Original Research Article

Study of Genetic diversity in Indian Barnyard millet genetic resources [*Echinochloa frumentacea (L.)*]

ABSTRACT

Sixty four Indian barnyard millet genetic resources were studied to assess the extent of genetic divergence for 18 quantitative traits using Mahalanobis D^2 Statistic . Sixty four genetic resources of Indian barnyard millet were evaluated during *kharif*, 2020 in a lattice square design, replicated twice at Regional Agricultural Research. Based on Tocher's method, the entire genetic materials were separated into eight distinct and non-overlapping clusters suggesting availability of genetic diversity. Cluster I has highest number of accessions (57) and the remaining were mono genotypic clusters II, III, IV, V, VI, VII and VIII containing only one accession each indicating high degree of heterogeneity among the genotypes. The widest inter-cluster distance was recorded between clusters IV and VII. Therefore, it is concluded that the genotypes to these clusters has to be intercrossed in order to create more diversity and improving grain yield in barnyard millet. The traits, grain yield per plant and panicle weight contributed maximum towards total divergence has scope of crop improvement through those traits Diversity of parent paly main role for the successful of any breeding programme. So the crosses can be made among the parents having widest divergence would more likely to yield desirable recombination in segregating generations.

Key words: D^2 Statistic, Genetic diversity, genetic resource and Indian barnyard millet.

INTRODUCTION

Barnyard millet serves as dual purpose for feed and fodder crop Bandyopadhya (2009).. It is mainly grown in India, China, Japan, and Korea. It is the fourth most produced minor millet, providing food security to many poor people across the world. Globally, India is the biggest producer of barnyard millet, both in terms of area (0.146 m ha−1) and production (0.147

mt) with average productivity of 1034 kg/ha during the last 3 years (IIMR, 2018). The major barnyard millet producing states in India are Uttarakhand, Madhya Pradesh, Karnataka, Uttar Pradesh and North east region of India. The cultivated species of barnyard millet viz., Indian barnyard millet (*Echinochloa frumentacea*) and second Japanese barnyard millet (*Echinochloa esculenta)* Sood *et al.* (2015).

Prevalence of genetic diversity is a prime requisite in any crop improvement programme. Multivariate analysis through D^2 statistic, provides a quantitative estimate of association between geographic and genetic diversity based on the generalized distance (Mahalanobis, 1936). It enables to discriminate between different cultivars according to the diversity prevalent in the germplasm collections and thus assist in the selection of genetically divergent parents for their exploitation in hybridization programme. In addition, principal component analysis may be used to classify the relationships between the traits in multi-trait systems and for identifying the patterns of data by reducing the number of dimensions. It also provides an insight into the process contributing differences in yield among the genotypes, a vital aspect in identification and selection of top ranking genotypes out of diverse germplasm base.

Now a days the crop gained importance due to its rich nutritional profile and high dietary fibre content. Watanable (1999) stated that the importance of barnyard millet has increased due to its highly rich nutritious grains and presence of strong antioxidative compounds. The barnyard millet contains 10.5% protein, 3.6% fat, 68.8% carbohydrate and 398 kcal/100 g energy. The total dietary fiber content was high (12.6%) including soluble (4.2%) and insoluble (8.4%) fractions Indian barnyard millet contains between 51.5% to 59.5% starch Ugare *et al*. (2014).The genetic divergence studies enable to assess the extent of genetic diversity prevalent in the genetic resources utilized for study.

Material and Methods

Sixty four genetic resources of Indian barnyard millet were evaluated during *kharif*, 2020 in a lattice square design, replicated twice at Regional Agricultural Research Station, Nandyal. The details of 64 genotypes are given in the annexure I. Data was collected on five randomly selected plants of each genotypes per replication for 18 quantitative traits like Days to 50% flowering, basal tillers, Days to maturity, Peduncle length (cm) Sood *et al.* (2015) in barnyard millet and Amarnath *et al*. (2019) in foxtail millet, flag leaf blade length(cm), flag leaf blade width(cm), Plant height (cm), Panicle length (cm), 1000 seed weight (gm), Panicle weight /plant (gm), Harvest Index(%),Lower raceme length (cm), Grain yield/plant (gm), Phosphorus, Calcium, Iron, Zinc mg/100g, Protein %.The analysis was done through software - WINDOWSTAT 9.2 version. The experimental design used for the study was lattice square design in two replication with randomization and the statistical analysis method used are ANOVA, D^2 statistics and Principal component analysis or canonical root analysis.

Results and Discussion

The ANOVA (Table 1) revealed significant differences among the genetic material for all the traits studied indicating considerable extent of variability in the germplasm accessions, which could be used in further breeding programmes. Based on relative magnitude of D^2 values, 64 genotypes were grouped into eight distinct and non-overlapping clusters (Table 2, Fig 1). Cluster I has highest number of accessions (57) and the others were mono genotypic clusters II, III, IV, V, VI, VII and VIII containing only one accession each indicating high degree of heterogeneity among the genotypes. The D^2 values of eight clusters are presented in the Table 3 and Fig 2. The intra-cluster distances were lower than the inter-cluster distances indicating the presence of widest genetic diversity between the clusters rather than within the clusters. The intra cluster distance (0) observed in clusters II, III, IV, V, VI, VII and VIII indicated the close resemblance between the germplasm accessions present in that cluster. Therefore, selection of parents which occupying in the same cluster may not be considered effective as it lacks diversity (Kumar et al. (2010). Inter-cluster distance values varied from 62.03 (cluster IV and cluster VI) to 401.29 (cluster VI and cluster VII). Hence, the germplasm accessions between cluster IV (TNEf-216, TNEf-202, TNEf-215) and cluster VII TNEf-218 has high degree of genetic diversity as they possessing maximum inter cluster distance between cluster VI and VII. This genotypes can be utilized under for hybridization programme for obtaining superior segregants. Similar finding were reported by Brunda *et al*. (2015), Devaliya *et al*. (2017), Mahanthesha *et al*. (2017 and Amarnath *et al*. (2019).

Cluster means for 18 traits per cluster were presented in Table 4. The clusters formed were distinct as maximum variation was observed in the clusters for the characters studied. The cluster I, observed maximum for protein content (8.7). Cluster II has maximum values for panicle length (25.7), lower raceme length (6), phosphorus content (284 mg) and iron content (18.3 mg). Cluster III has maximum panicle length (29.1). The mean for grain yield per plant (12.9) and zinc content (56.5) recorded highest in cluster V. The highest mean for days to 50% flowering (72.5), flag leaf blade width (2.5), plant height (122.1) and harvest index (34.8) are recorded in cluster VI. Cluster VII reported maximum values for peduncle length (23.9), 1000 seed weight (3.65), panicle weight (14.9), calcium content (22.7) and desired means for days to 50% flowering (41), and plant height (90.9) and days to maturity (81.0). Basal tillers (3.9) recorded highest mean in cluster VIII. The least values for days to 50% flowering (41), days to maturity (81) i.e earliness were reported in Cluster VII.

The result shows that no cluster has at least one genotype with all desirable characters, so the direct selection of genotype is not possible for immediate use. Therefore, the genotypes from divergent cluster has to be selected for hybridization programme for combining all characters. Similar reports were recorded by Murugan & Nirmalakumari (2006) and kavya (2016).

The relative contribution of various plant traits towards diversity are presented in the (Table 5 and Fig 3). All the characters studied, out them the trait grain yield per plant contributed maximum (16.6%) towards genetic diversity and next by panicle weight (15.7%) indicating that these traits can be used for the genetic improvement programme. Similar finding were published by Kumari and Singh (2015), Prabu *et al*. (2020), Manimekalai *et al*. (2018) and Mahanthesha *et al*. (2017) for grain yield / plant.

The canonical root analysis or principal component analysis (PCA) was used to verify the clustering pattern obtained by Mahalanobis D2 statistic. For 64 barnyard millet germplasm accessions, canonical root analysis was carried out as per the procedure outlined by Rao (1952). Seven canonical roots accounted for 75.9 per cent of total divergence (Table 6). The first, second, third and fourth roots accounted for 20.58, 15.20, 10.46, and 9.7 per cent respectively to total variability. The remaining canonical roots viz., fifth, sixth and seventh contributed 8.16, 6.49 and 5.2 per cent respectively towards the total variability. The mean values of canonical variates for three roots X, Y and Z were furnished in Table 7. Two dimensional (2D) and Three dimensional (3D) picture was constructed by plotting the mean values of vectors as in Fig 4. and Fig 5. The amount of contribution of different traits towards canonical vectors total divergence was presented in Table 8.

In the vector Z1, traits contributing towards total divergence positively were Days to 50% flowering (0.405), flag leaf blade length (0.111), flag leaf blade width (0.234), plant height (0.311), panicle length (0.219), harvest index (0.393) and protein (0.189) while the rest of the characters contributed negatively to the total diversity.

For the vector Z2, days to 50% flowering (0.143), basal tillers (0.206), peduncle length (0.276), flag leaf blade width (0.01766), plant height (0.0339), panicle length (0.227), panicle weight per plant (0.225), lower raceme length (0.466), phosphorus (0185) and iron (0229) contributed positively to the genetic diversity. While the traits viz., days to maturity, flag leaf blade length, 1000 grain weight, harvest index, grain yield / plant calcium, zinc and protein had contributed negatively to the diversity.

In the vector Z3, the traits viz., days to 50% flowering (0.345), peduncle length (0.139), flag leaf blade width (0.049), panicle weight per plant (0.187), harvest index (0.086), grain yield per plant (0.039), phosphorus (0.437) and zinc (0.172 had contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

In the vector Z4, the traits viz., days to 50% flowering (0.026), days to maturity (0.006), flag leaf blade width (0.487), panicle length (0.236), 1000 seed weight (0.391), lower raceme length (0.016), grain yield per plant (0.533), iron (0.008), zinc (0.053) and protein (0.075) had contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

For the vector Z5, the traits contributed towards total divergence were days to 50% flowering (0.014), peduncle length (0.633), flag leaf blade length (0.301), 1000 seed weight (0.226), harvest index (0.170), lower raceme length (0.104), grain yield per plant (0.174), phosphorus (0.327), calcium (0.157), iron (0.190) and protein (0.269) had contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

In the vector Z6, the trait days to 50% flowering (0.175), basal tillers (0.552), flag leaf blade length (0.430), flag leaf width (0.160), panicle weight per plant (0.051), grain yield per plant (0.394), calcium (0.017), iron (0.217), zinc (0.089) and protein (0.071) contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

For the vector Z7, the traits flag leaf blade length (0.200), plant height (0.300), panicle length (0.300), 1000 seed weight (0.100), panicle weight per plant (0.300), harvest index (0.100), phosphorus (0.100) and zinc (0.500) contributed positively to diversity. While rest of the characters showed negative contribution towards divergence.

For the vector Z1 to Z7 similar findings were reported by Prabu *et al*. (2020), Metha *et al*. (2005) in barnyard millet and Gopikrishana *et al*. (2021) in little millet.

Conclusion

Information on the relative contribution of various plant characters towards divergence (Table 5 and Fig 3) has also been reported to aid the breeder in choice of parents for hybridization and effective selections in the advance generations. Among all the characters studied, contributed maximum grain yield per plant (16.6%) towards genetic divergence followed by panicle weight per plant (15.7%) indicating feasibility of genetic improvement through those characters. Similar reports were published by Mahanthesha *et al*. (2017) for grain yield per plant.

Table .1. Analysis of variance for 18 morpho-physiological and biochemical characters studied in barnyard millet germplasm accessions

	DF	Days to 50% flowering	basal tillers	Days to maturity	peduncle length (cm)	FLB Length(cm)	FLB Width(cm)
Replications	1	6.498	0.17	6.216	0.028	1.123	0.023
Treatments (unadjusted)	63	106.721 **	0.788 **	106.202 **	12.791 **	12.886 **	0.122 **
Error (r.c.b.)	63	8.680 **	0.057 **	30.618 **	1.217 **	3.146 **	0.018 **
Blocks within Repllicated (adj)	14	10.312	0.073	35.729	1.354	3.791	0.022
Among (a)	7	11.495	0.034	39.991	1.771	3.003	0.013
Among (b)	7	9.129	0.112	31.468	0.937	4.579	0.031
Intrablock Error	49	8.213	0.053	29.157	1.178	2.962	0.017
Total	127	57.297 **	0.421 **	67.920 **	6.949 **	7.962 **	0.070 **

	DF	Plant height (cm)	Panicle length (cm)	1000 seed weight (gm)	panicle weight / plant (gm)	Harvest Index(%)	lower raceme length (cm)
Replications	1	5.53	0.025	0.057	0.512	3.073	0.107
Treatments (unadjusted)	63	389.058 **	18.084 **	0.459 **	6.365 **	10.119 **	1.707 **
Error (r.c.b.)	63	51.494 **	1.366 **	0.033 **	0.596 **	4.204 **	0.071 **
Blocks within Repllicated (adj)	14	50.592	1.833	0.032	0.765	5.529	0.066
Among (a)	7	37.696	2.954 *	0.033	0.622	7.957	0.043
Among (b)	7	63.487	0.712	0.03	0.908	3.1	0.09
Intrablock Error	49	51.751	1.233	0.034	0.547	3.826	0.073
Total	127	218.585 **	9.649 **	0.245 **	3.457 **	7.129 **	0.883 **

	DF	Grain yield/ plant (gm)	Phosphorus (mg/ 100g)	Calcium (mg/ 100g)	Iron (mg/ 100g)	Zinc (mg/ 100g)	Protein %
Replications	1	3.971	7.681	0.296	4.423	0.972	0.997
Treatments (unadjusted)	63	5.024 **	192.381 *	11.996 **	8.228 **	86.895 **	3.414 **
Error (r.c.b.)	63	1.138 **	106.989 **	1.660 **	1.297 **	10.480 **	0.476 **
Blocks within Repllicated (adj)	14	1.45	151.448	3.416 **	1.355	6.091	0.637

Among (a)	7	0.405	52.24	3.616 **	1.621	5.139	1.127 *
Among (b)	7	2.494 *	250.656 *	3.216 *	1.089	7.043	0.146
Intrablock Error	49	1.049	94.287	1.159	1.281	11.734	0.430
Total	127	3.088 **	148.567 *	6.777 **	4.760 **	48.312 **	1.937 **

Table 2. Clustering pattern of 64 barnyard millet genotypes by Tocher' method

Cluster No.	No.of genotypes	Genotype(s)
I	**57**	GEch-8, GEch-45, GEch-20, GEch-60,GEch-94, GEch-186, GEch-191, GEch-360, GEch-365, GEch-372, GEch- 416, GEch-418, GEch-393,GEch-383, GEch-567, GEch-568, GEch-566, GEch- 570,GEch-571, GEch-572, GEch-573, GEch-374, GEch-578, GEch-579, GEch-206, GEch-581, GEch-997, GEch-634, TNEf-190, TNEf-191, TNEf-192, TNEf-193, TNEf-194, TNEf-195, TNEf-196, TNEf-197, TNEf-198, TNEf-199, TNEf-201, TNEf-203, TNEf-204, TNEf-205, TNEf-206, TNEf-207, TNEf-208, TNEf-209, TNEf-210, TNEf-211, TNEf-212, TNEf-213, TNEf-214, TNEf-216, TNEf-217, TNEf-219, BM NDL-1, BM NDL-2,BM NDL-3, TNEf-318.
II	**1**	GEch-633
III	**1**	TNEf-200
IV	**1**	TNEf-216
V	**1**	TNEf-202
VI	**1**	TNEf-215
VII	**1**	TNEf-218
VIII	**1**	GEch-995

Table .3. Average intra and inter cluster distance for the barnyard millet accessions studied

Cluster Distances								
Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**
I	**92.23**	171.93	174.5	152.98	140.92	244.29	213.76	148.2
II		**0**	248.36	286.75	168.04	268.23	127.71	163.12
III			**0**	80.2	217.92	107.77	277.34	158.92
IV				**0**	287.28	62.03	360.53	168.53
V					**0**	328.08	126.78	113.43
VI						**0**	401.29	152.7
VII							**0**	207.48
VIII								0

Table .4. Cluster means with respect to yield and yield attributes among 64 barnyard millet germplasm accession

Cluster Means: Torcher method																	
Clusters	**DFF**	**BT**	**DTM**	**PL (cm)**	**FLB L (cm)**	**FLBW (cm)**	**PH (cm)**	**PAL (cm)**	**TSW (g)**	**PW (g)**	**HI (%)**	**LRL (cm)**	**GYP (gm)**	**Ph (mg/ 100g)**	**Ca (mg/ 100g)**	**Fe (mg/ 100g)**	**Zn (mg /100g)**	**Pr (%)**
I	48.17	1.94	88.24	17.56	26.92	2.2	118.25	18.46	2.48	10.1	33.66	3.23	8.69	276.13	19.69	16.72	45.12	8.75
II	42.5	2.7	82.5	20.23	24.35	2	118.45	25.72	2.95	11.2	31.43	6.02	9	284	18.05	18.3	54.1	8.53
III	69	1.4	109	23.25	29.17	2.38	121.66	18.3	2.7	14.4	34.25	2.7	12.15	279.5	16.1	16.7	55.55	7.53
IV	68.99	2	108.98	18.9	26.49	2.48	116.05	16.37	2.75	8.1	32.22	2.27	7.25	266	17.9	17.35	38.23	7.5
V	43.5	2.3	84	14.74	24.65	1.88	98.33	14.02	2.45	14.7	34.64	3.4	12.9	266	17.05	16.35	56.55	7.53
VI	72.5	2.5	112.5	18.95	27	2.53	122.17	17.29	2.3	10.9	34.89	3.82	8.75	267	18.35	16.95	41.95	6.83
VII	41	2.3	81	23.97	21.95	2.21	90.91	15.05	3.65	14.9	30.23	5	12.85	280	22.7	15.1	43.6	7
VIII	55.5	3.9	95.5	19.5	30	1.79	121.5	18.38	2.2	12.6	31.55	4.25	10.4	281.5	21.55	16.5	52.25	7.68

DFF Days to 50% Flowering, **BT** Basal tillers, **DTM** Days to maturity, **PL** Peduncle length, **FLBL** Flag leaf blade length, **FLBW** Flag leaf blade width, **PH** Plant height, **PAL** Panicle length, **TSW** 1000 seed weight, **PW** Panicle weight, **HI** Harvest index, **LRL** Lower raceme length, **GYP** Grain yield per plant , **Ph** Phosphorus mg/100g, **Ca** Calcium mg/100g, **Fe** Iron mg/100g, **Zinc** mg/100g, **Pr** Protein.

Table .5. Contribution of yield and its attributes towards total diversity in 64 barnyard millet germplasm accessions.

S.no	Characters	Contribution %	Times ranked 1st
1	Days to 50% flowering	0.4	7.1
2	Basal tillers	7.4	149.0
3	Days to maturity	2.3	46.4
4	Peduncle length (cm)	4.8	97.0
5	Flag Leaf Blade Length (cm)	0.2	4.0
6	Flag Leaf Blade Width (cm)	4.2	84.1
7	Plant height (cm)	1.8	36.1
8	Panicle length (cm)	0.2	3.0
9	1000 seed weight (gm)	6.3	127.0
10	Panicle weight /plant (gm)	15.7	317.0
11	Harvest Index (%)	13.5	272.0
12	lower raceme length (cm)	7.3	147.0
13	Grain yield/plant (g)	16.6	335.1
14	Phosphorus (mg/100g)	0.2	3.8
15	Calcium (mg/100g)	3.7	74.6
16	Iron (mg/100g)	2.3	46.4
17	Zinc (mg/100g)	6.1	122.0
18	Protein (%)	7.2	144.8

Table .6. Canonical vectors for 18 characters in 64 barnyard millet germplasm accessions

Parameters	Z_1	Z_2	Z_3	Z_4	Z_5	Z_6	Z_7
Eigene Value (Root)	3.70473	2.73658	1.8845	1.75198	1.47025	1.16972	0.9
% Var. Exp.	20.58185	15.20319	10.46943	9.73324	8.16807	6.49842	5.2
Cum. Var. Exp.	20.58185	35.78505	46.25448	55.98772	64.15578	70.65421	75.9
Characters							
Days to 50% flowering	0.40553	0.14318	0.34532	0.02626	0.01383	0.17468	0
basal tillers	-0.18463	0.20613	-0.0076	-0.31914	-0.0538	0.55239	0
Days to maturity	-0.39136	-0.17318	-0.33946	0.00617	-0.00573	-0.23601	0
peduncle length (cm)	-0.013	0.27683	0.13999	-0.08948	0.63295	-0.09399	0
FLB Length(cm)	0.11125	-0.14059	-0.2546	-0.17546	0.30118	0.42982	0.2
FLB Width(cm)	0.23477	0.01766	0.04979	0.4873	-0.21787	0.15969	0
Plant height (cm)	0.31174	0.03393	-0.26736	-0.19041	-0.10658	-0.18571	0.3
Panicle length (cm)	0.21917	0.22722	-0.32112	0.23562	-0.02406	-0.13507	0.3
1000 seed weight (g)	-0.28102	-0.02969	-0.1274	0.39129	0.22562	-0.16856	0.1
panicle weight /plant (g)	-0.21117	0.22571	0.18775	-0.06614	-0.28809	0.05128	0.3
Harvest Index(%)	0.39348	-0.11278	0.08662	-0.00875	0.17041	-0.2252	0.1
lower raceme length (cm)	-0.08338	0.46686	-0.24556	0.01618	0.10394	-0.06371	-0.1
Grain yield/plant (g)	-0.1167	-0.09104	0.03925	0.55332	0.174	0.39394	0
Phosphorus mg/100g	-0.1728	0.18516	0.43724	-0.00856	0.32679	-0.18849	0.1
Calcium mgs/100g	-0.03164	-0.46873	-0.0194	-0.23863	0.1569	0.01741	0.1
Iron mg/100g	0.04763	0.22991	-0.39911	0.00839	0.18985	0.21672	0
Zinc mg/100g	-0.25998	-0.19603	0.17271	0.05257	-0.04862	0.08949	0.5
Protein %	0.18902	-0.3485	-0.0497	0.07461	0.2689	0.07093	-0.1

Table .7. Canonical root values, per cent of variation and cumulative variation explained for 64 barnyard millet germplasm accessions

Eigene Value (Root)	3.70473	2.73658	1.8845	1.75198	1.47025	1.16972	0.9
% Var. Exp.	20.58185	15.20319	10.46943	9.73324	8.16807	6.49842	5.2
Cum. Var. Exp.	20.58185	35.78505	46.25448	55.98772	64.15578	70.65421	75.9

Table. 8. Mean values of canonical vectors for 64 barnyard millet germplasm accessions.

S. No	Genotype	X Vector	Y Vector	Z Vector
1	Gech-8	3.498	8.382	4.284
2	Gech-45	7.768	4.824	4.366
3	Gech-20	12.916	7.279	3.867
4	Gech-60	6.474	1.984	4.394
5	Gech-94	6.922	7.644	3.136
6	Gech-186	8.306	8.543	4.484
7	Gech-191	9.652	3.384	4.645
8	Gech-360	7.757	5.525	5.016
9	Gech-365	6.646	3.655	6.252
10	Gech-372	3.734	1.387	7.34
11	Gech-416	8.502	2.087	4.779
12	Gech-418	9.684	0.717	3.385
13	Gech-393	9.59	2.765	6.393
14	Gech-383	9.496	4.531	7.518
15	Gech-567	8.537	11.057	3.342
16	Gech-568	9.488	7.851	4.452
17	Gech-566	6.139	8.131	4.711
18	Gech-570	7.292	6.243	5.328
19	Gech-571	4.657	8.791	3.633
20	Gech-572	7.128	2.323	7.98
21	Gech-573	6.775	7.246	5.782
22	Gech-374	7.748	0.971	8.766
23	Gech-578	5.283	5.674	5.295
24	Gech-579	5.856	2.438	7.223
25	Gech-206	10.81	3.714	7.87
26	Gech-581	4.136	5.899	7.341
27	Gech-997	8.876	3.722	9.682
28	Gech-995	6.865	9.463	10.14
29	Gech-633	4.368	13.015	2.946
30	Gech-634	9.227	3.522	6.348
31	TNEf-190	13	7.703	4.216
32	TNEf-191	7.955	0.761	9.631
33	TNEf-192	8.372	0.477	8.543
34	TNEf-193	11.612	5.864	8.537
35	TNEf-194	10.029	8.875	3.463
36	TNEf-195	10.58	1.12	8.753
37	TNEf-196	7.056	4.011	9.506

38	TNEf-197	4.506	0.824	8.462
39	TNEf-198	7.218	2.899	7.302
40	TNEf-199	12.955	9.244	13.684
41	TNEf-200	5.465	3.245	7.604
42	TNEf-201	1.957	5.771	9.192
43	TNEf-202	9.821	1.178	6.593
44	TNEf-203	8.739	-1.358	6.474
45	TNEf-204	6.269	-0.664	8.218
46	TNEf-205	13.451	3.924	8.746
47	TNEf-206	5.075	2.972	7.818
48	TNEf-207	8.236	1.036	5.426
49	TNEf-208	12.432	8.324	10.1
50	TNEf-209	13.878	4.078	6.856
51	TNEf-210	6.454	3.584	6.496
52	TNEf-211	14.943	7.961	7.961
53	TNEf-212	10.781	3.091	9.663
54	TNEf-213	11.931	3.239	9.512
55	TNEf-214	16.194	12.923	11.406
56	TNEf-215	15.74	6.724	10.987
57	TNEf-216	4.806	4.074	6.465
58	TNEf-217	-1.178	9.54	9.022
59	TNEf-218	8.693	5.406	8.2
60	TNEf-219	7.336	2.049	5.76
61	BMNDL-1	7.827	4.863	7.876
62	BMNDL-2	7.838	3.764	5.07
63	BMNDL-3	12.781	3.813	7.165
64	TNEf-318	3.498	8.382	4.284

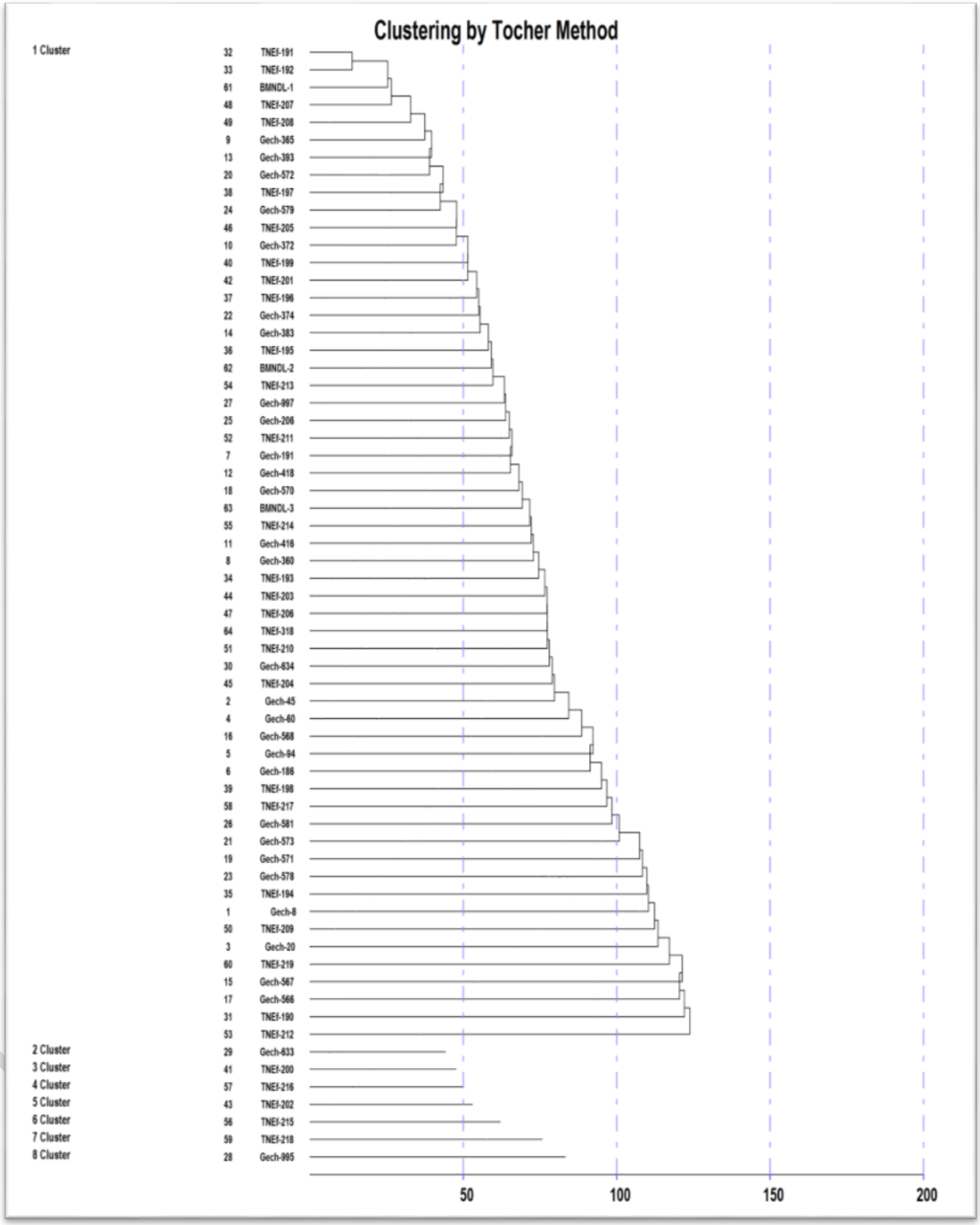

Fig .1. Clustering pattern of 64 barnyard millet germplasm accessions by Torchers method

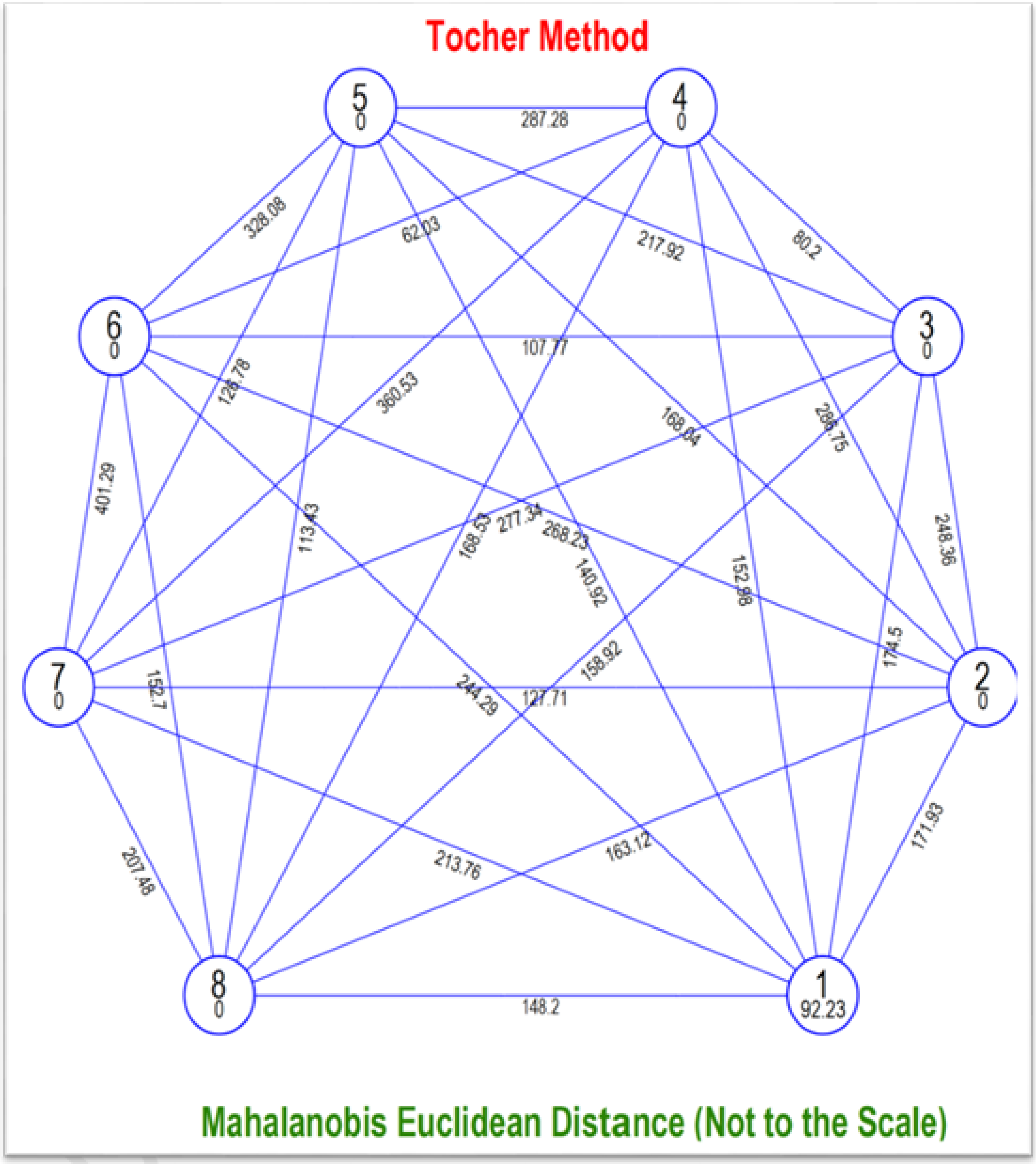

Fig .2. Cluster diagram showing average intra and inter cluster distances

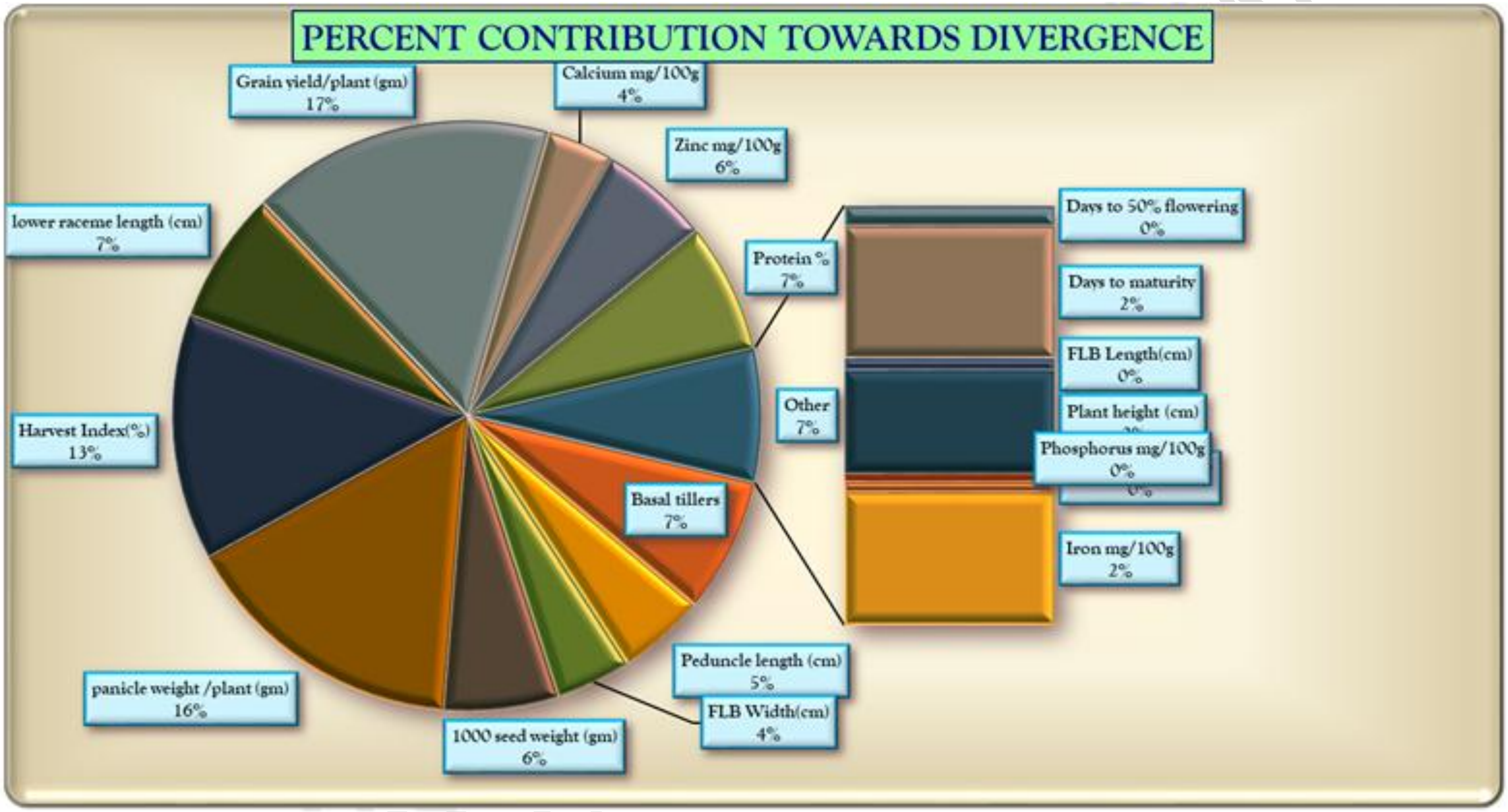

Fig .3. **Relative contribution of 18 characters to total genetic diversity in 64 barnyard millet germplasm accession**

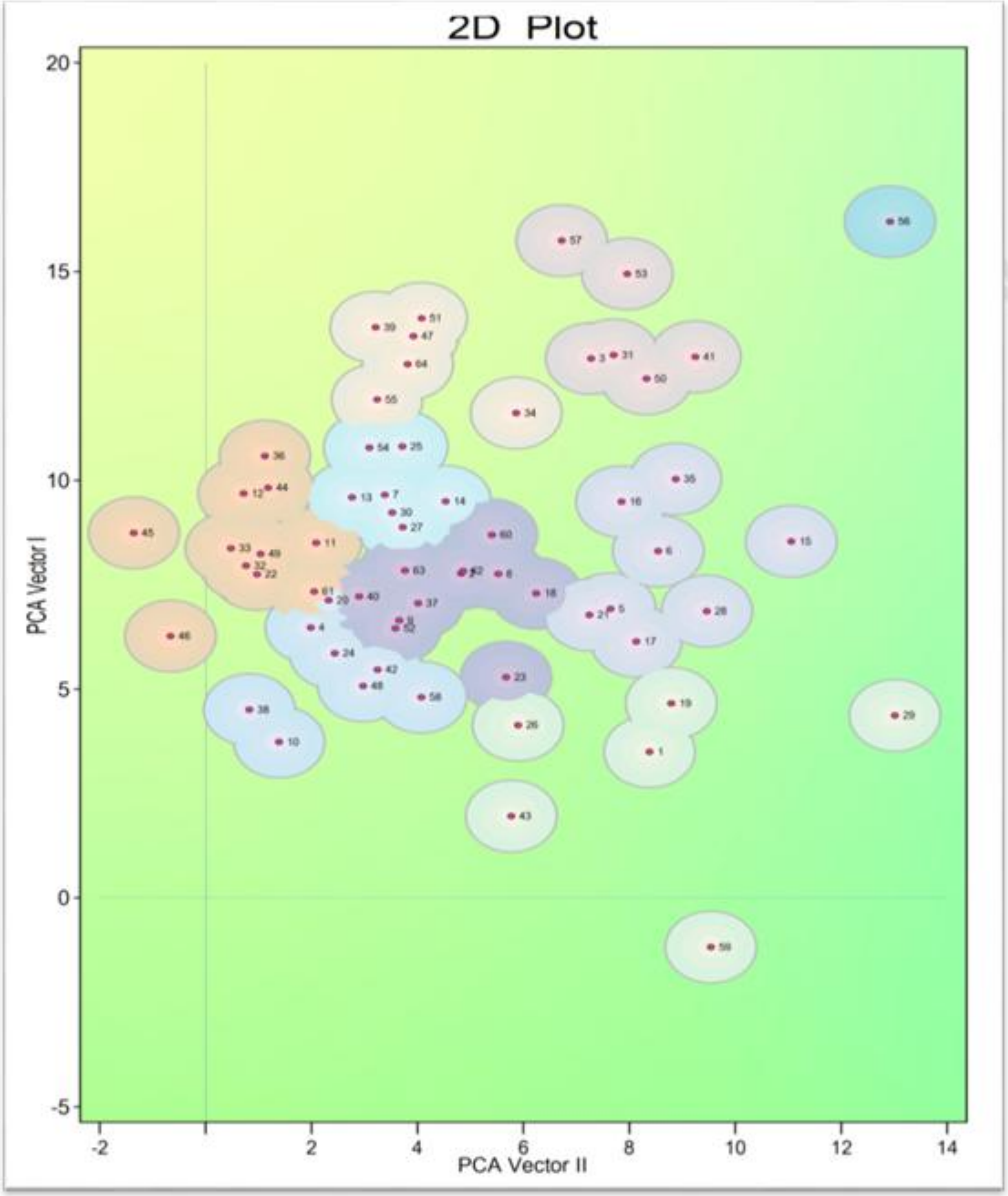

Fig 4. Two dimensional (2D) graph showing relative positions of 64 barnyard millet germplasm based on PCA scores

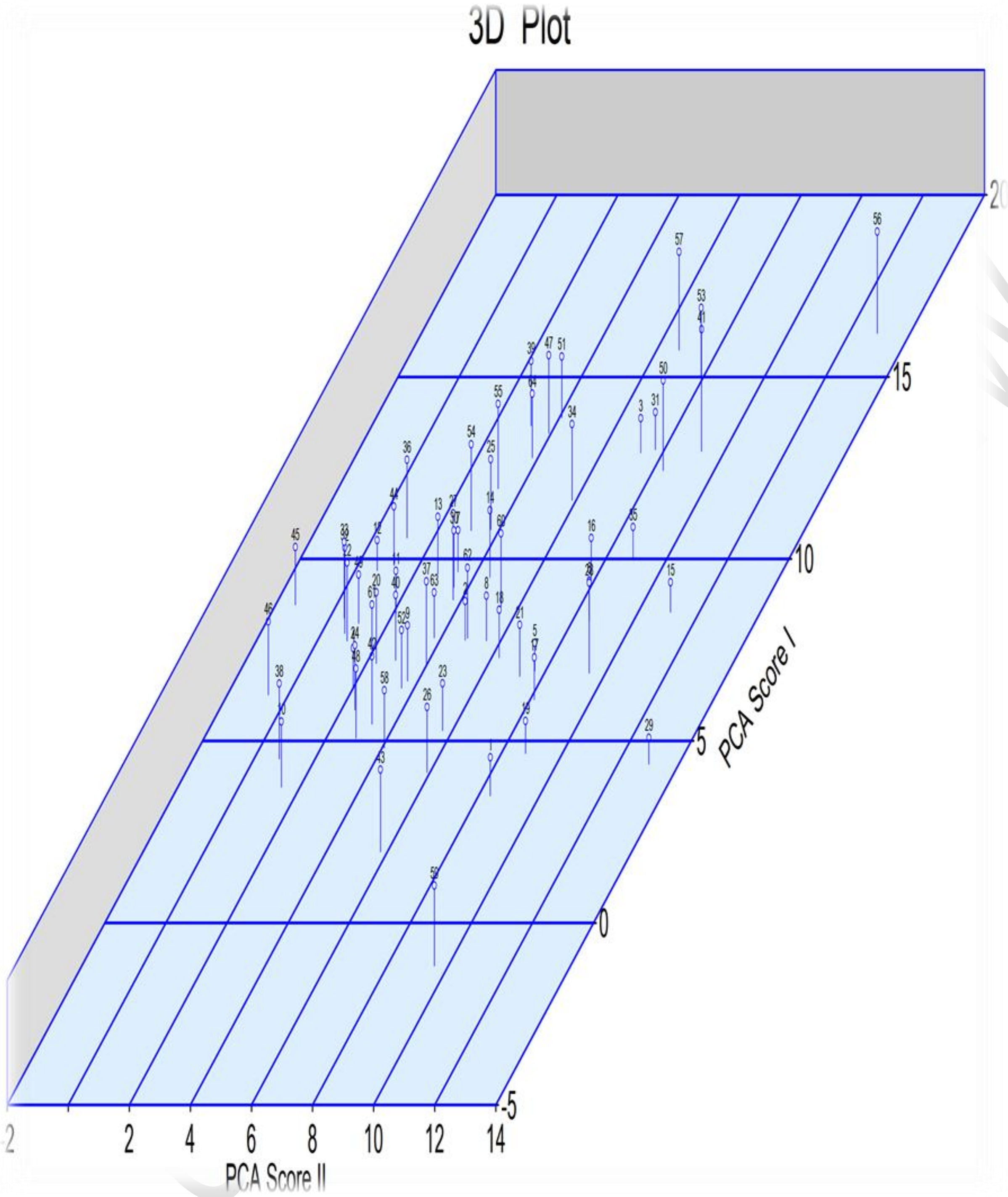

Fig 5. Three dimensional (3D) graph showing relative positions of 64 barnyard millet germplasm based on PCA score

Annexure I. Details of the 64 Indian barnyard millet genetic resources utilized for study

S.NO	Germplasm accession	Parentage/ Collection/Source
1	GEch-8	Dholi
2	GEch-45	Dholi
3	GEch-20	Dholi
4	GEch-60	NBPGR DS 67/82/22-2-83 (From GE ch 751)
5	GEch-94	Dholi
6	GEch-186	Almora
7	GEch-191	Almora
8	GEch-360	Almora
9	GEch-365	Almora
10	GEch-372	Almora
11	GEch-416	Almora
12	GEch-418	NBPGR Bihar (from GE ch 759)
13	GEch-393	Almora
14	GEch-383	Almora
15	GEch-567	Bihar
16	GEch-568	Bihar
17	GEch-566	Orissa
18	GEch-570	Orissa
19	GEch-571	Orissa
20	GEch-572	Orissa
21	GEch-573	Orissa
22	GEch-374	Almora
23	GEch-578	Rewa
24	GEch-579	Rewa
25	GEch-206	Almora
26	GEch-581	Rewa
27	GEch-997	India
28	GEch-995	India
29	GEch-633	Madhya Pradesh, Rewa
30	GEch-634	Madhya Pradesh, Rewa

31	TNEf-190	TNAU, Athiyandal
32	TNEf-191	TNAU, Athiyandal
33	TNEf-192	TNAU, Athiyandal
34	TNEf-193	TNAU, Athiyandal
35	TNEf-194	TNAU, Athiyandal
36	TNEf-195	TNAU, Athiyandal
37	TNEf-196	TNAU, Athiyandal
38	TNEf-197	TNAU, Athiyandal
39	TNEf-198	TNAU, Athiyandal
40	TNEf-199	TNAU, Athiyandal
41	TNEf-200	TNAU, Athiyandal
42	TNEf-201	TNAU, Athiyandal
43	TNEf-202	TNAU, Athiyandal
44	TNEf-203	TNAU, Athiyandal
45	TNEf-204	TNAU, Athiyandal
46	TNEf-205	TNAU, Athiyandal
47	TNEf-206	TNAU, Athiyandal
48	TNEf-207	TNAU, Athiyandal
49	TNEf-208	TNAU, Athiyandal
50	TNEf-209	TNAU, Athiyandal
51	TNEf-210	TNAU, Athiyandal
52	TNEf-211	TNAU, Athiyandal
53	TNEf-212	TNAU, Athiyandal
54	TNEf-213	TNAU, Athiyandal
55	TNEf-214	TNAU, Athiyandal
56	TNEf-215	TNAU, Athiyandal
57	TNEf-216	TNAU, Athiyandal
58	TNEf-217	TNAU, Athiyandal

59	TNEf-218	TNAU, Athiyandal
60	TNEf-219	TNAU, Athiyandal
61	BMNDL-1	Nandyal local
62	BMNDL-2	PLS from local
63	BMNDL-3	PLS from local
64	TNEf-318	TNAU, Athiyandal

Acknowledgment

The authors are highly thankful to Acharya N.G. Ranga Agricultural University, Guntur, Andhra Pradesh, India for providing barnyard millet genetic resources and assistance for the conduct of experiment.

References

Amarnath, K., Prasad, A.D. and Reddy, C.C.M., 2019. Assessment of genetic diversity in Indian Italian millet genetic resources [Setaria Italica (L.) Beauv]. *Electronic Journal of Plant Breeding*, *10*(1), pp.83-91.

Bandyopadhyay, B.B., 2009. Evaluation of barnyard millet cultivars for fodder yield under single and double cut treatments at higher elevation of hills. *Agricultural Science Digest*, *29*(1), pp.66-68.

Brunda, S.M., Kamatar, M.Y., Naveenkumar, K.L., Hundekar, R. 2015 Genetic diversity in the foxtail millet (*Setaria italica*) germplasm as determined by phonotypical traits. *The Ecoscan*. 8: 483-488.

Devaliya, S.D., Singh, M and Intawala, C.G. 2017. Genetic divergence studies in finger millet (*Eleusine coracana* (L.) Gaertn.). *International Journal of Current Microbiology and Applied Sciences*. 6(11): 2017-2022.

Gopikrishnan, A., Pandiyan, M., Thilagam, P., Veeramani, P. and Nanthakumar, S., 2021. Characterization of little millet (Panicum sumatrense) genetic diversity in yelagiri hills of Tamil Nadu. *Indian Journal of Plant Genetic Resources*, *34*(01), pp.59-63.

ICAR- Indian Institute of Millets Research. 2018. Annual Report: 2017-18. Rajendranagar, Hyderabad. pp. 11-13.

Kavya, P., Sujatha, M., Pandravada, S.R and Hymavathi, T.V. 2016. Exploiting genetic divergence in italian millet [*Setaria italica* (L.) P. Beauv.] elite germplasm lines: a neglected and a underutilised crop. *Environment and Ecology*. 35(3C): 2312-2315.

Kumari, S and Singh, S.K. 2015. Assessment of genetic diversity in promising finger millet (*Eleusine coracana* (L.) Gaertn) genotypes. *The Bioscan*. 10(2):825-830.

Kumar, D., Tyagi, V., Ramesh, B. and Pal, S., 2010. Genetic diversity in finger millet (Eleusine coracana L.). *Crop improvement*, *37*(1), pp.25-28.

Manimekalaia, M., M. Dhasarathanb, M., A. Karthikeyanb, A., Murukarthickc, Renganathana, V.G., Thangaraja, K., Vellaikumarb, S., Vanniarajana, C and Senthilb, N. 2018. Genetic diversity in the barnyard millet (*Echinochola frumentacea*) germplasms revealed by morphological traits and simple sequence repeat markers. *Current Plant Biology*. 14 (2018) 71–78.

Mahanthesha, M., Sujatha, M., Pandravada, S.R. and Meena, A.K. 2017. Study of genetic divergence in finger millet (*Eleusine coracana* (L.) Gaertn) germplasm. *International Journal of Pure and Applied Bioscience*. 5 (3):373-377.

Mehta, H., Tyagi, P.C. and Mohapatra, K.P., 2005. Genetic diversity in barnyard millet (Echinochloa frumentacea Roxb.). *Indian Journal of Genetics and Plant Breeding*, *65*(04), pp.293-295.

Murugan, R. and Nirmala kumari, A. 2006. Genetic divergence in italian millet. (Setaria italica (L.) Beauv). *Indian Journal of Genetics*. 66(4): 339- 340.

Prabu, R., Vanniarajan, C., Vetrivanthan, M., Gnanamalar, R.P., Shanmughasundaram, R and Ramalingam, J.2020. Association studies in barnyard millet (Echinochloa frumentacea (Roxb.) Link) for early maturity and yield contributing traits at high altitude region. *Electronic Journal of Plant Breeding*. Vol 11(1) :192-196 (2020).

Rao C. R. 1952. Advanced Statistical Methods in Biometrical Research, Ed. I, John Wiley and Sons, NelV York.

Sood, S., Khulbe, R.K., Kumar, A., Agrawal, P.K. and Upadhyaya, H.D., 2015. Barnyard millet global core collection evaluation in the submontane Himalayan region of India using multivariate analysis. *The Crop Journal*, *3*(6), pp.517-525.

Ugare R, Chimmad B, Naik R, Bharati P, Itagi S. Glycemic Index & Significance of Barnyard Millet (Echinochloa frumentacea) in type II Diabetics. Journal of Food Science and Technology, 2014, 51(2).

Watanabe, M., 1999. Antioxidative phenolic compounds from Japanese barnyard millet (Echinochloa utilis) grains. *Journal of Agricultural and Food Chemistry*, *47*(11), pp.4500-4505.