation estimates was slightly higher than genotypic coefficient of variation. High estimates of heritability (b.s.) was observed for all the characters studied except leaf/stem ratio. The traits green forage yield, plant height, number of internodes per plant, stem girth, leaf length, leaf width and number of leaves per plant showed high heritability estimates accompanied with high genetic advance percent of mean and high estimates of heritability coupled with moderate genetic advance percent of mean were observed for the characters *viz.*, days to 50% tasseling, days to 50% silking, L/S ratio, dry matter percentages and crude protein percentages. The characters *viz.*, days to 50% tasseling, days to 50% silking, plant height, stem girth, leaf length, leaf width, number of leaves per plant, number of internodes per plant, dry matter per cent and crude protein per cent showed significant positive correlation with green forage yield both at phenotypic and genotypic levels. The trait L/S ratio recorded significant negative correlation with green forage yield at only phenotypic level. L/S ratio recorded non-significant negative correlation with green forage yield only at genotypic level. Plant height, leaf length, leaf width and dry matter per cent recorded high magnitudes of direct effects accompanied by highly significant correlation with green forage yield at genotypic level, indicating true and perfect relationship between them. Thus suggesting that selection for these traits *viz.*, plant height, leaf length and dry matter per cent will be highly rewarding for improving the green forage yield.

**Keywords:** genotypes, variability, correlation, forage yield

**Introduction**

Maize (*Zea mays* L.) is an important cereal crop belongs to the tribe Maydeae, of the grass family, Poaceae. The plant is native to South America. *Zea mays* is the only species in the genus *Zea* with chromosome number  $2n=20$ . Maize is gaining importance in India as a feed crop. Its demand is increasing very fast particularly with the expansion of dairy, poultry and maize-based industries (Ahmed *et al.*, 2010) [3]. It is increasingly used as an animal feed and fodder crop for both green forage and silage. It has high production potentiality, wide adaptability and multiple uses (Gour *et al.*, 2006) [10]. It can be grown as a dual crop for grain as well as for fodder in India (Mahdi *et al.*, 2010) [17].

Forage maize is quick growing, succulent, sweet palatable, high yielding, nutritious and free from toxicants and can be safely fed to animals at any stage of crop growth (Devi, 2002) [8]. It is utilized in the form of grains, green fodder, silage, stover and pasturage. Green fodder provides adequate energy and proteins for growth of animals and milk production (Takawale *et al.*, 2009) [28]. Corn is an important feed for animal and poultry with high net energy content and low fibre content.

Germplasm, which is a prerequisite for any breeding programme, serves as a valuable source material as it provides scope for building of genetic variability. Study of variability, heritability and genetic advance in the germplasm will help to ascertain the real potential value of the genotype. Further, efficiency of selection in any breeding programme mainly depends upon the knowledge of association of the characters. Phenotypic correlation indicates the extent of the observation having relation between two characters while genotypic correlation provides an estimate of inherent association between the genes controlling any two characters. For formulating selection indices for genetic improvement of yield, the cause effect of the trait is very essential and can be done by path analysis.

**Corresponding Author:****SD Rathod**

PG Student, Mahatma Phule  
Krishi Vidyapeeth, Rahuri,  
Maharashtra, India

## Material and Methods

The field experiment was carried out at the research farm of AICRP on Forage Crops and Utilization, M.P.K.V., Rahuri, during *rabi* 2018-19. Present study was conducted among fifty four genotypes of forage maize including check variety African tall. For variability study, experiment was designed in randomized block design with two replications. In *rabi* 2018-19, each genotype was sown in two rows of 3 m length with 30 cm plant-to-plant distance and 60 cm inter row spacing.

Observations were recorded for 10 morphological characters, dry matter and crude protein content. Five randomly selected plants from each genotype were used to take observation except for days to 50 percent tasseling, 50 percent silking, dry matter and crude protein content, where observations were taken on the plot basis. Readings from five plants were averaged replication wise and the mean value was used for statistical analysis. Statistical analysis was performed by methods proposed by Panse and Sukhatme (1985) [20]. Variability parameters were estimated as suggested by Burton (1952), Johnson *et al.* (1955) and Allard (1960) [5, 12, 4]. Correlation coefficients were estimated as method suggested by Singh and Choudhari (1977) [27], while path coefficients

analysis was performed by methods of Dewey and Lu (1959) [7].

## Results and Discussion

### Estimates of Variability

The analysis of variance revealed significant treatment sum of squares for all the characters under study indicating an existence of a considerable variability for these characters in the genotypes. Estimation of phenotypic variance ( $\sigma^2_p$ ) and genotypic variance ( $\sigma^2_g$ ) were obtained for different traits. A wide range of variance was observed for all the traits. The highest variances ( $V_p$  and  $V_g$ ) were recorded for plant height (845.08 and 778.85) followed by leaf length (135.64 and 108.15), days to 50% tasseling (43.24 and 41.53) and days to 50 % silking (42.94 and 41.07) presented in **table 1**. Remaining characters showed low phenotypic and genotypic variance. Phenotypic variance was higher than genotypic variance for all the yield and yield contributing traits, indicating the influence of environmental factors on these traits. Less difference in the estimates of genotypic and phenotypic variance suggested that the variability present among the genotypes was mainly due to genetic reason with minimum influence of environment and hence heritable.

**Table 1:** Estimates of variability parameters for green forage yield and its contributing characters in fifty four forage maize genotypes

Sr. No.	Character	Mean	Range	Genotypic variance	Phenotypic variance	GCV	PCV	Heritability% (b.s) h <sup>2</sup>	Genetic Advance	Genetic Advance % of Mean
1	Days to 50 % tasseling	89.24	75.50-100.5	41.53	43.24	7.22	7.37	96.00	13.01	14.58
2	Days to 50 % silking	91.58	77.50-103.00	41.07	42.94	7.00	7.16	95.60	12.91	14.10
3	Plant height (cm)	123.80	76.50-221.50	778.85	845.08	22.54	23.48	92.20	55.19	44.58
4	No. of leaves/plant	11.97	8.30-15.60	2.38	2.69	12.89	13.71	88.40	2.99	24.95
5	No. of internodes/plant	10.40	7.05-14.40	2.67	3.12	15.71	16.97	85.80	3.12	29.98
6	Leaf length (cm)	73.04	53.95-101.70	108.15	135.64	14.24	15.95	79.70	19.13	26.19
7	Leaf width (cm)	8.42	6.79-11.19	1.03	1.25	12.05	13.27	82.40	1.90	22.53
8	Leaf:stem ratio	0.35	0.23-0.47	0.002	0.004	12.01	18.39	42.60	0.06	16.15
9	Stem girth (cm)	8.81	6.52-11.46	1.70	2.00	14.82	16.07	85.00	2.48	28.14
10	Dry matter content (%)	21.42	17.95-25.04	2.51	3.40	7.40	8.60	73.90	2.81	13.10
11	Crude Protein content (%)	8.30	6.24-9.74	0.43	0.64	7.94	9.62	68.10	1.12	13.50
12	Green forage yield/plant (kg)	0.482	0.234-1.171	0.05	0.06	47.08	48.69	93.50	0.45	93.78

The high GCV and PCV were estimated for green forage yield (47.08 and 48.69) followed by plant height (22.54 and 23.48). Moderate GCV and PCV were estimated in number of internodes per plant (15.71 and 16.97), stem girth (14.82 and 16.07), leaf length (14.24 and 15.95), leaf width (12.05 and 13.27) and leaf to stem ratio (12.01 and 18.39). However, crude protein content (7.94 and 9.62), dry matter content (7.40 and 8.60), days to 50% tasseling (7.22 and 7.37) and days to 50% silking (7.00 and 7.16) showed low GCV and PCV. The estimation of genotypic and phenotypic coefficient of variation indicates the amount of genetic and non-genetic variation present for different desirable characters. Higher magnitude of GCV and PCV for these traits indicated presence of high degree of variability and better scope for selection. Present findings were in accordance with reports of Kumar (1978), Rahman and Roquib (1987), Jha *et al.* (1997), Kapoor and Batra (2015), Kapoor (2017) and Ahalawat *et al.* (2018) [16, 23, 11, 14, 13, 2] who also reported high value of GCV and PCV for green forage yield, while Abirami (2005), Nagaraju (2012) [1, 19, 23], Kapoor and Batra (2015), Kapoor (2017) [14, 13] and Ahalawat *et al.* (2018) [2] reported high value of GCV and PCV for plant height.

The heritability (b.s.) estimates ranged between 42.60 per cent and 96.00 per cent. All character showed high heritability except L/S ratio. The character days to 50 per cent tasseling

recorded the highest estimate (96.00%) of heritability followed by day to 50 per cent silking (95.60%), green forage yield (93.50%), plant height (92.20%), number of leaves per plant (88.40%), number of internodes per plant (85.80%), stem girth (85.00%), leaf width (82.40%), leaf length (79.70%), dry matter content (73.90%) and crude protein content (68.10%). L/S ratio recorded the moderate estimate (42.60%) of heritability.

High heritability for days to 50% tasseling and silking and plant height was estimated in present study which was in accordance with Debnath (1987), Saikia and Sharma (2000), More (2003) and Nagaraju (2012) [6, 15, 18, 19], while for trait crude protein content, high heritability was reported by Krishnam (2001) and Kapoor and Batra (2015) [14].

According to Panse (1957) [21], such traits showing high heritability, governed predominantly by additive gene action and could be improved through individual plant selection and selection of these traits could be more effective for desired genetic improvement.

A perusal of genetic advances as percent of mean for all 12 quantitative traits under study was ranged from 13.10% (dry matter content) to 93.78% (green forage yield per plant). High value of genetic advance as percent of mean (GAM) was obtained in green forage yield per plant (93.78%) followed by plant height (44.58%), number of internodes per plant

(29.98%), stem girth (28.14%), leaf length (26.19%), number of leaves per plant (24.95%) and leaf width (22.53%), whereas, moderate GAM was observed for days to 50% tasseling (14.58%), days to 50% silking (14.10%), crude protein content (13.50%) and dry matter content (13.10%). The traits green forage yield, plant height, number of internodes per plant, stem girth, leaf length, leaf width and number of leaves per plant showed high heritability estimates accompanied with high genetic advance percent of mean which is due to additive gene action and direct selection for such traits is rewarding in crop improvement. Similar results were in accordance with Singh and Das (2000), Kappor and Batra (2015), Saief *et al.* (2015), Ahalawat *et al.* (2018) [2]. High estimates of heritability coupled with moderate genetic advance percent of mean were observed for the characters days to 50% tasseling, days to 50% silking, dry matter percentages and crude protein percentages. High heritability and moderate genetic advance as percent mean for crude protein content also reported by Satyanarayana *et al.* (2003) [26].

### Correlation coefficient

In the present investigation, correlation coefficient analysis measure the mutual relationship between various plant trait and to determine the component trait on which selection can be used for genetic improvement in yield while selecting the suitable plant type. It was revealed from the present study that, the genotypic correlation coefficients between most of the characters were higher in magnitude than the phenotypic correlation coefficients indicating strong inherent association between various characters studied and that the genotypic expression of the correlation was comparatively less

influenced by the environmental conditions. It was revealed that the green forage yield had significant and positive correlation both at genotypic and phenotypic level with plant height presented in table 2. The characters *viz.*, plant height (0.949, 0.917), leaf length (0.858, 0.792), dry matter per cent (0.820, 0.749), leaf width (0.792, 0.752), number of leaves per plant (0.770, 0.738), number of internodes per plant (0.739, 0.710), stem girth (0.715, 0.680), day to 50% silking (0.610, 0.586), day to 50% tasseling (0.598, 0.579), protein content (0.412, 0.394) showed significant positive association with green forage yield both at genotypic and phenotypic levels, respectively. It indicates dependence of these characters on each other. Desai and Patel (1997) [7] also reported that days to 50% tasseling, days to 50% silking, plant height, stem girth, leaf length, leaf width, number of leaves per plant and number of internodes per plant and dry matter yield showed significant positive association with green forage yield both at genotypic and phenotypic levels, respectively.

However, L/S ratio (-0.504) recorded non significantly negative correlation with green forage yield only at genotypic level. L/S ratio (-0.234) recorded significantly negative correlation with green forage yield at only phenotypic level. Patel and Shelke (1984) [22] also reported significantly negative correlation of leaf to stem ratio with green forage yield.

In present study the result on genotypic correlation were higher than the corresponding phenotypic correlation coefficient for most of the characters, indicated characters are useful in yield improvement. Teron *et al.* (2020) also observed high genotypic correlation coefficient than phenotypic correlation coefficient.

**Table 2:** Estimates of genotypic (above diagonal) and phenotype correlation coefficients (below diagonal) among green forage yield and yield contributing characters in fifty four maize genotypes

Character	Days to 50 % tasseling	Days to 50 % silking	Plant height (cm)	No. of leaves/plant	No. of internodes/plant	Leaf length (cm)	Leaf width (cm)	Leaf:: stem ratio	Stem girth (cm)	Dry matter content (%)	Crude protein content (%)	Green forage yield/plant (kg)
Days to 50 % tasseling	1.000	0.928**	0.583**	0.742**	0.687**	0.638**	0.588**	-0.137	0.463**	0.618**	0.006	0.598**
Days to 50 % silking	0.917**	1.000	0.594**	0.760**	0.691**	0.660**	0.601**	-0.141	0.480**	0.630**	0.027	0.610**
Plant height (cm)	0.562**	0.574**	1.000	0.821**	0.781**	0.833**	0.771**	-0.574**	0.621**	0.810**	0.391**	0.949**
No. of leaves/plant	0.702**	0.717**	0.786**	1.000	0.854**	0.863**	0.699**	-0.348**	0.629**	0.761**	0.163	0.770**
No. of internodes/plant	0.638**	0.641**	0.744**	0.801**	1.000	0.678**	0.665**	-0.451**	0.586**	0.697**	0.237*	0.739**
Leaf length (cm)	0.573**	0.593**	0.781**	0.804**	0.654**	1.000	0.638**	-0.293**	0.664**	0.771**	0.295**	0.858**
Leaf width (cm)	0.543**	0.555**	0.733**	0.674**	0.661**	0.613**	1.000	-0.691**	0.674**	0.755**	0.451**	0.792**
Leaf::stem ratio	-0.026	-0.030	-0.266*	-0.101	-0.108	0.023	-0.220*	1.000	-0.327**	-0.529**	-0.470	-0.504
Stem girth (cm)	0.438**	0.455**	0.607**	0.612**	0.584**	0.626**	0.627**	-0.007	1.000	0.647**	0.545**	0.715**
Dry matter content (%)	0.550**	0.554**	0.729**	0.713**	0.643**	0.689**	0.691**	-0.092	0.631**	1.000	0.346**	0.820**
Crude protein content (%)	0.010	0.029	0.367**	0.206*	0.272**	0.325**	0.432**	-0.057	0.533**	0.333**	1.000	0.412**
Green forage yield/plant (kg)	0.579**	0.586**	0.917*	0.738**	0.710**	0.792**	0.752**	-0.234*	0.680**	0.749**	0.393**	1.000

\*and \*\* significant at P= 5 and P = 1 level of significance, respectively

### Path Coefficient

In present study the trait plant height (0.749) recorded the maximum positive direct effect on green forage yield followed by leaf length (0.361), leaf width (0.233), number of internodes per plant (0.163), stem girth (0.146) and L/S ratio (0.113). However, day to 50% tasseling (0.034) and dry matter per cent (0.047) showed negligible positive direct effects on green forage yield presented in table 3. Path analysis and correlation studies revealed that plant height, leaf length and leaf width exhibited high direct effects on green forage yield and also recorded the significant correlation with green forage yield indicating true and perfect relationship

between them. The yield component leaf width and number of internodes per plant also exhibited the direct effects on green forage yield and recorded the significant correlation with green forage yield at both genotypic and phenotypic level. This also suggests that direct selection for these traits will help in improvement of yield in forage maize.

The character number of leaves per plant (-0.527) had high negative direct effect on green forage yield and negligible negative direct effect by crude protein percentage (-0.087) and day to 50% silking (-0.042).

Keeping in view all the above aspects, the genotypes *viz.*, 52095, 52217, 52336, 52483, 52507, 52623 and African Tall

in the present studies, deserve to be considered as potent parents for future crossing programme for improvement of

green forage yield and yield contributing characters.

**Table 3:** Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of component characters on green forage yield in fifty four maize genotypes

Character	Days to 50% tasseling	Days to 50% silking	Plant height (cm)	No. of leaves/plant	No. of internodes/plant	Leaf length (cm)	Leaf width (cm)	Leaf::stem ratio	Stem girth (cm)	Dry matter content (%)	Crude protein content (%)	Green forage yield/plant (kg)
Days to 50 % tasseling	0.034	-0.042	0.437	-0.391	0.112	0.230	0.137	-0.016	0.068	0.029	-0.001	0.598**
Days to 50 % silking	0.034	-0.042	0.445	-0.400	0.113	0.238	0.140	-0.010	0.070	0.030	-0.002	0.610**
Plant height (cm)	0.020	-0.025	0.749	-0.433	0.128	0.301	0.179	-0.065	0.091	0.039	-0.034	0.949**
No. of leaves/plant	0.026	-0.032	0.615	-0.527	0.139	0.311	0.163	-0.039	0.092	0.361	-0.014	0.770**
No. of internodes/plant	0.024	-0.029	0.585	-0.450	0.163	0.245	0.155	-0.051	0.086	0.033	-0.026	0.739**
Leaf length (cm)	0.022	-0.028	0.624	-0.455	0.111	0.361	0.148	-0.033	0.097	0.037	-0.039	0.858**
Leaf width (cm)	0.020	-0.025	0.577	-0.368	0.109	0.230	0.233	-0.079	0.099	0.036	-0.039	0.792**
Leaf::stem ratio	-0.005	0.006	-0.430	0.183	-0.074	-0.106	-0.161	0.113	-0.048	-0.025	0.041	-0.504
Stem girth (cm)	0.016	-0.020	0.466	-0.331	0.096	0.240	0.016	-0.037	0.146	0.031	-0.047	0.715**
Dry matter content (%)	0.021	-0.027	0.661	-0.401	0.114	0.278	0.176	-0.060	0.095	0.047	-0.030	0.820**
Crude protein content (%)	0.000	-0.001	0.293	-0.086	0.039	0.107	0.105	-0.053	0.080	0.016	-0.087	0.412**

Residual effect (R) = 0.186

### Conclusion

The traits green forage yield, plant height, number of internodes per plant, stem girth, leaf length, leaf width and number of leaves per plant showed high heritability estimates accompanied with high genetic advance percent of mean which is due to additive gene action and direct selection for such traits is rewarding in crop improvement. The yield components viz., plant height followed by leaf length, leaf width and number of internodes per tiller had high positive indirect effect through days to 50 per cent tasseling, days to 50 per cent silking, leaf length, leaf width, number of internodes per plant number of leaves per plant, stem girth, dry matter per cent and protein content.

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