International Journal of Chemical Studies

SD Rathod
PG Student, AICRP on Forage Crop and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

GC Shinde
Assistant Professor, Department of Agricultural Botany, AICRP on Forage Crop and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

SD Shinde
SRA, Department of Agricultural Statistics, MPKV, Rahuri, Maharashtra, India

Genetic diversity studies in forage maize genotypes

SD Rathod, GC Shinde and SD Shinde

Abstract
Fifty four genotypes of forage maize were evaluated at research farm of AICRP on Forage Crops and utilazation, M.P.K.V., Rahuri in a RBD design with two replications during the *rabi,* 2018-19. 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. Based on genetic distance (D^2 value) fifty four genotypes were grouped into seven clusters indicating wider genetic diversity in the germplasm collections of maize from different geographical origin. Out of seven clusters formed, Cluster I was the largest with 38 genotypes, followed by cluster VI with 7 genotypes, followed by cluster IV with 5 genotypes. Cluster II, III, V, and VII were monogenotypic. The clustering pattern indicated the absence of relationship between genetic diversity and geographical origin of genotypes. The maximum intra cluster distance was observed for cluster IV (D=7.71) followed by cluster I (D=7.19), followed by cluster VI (D=6.12). Whereas, the maximum inter cluster distance was observed between cluster IV and cluster VI (D=18.92) followed by cluster IV and cluster V (D=16.68), while lowest divergence was noticed between cluster II and VI (D=7.77). On basis of inter cluster distances, cluster mean and per se performance and divergence class observed in the present study, the genotypes *viz.,* 52095, 52217, 52336, 52483, 52507, 52623 and African tall were distinct and diverse and could be classified as promising genotypes. These genotypes may be used in crossing programme to achieve desired segregants in forage maize.

Keywords: D^2, clusters, diversity, protein, forage yield

Introduction
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) [6]. 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) [21]. 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. Mahalanobis D^2 analysis is very useful tool in studying the nature and cause of diversity prevalent in the available germplasm knowledge of genetic variability is very valuable in a planned breeding programme, since it helps in the choice of the best yield attributes either for selection or for hybridization.

Material and Methods
The field experiment was carried out at the AICRP on Forage Crops and Utilization, MPKV, Rahuri, during *rabi* 2018-19 to study the variability among fifty four genotypes of forage maize including check variety African tall. 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.

Corresponding Author:
SD Rathod
PG Student, AICRP on Forage Crop and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

Readings from five plants were averaged replication wise and the mean value was used for statistical analysis. Diversity analysis was done using Mahalanobis D^2 statistics (1936) [12]. Fifty four genotypes were grouped into 7 clusters as per Tocher's method as described by Rao (1952) [17]. The intra and inter cluster D values were worked out using Mahalanobis D^2 statistics.

Results and Discussion

The genetic divergence can be estimated by using an effective statistical tool, Mahalanobis D^2 statistics, which gives clear idea about the diverse nature of the population. The analysis of variance carried out for all twelve quantitative traits among 54 genotypes was presented in Table 1. The mean sum of squares due to genotypes showed highly significant differences for all twelve traits under study at 5% and 1% level of significance. Hence, presence of large amount of variability might be due to diverse source of materials taken for present study. This indicated that there is ample scope for selection of promising lines from the present gene pool for green forage yield and yield attributing traits. Significant differences among forage maize genotypes for forage yield and yield contributing traits were also reported by Roy (1953) [18], More (2003) [14], Nagaraju (2012) [15], Kapoor and Batra (2015) [10], Kapoor (2017) [9], Ahalawt et al. (2018) [1], Rahim (2019) [16] and Teron et al. (2020) [22].

Table 1: Analysis of variance for 12 characters of fifty four maize genotypes

Sr. No.	Character	Replication	Genotypes	Error
	DF	1	53	53
1	Days to 50% tasseling	0.330	84.770**	1.710
2	Days to 50% silking	0.230	84.010**	1.870
3	Plant height (cm)	4.880	1623.930**	66.220
4	No. of leaves/plant	0.009	5.070**	0.310
5	No. of internodes/plant	1.040	5.790**	0.440
6	Leaf length (cm)	5.530	243.790**	27.500
7	Leaf width (cm)	0.300	2.280**	0.220
8	Leaf::stem ratio	0.001	0.006**	0.002
9	Stem girth (cm)	0.110	3.700**	0.300
10	Dry matter content (%)	2.690	5.900**	0.880
11	Crude protein content (%)	0.110	1.070**	0.200
12	Green forage yield/plant (kg/plant)	0.020	0.110**	0.003

The knowledge of genetic diversity among the genotypes is essential for selecting parents for hybridization programme, especially in a cross pollinated crop like maize. Fifty four genotypes were grouped into 7 clusters (Table 2.) as per Tocher's method as described by Rao (1952) [17]. Cluster I was the largest with 38 genotypes, followed by cluster VI with 7 genotypes, followed by cluster IV with 5 genotypes. Cluster II, III, V, and VII were monogenotypic. These four genotypes maintained separate identity and they were not included with any other cluster and exhibited high genetic diversity with most of the other clusters.

Distribution of genotypes in different clusters was random but it has clearly shown relationship with the characters for which they were bred. It indicated that genetic diversity and geographic diversity are not related. The pattern of group constellation proved the existence of significant amount of variability. Earlier workers Sonawane et al. (1991) [20] and More (2003) [14] grouped 45 forage maize genotypes into 7 clusters, Gautam (2008) [7] grouped 135 genotypes into 15 clusters, Azad et al. (2012) [4] grouped 30 genotypes into 6 clusters, Shukla et al. (2014) [19] grouped 64 maize genotypes into 5 clusters and Ali et al. (2018) [3] 30 inbreds lines of maize into 4 clusters.

Table 2: Grouping of fifty four maize genotypes based on D^2 analysis

Cluster No.	Number of genotypes	Name of Genotypes
CL-I	38	52021,52045,52065,52068,52072,52081,52087,52093,52098,52113,52123,52141,52144,52169,52177,52180,52184,52191,52212,52219,52222,52224,5227,52250,52255,52285,52310,52339,52346,52347,52349,52357,52373, 52383,5243,52450,52485,52507,52623
CL-II	1	52217
CL-III	1	52095
CL-IV	5	52483, 52623, 52065, 52332, African tall
CL-V	1	52336
CL-VI	7	52014, 52230, 52237, 52063, 52018, 52117, 52200
CL-VII	1	52506

The intra and inter cluster D values were worked out using Mahalanobis D^2 statistics. The mean D values (Table 3.) cluster elements were used as measures of intra and inter cluster distance. The maximum intra cluster distance was observed for cluster IV (D=7.71) followed by cluster I (D=7.19), followed by cluster VI (D=6.12) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture. In the case of clusters II, III, V and VII the intra cluster distances are zero because of its monogenotypic nature.

The maximum inter cluster distance was observed between cluster IV and cluster VI (D=18.92) followed by cluster IV and cluster V (D=16.68), cluster III and cluster VI (D=16.33), cluster II and cluster VI (D=14.74), cluster IV and cluster VII (D=14.31) and cluster III and cluster V (D=14.23). These results suggest maximum divergence between genotypes of these indicating the fact that the genotypes resent in one cluster differ entirely from those present in other clusters. While lowest divergence was noticed between cluster II and IV (D=7.77).

Table 3: Average intra (bold) and inter cluster D values for seven clusters in fifty fourmaize genotypes

Cluster	CL-I	CL-II	CL-III	CL-IV	CL-V	CL-VI	CL-VII
CL-I	7.19	9.13	10.25	12.80	9.18	10.55	12.21
CL-II		0.00	9.81	7.77	13.06	14.74	12.89
CL-III			0.00	8.55	14.23	16.33	13.05
CL-IV				7.71	16.68	18.92	14.31
CL-V					0.00	8.37	8.77
CL-VI						6.12	12.23
Cl-VII							0.00

The present study revealed that days to 50% tasseling contributed maximum (33.33%) for divergence followed by L:S ratio (20.27%), stem girth (12.79%), leaf width (7.34%), plant height (6.08%) which contributed to 79.81% of total divergence. Minimum contribution towards the genetic divergence was to due green forage yield (5.87%) followed by leaf length (3.42%), No. of leaves (2.87%), protein content (2.45), No. of internodes (2.03%) and days to 50% silking (0.35%). This result was in accordance with Utkhede (1977) [23] and More (2003) [14] reported high contribution to the divergence by days to 50 and tasseling, high contribution due plant height was reported by Caraballoso *et al.* (2002) [5] and More (2003) [14]. High contribution to the divergence due to green forage yield was reported by Kumari and Shikha *et al.* (2018).

Table 4: Per cent contribution of 12 characters for divergence

Sr. No.	Source	Times ranked first	Contribution %
1	Days to 50% tasseling	477	33.33.
2	Days to 50% silking	5	0.35
3	Plant height (cm)	87	6.08
4	No. of leaves/plant	41	2.87
5	No. of internodes/plant	29	2.03
6	Leaf length (cm)	49	3.42
7	Leaf width (cm)	105	7.34
8	Leaf::stem ratio	290	20.27
9	Stem girth (cm)	183	12.79
10	Dry matter (%)	46	3.21
11	Protein content (%)	35	2.45
12	Green forage yield/plant (kg)	84	5.87

A comparison of the mean value of twelve characters of different clusters is presented in the Table 5. Considerable differences in cluster mean values were evident for all the characters. On the basis of inter cluster distances, cluster mean and divergence class observed in the present study, the genotypes *viz.,* 52095, 52217, 52336, 52483, 52507, 52623 and African Tall were distinct and diverse and could be classified as promising genotypes. These genotypes may be used in crossing programme to achieve desired segregants in forage maize.

Table 5: Mean values of the seven clusters for 12 characters in fifty four maize genotypes

Cluster No.	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)
CL-I	89.86	92.21	120.61	12.02	10.53	71.54	8.34	0.35	8.59	21.21	8.15	0.43
CL-II	97.50	99.50	155.75	12.85	11.90	87.72	9.95	0.38	11.45	25.00	8.71	0.76
CL-III	98.50	101.00	168.30	14.00	12.00	90.20	10.40	0.33	11.10	23.99	9.74	0.87
CL-IV	98.50	100.80	178.08	14.66	13.18	93.35	9.96	0.28	10.79	24.13	8.81	1.01
CL-V	80.50	83.00	131.95	10.65	7.20	66.85	7.30	0.31	7.35	20.31	7.90	0.31
CL-VI	79.36	81.57	82.45	9.50	7.81	60.28	7.26	0.38	7.99	19.85	8.40	0.26
CL-VII	80.00	83.00	178.50	12.10	10.15	92.10	9.45	0.35	9.35	21.95	9.17	0.92

Conclusion
On the basis of inter cluster distances, cluster mean and divergence class observed in the present study, the genotypes 52095, 52217, 52336, 52483, 52507, 52623 and African Tall were distinct and diverse and could be classified as promising genotypes. These genotypes may be used in crossing programme to achieve desired segregants in forage maize.

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