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RESEARCH ARTICLE

Assessment of Genetic Diversity in Finger Millet [*Eleusine coracana* (L.) Gaertn.] Genotypes

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Abstract

The experimental material comprised 148 diverse finger millet genotypes representing collections from all over India. All the genotypes were characterized for 19 grain yield and yield-related traits. They were evaluated to assess diversity among various genotypes at the Agricultural Research Station, Vizianagaram during *kharif,* 2019–20. Significant variations were observed for all the traits studied. Analysis of D^2 statistics grouped them into 22 clusters. Cluster I was the largest group with the maximum number of genotypes (103), followed by cluster XI and XIV with 13 and 11 genotypes, respectively, while 18 were solitary clusters. The inter-cluster distance was highest between clusters XVII and XXII, followed by clusters XIII and XXII. Among the 19 quantitative traits studied, the most important trait contributing to the divergence was ear length, followed by days to 50% flowering and grain yield. Based on mean values and inter-cluster distances, IC0329452 × IC0474832, IC043734 × IC0474832, IC0475882 × IC0474832, IC0474832 × IC028353 and IC0474832 × IC0478862 crosses are proposed to attain multiple desirable characters in a single genotype.

Keywords: Cluster, D^2 statistic, Finger millet, Genetic diversity.

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Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is the most important small millet crop. It is cultivated in more than 25 countries in Africa and Asia. India is a major producer of finger millet in Asia, occupying an area of 1193.70 thousand hectares with a production of 1982.90 thousand tonnes and productivity of 1661.00 kg per hectare (Anonymous, 2014). It is largely grown in the southern states of India. Finger millet gained its name as "Nutri-cereal" since the grains are nutritionally superior to many cereals in terms of protein (7–10%), calcium (344 mg/100 g), iron (3–4 mg/100 g) and other mineral content. It is also rich in phosphorus (283 mg/100 g) and potassium (408 mg/100 g). Moreover, carbohydrates in finger millet have the unique property of slow digestibility and are a good diet for diabetics. Finger millet is a drought-tolerant crop that can thrive with little water. It can also withstand high temperatures and thrive in poor, deteriorated soils. It may be grown in varied climates (Anuradha *et al*., 2021).

Despite having many health benefits, finger millet cultivation has been reduced and replaced by other commercial crops over the years. Now it is again gaining importance as people are becoming increasingly health-conscious. A decrease in the area can only be compensated for by increased productivity. Hence, finger millet improvement should be mainly focused on developing high-yielding varieties. The productivity of finger millet is also affected by a few diseases like a blast and banded blight, which are likely to

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cause more than 50% yield losses (Patro *et al.,* 2020). Though the ultimate aim of a breeder is to develop a high-yielding variety, the sustainability of a variety for a longer period in a farmer's field depends on its disease resistance to major diseases. As a result, developing a high-yielding variety with disease resistance is critical in the advancement of new finger millet cultivars. This can be achieved by exploiting the agrobiodiversity of finger millet lines for selecting genotypes with *per se* high yield and disease resistance or else for selecting genetically diverse parents with desirable characters to make crosses for creating variability. In this context, Mahalanobis D^2 statistics is an age-old effective tool utilized in quantifying the degree of divergence at a genetic level and also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). Genetic divergence is a tool to select diverse parents for utilization in specific hybridization to generate greater variability in self-pollinated crops. This in turn, provides scope for the breeder to select high-yielding varieties along with desirable traits. Hence, the present study was carried out to determine the nature and magnitude of genetic divergence among 148 finger millet genotypes under the Consortia Research Platform (CRP) agro biodiversity project.

Materials and Methods

The experimental material was comprised of 148 finger millet genotypes, including three checks, MR 6, GPU 67, and VL 352. They were obtained from the ICAR-Indian Institute of Millet Research, Hyderabad, which included diverse germplasm collected from different parts of the country (Table 1). All these genotypes were sown on 31.07.2019 at the Agricultural Research Station, Vizianagaram, Andhra Pradesh, located at latitude: 18.12′ N, longitude: 83.40′ E and an altitude of 63 m. MSL, comprising red sandy loam soil. The weather data for the location was presented in Figure 1. The layout was a completely randomized block design (RCBD) with two replications and a spacing of 30 cm between rows and 10 cm between plants. Each genotype was sown in two rows of 3 m in length. Fertilizers, DAP (87 kg/ha), MOP (42 kg/ha) and urea (22 kg/ha) were applied basally at the time of land preparation and the remaining 22 kg/ha of urea was applied three weeks after sowing. Standard management practices were followed, except for disease management. Observations were recorded on five plants and means were computed for the traits *viz.*, plant height (cm), number of productive tillers/plant, number of fingers/ear, ear length (cm), finger length (cm), finger width (cm), number of leaves/main tiller, flag leaf length (cm), flag leaf width (cm), length from top node to leaf sheath junction (cm), and peduncle length (cm). Days to 50% flowering and days to maturity were recorded by visualizing the entire plot. Fodder and grain yield were recorded per plot basis and then converted to per hectare. Disease data was recorded under natural field conditions. Leaf blast (Table 2) was recorded by using 0–5 scale and the percent disease index (PDI) was calculated by using the following formula:

PDI = Sum of all disease ratings/Total number of ratings × 100

Neck blast (%) = No. of infected panicles/Total no. of panicles × 100

Finger blast (%) = No. of infected fingers/Average number of fingers × 100

Banded blight (%) = No. of infected plants/Total number of plants × 100

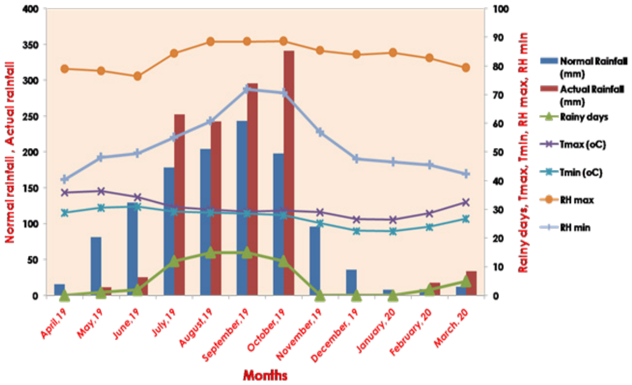

Figure 1: Weather data at the experimental site during kharif, 2019.

Mahalanobis D^2 statistic was used to assess the diversity among genotypes and were grouped into clusters using Tocher's method described by Rao (1952).

Results and Discussion

The variance analysis revealed significant differences among 148 genotypes for all the 19 characters included under study (Table 3), indicating that the experimental material consisted of more variation for all the traits. Similar results were obtained by Kumar *et al.*, (2010), Karad and Patil., (2013) and Anuradha *et al.*, (2020).

The quantitative assessment of genetic divergence was obtained by adopting the Mahalanobis D^2 statistic for yield and its contributing characteristics. These 148 genotypes were grouped into 22 clusters (Tables 3 and 4). Among various clusters, cluster I contained a maximum of 103 genotypes, followed by cluster XI consisting of 13 genotypes, cluster XIV with 11 genotypes, and cluster XIX with three genotypes, while the remaining clusters had a solitary genotype. It indicated that few genotypes were very diverse from others, contributing much to genetic diversity. Traits that contributed most to this diversity in these genotypes were discussed later. Two checks, *viz.*, MR 6 and VL 352, were grouped into the largest cluster I, and the remaining check, GPU 67, was grouped into the second largest cluster XI. It implies that the checks used in the study were also diverse. Similar results were reported earlier by Anantharaju and Meenakshiganesan (2008), Kumar *et al.*, (2010), Karad

Table 1: List of 148 finger millet genotypes and their origin.

S. No.	*Genotype ID*	*Accession Number*	*IC/EC Number*	*Country of Origin*	*State*
1	FIN 2853	GE 20	IC0476259	India	Unknown
2	FIN 2872	GE 188	IC0476362	India	Unknown
3	FIN 2891	GE 198	IC0476439	India	Unknown
4	FIN 2899	GE 108	IC0476484	India	Unknown
5	FIN 2901	GE 61	IC0476492	India	Unknown
6	FIN 2936	GE 162	IC0476623	India	Unknown
7	FIN 2960	GE 127	IC0476742	India	Bihar
8	FIN 2998	GE 10	IC0477078	India	Unknown
9	FIN 3003	GE 2	IC0477289	India	Unknown
10	FIN 3004	GE 125	IC0477419	India	Bihar
11	FIN 3007	GE 396	IC0475528	India	Tamil Nadu
12	FIN 3017	GE 276	IC0475790	India	Unknown
13	FIN 3022	GE 345	IC0475848	India	Unknown
14	FIN 3026	GE 363	IC0475937	India	Unknown
15	FIN 3062	GE 372	IC0476193	India	Unknown
16	FIN 3068	GE 374	IC0476246	India	Unknown
17	FIN 3086	GE 313	IC0476326	India	Unknown
18	FIN 3088	GE 280	IC0476333	India	Unknown
19	FIN 3090	GE 267	IC0476345	India	Unknown
20	FIN 3296	GE 527	IC0476587	India	Unknown
21	FIN 3318	GE 545	IC0475654	India	Unknown
22	FIN 3321	GE 676	IC0475716	India	Unknown
23	FIN 3336	GE 554	IC0475868	India	Unknown
24	FIN 3376	GE 679	IC0476124	India	Unknown
25	FIN 3422	GE 586	IC0476381	India	Unknown
26	FIN 3473	GE 724	IC0475746	India	Uttarakhand
27	FIN 3496	GE 776	IC0475802	India	Unknown
28	FIN 3525	GE 769	IC0476020	India	Unknown
29	FIN 3532	GE 782	IC0476095	India	Unknown
30	FIN 3538	GE 750	IC0476138	India	Unknown
31	FIN 3583	GE 861	IC0475407	India	Unknown
32	FIN 3608	GE 888	IC0475653	India	Unknown
33	FIN 3622	GE 916	IC0475759	India	Unknown
34	FIN 3639	GE 889	IC0475858	India	Unknown
35	FIN 3689	GE 866	IC0476213	India	Unknown
36	FIN 3726	GE 1059	IC0475382	India	Unknown
37	FIN 3765	GE 1007	IC0475697	India	Unknown
38	FIN 3321	GE 676	IC0475716	India	Unknown
39	FIN 3782	GE 1084	IC0475780	India	Unknown
40	FIN 3789	GE 961	IC0475814	India	Unknown
41	FIN 3793	GE 1022	IC0475826	India	Unknown
42	FIN 3847	GE 1093	IC0475246	India	Unknown
43	FIN 3848	GE 1199	IC0475251	India	Unknown
44	FIN 3855	GE 1185	IC0475344	India	Unknown

45	FIN 3856	GE 1117	IC0475355	India	Unknown
46	FIN 3871	GE 1131	IC0475416	India	Unknown
47	FIN 3883	GE 1167	IC0475477	India	Unknown
48	FIN 3901	GE 1197	IC0475620	India	Unknown
49	FIN 3928	GE 1174	IC0475882	India	Unknown
50	FIN 3952	GE 1175	IC0476459	India	Unknown
51	FIN 4203	GE 1551	IC0475019	India	Unknown
52	FIN 4213	GE 1564	IC0475073	India	Unknown
53	FIN 4219	GE 1557	IC0475125	India	Unknown
54	FIN 4260	GE 1528	IC0475436	India	Unknown
55	FIN 4288	GE 1671	IC0474816	India	Unknown
56	FIN 4303	GE 1666	IC0474956	India	Unknown
57	FIN 4331	GE 1603	IC0475164	India	Unknown
58	FIN 4336	GE 1584	IC0475201	India	Unknown
59	FIN 4349	GE 1638	IC0475270	India	Unknown
60	FIN 4462	GE 1780	IC0475095	India	Unknown
61	FIN 4482	GE 1741	IC0475244	India	Unknown
62	FIN 4483	GE 1773	IC0475252	India	Unknown
63	FIN 4491	GE 1795	IC0475374	India	Unknown
64	FIN 4493	GE 1712	IC0475386	India	Unknown
65	FIN 4498	GE 1723	IC0475473	India	Unknown
66	FIN 4512	GE 1869	IC0474775	India	Uttarakhand
67	FIN 4516	GE 1902	IC0474782	India	Unknown
68	FIN 4524	GE 1935	IC0474806	India	Unknown
69	FIN 4527	GE 1853	IC0474820	India	Unknown
70	FIN 4533	GE 1818	IC0474832	India	Unknown
71	FIN 4536	GE 1829	IC0474840	India	Unknown
72	FIN 4542	GE 1850	IC0474862	India	Unknown
73	FIN 4578	GE 1910	IC0474970	India	Unknown
74	FIN 4602	GE 1924	IC0475100	India	Unknown
75	FIN 4644	113/84-16	IC0478942	India	Unknown
76	FIN 4794	IE-2431	IC0473590	India	
77	FIN 4830	IE-2490	IC0473636	India	Unknown
78	FIN 4863	IE-2598	IC0473714	India	Unknown
79	FIN 4866	IE-2601	IC0473717	India	Unknown
80	FIN 4874	IE-2612	IC0473726	India	Unknown
81	FIN 4881	IE-2621	IC0473734	India	Unknown
82	FIN 4957	IE-2790	IC0473889	India	
83	FIN 4958	IE-2791	IC0473890	India	Unknown
84	FIN 4961	IE-2812	IC0473909	India	Unknown
85	FIN 5088	IE-3070	IC0474128	India	Unknown
86	FIN 5154	IE-3150(7-74-1)	IC0474199	India	Unknown
87	FIN 5158	IE-3154(10-5-4-1)	IC0474203	India	Unknown
88	FIN 5160	IE-3143-1	IC0479215	India	Unknown
89	FIN 5200	IE-3250	IC0474297	India	Unknown
90	FIN 5301	NC-57078	IC0007952	India	Unknown

91	FIN 5337	5/81 - 7	IC0049936	India	Tamil Nadu
92	FIN 5341	13/81 - 2	IC0049942	India	Karnataka
93	FIN 5406	96/81 - 2	IC0050000	India	Karnataka
94	FIN 5412	170-B	IC0071333	India	Kerala
95	FIN 5413	21/83-22175	IC0071338	India	Kerala
96	FIN 5425	A-1128	IC0087508	India	Sikkim
97	FIN 5433	C-2009450	IC0087540	India	Jharkhand
98	FIN 5453	GE-925	IC0478720	India	Unknown
99	FIN 5458	EKR- 180	IC0478760	India	Unknown
100	FIN 5460	GE-1019	IC0478764	India	Unknown
101	FIN 5461	EKEP- 10	IC0478776	India	Unknown
102	FIN 5462	GE-872	IC0478780	India	Unknown
103	FIN 5464	GE-629	IC0478790	India	Unknown
104	FIN 5514	GE-3196	IC0478792	India	Unknown
105	FIN 5540	GE-3311	IC0478444	India	Unknown
106	FIN 5562	GE-3372	IC0478809	India	Unknown
107	FIN 5578	GE-3548	IC0478442	India	Unknown
108	FIN 5596	GE-3990	IC0478656	India	Unknown
109	FIN 5599	GE-4073	IC0478693	India	Unknown
110	FIN 5601	GE-3736	IC0478710	India	Unknown
111	FIN 5601	GE-3736	IC0478710	India	Unknown
112	FIN 5620	GE-3839	IC0478883	India	Unknown
113	FIN 5668	GE-4492	IC0478862	India	Unknown
114	FIN 5717		IC0096774	India	Maharashtra
115	FIN 5731		IC0096815	India	Maharashtra
116	FIN 5732		IC0096817	India	Maharashtra
117	FIN 5735		IC0096827	India	Maharashtra
118	FIN 5736		IC0096844	India	Maharashtra
119	FIN 5849	96/82-25	IC0069594	India	Kerala
120	FIN 5893	K-2838TCR-425	IC0087530	India	Tamil Nadu
121	FIN 5960	GE-4736IE-2361	IC0473528	India	Unknown
122	FIN 5994	GE-4772IE-2410	IC0473571	India	Unknown
123	FIN 6077	GE-4867IE-2753	IC0473855	India	Unknown
124	FIN 6176	GE-4966IE-2958	IC0474034	India	Unknown
125	FIN 6188	GE-4979IE-3164	IC0474213	India	Unknown
126	FIN 6269	GE-5065IE-3333	IC0474370	India	Unknown
127	FIN 6347	M-112/81-6TCR-148	IC0069583	India	Karnataka
128	FIN 6364	M-132/84-8TCR-248-A (NC-71411X)	IC0071411-A	India	Unknown
129	FIN 6423	VRS-MF-872	IC0261985	India	Uttarakhand
130	FIN 6478	NSS-7890	IC0283815	India	Andhra Pradesh
131	FIN 6493	NSS-7928	IC0283853	India	Andhra Pradesh
132	FIN 6525	VR-MF-1371	IC0281756	India	Uttarakhand
133	FIN 6526	VR-MF-1373	IC0281758	India	Uttarakhand
134	FIN 6530	VR-MF-1383	IC0281768	India	Uttarakhand
135	FIN 6546	KVC-56	IC0329452	India	Himachal Pradesh

136	FIN 6558	JBT27/76	IC0331685	India	Jharkhand
137	FIN 6560	JBT27/94	IC0331687	India	Jharkhand
138	FIN 6563	JBT27/104	IC0331690	India	Jharkhand
139	FIN 6584	BS-9111	IC0308922	India	Andhra Pradesh
140	FIN 6585	BS-9143	IC0308929	India	Andhra Pradesh
141	FIN 6624	LS-47/2001	IC0344178	India	Maharashtra
142	FIN 6658	LS-41/2001	IC0344172	India	Maharashtra
143	FIN 6723	BAS-145	IC0345081	India	Andhra Pradesh
144	FIN 6754	VKS/SCC-8/13	IC0347252	India	Bihar
145	FIN 6772	DPRR-77	IC0361119	India	Uttarakhand
146	GPU 67			India	Karnataka
147	MR 6			India	Karnataka
148	VL 352			India	Uttarakhand

Table 2: Standard evaluation system (SES) scale for leaf blast disease.

Score	*Description*	*Reaction*
0	No lesions/symptoms on leaves	No disease/HR
1	Small brown specks of pinhead to slightly elongate, necrotic grey spots with a brown margin, less than 1% area affected	R
2	A typical blast lesion elliptical, 5–10 mm long, 1–5% of leaf area affected	MR
3	A typical blast region elliptical, 1–2 cm long, 6–25 % of leaf area affected	MS
4	26–50% leaf area affected	S
5	More than 50% of leaf area affected with coalescing lesions	HS

and Patil, (2013) and Anuradha *et al*., (2017). The origin of many genotypes was unknown (Table 1). However, it was observed that genotypes collected from Bihar, Tamil Nadu, Uttarakhand, Kerala, Jharkhand, Maharashtra, and Andhra Pradesh were grouped into different clusters irrespective of their origin. There was no parallelism between the origin of genotypes and grouping patterns. This is in accordance with the results of Shinde *et al*., (2013).

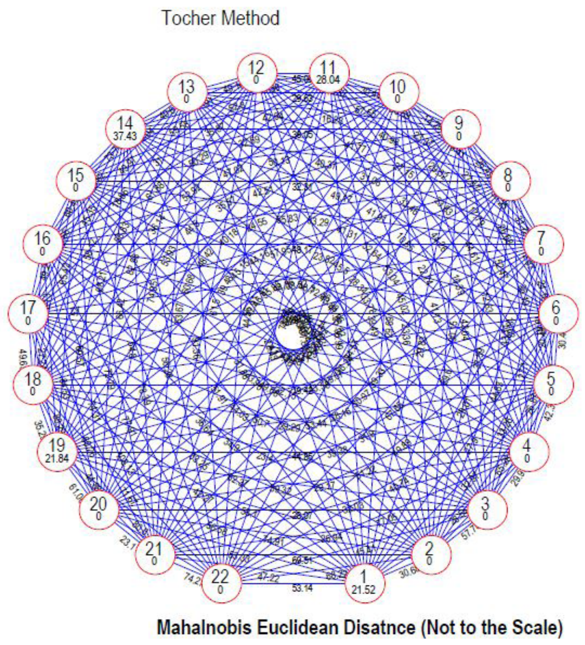

Figure 2: Intra and Inter cluster distance between 22 finger millet clusters

Intra and inter-cluster distances were worked out using D^2 values from divergence analysis (Table 5, Figure 2). The inter-cluster distance values ranged widely, with a minimum value of 10.39 between clusters IV and X and a maximum value of 108.13 between clusters XVII and XXII, indicating high diversity between the genotypes of XVII and XXII clusters. It was followed by clusters XIII and XXII (91.36) and XVII and XX (88.29). This suggested that there was wide genetic diversity between these clusters. The maximum heterosis is expected from the crosses with parents of these clusters. Cluster XXII, having a solitary genotype, was found to have a higher inter-cluster distance with almost 10 clusters (XVII, XIII, IX, XX, XV, XVI, IV, XXI, XXI, XVIII) recording more than 70 inter-cluster distance. The least inter-cluster distance with this cluster was observed with cluster VIII, which was also a solitary cluster. But even this inter-cluster distance was higher than the remaining 92 inter-cluster distances, implying that the genotypes from this cluster were highly diverse from the genotypes of remaining clusters. The cluster with the maximum number of genotypes recorded lesser inter-cluster distances, with the remaining other clusters indicating a low level of divergence. The intra-cluster distance ranged from 0 (solitary clusters) to 37.43 (XIV). Cluster XIV (37.43), followed by cluster XI (28.04), cluster XIX (21.84) and cluster I (21.52), recorded the next higher intra-

Table 3: ANOVA of 148 finger millet genotypes

Source of Variations	*df*	*Mean Squares*																		
		DFF	*DM*	*PH*	*NPT*	*NFE*	*EL*	*FL*	*FW*	*PDL*	*NJL*	*LN*	*FLL*	*FLW*	*GY*	*FY*	*LB*	*NB*	*FB*	*BB*
Treatments	147	67.94**	85.32**	82.34**	0.49**	2.38**	7.60**	7.55**	0.02**	6.27**	5.34**	14.08**	39.15**	0.02*	1910371**	4186643**	0.976**	27.88**	46.12**	13.25**
Replications	1	0.08	0.57	285.29	2.31	21.19	12.50	4.31	0.00	2.36	0.15	32.49	33.63	0.00	176217	3378	0.643	756.89	1935.97	669.12
Error	295	7.92	15.86	21.68	0.29	1.02	0.85	0.94	0.00	1.73	3.24	3.95	15.37	0.02	366225	1957735	0.149	8.02	14.21	4.54

Note: DFF: Days to 50% flowering; DM: Days to maturity; Plant height (cm); NPT: No. of productive tillers per plant; NFE: No. of finger per ear; EL: Ear length (cm); FL: Finger length (cm); Finger width (cm); PDL: Peduncle length (cm); NLJ: Length from the top node to leaf sheath junction (cm); LN: No. of leaves/main tiller ; FLL: Flag leaf length (cm); FLW: Flag leaf width (cm); GY: Grain yield (q/ha); FY: Fodder yield (q/ha), LB: Leaf blast (Grade); FB: Finger blast (%), Neck blast (%) and BB: Banded blight (%)

Table 4: Distribution of 148 genotypes of Finger millet into 22 different clusters on the basis of Mahalanobis D^2 Statistics

Cluster	*No. of genotypes*	*Genotypes*
I	103	GE-872 (IC0478780), FIN 5735 (IC0096827), EKEP- 10 (IC0478776), GE 125 (IC0477419), 96/82-25 (IC0069594), GE 1557 (IC0475125), GE 769 (IC0476020), GE 1666 (IC0474956), GE 280 (IC0476333), IE-2431 (IC0473590), GE 1850 (IC0474862), NC-57078(NC-57078), GE 1528 (IC0475436), IE-3070 (IC0474128), GE 1185 (IC0475344), GE 372 (IC0476193), GE 676 (IC0475716), GE 586 (IC0476381), FIN 5732 (IC0096817), VR-MF-1371 (IC0281756), GE 961 (IC0475814), GE 1723 (IC0475473), GE 1869 (IC0474775), BS-9143 (IC0308929), MR 6, 13/81 – 2 (IC0049942), VR-MF-1383 (IC0281768), GE-3736 (IC0478710), GE 1197 (IC0475620), GE-3372 (IC0478809), GE 527 (IC0476587), GE-629 (IC0478790), GE 861 (IC0475407), GE 267 (IC0476345), GE 363 (IC0475937), GE 125 (IC0477419), GE-4979IE-3164 (IC0474213), M-112/81-6TCR-148 (IC0069583), A-1128 (IC0087508), 5/81 – 7 (IC0049936), GE 1910 (IC0474970), BS-9111 (IC0308922), JBT27/76 (IC0331685), VL 352, EKR- 180 (IC0478760), GE 679 (IC0476124), GE 545 (IC0475654), GE-4772IE-2410 (IC0473571), GE 1175 (IC0476459), GE-3839 (IC0478883), JBT27/94 (IC0331687), LS-41/2001 (IC0344172), GE 554 (IC0475868), GE 1584 (IC0475201), GE 374 (IC0476246), GE 1935 (IC0474806), GE 1131 (IC0475416), GE 1059 (IC0475382), GE 724 (IC0475746), GE 198 (IC0476439), GE 1638 (IC0475270), GE 866 (IC0476213), GE-5065IE-3333 (IC0474370), GE-3311 (IC0478444), 96/81–2 (IC0050000), GE 1780 (IC0475095), VKS/SCC-8/13 (IC0347252), GE-4867IE-2753 (IC0473855), GE 1773(IC0475252), 113/84-16 (IC0478942), GE 1671 (IC0474816), GE1117 (IC0475355), GE 1084 (IC0475780), GE 2 (IC0477289), GE 1022 (IC0475826), GE 1167 (IC0475477),GE 1795 (IC0475374), M-132/84-8TCR-248-A(NC-71411X) (IC0071411-A), GE-1019 (IC0478764), BAS-145 (IC0345081), GE 1093 (IC0475246), IC0096844, IC0096774, IC0096815, GE-3548 (IC0478442), GE 1924 (IC0475100), GE-3990 (IC0478656), GE-4736IE-2361 (IC0473528), GE 782 (IC0476095), DPRR-77 (IC0361119), 6772, 21/83-22175 (IC0071338), IE-2601 (IC0473717), IE-2612 (IC0473726), IE-3143-1 (IC0479215), GE 345 (IC0475848), IE-2812 (IC0473909), GE 1199 (IC0475251), GE 1829 (IC0474840), GE 1741 (IC0475244), GE 127 (IC0476742), IE-2490 (IC0473636), IE-2598 (IC0473714), GE 1007 (IC0475697)
II	1	GE1174 (IC0475882)
III	1	GE 1853 (IC0474820)
IV	1	GE 776 (IC0475802)
V	1	GE 313 (IC0476326)
VI	1	C-2009450 (IC0087540)
VII	1	GE 10 (IC0477078)
VIII	1	K-2838TCR-425 (IC0087530)
IX	1	KVC-56 (IC0329452)
X	1	GE-925 (IC0478720)
XI	13	IE-2790 (IC0473889), VR-MF-1373(IC0281758), IE-2791 (IC0473890), GE 750 (IC0476138), GE 916 (IC0475759), IE-3150(7-74-1) (IC0474199), GE 889 (IC0475858), GE 162 (IC0476623), LS-47/2001 (IC0344178), NSS-7890 (IC0283815), 170-B (IC0071333), GPU 67, GE 1902 (IC0474782)
XII	1	GE 20 (IC0476259)

XIII	1	NSS-7928 (IC0283853)
XIV	11	GE 888 (IC0475653), GE 1551 (IC0475019), JBT27/104 (IC0331690), VRS-MF-872 (IC0261985), GE 1564 (IC0475073), GE-3196 (IC0478792), GE 188 (IC0476362), GE-3736 (IC0478710), IE-3250 (IC0474297), GE 61 (IC04764920), GE-4073 (IC0478693)
XV	1	IE-3154(10-5-4-1) (IC0474203)
XVI	1	GE 396 (IC0475528)
XVII	1	GE-4492 (IC0478862)
XVIII	1	GE 276 (IC0475790)
XIX	3	GE 1603 (IC0475164), GE 1712 (IC0475386), GE 108 (IC0476484)
XX	1	GE-4966IE-2958 (IC0474034)
XXI	1	IE-2621 (IC0473734)
XXII	1	GE 1818 (IC0474832)

Table 5: Intra and inter-cluster D2 values among 22 clusters with 148 finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes

Cluster	*I*	*II*	*III*	*IV*	*V*	*VI*	*VII*	*VIII*	*IX*	*X*	*XI*	*XII*	*XIII*	*XIV*	*XV*	*XVI*	*XVII*	*XVIII*	*XIX*	*XX*	*XXI*	*XXII*
I	21.52	30.68	28.01	28.54	32.97	27.90	29.01	29.60	29.83	29.69	36.99	31.89	28.43	31.88	51.91	36.64	33.25	42.27	56.58	53.33	47.22	53.14
II		0	57.78	29.24	65.28	33.26	44.83	37.62	30.15	23.36	39.49	55.62	40.40	41.70	23.96	44.03	34.9	62.37	58.10	74.91	69.51	68.22
III			0	29.95	19.06	26.87	27.10	33.31	43.04	41.13	45.02	33.78	41.96	35.67	77.46	49.66	50.70	23.40	59.32	28.07	26.94	45.41
IV				0	42.37	14.01	20.44	18.6	12.63	10.39	22.74	53.04	28.34	43.88	33.05	49.58	32.15	29.29	44.85	29.17	32.03	77.05
V					0	30.48	19.01	36.24	52.47	44.61	44.26	10.85	52.64	45.50	72.46	43.51	62.41	19.42	53.44	39.38	51.22	40.74
VI						0	24.16	12.90	26.68	17.79	23.83	33.46	41.91	41.31	23.82	48.3	49.86	32.29	43.58	28.16	31.9	49.89
VII							0	31.71	35.25	27.87	29.32	27.15	31.06	49.17	53.29	48.17	38.52	24.33	58.46	39.07	50.97	67.65
VIII								0	26.49	19.41	23.37	40.98	41.77	40.37	32.31	55.83	57.95	44.86	50.29	20.63	26.24	39.33
IX									0	14.29	36.69	57.55	16.23	38.05	50.13	42.51	24.55	44.16	55.88	59.3	43.52	84.57
X										0	30.44	46.32	29.63	42.94	32.69	47.02	35.57	40.18	45.15	46.81	47.59	60.44
XI											28.04	45.09	47.56	52.80	35.87	50.29	52.92	44.50	48.42	39.48	42.91	73.56
XII												0	49.16	47.91	59.58	31.00	61.88	36.14	53.93	60.68	61.5	44.56
XIII													0	40.61	73.04	49.97	18.86	58.83	82.98	74.05	53.67	91.36
XIV														37.43	73.77	46.82	45.35	58.12	68.21	66.42	54.8	56.28
XV															0	60.42	76.66	65.42	52.00	60.57	72.79	78.39
XVI																0	49.21	42.13	27.24	84.53	74.31	77.91
XVII																	0	49.65	72.44	88.29	60.26	108.13
XVIII																		0	35.29	38.45	44.88	71.67
XIX																			21.84	61.06	65.95	80.60
XX																				0	23.10	54.25
XXI																					0	74.27
XXII																						0

Table 6: Mean values of 22 clusters estimated by Tocher's method from 148 finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes

Cluster	*GY*	*DFF*	*DM*	*PH*	*NPT*	*NFE*	*EL*	*FL*	*FW*	*LNM*	*FLL*	*FLW*	*NJL*	*PDL*	*FY*	*LB*	*NB*	*FB*	*BB*
I	3705.7	69.2	102.1	69.6	3.4	7.2	8.1	6.4	0.9	14.1	40.0	1.2	9.7	9.4	7952.0	2.1	19.6	26.9	23.5
II	5250.0	84.0	116.0	70.7	3.4	7.4	7.5	6.2	1.0	15.4	43.2	1.1	11.4	10.2	7888.8	1.1	12.0	17.4	18.0
III	3105.6	56.0	91.0	71.6	3.3	7.4	9.9	7.5	0.9	13.1	34.8	1.1	12.7	8.8	5944.4	2.2	21.5	29.9	25.3
IV	3511.1	73.0	107.5	68.6	3.4	7.3	12.0	10.1	0.9	12.4	41.4	1.2	10.7	11.9	5166.6	2.5	20.6	28.8	25.2
V	1222.2	59.5	90.0	71.7	3.5	7.7	9.0	8.0	0.8	15.5	39.4	1.0	9.7	8.7	8444.4	3.1	25.3	33.8	27.0
VI	3188.9	71.5	106.0	67.6	2.8	7.9	11.8	9.6	1.0	14.2	34.8	1.0	7.2	10.4	7888.8	1.8	22.7	30.4	25.8
VII	1838.9	67.5	104.0	64.6	3.3	8.7	9.8	8.7	0.8	11.8	48.0	1.2	9.8	9.0	6555.5	2.9	24.9	34.5	27.4
VIII	4344.5	70.0	104.5	65.5	3.2	7.4	12.1	11.5	0.8	17.4	36.2	1.2	10.2	9.9	9833.2	1.5	17.8	24.4	23.1
IX	4994.4	72.5	108.5	69.2	3.4	5.5	9.7	8.8	0.8	12.9	42.4	1.2	7.1	12.5	5555.5	1.2	15.3	21.7	20.5
X	3694.5	76.0	111.0	68.9	2.5	7.3	10.2	8.7	0.8	15.2	41.1	1.2	10.0	12.7	6833.3	1.9	17.6	27.3	24.7
XI	3403.4	74.5	108.5	70.1	3.6	7.7	11.9	10.4	0.9	13.2	42.3	1.2	9.9	9.5	9358.9	2.4	20.4	28.1	23.9
XII	1416.7	66.5	97.0	73.5	2.7	6.7	7.9	6.6	0.8	15.6	37.9	1.1	7.9	5.8	9888.8	2.9	24.3	33.3	26.2
XIII	4350.0	70.0	104.5	61.0	2.5	5.8	8.0	6.0	0.6	9.4	43.1	1.3	8.1	10.8	6333.3	1.3	16.9	22.7	21.4
XIV	4791.9	66.7	98.2	70.1	3.7	7.1	7.7	6.1	0.9	13.8	38.7	1.1	9.6	10.6	9131.2	1.3	16.1	22.8	20.5
XV	3538.9	88.0	121.5	72.9	2.9	7.9	11.9	10.4	1.0	18.4	37.2	1.1	9.1	8.3	8166.6	2.3	20.3	25.8	23.0
XVI	3416.7	72.5	107.5	95.6	3.5	6.8	7.7	6.5	0.8	12.5	41.3	1.0	8.7	6.8	8777.7	2.7	20.9	29.4	24.1
XVII	4144.5	71.5	105.5	71.8	2.6	5.9	6.5	4.4	1.0	9.1	53.4	1.5	8.9	12.9	6944.4	1.6	18.0	24.9	23.1
XVIII	1711.1	61.0	97.5	85.8	3.2	6.7	10.7	8.8	1.0	15.8	47.5	1.1	12.0	9.6	5888.8	2.8	25.0	32.5	26.8
XIX	3122.2	73.2	106.7	100.8	3.2	8.5	11.7	9.9	1.0	14.9	42.9	1.1	10.4	9.8	9481.4	2.7	21.1	29.2	24.7
XX	3044.5	61.5	90.5	66.6	2.9	8.8	15.2	13.6	0.9	15.5	37.4	1.1	13.8	9.0	7722.2	2.8	23.5	31.2	26.0
XXI	4833.3	59.0	93.5	65.6	2.4	5.3	13.6	11.3	1.1	11.9	38.8	1.2	9.9	9.7	8499.9	1.8	14.1	19.6	21.2
XXII	4083.3	61.0	89.5	68.3	2.7	10.3	8.5	7.6	0.8	25.6	35.8	1.0	10.2	7.9	10499.9	1.5	18.0	25.3	22.2

cluster distances, while it was very low for cluster I, along with a lower inter-cluster distance, indicating its less usage in breeding. As usual, inter-cluster distances were higher than the intra-cluster distances, indicating the presence of wider genetic diversity between the clusters rather than within the clusters. Similar results were obtained by Wolie and Belete (2013) and Devaliya *et al*., (2017).

Cluster means indicate the average performance of all the genotypes present in a particular cluster. The cluster mean values for 19 characters are presented in Table 6. A large gap of 32 days existed between cluster XXII (89 days) and cluster XV (121 days) in maturity duration. Similarly, plant height ranged from 60.99 (cluster XIII) to 100.82 cm (cluster XIX), and the number of productive tillers per plant varied from 2.40 (cluster II) to 3.65 (cluster XIV). Larger variation was also noticed for many traits, *viz*., number of fingers per ear, length of the ear, finger length, finger width, number of leaves per main tiller, and flag leaf length.

The number of fingers per ear varied from 5.30 (cluster XXI) to 10.30 (cluster XXII), ear length ranged from 6.52 (cluster XVII) to 15.18 cm (cluster XX), finger length ranged from 4.42 (cluster XVII) to 13.63 cm (cluster XX), and finger width ranged from 0.60 (cluster XIII) to 1.08 cm (cluster XXI). The number of leaves per main tiller varied from 9.10 (cluster XVII) to 25.60 (cluster XXII), flag leaf length ranged from 34.75 (cluster III) to 53.40 cm (cluster XVII) while flag leaf width ranged from 0.95 (XXII) to 1.49 cm (cluster XVII). Length from top node to leaf sheath junction ranged from 7.14 (cluster IX) to 13.80 cm (cluster XX), peduncle length ranged from 5.84 (cluster XII) to 12.87 cm (cluster XVII). There was not much variation in disease incidence. However, grain and fodder yields varied more in between clusters. The average grain yield of cluster V (5250 kg/ha) was almost four times that of cluster V (1222 kg/ha). Similarly, the fodder yield of cluster IV (10499 kg/ha) was double that of cluster IV (5166 kg/ha). The mean performance of the clusters for 19 characters showed that the cluster II, consisting of a single genotype (IC0475882) had the highest grain yield (5250 kg/ha) and was characterized by low disease incidence for leaf blast grade (1.05), neck blast (12.03%), finger blast (17.42%), and banded blight (17.96%). Next, higher grain yields were recorded by clusters IX and XXI. The solitary cluster XIII (IC0283853) recorded the lowest plant height, while the solitary cluster XX (IC0474034) recorded longer ear length (15.18 cm) and finger length (13.63 cm). The solitary cluster XXII consisting of genotype IC0474832 recorded a higher fodder yield (10499 kg/ha) and was also characterized by a greater number of leaves per main tiller (25.60), a number of fingers per ear (10.30), and at the same time, it recorded earliness to maturity with short plant height. All these traits make this cluster very diverse from many other clusters. The cluster XVII with a single genotype (IC0478862) recorded the highest flag leaf length (53.40), flag leaf width (1.49), and peduncle length (12.87). High inter-cluster distance between clusters XXII and XVII can be evidenced because cluster XXII was characterized by early maturity, lower plant height, more number of leaves/plant, and a short and narrow flag leaf along with high fodder yield. In contrast, cluster XVII was with medium maturity, fewer fingers per ear, fewer leaves per main tiller but with a longer and broader flag leaf. The genotypes from these clusters can be used as diverse sources in future breeding programmes. Crossing may bring together the advantageous features of a single genotype, resulting in a larger heterosis because genotypes from both clusters recorded comparatively better yields and each one has individual merit.

Because each cluster is characterized by specific characters based on the improvement goal, genotypes from different clusters can be chosen while keeping the inter-cluster distance in mind. For example, to have a high yielding variety with low disease incidence, genotype IC0475882 from cluster II can be chosen and can be directly used in evaluation trials. In order to get high-yielding, disease-resistant early maturing variety, one has to opt for crossing either IC0329452 from cluster IX, IC043734 from cluster XXI or IC0475882 from cluster II with IC0474832 from cluster XXII, having inter-cluster distances of 84.67, 74.27, and 68.22, respectively. To develop a high-yielding, non-lodging, early

Table 7: Relative contribution of 19 characters towards divergence in finger millet [*Eleusine coracana* (L.) Gaertn.]

S. No	*Character*	*Times ranked*	*Contribution%*
1	Grain yield	1172	10.92%
2	Days to 50% flowering	2036	18.97%
3	Days to maturity	79	0.74%
4	Plant height	667	6.22%
5	Number of productive tillers	211	1.97%
6	Number of fingers per ear	244	2.27%
7	Ear length	2211	20.60%
8	Finger length	71	0.66%
9	Finger width	487	4.54%
10	Number of leaves per main tiller	647	6.03%
11	Flag leaf length	504	4.70%
12	Flag leaf width	226	2.11%
13	Node to leaf sheath junction	218	2.03%
14	Peduncle length	1058	9.86%
15	Fodder yield	405	3.77%
16	Leaf blast	76	0.71%
17	Neck blast	208	1.94%
18	Finger blast	165	1.54%
19	Blanded blight	46	0.43%

maturing variety, a cross between IC0474832 from cluster XXII and IC028353 from cluster XIII will be more effective with an inter-cluster distance of 91.36. Similar results were obtained by Kumar *et al.*, (2010), Rani *et al.*, (2014), Kumari and Singh (2015).

The percent contribution to genetic divergence was computed based on the number of times each of the 19 characters occurred in first place (Table 7). The results showed that the contribution of ear length per plant was the highest towards genetic divergence (20.60) by taking 2211 times to rank first. Similar results were reported by Mahanthesha *et al.*, 2017 and Devaliya *et al.*, 2017. Days to 50% flowering (18.97%) by 2036, grain yield (10.92%) by 1172 times. This implies that a lot of variation existed for ear length and days to 50% flowering while there was no variation for disease incidence.

Conclusion

It was observed that solitary cluster II consisted of a genotype, IC0475882, with high yield and disease resistance, which can be utilized directly after proper evaluation trials. To judiciously combine all the targeted traits into a single genotype, one has to go for hybridization between the selected genotypes from divergent clusters. On the basis of inter-cluster distances and mean values of clusters, crosses can be effected between IC0474832 and IC0478862; IC0329452 and IC0474832; IC043734 and IC0474832; IC0475882 and IC0474832; IC0474832 and IC028353 to have higher grain and fodder yield, disease resistance, earliness, and less plant height.

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