Augmenting the Pearl Millet Core Collection for Enhancing Germplasm Utilization in Crop Improvement

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ABSTRACT

Developing a core collection that represents the diversity of entire collection is an efficient approach to enhance the use of germplasm in crop improvement. Core collections are dynamic and need to be revised when additional germplasm and information become available. In the present study, the pearl millet [*Pennisetum glaucum* (L.) R. Br.] core collection, consisting of 1600 accessions selected from about 16,000 accessions characterized at the International Crops Research Institute for the Semi-Arid Tropics Genebank by 1998, was augmented by adding 501 accessions representing 4717 accessions assembled and characterized in the past 9 yr. The revised core consists 2094 accessions. (Five duplicate and two male sterile accessions were deleted from original core collection.) A comparison of mean data using Newman–Keuls test, variance using Levene's test, and distribution using χ^2 test indicated that the variation in the entire collection of 20,766 accessions was preserved in the revised core collection. A few important phenotypic correlations that may be under coadapted gene complexes were preserved in the revised core collection. The Shannon–Weaver diversity index for different traits was similar in the revised core and entire collection. The revised core collection was observed to be more valuable than the original core as it has sources of resistance for important diseases such as downy mildew. The revised core collection could be a point of entry to the proper exploitation of pearl millet genetic resources for crop improvement.

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Abbreviations: CR%, coincidence rate; ICRISAT, International Crops Research Institute for the Semi-Arid Tropics; VR%, variable rate.

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is an important cereal crop cultivated mostly in the arid and semiarid tropics of Africa and Asia for grain and forage and for forage in Korea and the Americas. It has immense potential for adaptation to the extreme limits of agriculture. It is cultivated mainly in Niger, Nigeria, Burkina Faso, Togo, Ghana, Mali, Senegal, the Central African Republic, Cameroon, Sudan, Botswana, Namibia, Zambia, Zimbabwe, and South Africa in Africa and India, Pakistan, and Yemen in Asia for grain and forage. Success in crop improvement programs depends largely on the extent of genetic variability available to the researchers. Because of its allogamous nature, pearl millet landraces are highly heterogeneous, resulting in large variability within and among these landraces. The remarkably large variability for agronomically important traits in the collection makes it a difficult crop to handle by genebank curators and breeders for both genetic conservation and utilization.

As the importance of genetic diversity for sustainable crop improvement and the potential threat to diversity from large-scale replacement of landraces by high-yielding cultivars was recognized, the collection and conservation of a large number of germplasm accessions was undertaken as a priority. Systematic efforts were made at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) to collect and conserve

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the available pearl millet diversity, and 20,844 accessions of cultivated and 750 accessions of wild relatives originating from 50 countries were assembled. In most crops, including pearl millet, entire crop diversity has not been collected and conserved ex situ, and efforts are ongoing to collect the remaining diversity. As a result, the amount of genetic diversity conserved in ex situ collections is increasing (Cox et al., 1986; Duvick, 1984). A large gap exists, however, between availability and actual use of the materials (Peeters and Galwey, 1988; Wright, 1997; Upadhyaya et al., 2006; Upadhyaya et al., 2007). This is true for different crops in national programs as well as in the international breeding programs. Jiang and Duan (1998) in China and Upadhyaya et al. (2003) at ICRISAT, for example, reviewed the use of groundnut (*Arachis hypogaea* L.) germplasm in crop improvement. In China, the introduced germplasm and wild relatives have seldom been used in crop improvement (Jiang and Duan, 1998), and at ICRISAT <1% of groundnut germplasm was used in breeding during 1976 to 2001. In several other crops, such as wheat (*Triticum aestivum* L.) (Dalrymple, 1986), spring barley (*Hordeum vulgare* L.) (Vellve, 1992), maize (*Zea mays* L.) (Dowswell et al., 1996), pigeonpea (*Cajanus Cajan* L.) (Shiv Kumar et al., 2004), and chickpea (*Cicer arietinum* L.) (Upadhyaya et al., 2006) limited use of germplasm has been reported. In pearl millet, a very few of the 21,594 germplasm accessions have been utilized in development of cultivars (Bhattacharjee et al., 2007). The plant breeders prefer to work with their own lines rather than exotic materials (Cox et al., 1988; Duvick, 1995). This approach has resulted in narrowing the genetic base of cultivated pearl millet, which needs to be broadened through greater use of variability conserved in genebanks.

The main reason for the low use of germplasm is the large size of collections and the unavailability of information on traits of economic importance to enable breeders to choose parents for use in breeding programs (Goodman, 1990; Peeters and Williams, 1984). To overcome size-related problems, Frankel (1984) proposed the development of a core collection (10% of an entire collection) that represents the diversity of the crop. The core collection can be extensively evaluated, and the information derived can be used to plan a more efficient utilization of the entire collection (Tohme et al., 1995; Brown, 1989; Upadhyaya et al. 2001b, 2005; Upadhyaya, 2005). Core collections are dynamic and should be revised as additional accessions and information become available (Upadhyaya et al., 2001a) for proper and enhanced utilization of germplasm. A core collection of pearl millet was developed in 1998 using data available through 31 Dec. 1997 for 11 agronomic traits on 16,063 accessions (total accessions available: 20,642) (Bhattacharjee et al., 2007). However, this collection was published after almost 10 years (Bhattacharjee et al., 2007). Meanwhile, concerted efforts were made to collect and assemble additional germplasm and complete the characterization and evaluation of pearl millet germplasm for different morphological and agronomic characteristics. Thus, we have additional data on 4717 accessions for 10 morphological and 12 agronomic traits. The main aim of this study was to augment the pearl millet core collection developed by Bhattacharjee et al. (2007) by adding additional accessions representing new 4717 accessions in such a way that not only does the added sample represent the new accessions but the new core represents the entire collection of pearl millet as June 2007.

MATERIALS AND METHODS

The ICRISAT genebank conserves 21,594 pearl millet accessions from 50 countries. Of these, 20,844 accessions are cultivated, including 78 male sterile accessions. Bhattacharjee et al. (2007) developed a pearl millet core collection (1600 accessions) using data on 11 quantitative traits for 16,063 accessions that included 14 male sterile lines. That core collection consisted of five accessions that were duplicate and two accessions that were male sterile. In our study, we excluded these seven accessions, and the core we used for updating consisted of 1593 accessions. We now have full characterization data for 10 morphological and 12 agronomic traits on an additional 4717 accessions (total: 20,766 accessions, excluding 78 male steriles). The newly acquired and characterized 4717 were used to select the representative sample that when added to the 1593 core accessions, results in a revised core collection that represents the entire collection.

The 4717 additional accessions were characterized and evaluated in an augmented design, repeating one of the three control cultivars ('ICTP 8203', 'WC C 75', 'Raj 171') after every 10 test entries, in the alfisol-Patancheru Soil Series (Udic Rhodustolf) fields in the rainy (June–October) and postrainy (November–March) seasons at Patancheru (18°N, 78°E, 545 m above sea level, and 600 km away from sea), Andhra Pradesh, India. Data for the two seasons for plant height, days to 50% flowering, panicle length, and width were considered separately because of the large differences for these traits between rainy and postrainy seasons (Appa Rao et al., 1986). Four other traits (number of productive and total tillers, panicle exsertion, and 1000-seed weight) were recorded only in the rainy season. Each plot consisted of two 4-m rows, with row spacing of 75 cm and plant-to-plant spacing of 10 cm. Care was taken to ensure uniform planting depth of 3 cm. The experimental field received 150 kg di-ammonium phosphate as a basal dose at the time of field preparation and 100 kg urea as topdressing 20 d after sowing. The experiments received life-saving irrigation in the rainy season and about 12 irrigations in the postrainy season, each irrigation with 5 cm water depth. The crop was protected from weeds.

Data on 10 morphological traits (synchrony of panicle maturity, panicle shape, spikelet density, bristle length, seed shape, seed color, endosperm texture, fodder yield potential, seed yield potential, and overall plant aspect) and 12 agronomic traits (days to 50% flowering in rainy and postrainy, plant height in rainy and postrainy, number of total and productive tillers, panicle length and width in rainy and postrainy, panicle exsertion, and 1000-seed weight) were recorded following pearl

millet descriptors (IBPGR and ICRISAT, 1993). In each accession, five representative plants were selected to record observations on plant height (cm), panicle exsertion, length and width, and number of total and productive tillers. Days to 50% flowering (days from sowing to the stage when 50% of plants have begun flowering), and 1000-seed weight (g) were recorded on a plot basis. Synchrony of panicle maturity, bristle length, fodder yield potential, seed yield potential, and overall plant aspect are visual observations, recorded over plot basis as score on a 1 to 9 scale, where 1 = poorest and 9 = best.

Phenotypic distance matrix was created for 4717 accessions following the procedure described by Johns et al. (1997), which is based on Gower's (1985) method. For each trait, the distance between two accessions was calculated as the difference between phenotypic values divided by the range of that trait. Thus, the distance for the traits was on a 0 to 1 scale. The distance matrixes was constructed by adding individual trait distances for each pair and dividing by the number of traits scored in both lines. This distance matrix was subjected to hierarchical cluster algorithm of Ward (1963) at an R^2 of 0.75 using SAS 9.1.3. (SAS Institute, 2006). This method optimizes an objective function because it minimizes the sum of squares between groups. The proportional sampling strategy was used, and approximately 10% of the accessions or a minimum of one from each cluster was randomly selected to form a representative sample of 4717 accessions.

Frequencies for country of origin and regions were calculated and compared for the entire collection and revised core collection using χ^2 tests (Table 1). Yates correction was applied where the number of accessions in the entire collection was less than five. Frequency distributions of classes for all the morphological traits were evaluated by the χ^2 test (Table 2). The means for the entire and revised core, newly characterized and its representative sample, were compared by Newman–Keuls procedure (Newman, 1939; Keuls, 1952). Homogeneity of variances was tested by Levene's test (Levene, 1960). The coincidence rate (CR%) and the variable rate (VR%) were calculated to compare newly acquired and characterized with its representative sample and the entire collection with the revised core collection (Hu et al., 2000). The Shannon–Weaver diversity index (H') (Shannon and Weaver, 1949) was used to measure and compare the phenotypic diversity in the 4717 accessions with sample of 501 and the entire collection with the revised core collection. The phenotypic correlations among different traits were estimated separately to determine whether the associations, which may be under the same genetic control, were conserved in the revised core collection.

RESULTS AND DISCUSSION

The strategy we used in clustering the 4717 accessions resulted in 132 clusters. The number of accessions in the clusters ranged from 3 (in five clusters) to 162 (in one cluster). The number of clusters with 3 to 50 accessions was 98; with 51 to 100 accessions was 30; and with 101 to 162 accessions was 4. Proportional strategy of selecting randomly from each cluster resulted in 501 accessions representing the 4717 (10.6%) accessions. The revised pearl millet core collection thus consisted of 2094 accessions: 501 accessions added to 1593 accessions of pearl millet core collection of Bhattacharjee et al. (2007). The revised core of 2094 accessions was compared with the entire collection (20,766) for different parameters to assess its representativeness, as explained below.

Geographic Origin

The revised core consists of accessions from 46 countries, with better representation of geographical distribution of the species in the entire collection than in the earlier core collection, which consisted of accessions from only 25 countries (Bhattacharjee et al., 2007). The frequency distribution of accessions from different countries in the revised core (2094) and the entire collection (20766), as assessed by the χ^2 test, were nonsignificant for 49 countries (P = 0.076 to 1.000), all countries with the exception of Togo (P = 0.027) (Table 1), indicating representative similarity between the revised core and the entire collection. The χ^2 test also indicated that all regions with exception of East Africa (P = 0.032) and southern Africa (P = 0.018), were well represented in the revised core collection. The χ^2 probabilities for the nine geographic regions (central Africa, North Africa, West Africa, Americas, East Asia, South Asia, West Asia, Europe, and Oceania) were nonsignificant (P = 0.227–0.828). Accessions from East Africa (187, P = 0.032) were overrepresented, and those from southern Africa (255; P = 0.018) were underrepresented in the revised core collection. The χ^2 due to heterogeneity for all the 11 geographic regions was nonsignificant (P = 0.372–0.968), indicating that the countries within each region were represented adequately. The overall χ^2 (22.059 at 48 df) was nonsignificant (P = 0.999). The overall composition of the revised core reflects the predominance of accessions from East Africa, southern Africa, West Africa, and South Asia in the revised core 187 to 788, which is in accordance with the entire collection (1585 to 7948) (Table 1).

Frequency Distribution of Morphological Descriptor

Frequency distribution of classes for all the morphological traits between the entire (20,766) and revised core (2094), and between newly characterized accessions (4717) and its representative sample (501) was tested using χ^2 tests. The χ^2 probabilities for distribution of classes in all 10 morphological traits were nonsignificant (0.088–0.943) between entire (20766) and revised core (2094) (Table 2) and except for bristle length (P = 0.004) for all the traits (0.097–0.992) between newly characterized accessions (4717) and its representative sample (501) (data not shown). The χ^2 probabilities in the earlier core collection of 1600 accessions were calculated and were significant for all the 10 morphological traits (data not shown). This indicates that the revised core collection, rather than the earlier core, represents the distribution of all 10 morphological descriptors.

Table 1. Frequency distribution of accessions in different regions and countries in the entire and core collections of pearl millet, χ^2 values, and probabilities.

Region	Country within region	Entire collection	Core collection	df	χ^2	*P*
Central Africa		1,169	115	1	0.070	0.7908
	Central African Republic	142	11	1	0.631	0.4269
	Cameroon	911	91	1	0.021	0.8840
	Congo	8	1	1	0.058	0.8103
	Chad	97	11	1	0.223	0.6370
	Zaire	11	1	1	0.006	0.9371
	Heterogeneity			4	0.869	0.9290
East Africa		1,585	187	1	4.619	0.0316
	Malawi	298	35	1	0.001	0.9787
	Sudan	587	70	1	0.008	0.9287
	Tanzania	478	56	1	0.003	0.9581
	Uganda	118	13	1	0.061	0.8049
	Ethiopia	2	1	1	0.295	0.5867
	Kenya	98	11	1	0.027	0.8687
	Somalia	4	1	1	0.002	0.9674
	Heterogeneity			6	4.222	0.6466
North Africa		15	3	1	1.463	0.2265
	Algeria	5	1	1	0.000	1.0000
	Morocco	4	1	1	0.113	0.7373
	Tunisia	6	1	1	0.033	0.8551
	Heterogeneity			2	1.317	0.5177
Southern Africa		2,932	255	1	5.591	0.0181
	Botswana	82	7	1	0.002	0.9607
	Mozambique	31	3	1	0.034	0.8532
	Namibia	1,118	86	1	1.298	0.2546
	Zambia	155	20	1	3.153	0.0758
	Zimbabwe	1,384	124	1	0.110	0.7406
	South Africa	162	15	1	0.059	0.8083
	Heterogeneity			5	0.935	0.9676
West Africa		6,429	672	1	0.867	0.3517
	Benin	46	6	1	0.295	0.5868
	Burkina Faso	860	80	1	1.089	0.2968
	Cape Verde	2	1	1	0.405	0.5246
	Ghana	283	37	1	1.861	0.1725
	Gambia	15	2	1	0.119	0.7300
	Mali	1,048	112	1	0.055	0.8144
	Mauritania	6	1	1	0.222	0.6378
	Niger	1,132	110	1	0.586	0.4441
	Nigeria	2,065	236	1	1.882	0.1701
	Senegal	393	40	1	0.028	0.8663
	Sierra Leone	59	9	1	1.301	0.2540
	Togo	520	38	1	4.920	0.0265
	Heterogeneity			11	11.896	0.3715
Americas		219	24	1	0.166	0.6834
	Brazil	2	1	1	0.360	0.5486
	USA	207	22	1	0.021	0.8857
	Mexico	10	1	1	0.008	0.9270

Means and Variances

Differences between the means of the newly characterized accessions (4717) and its representative sample (501) were found to be nonsignificant for all the 12 agronomic traits (data not shown). Further, the differences between the means of entire (20,766) and revised core (2094) collections were nonsignificant for all the traits except plant height in the rainy and postrainy seasons (Table 3). The earlier core collection when compared with the entire collection (20,766 accessions) differed significantly for mean number of days to 50% flowering and plant height in the rainy season and for panicle exsertion and panicle width in the postrainy season. The variances of nine agronomic traits (days to flowering–rainy, plant height–rainy, number of total and productive tillers, panicle exsertion, panicle length and width in rainy and postrainy seasons, and 1000-seed weight) were homogeneous for the newly acquired and characterized accessions (4717) and its representative sample (501) (data not shown). The variances for entire and revised core were homogenous for all the traits except plant height in the postrainy season (Table 3). This indicates that the revised core is better representative of the entire collection than the earlier core collection (Bhattacharjee et al., 2007) in which the variances of 7 of the 11 agronomic traits were significantly different than the entire collection. Further, the number of traits for which significance for mean (2 out 12, 16.7%) and variances (0 out of 12, 0%) was less than 20% in this study, confirming that the revised core is a representative of the entire collection (Hu et al., 2000).

Shannon–Weaver Diversity Index

The Shannon–Weaver diversity index (H') was calculated to compare the phenotypic diversity among characters in the entire collection, revised core collection, and in the 4717 newly characterized accessions and its representative sample, separately. The index is used in genetic studies as a convenient measure for both allelic richness and evenness. A low H' indicates an extremely unbalanced frequency classes for an individual trait and a lack of genetic diversity. The average H' index for the revised core collection was 0.617 ± 0.027 for qualitative traits and 0.562 ± 0.021 for quantitative traits, compared with 0.611 ± 0.027 and 0.568 ± 0.021 in the entire collection (Table 4). The H' for 11 quantitative traits in the earlier core collection was 0.590 ± 0.056 (Bhattacharjee et al., 2007). The overall H' was 0.589 ± 0.017 in both the entire and the revised core collection, indicating that the revised core collection captured adequate diversity. This suggests that the revised core collection is representative of the entire collection. The overall H' was 0.520 ± 0.018 in the acquired and characterized accessions and 0.518 ± 0.020 in its representative sample (data not shown).

Variable Rate and Coincidence Rate

The coefficients of variation for most of the traits were higher in the revised core collection than the entire collection, resulting in a VR% of 103.0% for agronomic traits (Table 4). Similarly, it was higher in the representative samples of newly characterized accessions, resulting in a VR% of 109.0% for agronomic traits. The variances and coefficients of the variation in the selected collection should be higher than in the entire collection (Hu et al., 2000). More than 90% range variation was captured in nine agronomic traits in the revised core collection. The high CR% (92.7%) for agronomic traits that was captured in the revised core collection (Table 4) (compared with 87.2% in the earlier core collection; Bhattacharjee et al., 2007) reaffirmed the adequacy of the revised core collection. The CR% captured by the representative samples of newly acquired and characterized accessions was 95.0% for agronomic traits, confirming that the sampling from the 4717 accessions was adequate and that the revised core was representative of the entire collection.

Correlation Coefficients

Phenotypic correlations were performed for all the traits in the entire collection, revised core, newly characterized accessions, and its representative sample, independently. With 20,764 degree of freedom, several correlations in the entire collection ($r = >0.011$) were significant at $P = 0.05$; at 2092 degrees of freedom in the revised core collection, several correlations ($r = >0.036$) were significant at $P = 0.05$. However, the proportion of variance in one trait that can be attributed to its linear relationship with a second trait is indicated by the square of correlation coefficient (coefficient of determination, Snedecor and Cochran, 1980). Considering the criterion correlation coefficients with an absolute value >0.707 have been suggested to be as meaningful (Skinner et al., 1999), so that one trait is predicted more than 50% of variation in the other. In our study, we found such high correlation coefficients in the entire and revised core collection (Table 5) and in the newly characterized accessions and representative sample (data not shown) between number of total tillers and number of productive tillers, and between panicle length rainy and postrainy (Table 5). This shows that the associations observed in the entire collection were preserved in the revised core collection and that associations observed in newly acquired and characterized accessions were preserved in its representative sample. This will be helpful in economizing germplasm characterization by eliminating the highly correlated traits and using a few easily measurable traits.

The resources available for evaluation of germplasm are limited. Therefore, the evaluation of large-sized collections is difficult, time consuming, and resource intensive. Development of a core collection has been suggested as a way to overcome size-related problems and enhance efficiency of evaluation. Core collections are dynamic, and it is useful to revise them periodically as and when new germplasm and information on characterization and evaluation become available. This revised core collection (2094 accessions),

Table 1. Continued.

Region	Country within region	Entire collection	Core collection	df	χ^2	*P*
	Heterogeneity			2	0.223	0.8947
East Asia		16	1	1	0.233	0.6292
	Korea, Republic of	1	0	1	0.063	0.8026
	Union of Soviet Socialist Republics†	15	1	1	0.004	0.9485
	Heterogeneity			1	0.167	0.6832
South Asia		7,948	788	1	0.226	0.6345
	India (India + ICRISAT)	7,769	774	1	0.018	0.8926
	Pakistan	168	13	1	0.803	0.3703
	Maldives	1	0	1	0.099	0.7529
	Myanmar	10	1	1	0.000	0.9931
	Heterogeneity			3	0.748	0.8619
West Asia		400	43	1	0.176	0.6748
	Lebanon	108	10	1	0.223	0.6366
	Turkey	2	0	1	0.215	0.6429
	Yemen, Republic of	290	33	1	0.107	0.7438
	Heterogeneity			2	0.369	0.8315
Europe		45	5	1	0.047	0.8282
	Germany	3	1	1	0.083	0.7728
	France	11	2	1	0.495	0.4817
	United Kingdom	31	2	1	0.606	0.4364
	Heterogeneity			2	1.137	0.5664
Oceania	Australia	8	1	1	0.054	0.8163
Heterogeneity				10	13.513	0.1964
Total		20,766	2094	48	22.059	0.9990

†Accessions from Union of Soviet Socialist Republics were collected before 1992

Table 2. Frequency distribution of different morphological descriptors, χ^2 values, and probabilities in entire and core collection of pearl millet.

Character	df	χ^2	*P*
Between entire 20,766 accessions and core 2094 accessions			
Synchrony of panicle maturity	8	10.246	0.248
Panicle shape	8	7.464	0.488
Spikelet density	8	8.805	0.359
Bristle length	8	10.929	0.206
Seed shape	4	0.764	0.943
Seed color	9	14.879	0.094
Endosperm texture	8	7.73	0.46
Fodder yield potential	8	5.15	0.742
Seed yield potential	8	13.756	0.088
Overall plant aspect	7	9.412	0.224

Table 3. Range, means and variances in entire and core collections of pearl millet.

Character†	Range		Mean‡		Variance§			
	Entire	Core	Entire	Core	Entire	Core	Value	*P*
	Entire 20766 accessions and core 2094 accessions							
Days to flower–R	33–159	33–157	72.9a	72.7a	570.09	540.49	2.17	0.14
Days to flower–PR	32–138	32–135	71.4a	71.2a	123.72	134.02	3.43	0.06
Plant height (cm)–R	30–490	35–490	246.6a	243.3b	4396.58	4614.52	2.37	0.12
Plant height (cm)–PR	25–425	25–425	160.3a	158.5b	1297.71	1446.67	7.70	0.01
Total tillers (no.)	1–35	1–35	2.7a	2.7a	3.12	3.36	0.03	0.60
Productive tillers (no.)	1–19	1–19	2.1a	2.1a	1.27	1.41	1.15	0.28
Panicle exsertion (cm)	–45–29	–32–22	3.7a	3.5a	43.34	45.21	1.12	0.29
Panicle length (cm)–R	5–135	5–120	28.2a	28.2a	113.00	123.99	2.03	0.15
Panicle length (cm)–PR	4–125	5–115	25.5a	25.3a	109.65	112.54	0.15	0.70
Panicle width (mm)–R	8–58	10–55	24.0a	23.9a	22.75	22.84	0.01	0.94
Panicle width (mm)–PR	8–61	8–52	22.9a	22.8a	25.73	26.22	0.15	0.69
1000-seed weight (g)	1.5–21.25	2.9–19.3	8.5a	8.5a	4.97	5.05	0.14	0.71

†R, rainy season; PR, postrainy season.

‡Means were tested using Newman–Keuls test. Means followed by different letters were significant at $p = 0.05$.

§Variances were tested using Levene's test.

Table 4. Shannon–Weaver diversity index (*H*) in entire and core collection, range, and coefficient variation % captured in pearl millet core collection.

Character	H		CR%†	VR%†
	Entire	Core		
Qualitative				
Synchrony of panicle maturity	0.616	0.623	87.5	101.6
Panicle shape	0.561	0.567	100.0	103.6
Spikelet density	0.632	0.640	100.0	101.8
Bristle length	0.443	0.448	100.0	103.0
Seed shape	0.690	0.691	100.0	100.4
Seed color	0.567	0.574	100.0	99.6
Endosperm texture	0.772	0.769	87.5	100.0
Fodder yield potential	0.648	0.647	87.5	100.3
Seed yield potential	0.587	0.604	87.5	104.8
Overall plant aspect	0.590	0.607	100.0	104.8
Mean-qualitative	0.611	0.617	95.0	102.0
SE	0.027	0.027	2.04	0.62
Quantitative‡				
Days to flower–R	0.581	0.596	98.4	97.6
Days to flower–PR	0.615	0.611	97.2	104.3
Plant height (cm)–R	0.625	0.631	98.9	103.8
Plant height (cm)–PR	0.630	0.616	100.0	106.8
Total tillers (no.)	0.427	0.414	100.0	102.5
Productive tillers (no.)	0.431	0.436	100.0	103.3
Panicle exsertion (cm)	0.601	0.560	73.0	108.8
Panicle length (cm)–R	0.555	0.557	88.5	104.9
Panicle length (cm)–PR	0.551	0.548	90.9	102.0
Panicle width (mm)–R	0.606	0.601	90.0	100.7
Panicle width (mm)–PR	0.623	0.616	83.0	101.6
1000-seed wt. (g)	0.613	0.611	83.0	101.1
Mean—quantitative	0.568	0.562	92.7	103.3
SE	0.021	0.021	2.53	0.85
Mean—all	0.589	0.589	93.3	102.6
SE	0.017	0.017	1.66	0.54

†CR% = coincidence rate; VR% = variable rate.

‡R, rainy season; PR, postrainy season.

which represents 10.1% of entire collection (20766 accessions) in the ICRISAT genebank, provides an easy access to enhance and accelerate the utilization of pearl millet genetic resources. The revised core collection represents the entire collection better than the core collection using data on 16,063 accessions that was available up to 1997 (Bhattacharjee et al., 2007). A comparison of two core collections, the earlier one (Bhattacharjee et al. [2007], based on 1997 data) and the present revised core collection, in terms of useful germplasm such as resistant to different diseases would illustrate the importance of this research. Downy mildew [caused by *Sclerospora graminicola* (Sacc.) Schroet.], for example, is the most widespread and destructive disease of pearl millet in India and western Africa (Rachie and Majumdar, 1980). Grain yield losses of 10 to 60% have been reported in various countries in Asia and Africa (Nene and Singh, 1976). None of the 47 accessions resistant to downy mildew were included in the earlier core collection, whereas 12 accessions resistant to downy mildew were included in the revised core collection. This was mainly due to the clustering in the 4717 accessions from which 501 were sampled to constitute the revised core collection.

The core collection could be of immense value particularly in projects involving the screening of germplasm for sources of desirable traits in pearl millet. Breeding for resistance to various biotic and abiotic stresses is one of the most important objectives in pearl millet breeding. Breeding for downy mildew resistance is the most important objectives in most pearl millet breeding programs in Asia and Africa. IP 21206, IP 21190, and IP 21170, the three accessions resistant to downy mildew, were selected as part of this core collection. These three accessions belong to cluster 23. There are 85 accessions in this cluster, which could be a valuable source of downy mildew resistance. The information on clusters from which a particular type

of germplasm accessions with trait of interest has been identified will assist researchers in looking extensively for more accessions with similar traits. Also, the core collection could provide an efficient subset of germplasm when it is not feasible to screen the entire germplasm collection economically. For example, for downy mildew resistance, only 2800 accessions that flower at ICRISAT Center, Patancheru, were screened between 1976 and 1994 (Singh et al., 1997). It will take at least nine more years to screen the entire collection (2000 accessions per year). However, following the core collection approach, finding information on variability in the entire collection, as well as possibly identifying some new sources of resistance, could be accomplished in a single year and with drastically reduced resources.

The establishment of the revised pearl millet core collection may help in tackling new biotic and abiotic constraints. Since the core collection represents the entire collection, and seeds can be multiplied and made available, it can be screened and the new sources identified rapidly. The reserved collection can also be exploited for additional sources by screening the accessions in the cluster from which the source in the core has been detected. The core collection can also be used for molecular characterization to study the population structure and to identify genetically diverse parents for making crosses to generate recombinant inbred lines for mapping, enhancing the trait, and broadening the genetic base of cultivars. The revised core collection along with country of origin is available at http://www.icrisat.org/Pearl-Millet/Pearlmillet/coreMillet.htm.

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Table 5. Correlation coefficients in the entire (20766) collection and core (2094) collection of pearl millet among 12 agronomic traits.†

Collection	Trait‡	Days to flower R	Days to flower PR	Plant height R	Plant height PR	Total tillers	Productive tillers	Panicle exsertion	Panicle length R	Panicle length PR	Panicle width R	Panicle width PR	1000-seed wt.
		d		cm		no.		cm			mm		g
Entire	Days to flower–PR	0.216	1.000										
Core	Days to flower–PR	0.257	1.000										
Entire	Plant height (cm)–R	0.586	0.080	1.000									
Core	Plant height (cm)–R	0.568	0.051	1.000									
Entire	Plant height (cm)–PR	0.038	0.297	0.311	1.000								
Core	Plant height (cm)–PR	0.072	0.300	0.330	1.000								
Entire	Total tillers (no.)	−0.049	−0.078	−0.154	−0.179	1.000							
Core	Total tillers (no.)	−0.085	−0.086	−0.181	−0.190	1.000							
Entire	Productive tillers (no.)	−0.060	−0.114	−0.177	−0.209	0.890	1.000						
Core	Productive tillers (no.)	−0.099	−0.127	−0.207	−0.220	0.913	1.000						
Entire	Panicle exsertion (cm)	−0.166	−0.208	−0.164	−0.120	0.220	0.224	1.000					
Core	Panicle exsertion (cm)	−0.166	−0.220	−0.131	−0.181	0.231	0.235	1.000					
Entire	Panicle length (cm)–rainy	0.105	0.205	0.357	0.355	−0.310	−0.317	−0.472	1.000				
Core	Panicle length (cm)–rainy	0.108	0.188	0.355	0.393	−0.309	−0.321	−0.481	1.000				
Entire	Panicle length (cm)–postrainy	0.124	0.277	0.289	0.480	−0.322	−0.340	−0.440	0.769	1.000			
Core	Panicle length (cm)–postrainy	0.122	0.247	0.279	0.512	−0.318	−0.331	−0.489	0.768	1.000			
Entire	Panicle width (mm)–rainy	−0.073	0.042	0.173	0.154	−0.266	−0.264	−0.212	0.173	0.167	1.000		
Core	Panicle width (mm)–rainy	−0.089	0.041	0.150	0.158	−0.224	−0.223	−0.209	0.161	0.158	1.000		
Entire	Panicle width (mm)– postrainy	0.034	0.149	0.124	0.278	−0.249	−0.258	−0.175	0.095	0.231	0.563	1.000	
Core	Panicle width (mm)– postrainy	0.028	0.123	0.113	0.294	−0.242	−0.247	−0.200	0.106	0.236	0.571	1.000	
Entire	1000-seed wt. (g)	0.137	−0.199	0.247	0.011	−0.176	−0.161	−0.053	0.125	0.104	0.352	0.267	1.000
Core	1000-seed wt. (g)	0.124	−0.229	0.249	0.047	−0.172	−0.153	−0.038	0.122	0.099	0.319	0.265	1.000

†Correlation coefficients > 0.016 and 0.011 are significant at 0.01 and 0.05 probabilities, respectively in the entire collection at df 20, 764 and Correlation coefficients > 0.051 and 0.036 at 0.01 and 0.05 probabilities, respectively in the core collection at df 20292.

‡R, rainy season; PR, postrainy season.

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