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GENETIC STUDIES ON GREEN FODDER YIELD AND QUALITY TRAITS IN FORAGE MAIZE (*ZEA MAYS* L.)

Yogendra Prasad*, Sunil Kumar, Ravi Kumar, Kamleshwar Kumar, Surya Prakash, and C. S. Mahato
Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi, Jharkhand 834 006, India
*Corresponding author E-mail: yogendraprasad_bau@rediffmail.com

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ABSTRACT

An experiment was conducted to evaluate the genetic divergence in 33 genotypes of fodder maize (*Zea mays* L.) through genetic variability, D^2 and principal component Analysis (PCA). The Experiment was laid out in RBD with three replications during kharif 2025 at Forage Research Farm, RVC, Birsa Agricultural University, Ranchi. Observations were recorded on eight biometrical traits and quality trait. The genotypes were significantly different for all the characters; this indicates that there is scope for further genetic studies. The maximum inter-cluster distance was observed for cluster between VI & VII (53.07) followed by cluster VII & IX (49.17), cluster I & VI (46.62) and cluster I & IX (44.49) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture. All the genotypes were grouped in to nine clusters. Cluster-III was the largest with eight genotypes, followed by cluster-II with seven genotypes; cluster-IV with six genotypes, Cluster-I & V having three genotypes each, cluster-VII & IX having two genotypes each and cluster-VI & cluster VIII was mono genotypic. The maximum contribution towards divergence was observed by plant height contributed maximum (54.92%) for divergence followed by days to 50 % flowering (32.20%), crude protein (%) (6.06 %), GFY (q/ha/day) (5.49 %) and DMY (q/ha) (1.33 %) to total divergence 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 (%). On the basis of cluster mean and divergence observed in the present study, the genotypes viz., IFH-11-244, KDFM-11 and IFH-11-247 were distinct and diverse and could be classified as promising genotypes.

***Keywords* :** D^2, clusters, diversity, crude protein, forage yield.

Introduction

Maize (*Zea mays* L.) is a quick growing; succulent, high yielding, nutritional and toxin- free fodder crop (Arya *et al*., 2020). It is world's third most important cereal after wheat and rice and known as "Queen of Cereals". Maize crop used as a fodder, rich source of energy and protein to dairy animals and can be safely fed at any stages of crop growth (Chaudhary *et al.*, 2016) particularly from tasseling stage onwards (Prasad *et al*., 2021). The increasing demand for quality green fodder driven by dairy intensification and changing climate pattern necessitates the efficient utilization of diverse germplasm resources to breed high-yielding, nutritionally superior fodder cultivars. The importance of exploring available variability for green fodder yield, dry matter content and other morphological attributes are well emphasized (Singh *et al*., 2021). Genetic diversity analysis provides relevant information for crop improvement revealing the extent of divergence among genotypes, the presence of distinct group within a population and the potential of specific lines to serve as parents for generating heterotic combinations. Keeping in this view, an attempt was made to assess the degree and extent of genetic divergence for several green fodder yield contributing traits among the available fodder maize genotypes. The magnitude of genetic diversity can be assessed using statistical tool such as principal component analysis (PCA) and cluster analysis.

A wide range of diversity is found among the maize genotypes under study at both phenotypic and genotypic level. The knowledge of genetic diversity in maize is important for the understanding of genetic structure which subsequently helps the breeder in choosing desirable parents to select the relevant breeding programme (Al Badeiry *et al*., 2014). Diverse genotypes can be used to produce superior hybrids/lines, segregating population with high variability and introgression of desirable traits/genes. Therefore, there is a need to evaluate the available genotypes for the extent of genetic diversity. Mahalanobis (1936) D^2 statistics is a handy tool to study the nature and magnitude of diversity present in the available germplasm. The knowledge of genetic variability is a pre-requisite for any breeding programme since, it helps in choosing the best yield attributes either for selection or hybridization. In this context, the present study aims to assess the extent and pattern of genetic diversity in diverse fodder maize germplasm panel using PCA for key fodder-related traits. This analysis is intended to guide the selection of genetically divergent accessions, enhance breeding efficiency and contribute to the development of maize varieties optimized for high biomass yield and also improved forage quality.

Material and Methods

An experiment was conducted at Fodder Farm (RVC) of Birsa Agricultural University, Jharkhand during kharif 2024. 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 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 30 maize entries tested in different part of India, where each entry was accommodated in a 7.2 m^2 plot size containing 6 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. Observations were recorded on eight biometrical traits and quality traits from five randomly selected plants were averaged over replication and mean value was used for statistical analysis with respect to days to 50 per cent flowering, plant height (cm), green fodder yield (q/ha), green fodder yield (q/ha/day), dry matter yield (q/ha), dry matter yield (q/ha/day), leaf /stem ratio, and crude protein content (%). D^2 statistics given by Mahalanobis was used for divergence analysis. Thirty-three genotypes were grouped into nine clusters as per Tocher’s method. The intra and inter-cluster distance were worked out by using Mahalanobis D^2 statistics.

Results and Discussion

Genetic variability studies provide basic information about the genetic properties of the population on which breeding procedures are used for further improvement of the crop. All the data of eight biometrical and quality traits of fodder maize were subjected to an analysis of variance. The analysis of variance carried out for all the eight quantitative traits among thirty-three genotypes are presented in Table-2. ANOVA revealed significant differences among genotypes for all the traits under studied. The wide range of mean values were observed for the traits viz., GFY (327.1 to 504.8 q/ha), plant height (120.27 to 210.87 cm), days to 50 % flowering (52.3 to 70.3 days), dry matter yield (78.8-128.5 q/ha) and Crude protein (5.58 to 10.26 %). Table-3 indicated that the phenotypic variance was slightly higher than genotypic variance for green fodder yield and its associated traits, indicating that these traits are influenced by the environmental factors. The highest genotypic and phenotypic variance was recorded for green fodder yield (2137.7 to 3508.1), respectively followed by dry matter yield (189.92 to 291.86), respectively, plant height 638.83 to 642.89), respectively and crude protein (1.13 to 1.20), respectively with lesser difference value exist between the genotypic and phenotypic variance. 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 minimal influence of environment. Similar results were reported by Rathod *et al*. (2021) in fodder maize. The quantity of genetic and non-genetic variation is determined by estimating genotypic and phenotypic coefficient of variations as suggested by Burton (1952). Higher GCV and PCV magnitudes for these traits indicated a high degree of diversity and more scope for selection. The obtained results of higher GCV and PCV for green fodder yield (10.66 to 13.66) revealed that the green fodder yield is controlled by additive gene action and hence the selection might be effective. Moderate GCV and PCV were obtained for the traits such as plant height (15.75 to 15.80), leaf stem ratio (0.57 to 5.60), days to 50 % flowering (7.70 to 7.75) and crude protein percentage (14.55 to 14.99). Similar findings for plant height and leaf length were reported by Kapoor and Batra (2015) and for crude protein by Chakrovorty and Neog (2015) and Murugan *et al.* (2010) for green fodder yield.

Heritability is the ratio of genotypic variance to the total variance. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1960). The trait days to 50 % flowering and plant height (0.99 %) recorded the highest estimate of heritability followed by crude protein (0.94 %), green fodder yield q/ha/day (0.95 %) and green fodder yield q/ha (0.61 %). Similar results for plant height reported by Prakash *et al.* (2019) and for plant height and green fodder yield also reported by Ali *et al.* (2015) in fodder maize. It indicates that improvement of these characters would be effective through phenotypic selection due to additive gene action.

Genetic advance is a measure of genetic gain under selection. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al.,* 1955). High heritability coupled with high genetic advance were recorded for the trait green fodder yield (74.35 %) followed by plant height (52.90%) and dry matter yield (22.90 %). It indicates that the genes for these traits are controlled by additive gene action and selection may be effective. Similar results were reported by Ali *et al.* (2015). Therefore, the direct selection for green fodder yield and plant height would be effective.

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 three genotypes were grouped into nine Clusters (Table-5) as per Tocher’s method described by Rao (1952). Cluster-III was the largest with eight genotypes, followed by cluster-II with seven genotypes; cluster-IV with six genotypes, cluster-I & V having three genotypes each, cluster-VII & IX having two genotypes each and cluster-VI & cluster VIII 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. Similarly Prasad, (2021) divided 19 maize genotypes into five clusters.

Mahalanobis D^2 statistics was used to calculate intra and inter cluster distances within and between the genotypes, respectively. The mean D^2 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 VI & VII (53.07) followed by cluster VII & IX (49.17), cluster I & VI (46.62) and cluster I & IX (44.49) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture. In the case of clusters VI & VIII 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 resent in one cluster differ entirely from those present in other clusters. While lowest divergence was noticed between cluster I (8.36) and II (8.70).

The present study revealed that plant height contributed maximum (54.92%) for divergence followed by days to 50 % flowering (32.20%), CP (%) (6.06%), GFY (q/ha/day) (5.49 %) and DMY (q/ha) (1.33 %) 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.* (2021) and More (2003).

The cluster means for eight quantitative traits studied in thirty three 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-8. Cluster VII shows the highest characters mean for plant height (cm), GFY (q/ha) DMY (q/ha) and CP (%). Cluster IX exhibited highest character mean for days to 50 % flowering, cluster VIII shows the highest characters mean for GFY (q/ha/day) and DMY (q/ha/day) whereas, Cluster-III exhibited highest character mean for Leaf stem ratio. Hence, it is obvious from the result that, cluster VII may be used as one of the parent in crossing programme to enhance the GFY, DMY, plant height and CP (%),Cluster VIII may be used as the parent for enhancing the GFY and CP (%). High contribution to the divergence was due to green forage yield as reported by Kumari *et al.* (2018) and Rathod *et al.* (2021).

On the basis of cluster mean and divergence observed in the present study, the genotypes viz., IFH-11-244, KDFM-11 and IFH-11-247 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.

Table 1: Range and mean of eight characters in Fodder Maize

Sl.No.	Characters	Range	Mean	CV (%)
1.	Days to 50% flowering	52.33 - 70.30	58.47	0.89
2.	Plant ht. (cm)	120.27 - 210.87	160.43	1.26
3.	GFY (q/ha)	327.10-504.83	433.47	8.54
4.	GFY (q/ha/day)	5.78-8.84	7.45	3.00
5.	DMY (q/ha)	78.80-128.53	112.61	8.96
6.	DMY (q/ha/day)	1.42-2.40	1.92	11.82
7.	Leaf/stem ratio	0.92-1.10	0.99	5.63
8.	Crude protein (%)	5.58-10.26	7.32	3.50

Table 2: Analysis of variance for eight characters in Fodder Maize

Sl.No.	Characters	Mean sum of Squares		
		Replication (df=2)	Treatments (df=32)	Error(df=64)
1.	Days to 50% flowering	1.23	1956.02	17.43
2.	Plant ht. (cm)	10.91	61457.83	259.79
3.	GFY (q/ha)	5650.05	249073.32	87705.55
4.	GFY (q/ha/day)	1.59	97.47	3.20
5.	DMY (q/ha)	644.47	21494.11	6524.34
6.	DMY (q/ha/day)	0.69	8.69	3.29
7.	Leaf/stem ratio	0.017	0.096	0.198
8.	Crude protein (%)	1.28	111.05	4.50

Table 3: Estimation of genetic parameters of Eight characters of Fodder Maize

Sl. No	Characters	σ^2 p	σ^2 g	PCV	GCV	Heritability (Broad Sence)	Genetic advanced at 5 (%)	Genetic Advanced as % of mean (5%)
1.	Days to 50% flow.	20.56	20.28	7.75	7.70	0.99	9.26	15.83
2.	Plant ht. (cm)	642.89	638.83	15.80	15.75	0.99	52.90	32.35
3.	GFY (q/ha)	3508.11	2137.71	13.66	10.66	0.61	74.35	17.15
4.	GFY (q/ha/day)	1.05	0.99	13.74	13.41	0.95	2.01	26.96
5.	DMY (q/ha)	291.86	189.92	15.17	12.24	0.65	22.90	20.33
6.	DMY (q/ha/day)	0.12	0.07	18.42	14.13	0.59	0.43	22.32
7.	Leaf/stem ratio	0.003	0.000	5.60	0.57	-0.01	-0.001	-0.12
8.	Crude protein (%)	1.20	1.13	14.99	14.55	0.94	2.13	29.09

Table 4: Mean Table

Sl. No.	Entries	Days to 50 % Flow.	Plant ht. (cm)	GFY (q/ha)	GFY (q/ha/day)	DMY (q/ha)	DMY (q/ha/day)	Leaf/stem ratio	CP (%)
1	MFH-2445	64	148.8	429.9	6.68	115.5	1.80	0.98	5.70
2	IFH-11-246	66	163.3	456.9	6.96	118.2	1.80	1.00	6.16
3	OUFM-24	58	198.8	480.6	8.24	125.6	2.15	0.99	5.25
4	COHM-8	56	146.3	398.6	7.08	110.8	1.97	1.03	5.70
5	JHFM-24-1	65	179.6	447.2	6.85	117.2	1.79	0.98	7.07
6	AH-4754	54	143.7	440.3	8.15	118.0	2.19	1.03	7.30
7	ADFM-8	52	167.9	462.5	8.84	125.8	2.40	0.99	5.70
8	IFH-11-243	58	164.2	391.0	6.70	102.2	1.75	0.99	7.07
9	PMC-17	59	199.3	485.4	8.27	129.8	2.21	1.01	6.16
10	DFH-24-2	61	125.7	361.8	5.93	98.9	1.62	1.01	7.07
11	MAH-20-32	55	148.1	443.1	8.10	126.7	2.32	0.99	5.70
12	IFH-11-241	60	169.0	435.4	7.22	109.1	1.81	1.00	7.07
13	PFM-17(JC-12)	57	166.5	492.4	8.59	117.2	2.04	1.01	7.53
14	KDFM-10	54	158.0	409.0	7.53	103.1	1.90	1.10	6.84
15	JHFM-24-2	66	130.6	366.7	5.53	94.4	1.42	0.97	7.76
16	AFH-10	54	139.2	379.2	6.98	84.2	1.55	0.92	8.21
17	DFH-24-1	57	129.5	347.2	6.09	88.9	1.56	0.96	7.53
18	NFM-112	59	173.1	422.2	7.16	106.1	1.80	0.96	7.30
19	AH-4733	56	200.1	483.3	8.58	124.4	2.21	0.96	7.98
20	KDFM-11	59	215.1	502.1	8.56	120.8	2.06	0.96	10.26
21	IFH-11-244	61	210.9	504.9	8.28	138.0	2.26	1.00	9.12
22	IFH-11-247	59	175.1	493.7	8.32	130.3	2.20	0.98	7.53

23	TNFMH-2308	60	124.8	404.9	6.71	102.6	1.70	1.01	8.44
24	AH-4750	55	162.0	397.9	7.28	108.5	1.98	0.97	7.98
25	BAUFM-23-8	53	120.3	376.4	7.10	103.1	1.95	0.97	8.21
26	IFH-11-242	61	149.6	365.3	6.02	90.6	1.49	1.00	7.76
27	JH-20088	53	158.7	461.8	8.77	122.2	2.32	1.00	6.61
28	MAH-20-45	52	158.0	462.5	8.84	115.3	2.20	1.02	7.98
29	IFH-11-245	61	160.5	486.1	7.97	125.1	2.05	0.97	8.21
30	ADFM-7	56	179.3	493.7	8.76	133.6	2.37	0.98	8.90
31	JHFM-24-3	62	166.5	489.6	7.85	128.6	2.06	0.97	6.84
32	J-1006 (NC)	53	126.3	327.1	6.17	78.7	1.49	1.01	7.30
33	African Tall (NC)	70	135.5	406.2	5.78	102.4	1.46	0.94	7.30
	Mean	**58**	**160.4**	**433.5**	**7.41**	**112.6**	**1.93**	**0.99**	7.32

Table 5: No. and Name of Genotypes in different Cluster

Cluster	No. of Genotype	Name of Genotype
Cluster- I	3	OUFM-24, PMC-17, AH-4733
Cluster- II	7	IFH-11-241, NFM-112, IFH-11-243, IFH-11-245, JHFM-24-3, IFH-11-247,PFM-17
Cluster- III	8	JH-20088, MAH-20-45, KDFM-10, AH-4750, AH-4754, MAH-20-32, COHM-8, ADFM-8
Cluster- IV	6	DFH-24-2, TNFMH-2308, DFH-24-1,IFH-11-242, AFH-10, J-1006
Cluster- V	3	MFH-2445, IFH-11-246, JHFM-24-1
Cluster- VI	1	BAUFM-23-8
Cluster- VII	2	KDFM-11, IFH-11-247
Cluster- VIII	1	ADFM-7
Cluster- IX	2	JHFM-24-2, African Tall

Table 6: Independent character contribution towards divergence

Source	Times Ranked 1st	Contribution (%)
Days to 50% flow.	170	32.20
Plant ht. (cm)	290	54.92
GFY (q/ha)	0	0.00
GFY (q/ha/day)	29	5.49
DMY (q/ha)	7	1.33
DMY (q/ha/day)	0	0.00
Leaf/stem ratio	0	0.00
Crude protein (%)	32	6.06

Table 7: Inter and Intra Cluster Distances

Cluster	Cluster - I	Cluster - II	Cluster - III	Cluster - IV	Cluster - V	Cluster - VI	Cluster - VII	Cluster - VIII	Cluster - IX
Cluster- I	8.36	19.76	26.85	40.70	26.39	46.62	15.58	16.40	44.49
Cluster- II	19.76	8.70	16.77	24.43	15.44	31.52	26.50	14.73	28.30
Cluster- III	26.85	16.77	10.84	21.72	26.00	22.85	35.30	18.09	34.50
Cluster- IV	40.70	24.43	21.72	13.30	27.49	16.04	47.11	31.63	23.56
Cluster- V	26.39	15.44	26.00	27.49	12.03	37.35	32.70	25.82	21.70
Cluster- VI	46.62	31.52	22.85	16.04	37.35	0.00	**53.07**	34.75	33.60
Cluster- VII	15.58	26.50	35.30	47.11	32.70	**53.07**	9.21	19.79	49.17
Cluster- VIII	16.40	14.73	18.09	31.63	25.82	34.75	19.79	0.00	39.32
Cluster- IX	44.49	28.30	34.50	23.56	21.70	33.60	49.17	39.32	9.62

Table 8: Cluster Means Table

Cluster	Cluster - I	Cluster - II	Cluster - III	Cluster - IV	Cluster - V	Cluster - VI	Cluster - VII	Cluster - VIII
Cluster- I	57.78	199.40	483.09	126.67	8.36	0.99	6.57	2.19
Cluster- II	59.67	167.85	458.63	116.93	7.69	0.98	7.33	1.88
Cluster- III	53.92	155.32	434.46	116.34	8.07	1.02	6.69	2.16
Cluster- IV	57.72	132.52	364.22	90.66	6.32	0.98	7.72	1.57
Cluster- V	65.11	163.90	444.68	116.90	6.83	0.99	6.31	1.80
Cluster- VI	53.00	120.27	376.40	103.23	7.10	0.97	8.21	1.95
Cluster- VII	59.83	213.00	503.45	129.40	8.42	0.98	9.69	2.16
Cluster- VIII	56.33	179.27	493.73	133.67	8.76	0.98	8.90	2.37
Cluster- IX	68.33	133.07	386.43	98.38	5.66	0.96	7.53	1.44

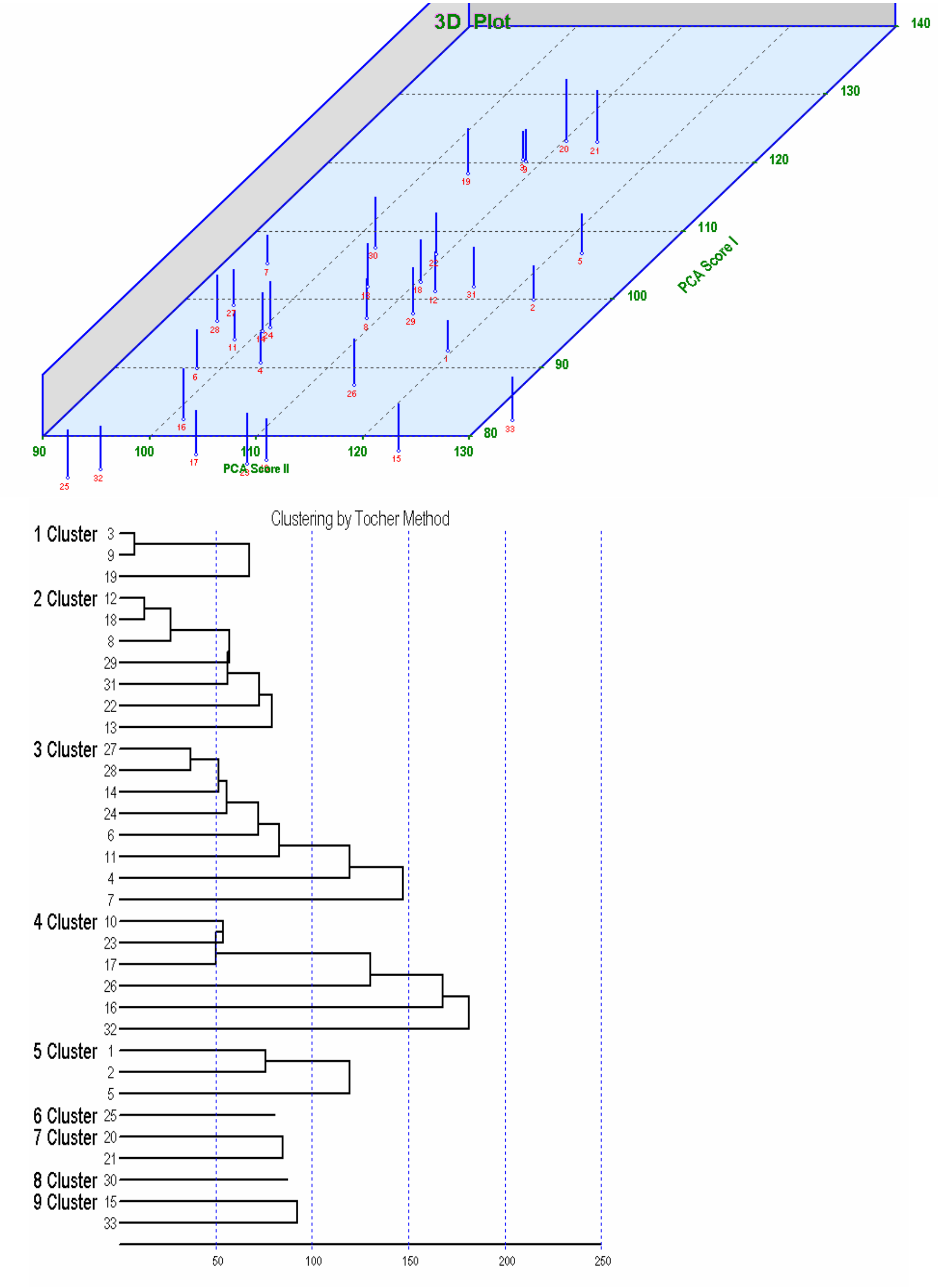

Fig. 1: 3D Plot and clustering by Tocher method

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