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Establishing a core collection of foxtail millet to enhance the utilization of germplasm of an underutilized crop

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Abstract

Foxtail millet (*Setaria italica* (L.) Beauv.) is one of the ten small millets and is cultivated in 23 countries. The foxtail millet is valued as a crop of short duration, which is good as food, feed and fodder. In general, grain yield levels of foxtail millet are low in comparison with other staple cereals. The greater use of diverse germplasm in breeding is suggested as a means to improve the productivity of this crop. The International Crops Research Institute for the Semi-Arid Tropics genebank is presently holding 1474 cultivated germplasm accessions from 23 countries. To utilize this diversity in research, a core collection (10% of the entire collection) was established using the taxonomic and qualitative traits data. The germplasm accessions were stratified into three taxonomic races (Indica, Maxima and Moharia). Principal coordinate analysis was performed on 12 qualitative traits for each of the biological races, separately that resulted in the formation of 29 clusters. From each cluster, 10% of the accessions were selected to constitute a core collection of 155 accessions. The composition and diversity of the core collection was validated by the χ^2-tests of the frequencies of origin, races, subraces and data on qualitative traits. The analysis of the quantitative traits for mean, range, variance, Shannon–Weaver diversity index and phenotypic associations indicated that the diversity from the entire collection was optimally represented in the core collection. The core subset will be evaluated in replicated trials to make a more precise assessment of diversity and further efforts to identify the sources of agronomic and grain nutritional traits for utilization in breeding programmes.

Keywords: diversity index; foxtail millet; germplasm diversity; phenotypic correlation; *Setaria italica*

Introduction

Foxtail millet (*Setaria italica* (L.) Beauv.) is one of the ten small-grained cereals (small millets), which is grown as a food crop in Asia and for animal feed in the USA and Europe. The naming of this taxon evolved as the millet having panicles resembling a fox's tail in appearance i.e. a long panicle with soft, long and erect hairs. China, India and Japan are the chief foxtail millet growing countries. The foxtail millet is believed to have first domesticated in the Central China (Chang, 1973; Ho, 1975). Taxonomically, foxtail millet comprised two subspecies, *S. italica* subsp. *italica* and subsp. *viridis*. The subspecies *viridis* is considered as the progenitor of the cultivated form.

Based on the comparative morphology of the foxtail millet accessions, Prasada Rao *et al.* (1987) have suggested that there are three races of foxtail millet: (i) race Moharia is common in Europe, southeast

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Russia, Afghanistan and Pakistan; (ii) race Maxima is common in eastern China, Georgia (Eurasia), Japan, Korea, Nepal and northern India (it has also been introduced in the USA); and (iii) race Indica is found in the remaining parts of India and Sri Lanka.

It is difficult to make precise estimates of the area under this crop worldwide, because the area under all the millets is generally reported together. However, the Consultative Group on International Agricultural Research have recently (2006) estimated that foxtail millet is cultivated on about 4.90 m ha annually (available online only at http://www.cgiar.org/research/res_millet.html). China ranks first in the area and production of foxtail millet. The area of 8.09 m ha in 1936 under foxtail millet has subsequently declined to 4.09 m ha in 1983. However, there has been a further upward trend in the area under this crop since 1982 (Jiaju, 1989). In India, foxtail millet is grown on about 1 m ha. The grain is used both for food and feed. A seed oil content of 5.45%, with a range between 4.0 and 7.3% has been reported in the germplasm (Seetharam *et al.*, 1983). The seeds are also a rich source of protein (12.3%) and minerals (3.3%; Rai, 2002). In general, foxtail millet is valued as a crop of short growth duration, which is fairly resistant to insect pests and diseases, and the grains make a nutritious and healthy food. Ramprasad (2005) has highlighted the folk medicine value of the foxtail millet grains.

Foxtail millet has received little research attention in the past years and continues to be a neglected and underutilized crop given its potential. The grain yields are generally low in comparison with other staple cereals; however, yield levels of 1500–2250 kg/ha have been reported from China (Jiaju, 1989). In view of the several merits, this crop deserves increased research attention. The germplasm characterization is now essential in order to breed high yielding varieties. The genebank at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) is presently holding 1474 accessions of foxtail millet from 23 countries. These accessions need to be evaluated in multilocational trials to identify suitable parental material for use in breeding programmes. However, evaluating the entire collection of this size is a cumbersome and long task. A core collection approach (Frankel, 1984) can be used to overcome this problem efficiently. Though the germplasm collection of 1474 accessions of cultivated foxtail millet is not large when compared with other crops like sorghum in ICRISAT genebank, yet it is large in view of the current low research priority accorded to this crop. The core collection, thus formed, can be evaluated extensively at a relatively low cost and the information derived could be used as a guide towards more efficient utilization of the entire collection (Brown, 1989). The core collections of various crops have been developed (see Upadhyaya, 2004) including the other small millets – finger millet (Upadhyaya *et al.*, 2006a). In this paper, we describe the strategy in developing the core collection of foxtail millet using passport information and the data on taxonomical and 12 qualitative traits.

Materials and methods

The Rajendra S. Paroda genebank at ICRISAT, Patancheru, India holds 1474 accessions of the cultivated foxtail millet originating from 23 countries. These accessions were assembled in the ICRISAT genebank over the period from 1976 to 2001. As the number of accessions grew in the collection, they were characterized for 12 qualitative (discrete classes) and 11 quantitative (continuous variation) traits in 1980 (400 accessions), 1984 (317 accessions), 1987 (569 accessions), 1989 (102 accessions) and 2002 (86 accessions). The characterization site, Patancheru, is located at 18°N and 78°E, at an altitude of 545 m, and about 600 km from the sea. Annual rainfall is about 750 mm, most of which occurs during June–September. The germplasm accessions were sown on red soils (alfisols), 75 cm apart on ridges, each accession occupying a single row of 4 m length, plant-to-plant spacing being 10 cm. An application of 20 kg N_2 and 50 kg P_2O_5 per ha was made as basal fertilizer and 45 kg N_2 was applied as a top dressing. In all years, sowings were done towards the end of July. Irrigation and hand weeding were given when necessary. The crops were essentially free of disease or insect pests, and no chemical sprays were applied.

The data were recorded on 12 qualitative and 11 quantitative traits following the descriptors of *S. italica* and *Setaria pumila* (IBPGR, 1985). The data on all the 12 qualitative traits (plant pigmentation, leaf colour, growth habit, culm branching, bristle length, panicle lobing, inflorescence compactness, lobe compactness, grain colour, plant lodging, leaf senescence and overall plant aspect) and days to flowering (quantitative trait) were recorded on a plot basis. The data on basal tiller number (quantitative trait) were recorded on five representative plants in the plot. The remaining nine quantitative traits (plant height, flag leaf blade length and width, flag leaf sheath length, peduncle length, panicle exsertion, inflorescence length and width and weight of five panicles) were recorded on the main culms of the five representative plants in the plots. During field evaluation, the accessions were classified into their taxonomical races and subraces.

The germplasm accessions were stratified into three taxonomical races (Indica: 996 accessions, Maxima: 235 accessions and Moharia: 243 accessions). The data on the 12 qualitative traits were analyzed using principal

coordinate analysis on the accessions in each of the three races, separately, and used in constituting the core subset as the expression of these traits is least influenced by genotype × environment interactions. However, for the validation of the core composition, the data on geographic origin (West Asia, East Asia, Russia and the CIS, South and Southeast Asia, Africa, the Americas, Europe and unknown origin), qualitative as well as quantitative traits was used.

A hierarchical cluster analysis (Ward, 1963) was conducted on the scores of the first five principal coordinates delineating all the accessions into 29 clusters. From each cluster, about 10% of the accessions were randomly selected to form the core collection. In clusters having less than ten accessions, at least one was included in the core collection. The frequency of the accessions according to the origin by geographical region, country and affiliation to biological races and subraces in the entire and core collections was analyzed by the χ^2-test. Yates' (1934) correction was applied when the frequency in a class (entire collection) was less than five. The means of the entire and core collections were compared using the Newman–Keuls procedure (Newman, 1939; Keuls, 1952) for all the 11 quantitative traits. The homogeneity of variances of the entire and core collections was tested with the Levene's (1960) test. The percentage of significant differences between the entire collection and the core subset were calculated for the mean difference (MD %), variance difference (VD %), variable rate (VR %) and coincident rate (CR %; Hu *et al.*, 2000). The diversity index (H') of Shannon and Weaver (1949) was estimated and used as a measure of phenotypic diversity in both the entire and core collections for each trait. The phenotypic correlations between traits in the entire and core collections were estimated separately. This was done to assess the extent to which the trait associations (presumed to be under genetic control) were captured in the core collection.

Table 1. Number and percentage of accessions from different regions and countries (within region) in entire and core collections of the foxtail millet germplasm

Region/country	Entire	Core	χ^2	*P*
West Asia	189 (12.8)	20 (12.9)	0.001	0.978
Afghanistan	17 (9.0)	2 (10.0)	0.022	0.881
Iran	2 (1.1)	1 (5.0)	0.393	0.531
Lebanon	33 (17.5)	3 (15.0)	0.069	0.792
Syria	116 (61.4)	12 (60.0)	0.006	0.937
Turkey	21 (11.1)	2 (10.0)	0.022	0.882
Heterogeneity			0.512	0.972
East Asia	110 (7.5)	11 (7.1)	0.028	0.868
China	58 (52.7)	6 (54.5)	0.007	0.934
Korea	52 (47.3)	5 (45.5)	0.008	0.930
Heterogeneity			0.013	0.909
Russia and CIS	67 (4.5)	7 (4.5)	0.000	0.986
South and Southeast Asia	1031 (69.9)	103 (66.5)	0.271	0.603
India	933 (90.5)	93 (90.3)	0.000	0.983
Nepal	21 (2.0)	2 (1.9)	0.005	0.946
Pakistan	29 (2.8)	3 (2.9)	0.004	0.952
Sri Lanka	14 (1.4)	1 (1.0)	0.114	0.736
Myanmar	6 (0.6)	1 (1.0)	0.268	0.605
Taiwan	28 (2.7)	3 (2.9)	0.015	0.904
Heterogeneity			0.134	0.999
Africa	13 (0.9)	4 (2.6)	5.071	0.024
Ethiopia	1 (7.7)	1 (25.0)	0.057	0.811
Kenya	8 (61.5)	1 (25.0)	1.207	0.272
Malawi	1 (7.7)	1 (25.0)	0.057	0.811
South Africa	3 (23.1)	1 (25.0)	0.305	0.581
Heterogeneity			3.445	0.328
America/USA	47 (3.2)	5 (3.2)	0.014	0.905
Europe	15 (1.0)	4 (2.6)	3.721	0.054
United Kingdom	4 (26.7)	1 (25.0)	0.149	0.700
Hungary	9 (60.0)	1 (25.0)	0.447	0.504
Spain	1 (6.7)	1 (25.0)	0.381	0.537
Switzerland	1 (6.7)	1 (25.0)	0.204	0.651
Heterogeneity			2.540	0.468
Unknown	2 (0.1)	1 (0.6)	0.399	0.528

Results

The entire collection of foxtail millet in the ICRISAT genebank (1474 accessions) was grouped into 29 clusters. Race wise, the number of clusters was 12 (1–12) in Indica, 11 (13–23) in Maxima and 6 (24–29) in Moharia. The number of accessions in clusters ranged between 7 and 134. From each cluster, 10%, or at least one accession, was included in the core collection resulting in a selection of 155 accessions, which is 10.51% of the entire collection. The number of core accessions in individual clusters ranged from 1 to 14. The list of 155 core collection accessions with the data on race, subrace and the country of origin is given in Supplementary Table S1, available online only at http://journals.cambridge.org.

The χ^2-values of frequency distribution for the 12 qualitative traits (plant pigmentation, leaf colour, growth habit, culm branching, bristle length, panicle lobing, inflorescence compactness, lobe compactness, grain colour, lodging, senescence and over all plant aspect) and trait classes (three to six classes) were non-significant, suggesting that the representation of diversity from the entire to the core collections was adequate (Supplementary Table S2, available online only at http://journals.cambridge.org). The entire collection of foxtail millet is represented by 23 countries spread over Asia, Africa, Europe and North America. Seven countries (Ethiopia, Iran, Malawi, South Africa, Spain, Switzerland and UK) and the group of accessions with unknown origin, had less than five accessions in the entire collection. A χ^2-test was carried out to determine whether the sampling of accessions in the core collection represented the entire collection satisfactorily. The χ^2-value was non-significant for all regions except Africa. The accessions from Africa were over represented in the core collection. There were 13 accessions from Africa, and the clustering based on 12 qualitative traits delineated into four clusters, having 1, 8, 1 and 3 accessions, individually. Including at least one accession from each of these clusters resulted in higher (significant) representation in the core collection from this region. The heterogeneity for all the regions was non-significant ($P = 0.328–0.999$). The countries within the regions and the unknown group had non-significant χ^2-values, indicating that all the countries were optimally represented in the core collection (Table 1).

In foxtail millet, the race Indica is characterized by tall plants (average 122 cm) with three to four tillers and 18 cm long panicles. On a panicle, spikelets are loosely arranged and have three bristles below each spikelet (Prasada Rao *et al.*, 1987). The germplasm collection in ICRISAT genebank is dominated by this race with 996 accessions (67.57%). The race Moharia is phenotypically similar to subsp. *viridis*, except that the latter has the grain-shattering feature. The plants are relatively short (about 60 cm), producing about nine tillers and also having a tendency to produce culm branches. The panicles are about 8 cm long and compact in appearance (Prasada Rao *et al.*, 1987). This race is represented by 243 accessions (16.49%) in the ICRISAT genebank. The race Maxima is highly variable. It is identifiable by closely arranged spikelets on long panicles, giving the panicles a tightly lobed appearance. On average, plants grow mid-tall (85 cm) with one to two unbranched tillers and with panicles of 15 cm length. The race Maxima is represented by 235 accessions (15.94%) of the foxtail millet germplasm in the ICRISAT genebank. These races were adequately represented in the core collection having 102

Table 2. Number (percentage) of accessions belonging to different races and subraces (within race) in entire and core collections of the foxtail millet germplasm

Race/subrace	Entire collection	Core collection	χ^2	Prob.
Indica	996 (67.57)	102 (65.81)	0.071	0.789
Heterogeneity			4.289	0.232
Erecta	4 (0.40)	2 (1.96)	2.902	0.089
Glabra	137 (13.76)	16 (15.69)	0.277	0.599
Nana	838 (84.14)	81 (79.41)	0.271	0.603
Profusa	17 (1.71)	3 (2.94)	0.911	0.340
Maxima	235 (15.94)	24 (15.48)	0.020	0.886
Heterogeneity			0.559	0.756
Assamense	2 (0.85)	1 (4.17)	0.428	0.513
Compacta	208 (88.51)	20 (83.33)	0.073	0.788
Spongiosa	25 (10.64)	3 (12.50)	0.078	0.780
Moharia	243 (16.49)	29 (18.71)	0.465	0.495
Heterogeneity			1.321	0.517
Aristata	79 (32.51)	11 (37.93)	0.262	0.609
Fusiformis	1 (0.41)	1 (3.45)	1.214	0.271
Glabra	163 (67.08)	17 (58.62)	0.309	0.578

Table 3. Range, means, and variances in entire collection and core collection of the foxtail millet germplasm

Character	Range		Mean[1]		Variance[2]			
	Entire collection	Core collection	Entire collection	Core collection	Entire collection	Core collection	*F* Value	Prob
Days to flowering (no)	32–135	33–135	53.2 ± 0.28	53.8 ± 1.00	115.35	155.72	1.76	0.185
Plant height (cm)	25–215	35–190	110.4 ± 0.83	112.0 ± 2.44	1009.43	925.16	0.64	0.422
Basal tillers number (no)	1–52	1–41	6.8 ± 0.14	6.9 ± 0.41	28.02	25.95	0.07	0.796
Flag leaf blade length (cm)	30–520	80–520	287.1 ± 2.06	291.8 ± 6.78	6239.38	7122.69	1.28	0.257
Flag leaf blade width (cm)	5–40	10–40	20.6 ± 0.15	20.7 ± 0.49	34.29	37.85	0.56	0.453
Flag leaf sheath length (cm)	50–260	60–245	139.8 ± 0.83	141.3 ± 2.40	1009.04	895.73	0.72	0.396
Peduncle length (cm)	80–500	120–500	299.0 ± 1.48	305.7 ± 4.54	3229.80	3189.43	0.02	0.892
Panicle exsertion (cm)	10–360	60–350	160.5 ± 1.35	167.1 ± 4.03	2684.49	2521.03	0.25	0.620
Inflorescence length (cm)	10–390	30–350	165.2 ± 1.48	167.9 ± 4.83	3231.58	3620.11	0.73	0.394
Inflorescence width (cm	5–120	7–120	19.7 ± 0.19	20.6 ± 0.88	53.80	119.49	4.66	0.031
Weight of five panicles (g)	0.6–116.5	0.75–100.1	31.1 ± 0.49	30.4 ± 1.49	359.42	344.71	0.11	0.741

[1]Means were tested using Newman–Keuls test and were non-significant for all characters. [2]Variances were tested by Levene's test.

accessions of Indica (65.81%), 29 accessions of Moharia (18.71%) and 24 accessions of Maxima (15.48%). The χ^2-values for the races for frequency distribution between the entire and the core collections were non-significant ($\chi^2 = 0.071$, 0.020 and 0.465, and $P = 0.789$, 0.886 and 0.495 for Indica, Maxima and Moharia, respectively), revealing that the sampling technique to constitute the core collection was effective. Considering the representation of the foxtail millet germplasm at subrace level, race Indica comprised four subraces, namely, Erecta, Glabra, Nana and Profusa. Of these subraces, Nana is predominant (79.41%) followed by Glabra (15.69%). The race Moharia comprised three subraces, of which Glabra is more common (58.62%) followed by Aristata (37.93%) and Fusiformis (3.45%). The race Maxima also comprised three subraces, of which Compacta is more common (83.33%) and the other two subraces are Spongiosa (12.50%) and Assamense (4.17%). The frequency distribution of the accessions by subraces within races in the entire and core collections indicated a good fit, again suggesting that the core collection represented the entire collection at the subrace level also (Table 2).

Differences between the means of the entire and core collections were non-significant for all the 11 quantitative traits (Table 3). The homogeneity test of the variances between the entire and core collections revealed homogeneity of the variances for all quantitative traits except for the inflorescence width. This indicated a VD % of only 9% (<20%; Hu *et al*., 2000) with the variance in the core being greater than the entire collection. The CR value of 87.7% (>80%) and VR of 104% in the core (Table 4) indicated a fairly high representation of diversity from the entire collection to the core subset.

The estimates of Shannon–Weaver diversity index (H') reveal the allelic richness and evenness in a population. Overall, the H' estimates for all the 23 traits, and the

Table 4. Coincident rate percentage and variable rate percentage of 11 quantitative traits of the core collection of the foxtail millet germplasm

Trait	CR (%)	VR (%)
Days to flowering (no)	99.0	114.8
Plant height (cm)	81.6	94.4
Basal tillers number	78.4	94.8
Flag leaf blade length (cm)	89.8	105.1
Flag leaf blade width (cm)	85.7	104.6
Flag leaf sheath length (cm)	88.1	93.2
Peduncle length (cm)	90.5	97.2
Panicle exsertion (cm)	82.9	93.1
Inflorescence length (cm)	84.2	104.2
Inflorescence width (cm)	98.3	142.2
Weight of five panicles (g)	85.7	99.9
Mean ± SE	87.65 ± 1.95	103.95 ± 4.32

qualitative (12) traits, separately corresponded well between the entire and core collections. The mean H' for quantitative traits was 0.588 ± 0.016 and 0.575 ± 0.018 for the entire and core collections, respectively. The values are nearly similar, revealing that the diversity of the entire collection has been effectively sampled in constituting the core collection (Supplementary Table S3, available online only at http://journals.cambridge.org).

Phenotypic correlations were calculated between the 11 quantitative traits in the entire and core collections separately (Supplementary Table S4, available online only at http://journals.cambridge.org). In the entire and core collections, 53 and 41 correlations, respectively, were significant at the 1% level of significance. The significance levels in the entire and the core collections were different due to the different numbers of degree of freedom, 1472 for the entire collection and 153 for the core collection, and hence, the correlations between the two sets could be considered having a similar trend.

Discussion

Foxtail millet is an important crop in some niches, namely, northern hills, Assam and Andhra Pradesh in India, and Northeast provinces of China; however, the precise estimates of the area under cultivation are not available. For productivity also, except from China, where grain yield as high as 2250 kg/ha has been reported (Jiaju, 1989), the information is not available. The grains of foxtail millet are nutritious and they also possess high dietary values, e.g. high oil contents (5.45%; Seetharam *et al.*, 1983), protein (12.3%), minerals (3.3%; Rai, 2002), crude fibre (10.8%) and iron (49 mg/kg of grain; Beghel *et al.*, 1985). The grains also make an ideal food for people suffering from diabetes and gastric problem as well used to treat chickenpox (Ramprasad, 2005). In general, this crop is valued for its short duration, cultivated with limited farm inputs and remaining free from any disease or insect pest. In view of the several merits of this crop and a very limited research undergone, foxtail millet deserves greater attention. There is a need to identify the germplasm accessions with economic traits that can be used in breeding cultivars with high and stable yields. The core collection, which has reduced number of accessions, though containing almost full diversity, can be used for such purposes cost effectively.

Our results indicated that the germplasm collection at ICRISAT possess good amount of diversity for important agronomic traits (Table 3 and Supplementary Table S3, available online only at http://journals.cambridge.org) and serves as a good basis for developing a core collection. The present core collection of 155 accessions is a good representative of the entire collection as indicated by the non-significant differences in the means and homogeneity of variances of the entire and core collections. The negligible estimates of MD (0%), VD (9%) and low discrepancy of CR (87.7%) and VR (104%) suggest that the variability on the 11 quantitative traits have been captured in the core collection and corresponds well with the hypothesis of Hu *et al.* (2000). They considered a core collection to be the representative of the entire collection when no more than 20% of the traits have different means and variances (significant at 0.05) and the CR and VR % retained by the core collection are no $<80\%$.

The trend of similar phenotypic correlations in the core and entire collections in the present study supported the hypothesis put forward by Ortiz *et al.* (1998) that the adequate and proper sampling is essential in developing a representative core collection, requires consideration of the sampling of phenotypic associations arising out of coadapted gene complexes. The information from phenotypic correlations can also be used to identify traits, which need not be recorded in the initial characterization, when information is revealed by an easily measurable associated trait. 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 the correlation coefficient (Snedecor and Cochran, 1980). Furthermore, the correlation coefficients with an absolute value >0.71 or <-0.71 have been suggested to be meaningful (Skinner *et al.*, 1999), so that 50% of the variation in one trait is predicted by the other. In the present study, three meaningful correlations ($r > 0.71$) were: (i) plant height *vs.* inflorescence length, (ii) flag leaf blade length *vs.* inflorescence length, and (iii) peduncle length *vs.* panicle exsertion in the entire and core collections. The examination of these combinations revealed that the inflorescence length corresponds well with the plant height and the flag leaf blade length and peduncle length corresponds well with the panicle exsertion. Hence, to be cost effective and reduce some redundancy in the foxtail millet research in the future, of the five traits involved in the three trait pairs, panicle exsertion and inflorescence length need not be recorded. This corresponds well with a study on finger millet germplasm (Upadhyaya *et al.*, 2006a), where the peduncle length was correlated with the panicle exsertion and the inflorescence length with the length of the longest finger and concluded that the two traits, panicle exsertion and longest finger length could be ignored in initial characterization studies.

The present core collection has merits as this has been developed based on germplasm characterization and clustering and expected to be more efficient than the core developed using the passport data and random selection of accessions (Diwan *et al.*, 1995). Furthermore, this core has high level of representativeness of the entire

collection and is likely to provide easy access to the entire collection.

In view of the limited resources available for agricultural research in developing countries, especially for a low priority crop such as foxtail millet, the core collection will provide a good working collection that can be extensively characterized for all economically important traits including the reactions to various stress factors and for nutritional traits, such as protein, β-carotene, iron and zinc contents. The molecular characterization of the core collection would help in revealing the population structure and in assessing the genetic diversity at DNA level with reduced resources. In fact, the characterization data on morphological, agronomical, biochemical and molecular traits should be integrated because the different types of traits provide complementary information (Singh *et al.*, 1991). The tolerance to high and low temperatures is going to be an important factor in view of global climate change. The core collection due to its drastically reduced size can be conveniently evaluated to identify tolerant/resistant sources using lesser resources. With the use of the core and mini core collections of chickpea (Upadhyaya and Ortiz, 2001), sources of high grain yield (Upadhyaya *et al.*, 2007), tolerance to drought (Kashiwagi *et al.*, 2005) and diseases (Pande *et al.*, 2006) have been identified. Similarly, new sources of tolerance to drought (Upadhyaya, 2005) and low temperature at germination (Upadhyaya *et al.*, 2009b), and for early maturity (Upadhyaya *et al.*, 2006b), were identified in the groundnut core and mini core collections. For additional sources of useful traits, the accessions from the reserve collections (remaining part of the entire collection) can also be examined selectively from the same cluster from which the accession in the core collection has been identified. The core collection is expected to facilitate efficient access to the germplasm by the user community. This core collection is not static and should be revised periodically when new accessions and information becomes available as in the case of pearl millet (Upadhyaya *et al.*, in press).

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