



GENETIC DIVERSITY STUDIES IN MAIZE (*ZEA MAYS* L.) FOR GREEN FODDER YIELD AND ATTRIBUTING TRAITS

Yogendra Prasad*¹, Ravi Kumar², Kamleshwar Kumar³, Sanjay Kumar⁴, Sunil Kumar⁵ and Surya Prakash⁶

^{1,2,3,6}Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi, Jharkhand 834 006, India.

⁴Department of Plant Breeding and Genetics, MBAC, Agwanpur, Saharsa-852201, Bihar, India.

⁵Department of Plant Breeding and Genetics, Veer Kunwar Singh College of Agriculture, Dumraon (Buxar), Bihar 802136, India.

Corresponding Author: Yogendra Prasad

Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi, Jharkhand 834 006, India.

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ABSTRACT

Fifteen maize (*Zea mays* L.) genotypes were evaluated for Genetic Diversity Studies at Forage Research Farm, RVC, Birsa Agriculture University, Ranchi. The Experiment was laid out in RBD with three replications. The genotypes were significantly different for all the characters, this indicates that there is scope for further genetic studies. All the genotypes were grouped in to four clusters. Cluster-I having the largest genotype (i.e seven genotypes), Cluster-IV having four genotypes, Cluster-II having three genotypes and Cluster-I having one genotype. The maximum contribution towards divergence was observed by Dry matter yield (49.52 %) followed by leaf /stem ratio (15.24 %), Crude protein (12.38 %), Dry matter yield (q/ha/day) (11.43 %), Days to 50 % flowering (9.95 %). The genotypes DMRH-1140, IIMRFH-17-1 and IMH-1527 were the most promising ones and their adaptation to the agro-ecological condition of Jharkhand. This can bring substantial increase in green fodder yield and crude protein (%).

KEYWORD: D², Diversity, Cluster.

INTRODUCTION

Maize (*Zea mays* L.), among the different fodder crops is regarded as one of the important dual purpose crop, used in human diet as well as animal feed. Maize has the potential to supply large amount of energy-rich forage for daily animal diets and its fodder can safely be fed at all stages of growth. 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 energy content and low fibre content.

Mahalanobis (1936) D² analysis is very useful tool to study the nature and magnitude of diversity prevalent in the available germplasm. Knowledge of genetic variability is pre-requisite for breeding programme, since it helps in the choice of the best yield attributes either for selection or hybridization.

MATERIAL AND METHODS

The present investigation was carried out at Fodder Farm (RVC) of Birsa Agricultural University, Jharkhand. Geographically, Ranchi district is situated in a plateau region with latitude 23°17' N and 85°10' E longitude at an altitude of about 625 metres above mean sea level. The area on an average receives 1398 mm of rainfall. The climate of the area is sub-tropical humid. The experimental materials in the present study comprised of two composite forage as check varieties viz., African Tall and J-1006 along with 13 maize entries tested in different part of India, where each entry was accommodated in 7.2 m² plot size containing 6 rows of 4 m length with inter-row spacing of 30 cm with three replications. Recommended dose of fertilizer N: P: K, 80: 40: 20 kg/ha was provided to obtain normal growth of the crop. 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 40 days of sowing. Five randomly selected plants from the rows of a plot for each genotype were tagged for recording the observations on plant population (m^2), days to 50 per cent flowering, plant height (cm), green fodder yield (q/ha), dry matter yield

(q/ha/day), dry matter yield (%), leaf /stem ratio, green forage yield (q/ha/day) and crude protein content (%). D^2 analysis was used by Mahalanobis (1936). Fifteen genotypes were grouped into four clusters as per Tocher's method as described by Rao (1952). The intra and inter-cluster distance were worked out by using Mahalanobis D^2 statistics.

Table 1: Analysis of variance for 10 characters in Fodder Maize.

Sl. No.	Characters	Mean sum of Squares		
		Replication (df=2)	Treatments (df=14)	Error (df=28)
1.	Plant population (m^2)	1.26	14.46	8.84
2.	Days to 50 % Flowering	1.37	411.64	11.95
3.	Plant Height (cm)	16.21	2839.17	559.37
4.	GFY (q/ha)	0.72	48974.97	453.26
5.	GFY (q/ha/day)	0.02	22.68	0.09
6.	DMY (q/ha)	0.96	3590.12	19.92
7.	DMY (q/ha/day)	0.03	33.61	0.16
8.	DMY (%)	0.14	176.43	3.80
9.	CP (%)	0.01	55.59	0.62
10.	Leaf/Stem ratio	20.40	557.79	497.48

Table 2: Range and mean of 10 characters in Forage Maize.

Sl. No.	Characters	Range	Mean	CV (%)
1.	Plant population (m^2)	5.20 - 7.93	6.36	8.83
2.	Days to 50 % Flowering	48.33 - 60.00	53.02	1.23
3.	Plant Height (cm)	177.8 - 204.1	185.15	2.41
4.	GFY (q/ha)	129.2 - 263.8	210.10	1.91
5.	GFY (q/ha/day)	2.40 - 5.15	3.98	1.48
6.	DMY (q/ha)	29.50 - 61.80	44.88	1.87
7.	DMY (q/ha/day)	3.40 - 6.50	4.41	1.74
8.	DMY (%)	16.83 - 23.7	21.49	1.71
9.	CP (%)	5.69 - 9.19	7.39	2.01
10.	Leaf/Stem ratio	0.42 - 0.59	0.47	8.52

Table-3: Cluster mean for 10 characters in Forage Maize.

Sl. No.	Character	Plant population	Days to 50% Flowering	Plant ht. (cm)	GFY (q/ha)	GFY (q/ha/day)	DMY (q/ha)	DMY (q/ha/day)	DMY (%)	CP (%)	Leaf stem ratio
1.	Cluster-I	6.59	52.52	186.95	203.14	3.87	44.08	4.61	21.92	7.28	0.48
2.	Cluster-II	6.16	56.55	182.77	198.12	3.50	35.96	3.50	18.22	7.80	0.45
3.	Cluster-III	6.33	53.67	178.73	129.15	2.41	29.50	3.90	23.17	7.65	0.50
4.	Cluster-IV	6.12	51.08	185.40	251.52	4.92	56.80	4.90	22.75	7.21	0.47

Table- 4: Number and name of genotypes in different cluster.

Cluster	No. of genotypes	Genotype
I	7	IAFM-2015-15, IMH-1526, KDFM-2, J-1006, IIMRFH-17-3, IIMRFH-17-2, IAFM-2015-26
II	3	TSMF 16-3, African Tall, TNFM 132-4
III	1	BAUFM-1
IV	4	IMH-1527, IMRFH-17-1, HPFM-8, DMRH-1410

Table- 5: Inter and Intra Cluster Distance.

Cluster	I	II	III	IV
I	962.170	1536.799	3191.416	2764.963
II		413.151	2359.678	4684.449
III			0.000	9466.463
IV				1481.270

Table- 6: Independent character contribution towards divergence.

Sl. No.	Source	Times Ranked ^{1st}	Contribution (%)
1.	Plant population (m ²)	0	0.00
2.	Days to 50 % Flowering	1	9.95
3.	Plant Height (cm)	0	0.00
4.	GFY (q/ha)	0	0.00
5.	GFY (q/ha/day)	0	0.00
6.	DMY (q/ha)	52	49.52
7.	DMY (q/ha/day)	12	11.43
8.	DMY (%)	7	6.67
9.	CP (%)	13	12.38
10.	Leaf/Stem Ratio	16	15.24

RESULTS AND DISCUSSION

The genetic divergence can be estimated by using an effective statistical tool, Mahalanobis D² statistics, which gives clear idea about the diverse nature of the population. The analysis of variance carried out for all the ten quantitative traits among fifteen genotypes are presented in Table-1. The mean sum of squares due to genotypes showed highly significant differences for all the ten traits under study. Hence, presence of large amount of variability might be due to diverse source of materials taken for the 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 More (2003), and Rathod *et al.* (2021).

The knowledge of genetic diversity among the genotypes is essential for selection of parents for hybridization programme, especially in a cross pollinated crop like maize. Fifteen genotypes were grouped into 4 clusters (Table-4) as per Tocher's method described by Rao (1952). Cluster I was the largest with 7 genotypes, followed by cluster IV with 4 genotypes, followed by cluster II with 3 genotypes. Cluster III was mono-genotypic. Distribution of genotypes in different clusters was random but it has clearly shown relationship with the characters for which they were bred. It indicates 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) and More (2003) grouped 45 forage maize genotypes into 7 clusters, Azad *et al.* (2012) grouped 30 genotypes into 6 clusters, and Rathod *et al.* (2021) 54 genotypes of maize into 7 clusters.

The intra and inter-cluster distance values were worked out using Mahalanobis D² statistics. The mean D² values (Table-6) cluster elements were used as measures of intra and inter-cluster distance. The maximum inter-cluster distance was observed for cluster between III & IV (9466.463) followed by cluster II & IV (4684.449), followed by cluster I & III (3191.416) and followed by Cluster II & III (2359.678) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture. In the case of clusters III & III the intra -cluster distances are zero because of its mono-genotypic nature. These results suggest that maximum divergence between genotypes of these indicating the fact that the genotypes present in one cluster differ entirely from those present in other clusters. While lowest divergence was noticed between cluster II and II (413.151).

The present study revealed that DMY (q/ha) contributed maximum (49.52%) for divergence followed by leaf /stem ratio (15.24%), CP (%) (12.38 %), DMY (q/ha/day), (11.43 %), Days to 50 % flowering (9.95) and DMY % (6.67 %) to total divergence. This result was in accordance with Utkhede (1977) and More (2003) reported high contribution to the divergence by days to 50 % flowering, high contribution due to plant height was reported by Rathod *et al.* and More (2003).

The cluster means for ten quantitative traits studied in fifteen genotypes of maize revealed considerable differences among the entire clusters. Cluster wise mean and over all cluster mean for the characters are presented in Table-3. Cluster I shows the highest characters mean for plant height (cm) and plant population. Cluster II exhibited highest character mean for days to 50 % flowering and crude protein (%), Cluster III shows the highest characters mean for DMY (%) and leaf /stem

ratio whereas, Cluster- IV exhibited highest character mean for GFY (q/plot), GFY (q/ha/day) and DMY (q/ha). Hence, it is obvious from the result that, Cluster IV may be used as one of the parent in crossing programme to enhance the GFY, DMY and plant height, genotype belong to Cluster II may be used as the parent for enhancing the CP (%). High contribution to the divergence was due to green forage yield as reported by Kumari *et al.* and Rathod *et al.* (2021).

On the basis of cluster mean and divergence observed in the present study, the genotypes viz., *DMRH-1140*, *IIMRFH-17-1* and *IMH-1527* were distinct and diverse and could be classified as promising genotypes. These genotypes may be used in crossing programme to achieve the desired segregants in forage maize.

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