Research Paper

Genetic Diversity of Local and Exotic Finger Millet [*Eleusine coracana* (L.) Gaertn.] Germplasm in Sri Lanka Revealed by SSRs

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Abstract

Finger millet is a highly valuable future crop consisting of vast genetic and genomic diversity. Genotypic analysis of 73 local and exotic finger millet accessions collected from the Plant Genetic Resources Center (PGRC) and farmer cultivars in Sri Lanka was carried out using 19 SSR markers. The PCR products were separated and visualized on a 6% polyacrylamide gel with staining. An average of 3.11 alleles per locus was observed for 12 polymorphic markers. The average Polymorphic Information Content (PIC) was 29%. The highest number of alleles per locus, the highest PIC, and the highest gene diversity were observed in the SSR marker UGEP24 followed by UGEP15. AC009304, AC007116, AC000927, TVFM-01 AC009311, AC000504, and AC007116 accessions showed five rare alleles for four SSR markers. Irrespective of the place of origin, the local and exotic accessions were grouped together in the dendrogram. Except for the farmer cultivars collected from Mahiyangana, other accessions collected from the same location/district were grouped in different main groups. The AC009304 with exotic origin exhibited the highest genetic distance from all the other accessions. The higher genetic diversity, observed within the district/ location and the presence of similar alleles among the local and exotic accessions are vital for systematic conservation of finger millet germplasm and utilization of trait-specific accessions in a breeding program of Sri Lanka.

Keywords: Finger millet, Genetic diversity, Genetic distance, SSR markers

Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn.] is a highly valuable future crop consisting of vast genetic and genomic diversity. It is considered as an important component of food security in rural farming communities. The hardy nature of the finger millet crop can withstand abiotic stresses such as drought, salinity, high temperature, and water lodging thus it gives assured production under stressful conditions (Sood *et al*., 2016). At present, 36,873 finger millet germplasm accessions are conserved in national and international genebanks (Vetriventhan *et al*., 2020). The finger millet genome has been sequenced and it is one of the largest (1.5 Gb) among the other millet genome such as foxtail millet, proso millet, teff and Japanese barnyard millet (Vetriventhan *et al*., 2020).

Dida *et al*. (2008) used 45 SSR markers to understand the genetic relationship of 79 finger millet accessions from Africa and Asia, and found three distinguished sub-populations. Bharathi (2011) genotyped a finger millet global composite collection of 1,000 accessions using 20 SSR markers and developed a reference set of 300 accessions. Assessment of genetic diversity and population structure of 67 Indian and African finger millet germplasm by using SSR markers showed average gene diversity of 0.471, and observed 19 rare and nine unique alleles, which can be used as a potential source for improvement of finger millet (Arya *et al*., 2013).

Wakista *et al*. (2015) used 31 SSR markers to assess the genetic diversity of 48 finger millet accessions collected from the PGRC of Sri Lanka with different geographical origins. However, at the PGRC, Sri Lanka, there are 551 finger millet accessions (PGRC, 2019). Hence, the analysis of the genetic diversity of more finger millet germplasm accessions in Sri Lanka is important for finger millet improvements and conservation. Therefore, the objective of this study was to assess the genetic diversity of 73 local (52 accessions from 14 districts) and exotic (21 accessions from India, Nepal and Zimbabwe) finger millet accessions based on 19 simple sequence repeat (SSR) markers.

Materials and Methods

Molecular characterization of finger millet accessions

The finger millet germplasms were collected from Plant Genetic Resources Center, Sri Lanka, and a few farmer cultivars were collected from Mahiyanganaya and Killinochchiya (Table 1). The laboratory analysis was conducted at the Biotechnology laboratory of Field Crops Research and Development Institute, Mahailluppallama.

DNA extraction

The DNA extraction of finger millet accessions was done using the Promega Wizard® Genomic DNA Purification Kit (A1120) according to the manufacturer's protocol (Promega, USA).

Table 1. Finger millet germplasm accessions used for genotypic characterization

Collected district/ Area	Number of Accessions	PGRC accession number
Ampara	1	011774
Anuradhapura	5	012038, 012189, 012269, 012401, 007071
Badulla	3	006581, 007090, 000965
Batticaloa	1	011087
Hambantota	3	000152, 000192, 000955
Jaffna	3	012968, 002383, 002384
Kandy	3	011350, 012248, 007823
Killinochchi	4	TVFM -01, TVFM013-1, TVFM-02, TVFM-04,
Kurunagala	2	000418, 0007078
Mahiyanganaya (Farmer cultivars)	4	M1, M2, M4, M7
Matale	3	011334, 011342, 000353
Monaragala	6	000108 (Oshada), 011252, 011821, 000127, 012927, 008470
Nuwara Eliya	6	001051, 012282, 012465, 001460, 000504, 009079
Polonnaruwa	4	10453, 012605, 012629, 007769
Ratnapura	3	001329, 008613, 008630
Local unknown	1	011819
Exotic unknown	6	012591, 012593, 012639, 001906, 009304, 009311
India	7	010326 (Rawana), 012495, 000910, 000923, 000926, 000927, 000964
Nepal	2	012428, 012494,
Zimbabwe	6	007109, 007110, 007111, 007112, 007116, 007117
Total	73	

Approximately 100 mg of leaf samples obtained from newly expanded leaves of 13 to 15 days old finger millet seedlings, were used to extract genomic DNA. The DNA quality and quantity were determined by agarose gel electrophoresis (0.8% w/v) and spectrophotometry (Nano-drop® 1000-Thermo Scientific, USA).

SSR marker analysis

Nineteen SSR markers, developed by Dida *et al*. (2007) were used to analyze the molecular diversity (Table 2).

Steps of Polymerase Chain Reaction (PCR)

The PCR was set up in a 10 µL reaction mixture constituting of 1x PCR buffer, 2mM $MgCl_2$, 200µM dNTPs, 250 nM of forward and reverse primer each, 1 unit Taq DNA polymerase 500 u/µL (Promega, USA). The PCR amplification conditions were initial denaturation at 94 °C for 3 min followed by 10 cycles of denaturation at 94 °C for 30 sec, touchdown annealing starting at 62 °C for 30 sec, decreasing 0.7 °C/cycle, extension at 72 °C for 1 min followed by 35 cycles at an annealing temperature of 55 °C and final extension at 72 °C for 4 min (Dida *et al*., 2007). PCR products were separated on 6% polyacrylamide (denaturing) gels and visualized by staining with Ethidium Bromide (0.5 mg ml^{-1}). The 50 bp DNA ladder was used to compare the bands.

Table 2. Simple Sequence Repeat (SSR) marker, allele size range, repeat motif and sequences of forward and reverse primer

No.	Primer	Allele size	Repeat motif	Primer Forward	Primer Reverse
1	UGEP33	211-237	$(TC)_{18}$	TAGCCCGTTTGCTTGTTTTG	AAGGCCCTAGAACGTCAAGC
2	UGEP96	246-310	$(CT)_{10}$	TAATGGGCCTAATGGCAATG	CAAAATCCGAGCCAAGATTC
3	UGEP56	175-183	$(GT)_{12}$	CTCCGATACAGGCGTAAAGG	ACCATAATAGGGCCGCTTG
4	UGEP3	220-222	$(CA)7N12(GA)_{15}$	CCACGAGGCCATACTGAATAG	GATGGCCACTAGGGATGTTG
5	UGEP68	254-258	$(CT)_{14}$	CGGTCAGCATATAACGAATGG	TCATTGATGAATCCGACGTG
6	UGEP46	179-191	$(GA)_{14}$	CAAGTCAAAACATTCAGATGG	CCACTCCATTGTAGCGAAAC
7	UGEP27	267-285	$(GA)_{19}$	TTGCTCTGAGGTTGTGTTGC	TCAAGCATAGTGCCCTCCTC
8	UGEP31	254-260	$(GA)_{12}$	ATGTTGATAGCCGGAAATGG	CCGTGAGCCTCGAGTTTTAG
9	UGEP57	467-473	$(AG)_{16}$	CCATGGGTTCATCAAACACC	ACATGAGCTCGCGTATTGC
10	UGEP15	195-203	$(CT)_{22}$	AAGGCAATCTCGAATGCAAC	AAGCCATGGATCCTTCCTTC
11	UGEP64	233-245	$(CT)_{23}$	GTCACGTCGATTGGAGTGTG	TCTCACGTGCATTTAGTCATTG
12	UGEP73	176-194	$(CT)_4CC(CT)_{10}$	GGTCAAAGAGCTGGCTATCG	ACCAGAACCGAATCATGAGG
13	UGEP110	204-216	$(CT)_{12}$	AAATTCGCATCCTTGCTGAC	TGACAAGAGCACACCGACTC
14	UGEP106	182-190	$(AC)_{12}$	AATTCCATTCTCTCGCATCG	TGCTGTGCTCCTCTGTTGAC
15	UGEP20	146-158	$(GA)_{20}$	GGGGAAGGCAATGATATGTG	TTGGGGAGTGCCAACAATAC
16	UGEP81	287-295	$(GT)_{12}$	AAGGGCCATACCAACACTCC	CACTCGAGAACCGACCTTTG
17	UGEP24	171–223	$(GA)_{26}$	GCCTTTTGATTGTTCAACTCG	CGTGATCCCTCTCCTCTCTG
18	UGEP102	170-198	$(TG)_{17}$	ATGCAGCCTTTGTCATCTCC	GATGCCTTCCTTCCCTTCTC
19	UGEP107	224-240	$(GA)_{15}$	TCATGCTCCATGAAGAGTGTG	TGTCAAAAACCGGATCCAAG

Source: Dida et al. (2007)

Allele scoring

The alleles were scored manually based on the size of each PCR amplified fragment and used for further analysis. Then the presence and absence of detected alleles per marker to each accession were converted to a 0, 1 scale.

Molecular marker data analysis of local finger millet germplasm accessions

Allele scores for respective SSR markers were analyzed using the PowerMarker® version 3.25 Software (Liu, 2005).

Polymorphism Information Content (PIC)

The polymorphism information content (PIC) was estimated as follows (Bostein *et al.*, 1980)

$$PIC=1-\sum_{i=1}^{k} Pi^2 - \sum_{i=1}^{k-1}\sum_{i+1}^{k} 2Pi^2 Pj^2$$

Where, *Pi* - frequency of i^{th} allele

Rare allele frequency

Allele frequency was calculated based on the allele count divided by the total number of alleles. The percentage of polymorphic allele frequency is less than 2% (0.02) is considered a rare allele in this study (Mohommadi and Prasanna, 2003).

Molecular diversity analysis

The allelic data were used to produce a distance matrix based on Nei genetic distance (Nei and Takezaki, 1983) and a phylogenetic tree was obtained by Neighbor-joining method using PowerMarker version 3.25.

Results and Discussion

Allelic diversity of finger millet germplasm

Of the 19 markers tested, six SSR makers, UGEP31, UGEP73, UGEP56, UGEP96, UGEP64, and UGEP68 were monomorphic. Furthermore, the marker, UGEP20 failed to amplify in most of the samples. Hence, these seven SSR markers were removed from the detailed analysis. Allele sizes ranged from about 150 bp (UGEP24) to about 430 bp (UGEP57) for 73 finger millet accessions studied. The summary statistics of 12 polymorphic markers are given in Table 3. These SSR markers used in this study were genomic markers. Hence, they are dispersed throughout the genome of the finger millet (Dida *et al*., 2007). Therefore, they are capable of detecting "true gene diversity" available inside or adjacent to the genes compared to random genome markers such as RFLP or RAPD (Thiel *et al*., 2003).

The total number of alleles detected in the present study was 36 for twelve polymorphic SSR markers. The maximum number of alleles (5) was detected with UGEP24. The average number of alleles per locus was 3.0 for polymorphic markers. Nethra *et al*. (2014) and Ramakrishna *et al*. (2016) reported that the average number of alleles per locus was 3.11 and 2.9, respectively for the most diverse finger millet germplasm including *E. africana* and *E. indica* using SSRs. Similarly, Warkista *et al*. (2017) reported average alleles per locus as 2.6 for 20 Sri Lankan germplasm collected from 4 districts using the SSR technique. A comparatively large number of alleles per locus were ranging from, 7 - 21, 3 - 23 and 6 – 22 which have been reported by Bharathi, (2011), Manyasa *et al*. (2015) and Lule *et al*. (2014) respectively with capillary electrophoresis using an ABI Prism® 3730 Genetic analyzer (Applied Biosystems, USA). The reason for scoring of a higher number of alleles per marker was due to the analysis of diverse finger millet germplasm including land landraces and wild *Eleusine* species.

The average Polymorphic Information Content (PIC) of the present study was 29%. The highest number of alleles per locus and the highest PIC value were observed with the SSR marker UGEP24 (0.68) followed by UGEP15 (0.63). However, these values were lower compared to the studies conducted by Panwar *et al*. (2010) using 10 SSRs for 83 germplasm obtained from India and Africa, which showed 70.6% polymorphism. However, SSR (UGEP markers) diversity analysis studies of a fairly large number of germplasm showed an average polymorphism of 53% and 60.6% (Manyasa, 2015; Bharathi, 2011). The high polymorphism indicates the wide diversity among accessions. Similarly, the highest gene diversity was observed with UGEP24 and UGEP15 markers (Table 3).

The heterozygosity was not observed for all the markers. The finger millet is a highly self-pollinated crop and natural cross-pollination is very low, only around 1% (Jansen and Ong 1996; Upadhyaya *et al*., 2008). The DNA was extracted from a bulk sample of seedlings from the seeds of a single ear (panicle), multiplied in the previous season, and off types were removed.

Table 3. Summary of genetic diversity parameters across 73 different finger millet accessions for 12 SSR markers

Marker	Major allele. frequency	Allele No	Gene diversity	PIC
UGEP110	0.96	3.00	0.08	0.08
UGEP 106	0.96	2.00	0.08	0.08
UGEP81	0.89	3.00	0.20	0.19
UGEP46	0.99	2.00	0.03	0.03
UGEP3	0.95	3.00	0.10	0.10
UGEP107	0.82	4.00	0.31	0.29
UGEP102	0.58	3.00	0.54	0.45
UGEP57	0.62	2.00	0.47	0.36
UGEP33	0.84	3.00	0.28	0.25
UGEP27	0.75	2.00	0.37	0.30
UGEP24	0.44	5.00	0.70	0.66
UGEP 15	0.47	4.00	0.68	0.63
Mean	0.77	3.00	0.32	0.29

PIC = Polymorphism Information Content

Therefore, the heterozygosity observed due to physical mixtures of off types was none in this study. Previous studies have shown that the different levels of heterozygosity may be observed due to the reason that some markers can be mapped both A and B genome of finger millet being an allotetraploid (Dida *et al*., 2008). Apart from that some land races involved in those studies still carry the residual heterozygosity for some SSR markers (Bharathi, 2011).

A rare allele (polymorphic allele frequency <2%) has been observed for some SSR markers (Mohommadi and Prasanna, 2003). The rare alleles can be held genes for special traits such as pest and disease resistance and tolerance to drought (Bharathi, 2011). The marker UGEP46 showed a rare allele in AC009304 accession, which is an exotic germplasm from an unknown source. The marker UGEP110 also showed two rare alleles in exotic accessions of AC7116 (Zimbabawe), AC000927 (India) and farmer cultivar TVFM-01 from Killinochchi. The marker UGEP3 exhibited a rare allele in exotic accession AC009311. Marker UGEP33 showed a rare allele in AC504 (Nuwara Eliya) and AC007111 (Zimbabwe) (Table 4). The AC009304 (exotic) with a rare allele showed a higher flag leaf length, flag leaf width, plant height, and a lower number of tillers (Kumari *et al*., 2018). The AC000927 (India) with a rare allele attributed to a higher 1000 grain weight and AC009311 showed lower number of tillers (Kumari *et al*., 2018). The global composite collection of 1,000 germplasm from Africa and India showed 110 rare alleles in 104 accessions (Bharathi, 2011).

Table 4. Allele frequencies for SSR markers for 73 finger millet accessions

SSR marker	Allele frequency				
	Allele* 1	Allele 2	Allele 3	Allele 4	Allele 5
UGEP15	0.164	0.247	0.466	0.123	
UGEP24	0.425	0.068	0.205	0.247	0.055
UGEP27	0.247	0.753			
UGEP33	0.027	0.836	0.137		
UGEP57	0.616	0.384			
UGEP102	0.370	0.562	0.068		
UGEP 107	0.041	0.096	0.822	0.041	
UGEP3	0.014	0.945	0.041		
UGEP46	0.986	0.014			
UGEP81	0.068	0.890	0.041		
UGEP106	0.959	0.041			
UGEP110	0.014	0.959	0.027		

**Alleles were named as 1,2,3... etc. based on the lowest to highest base pair number, respectively, scored by manually*

Population diversity of finger millet germplasm

Phylogenetic tree based on Nei genetic distance among 73 accessions of the collection was divide in to three main

groups (1, 2 and 3). Then each group was subdivided into 2 clusters; C_1, C_2, C_3, C_4, C_5 and C_6 , respectively from the groups 1,2 and 3 (Figure 1 and Table 5). The three main groups consisted of 15, 27, and 31 accessions, respectively. Among the 15 accessions in group 1, ten accessions belonged to exotic germplasm whereas C_2 of group 1 consisted of 5 exotic accessions from Zimbabwe one exotic accession from genebank International Crops Research Institute for Semi-Arid Tropics (ICRISAT) collection, and one local farmer cultivar from Killinochchi. The C_1 of group 1 comprised of equal proportions of local [AC000108, *Oshadha*, from Monragala), AC007090 (Badulla), TVFM-01 (Killinochchi)] and exotic germplasm from Zimbabwe, India and Nepal. Main group 2 contained 27 germplasm accessions mostly from Sri Lanka and only 3 of them were of exotic origin [AC007111 (Zimbabwe), AC012495 (India), AC000926 (India)]. The 7 of 31 germplasm in group 3 were exotic from India, Nepal, and Zimbabwe. The local accessions from different districts were grouped in clusters 5 and 6 (Table 5). The six studied accessions from Nuwara Eliya were grouped in groups 2 and group 3. The four accessions from Killinochchi were grouped in groups 1 and 2. However, the farmer cultivars collected from Mahiyanganaya were grouped into 3rd group but in two separate subgroups (clusters). Hence, irrespective of the district of collection and location of origin the local and exotic germplasms were grouped in same clusters. In contrast, the accessions from districts or location were grouped in different clusters as well.

Based on morphological characterization study conducted for these accessions showed that the accessions grouped in the same group were morphologically different for qualitative traits such as days to flowering, panicle shape, pigmentation, and grain color and quantitative traits such as plant height, yield, finger length, flag leaf length, ear weight, panicle exertion, peduncle length and 1000 grain weight (Kumari *et al*., 2018: Kumari *et al*., 2021). The results of the present study can be supported by the observation of past studies of morphological and molecular diversity (using 19 UGEP SSR markers) analysis of 340 east African finger millet germplasm showing that there was no identified link between a marker and morphological traits (Manyasa *et al.*, 2015).

Further, PGRC finger millet accessions with numbers less than AC006000 were collected or introduced during 1987 to 1990, numbers between AC006000 to AC010100 were collected between 1990 to 2000, numbers between AC010101 to AC012800 were collected or introduced between the year 2001 to 2007, and the accessions with the number greater than AC012800 were introduced or locally collected after 2007. Therefore, the grouping of exotic accessions with local accessions was not evident by the previous exotic introduction to local regions and re-collection as these accessions were collected in different time periods. The *Rawana* (AC010326) is the officially released variety of Indian origin. In addition, exotic accessions were evaluated in a breeding program at Field Crops Research and Development Institute, Mahailluppallama (Anonymous, 2003).

Table 5. Cluster formation of accessions under different groups and clusters based on SSR markers

Group	Cluster	Total No. acc.	No. of Exotic acc.	No. of local acc.	Accessions number and origin*
1	1	8	4	4	000108(MON), 001906 (EXOUN), 007090(BADU), 007769 (POL), 000927 (EXO-IN), 012428(EXO-NEP), 012639 (EXOUN), TVFM -01(KILLI)
1	2	7	6	1	007109 (EXO-ZIM), 007110 (EXO-ZIM), 007116(EXO-ZIM), 007117 (EXO-ZIM), _009304 (EXOUN), 009311 (EXOUN), KILLI_TVFM013-1
2	3	14	2	12	000127 (MON), 000504(NELYA), 000910 (EXO-IN), 001329 (RAT), 002383(JAFF), 002384(JAFF), 012968(JAFF), 007111(EXO-ZIM), 007823(KAN), 008470(MON), 009079 (NELYA), 0011087 (BATI), 0012465(NELYA), TVFM-02(KILLI)
2	4	13	1	12	000152(HAM), 000192(HAM), 000353(MAT), 000926(EXO-IN), 000965(BADU), 0001051(NELYA), 0001460(NELYA), 000418 (KURU), 008613(RAT), 008630 (RAT), 010453(POL), 012038(ANU), TVFM-04 (KILLI)
3	5	17	2	15	000923(EXO-IN), 007078(KURU), 011252(MON), 011334 (MAT), 011342 (MAT), 011350 (KAN), 011819 (LOCUN), 011821(MON), 012189(ANU), 011819(UNL), 012282(NELYA), 012401(ANU), 012494(EXO-NEP), 012591 (EXOUN), 012629(POL), 012927 (MON), M2 (MAHI)
3	6	14	5	9	000955(HAM), 000964(EXO-IN), 006581(BADU), 007071 (ANU), 007112(EXO-ZIM), 010326 (EXO-IN), 011774 (AMP), 012248 (KAN), 012495(EXO-IN), 012593 (EXOUN9), 012605(POL), M1 (MAHI), M4 (MAHI), M7 (MAHI)

**ANU=Anuradhapura, AMP=Ampara, BAT=Baticolo, EXO-IN=Exotic India, EXO-NEP= Exotic Nepal, EXO-ZIM=Exotic Zimbabwe, EXOUN= Exotic unknown origin, UNL=Local unknown origin, HAM=Hambantota, KUR=Kurunegala, JAFF=Jaffana, KAN=Kandy, MON=Monaragala, MAT=Matale, NELYA=Nuwara Eliya, POL=Polonnaruwa, RAT=Ratnepura. TVFM= farmer cultivar from Killinochchi and Jaffna, MAHI=M1-M9 farmer cultivar from Mahiyanganaya*

Nei's frequency-based distance matrix showed that the highest distance (0.8333) was observed between AC009304 (exotic germplasm from ICRISAT collection (IE48509)) and AC910 (from India). Further, the AC009304 collection showed a comparatively higher distance from all the other studied accessions too. The morphological evaluation of AC009304 showed a higher plant height, flag leaf length, flag leaf width, and a lower number of tillers compared to other studied accessions (Kumari *et al*., 2018). Whereas, the lowest (0.00) distance was observed between following locally collected accessions, AC007769 (Polonnaruwa) and AC012296 (Anuradhapura); M1 (Farmer variety from Mahiyanganaya) and AC011774 (Ampara); AC108 (Monaragala) and AC012269 (Anuradhapura); AC011087

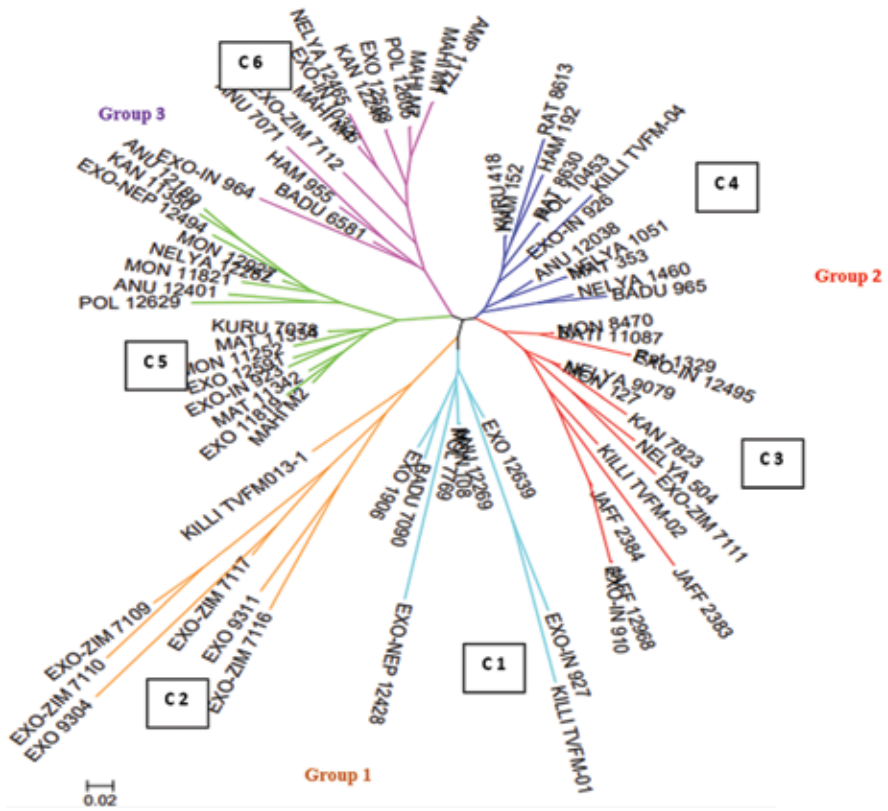

Figure 1. Dendrogram based on Neighbor-joining consensus tree based on the simple matching dissimilarity matrix

ANU=Anuradhapura, AMP=Ampara, BAT=Baticolo, EXO-IN=Exotic India, EXO-NEP= Exotic Nepal, EXO-ZIM=Exotic Zimbabwe, EXO= Exotic unknown origin, HAM=Hambantota, KUR=Kurunegala, JAFF=Jaffana, KAN=Kandy, MON=Monaragala, MAT=Matale, NELYA=Nuwara Eliya, POL=Polonnaruwa, RAT=Ratnepura. TVFM= farmer cultivar from Killinochchi and Jaffna, MAHI=M1-M9 farmer cultivar from Mahiyanganaya

(Baticoloa) and AC008470 (Monaragala); AC000152 (Hambantota) and AC000418 (Kurunegala); AC007078 (Kurunegala) and AC011334 (Matale); AC000353 (Matale) and AC001051 (Nuwara Eliya); AC000108 (Monaragala) and AC007769 (Polonnaruwa); AC000127 (Monaragala) and AC009079 (Nuwara Eliya); AC012927 (Monaragala) and AC012282 (Nuwara Eliya). Further, the lowest distance (0.000) was observed between following local and exotic accessions, AC012968 (Jaffna) and AC000910 (India) which showed similar morphological traits such as ultra-short days to flowering (51-52 days), purple pigmentation, top curved panicle shape with lower grain yield (Kumari *et al*., 2018). AC012248 (Kandy) and AC012593 (Exotic unknown) showed similar morphological traits as well (Kumari *et al*., 2018). Even though, AC001329 (Ratnapura) and AC012495 (India) showed a lower distance value, these two accessions showed a marked difference in morphological traits. Though these accession pairs showed the lowest genetic distance for studied 12 SSR markers, most of them were morphologically different from each

other (Kumari *et al.*, 2018). Hence, genetic delineation of accessions can be improved by the use of more SSR markers (Manyasa *et al*., 2015).

Wakista *et al*. (2017), found that the pattern of clustering of 21 Sri Lankan finger millet accessions based on molecular markers had no impact on the geographical region/ district of collection. The present study has included only three accessions that Wakista *et al*. (2017) used. Similarly, Arya *et al*. (2012) reported the clustering of south Indian accessions with African lowland types and north/highland Indian accessions with that of African highlands. A total of 479 polymorphic loci were generated using the 50 RAPD primers for 32 Indian finger millet germplasm from different states of India clustered into two groups (Babu *et al*., 2007). Ramakrishnan *et al*. (2016), reported that three clusters were formed for 128 Indian and non-Indian germplasm when 87 genomic SSR markers were used and the non-Indian genotypes were grouped with Indian genotypes. Hence, the potential of RAPD, SSR, and gene-based markers for characterizing germplasm, estimating of genetic diversity, and narrowing down the vast germplasm into distinct core groups has been identified in many studies worldwide (Panwar *et al*., 2010; Naga *et al*., 2012).

Conclusions

The molecular diversity analysis showed an average of 3.6 alleles per locus with 12 polymorphic markers for 73 local (from 14 districts) and exotic (India, Nepal and Zimbabwe) finger millet germplasm. Irrespective of the place of collection, the finger millet accessions are grouped into three main groups. Local accessions were sub-grouped with germplasm from India, Nepal and Zimbabwe and it indicates that alleles present in India and African finger millet germplasm are present in the local accessions as well. Further, local accessions within the same location have shown a higher genomic distance. Incorporation of important traits through hybridization between local and exotic accessions in different clusters can be done and true crosses can be identified using studied SSR markers in breeding of finger millet. Hence, the molecular diversity present in finger millet accessions available in the Plant Genetic Resources Centre of Sri Lanka can be utilized along with their morphological traits for the selection and development of trait-specific promising finger millet varieties for dryland farming in Sri Lanka.

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