RESEARCH

Developing a Mini-Core Collection in Finger Millet Using Multilocation Data

H. D. Upadhyaya,* N. D. R. K. Sarma, C. R. Ravishankar, T. Albrecht, Y. Narasimhudu, S. K. Singh, S. K. Varshney, V. G. Reddy, S. Singh, S. L. Dwivedi, N. Wanyera, C. O. A. Oduori, M. A. Mgonja, D. B. Kisandu, H. K. Parzies, and C. L. L. Gowda

ABSTRACT

Finger millet [*Eleusine coracana* (L.) Gaertn.], among small millets, is the most important food crop in some parts of Asia and Africa. The grains are a rich source of protein, fiber, minerals, and vitamins. A core collection of 622 accessions was developed. The aim of this study was to develop a mini-core collection using multilocational evaluation data of the core collection. Six hundred and twenty-two accessions together with six controls (four common and two location-specific) were evaluated for 20 morphological descriptors at five agroecologically diverse locations in India during the 2008 rainy season. The experiment was conducted in α design with two replications at Patancheru and in augmented design with one of the six controls repeated after every nine-test entry at other locations. The hierarchical cluster analysis of data using phenotypic distances resulted in 40 clusters. From each cluster, ~10% or a minimum of 1 accession was selected to form a mini-core, which was comprised of 80 accessions. The comparison of means, variances, frequency distribution, Shannon–Weaver diversity index (H`), and phenotypic correlations revealed that the mini-core captured the entire diversity of the core collection. This mini-core collection is an ideal pool of diverse germplasm for identifying new sources of variation and enhancing the genetic potential of finger millet.

H.D. Upadhyaya, V.G. Reddy, S. Singh, S.L. Dwivedi, and C.L.L. Gowda, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, 502324 AP, India; N.D.R.K. Sarma, Agricultural Research Station, Vizianagaram, 535001, AP, India; C.R. Ravishankar, Zonal Agricultural Research Station, Mandya, 571405, Karnataka, India; T. Albrecht and H.K. Parzies, Univ. of Hohenheim, Institute of Plant Breeding, Seed Science and Population Genetics, Fruwirthstr. 21, D-70599, Stuttgart, Germany; Y. Narasimhudu, Regional Agricultural Research Station, Nandyal, 518502, AP, India; S.K. Singh and S.K. Varshney, Rajendra Agricultural Univ., Dholi, 843121, Bihar, India; N. Wanyera, National Semi-Arid Resources Research Institute (NASARRI), PO Soroti, Uganda; C.O.A. Oduori, Kenya Agricultural Research Institute (KARI), PO Box 169, Kakamega, Code 50100, Kenya; M.A. Mgonja, ICRISAT Regional Office for Eastern and Southern Africa, United Nations Ave., World Agroforestry Center, Gigiri PO Box 39063-00623, Nairobi, Kenya; and D.B. Kisandu, Agricultural Research Institute (ARI), Uyole, PO Box 400, Mbeya, Tanzania. Received 27 Nov. 2009. *Corresponding author (h.upadhyaya@cgiar.org).

Abbreviations: BLUPs, best linear unbiased predictors; CR%, coincidence rate; H`, Shannon–Weaver diversity index; ICRISAT, International Crops Research Institute for the Semi-Arid Tropics; MD%, mean difference percentage; P, probability; REML, residual maximum likelihood; VD%, variance difference percentage; VR%, variable rate.

Finger millet [*Eleusine coracana* (L.) Gaertn.] is an important food crop in the lives of some of the world's poorest inhabitants. It is widely grown in India, Myanmar, Nepal, Sri Lanka, China, and Japan in Asia and Uganda, Tanzania, Kenya, Ethiopia, Rwanda, Zaire, Eritrea, and Somalia in Africa. The crop was

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domesticated around 5000 yr BC in the Western Uganda and Ethiopian highlands and from there reached to the west cost of India around 3000 BC (Hilu and deWet, 1976a). Finger millet is allotetraploid with chromosome number $2n = 4x = 36$ and evolved from a cross between two diploid species, *E. indica* (AA) and *E. floccifolia* or *E. tristachya* (BB), as genome donors (Chennaveeraiah and Hiremath, 1973, 1974; Hilu and deWet, 1976b; Hiremath and Salimath, 1992). The grains are a rich source of seed protein, fiber, minerals (calcium, iron, and manganese), and amino acids (tryptophan, cystine, and methionine) and are mostly used for making chapattis, cakes, puddings, or porridge. The nutritional quality of finger millet grain makes it an ideal food for expectant women, breast-feeding mothers, children, the sick, and diabetics (National Research Council, 1996). It is a major component in the preparation of food for HIV patients in Eastern Africa. The finger millet grains in some parts of Africa and Asia are used for producing beer or liquor (Hilu and deWet, 1976a). Finger millet has also been used as a folk remedy for many diseases (Watt and Breyer-Brandwijk, 1962). The finger millet straw is a highly nutritious fodder.

The species *E. coracana* consists of two subspecies, *africana* and *coracana*. The subspecies *africana* has two wild races, *africana* and *spontanea*, while subspecies *coracana* has no wild races but four cultivated races: *elongata*, *plana*, *compacta*, and *vulgaris*. The races have been further divided into subraces, which include *laxa*, *reclusa*, and *sparsa* in race *elongata*; *seriata*, *confundere*, and *grandigluma* in race *plana*; and *liliacea*, *stellata*, *incurvata*, and *digitata* in race *vulgaris*. The race *compacta* has no subraces (Prasada Rao and de Wet, 1997). These races and subraces can be differentiated from one another by inflorescence morphology (Prasada Rao et al., 1993).

The genebank of International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) at Patancheru (India) holds 5940 accessions of finger millet from 23 countries. Using 14 quantitative traits data on these accessions, Upadhyaya et al. (2006a) established a core collection in finger millet, which consists of 622 accessions representing geographical regions and biological races from the entire collection. Accessions from Africa (58.7%) and Asia (35.8%) were predominant in the core, while those from America and Europe were represented by 0.8 to 1.1% only. About 3.5% of the accessions in the core collection were of unknown origin. The subsp. *coracona* accessions were represented by 97.4%, while those from subsp. *africana* were 2.6% only. The accessions within subsp. *coracona* were predominated by race *vulgaris* (62.5%), followed by *plana* (16.8%), *compacta* (12.4%), and *elongata* (8.3%).

Cultivated finger millet has a narrow genetic base, most probably owing to a bottleneck associated with its domestication (references cited in Dida et al., 2008). Genetically diverse germplasm with beneficial traits should become available to breeders for enhancing the genetic base of finger millet. The core collection in finger millet consists of 622 accessions, which is still large for multilocation evaluations. To overcome the latter problem, Upadhyaya and Ortiz (2001) developed a two-stage strategy: first to develop a core collection using characterization data from the entire collection and then to evaluate core collection accessions for various traits to develop a mini-core collection. In both stages, the intention is to ensure that over 80% of the variability from the entire collection (for developing core) or from the core collection (for developing mini core) is sampled.

The aim of the present investigation was to construct a mini-core collection for diverse uses in crop improvement by using multilocation evaluation data of the core collection on morpho-agronomic traits at agroecologically diverse locations in major finger millet growing states in India.

MATERIALS AND METHODS

Six hundred and twenty-two accessions of the finger millet core collection along with six controls were evaluated at five locations in India during the 2008 rainy season. The test locations included were Patancheru (17.3° N, 78.5° E), Nandyal (15.3° N, 78.3° E), and Vizianagaram (18.7° N, 83.3° E) in Andhra Pradesh, Mandya (12.3° N, 76.5°E) in Karnataka, and Dholi (24.9° N, 72.1° E) in Bihar. The four common controls were PR 202, RAU 8, VL 149, and VR 708, while the two other controls were location-specific. The experiment was conducted in α design (Patterson and Williams, 1976) with two replications at Patancheru and in augmented design (Federer, 1956) with one of the six control cultivars repeated after every nine-test entry at four locations. Each plot consisted of one row of 4 m. Row-to-row spacing was maintained at 30 cm at Mandya, Nandyal, and Vizianagaram; 40 cm at Dholi; and 60 cm at Patancheru. Plant-to-plant spacing within row was fixed at 10 cm. Basal fertilizer of 20 kg N and 50 kg P and a top dressing of 50 kg N ha^{-1} were applied after 30 d of sowing. Experiments were kept free from weeds and insect pests. Irrigation was applied as and when necessary. Data on 5 qualitative (plant pigmentation, growth habit, inflorescence compactness, culm branching, and grain color) and 15 quantitative (days to flowering, plant height, basal tillers, flag leaf blade length and width, flag leaf sheath length, peduncle length, panicle exertion, inflorescence length and width, length and width of longest finger, panicle branches, grain yield, and overall plant aspect score) traits were recorded following finger millet descriptors (IBPGR, 1985). Data on plant pigmentation and growth habit were recorded after days to 50% flowering. Grain characteristics were recorded at postharvest stage in the laboratory. The number of days to flowering was recorded as the number of days from sowing to the date when 50% of plants in a plot had started flowering. Data on plant height, basal tillers, flag leaf blade length and width, flag leaf sheath length, peduncle length,

panicle exertion, inflorescence length and width, length and width of longest finger, fingers per ear, and grain yield per plant were recorded on five representative plants. Grain yield of five plants was added to the plot yield to determine total plot yield in kilograms per hectare. Panicle exertion was measured as the length of exposed peduncle from the flag leaf to the base of the panicle. Panicle length and width were measured at maturity as the maximum length from the base to the tip of the panicle and maximum width in the natural position. For quantitative traits, the averages of five plants per plot were computed that were used for statistical analyses.

The random model of residual maximum likelihood (REML) (Patterson and Thompson, 1971) in GenStat 10 (http://www.genstat.co.uk; verified 9 June 2010) (Payne et al., 2007) was used to analyze data of 15 quantitative traits for individual locations. Meta-analysis of the combined data from all five locations was performed and variance components of the random effects were estimated using maximum likelihood (DerSimonian and Laird, 1986; Hardy and Thompson, 1996; Whitehead, 2002; Payne and Senn, 2007). Environments were considered fixed and the significance was evaluated using Wald statistic. Variance components owing to genotype (σ^2g) and its standard errors (SE) were estimated for individual and combined (meta) analysis. Best linear unbiased predictors (BLUPs) (Schönfeld and Werner, 1986) for individual location and combined (meta) analysis were worked out for all quantitative traits. A Gower's (1985) dissimilarity matrix was created for 616 accessions (6 wild accessions were excluded from the analysis) using 5 qualitative and 15 quantitative traits. Data on qualitative traits were transformed to a numerical scale (IBPGR, 1985) to calculate the dissimilarity matrix, which was subjected to hierarchical cluster algorithm (Ward, 1963) at an R^2 (squared multiple correlation value) of 0.75. This method optimizes an objective function because it minimizes the sum of squares between groups. A proportional sampling strategy of selecting the representative accessions was used, and ~10% of the accessions or a minimum of one accession from each cluster was randomly selected to form a mini-core collection. Proportional strategy is more efficient than other sampling strategies (Grenier et al., 2001), it captures more alleles, and it often has lower variance (Cochran, 1977). Furthermore, it has also been suggested in case of undifferentiated loci (Brown, 1989).

The 23 countries of origin of the core collection accessions were grouped into four regions: Africa, Asia, America, and Europe. The origin of accessions in a fifth group was not known. Frequencies of geographic regions, countries within regions, races, subraces within races, and all the qualitative traits in the core and mini-core collections were tested by χ^2. Yates (1934) correction was applied if the number of accessions for a given class in the core or mini-core collection was less than five. Means for the core and mini-core collections were compared by the Newman-Keuls procedure (Newman, 1939; Keuls, 1952). Homogeneity of variances was tested by Levene's test (Levene, 1960). The variance difference (VD%), mean difference (MD%), coincidence rate (CR%), and variable rate (VR%) were calculated to compare the core and mini-core collections (Hu et al., 2000). The VR% compares the coefficient of variation values for individual traits measured in the core with the mini-core to determine how well the variance is represented in the mini-core collection, while the CR% indicates whether the distribution ranges of each trait in the mini-core are well represented when compared with the core collection. Shannon and Weaver's (1949) diversity index (H`) was used to measure and compare the phenotypic diversity for each trait in the core and mini-core collections. Phenotypic correlations among 15 quantitative traits in the core and mini-core collections were estimated separately to determine whether associations that may be under the same genetic control were conserved in the mini-core collection (Ortiz et al., 1998).

RESULTS AND DISCUSSION

Residual maximum likelihood analysis of individual locations indicated that the genotypic variance for most of the traits, except for plant height, flag leaf length and width, peduncle length, width of longest finger, and fingers per ear at Nandyal; flag leaf blade length at Dholi; width of longest finger at Mandya; and basal tillers and fingers per ear at Vizianagaram were significant in all five environments (Table 1). In pooled (meta) analysis, both genotypic effects (except for inflorescence width) and genotype × environment interaction effects were significant for all the traits (Table 1). Highly significant ($P < 0.001$) Wald statistics revealed that the environments differed significantly.

The phenotypic distance matrix (Gower, 1985) for 20 traits involving 616 accessions (6 wild accessions were excluded from the analysis) was subjected to hierarchical cluster analysis (Ward, 1963), which resulted in classifying 616 accessions of the core collection into 40 clusters, with the number of accessions in the individual cluster ranging from 5 to 36. A mini-core collection of 80 accessions (sampling 1 to 4 accessions from 40 clusters) was formed using the sampling strategy of 10% or a minimum of 1 accession from each cluster. It represented 12.86% of core collection accessions or 1.34% of the entire collection accessions of finger millet in the ICRISAT genebank. The differences between means of the core and mini-core collections were found to be nonsignificant for all the traits, while variances between the core and mini-core collections were homogeneous for all traits (except for width of the longest finger) (Table 2), resulting in 0% MD% and 6.7% VD%, well below the 20% acceptable rate (Hu et al., 2000) (Table 3). The mini-core collection represented, on average, 82.0 ±4.08% range variation for 15 traits from the core collection (Table 3).

The H` was calculated to compare phenotypic characters in the core and mini-core collections. The index is used in genetic studies as a convenient measure of both allelic richness and evenness. A low H` indicates an extremely

Table 1. Variance due to genotype (g), environment (e), and g x e interaction for 15 quantitative traits among 616 finger millet [*Eleusine coracana* (L.) Gaertn.] core collection accessions evaluated at five locations, 2008 rainy season, India.

Trait	Dholi	Mandya	Nandyal	Patancheru	Vizianagaram	Meta analysis	Environment		
	σ^2g	σ^2g	σ^2g	σ^2g	σ^2g	σ^2g	σ^2g x e	Wald statistics	*P*
Days 50% flowering	118.31**	601.27**	59.74**	56.86**	62.41**	36.88**	28.79**	1611.03	< 0.001
Plant height (cm)	1990.27**	2064.00**	7.50	94.74**	146.34**	56.70**	77.90**	77.22	< 0.001
Basal tiller (no.)	1.32**	1.14**	2.93**	0.21*	0.58	0.25**	0.70**	130.81	< 0.001
Flag leaf blade length (mm)	972.00	38.82**	39.00	1360.00**	19.57**	289.00**	21851.00**	48.79	< 0.001
Flag leaf blade width (mm)	2.37**	0.13**	0.19	0.19**	0.51**	0.06*	0.32**	149.60	< 0.001
Flag leaf sheath length (mm)	134.60**	1.37**	161.97**	82.70**	1.48**	20.10**	134.00**	488.23	< 0.001
Peduncle length (mm)	13,263.70**	1.40**	87.10	551.00**	12.63**	34.00**	119.00**	1284.77	< 0.001
Inflorescence exertion (mm)	614.70**	1.43**	127.40**	205.00**	2946.00**	22.00**	132.00**	948.94	< 0.001
Inflorescence length (mm)	348.61**	–†	211.70**	295.90**	3.50**	201.00**	92.30**	37.30	< 0.001
Inflorescence width (mm)	112.69**	–	6.31**	121.70**	0.09**	1.38	18.24**	91.08	< 0.001
Length of longest finger (mm)	311.40**	3.47**	142.85**	314.70**	2.41**	140.50**	158.90**	212.01	< 0.001
Width of longest finger (mm)	13.20**	42.00	0.18	1.15**	0.02**	0.19**	1.61**	6362.26	< 0.001
Finger per ear (no.)	1.01**	1.36**	0.09	1.07**	0.54	0.23**	0.81**	401.62	< 0.001
Grain yield (kg ha-1)	179,713.00**	570,618.00**	83,204.00*	291,203.00**	84.60**	115,279.00**	175,551.00**	605.96	< 0.001
Plant aspect score	0.91**	0.25**	5.88*	9.03*	0.41**	0.03**	0.26**	666.61	< 0.001

*Significant at $P = 0.05$.

**Significant at $P = 0.01$.

†– = data not available.

unbalanced frequency of classes for an individual trait and a lack of genetic diversity. The average H` for 15 quantitative traits in the mini-core collection (0.585 ±0.0097) was comparable to the core collection (0.610 ±0.0061), indicating that the diversity of the core was represented in the mini-core collection (Table 3). The previous studies also reported similar or slightly lower H` in mini-core than core collections (Upadhyaya et al., 2002, 2006b, 2009b). The variances and coefficient of variation in the selected subset should be higher than the initial collection (Hu et al., 2000). In the present study, high coincidence rate of variation (84 to 100%) for 10 of the 15 quantitative traits and higher variable rate (86.4 to 128.9) for all the 15 traits captured in the mini-core collection further confirmed that the mini-core was representative of the core collection (Table 3).

The similarity of distribution frequencies between the core and mini-core collections was tested using χ^2, which was nonsignificant between geographic regions as well as countries within regions, indicating that accessions from the regions or those from countries within regions were well represented in the mini-core collection (Table 4). Biologically, the finger millet core collection accessions are represented by four races and 10 subraces. The χ^2 probabilities of the frequency distribution of races and subraces accessions of core and mini-core collections revealed that core collection accessions from both races and subraces were well represented in the mini-core collection (Table 5). Furthermore, the nonsignificant χ^2 probabilities of the frequency distribution of five qualitative traits (pigmentation, growth habit, culm branching, inflorescence compactness and shape, and grain color) in core and mini-core collections revealed that these traits were well represented in the mini-core collection (Table 6).

Proper and adequate sampling of accessions in the core collection from the entire collection helps conserve phenotypic associations arising from coadapted gene complexes (Ortiz et al., 1998). In the present study, there was a fair degree of similarity in phenotypic correlation coefficients among 15 quantitative traits (data not presented), suggesting that this mini-core collection has preserved most of the coadapted gene complexes controlling these associations. Further, the proportion of variance in one trait that can be attributed to its relationship with a second trait is indicated by the square of the correlation coefficient (Snekecor and Cochran, 1980), and the estimate of this value as greater than 0.71 or lower than -0.71 has been suggested as a meaningful correlation (Skinner et al., 1999). Few correlation coefficients (plant height and peduncle length, peduncle length and inflorescence exertion, inflorescence length and length of longest finger) in the present study were close to this value in both the core and mini-core collections, with coefficients, in general, greater in mini-core than core collection.

The mini-core collection (80 accessions) reported here adequately preserved the variation from the core collection

Table 2. Comparison of range, means, and variances for 15 quantitative traits in finger millet [*Eleusine coracana* (L.) Gaertn.] core and mini-core collections.

Trait	Range		Mean		Variance			
	Core	Mini-core	Core	Mini-core	Core	Mini-core	*F* value	*P*
Days to 50% flowering	51.24–96.37	51.24–93.73	74.19a†	73.44a	39.94	46.77	0.51	0.474
Plant height (cm)	71.46–134.04	72.66–113.31	99.87a	97.94a	62.91	74.66	0.72	0.398
Basal tiller (no.)	3.34–6.73	3.56–5.45	4.37a	4.37a	0.21	0.19	0.23	0.633
Flag leaf blade length (mm)	257.98–401.38	264.98–385.9	336.09a	335.84a	482.19	597.14	1.59	0.208
Flag leaf blade width (mm)	9.85–11.69	9.85–11.62	11.03a	11.03a	0.03	0.05	1.88	0.170
Flag leaf sheath length (mm)	85.22–123.77	89.54–113.49	102.22a	101.88a	30.81	22.87	2.17	0.141
Peduncle length (mm)	184.50–210.83	185.34–208.11	198.57a	197.89a	26.12	24.48	0.20	0.653
Inflorescence exertion (mm)	119.47–147.21	121.12–145.56	134.50a	134.24a	25.70	22.75	0.56	0.455
Inflorescence length (mm)	50.99–166.48	55.62–166.48	79.09a	79.76a	188.83	246.30	0.63	0.427
Inflorescence width (mm)	46.98–57.15	50.53–56.69	53.05a	52.91a	1.50	1.38	0.18	0.669
Length of longest finger (mm)	45.67–139.73	49.79–139.73	71.12a	70.41a	151.90	171.99	0.14	0.710
Width of longest finger (mm)	12.39–16.86	13.31–16.17	14.16a	14.21a	0.24	0.25	0.01	0.623
Fingers per ear (no.)	6.13–9.41	6.13–9.41	7.49a	7.46a	0.27	0.37	3.43	0.064
Grain yield (kg ha^{-1})	691–2710.19	691–2430.05	1526.50a	1522.85a	126,779.20	111,861.23	0.53	0.468
Plant aspect score	2.43–3.73	2.43–3.68	3.09a	3.08a	0.05	0.06	0.34	0.562

†Means followed by the same letter are not significantly different at $P = 0.05$.

Table 3. Coincidence rate (CR%), variable rate (VR%), and Shannon–Weaver diversity index (H`) of 15 quantitative traits in finger millet [*Eleusine coracana* (L.) Gaertn.] core and mini-core collections.

Traits	VR%	CR%	H	
			Core	Mini-core
Days to 50% flowering	109.3	94.2	0.6160	0.6130
Plant height (cm)	111.1	65.0	0.6264	0.5915
Basal tiller (no.)	94.7	55.8	0.6107	0.5934
Flag leaf blade length (mm)	111.4	84.3	0.6335	0.5868
Flag leaf blade width (mm)	128.9	96.2	0.5518	0.5086
Flag leaf sheath length (mm)	86.4	62.1	0.6253	0.6072
Peduncle length (mm)	97.1	86.5	0.6132	0.6037
Inflorescence exertion (mm)	94.3	88.1	0.6299	0.6192
Inflorescence length (mm)	113.3	96.0	0.5742	0.5218
Inflorescence width (mm)	96.1	60.6	0.6319	0.6147
Length of longest finger (mm)	107.5	95.6	0.5796	0.5331
Width of longest finger (mm)	101.5	64.0	0.6013	0.5565
Fingers per ear (no.)	118.1	100.0	0.6226	0.6247
Grain yield (kg ha^{-1})	94.2	86.1	0.6101	0.5887
Plant aspect score	105.8	96.2	0.6213	0.6164
Mean ±SE	104.6 ±2.89	82.0 ±4.08	0.610 ±0.0061	0.585 ±0.0097

(616 accessions) (Upadhyaya et al., 2006a) and from the entire collection of finger millet germplasm (5940 accessions) maintained in the ICRISAT genebank at Patancheru, India. The development of a mini-core in finger millet has dramatically reduced the number of entries to be evaluated and thus provided a pool of diversity that can be extensively evaluated for economically important traits. The multilocation evaluation of this mini-core for biotic and abiotic stresses and for agronomic traits is underway in Kenya, Uganda, Tanzania, and India to identify new sources of variation for use in crop improvement programs. In other crops, when mini-core collections were evaluated, researchers were able to identify new sources of variation, for example, drought tolerance in chickpea and groundnut; salinity tolerance in chickpea, groundnut, and pigeonpea; low temperature tolerance (at germination) in groundnut; resistance to pest (pod borer) and diseases (*Ascochyta* blight, *Botrytis* gray mold, dry root rot, and *Fusarium* wilt) in chickpea; early maturity and/or large-seed size in chickpea and groundnut; and large-seed size and high grain yield in chickpea (reviewed in Upadhyaya et al., 2009a). This mini-core collection can also be used for molecular characterization to select genetically diverse germplasm to maximize diversity and broaden the genetic base of finger millet cultivars. Table 7 provides the passport information of the accessions included in the finger millet mini-core collection. Researchers can receive limited seeds of the finger millet mini-core accessions, free of charge, from the genebank at ICRISAT, Patancheru, India, following the terms and conditions of the Standard Material Transfer Agreement.

Table 4. Frequency and χ^2 probability of finger millet [*Eleusine coracana* (L.) Gaertn.] core and mini-core collections accessions representing regions and countries within region.

Region/country	Core	Mini-core	df	χ^2	*P*
Africa	359	49	1	0.121	0.728
Burundi	1	0	1	2.968	0.085
Ethiopia	3	1	1	0.020	0.888
Kenya	107	8	1	2.987	0.084
Malawi	23	4	1	0.236	0.627
Mozambique	1	0	1	2.968	0.085
Nigeria	5	1	1	0.148	0.701
Senegal	1	1	1	0.968	0.325
South Africa	1	0	1	2.968	0.085
Tanzania	3	0	1	2.020	0.155
Uganda	81	10	1	0.101	0.751
Zaire	1	0	1	2.968	0.085
Zambia	21	3	1	0.006	0.938
Zimbabwe	111	21	1	2.259	0.133
Heterogeneity			12	20.295	0.062
Asia	223	27	1	0.133	0.715
India	149	17	1	0.060	0.807
Maldives	1	1	1	1.186	0.276
Nepal	70	9	1	0.032	0.858
Pakistan	1	0	1	3.186	0.074
Sri Lanka	2	0	1	2.275	0.132
Heterogeneity			4	6.606	0.158
United States	5	1	1	0.189	0.664
Europe	7	1	1	0.009	0.924
Germany	1	1	1	0.893	0.345
Italy	3	0	1	2.012	0.156
United Kingdom	3	0	1	2.012	0.156
Heterogeneity			2	4.908	0.086
Unknown	22	2	1	0.257	0.612

Table 5. Frequency and χ^2 probability of finger millet [*Eleusine coracana* (L.) Gaertn.] core and mini-core accessions representing races and subraces within races.

Race/subrace	Core	Mini-core	df	χ^2	*P*
Compacta	62	7	1	0.137	0.711
Elongata	51	7	1	0.021	0.884
Laxa	6	1	1	0.038	0.846
Reclusa	24	4	1	0.151	0.697
Sparsa	21	2	1	0.270	0.603
Heterogeneity			2	0.438	0.803
Plana	103	13	1	0.011	0.918
Confundere	89	9	1	0.444	0.505
Grandigluma	5	2	1	2.970	0.085
Seriata	9	2	1	0.657	0.418
Heterogeneity			2	4.060	0.131
Vulgaris	400	53	1	0.021	0.884
Digitata	146	18	1	0.094	0.760
Incurvata	169	23	1	0.016	0.898
Liliacea	31	5	1	0.194	0.660
Stellata	54	7	1	0.003	0.954
Heterogeneity			3	0.286	0.963

Table 6. Frequency distribution and χ^2 probability of finger millet [*Eleusine coracana* (L.) Gaertn.] core and mini-core accessions representing qualitative traits.

	Number of accessions				
Trait	Core	Mini-core	df	χ^2	*P*
Plant pigmentation			1	0.203	0.652
Green	401	54	1	0.071	0.790
Purple	215	26	1	0.132	0.716
Growth habit			2	1.910	0.385
Decumbent	85	14	1	0.794	0.373
Erect	523	64	1	0.226	0.634
Prostrate	8	2	1	0.889	0.346
Culm branching			2	2.655	0.265
High	424	52	1	0.171	0.680
Low	23	1	1	1.322	0.250
Medium	169	27	1	1.163	0.281
Inflorescence compactness and shape			7	2.236	0.946
Compact	9	1	1	0.024	0.876
Fisty	51	7	1	0.021	0.884
Incurved	212	28	1	0.008	0.929
Long open	15	1	1	0.461	0.497
Pendulous	21	1	1	1.094	0.296
Short open	60	10	1	0.626	0.429
Top curved	248	32	1	0.001	0.971
Grain color			4	2.486	0.647
Dark brown	55	7	1	0.003	0.957
Light brown	351	45	1	0.007	0.931
Ragi brown	58	6	1	0.312	0.577
Reddish brown	137	18	1	0.002	0.961
White	15	4	1	2.161	0.142

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Table 7. Pattern of distribution of mini-core accessions into forty clusters and passport information of the 80 accessions included in finger millet [*Eleusine coracana* (L.) Gaertn.] mini-core collection.

IE no.	Cluster no.	Country	Race	Subrace
501	3	India	*Vulgaris*	*Stellata*
518	1	India	*Vulgaris*	*Incurvata*
1055	8	Unknown	*Vulgaris*	*Digitata*
2034	19	India	*Vulgaris*	*Incurvata*
2042	6	India	*Vulgaris*	*Incurvata*
2217	1	India	*Vulgaris*	*Stellata*
2296	21	India	*Vulgaris*	*Digitata*
2312	15	India	*Elongata*	*Sparsa*
2430	25	Kenya	*Vulgaris*	*Digitata*
2437	38	Kenya	*Plana*	*Confundere*
2457	32	Kenya	*Compacta*	–
2572	22	Kenya	*Plana*	*Grandi-gluma*
2589	29	United States	*Plana*	*Seriata*
2606	21	Malawi	*Vulgaris*	*Incurvata*
2619	22	Malawi	*Vulgaris*	*Incurvata*
2710	13	Malawi	*Plana*	*Confundere*
2790	7	Malawi	*Elongata*	*Laxa*
2821	1	Nepal	*Compacta*	–
2871	33	Zambia	*Compacta*	–
2872	13	Zambia	*Vulgaris*	*Digitata*
2911	17	Zambia	*Vulgaris*	*Incurvata*
2957	16	Germany	*Vulgaris*	*Liliacea*
3045	18	India	*Vulgaris*	*Liliacea*
3077	20	India	*Vulgaris*	*Incurvata*
3104	2	India	*Vulgaris*	*Incurvata*
3317	26	Zimbabwe	*Vulgaris*	*Digitata*
3391	13	Zimbabwe	*Vulgaris*	*Digitata*
3392	10	Zimbabwe	*Compacta*	–
3470	12	India	*Vulgaris*	*Stellata*
3475	28	India	*Vulgaris*	*Incurvata*
3614	25	Unknown	*Plana*	*Confundere*
3721	26	Uganda	*Compacta*	–
3945	23	Uganda	*Plana*	*Confundere*
3952	38	Uganda	*Plana*	*Confundere*
3973	34	Uganda	*Vulgaris*	*Stellata*
4028	38	Uganda	*Vulgaris*	*Incurvata*
4057	26	Uganda	*Plana*	*Seriata*
4073	25	Uganda	*Elongata*	*Reclusa*
4121	36	Uganda	*Plana*	*Confundere*
4329	12	Zimbabwe	*Vulgaris*	*Incurvata*
4491	7	Zimbabwe	*Elongata*	*Reclusa*
4497	31	Zimbabwe	*Vulgaris*	*Digitata*
4545	30	Zimbabwe	*Compacta*	–
4565	40	Zimbabwe	*Elongata*	*Reclusa*
4570	26	Zimbabwe	*Plana*	*Confundere*
4622	24	Zimbabwe	*Compacta*	–
4646	37	Zimbabwe	*Plana*	*Grandi-gluma*
4671	21	India	*Vulgaris*	*Digitata*
4734	9	India	*Vulgaris*	*Digitata*
4757	28	India	*Vulgaris*	*Stellata*
4795	25	Zimbabwe	*Vulgaris*	*Digitata*
4797	18	Maldives	*Vulgaris*	*Liliacea*
4816	21	India	*Elongata*	*Reclusa*
5066	27	Senegal	*Vulgaris*	*Incurvata*
5091	31	Zimbabwe	*Vulgaris*	*Digitata*
5106	11	Zimbabwe	*Vulgaris*	*Incurvata*
5201	9	India	*Vulgaris*	*Digitata*
5306	36	Zimbabwe	*Vulgaris*	*Digitata*
5367	14	Kenya	*Vulgaris*	*Liliacea*
5537	4	Nepal	*Vulgaris*	*Stellata*
5817	5	Nepal	*Vulgaris*	*Incurvata*
5870	14	Nepal	*Vulgaris*	*Digitata*
6059	38	Nepal	*Vulgaris*	*Digitata*
6082	14	Nepal	*Plana*	*Confundere*
6154	34	Nepal	*Vulgaris*	*Incurvata*
6165	28	Nepal	*Vulgaris*	*Incurvata*
6221	6	Nepal	*Vulgaris*	*Stellata*
6240	23	Zimbabwe	*Vulgaris*	*Incurvata*
6294	12	Zimbabwe	*Vulgaris*	*Incurvata*
6326	13	Zimbabwe	*Vulgaris*	*Digitata*
6337	19	Zimbabwe	*Vulgaris*	*Incurvata*
6350	28	Zimbabwe	*Vulgaris*	*Incurvata*
6421	36	Uganda	*Vulgaris*	*Digitata*
6473	33	Uganda	*Plana*	*Confundere*
6514	11	Zimbabwe	*Vulgaris*	*Incurvata*
6533	39	Nigeria	*Elongata*	*Sparsa*
7018	27	Kenya	*Vulgaris*	*Incurvata*
7079	40	Kenya	*Vulgaris*	*Liliacea*
7320	35	Kenya	*Vulgaris*	*Digitata*
7508	14	Ethiopia	*Vulgaris*	*Incurvata*

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