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Genetic diversity studies in maize (*Zea mays* L.) for green fodder yield and its quality traits

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Abstract

The experimental material for present study consisted of 32 genotypes of maize for genetic diversity. Observations were recorded on five quantitative and one quality parameters during Kharif 2022 at RVC Fodder Farm, Birsa Agriculture University, Ranchi (Jharkhand) in three replications and in RBD design. 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 seven clusters. Cluster-I having the largest genotype (i.e eighteen genotypes), Cluster-II having six genotypes, Cluster-IV having four genotypes and Cluster-III, V, VI and VII having one genotype each. The maximum inter-cluster distance was observed for cluster between II & IV (262.94) followed by cluster II & III (169.20) and cluster II & V (144.90) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture. The maximum contribution towards divergence was observed by Plant height (56 %) followed by Days to 50 % Flowering (18.75 %), Leaf /Stem ratio (15.24 %), Crude protein (12.38 %), Green Fodder Yield (3.02 %) and Dry matter yield (q/ha/day) (1.61 %). The genotypes MAH 15-84, IFH 10-21 K2, ADFM-4 and KDFM-8 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 (%). This study gives an insight into the diversity pattern of advance maize lines which will be helpful for further utilisation in breeding programme.

Keywords: GCV, PCV, diversity, heritability

Introduction

Maize (*Zea mays* L.) is an important fodder crop which provide better nutrition quality along with good quantity of biomass. Commonly known as queen of cereals due to its productivity and utility value, maize is globally grown in different seasons for diverse uses in different agro-ecological conditions (Langade, *et al.*, 2013) [5]. Fodder crops are an important component of agricultural economy as they help in sustainable development of livestock sector. In India, it is used as green fodder, hay and silage for animals. In India, it is used as green fodder, hay and silage for animal. The demand of fodder maize is increasing very fast particularly with the expansion of dairy, poultry and maize-based industries (Ahmed *et al.*, 2010) [1]. It has high production potentiality, wide adaptability and multiple uses (Gour *et al.*, 2006) [3]. Green fodder provides adequate energy and proteins for growth of animals and milk production (Takawale *et al.*, 2009) [11]. Presently there is a chronic shortage of green fodder in the country and therefore, silage may play a critical role in filling the wide gap in availability and requirement of quality green forages for animals.

Mahalanobis (1936) [6] 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.

Materials and Methods

The present investigation was carried out at Fodder Farm (RVC) of Birsa Agricultural University, Jharkhand. Geographically, the 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 site is sub-tropical humid. The experimental materials in the present study comprised of two composite forage as check varieties viz., African Tall & J-1006 and one hybrid check COHM-8 along with 29 maize entries tested in different part of India, where each entry was accommodated in a 9.6 m² plot size containing 8 rows of 4 m length with an inter-row spacing of 30 cm with three replications. The recommended dose of fertilizer N: P: K, 80: 40: 20 kg/ha was given to achieve average growth of the crop. Full dose of phosphatic and potassic fertilizers and a half dose of nitrogenous fertilizer were applied at the time of final land preparation as basal dose. The remaining half of nitrogenous fertilizer was top-dressed 40 days after sowing. Five randomly selected plants from the rows of a plot for each genotype were tagged for recording the observations on plant population (m²), days to 50 per cent flowering, plant height (cm), green fodder yield (q/ha), dry matter yield (q/ha/day), leaf /stem ratio and crude protein content (%). Thirty two genotypes were grouped into seven clusters as per Tocher's method described by Rao (1952) [8]. The intra and inter-cluster distance were worked out by using Mahalanobis D² statistics.

Results and Discussion

The genetic divergence can be estimated by using an effective statistical tool, Mahalanobis D² statistics, which gives a clear idea about the diverse nature of the population. The analyses of variance were carried out for all the six traits among thirty two genotypes are presented as per Table-1. The mean sum of squares due to genotypes showed significant differences for all the six traits under study. Hence, a large amount of variability might be due to the diverse source of materials taken for the present study. This indicated ample scope for selecting promising lines from the current 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) [7], and Rathod *et al.* (2021) [9].

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. Thirty two genotypes were grouped into seven clusters Cluster-I having the largest genotype (i.e. eighteen genotypes), Cluster-II having six genotypes, Cluster-IV having four genotypes and Cluster-III, V, VI and VII having one genotype each.

The intra and inter-cluster distance values were worked out using Mahalanobis D² statistics. The mean D² values (Table-7) cluster elements were used as measures of intra and inter-cluster distance. The maximum inter-cluster distance was observed for cluster between II & IV (262.94) followed by cluster II & III (169.20) and cluster II & V (144.90) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture. These results suggest that maximum divergence between genotypes of these indicating that the genotypes present in one cluster differ entirely from those present in other clusters. While lowest divergence was noticed between cluster I (27.19) and cluster V & cluster VI (27.62). Earlier workers reported similar findings for different clustering patterns and criterion for selection of parents in hybridization programme for yield improvement (Barua *et al.*, 2017; Singh, *et al.*, 2020) [2, 10]. In the case of cluster III, V, VI and VII the cluster distances are zero because of its mono-genotypic nature. Similar study was also observed by Yogendra *et al.* (2021) [13].

The present study revealed that the maximum contribution towards divergence was observed in Plant height (56 %) followed by Days to 50 % Flowering (18.75 %), Leaf /Stem ratio (15.24 %), Crude protein (12.38 %), Green Fodder Yield (3.02 %) and Dry matter yield (q/ha/day) (1.61 %). High contribution to the divergence was due to green forage yield, as reported by Kumari *et al.* and Rathod *et al.* (2021) [9].

The cluster means for six quantitative traits studied in thirty two genotypes of maize revealed considerable differences among the clusters. Cluster wise mean and over all cluster mean for the characters are presented in Table-6. Cluster II shows the highest characters mean for plant height and green fodder yield. Cluster III shows the highest characters mean for dry matter yield. Cluster VII exhibited the highest characters mean for leaf stem ratio and Cluster VI shows the highest characters mean for crude protein percentage. Divergence analysis assisted in identification of diverse groups among the genotypes under evaluation and reflected for the prospective utilization in hybridization programme.

On the basis of cluster mean and divergence observed in the present study, the genotypes MAH 15-84, IFH 10-21 K2, ADFM-4 and KDFM-8 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 (%). This study gives an insight into diversity pattern of advance maize lines which will be helpful for further utilisation in breeding programme.

Table 1: Analysis of variance for six characters in Fodder Maize

Sl. No.	Characters	Mean sum of Squares		
		Replication (df=2)	Treatments (df=14)	Error (df=28)
1.	Days to 50 % Flowering	0.291	22.714	0.431
2.	Plant Height (cm)	18.063	1280.942	6.789
3.	GFY (q/ha)	6.331	15.258	1.772
4.	DMY (q/ha)	4.291	53.534	8.098
5.	Leaf/Stem ratio	0.001	0.021	0.001
6.	CP (%)	0.152	3.149	0.190

Table 2: Range and mean of six characters in Forage Maize

Sl. No.	Characters	Range	Mean	CV (%)
1.	Days to 50 % Flowering	49.33-60.67	54.24	1.2
2.	Plant Height (cm)	116.27-204.07	169.60	1.5
3.	GFY (q/ha)	11.27-20.00	15.35	8.7
4.	DMY (q/ha)	40.00-54.33	47.64	6.0
5.	Leaf/Stem ratio	0.52-0.91	0.61	4.0
6.	CP (%)	6.30-10.58	7.61	5.3

Table 3: Estimation of genetic parameters of six characters of Forage Maize

Sl. No.	Characters	$\sigma^2 p$	$\sigma^2 g$	PCV	GCV	Heritability (Broad sense)	Genetic Advanced as % of mean (5%)
1.	Days to 50 % Flowering	7.859	7.427	5.168	5.024	0.95	10.06
2.	Plant Height (cm)	431.507	424.717	12.248	12.151	0.99	24.83
3.	GFY (q/ha)	6.267	4.495	16.309	13.812	0.72	24.09
4.	DMY (q/ha)	26.576	18.478	10.822	9.024	0.70	15.50
5.	Leaf/Stem ratio	0.007	0.006	14.082	13.500	0.92	26.66
6.	CP (%)	1.156	0.996	14.137	13.124	0.86	25.10

Table 4: Number and name of genotypes in different cluster

Cluster	No. of genotypes	Genotype
I	18	RCRMH-17, PMC-15, PFM-14, AFM-19, KDFM-8, IFH 10-21 K2, HPFM-12, PMC-16, RCRMH-2, JH-17011, AH-4668, IFH 10-21 K1, J-1006, BMC-1853, AH-1625, AFH-1, ADC-5, ADFM-4
II	6	PMC-14, AFM-23, Baif Maize-7, CHCF-2208, COHM-8, MFM 18-4
III	1	AH 4688
IV	4	AH4686, MAH 15-84, MHF 22-1, AH-4687
V	1	African Tall
VI	1	HPFM-12
VII	1	ADFM-5

Table 5: Independent character contribution towards divergence

Sl. No.	Source	Times Ranked 1 st	Contribution (%)
1.	Days to 50 % Flowering	93	18.75
2.	Plant Height (cm)	278	56.05
3.	GFY (q/ha)	15	3.02
4.	DMY (q/ha)	8	1.61
5.	Leaf/Stem ratio	50	11.90
6.	CP (%)	43	8.67

Table 6: Cluster mean for 6 characters in Forage Maize

Sl. No.	Character	Days to 50% Flow	Plant ht. (cm)	Green Fodder yield (kg/plot)	DMY Yield (g/plot)	Leaf Stem ratio	Crude Protein (%)
1.	Cluster-I	53.65	168.91	15.47	49.04	0.59	7.38
2.	Cluster-II	54.22	198.99	16.09	46.61	0.65	8.07
3.	Cluster-III	56.67	155.37	14.07	41.00	0.73	6.30
4.	Cluster-IV	52.58	132.37	14.53	49.42	0.61	7.93
5.	Cluster-V	59.67	162.20	11.50	36.00	0.61	7.30
6.	Cluster-VI	60.67	171.77	16.50	46.00	0.55	9.07
7.	Cluster-VII	57.33	173.93	16.10	41.33	0.99	7.82

Table 7: Cluster Distance for 7 characters in Forage Maize

Sl. No.	Character	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII
1.	Cluster-I	27.19	77.02	66.50	102.01	66.42	60.76	94.99
2.	Cluster-II	77.02	42.72	169.20	262.94	144.90	104.67	140.79
3.	Cluster-III	66.50	169.20	0.00	67.68	30.31	82.03	32.30
4.	Cluster-IV	102.01	262.94	67.68	43.99	107.57	144.76	144.43
5.	Cluster-V	66.42	144.90	30.31	107.57	0.00	27.62	71.95
6.	Cluster-VI	60.76	104.67	82.03	144.76	27.62	0.00	104.88
7.	Cluster-VII	94.99	140.79	32.30	144.43	71.95	104.88	0.00

Conclusion

In conclusion, the utilization of Mahalanobis D2 statistics proved effective in estimating genetic divergence among thirty-two maize genotypes, revealing significant differences across six key traits. This variability underscores the potential for selecting promising lines to enhance green forage yield and related attributes. The clustering analysis facilitated grouping genotypes based on their genetic distances, indicating potential variations in genetic architecture among clusters. Plant height emerged as the primary contributor to genetic divergence, followed by other traits such as flowering time and crude protein content. Cluster-wise analysis highlighted distinct trait means among genotypes, aiding in the identification of promising candidates for hybridization programs. Among the genotypes evaluated, MAH 15-84, IFH 10-21 K2, ADFM-4, and KDFM-8 demonstrated promising characteristics for adaptation and yield improvement in Jharkhand's agro-ecological conditions. This study provides valuable insights into the diversity patterns of advanced maize lines, offering a roadmap for their strategic utilization in breeding programs to enhance maize productivity and quality.

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