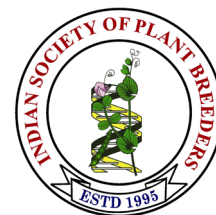# Electronic Journal of Plant Breeding

Research Article

A multivariate approach to assess the genetic diversity in finger millet [*Eleusine coracana* (L.) Gaertn.] germplasm accessions

T. E. Nagaraja[1*], Sujata Bhat[2], C. Nandini[3], H. S. Saritha[4] and S. Gazala Parveen[5]

[1]ICAR-AICRP on Small Millets, ZARS, University of Agricultural Sciences, GKVK, Bengaluru, India,560065
*E-Mail: tenagaraja@gmail.com

Abstract
Finger millet [*Eleusine coracana* (L.) Gaertn.], a staple cereal amongst the rural population of large parts of Africa and South Asia. It is well-known for its nutritional status, especially abundant quantities of iron and calcium. Despite these advantages, finger millet is far from extensive conventional crop improvement programs. To popularize finger millet production and increase its productivity, primarily, the characterization of its germplasm is crucial. In the present study, 587 finger millet genotypes collected from different sources were analyzed for various estimates of genetic variability parameters, genetic divergence through K-means clustering followed by principal component analysis (PCA). The analysis of variance revealed substantial amount of genetic variability for the seven quantitative traits among 587 finger millet germplasm accessions. The genotypes were classified into two clusters following K-means clustering algorithm. The cluster I had higher number of genotypes (343) than cluster II (244). Thus, the grouping of accessions shall be of practical value to finger millet researchers to select and tap the genetic potential of elite accessions from different clusters as donor parentsin crossing programs. Based on PCA, three principal components (PC) with eigen values greater than one contributed 72.55% of the total variability. The PC1 accounted highest proportion of total variance (40.82 %), followed by PC2, PC3, PC4, PC5, PC6 and PC7that revealed 16.74 %, 14.98 %, 11.06 %, 9.19 %, 7.12% and 0.06 % variation, respectively.

Keywords: Finger millet, Summary statistics, Phenotypic Correlation, Principal Component Analysis, K-means cluster.

INTRODUCTION

Finger millet (*Eleusin ecoracana*(L.) Gaertn.), familiar as ragi in India, rapoko in South Africa and dagusa in Ethiopia (Ignacimuthu and Ceasar, 2012) is an allotetraploid crop (2n=4x=36) derived from *E. coracana* subsp. *africana*. Due to the appearance of the"finger-like" branching of the panicle, it is referred as finger millet. It was domesticated 5000 years ago in western Uganda and Ethiopian highlands (Mehra 1963; Hilu and deWet 1976; Hilu *et al.*, 1979). It is a popular staple food crop among rural population. It has gained popularity as an agronomically sustainable crop, due to ease of cultivation in degraded land with sparse inputs and immense capacity to withstand drought and saline conditions (Dida *et al.*, 2008).

Finger millet accounts for12% of the global millet area and is grown in >25 countries in Eastern and Southern Africa and across Asia from the near East to the far East. The major finger millet-producing countries are Uganda, India, Nepal and China (www.cgiar.org/our-research/crop-factsheets/millets/). It is grown across India, in an area of 890.94 hectares with a production of 1238.70 tonnes and 1390 kg/ha productivity (Indiastat, 2019).

Considering the nutritional profile, finger millet is regarded as a "Super Cereal" with ample of minerals and micronutrients (National Research Council, 1996; Sood *et al.,* 2017; Kumar *et al.,* 2016). The calcium content present in finger millet is ten folds higher than that

of rice, wheat and maize (Kurien *et al.,* 1959). Abundant quantities of iron and fiberare also present. By virtue of possessing low glycemic index (GI), it is a popular diabetic diet (Chandrasekara and Shahidi, 2010). Due to its ability to thrive well in poor soil, low rainfall conditions without affecting its nutrition status it is regarded as a climate-smart crop.

Any crop improvement program primarily relies on the genetic resources available for the crop in question. Its progress is determined by the amplitude of genetic variability available in the germplasm. For this, evaluation of germplasm for various quantitative/qualitative traits to identify the sources of desirable genes is essential. The data generated from such characterization/evaluation studies is used to ascertain the patterns of genetic variability along with the genetic relationships among germplasm collections. The multivariate hierarchical cluster analysis helps in grouping the genotypes based on similarity, while the principal component analysis (PCA) assesses the genetic diversity pattern obtained by clustering. In this view, the current study characterized 587 finger millet germplasm accessions for seven quantitative traits to understand their association *via* PCA and cluster analysis that shall assist in classifying the available germplasm into distinct groups on the basis of the extent of diversity. This information shall be of use to recognize finger millet genotypes that shall help to wide nits genetic pool and initiate further genetic refinement programs.

MATERIALS AND METHODS

Experimental material: The experimental material for the current investigation consisted of 587 (584 accessions + 3 checks) finger millet germplasm accessions (**Table 1**) representing collections across India, Uganda, Ethiopia, Kenya, Tanzania, Zimbabwe, Mozambique and Mexico (**Table 2**) that are maintained at National Active Germplasm Site, Project Coordinating Unit, All India Coordinated Research Project (AICRP) on Small Millets, University of Agricultural Sciences, GKVK, Bangalore.

Evaluation of experimental material: This study was executed at Zonal Agricultural Research Station (ZARS), University of Agricultural Sciences, GKVK, Bangalore located at 13⁰ 05" N latitude and 77⁰ 34" E longitude, during *Kharif*-2018. The location is at an altitude of 924 meters above mean sea level. The 584 germplasm accessions were sown in 13 blocks in augmented design (Federer, 1961); each block consisted of 45 accessions (except the last block that had 44 genotypes) and 3 standard checks (GPU 45, GPU 67 and PR 202). Each accession was sown in single row of 3m length spaced 30cm apart. The proposed package of practice was followed to raise a healthy crop. Five plants were indiscriminately selected to record observations on days to 50% flowering, days to maturity, plant height (cm), number of productive tillers, main ear length(cm), number of fingers per ear and grain yield per plant (g).

Table 1. List of 587 finger millet germplasm accessions used in the current study

Code	Genotypes	Code	Genotypes	Code	Genotypes	Code	Genotypes
1	GE 474	148	GE 4868	295	GE 5155	442	GE 5915
2	GE 4657	149	GE 4871	296	GE 5159	443	GE 5916
3	GE 4667	150	GE 4872	297	GE 5700	444	GE 5917
4	GE 4668	151	GE 4873	298	GE 5702	445	GE 5920
5	GE 4669	152	GE 4875	299	GE 5704	446	GE 5922
6	GE 4670	153	GE 4876	300	GE 5705	447	GE 5923
7	GE 4671	154	GE 4877	301	GE 5706	448	GE 5924
8	GE 4672	155	GE 4878	302	GE 5707	449	GE 5925
9	GE 4673	156	GE 4879	303	GE 5708	450	GE 5926
10	GE 4677	157	GE 4883	304	GE 5710	451	GE 5927
11	GE 4678	158	GE 4884	305	GE 5711	452	GE 5928
12	GE 4679	159	GE 4885	306	GE 5712	453	GE 5929
13	GE 4680	160	GE 4887	307	GE 5716	454	GE 5930
14	GE 4682	161	GE 4888	308	GE 5717	455	GE 5931
15	GE 4684	162	GE 4889	309	GE 5718	456	GE 5933
16	GE 4685	163	GE 4890	310	GE 5721	457	GE 5934
17	GE 4687	164	GE 4891	311	GE 5722	458	GE 5935
18	GE 4688	165	GE 4895	312	GE 5724	459	GE 5936
19	GE 4690	166	GE 4896	313	GE 5726	460	GE 5938

Table 1. Continued..

Code	Genotypes	Code	Genotypes	Code	Genotypes	Code	Genotypes
20	GE 4691	167	GE 4897	314	GE 5727	461	GE 5939
21	GE 4692	168	GE 4898	315	GE 5728	462	GE 5940
22	GE 4693	169	GE 4900	316	GE 5730	463	GE 5942
23	GE 4694	170	GE 4901	317	GE 5732	464	GE 5943
24	GE 4696	171	GE 4902	318	GE 5733	465	GE 5944
25	GE 4697	172	GE 4904	319	GE 5741	466	GE 5945
26	GE 4698	173	GE 4906	320	GE 5742	467	GE 5946
27	GE 4701	174	GE 4907	321	GE 5743	468	GE 5947
28	GE 4702	175	GE 4908	322	GE 5747	469	GE 5948
29	GE 4703	176	GE 4909	323	GE 5751	470	GE 5949
30	GE 4704	177	GE 4911	324	GE 5752	471	GE 5951
31	GE 4706	178	GE 4912	325	GE 5753	472	GE 5952
32	GE 4709	179	GE 4924	326	GE 5754	473	GE 5953
33	GE 4710	180	GE 4925	327	GE 5755	474	GE 5954
34	GE 4711	181	GE 4926	328	GE 5756	475	GE 5957
35	GE 4712	182	GE 4929	329	GE 5757	476	GE 5958
36	GE 4714	183	GE 4930	330	GE 5758	477	GE 5959
37	GE 4715	184	GE 4932	331	GE 5759	478	GE 5960
38	GE 4717	185	GE 4933	332	GE 5760	479	GE 5964
39	GE 4718	186	GE 4934	333	GE 5761	480	GE 5965
40	GE 4719	187	GE 4935	334	GE 5762	481	GE 5969
41	GE 4720	188	GE 4937	335	GE 5763	482	GE 5972
42	GE 4722	189	GE 4938	336	GE 5764	483	GE 5973
43	GE 4724	190	GE 4940	337	GE 5766	484	GE 5974
44	GE 4725	191	GE 4941	338	GE 5767	485	GE 5978
45	GE 4726	192	GE 4947	339	GE 5768	486	GE 5979
46	GE 4727	193	GE 4948	340	GE 5770	487	GE 5983
47	GE 4728	194	GE 4951	341	GE 5771	488	GE 5989
48	GE 4729	195	GE 4954	342	GE 5772	489	GE 5990
49	GE 4731	196	GE 4955	343	GE 5773	490	GE 5991
50	GE 4732	197	GE 4956	344	GE 5774	491	GE 5992
51	GE 4733	198	GE 4958	345	GE 5775	492	GE 6004
52	GE 4735	199	GE 4959	346	GE 5776	493	GE 6005
53	GE 4736	200	GE 4960	347	GE 5777	494	GE 6006
54	GE 4737	201	GE 4964	348	GE 5778	495	GE 6007
55	GE 4738	202	GE 4966	349	GE 5779	496	GE 6009
56	GE 4740	203	GE 4967	350	GE 5780	497	GE 6010
57	GE 4743	204	GE 4969	351	GE 5781	498	GE 6012
58	GE 4745	205	GE 4971	352	GE 5782	499	GE 6013
59	GE 4746	206	GE 4972	353	GE 5783	500	GE 6014
60	GE 4748	207	GE 4973	354	GE 5784	501	GE 6015
61	GE 4749	208	GE 4974	355	GE 5785	502	GE 6017
62	GE 4750	209	GE 4975	356	GE 5786	503	GE 6018
63	GE 4751	210	GE 4977	357	GE 5787	504	GE 6021
64	GE 4753	211	GE 4978	358	GE 5788	505	GE 6022
65	GE 4754	212	GE 4979	359	GE 5790	506	GE 6023

Table 1. Continued..

Code	Genotypes	Code	Genotypes	Code	Genotypes	Code	Genotypes
66	GE 4756	213	GE 4981	360	GE 5791	507	GE 6024
67	GE 4758	214	GE 4982	361	GE 5793	508	GE 6025
68	GE 4760	215	GE 4986	362	GE 5794	509	GE 6027
69	GE 4761	216	GE 4987	363	GE 5795	510	GE 6028
70	GE 4764	217	GE 4989	364	GE 5796	511	GE 6029
71	GE 4770	218	GE 4990	365	GE 5797	512	GE 6030
72	GE 4771	219	GE 4991	366	GE 5799	513	GE 6031
73	GE 4772	220	GE 4992	367	GE 5800	514	GE 6032
74	GE 4774	221	GE 4993	368	GE 5801	515	GE 6033
75	GE 4775	222	GE 4994	369	GE 5802	516	GE 6034
76	GE 4776	223	GE 4996	370	GE 5806	517	GE 6035
77	GE 4777	224	GE 4997	371	GE 5807	518	GE 6037
78	GE 4778	225	GE 4998	372	GE 5808	519	GE 6038
79	GE 4781	226	GE 5000	373	GE 5809	520	GE 6039
80	GE 4782	227	GE 5003	374	GE 5811	521	GE 6041
81	GE 4784	228	GE 5004	375	GE 5812	522	GE 6042
82	GE 4785	229	GE 5006	376	GE 5813	523	GE 6043
83	GE 4786	230	GE 5007	377	GE 5814	524	GE 6044
84	GE 4790	231	GE 5008	378	GE 5815	525	GE 6045
85	GE 4792	232	GE 5010	379	GE 5816	526	GE 6046
86	GE 4793	233	GE 5012	380	GE 5818	527	GE 6048
87	GE 4794	234	GE 5013	381	GE 5819	528	GE 6049
88	GE 4795	235	GE 5015	382	GE 5820	529	GE 6050
89	GE 4796	236	GE 5017	383	GE 5822	530	GE 6051
90	GE 4797	237	GE 5018	384	GE 5823	531	GE 6052
91	GE 4799	238	GE 5019	385	GE 5825	532	GE 6053
92	GE 4801	239	GE 5020	386	GE 5826	533	GE 6054
93	GE 4802	240	GE 5021	387	GE 5827	534	GE 6055
94	GE 4803	241	GE 5023	388	GE 5830	535	GE 6056
95	GE 4804	242	GE 5025	389	GE 5834	536	GE 6057
96	GE 4805	243	GE 5027	390	GE 5835	537	GE 6058
97	GE 4806	244	GE 5028	391	GE 5838	538	GE 6059
98	GE 4807	245	GE 5029	392	GE 5839	539	GE 6061
99	GE 4808	246	GE 5030	393	GE 5842	540	GE 6062
100	GE 4809	247	GE 5031	394	GE 5843	541	GE 6063
101	GE 4810	248	GE 5032	395	GE 5844	542	GE 6064
102	GE 4811	249	GE 5033	396	GE 5845	543	GE 6066
103	GE 4812	250	GE 5034	397	GE 5846	544	GE 6067
104	GE 4813	251	GE 5036	398	GE 5847	545	GE 6080
105	GE 4815	252	GE 5037	399	GE 5848	546	GE 6142
106	GE 4817	253	GE 5038	400	GE 5849	547	GE 6228
107	GE 4820	254	GE 5039	401	GE 5850	548	GE 6252
108	GE 4821	255	GE 5040	402	GE 5851	549	GE 6288
109	GE 4822	256	GE 5041	403	GE 5852	550	GE 6295
110	GE 4823	257	GE 5049	404	GE 5853	551	GE 6298
111	GE 4824	258	GE 5050	405	GE 5854	552	GE 6307

Table 1. Continued..

Code	Genotypes	Code	Genotypes	Code	Genotypes	Code	Genotypes
112	GE 4825	259	GE 5056	406	GE 5855	553	GE 6309
113	GE 4826	260	GE 5069	407	GE 5856	554	GE 6322
114	GE 4827	261	GE 5074	408	GE 5857	555	GE 6324
115	GE 4828	262	GE 5078	409	GE 5859	556	GE 6327
116	GE 4829	263	GE 5079	410	GE 5860	557	GE 6331
117	GE 4830	264	GE 5087	411	GE 5861	558	GE 6341
118	GE 4831	265	GE 5091	412	GE 5862	559	GE 6364
119	GE 4832	266	GE 5093	413	GE 5863	560	GE 6375
120	GE 4833	267	GE 5094	414	GE 5865	561	GE 6389
121	GE 4834	268	GE 5095	415	GE 5868	562	GE 6407
122	GE 4835	269	GE 5096	416	GE 5878	563	GE 6413
123	GE 4837	270	GE 5097	417	GE 5879	564	GE 6416
124	GE 4838	271	GE 5098	418	GE 5882	565	GE 6475
125	GE 4839	272	GE 5099	419	GE 5884	566	GE 6484
126	GE 4840	273	GE 5103	420	GE 5886	567	GE 6486
127	GE 4841	274	GE 5104	421	GE 5888	568	GE 6487
128	GE 4843	275	GE 5105	422	GE 5889	569	GE 6488
129	GE 4845	276	GE 5112	423	GE 5890	570	GE 6489
130	GE 4846	277	GE 5116	424	GE 5891	571	GE 6490
131	GE 4848	278	GE 5118	425	GE 5892	572	GE 6491
132	GE 4849	279	GE 5123	426	GE 5894	573	GE 6492
133	GE 4852	280	GE 5124	427	GE 5895	574	GE 6493
134	GE 4853	281	GE 5126	428	GE 5898	575	GE 6494
135	GE 4854	282	GE 5127	429	GE 5901	576	GE 6495
136	GE 4855	283	GE 5131	430	GE 5902	577	GE 6497
137	GE 4856	284	GE 5132	431	GE 5904	578	GE 6498
138	GE 4857	285	GE 5134	432	GE 5905	579	GE 6499
139	GE 4858	286	GE 5135	433	GE 5906	580	GE 6500
140	GE 4859	287	GE 5137	434	GE 5907	581	GE 6503
141	GE 4860	288	GE 5138	435	GE 5908	582	GE 6504
142	GE 4861	289	GE 5139	436	GE 5909	583	GE 6505
143	GE 4862	290	GE 5140	437	GE 5910	584	GE 6509
144	GE 4863	291	GE 5141	438	GE 5911	585	GPU 67
145	GE 4865	292	GE 5142	439	GE 5912	586	GPU 45
146	GE 4866	293	GE 5146	440	GE 5913	587	PR 202
147	GE 4867	294	GE 5150	441	GE 5914		

Statistical analysis: Summary statistics was estimated using Microsoft Excel. The analysis of variance (ANOVA) was performed for all the seven quantitative traits (Federer and Raghavarao, 1975). Estimates of genetic variability were obtained for all the seven traits. The PCA was computed to find out the relative importance of different traits in capturing the variation in entire germplasm. The data obtained was also disposed for K-means clustering. The analysis was performed in R software *version* 4.0.2.

RESULTS AND DISCUSSION

Analysis of variance: The data obtained on seven quantitative traits from 587 finger millet germplasm accessions was used for analysis of variance. Presence of sufficient genetic variability in the accessions was confirmed by significant differences obtained for all the traits evaluated (**Table 3**). A successful plant breeding programme typically hinges on the presence of genetic variability, this aid in the identification and selection of desired genotypes.

Table 2. Details of the source of finger millet germplasm accessions used in the study

Source	Number of accessions
Uganda	26
Kenya	76
Malawi	61
Ethiopia	16
Zambia	50
Zimbabwe	45
Mozambique	1
Tanzania	12
Mexico	3
India	268
Unkown	29
Total	**587**

Table 3. Analysis of variance of the quantitative traits evaluated in 587 finger millet germplasm accessions

Trait	Blocks (eliminating treatments)	Treatment (eliminating blocks)	Residuals
Degrees of freedom	12	586	33
Days to 50% flowering	1740.09**	68.37**	0.00
Days to maturity	1736.60**	65.97**	0.00
Number of productive tillers	0.76**	4.81**	0.00
Plant height (cm)	361.44**	1344**	0.00
Main ear length (cm)	3.39**	0.12**	0.00
Number of fingers /ear	1.18**	5.44**	0.00
Grain yield/plant (g)	33.41**	14.39**	0.00

Genetic variability parameters: The traits' mean and range of the finger millet accessions showed considerable differences, signifying the genotypes used in the current study are genetically diverse (**Fig. 1 and Table 4**).Similar results for summary statistics of various traits were reported in previous studies on finger millet genotypes (Kebere *et al.,* 2006; Nirmalakumari *et al.,* 2010; Ganapathy *et al.,* 2011; Shinde *et al.,* 2014). The accessions are highly variable for number of productive tillers, main ear length and grain yield/plant as stipulated by estimates of PCV (>20%; **Table 4**). All the traits possessed higher broad sense heritability (> 60%) except days to maturity (52.39 %; **Table 4**). The traits *viz*., number of productive tillers, main ear length and grain yield/plant expressed higher estimates GCV and broad sense heritability, compared to other traits, implying a narrow influence of environment on the genes governing them. In this study, a combination of high heritability and high genetic advance estimates were obtained for grain yield/plant. Hence, indicating that the traits are regulated by additive gene action. Similarly, high GCV, heritability and GAM estimates were found for ear-heads/plant (John, 2006), grain yield/plant (Kadam *et al.,* 2010; and Dagnachew *et al.,* 2012), and ear-heads/plant (Andualem *et al.,* 2013).

Cluster analysis:The most popular approach to organize genotypes into contrasting categories is "K-means clustering". The average silhouette method indicated that the optimum number of clusters for the 587 finger millet genotypes evaluated for seven quantitative traits are two (**Fig. 2**; **Table 5**). Higher number of accessions were retained in cluster I (343) than cluster II (244). The traits' mean differences between clusters was significant (**Table 6**).The mean of number of productive tillers and grain yield/plant are higher and that of days to 50 % flowering and days to maturity are lower in cluster II compared to cluster I, indicating the suitability of this cluster II in deriving early flowering and high yielding finger millet accessions with early maturity. The differences between the two clusters were significant for traits' variances except for number of productive tillers, plant height and grain yield/plant (**Table 7**). The variances were higher for days to 50% flowering, days to maturity, number of productive tillers, plant height and grain yield/plant, indicating ample scope of selection for these traits in cluster II.

However, sufficient variability is indicated in the 587 finger millet germplasm accessions, the genotypes are grouped under only two clusters, this might be due to
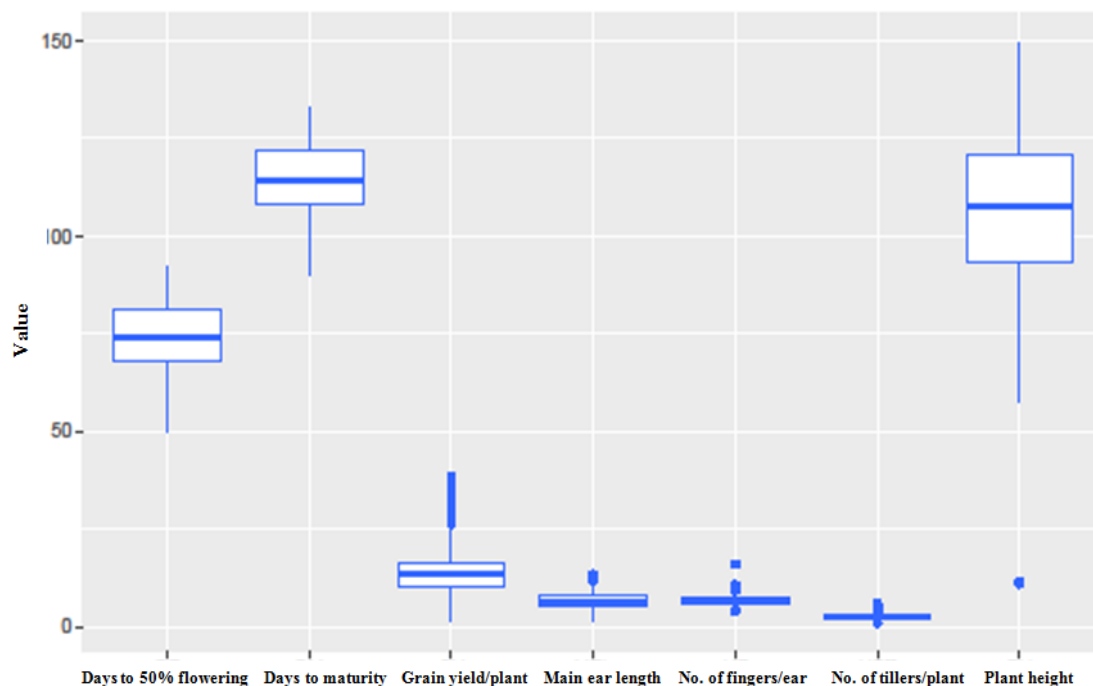
Fig. 1. Box-Whisker plot depicting the summary statistics of the seven quantitative traits evaluated in 587 finger millet germplasm accessions

Table 4. Summary statistics and estimates of genetic variability components for various quantitative traits evaluated in 587 finger millet germplasm accessions

Trait	Range		Mean±SE	GCV	PCV	h²b (%)	GA	GAM
	Minimum	Maximum						
Days to 50% flowering	50.00	92.00	73.17±0.40	13.26	13.14	75.23	20.01	27.35
Days to maturity	90.00	133.00	113.90±0.40	8.53	10.25	52.39	20.04	17.59
Number of productive tillers	1.00	6.00	2.37±0.03	32.38	30.28	78.36	1.58	66.80
Plant height (cm)	11.00	149.60	106.10±0.78	17.84	19.56	84.25	39.06	36.81
Main ear length (cm)	1.60	13.30	6.69±0.07	27.19	24.98	70.23	3.75	56.10
Number of fingers /ear	4.00	16.00	6.81±0.04	15.18	18.25	91.28	2.13	31.31
Grain yield/plant (g)	1.43	38.29	13.82±0.24	41.75	40.12	95.46	11.91	86.14

narrow genetic distance between them. Likewise, Karad and Patil (2013) grouped 65 finger millet genotypes into five groups based on twelve morphological traits. Patil *et al.*(2017) reported genetic divergence on 65 finger millet accessions and grouped them into five clusters. Previously, Anuradha *et al.*(2017) reported six clusters while studying 25 finger millet genotypes and described different ranges of eight morphological traits.

Inter- and intra- cluster distance: It is suggested that attempting crosses between genotypes belonging to different clusters results in heterotic combinations (Venkatesh *et al.,* 2014).But, exploitation of heterosis in finger millet which is highly self-pollinated is a

tedious task on commercial scale. Parents chosen from clusters with high inter-cluster distance are likely to yield worthwhile recombinants in the successive generations, that can be further bred as homozygous varieties. The intra-cluster heterogeneity of cluster II (22.10) was higher as compared to that of cluster I (20.07; **Table 8**). The inter-cluster distance (39.69) between cluster I and II was higher than intra-cluster distances, explaining the existence of a greater diversity between them.

Principle component analysis: Principal component analysis was effectuated to pinpoint the most contributing traits to the total variability. The PCA helps to strengthen the findings from the cluster analysis and exhibits the

Table 5. Clustering of 587 finger millet accessions into two clusters using 7 quantitative traits

Cluster	Number of genotypes	Name of the genotype
Cluster I	343	GE 474 GE 4657 GE 4667 GE 4668 GE 4669 GE 4670 GE 4671 GE 4672 GE 4673 GE 4677 GE 4678 GE 4680 GE 4682 GE 4684 GE 4685 GE 4687 GE 4688 GE 4692 GE 4693 GE 4694 GE 4696 GE 4697 GE 4698 GE 4701 GE 4702 GE 4703 GE 4706 GE 4709 GE 4710 GE 4711 GE 4712 GE 4714 GE 4715 GE 4717 GE 4718 GE 4719 GE 4720 GE 4722 GE 4724 GE 4725 GE 4726 GE 4727 GE 4728 GE 4729 GE 4731 GE 4732 GE 4733 GE 4735 GE 4736 GE 4737 GE 4738 GE 4740 GE 4743 GE 4745 GE 4746 GE 4748 GE 4749 GE 4750 GE 4751 GE 4753 GE 4754 GE 4756 GE 4758 GE 4760 GE 4761 GE 4764 GE 4770 GE 4771 GE 4772 GE 4774 GE 4775 GE 4776 GE 4777 GE 4778 GE 4781 GE 4782 GE 4784 GE 4785 GE 4786 GE 4790 GE 4792 GE 4793 GE 4794 GE 4796 GE 4797 GE 4799 GE 4801 GE 4802 GE 4803 GE 4804 GE 4805 GE 4806 GE 4807 GE 4808 GE 4809 GE 4810 GE 4811 GE 4812 GE 4813 GE 4815 GE 4817 GE 4820 GE 4821 GE 4822 GE 4823 GE 4824 GE 4825 GE 4826 GE 4827 GE 4828 GE 4829 GE 4830 GE 4831 GE 4832 GE 4833 GE 4834 GE 4835 GE 4837 GE 4838 GE 4839 GE 4840 GE 4841 GE 4843 GE 4845 GE 4846 GE 4848 GE 4849 GE 4852 GE 4853 GE 4854 GE 4855 GE 4856 GE 4857 GE 4859 GE 4860 GE 4861 GE 4862 GE 4863 GE 4865 GE 4866 GE 4867 GE 4868 GE 4871 GE 4872 GE 4873 GE 4875 GE 4876 GE 4877 GE 4878 GE 4879 GE 4883 GE 4884 GE 4885 GE 4888 GE 4889 GE 4890 GE 4891 GE 4895 GE 4896 GE 4897 GE 4898 GE 4900 GE 4901 GE 4902 GE 4904 GE 4906 GE 4907 GE 4908 GE 4909 GE 4911 GE 4912 GE 4924 GE 4925 GE 4926 GE 4929 GE 4930 GE 4933 GE 4934 GE 4937 GE 4938 GE 4940 GE 4941 GE 4947 GE 4948 GE 4951 GE 4954 GE 4955 GE 4956 GE 4958 GE 4960 GE 4964 GE 4966 GE 4967 GE 4969 GE 4972 GE 4974 GE 4975 GE 4977 GE 4978 GE 4979 GE 4981 GE 4982 GE 4986 GE 4987 GE 4989 GE 4990 GE 4991 GE 4992 GE 4993 GE 4994 GE 4996 GE 4997 GE 4998 GE 5000 GE 5003 GE 5004 GE 5010 GE 5012 GE 5013 GE 5015 GE 5019 GE 5025 GE 5027 GE 5028 GE 5030 GE 5032 GE 5033 GE 5034 GE 5036 GE 5079 GE 5087 GE 5091 GE 5093 GE 5094 GE 5095 GE 5096 GE 5097 GE 5098 GE 5099 GE 5112 GE 5116 GE 5118 GE 5123 GE 5124 GE 5126 GE 5127 GE 5131 GE 5132 GE 5134 GE 5137 GE 5139 GE 5140 GE 5141 GE 5142 GE 5146 GE 5150 GE 5155 GE 5159 GE 5702 GE 5704 GE 5705 GE 5722 GE 5727 GE 5728 GE 5730 GE 5732 GE 5733 GE 5752 GE 5762 GE 5771 GE 5772 GE 5784 GE 5785 GE 5787 GE 5794 GE 5795 GE 5796 GE 5797 GE 5799 GE 5800 GE 5801 GE 5802 GE 5806 GE 5807 GE 5809 GE 5811 GE 5812 GE 5814 GE 5815 GE 5816 GE 5818 GE 5822 GE 5823 GE 5834 GE 5835 GE 5844 GE 5847 GE 5849 GE 5850 GE 5851 GE 5855 GE 5856 GE 5862 GE 5882 GE 5901 GE 5902 GE 5904 GE 5905 GE 5909 GE 5910 GE 5911 GE 5912 GE 5913 GE 5914 GE 5916 GE 5922 GE 5923 GE 5928 GE 5930 GE 5934 GE 5936 GE 5940 GE 5983 GE 5989 GE 5990 GE 5991 GE 5992 GE 6005 GE 6023 GE 6024 GE 6025 GE 6029 GE 6295 GE 6298 GE 6331 GE 6364 GE 6375 GE 6407 GE 6413 GE 6416 GE 6505 GE 6509 PR 202

| Cluster	Number of genotypes	Name of the genotype					
Cluster II	244	GE 4679	GE 4690	GE 4691	GE 4704	GE 4795	GE 4858
		GE 4887	GE 4932	GE 4935	GE 4959	GE 4971	GE 4973
		GE 5006	GE 5007	GE 5008	GE 5017	GE 5018	GE 5020
		GE 5021	GE 5023	GE 5029	GE 5031	GE 5037	GE 5038
		GE 5039	GE 5040	GE 5041	GE 5049	GE 5050	GE 5056
		GE 5069	GE 5074	GE 5078	GE 5103	GE 5104	GE 5105
		GE 5135	GE 5138	GE 5700	GE 5706	GE 5707	GE 5708
		GE 5710	GE 5711	GE 5712	GE 5716	GE 5717	GE 5718
		GE 5721	GE 5724	GE 5726	GE 5741	GE 5742	GE 5743
		GE 5747	GE 5751	GE 5753	GE 5754	GE 5755	GE 5756
		GE 5757	GE 5758	GE 5759	GE 5760	GE 5761	GE 5763
		GE 5764	GE 5766	GE 5767	GE 5768	GE 5770	GE 5773
		GE 5774	GE 5775	GE 5776	GE 5777	GE 5778	GE 5779
		GE 5780	GE 5781	GE 5782	GE 5783	GE 5786	GE 5788
		GE 5790	GE 5791	GE 5793	GE 5808	GE 5813	GE 5819
		GE 5820	GE 5825	GE 5826	GE 5827	GE 5830	GE 5838
		GE 5839	GE 5842	GE 5843	GE 5845	GE 5846	GE 5848
		GE 5852	GE 5853	GE 5854	GE 5857	GE 5859	GE 5860
		GE 5861	GE 5863	GE 5865	GE 5868	GE 5878	GE 5879
		GE 5884	GE 5886	GE 5888	GE 5889	GE 5890	GE 5891
		GE 5892	GE 5894	GE 5895	GE 5898	GE 5906	GE 5907
		GE 5908	GE 5915	GE 5917	GE 5920	GE 5924	GE 5925
		GE 5926	GE 5927	GE 5929	GE 5931	GE 5933	GE 5935
		GE 5938	GE 5939	GE 5942	GE 5943	GE 5944	GE 5945
		GE 5946	GE 5947	GE 5948	GE 5949	GE 5951	GE 5952
		GE 5953	GE 5954	GE 5957	GE 5958	GE 5959	GE 5960
		GE 5964	GE 5965	GE 5969	GE 5972	GE 5973	GE 5974
		GE 5978	GE 5979	GE 6004	GE 6006	GE 6007	GE 6009
		GE 6010	GE 6012	GE 6013	GE 6014	GE 6015	GE 6017
		GE 6018	GE 6021	GE 6022	GE 6027	GE 6028	GE 6030
		GE 6031	GE 6032	GE 6033	GE 6034	GE 6035	GE 6037
		GE 6038	GE 6039	GE 6041	GE 6042	GE 6043	GE 6044
		GE 6045	GE 6046	GE 6048	GE 6049	GE 6050	GE 6051
		GE 6052	GE 6053	GE 6054	GE 6055	GE 6056	GE 6057
		GE 6058	GE 6059	GE 6061	GE 6062	GE 6063	GE 6064
		GE 6066	GE 6067	GE 6080	GE 6142	GE 6228	GE 6252
		GE 6288	GE 6307	GE 6309	GE 6322	GE 6324	GE 6327
		GE 6341	GE 6389	GE 6475	GE 6484	GE 6486	GE 6487
		GE 6488	GE 6489	GE 6490	GE 6491	GE 6492	GE 6493
		GE 6494	GE 6495	GE 6497	GE 6498	GE 6499	GE 6500
		GE 6503	GE 6504	GPU 67	GPU 45		
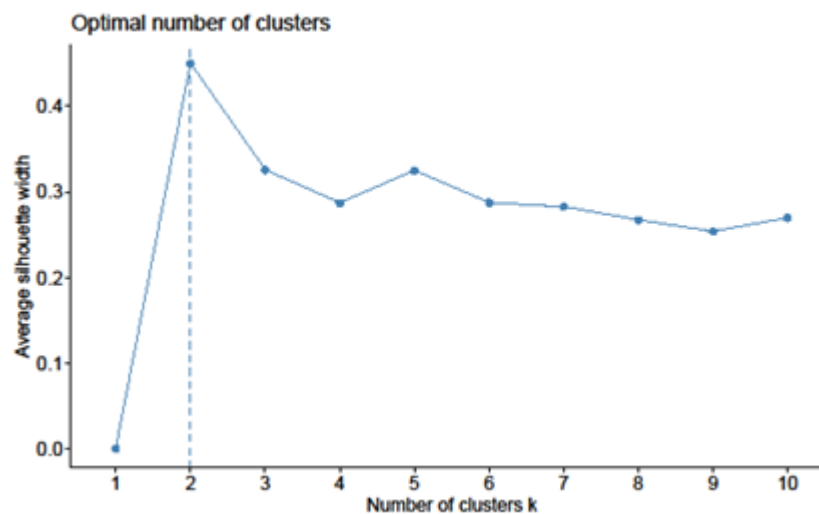
Fig. 2. Determination of optimum clusters by average silhouette method

Table 6. Comparison of the quantitative trait means between the two clusters

Trait	Cluster I	Cluster II	'T' statistic	Probability
Days to 50% flowering	78.58	65.58	21.28	0.00
Days to maturity	119.31	106.29	21.32	0.00
Number of productive tillers	2.23	2.56	-5.27	0.00
Plant height (cm)	118.73	88.34	31.52	0.00
Main ear length (cm)	7.39	5.68	12.64	0.00
Number of fingers/ear	6.95	6.60	4.12	0.00
Grain yield/plant (g)	12.15	13.94	3.71	0.00

Table 7. Comparison of the quantitative trait variances between the two clusters

Trait	Cluster I	Cluster II	'F' statistic	Probability
Days to 50% flowering	40.67	71.04	0.57	0.00
Days to maturity	40.54	71.06	0.57	0.00
Number of productive tillers	0.52	0.64	0.81	0.08
Plant height (cm)	121.48	147.89	0.82	0.09
Main ear length (cm)	3.29	1.60	2.05	0.00
Number of fingers/ear	1.20	0.81	1.48	0.00
Grain yield/plant (g)	32.48	34.19	0.95	0.67

Table 8. Inter- and intra- cluster distance among the two clusters obtained

Cluster	Cluster I	Cluster II
Cluster I	20.07	39.69
Cluster II	-	22.10

principal contributors towards variability between the genotypes (Mahajan and Mehan 1980) by reducing large data sets and finding only few significant independent variables without disturbing its original variability. Three principal components with eigen values greater than one contributed 72.55 percent of the total variability among 587 genotypes evaluated for 7 quantitative traits. The following traits contributed positively to PC1 that had 40.82 percent variation proportion to the total variability: days to 50% flowering (0.54), days to maturity (0.54) and plant height (0.44). In PC2, accounting for 16.74 percent of the total variability, grain yield/plant (0.67) and number of fingers/ear (0.65) contributed positively to the total variation (**Table 9**). The trait days to 50% flowering, days to maturity and plant height contributed majorly to the first two principal component analyses (**Fig. 3**).

Biplot analysis: The genotype 470 (GE 5949) significantly contributed in a positive direction in PC1, however inversely in PC2. The genotype 70 (GE 4764) contributed significantly in a negative direction in both PC1 and PC2 (**Fig. 4**). The genotypes 471 (GE 5951) and 475 (GE 5957) had also contributed positively to both PC1 and PC2. This illustrates the contribution of each genotype in

the total variation among different principal components. The genotype 470 (GE 5949) was distantly related to the genotype 70 (GE 4764), selection of these two diverse genotypes would be effective for improving grain yield in finger millet because they possessed the most deserving complement traits of each other.

The output of thea nalysis of variance and estimates of genetic variability parameters in the current study implied the existence of ample genetic diversity among 587 finger millet accessions, indicating their efficiency in use as parents in subsequent breeding programmes through selection and hybridization. This was evident as a result of high heritability and high genetic advance estimates for grain yield/plant. The K-means clustering, grouped the finger millet accessions into two clusters. The mean differences between clusters were significant for all traits. High variances for days to 50% flowering, days to maturity and grain yield/plant in cluster II, signified the scope of selection for these traits. Three principal components with eigen values greater than one contributed 72.55 percent of the total variability among 587 genotypes evaluated for seven quantitative traits. Days to 50% flowering, days to maturity and plant height contributed significantly to the total genetic variability and divergence. Therefore,
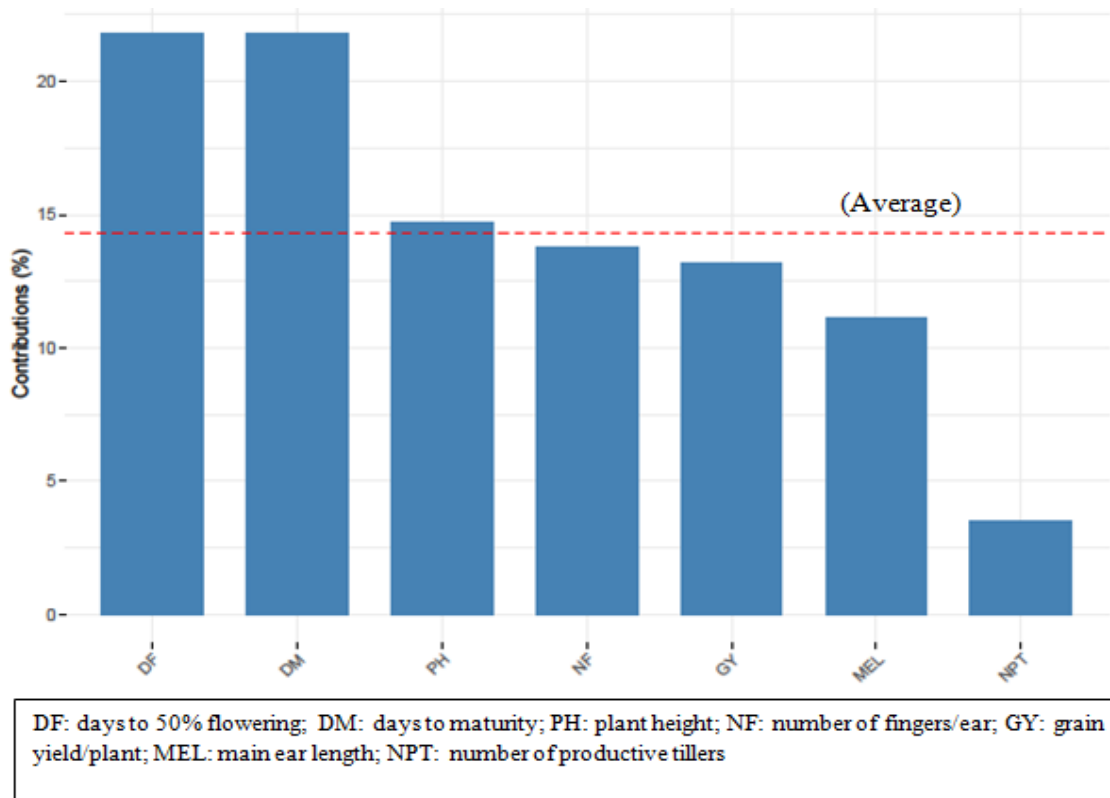
DF: days to 50% flowering; DM: days to maturity; PH: plant height; NF: number of fingers/ear; GY: grain yield/plant; MEL: main ear length; NPT: number of productive tillers

Fig. 3. Contribution of the seven quantitative traits evaluated in 587 finger millet germplasm accessions to the principal component 1 and 2
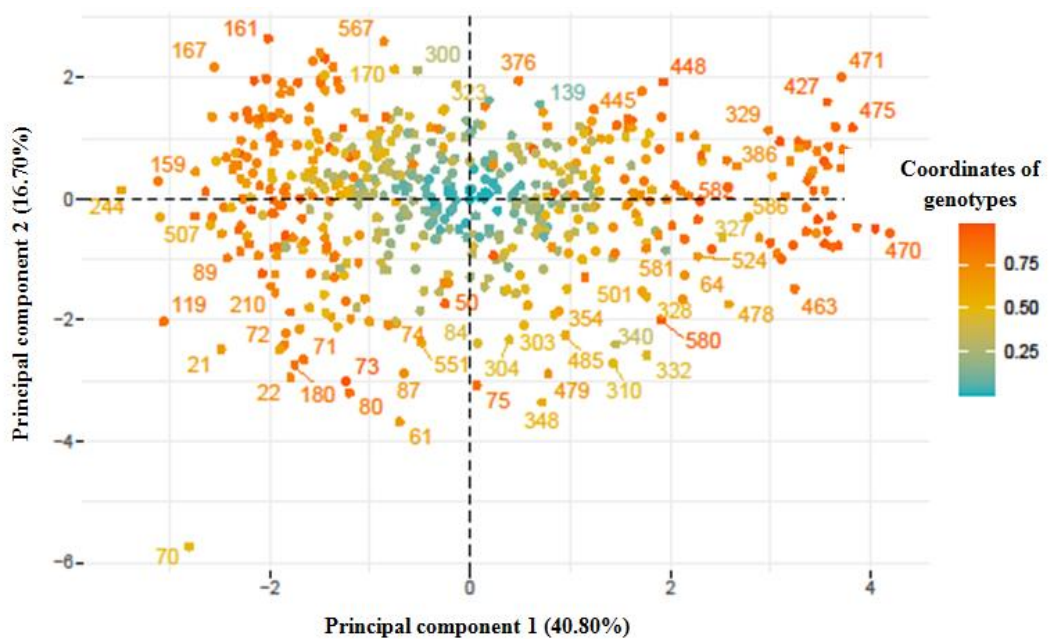

Fig. 4. Distribution of 587 finger millet accessions across Principal components 1 and 2

Table 9. Principal component analysis showing the contribution of morphological traits to the total variation among the finger millet accessions

Communality	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Days to 50% flowering	0.54	-0.19	-0.13	-0.19	-0.28	-0.17	-0.70
Days to maturity	0.54	-0.19	-0.14	-0.19	-0.28	-0.17	0.70
No. of productive tillers	-0.22	0.01	-0.73	0.46	-0.43	0.07	0.00
Plant height (cm)	0.44	0.13	-0.10	0.10	0.22	0.84	0.00
Main ear length (cm)	0.38	0.17	-0.08	0.59	0.50	-0.45	0.00
No. of fingers /ear	0.14	0.65	0.44	0.24	-0.54	-0.01	0.00
Grain yield per plant (g)	-0.013	0.67	-0.45	-0.53	0.20	-0.14	0.00
Eigen value	2.85	1.17	1.04	0.77	0.64	0.49	0.00
Proportion of variance	40.82	16.74	14.98	11.06	9.19	7.12	0.06
Cumulative variance (%)	40.82	57.56	72.55	83.61	92.81	99.93	100.00

emphasis should be given these characters when selection is exercised in finger millet crop improvement programmes. Performing genetic divergence studies before starting up a new breeding programme will help to determine the amount of existence of genetic diversity in it, thereby reducing the cost of money and time in crop improvement programmes.

REFERENCES

Anuradha, N., Patro, T.S.S.K., Divya, M., Sandhya Rani, Y. and Triveni, U. 2017. Morphological diversity analysis in finger millet (*Eleusine coracana* (L.) Gaertn.). *Frontiers in Crop Improvement,* **5**(1):67–70.

Chandrasekara, A. and Shahidi, F. 2010. Content of insoluble bound phenolics in millets and their contribution to antioxidant capacity. *Journal of Agricultural and Food Chemistry,* **58**:6706–6714. [Cross Ref]

Dagnachew, L., Kassahun, T., Masresha, F. and Santie, D.V. 2012. Multivariate analysis for quantitative traits in finger millet (*Eleusine coracana* subsp. *coracana*) population collected from Eastern and Southeastern Africa: detection for patterns of genetic diversity. *International Journal of Agricultural Research, Innovation and Technology,* **6**:303-314. [Cross Ref]

Dida, M.M., Wanyera, N., Dunn, M.L.H., Bennetzen, J.L. and Devos, K.M. 2008. Population structure and diversity in finger millet (*Eleusine coracana*) germplasm. *Tropical Plant Biology,* **1**:131–141. [Cross Ref]

Federer, W.T. 1961. Augmented designs with one-way elimination of heterogeneity. *Biometrics,* **17**: 447–473. [Cross Ref]

Federer, W.T. and Raghavarao, D. 1975.On Augmented Designs. *Biometrics,* **31**:29-35. [Cross Ref]

Ganapathy, S.,Nirmalakumari, A. and Muthiah, A.R. 2011. Genetic variability and inter relationship analysis for economic traits in finger millet germplasm. *World Journal of Agricultural Sciences,* **7**(2):185-188.

Hilu, K.W. and De Wet, J.M.J. 1976. Racial evolution of finger millet, *Eleusine coracana*. *American Journal of Botany,* **63**:1311–1318. [Cross Ref]

Hilu, K.W., de Wet, J.M.J. and Harlan, J.R. 1979. Archaeobotanical studies of *Eleusine coracana* ssp. *coracana* (finger millet). *American Journal of Botany,* **66**: 330–333. [Cross Ref]

Ignacimuthu, S. and Ceasar, S.A. 2012. Development of transgenic finger millet (*Eleusine coracana* (L.) Gaertn.) resistant to leaf blast disease. *Journal of Biosciences,* **37**(1):135-147. [Cross Ref]

John, K. 2006. Variability and correlation studies in quantitative traits of finger millet (*Eleusine coracana* Gaertn). *Agricultural Science Digest,* **26**(3): 166-169.

Kadam, D.D., Nigade, R. D. and Karad, S. R. 2010. Study on variation and selection parameters in ragi genotypes (*Eluesine coracana)*. *International journal of agricultural sciences,* **6**(2):383-385.

Karad, S.R. and Patil, J. V. 2013. Assessment of genetic diversity among finger millet (*Eleusine coracana* L.) genotypes. *International Journal of Integrative Science Innovation and Technology,* **4**:37-43.

Kebere, B., Prapa, S., Wasana, W. and Vipa, H. 2006. Genetic variation, heritability and path analysis in Ethiopian finger millet [*Eleusine coracana*(L.) Gaertn] landraces. *Kasetsart Journal of Natural Sciences,***40**:322-334.

Kumar, A., Metwal, M., Kaur, S., Gupta, A.K., Puranik, S., Singh, S., Singh, M., Gupta, S., Babu, B.K., Sood, S. and Yadav, R. 2016. Nutraceutical value of finger millet (*Eleusine coracana* (L.) Gaertn.), and their improvement using omics approaches. *Frontiers in Plant Science*,**7**:934. [Cross Ref]

Kurien, P.P., Joseph, K., Swaminathan, M. and Subrahmanyan, V. 1959. The distribution of nitrogen, calcium and phosphorus between the husk and endosperm of *ragi* (*Eleusine coracana*). *Journal of Food Science and Technology-Mysore,* **8**:353–355.

Mahajan, R. and Mehan, D. 1980. Principal component analysis in rice. *Crop Improvement,***7**:83–87.

Mehra, K.L. 1963. Consideration of the African origin of *Eleusine coracana* (L.) Gaertn. *Current Science,***32**:300–301.

Nirmalakumari, A., Salini, K. and Veerabadhiran, P. 2010. Morphological characterization and evaluation of little millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz.) germplasm. *Electronic Journal of Plant Breeding,* **1**(2):148-155.

Patil, H. E., Patel, B.K. and Savankumar, N. P. 2017. Assessment of genetic diversity in finger millet (*Eleusine coracana* L.) through multivariate analysis approach, *International Journal of Economic Plants*, **04**(04):148-151.

Shinde, S.R., Desai, S.V. and Pawar, R.M. 2014. Genetic variability and character association in finger millet [*Eleusine coracana* (L.) Gaertn]. *International Journal of Plant Sciences*, **9**(1):13-16.

Sood, S., Kant, L. and Pattanayak, A. 2017. Finger millet (*Eleusine coracana* (L.) Gaertn)-a minor crop for sustainable food and nutritional security. *Asian Journal of Chemistry,***29**(4):707–710. [Cross Ref]

Venkatesh, L.,Niranjana, M. and Nehru, S.D. 2014. Analysis of genetic diversity in grain amaranth (*Amaranthus* spp.). *Indian Journal ofGenetics*,**74**(4):522-525. [Cross Ref]