Formation of Core Set in Finger Millet (*Eleusine coracana* (L.) Gaertn.) Germplasm using Geographical Origin and Morpho-agronomic Characters

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Finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm collection involving 4511 accessions at National Active Germplasm Collection Site (NAGS), Project Co-ordination Cell (Small millets), UAS, Bangalore were evaluated for different morpho-agronomic characters over the years. A core set of 551 accessions was formed using this evaluated data by cluster analysis and PCA scoring. Majority of the accessions have Indian origin. The core set formed was true representative of the entire collection and the procedure followed in its formation was appropriate as the statistical analysis indicated that core set did not differ significantly from entire collection. The total diversity present in the entire collection was completely captured in core set. Character association studies revealed that the associations among yield and yield contributing characters found in entire collection were also found in core set. The characters *viz.*, plant height, culm thickness, number of leaves, flag leaf sheath width, flag leaf blade length and width, leaf blade width, days to 50 per cent flowering and days to maturity could be used as indirect selection for high seed yield.

Key Words: Finger millet, Core Set, Diversity, Correlation

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an important food crop in Southern Asia and Eastern Africa. Finger millet popularly known as ragi, ranks third in importance after sorghum and pearl millet, both in area and production providing staple for a large section of farming community in many parts of India. The cultivation of this crop is more widespread compared to other millets and grows from sea level in South India to high lands of Himalayas.

The crop has dual importance as source of food grain as well as straw. Finger millet grain is very nutritious with good quality protein, calcium and other minerals. The cultivated *E. coracana* is a tetraploid (2n=4x=36) and has morphological similarity to both *E. indica* (2n=18) and *E. africana* (2n=36) and is highly variable in its primary centre of origin in Africa and secondary centre of origin in India. India is the major producer of finger millet contributing nearly 60 per cent of the global production.

The success in plant breeding research is closely linked to the availability of appropriate germplasm. Realizing this, National Active Germplasm Collection Site (NAGS), Project Co-ordination Cell, All India Co-ordinated Small Millets Improvement Project (AICSMIP), Bangalore has made an effort in the assemblage of large collection of finger millet germplasm at global level (4511 accessions). Collection and conservation of large number of germplasm pose several problems in various germplasm related activities. To overcome these problems, the concept of developing core collection from the entire germplasm as suggested by Otto Frankel (1984) has been considered as effective strategy for enhancing the utility of germplasm. Considering the importance of finger millet as food and feed crop, especially to harsh agricultural regions in the country, an effort was made to develop a core set from the entire collection of 4511 accessions at Bangalore using all available information on geographical origin and evaluated data on agro-morphological characters.

Materials and Methods

Characterization and Evaluation of Finger Millet Accessions

A total of 4511 accessions of finger millet which includes extensive collections from various parts of Indian subcontinent, African and Asian countries maintained at NAGS, AICSMIP, Bangalore were evaluated at Main Research Station, Gandhi Krishi Vigyan Kendra, Bangalore over the years from 1987 to 2005. The accessions were grown in an augmented design (Federer, 1966) for evaluation. Each accession was grown in one row of 3 m length. The row to row distance was kept at 30 cm and plant to plant distance was kept at 10 cm. Data on 27 descriptors were recorded following the procedures

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given in the Descriptors for finger millet (IBPGR, 1983), FAO, Rome.

For characterization and evaluation, fifteen quantitative characters *viz.*, plant height (cm), culm thickness (cm), number of productive tillers, number of leaves, flag leaf sheath length (cm), flag leaf sheath width (cm), flag leaf blade length (cm), flag leaf blade width (cm), leaf blade length (cm), leaf blade width (cm), peduncle length (cm), number of fingers per ear, days to 50 per cent flowering, days to maturity, grain yield per plant (g) and twelve qualitative characters *viz.*, growth habit, plant pigmentation at flowering, culm branching, ear size, ear shape, grain covering by glumes, grain colour, grain shape, grain surface, grain uniformity, pericarp persistence on seed at maturity, synchrony of ear maturity in each accession were considered for formation of core set.

Formation of Core Set

The initial grouping of accessions was attempted using characterization data such as plant pigmentation, grain colour, grain shape, ear shape etc. The groups thus formed were further subjected to cluster analysis using SYSTAT 9 package. Cluster having large number of accessions was further subjected to Principal Component Analysis (PCA) using package SPLUS 2000. Using PCA scores, around 10 per cent of the accessions in each cluster were selected for inclusion in the core set. The geographical distribution of germplasm accessions in entire collection and the core set were studied. State wise grouping of Indian collections and country wise grouping were made and per cent contribution of accessions from each region was worked out.

Statistical Analysis

The data on quantitative characters was subjected to statistical analysis to calculate mean, range and variance in the entire collection and the core set. The means of the entire collection and core set were compared using Newman–Keuls procedure (Newman, 1939 and Keuls, 1952) for all the fifteen quantitative characters. The homogeneity of variances in the entire collection and core set was tested with Levene's test (Levene, 1960).

Regarding characterization of qualitative characters; according to the finger millet Descriptors, germplasm accessions were counted for each sub-descriptor and their frequencies were worked out both in the entire collection and the core set. Chi-square (χ^2) test was applied to test whether the expected frequencies of accessions under different sub descriptors were present in the core set formed.

The frequency distribution for 15 quantitative characters and also for 12 qualitative characters under different sub-descriptors was calculated. Using this data, Shannon and Weaver (1949) diversity index (H′) was estimated and used as a measure of phenotypic diversity in the entire collection and core set for each character. The phenotypic correlations among yield and yield contributing characters in entire collection and core set were estimated separately, as suggested by Al-Jibourie *et al.* (1958) to know the extent of character associations.

Results and Discussion

A total of 551 accessions of core set was formed from the global collection of 4511 accessions and it constituted 12 per cent of the entire collection. Based on the origin, the accessions of both entire collection and core set were classified according to state wise and also country wise and are presented in Table 1. In the entire collection, maximum number of accessions were from Asia, especially from India. In Indian collections, maximum accessions were collected from Uttar Pradesh, followed by Karnataka and Tamil Nadu. Other states also contributed in small numbers to the entire collections. Africa contributed 27.87 per cent of accessions to the entire collection. Within Africa, maximum accessions were from Malawi and Kenya.

Regarding geographical distribution of germplasm accessions in core set, same trend was observed as in case of entire collection. Maximum accessions were from India (383) followed by African countries. In India, similar trend of distribution of accessions was observed. More number of accessions was from Uttar Pradesh (24.86%) followed by Karnataka (15.06 %) and Tamil Nadu (9.98%). The distribution of accessions in African countries was also similar to that of entire collection. Two countries *viz.*, Malawi (9.98%) and Kenya (8.71%) contributed more accessions to the core set. The similar trend of distribution of accessions according to their origin in both entire collection and core set indicates that the core set truly represents the entire collection and the procedure followed to constitute the core set was appropriate.

Mean, range and variance for 15 quantitative characters in both entire collection and core set is presented in Table 2. Based on Newman-Keuls test, non-significant differences were observed between the entire

Table 1. Number and Percentage of Accessions Present in Different Countries/Continents of Entire Collection and Core Set of Finger Millet Germplasm

S. No.	Continent / Country / State	Entire	Percentage	Core	Percentage
I. Asia					
1	India				
	a) Andhra Pradesh	168	3.72	21	3.81
	b) Bihar	246	5.45	11	2.00
	c) Delhi	54	1.20	3	0.54
	d) Gujarat	17	0.38	2	0.36
	e) Himachal Pradesh	18	0.40	2	0.36
	f) Jammu & Kashmir	6	0.13	1	0.18
	g) Karnataka	654	14.50	83	15.06
	h) Kerala	36	0.8	4	0.73
	i) Madhya Pradesh	121	2.68	9	1.63
	j) Maharashtra	244	5.41	37	6.72
	k) NEFA	16	0.35	1	0.18
	l) Orissa	85	1.88	11	2.00
	m) Punjab	5	0.11	–	–
	n) Rajastan	1	0.02	–	–
	o) Sikkim	44	0.98	6	1.09
	p) Tamil Nadu	451	10.00	55	9.98
	q) Unknown states	12	0.27	–	–
	r) Uttar Pradesh	1051	23.30	137	24.86
	s) West Bengal	2	0.04	–	–
	Total (India)	**3231**	**71.62**	**383**	**69.51**
2	Japan	3	0.07	3	0.54
3	Nepal	8	0.18	–	–
4	Sri Lanka	12	0.27	3	0.54
	Total (Asia)	**3254**	**72.13**	**389**	**70.60**
II. Africa					
1	Burundi	1	0.02	–	–
2	Ethiopia	16	0.35	2	0.36
3	Kenya	379	8.40	48	8.71
4	Malawi	412	9.13	55	9.98
5	Mozambique	1	0.02	–	–
6	Sudan	7	0.16	–	–
7	Tanzania	23	0.51	4	0.73
8	Uganda	181	4.02	24	4.36
9	Unknown African country	54	1.20	10	1.81
10	Zambia	92	2.04	12	2.18
11	Zimbabwe	91	2.02	7	1.27
	Total (Africa)	**1257**	**27.87**	**162**	**29.40**
	GRAND TOTAL	**4511**		**551**	

and core set for all the quantitative characters studied. The homogeneity test (Levene's test) revealed that the variance of entire collection was homogenous with the variance of core set for all the quantitative characters studied. The range for the characters studied in the core set was similar to the range in the entire collection for all the quantitative characters studied. Scores were recorded for 12 qualitative characters (morpho-agronomic) for both entire and core collection according to the Descriptors for finger millet and presented in Table 3. The chi-square (χ^2) value for frequency distribution of accessions under different sub-descriptors of entire collection and that of core set revealed non significant differences for all the qualitative characters studied. All these tests indicate that the core set formed represents the entire collection of finger millet.

Estimates of Shannon-Weaver diversity index (H′) for all the characters both in entire and core set are presented in Table 4. This index indicates the presence of genetic diversity for a character. The indices for all the characters in core set were similar to that in entire collection. The average of H′ values for 15 quantitative characters and 12 qualitative characters in core set was also similar to that in entire collection. This indicates that the diversity present in the entire collection was represented in the core set formed.

Table 2. Comparison of Mean, Range and Variance for the Quantitative Characters in the Entire Collection and Core Set of Finger Millet Germplasm

S. No.	Character	Mean			Range		Variance		
		Entire	Core	T test	Entire	Core	Entire	Core	F test
1	Plant height (cm)	94.79 ± 0.26	95.85 ± 0.848	NS	33.0 – 153.0	33.0 – 153.0	311.03	396.02	NS
2	Culm thickness (cm)	0.85 ± 0.002	0.86 ± 0.007	NS	0.4 – 1.9	0.4 – 1.9	0.02	0.03	NS
3	Number of productive tillers	3.94 ± 0.019	3.96 ± 0.052	NS	1.0 – 10.0	1.0 – 9.0	1.59	1.60	NS
4	Number of Leaves	9.75 ± 0.028	9.89 ± 0.087	NS	4.0 – 17.0	4.0 – 16.0	3.430	4.22	NS
5	Flag leaf sheath length (cm)	10.15 ± 0.031	10.21 ± 0.086	NS	2.0 – 28.0	4.6 – 17.0	4.28	4.31	NS
6	Flag leaf sheath width (cm)	1.09 ± 0.002	1.095 ± 0.006	NS	0.4 – 1.7	0.7 – 1.7	0.02	0.02	NS
7	Flag leaf blade length (cm)	33.95 ± 0.105	34.63 ± 0.349	NS	11.5 – 60.5	14.9 – 60.5	49.90	67.20	NS
8	Flag leaf blade width (cm)	1.03 ± 0.002	1.047 ± 0.008	NS	0.5 – 2.0	0.6 – 2.0	0.02	0.03	NS
9	Leaf blade length (cm)	45.92 ± 0.114	45.1 ± 0.390	NS	20.9 – 70.2	21.0 – 70.2	58.12	83.60	NS
10	Leaf blade width (cm)	1.18 ± 0.002	1.196 ± 0.008	NS	0.5 – 2.0	0.6 – 2.0	0.03	0.03	NS
11	Peduncle length (cm)	22.82 ± 0.055	22.92 ± 0.162	NS	9.2 – 41.0	9.2 – 34.0	13.84	14.43	NS
12	Finger number	7.01 ± 0.018	7.01 ± 0.053	NS	3.0 – 13.0	3.0 – 11.0	1.44	1.54	NS
13	Days to 50% flowering	59.79 ± 0.106	60.45 ± 0.337	NS	40.0 – 79.0	44.0 – 78.0	50.79	62.59	NS
14	Days to maturity	102.20 ± 0.146	103.06 ± 0.468	NS	80.0 – 129.0	80.0 – 128.0	96.51	120.87	NS
15	Grain yield per plant (g)	12.90 ± 0.100	13.54 ± 0.342	NS	1.0 – 48.8	1.7 – 45.2	45.37	64.43	NS

NS: Non significant at P = 0.05

Table 3. Descriptors, Descriptor State, Score Code and Phenotypic Proportions in Entire Collection (E) and Core Set (C) of Finger Millet Germplasm

S.No.	Descriptor	Descriptor state	Score code	E	C	χ^2
1	Growth habit	Decumbent	3	1786	228	
		Erect	5	2671	314	1.7809^{NS}
		Prostrate	7	54	9	
2	Plant pigmentation	Non pigmented	0	3049	377	
	at flowering	Pigmented	1	1462	174	0.1736^{NS}
3	Culm branching	Absent	0	2170	286	
		Present	1	2341	263	3.4958^{NS}
4	Ear shape	Droopy	1	93	17	
		Open	2	1581	190	
		Semi-compact	3	2381	274	8.1047^{NS}
		Compact	4	379	56	
		Fist	5	77	14	
5	Ear size	Small	3	1108	127	
		Intermediate	5	2865	340	4.6398^{NS}
		Large	7	538	85	
6	Grain covering by	Exposed	3	647	93	
	Glumes	Intermediate	5	2252	264	2.9585^{NS}
		Enclosed	7	1612	194	
7	Grain colour	White	1	16	5	5.0450^{NS}
		Light brown	2	1795	212	
		Copper brown	3	1710	210	
		Purple brown	4	990	123	
8	Grain shape	Round	1	2959	364	
		Reniform	2	1498	181	0.1215^{NS}
		Ovoid	3	54	6	
9	Grain surface	Smooth	1	4120	506	
		Wrinkled	2	391	45	0.2185^{NS}
10	Grain uniformity	Not uniform	0	1075	122	
		uniform	1	3436	429	0.8235^{NS}
11	Pericarp persistence	Non persistent	0	903	108	
	on seed after	Partially persistent	3	2950	370	1.0007^{NS}
	threshing	Persistent	7	657	73	
12	Synchrony of ear	Non synchronous	0	1863	227	0.0050^{NS}
	maturity	Synchronous	1	2648	324	

^{NS}: Non significant at P = 0.05

Table 4. Shannon–Weaver Diversity Index (H') for 15 Quantitative and 12 Qualitative Characters in the entire Collection and Core Set of Finger Millet

S.No.	Character	Shannon–Weaver Index	
		Entire	Core
	Quantitative character		
1	Plant height	1.808	1.917
2	Culm thickness	1.283	1.445
3	Number of productive tillers	1.613	1.588
4	Number of Leaves	1.504	1.651
5	Flag leaf sheath length	1.214	1.220
6	Flag leaf sheath width	1.528	1.588
7	Flag leaf blade length	1.782	1.904
8	Flag leaf blade width	1.415	1.500
9	Leaf blade length	1.857	2.013
10	Leaf blade width	1.386	1.448
11	Peduncle length	1.535	1.536
12	Number of fingers	1.583	1.620
13	Days to 50% flowering	1.975	2.057
14	Days to Maturity	2.069	2.187
15	Grain yield	1.646	1.802
	Mean ± SE	**1.613 ±0.064**	**1.698 ±0.070**
	Qualitative character		
1	Growth habit	0.730	0.753
2	Plant pigmentation at flowering	0.630	0.624
3	Culm branching	0.692	0.693
4	Ear size	0.887	0.924
5	Ear shape	1.062	1.148
6	Grain covering by glumes	0.993	1.020
7	Grain colour	1.087	1.113
8	Grain shape	0.696	0.688
9	Grain surface	0.295	0.281
10	Grain uniformity	0.549	0.529
11	Pericarp persistence on seed at maturity	0.880	0.854
12	Synchrony of ear maturity	0.678	0.677
	Mean ± SE	**0.765 ±0.066**	**0.775 ±0.072**
	Overall mean ± SE	**1.236 ±0.094**	**1.288 ±0.103**

The effect of each yield contributing characters on yield improvement in finger millet was analyzed through character association studies. Estimates of phenotypic correlation coefficients for 15 quantitative characters in both entire and core set are presented in Table 4. Out of 105 correlations, 64 correlations were significant in both entire and core set. This indicates a good representation of phenotypic correlations of characters from entire collection to the core set. The characters namely, culm thickness, number of productive tillers, number of leaves, flag leaf sheath width, flag leaf blade length and width, leaf blade width, days to 50 per cent flowering, days to maturity were positively associated and flag leaf sheath length was negatively associated with grain yield in both entire and core set. But, plant height was positively correlated with grain yield only in core set.

Among different characters studied, the significant correlations between characters found in entire collections were also found in core set. Characters *viz.*, plant height, culm thickness, number of leaves, flag leaf blade length, flag leaf blade width, days to 50% flowering and days to maturity were correlated with each other in both entire collection and core set. Hence in future characterization of finger millet germplasm, plant height, culm thickness, number of leaves, flag leaf sheath width, flag leaf blade length and width, leaf blade width, days to 50 per cent flowering and days to maturity could be used as indirect measure to select for high yield.

It can be concluded that the core set involving 551 accessions formed from 4511 accessions of entire collection of finger millet is a true representative of entire collection and has all the diversity present in the entire collection. The core set thus selected comprised accessions with higher diversity representing the entire coverage of variability giving accurate reproducible list of entries of core whenever repeated. This avoids the repeating of useful alleles thus enhancing their richness. Hence this core set can be used in future for effective screening of the finger millet germplasm for identifying the sources of desirable characters. The method followed in the formation of core set was correct and core set represents the entire set.

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