Establishing a core set from global collection of finger millet [*Eleusine coracana* (L.) Gaertn]

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ABSTRACT

In the present investigation core set of finger millet germplasm was formed using data on geographical distribution and agro-morphological traits by using software called Power Core (v.1.0) which yielded core set consisting of 221 accessions. In the core set formed, majority of the accessions were from Asian continent. Percentage of significance difference between the entire collection and core set for means and variances suggested that the core collection represents the entire collection. Coincident rate for distribution of ranges, variable rate for coefficient of variation values, Newman-Keuls' test for means, Levene's test for variances, Chi-square test for frequency distribution analysis and Shannon-Weaver diversity index for different traits indicated that the variation available in the entire collection has been preserved in the core set. This indicates that the method followed in the formation of core set by using the software 'Power Core' (v.1.0) was appropriate and core set represents the entire collection.

Key words : Core set, Diversity index, Finger millet, Power core

INTRODUCTION

Finger millet [*Eleusine coracana* (L.) Gaertn.] is an important food crop in Africa and South Asia. It is a hardy crop that can be grown in diverse environments from almost at sea level in South India to high lands of Himalayas. It has dual importance as a source of food grain as well as straw. Finger millet provides staple food for a large section of farming community in many parts of India. The native home of finger millet is presumed to be highlands of Central Africa and India is often considered as secondary centre of diversity.

Finger millet is very nutritious with good quality protein, plentiful minerals, dietary fibres, phytochemicals and vitamins. The grain has very good malting qualities providing opportunities in expanding its utility range in food processing and value addition. It is used in the production of beer, porridge, soup, bread, cake and pudding. Despite all these merits, this crop has been neglected from the main stream of crop improvement programme. One of the means to boost its production and productivity is to enhance utilization of finger millet germplasm to breed superior varieties.

Recognizing the importance of collection, conservation and easy access of finger millet germplasm to the breeders, the All India Co-ordinated Small Millets

Improvement Project (AICSMIP) established a germplasm unit at Bangalore in 1979 which has finger millet collection exceeding 6500 accessions. With the rapid increase in the number of accessions contained in crop germplasm collections, redundant resources have become an obstacle to the effective maintenance and utilization of these collections. Realizing this difficulty, the concept of forming core collection forms a very effective alternative from the point of enhancing the utility of conserved germplasm. The use of core collections to improve access to large, unwieldy collections, originally envisioned by Sir Otto Frankel (1984). A core collection consists of a limited number of accessions derived from a whole germplasm collection, chosen to represent the genetic spectrum in the whole collection and includes as much as possible of its genetic diversity.

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 core set from the entire collection. The core set was developed from the entire collection of 4511 accessions at Bangalore using all available information on geographical origin and evaluated data on agro-morphological characters. The objective of this study was to develop a core set of finger millet germplasm accessions by utilizing PowerCore (v.1.0) software and to compare the core set developed

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with entire collection based on phenotypic variation.

MATERIALS AND METHODS

Formation and evaluation of core set:

Germplasm accessions in finger millet evaluated at Project Co-ordination Cell (Small Millets), AICSMIP, Bangalore were used in the study. Totally 4511 accessions were evaluated in different years from 1987 to 2005 for both qualitative and quantitative traits at the Zonal Agricultural Research Station, GKVK, Bangalore. The evaluated data of six years *viz.,* 1987, 1988, 1989, 1990, 2002 and 2003 was used to form the core set by using the software 'PowerCore'(v.1.0) which was developed by Genetic Resource Division, Rural Development Administration, Republic of Korea. The design concept and implementation strategy of 'PowerCore' and the validation on the outcome in comparison with other methods has been well described by Kyu – Won Kim *et al.* (2007). Data on twenty seven descriptors available for these accessions were used for forming core germplasm (Anonymous, 1985), FAO, Rome. A core set of 221 accessions was formed by running each six years data separately.

PowerCore software uses the NET Frame work version 1.1 environment and is freely available for the MS windows platform (http://genebank.rda.go.kr/ 'powercore'/). This new method is used for the establishment of core and allele mining set by the advanced M (Maximization) strategy implemented through a modified Heuristic Algorithm. The experiment was laid out in a 15 x 15 simple lattice design with two replications (Cochran and Cox, 1957).

For characterization and evaluation, 18 quantitative characters *viz.,* plant height (cm), culm thickness (cm), number of productive tillers, flag leaf blade length (cm), flag leaf blade width (cm), peduncle length (cm), finger number, finger length (cm), finger width (cm), days to 50 per cent flowering, test weight (g), straw yield per plant (g), ear weight (g), grain yield per plant (g), total biomass (g), harvest index, blast on neck (%), blast on finger (%) 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, synchrony of ear maturity in each accession were considered.

Comparison of formulated core set with entire collection:

The accessions in the entire collection and core set were classified according to their place of origin and their percentages were calculated and compared. The quantitative data were subjected to statistical analysis to estimate mean, range, coefficient of variability and variance and the same were compared to determine whether the core sets formed represents the entire collection for the diversity present. The mean data of entire collection and core set was compared using Newman-Keuls test and Levene's (1960) test was used to test the homogeneity of variance of entire collection and core set.

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 entire and core set given in Table 1. The ratio of different sub descriptors of qualitative traits of entire collection and core set were compared using chi-square test (χ^2). Chi-square 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 quantitative characters and also for qualitative characters under different sub-descriptors was calculated. Using this data, Shannon and Weaver (1949) diversity index (H') was estimated for both qualitative and quantitative characters.

RESULTS AND DISCUSSION

A core set of finger millet consisting of 221 accessions was formed from the entire collection of 4511 accessions by using the software called 'PowerCore' (v.1.0). The core set constituted 4.89 per cent of the entire collection. Geographical regions, countries, number of accessions and their percentage of core set as compared to entire collection are presented in Table 1. Regarding geographical distribution of germplasm accessions in entire collection, maximum accessions were from Asian continent (3254 and 72.13%) followed by African countries (1257 and 27.87%). Among Asian countries, more number of accessions was from India (3231 and 71.62%). In Indian subcontinent, Uttar Pradesh (1051 and 23.30%) was represented with more number of accessions followed by Karnataka (654 and 14.50%) and Tamil Nadu (451 and 10 per cent), while other states represented with less number of accessions. Among African countries, Malawi (412 and 9.13%) Kenya (379 and 8.4%) and Uganda (181 and 4.02%) represented with more number of accessions.

The total number of accessions in core set was 221 which included entries from seven different countries representing most of the geographic regions where finger millet is grown. The composition of the core collection

Table 1 : Number and percentage of accessions contributed from different countries / continents to entire collections and core set of finger millet germplasm

Sr. No.	Continent / Country / State	Entire	Percentage	Core	Percentage
Asia					
1	India				
	Andhra Pradesh	168	3.72	10	4.53
	Bihar	246	5.45	16	7.24
	Delhi	54	1.20	2	0.91
	Gujarat	17	0.38	-	-
	Himachal Pradesh	18	0.40	-	-
	Jammu & Kashmir	6	0.13	1	0.45
	Karnataka	654	14.50	33	14.93
	Kerala	36	0.8	1	0.45
	Madhya Pradesh	121	2.68	6	2.72
	Maharashtra	244	5.41	13	5.88
	North eastern states	16	0.35	-	-
	Orissa	85	1.88	3	1.36
	Punjab	5	0.11	-	-
	Rajasthan	1	0.02	-	-
	Sikkim	44	0.98	3	1.36
	Tamil Nadu	451	10.00	21	9.5
	Unknown states	12	0.27	1	0.45
	Uttar Pradesh	1051	23.30	49	22.17
	West Bengal	2	0.04	-	-
	Total (India)	3231	71.62	159	71.95
2	Japan	3	0.07	-	-
3	Nepal	8	0.18	-	-
4	Sri Lanka	12	0.27	-	-
	Total (Asia)	3254	72.13	159	71.95
Africa					
1	Burundi	1	0.02	-	-
2	Ethiopia	16	0.35	2	0.91
3	Kenya	379	8.40	19	8.59
4	Malawi	412	9.13	20	9.05
5	Mozambique	1	0.02	-	-
6	Sudan	7	0.16	-	-
7	Tanzania	23	0.51	-	-
8	Uganda	181	4.02	9	4.07
9	Unknown African country	54	1.20	2	0.91
10	Zambia	92	2.04	5	2.26
11	Zimbabwe	91	2.02	5	2.26
	Total (Africa)	1257	27.87	62	28.05
	Grand total	4511		221	

reflects the predominance of accessions from India and some of the African countries both representing the dry semi-arid tropical ecology. Among the continents, maximum accessions were from Asia (India – 159 and 71.95%) followed by African countries (62 and 28.05%). In India, more number of accessions was from Uttar Pradesh (49 and 22.17%), Karnataka (33 and 14.93%) and Tamil Nadu (21 and 9.5%). The distribution of accession in African countries was also similar to that of

entire collection. Two countries *viz.,* Malawi (20 and 9.05%) and Kenya (19 and 8.59%) contributed more accessions to the core set. Similar trend of distribution of accessions according to their origin in both entire collection and core set implies that core set truly represents the entire collection indicating that sampling technique followed to constitute the core was appropriate.

The percentage of significance difference between the entire collection and core set was calculated for the

Table 2 : Number of accessions selected as core set from the data of different years and properties of core set

Year of evaluation	Number of accessions			Mean difference (%)	Variance difference (%)	Coincidence rate (%)	Variable rate (%)	Coverage (%)
	Total	Core	Percentage					
1987	992	46	4.64	5.92	31.07	96.71	73.64	100
1988	993	38	3.83	4.84	29.22	97.33	74.66	100
1989	958	32	3.34	6.70	30.25	96.43	75.95	100
1990	997	28	2.81	6.77	34.58	96.38	73.40	100
2002	638	68	10.66	15.59	44.78	96.12	64.29	100
2003	502	9	1.79	12.54	48.87	95.95	58.01	100
Total	5080	221	4.35					

Table 3 : Comparison of mean, range and variance for the quantitative characters in the entire collection and core set of finger millet germplasm

Sr. No.	Character	Mean ± SE		t test	Range		Variance		F test
		Entire	Core		Entire	Core	Entire	Core	
1.	Plant height (cm)	94.79 ± 0.26	96.02 ± 1.34	0.918[NS]	33.0 – 153.0	33.0 -153.0	311.03	398.23	0.781[NS]
2.	Culm thickness (cm)	0.85 ± 0.002	0.87 ± 0.014	1.428[NS]	0.4 – 1.9	0.4 – 1.9	0.02	0.04	0.500[NS]
3.	Number of productive tillers	3.94 ± 0.019	4.05 ± 0.09	1.222[NS]	1.0 – 10.0	1.0 – 9.0	1.59	1.63	0.975[NS]
4.	Number of leaves	9.75 ± 0.028	9.9 ± 0.142	1.056[NS]	4.0 – 17.0	4.0 – 16.0	3.430	4.51	0.762[NS]
5.	Flag leaf blade length (cm)	33.95 ± 0.105	34.78 ± 0.56	1.482[NS]	11.5 – 60.5	14.9 – 60.5	49.90	69.3	0.720[NS]
6.	Flag leaf blade width (cm)	1.03 ± 0.002	1.05 ± 0.015	1.333[NS]	0.5 – 2.0	0.6 – 2.0	0.02	0.052	0.385[NS]
7.	Peduncle length (cm)	22.82 ± 0.055	23.28 ± 0.262	1.755[NS]	9.2 – 41.0	9.2 – 38.0	13.84	15.23	0.908[NS]
8.	Finger number per ear	7.01 ± 0.018	7.10 ± 0.087	1.035[NS]	3.0 – 13.0	3.0 – 11.0	1.44	1.68	0.857[NS]
9.	Days to 50% flowering	59.79 ± 0.106	60.83 ± 0.543	1.915[NS]	40.0 – 79.0	44.0 – 78.0	50.79	65.23	0.778[NS]
10.	Days to maturity	102.20 ± 0.146	103.6 ± 0.753	1.859[NS]	80.0 – 129.0	82.0 – 128.0	96.51	125.34	0.769[NS]
11.	Grain yield per plant (g)	12.90 ± 0.100	14.02 ± 0.614	1.824[NS]	1.0 – 48.8	1.7 – 45.2	45.37	83.26	0.545[NS]

NS=Non-significant

mean difference percentage (MD %) and the variance difference percentage (VD %) (Hu *et al.,* 2000). The coincidence rate (CR %) and the variable rate (VR %) were calculated to evaluate the properties of core collection. For the validation, different statistical parameters were analyzed to compare the mean and variance ratio between core and entire collection and presented in Table 2. For the present study maximum number of classes (10) for each variable was used so that more diversity can be captured in the core sets. The results showed that there was no significant difference (α=0.05) for the means of all traits between each of the six core collections and the entire collections. Coincidence rate (CR %) values for all core collections is greater than 80 per cent. Further, core collection with a large VD and VR per cent is considered to provide a good representation of the genetic diversity of the entire collection suggesting that variation observed in core collection was higher than the entire collection and the selected accession were more dispersed and diverse. The VR per cent for all the core

collections indicated that the coefficient of variation for all the traits in all the six core collections were greater in core collections compared to entire collections which indicates that the sample six of the core set was adequate. The core sets resulted showed 100 per cent coverage for all the six core collection. Therefore, it is evident that the properties of core collection developed by 'PowerCore' were stable and feasible.

Mean, range and variance for 15 quantitative characters in both entire collection and core set is presented in Table 3. Based on Newman-Keuls test, non-significant differences were observed between the entire and core set for all the quantitative characters studied. 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 10 qualitative characters

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Table 4 : Descriptors, descriptor state, score code and phenotypic proportions in entire collection (E), and core (C) of finger millet germplasm

Sr. No.	Descriptor	Descriptor state	Score code	E	C	χ^2
1.	Growth habit	Decumbent	3	1786	93	2.4384[NS]
		Erect	5	2671	127	
		Prostrate	7	54	5	
2.	Plant pigmentation at flowering	Non pigmented	0	3049	151	0.0236[NS]
		Pigmented	1	1462	74	
3.	Culm branching	Absent	0	2170	114	0.5916[NS]
		Present	1	2341	111	
4.	Ear shape	Droopy	1	93	6	7.8552[NS]
		Open	2	1581	73	
		Semi-compact	3	2381	117	
		Compact	4	379	20	
		Fist	5	77	9	
5.	Ear size	Small	3	1108	59	0.3599[NS]
		Intermediate	5	2865	139	
		Large	7	538	27	
6.	Grain covering by glumes	Exposed	3	647	35	0.2709[NS]
		Intermediate	5	2252	111	
		Enclosed	7	1612	79	
7.	Grain colour	White	1	16	2	3.5602[NS]
		Light brown	2	1795	92	
		Copper brown	3	1710	90	
		Purple brown	4	990	41	
8.	Grain shape	Round	1	2959	162	4.3409[NS]
		Reniform	2	1498	60	
		Ovoid	3	54	3	
9.	Grain surface	Smooth	1	4120	204	0.1259[NS]
		Wrinkled	2	391	21	
10.	Synchrony of ear maturity	Non synchronous	0	1863	93	0.0001[NS]
		Synchronous	1	2648	132	

NS : Non-signifiant

for both entire and core collection according to the Descriptors for finger millet and presented in Table 4. 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 indicated that the core set formed represents the entire collection of finger millet.

Estimates of Shannon and Weaver (1949) diversity index (H') for all the characters both in entire and core set are presented in Table 5. 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 9 quantitative characters and 10 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.

It can be concluded that, the core set involving 221 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. Hence, this core set can be used in future for effective screening of the finger millet germplasm for identifying the sources of desirable characters. This indicates that the method followed in the formation of core set by using the software 'PowerCore' (v.1.0) was correct and core set represents the entire collection. Thus, 'PowerCore' (v.1.0) is a new faster approach for developing core collection, which effectively simplifies

Sr. No.	Characters	Shannon–weaver diversity index	
		Entire	Core
	Quantitative character		
1.	Plant height	1.808	2.016
2.	Culm thickness	1.283	1.379
3.	Number of productive tillers	1.613	1.037
4.	Flag leaf blade length	1.782	1.736
5.	Flag leaf blade width	1.415	1.986
6.	Peduncle length	1.535	1.885
7.	Number of fingers per ear	1.583	1.795
8.	Days to 50% flowering	1.975	2.133
9.	Grain yield per plant	1.646	1.507
	Mean ± SE	1.627 ± 0.07	1.719 ± 0.117
	Qualitative character		
1.	Growth habit	0.730	0.773
2.	Plant pigmentation at flowering	0.630	0.633
3.	Culm branching	0.692	0.693
4.	Ear size	0.887	0.903
5.	Ear shape	1.062	1.146
6.	Grain covering by glumes	0.993	1.006
7.	Grain colour	1.087	1.084
8.	Grain shape	0.696	0.647
9.	Grain surface	0.295	0.310
10.	Synchrony of ear maturity	0.678	0.678
	Mean ± SE	0.775 ± 0.076	0.787 ± 0.080
	Overall mean ± SE	1.178±0.112	1.229 ± 0.129

Table 5 : Shannon–Weaver diversity index (H') for 9 quantitative and 10 qualitative characters in the entire collection and core set of finger millet

the generation process of a core set with a reduced number of core entries and maintaining high per cent of diversity to other methods used.

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