

STUDIES ON GENETIC VARIABILITY IN FORAGE MAIZE (*ZEA MAYS L.*)

M. CHAKROVORTY*¹ AND S. BORA NEOG

Department of Plant Breeding & Genetics

Assam Agricultural University,

Jorhat-785 013 (Assam), India

*(e-mail : manoshiaub@gmail.com)

(Received : 20 June 2015; Accepted : 26 September 2015)

SUMMARY

The present study revealed significant variation for all the traits except leaf area ratio and leaf : stem ratio. A higher estimate of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was obtained for per day productivity of dry matter yield. High heritability coupled with high genetic advance was exhibited by per day productivity of green forage yield and per day productivity of dry matter yield. This indicated that these characters were under the control of additive gene action. The mean performance of all the genotypes revealed that JCM-09-1 produced the highest green forage yield along with the highest per day productivity of green forage yield.

Key words : Genetic variability, per day productivity, green forage yield, forage maize

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). 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). It can be grown as a dual crop for grain as well as for fodder in India (Mahdi *et al.*, 2010). 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; Patel *et al.*, 2007). 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). Corn is an important feed for animal and poultry with high net energy content and low fibre content.

In India, the high forage yielding maize varieties viz., African Tall and J-1006 have been cultivated over the years as fodder maize. Considering the higher demand of feed in recent years and the better quality of maize as fodder, evolution of fodder maize varieties better than the existing ones has been considered to be of utmost importance. Evaluation of more and more maize germplasms from different regions is very much important for selecting better ones for fodder purpose.

Introgression of new genes for fodder quality from the selected maize germplasms to an adapted variety will pave the way for developing fodder maize varieties with high yield and forage quality. Better germplasm identified from performance trial may also be used directly as variety after years of evaluation in station breeding programme, multi-locational trial and on-farm testing. Germplasms are the basic raw material in any crop improvement programme. Characterization and evaluation are important pre-requisites for its effective utilization and also to identify sources of useful genes. Progress in any crop improvement programme depends mainly on the variability existing in the base population. Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. Heritability gives the information on the kind and magnitude of genetic variation in quantitative traits. Both heritability and genetic advance will be helpful in discerning the type of gene action and in formulating suitable breeding procedure. The study of variability, heritability and genetic advance in the germplasms will help to ascertain the real genetic potential value of the germplasm.

The present investigation was carried out at Instructional-cum-Research (ICR) Farm of Assam Agricultural University, Jorhat during **kharif** 2011.

¹T41, Third Floor, Khirki Extension, Malviya Nagar, Delhi-110 017, India.

Geographically, the farm is situated at 26°46' N latitude and 94°13' E longitude with altitude of 86.6 m. The climate of the area is sub-tropical humid. The experimental materials in the present study comprised two check varieties viz., African Tall and J-1006 along with 56 maize germplasms collected from different regions of north-east India. The maize germplasms used in the present study with their place of collection are presented in Table 1.

The experiment was laid out in an augmented design (Federer, 1957) with seven blocks and the two check varieties were repeated in each block. Each block had 10 plots with each plot having a size of 3 x 3 m. The row to row spacing was maintained at 50 cm and plant to plant was maintained at 20 cm. The fertilizer dose at a rate of N 80 : P₂O₅ 40 : K₂O 40 kg/ ha was given. Full dose of phosphatic and potassic fertilizers along with half dose of nitrogenous fertilizer were applied at the time of final land preparation as basal dose and the

remaining half of nitrogenous fertilizer was top dressed after 45 days of sowing. Ten randomly selected plants from the middle of the rows of a plot for each genotype were tagged for recording observations on days to 50 per cent flowering, plant height (cm), stem girth (cm), leaves per plant, leaf width (cm), leaf area (cm), leaf area ratio, leaf : stem ratio, green forage yield (g), per day productivity of green forage (g), dry matter yield (g), per day productivity of dry matter (g), total carbohydrate content (g), crude protein content (%) and crude fibre content (%).

The plot means were calculated for all the characters and the analysis of variance (ANOVA) for augmented design was carried out following Federer (1957). Genotypic and phenotypic coefficients of variations were estimated by the formula given by Burton (1952). Heritability in broad sense was calculated according to Hanson *et al.* (1956) and genetic advance was estimated by the formula of Johnson *et al.* (1955).

TABLE 1
List of genotypes with their place of collection

S. No.	Genotypes	Place of collection	S. No.	Genotypes	Place of collection
1.	African Tall*	BAIF, Pune	30.	JCM-09-28	Arunachal Pradesh
2.	J-1006*	IGFRI, Jhansi	31.	JCM-09-29	Arunachal Pradesh
3.	JCM-09-1	Arunachal Pradesh	32.	JCM-09-30	Arunachal Pradesh
4.	JCM-09-2	Arunachal Pradesh	33.	JCM-09-31	Arunachal Pradesh
5.	JCM-09-3	Arunachal Pradesh	34.	JCM-09-32	Arunachal Pradesh
6.	JCM-09-4	Arunachal Pradesh	35.	JCM-09-33	Arunachal Pradesh
7.	JCM-09-5	Arunachal Pradesh	36.	JCM-09-34	Mizoram
8.	JCM-09-6	Arunachal Pradesh	37.	JCM-09-35	Arunachal Pradesh
9.	JCM-09-7	Arunachal Pradesh	38.	JCM-09-36	Arunachal Pradesh
10.	JCM-09-8	Arunachal Pradesh	39.	JCM-09-37	Arunachal Pradesh
11.	JCM-09-9	Arunachal Pradesh	40.	JCM-09-38	Manipur
12.	JCM-09-10	Arunachal Pradesh	41.	JCM-09-39	Arunachal Pradesh
13.	JCM-09-11	Arunachal Pradesh	42.	JCM-09-40	Arunachal Pradesh
14.	JCM-09-12	Arunachal Pradesh	43.	JCM-09-41	Arunachal Pradesh
15.	JCM-09-13	Arunachal Pradesh	44.	JCM-09-42	Arunachal Pradesh
16.	JCM-09-14	Arunachal Pradesh	45.	JCM-09-43	Manipur
17.	JCM-09-15	Arunachal Pradesh	46.	JCM-09-44	Mizoram
18.	JCM-09-16	Arunachal Pradesh	47.	JCM-09-45	Nagaland
19.	JCM-09-17	Arunachal Pradesh	48.	JCM-09-46	Mizoram
20.	JCM-09-18	Arunachal Pradesh	49.	JCM-09-47	Assam
21.	JCM-09-19	Arunachal Pradesh	50.	JCM-09-48	Assam
22.	JCM-09-20	Arunachal Pradesh	51.	JCM-09-49	Assam
23.	JCM-09-21	Arunachal Pradesh	52.	JCM-09-50	Assam
24.	JCM-09-22	Arunachal Pradesh	53.	JCM-09-51	Assam
25.	JCM-09-23	Arunachal Pradesh	54.	JCM-09-52	Nagaland
26.	JCM-09-24	Arunachal Pradesh	55.	JCM-09-53	Nagaland
27.	JCM-09-25	Arunachal Pradesh	56.	JCM-09-54	Arunachal Pradesh
28.	JCM-09-26	Arunachal Pradesh	57.	JCM-09-55	Nagaland
29.	JCM-09-27	Arunachal Pradesh	58.	JCM-09-56	Nagaland

*Indicates check variety.

TABLE 2
Estimates of genetic parameters for different characters in forage maize

Character	Mean±SE	PCV (%)	GCV (%)	$h^2_{b.s.}$ (%)	GA (% of mean)
D50F (day)	67.45±1.29	13.21	13.10	98.31	26.76
PH (cm)	198.10±5.47	19.62	19.56	99.43	40.18
SG (cm)	2.17±0.05	17.18	16.13	88.16	31.21
L/P	10.26±0.32	20.32	16.53	66.17	27.70
LW (cm)	8.35±0.21	12.79	7.80	37.22	9.80
LA (cm ²)	428.87±13.85	17.38	16.51	90.28	32.32
CP (%)	9.88±0.34	20.93	20.36	94.62	40.79
CF (%)	28.29±0.93	24.14	23.95	98.41	48.94
TC (%)	11.18±0.39	23.45	22.22	89.75	43.35
DMY (kg/ha)	23.73±2.52	34.93	32.37	85.89	61.80
DMP _y (kg/ha/day)	0.80±0.04	38.65	36.73	90.31	71.90
GFP _y (kg/ha/day)	2.99±0.14	33.88	31.66	93.44	65.21
GFY (kg/ha)	197.25±7.38	25.45	24.40	95.87	49.99

D50F : Days to 50 per cent flowering, PH : Plant height, SG : Stem girth, L/P : Leaves per plant, LW : Leaf width, LA : Leaf area, CP : Crude protein, CF : Crude fibre, TC : Total carbohydrate, DMY : Dry matter yield, DMP_y : Per day productivity of dry matter yield, GFP_y : Per day productivity of green forage yield and GFY : Green forage yield.

The genetic variability is a pre-requisite for any effective selection scheme. In the present study, there were highly significant differences among the genotypes for all the characters except leaf area ratio and leaf : stem ratio, which did not show significant variation. Leaf area ratio and leaf : stem ratio were not considered in further analyses. The estimates of genotypic and phenotypic coefficients of variation, heritability in broad sense and expected genetic advance (as % of mean) for all characters are presented in Table 2.

In the present study, the magnitude of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) indicating low to medium influence of environment on the characters except L/P and LW for which environmental effect appeared profound. Murugan *et al.* (2010), Srivas and Singh (2010) and Tomar and Prodhana (2012) also obtained higher PCV as compared to GCV indicating the influence of environment on the characters they studied. Among the genotypes under study, dry matter yield, per day productivity of dry matter and per day productivity of green forage showed high genotypic and phenotypic coefficients of variation. Ali *et al.* (2006) obtained high GCV and PCV for dry matter yield in forage maize. Moderate genotypic coefficient of variation and phenotypic coefficient of variation were observed for green fodder yield, crude fibre content, total carbohydrate and crude protein content. Murugan *et al.* (2010) obtained moderate GCV and PCV for forage yield and crude protein content in forage maize. Nagabhushan *et al.* (2011) also obtained moderate GCV

and PCV for green forage yield in maize. Low GCV and PCV were obtained for plant height, leaf area, stem girth, days to 50 per cent flowering and leaf width.

In the present study, heritability estimates were recorded high for most of the characters viz., plant height, crude fibre content, days to 50 per cent flowering, green forage yield, crude protein content, per day productivity of green forage, per day productivity of dry matter and leaf area. High heritability of plant height, green forage yield, dry matter yield and stem girth was obtained by Ali *et al.* (2006) in forage maize. Idris *et al.* (2011) obtained high heritability for days to 50 per cent flowering in forage maize. Nagabhushan *et al.* (2011) obtained high heritability for green fodder yield and grain yield/plant in dual purpose forage maize. Moderately high heritability for total carbohydrate content, stem girth and dry matter yield indicated that these characters were also influenced by the environment and thus, more precise evaluation will be needed for improvement of these characters. Low estimates of heritability were found for leaves/plant and leaf width and this indicated the preponderance of environmental influence on these characters. Genetic advance as percentage of mean was high for the characters viz., per day productivity of dry matter, per day productivity of green forage and dry matter yield. Ali *et al.* (2006) and Srivas and Singh (2010) also obtained high genetic advance for dry matter yield in forage maize.

In this study, high heritability (>90%) and high genetic advance (>60%) were obtained for per day productivity of dry matter and per day productivity of

green forage. Genotypic coefficients of variation (GCV) for these characters were also high. Thus, selection for these characters might accumulate more additive genes leading to further improvement of their performance and these characters may be used as selection criteria in forage maize breeding programme. High heritability with moderate genetic advance (>40% but <60%) was obtained for plant height, crude protein content, crude fibre content and green forage yield. This indicated that most likely the heritability of these characters was due to additive gene effects and selection might be effective. Moderate heritability (>80% but <90%) coupled with high genetic advance was obtained for dry matter yield. The GCV of this character was also found high. It revealed that this character was governed by additive gene effects and the selection might be effective in such case. Therefore, based on the study of genetic parameters in this population of genotypes, it could be inferred that direct selection for per day productivity of dry matter, per day productivity of green forage and dry matter yield would be effective to bring about improvement of the crop. The other characters that could be effective selection criteria were green forage yield, crude fibre content, crude protein content and plant height. Ali *et al.* (2006) obtained high heritability with high genetic advance for plant height, dry matter yield and green forage yield. Murugan *et al.* (2010) obtained it for plant height and grain protein content. Srivas and Singh (2010) obtained high heritability and high genetic advance for dry matter yield and plant height.

ACKNOWLEDGEMENTS

The authors are grateful to Director of Post Graduate Studies (DPGS), Assam Agricultural University and the Head of Department (HOD), Dept. of Plant Breeding & Genetics, Assam Agricultural University, for guidance, encouragement and providing necessary facilities during the course of study.

REFERENCES

- Ahmed, S., A. B. Malaviya, and A. B. Majumdar. 2010 : Genetic divergence and variability in fodder maize. *Forage Res.*, **35** : 223-226.
- Ali, S., H. Rahman, Raziuddin, S. S. Shah, and G. Hassan, 2006 : Estimates of variability, heritability and genetic advance for fodder traits in two maize populations. *Pak. J. Biol. Sci.*, **9** : 2618-2623.
- Burton, G. W. 1952 : Quantitative inheritance in grasses. *Proc. 6th Grassld. Cong.*, **1** : 277-281.
- Devi, L. G. 2002 : Forage yield of maize (*Zea mays* L.) as influenced by nitrogen levels and biofertilizers. *Forage Res.*, **27** : 263-266.
- Federer, W. T. 1957 : *Experimental Design (Theory and Practices)*, Indian edn. Oxford and IBH Publishing Co.
- Gour, V., P. C. Patel, M. R. Patel, and N. N. Patel. 2006 : Effect of sowing date and harvesting stage on forage yield and quality of maize. *Forage Res.*, **31** : 267-268.
- Hanson, C. H., H. F. Robinson, and R. E. Comstock. 1956 : Biometrical studies of yield in segregating population of Korean lespedeza. *Agron. J.*, **56** : 248.
- Idris, A. E. and A. I. Abuali. 2011 : Genetic variability for vegetative and yield traits in maize (*Zea mays* L.) genotypes. *Int. Res. J. Agric. Sci. and Soil Sci.* **1** : 408-411.
- Johnson, H. W., H. F. Robinson, and R. E. Comstock, 1955 : Estimates of genetic and environmental variabilities in soybean. *Agron. J.*, **47** : 314-318.
- Mahdi, S. S., B. Hasan, R. A. Bhat, and M. A. Aziz. 2010 : Yield and economics of fodder maize as influenced by nitrogen and seed rate and zinc under temperate condition. *Forage Res.*, **36** : 22-25.
- Murugan, S., J. Padmanaban, and S. Manirajan. 2010 : Genetic variability and heritability studies in F₂ and F₃ generations of QPM and non-QPM maize crosses. *Int. J. Plant Sci.*, **5** : 290-293.
- Nagabhushan, N. M. Mallikarjuna, C. Haradari, M. S. Shashibhaskar, and G. D. Prahalada. 2011 : Genetic variability and correlation studies for yield and related characters in single cross hybrids of maize (*Zea mays* L.). *Curr. Biotica*, **5** : 157-163.
- Patel, A. S., A. C. Sadhu, M. R. Patel, and P. C. Patel. 2007 : Effect of zinc, FYM and fertility levels on yield and quality of forage maize (*Zea mays* L.). *Forage Res.*, **32** : 209-212.
- Srivas, S. K., and U. P. Singh. 2010 : Genetic variability, correlation coefficient and path analysis of seed and its component traits in forage maize (*Zea mays* L.). *Indian J. Plant Genetic Resources*, **23** : 217-220.
- Takawale, P. S., J. S. Desale, and V. K. Kauthale. 2009 : Assessment of unpiloted maize (*Zea mays* L.) germplasm and its utilization in heterosis for forage traits. *Indian J. Genet.*, **69** : 159-161.
- Tomar, U. S., and H. S. Proadhan. 2012 : Estimation of genetic variability parameters and analysis of genetic architect of green ear yield and its different components in green maize (*Zea mays* L.). *Plant Archives*, **12** : 205-208.