RESEARCH ARTICLE

SABRAO Journal
of Breeding and Genetics
47 (2) 79-88, 2015

FINGER MILLET GERMPLASM CHARACTERIZATION AND EVALUATION USING PRINCIPAL COMPONENT ANALYSIS

V. ULAGANATHAN[1*] and A. NIRMALAKUMARI[2]

[1]Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, India.
[2]Centre of Excellence in Millets, Atthiyandal, Tamil Nadu Agricultural University, Coimbatore, India.
*Corresponding author's email: ulagunbourne@gmail.com

SUMMARY

Finger millet is an important crop in the developing world especially in Africa and Asia. The aim of this study was to characterize 305 finger millet genotypes using multivariate traits. The maximum coefficient of variation was recorded for grain yield per plant. High variability observed for most of the characters indicated the scope of improvement of these characters by direct selection. Phenotypic correlation between grain yield per plant was highly significant and positively associated with days to flowering, productive tillers per plant, plant height, 1000-grain weight, flag leaf sheath length, days to maturity, flag leaf blade length and finger width. The principal component analysis revealed that the first 4 components with eigen value of greater than 0.65 contributed about 87.8% of total variability. The proportions of the total variance attributable to the first 4 principal components were 66.7, 10.7, 5.5 and 5.0% respectively. The characters including grain yield per plant, 1000-grain weight, productive tillers per plant, days to flowering, days to maturity, finger number per panicle, finger length and finger width were the most important traits contributing for the overall variability. This implied that these traits should be given emphasis in finger millet improvement program. Cluster analysis grouped 305 genotypes into 16 different clusters through multivariate hierarchical clustering. Cluster VII, X, XIII and XVI formed solitary clusters which revealed the presence of wide diversity for various characters among these accessions. The variability existing in the finger millet germplasm provide opportunities for breeders to select specific donors for genetic improvement.

Key words: Variability, phenotypic correlation, quantitative traits, principal component analysis, cluster analysis, genetic improvement

Key findings: The genotypes TNEc 1242, TNEc 1872, TNEc 1747 and TNEc 2092 found to be more variable. Recombination breeding using these parents provides segregants with rare combination of traits of interest towards maximizing grain yield potential.

Manuscript received: August 8, 2014; Decision on manuscript: October 9, 2014; Manuscript accepted: January 7, 2015.
© Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2015

Communicating Editor: Bertrand Collard

INTRODUCTION

Finger millet is one of the most important small millets crop grown in large areas of the developing world especially in Africa and Asia. It has the ability to produce higher yield than other crops under multiple stresses such as drought, soil acidity and land marginality (Barbeau and Hilu, 1993; Upadhyaya *et al.*, 2006). Moreover, it has high nutritional value and excellent storage qualities (Dida *et al.*, 2007). In India, it is cultivated on 1.8 million ha

with a production of 2.19 million tons and average productivity of 1489 kg per ha (Directorate of Economics and Statistics, GOI, 2010-11).

In any crop, germplasm resource not only serves as a valuable source of useful genes but also provides scope for building up a basic population of wide genetic variability. Bringing improvement over existing crop varieties is a continuous process in plant breeding. To achieve this objective, the breeder has to identify diverse parents having high genetic variability for combining desirable characters. Therefore, knowledge of sound genetic diversity is essential for undertaking any recombination breeding program. In earlier days, geographical diversity was considered as a measure of genetic diversity but recently it is observed that genetic materials from same eco geographic origin also possess diverse genetic makeup and it is not uncommon that the genetic materials of different eco geographic origin possess similar genetic architecture due to free and easy material transfer facilities.

The usefulness of multivariate analysis for the study of morphologically complex individual and for measuring the degree of divergence between biological populations has been shown in different fields of research. Multivariate statistical techniques which simultaneously analyze multiple measurements on each individual under investigation are widely used in analysis of genetic diversity irrespective of whether it is morphological, biochemical or molecular marker-based and subsequently, classification of germplasm collections. Among the multivariate techniques, principal component analysis (PCA) and cluster analysis had been shown to be very useful in selecting genotypes for breeding program that meet the objective of a plant breeder (Mohammadi and Prasanna, 2003). PCA may be used to reveal patterns and eliminate redundancy in data sets (Adams, 1995) as morphological and physiological variations routinely occur in crop species. Cluster analysis is commonly used to study genetic diversity and for forming core subset for grouping accessions with similar characteristic into one homogenous category. Clustering is also used to summarize information on relationships between objects by grouping similar units so that the relationship may be easily understood and communicated. Multivariate analysis has been used frequently for genetic diversity analysis in many crops such as finger millet (Dagnachew *et al*., 2012b) and rice (Gana *et al.,* 2013).

The important objective of any plant scientist is to identify an optimum number of plant traits which are sufficient to explain the maximum variability in the crop growth from sowing to harvest. This study was undertaken to run a classification analysis on the finger millet genotypes by means of descriptive statistic and to understand the association of various characters, PCA and cluster analysis which would enable breeders to classify the available germplasm into distinct groups on the basis of their genetic diversity.

MATERIALS AND METHODS

This study was conducted to characterize 300 finger millet germplasm accessions out of 2664 collected from different geographical regions maintained at Small Millets Unit of Department of Millets, Tamil Nadu Agricultural University, Coimbatore, India. A total of 300 finger millet germplasm has been selected based on the yield characters like plant height, productive tillers per plant, finger number per panicle, finger length, days to maturity and grain yield per plant. For evaluation and characterization these 300 germplasm accessions and 5 check varieties were grown in augmented block design during *kharif*, 2011. The germplasm accessions were divided into 12 blocks, each consisted of 25 accessions and 5 check varieties namely CO (Ra) 14, CO 9, GPU 28, TRY 1 and Paiyur 2. Each accession was grown in single rows of 3 m length with a spacing of 30 cm x 10 cm. Observations were recorded from 5 randomly selected plants in each accession for 13 quantitative characters such as plant height (cm), productive tillers per plant, flag leaf sheath length (cm), flag leaf sheath width (cm), flag leaf blade length (cm), flag leaf blade width (cm), finger number per panicle, finger length (cm), finger width (mm), days to maturity, 1000 grain weight (g) and grain yield per plant (g) as per the descriptors for *Eleusine coracana*

(IBPGR, 1985) except days to flowering. Days to flowering was noted on single row basis.

The data collected for all quantitative characters were subjected to analysis of variance for augmented block design according to the method suggested by Federer and Raghavarao (1975). The major descriptive statistics such as mean, range, standard deviation and coefficient of variation were worked out by adopting the standard methods (Panse and Sukhatme, 1964). Phenotypic correlation coefficients were calculated using the formula as suggested by Johnson *et al*. (1955). The principal component analysis was computed using the software statistical package for the social sciences (SPSS) 16.0 package (Levesque, 2007). As suggested by Johnson and Wichern (1988), principal components with eigen values less than one was considered. Mean values of 305 genotypes for 13 quantitative traits were subjected to multivariate hierarchical cluster analysis computed using the software numerical taxonomy and multivariate analysis system (NTSYS) pcv2.02i (Rohlf, 1998).

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences among the genotypes for all characters under study. This indicated germplasm accessions studied were genetically diverse and the considerable amount of variability existed in the experimental material hence there is an opportunity for plant breeder to undertake further breeding activities like hybridization program. Substantial variations in finger millet have been reported in previous studies by Naik *et al.* (1994) and Prasad Rao *et al.* (1994). The range, mean, standard deviation and coefficient of variation for 13 quantitative traits in 305 finger millet genotypes are presented in Table 1. Flag leaf blade length exhibited the widest range where the genotype TNEc 0180 (14.6 cm) had the lowest and TNEc 0407 (54.2 cm) had the highest values followed by grain yield per plant. The genotypes TNEc 1776 (13.7 g) and TNEc 2161 (47.8 g) recorded low and high values respectively for grain yield per plant. Similar results on wide range of variations for plant height and grain yield per plant (Narasmba Rao and Parathasarathi, 1968), finger length and number (Kebede and Menkir, 1986) and plant height and productive tillers (Prasada Rao *et al.,* 1994) were reported earlier. Such diversity within the finger millet genotypes tested would provide ample opportunities for future genetic improvement of the crop through direct selection from the accessions and/or following traits recombination through intra-specific hybridization for desirable traits. The maximum coefficient of variation was found in grains yield per plant (26.3%). Hence, there is scope for selecting high yielding potential genotypes.

Grain yield is a complex character influenced by a large number of other component characters. A knowledge on the association between yield and other biometrical traits and also among component traits helps in improving the efficiency of selection. The correlation between characters may exist due to various reasons such as pleiotropy, genetic linkage and association of loci or blocks of loci governing variability for different characters located on same chromosome. It has been generally accepted that correlation between different characters represents a coordination of physiological processes which is often achieved through gene linkages. The association of all morphological traits was estimated by correlation analysis (Table 2). Among the 13 morphological traits studied, days to flowering (0.93), productive tillers per plant (0.92), plant height (0.91), 1000 grain weight (0.90), flag leaf sheath length (0.85), days to maturity (0.83), flag leaf blade length (0.78) and finger width (0.30) had significant and positive correlations with grain yield per plant at $P = 0.01$ level. Earlier workers have also reported significant positive association of grain yield per plant with days to flowering, flag leaf sheath length, flag leaf blade length and 1000-grain weight (Kadam *et al.,* 2009) and productive tillers per plant (Dagnachew *et al.,* 2012a). Maximum positive correlation observed for most of the characters with grain yield per plant indicated that all these characters could be simultaneously improved and it also suggested that increase in any one of them would lead to improvement of other character.

Table 1. Patterns of genetic variability for 13 quantitative traits in 305 finger millet genotypes.

Characters	Mean	Minimum	Maximum	Range	SD	CV (%)
Days to flowering	80.0	62.0	83.0	21.0	5.1	7.2
Plant height (cm)	91.2	62.7	114.7	52.0	12.0	13.2
Productive tillers per plant	9.3	6.0	14.0	8.0	1.8	19.7
Flag leaf sheath length (cm)	10.1	7.0	14.7	7.7	1.7	16.9
Flag leaf sheath width (cm)	1.0	0.7	1.4	0.7	0.2	15.7
Flag leaf blade length (cm)	30.2	14.6	54.2	39.6	7.2	23.8
Flag leaf blade width (cm)	1.0	0.7	1.5	0.8	0.2	15.7
Finger number per panicle	8.6	6.0	12.7	6.7	1.4	15.9
Finger length (cm)	8.8	6.1	12.6	6.5	1.5	17.1
Finger width (mm)	10.1	7.0	13.0	6.0	1.3	12.4
Days to maturity	101.0	88.0	113.0	25.0	5.1	5.1
1000 grain weight (g)	2.5	1.5	3.6	2.1	0.4	15.4
Grain yield per plant (g)	29.4	13.7	47.8	34.2	7.7	26.3

SD - Standard deviation; CV - Coefficient of variation

Table 2. Phenotypic correlation coefficients for different traits in 305 finger millet genotypes.

Characters	DF	PH	PT	FLSL	FLSW	FLBL	FLBW	FN	FL	FW	DM	TGW	GYP
DF	1.00	0.84**	0.85**	0.81**	-0.70**	0.76**	-0.66**	-0.47**	-0.42**	0.26**	0.91**	0.84**	0.93**
PH		1.00	0.85**	0.92**	-0.82**	0.85**	-0.79**	-0.51**	-0.45**	0.28**	0.74**	0.83**	0.91**
PT			1.00	0.78**	-0.71**	0.70**	-0.65**	-0.49**	-0.44**	0.25**	0.75**	0.84**	0.92**
FLSL				1.00	-0.76**	0.86**	-0.70**	-0.44**	-0.39**	0.20**	0.71**	0.75**	0.85**
FLSW					1.00	-0.71**	0.82**	0.45**	0.37**	-0.24**	-0.63**	-0.70**	-0.75**
FLBL						1.00	-0.64**	-0.37**	-0.31**	0.18**	0.70**	0.69**	0.78**
FLBW							1.00	0.43**	0.32**	-0.19**	-0.58**	-0.66**	-0.70**
FN								1.00	0.69**	-0.42**	-0.43**	-0.60**	-0.55**
FL									1.00	-0.35**	-0.39**	-0.55**	-0.49**
FW										1.00	0.25**	0.28**	0.30**
DM											1.00	0.75**	0.83**
TGW												1.00	0.90**
GYP													1.00

* Significant at $P = 0.05$ ** Significant at $P = 0.01$

DF - Days to flowering , PH- Plant height (cm) , PT - Productive tillers per plant, FLSL - Flag leaf sheath length (cm), FLSW - Flag leaf sheath width (cm), FLBL - Flag leaf blade length (cm), FLBW - Flag leaf blade width (cm), FN - Finger number per panicle, FL - Finger length (cm), FW - Finger width (mm), DM - Days to maturity, TGW – 1000-grain weight (g), GYP - Grain yield per plant (g)

For example, grain yield per plant which was positively correlated with plant height, flag leaf sheath length and flag leaf blade length indicating that finger millet growth at vegetative stage is also important and crucial for the physiological process that determines the output of its performance in terms of yield and other physiological attributes that contributes to its development. Perusal on correlation among component characters revealed that strong associations among desirable component characters are present especially with days to flowering and productive tillers per plant. Hence, selection criteria should consider all these characters for the improvement of grain yield in finger millet.

Significant negative correlation observed for flag leaf sheath width (-0.75), flag leaf blade width (-0.70), finger number per panicle (-0.55) and finger length (-0.49) with grain yield per plant (P = 0.01) indicated increase in one character would lead to decrease in another character. Negative association for flag leaf sheath width and flag leaf blade width with grain yield per plant was beneficial ssociation because wider flag leaf sheath width may pose problem require more energy for complete emergence of the panicle which will result in reduced thousand grain weight and /or grain yield per plant. Similarly, panicle length having negative and significant correlation with grain yield per plant was reported by Nirmalakumari *et al.,* (2010) in little millet.

The principal component analysis is a technique which identifies plant traits that contribute most of the observed variation within a group of genotypes. This tool has a practical application in the selection of best genotypes for breeding purpose. The results of PCA revealed that the first 4 components with eigen value of greater than 0.65 contributed about 87.8% of total variability in 305 genotypes involving all the 13 quantitative traits studied (Table 3). The importance of traits towards the PC could be seen from the corresponding eigen values which are presented in Table 4. The first principal component accounted for 66.7% of the total variation in the population. Grain yield per plant (0.96) contributed more to the variation followed by plant height (0.95), days to flowering (0.92), 1000 grain weight (0.91), productive tillers per plant and flag leaf sheath length (0.90), days to maturity (0.85), flag leaf sheath width, flag leaf blade length (0.84) and finger width (0.34) had the highest loadings in PC1 indicating their significant importance for these components. These traits had the largest participation in the divergence and carried the largest portion of its variability. All other characters contributed negative to the first component.

Table 3. Principal components showing the Eigen values, proportion of variation and total variation across axis.

Principal component	Eigen value	Variation (%)	Total variation explained across axis
1	8.67	66.7	66.7
2	1.39	10.7	77.4
3	0.71	5.5	82.8
4	0.65	5.0	87.8
5	0.39	3.0	90.8
6	0.30	2.3	93.1
7	0.29	2.2	95.4
8	0.17	1.3	96.7
9	0.15	1.2	97.9
10	0.12	0.9	98.8
11	0.07	0.5	99.3
12	0.06	0.4	99.7
13	0.03	0.3	100.0

Table 4. Principal component analysis for 13 quantitative traits in 305 finger millet genotypes – non-rotated loadings.

Character	Principal component			
	PC1	PC2	PC3	PC4
Days to flowering	0.92	0.11	-0.01	0.27
Plant height (cm)	0.95	0.11	0.05	-0.10
Productive tillers per plant	0.90	0.07	-0.05	0.16
Flag leaf sheath length (cm)	0.90	0.20	0.02	-0.06
Flag leaf sheath width (cm)	0.84	-0.13	-0.12	0.37
Flag leaf blade length (cm)	0.84	0.26	0.07	-0.02
Flag leaf blade width (cm)	-0.79	-0.16	-0.09	0.46
Finger number per panicle	-0.62	0.62	0.22	0.15
Finger length (cm)	-0.55	0.65	0.37	0.06
Finger width (mm)	0.34	-0.63	0.69	0.09
Days to maturity	0.85	0.09	0.01	0.35
1000 grain weight (g)	0.91	-0.07	-0.13	0.11
Grain yield per plant (g)	0.96	0.04	-0.03	0.15

Second principal component contributed 10.7% of the total variation. Characters that contributed to the second component include finger length (0.65), finger number per panicle (0.62), flag leaf blade length (0.26), flag leaf sheath length (0.20), plant height and days to flowering (0.11). The third principal component accounted for 5.5% of the total variation in the population. Finger width contributed the highest (0.69) followed by finger length (0.37) while finger number per panicle contributed less variation. Likewise, the fourth principal component contributed 5.0% of the total variation. The major characters that contributed highly to the variation include flag leaf blade width (0.46), flag leaf sheath width (0.37), days to maturity (0.35), days to flowering (0.27), productive tillers per plant (0.16), finger number per panicle and grain yield per plant (0.15) while 1000-grain weight (0.11) contributed least to the variation. Similar findings with regard to grain yield per plant, plant height, days to flowering and productive tillers per plant were reported by Salini *et al.,* (2010) in prosomillet. The traits such as grain yield per plant and plant height as earlier reported by Khavari Khorasani *et al.,* (2011) in maize and days to maturity was reported by Azad *et al.,* (2012) in maize.

Principal component analysis in this study confirmed the first principal components contributed maximum number of characters towards genetic diversity and these traits could be effectively used for further breeding programs to create more variability. Grain yield per plant, plant height, days to flowering, 1000-grain weight, productive tillers per plant, flag leaf sheath length, days to maturity, flag leaf sheath width and flag leaf blade length were the most important traits contributing for the overall variability observed among the genotypes. Characters with high variability are expected to provide high level of transgressive segregation in breeding populations. This is important for breeders to investigate high yielding, early maturing and dwarf varieties through conventional breeding. Several authors indicated that different morphological traits for the different crops have contribution for the overall variability (Negash *et al.,* 2005; Assefa *et al.,* 2003).

The tri-dimensional spatial figuration shows 5 basic clusters of the characters studied (Figure 1). The cluster I had 3 characters in a group (plant height, flag leaf sheath length and flag leaf blade length) and cluster II had 5 characters in another group (grain yield per plant, productive tillers per plant, 1000-grain weight, days to maturity and days to flowering). In cluster III (finger length and finger number per panicle) and IV (flag leaf sheath width and

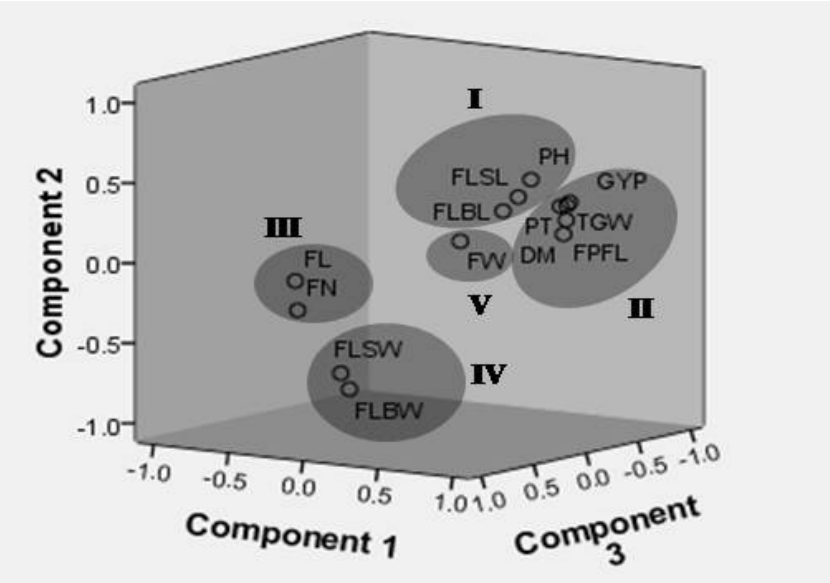

Figure 1. Three-dimensional graph showing the grouping of the 13 traits studied.

FPFL - Days to flowering. PH - Plant height (cm), PT - Productive tillers per plant, FLSL - Flag leaf sheath length (cm), FLSW- Flag leaf sheath width (cm), FLBL - Flag leaf blade length (cm), FLBW- Flag leaf blade width (cm), FN - Finger number per panicle, FL- Finger length (cm) , FW - Finger width (mm) DM - Days to maturity, TGW – 1000-grain weight (g), GYP - Grain yield per plant (g)

flag leaf blade width) had 2 characters each. Cluster V had the one character namely finger width. In the figure shows characters within the cluster are closely associated likewise finger length and finger number per panicle falls under the same cluster. Likewise finger length and finger width are comes under different clusters (III and V) it shows the characters between the groups are more divergent. The grain yield is mainly determined by productive tillers per plant and 1000-grain weight. The productive tillers per plant, 1000-grain weight, days to maturity and days to flowering were associated within the same group. The results showed that cluster II traits could be used for selecting high yielding as well as early maturing lines.

Based on cluster analysis, 305 genotypes were separated into 16 clusters through multiple hierarchical using similarity coefficient matrix at 3 (Table 5). The clustering pattern could be utilized in choosing the diverse genotypes which were likely to generate the highest possible variability for various economic characters. Cluster III was the largest comprising of 73 genotypes followed by cluster I with 68 genotypes, cluster XI with 45 genotypes, cluster VI with 40 genotypes, cluster VIII with 18 genotypes, cluster XII with 16 genotypes, cluster XV with 14 genotypes, cluster IX with 10 genotypes, cluster XIV with 7 genotypes, cluster II with 5 genotypes, cluster IV with 3 genotypes and cluster V with 2 genotypes. The genotypes namely TNEc 1242, TNEc 1872, TNEc 1747 and TNEc 2092 formed solitary clusters which revealed the presence of wide diversity for various characters among these accessions. Hybridization using genotypes belonging to VII, X, XIII and XVI clusters might be used for exploitation of hybrid vigor. The random pattern of distribution of accessions into various clusters from different eco-geographic regions revealed that there was no association between genetic diversity and geographic diversity. The nature of selection forces operating under one eco-geographical region seemed to be similar to that of other regions since the accessions from different geographical regions were grouped together into same clusters. This could be due to the similarity of conditions under which the types were breed and domesticated in different localities. Similar results were reported by Salini *et al.,* (2010) using 364 proso millet genotypes were grouped into17 clusters.

Table 5. Constituents of 16 clusters in 305 finger millet genotypes based on 13 quantitative characters.

Clusters	Number of genotypes	Constituent accessions
I	68	TNEc 0009, TNEc 1860, TNEc 0933, TNEc 1043, TNEc 1762, TNEc 0074, TNEc 0783, TNEc 0941, TNEc 1051, TNEc 1665, TNEc 0818, TNEc 1789, TNEc 1283, TNEc 0504, TNEc 1756, TNEc 1267, TNEc 0502, TNEc 0914, TNEc 0969, TNEc 1638, TNEc 1577, TNEc 1952, TNEc 0545, TNEc 1034, TNEc 2063, TNEc 1102, TNEc 0938, TNEc 0565, TNEc 0961, TNEc 1989, TNEc 1063, TNEc 2155, TNEc 0804, TNEc 2058, TNEc 1035, TNEc 2110, TNEc 1129, TNEc 1181, TNEc 1744, TNEc 1183, CO(Ra) 14, TNEc 0513, TNEc 0857, TNEc 0860, TNEc 0522, TNEc 0533, TNEc 0563, TNEc 0029, TNEc 1161, TNEc 0213, TNEc 0884, TNEc 1767, TNEc 1988, TNEc 0134, TNEc 2118, TNEc 0505, TNEc 2054, TNEc 1842, TNEc 0512, TNEc 1268, TNEc 0574, TNEc 0677, TNEc 2005, TNEc 0959, TNEc 0384, TNEc 1714, TNEc 1188, TNEc 0313
II	5	TNEc 0032, TNEc 0836, TRY 1, PAIYUR 2, TNEc 1953
III	73	TNEc 0033, TNEc 2041, GPU 28, CO 9, TNEc 0039, TNEc 1057, TNEc 2157, TNEc 0495, TNEc 1795, TNEc 1021, TNEc 0942, TNEc 1738, TNEc 0271, TNEc 1743, TNEc 0680, TNEc 0902, TNEc 1047, TNEc 1163, TNEc 1797, TNEc 1237, TNEc 1895, TNEc 0562, TNEc 0794, TNEc 0583, TNEc 0962, TNEc 1873, TNEc 1059, TNEc 1062, TNEc 0111, TNEc 0819, TNEc 0191, TNEc 1041, TNEc 1154, TNEc 1582, TNEc 1697, TNEc 0530, TNEc 0724, TNEc 1085, TNEc 1912, TNEc 0856, TNEc 1981, TNEc 0791, TNEc 1819, TNEc 1280, TNEc 1903, TNEc 0939, TNEc 0990, TNEc 1133, TNEc 0275, TNEc 0521, TNEc 1739, TNEc 0361, TNEc 1192, TNEc 0993, TNEc 0977, TNEc 1635, TNEc 1659, TNEc 1667, TNEc 1722, TNEc 1851, TNEc 0126, TNEc 1199, TNEc 1044, TNEc 0193, TNEc 0540, TNEc 2153, TNEc 1225, TNEc 1554, TNEc 1769, TNEc 1215, TNEc 1176, TNEc 1950, TNEc 1979
IV	3	TNEc 0986, TNEc 0987, TNEc 1609
V	2	TNEc 1584, TNEc 1607
VI	40	TNEc 0030, TNEc 1261, TNEc 1770, TNEc 1763, TNEc 0220, TNEc 0838, TNEc 1783, TNEc 0989, TNEc 1159, TNEc 1678, TNEc 0854, TNEc 1086, TNEc 1040, TNEc 1902, TNEc 0837, TNEc 1914, TNEc 2049, TNEc 0127, TNEc 0775, TNEc 0998, TNEc 0997, TNEc 1039, TNEc 1868, TNEc 1806, TNEc 0936, TNEc 0991, TNEc 1012, TNEc 0996, TNEc 1737, TNEc 1083, TNEc 1778, TNEc 0855, TNEc 1127, TNEc 1760, TNEc 1084, TNEc 1881, TNEc 1994, TNEc 1811, TNEc 1011, TNEc 1869
VII	1	TNEc 1242
VIII	18	TNEc 0080, TNEc 1791, TNEc 0974, TNEc 1583, TNEc 1036, TNEc 1730, TNEc 1087, TNEc 1093, TNEc 1174, TNEc 1774, TNEc 1793, TNEc 1768, TNEc 1910, TNEc 0117, TNEc 0908, TNEc 2215, TNEc 1167, TNEc 1522
IX	10	TNEc 0416, TNEc 0531, TNEc 0722, TNEc 0995, TNEc 2047, TNEc 1001, TNEc 1018, TNEc 2100, TNEc 1776, TNEc 1082
X	1	TNEc 1872
XI	45	TNEc 0018, TNEc 2035, TNEc 0631, TNEc 0227, TNEc 0602, TNEc 1944, TNEc 1621, TNEc 0419, TNEc 0629, TNEc 1020, TNEc 2036, TNEc 1305, TNEc 2055, TNEc 1306, TNEc 2089, TNEc 0087, TNEc 0397, TNEc 0147, TNEc 0180, TNEc 1857, TNEc 2097, TNEc 0166, TNEc 0274, TNEc 2187, TNEc 0205, TNEc 0214, TNEc 0251, TNEc 1226, TNEc 1633, TNEc 1307, TNEc 0308, TNEc 0601, TNEc 0578, TNEc 0707, TNEc 1977, TNEc 0509, TNEc 1639, TNEc 1968, TNEc 0153, TNEc 0520, TNEc 0570, TNEc 0881, TNEc 1252, TNEc 1312, TNEc 1759
XII	16	TNEc 0152, TNEc 0399, TNEc 1761, TNEc 0231, TNEc 0776, TNEc 0910, TNEc 0788, TNEc 0406, TNEc 0786, TNEc 2161, TNEc 0161, TNEc 0386, TNEc 0216, TNEc 0395, TNEc 1980, TNEc 1865
XIII	1	TNEc 1747
XIV	7	TNEc 0409, TNEc 0418, TNEc 1905, TNEc 0414, TNEc 2065, TNEc 0508, TNEc 0567
XV	14	TNEc 0089, TNEc 0756, TNEc 1909, TNEc 0907, TNEc 2150, TNEc 2156, TNEc 0992, TNEc 0407, TNEc 0921, TNEc 2158, TNEc 2135, TNEc 0754, TNEc 0787, TNEc 2179
XVI	1	TNEc 2092

CONCLUSION

Germplasm evaluation and characterization is important for plant breeders and multivariate statistical analysis provides a means for estimating morphological diversity between germplasm accessions. These tools are useful for the evaluation of potential breeding value of germplasm. However, this study suggests the need for breeders to exploit germplasm from distinct groupings for the development of improved varieties. Principal component analysis indicated that there was genetic variation for all traits within the accessions use in this study. Intercrossing between genotypes of diverse clusters would generate a broad spectrum of variability for effective selection in the segregating generations for the development of high yielding cultivars. The genotypes TNEc 1242, TNEc 1872, TNEc 1747 and TNEc 2092 formed solitary clusters and found to be more variable. Thus, crosses among the genotypes would exhibit high heterosis and may produce new recombinants with desired characters.

ACKNOWLEDGEMENTS

The authors would like to acknowledge International Development Research Centre (IDRC) and Canadian International Development Agency (CIDA), Canada for funding the research work.

REFERENCES

Adams MW (1995). An estimate of homogeneity in crop plants with special reference to genetic vulnerability in dry season. *Phseolus vulgaris*. *Euphytica,* 26: 665-679.

Assefa K, Arnulf M, Tefera H (2003). Multivariate analysis of diversity of tef (*Eragrostis tef (Zucc.)* Trotter) germplasm from western and south western Ethiopia. *Hereditas,* 138: 228-236.

Azad MK, Biswas BK, Alam NS, Alam KS (2012). Genetic Diversity in Maize (*Zea mays* L.) Inbred Lines. *The Agriculturists* 10(1): 64-70.

Barbeau WE, Hilu KW (1993). Protein, calcium, iron and amino acid content of selected wild and domesticated cultivars of Wnger millet. *Plant Foods Hum. Nutr.* 43: 97-104.

Dagnachew Lule, Kassahun Tesfaye, Masresha Fetene and Santie De Villiers (2012a). Inheritance and Association of Quantitative Traits in Finger Millet (*Eleusine coracana* Subsp. *Coracana*) Landraces Collected from Eastern and South Eastern Africa. *Int. J. Genet.* 2(2): 12-21.

Dagnachew Lule, Kassahun Tesfaye, Masresha Fetene and Santie De Villiers (2012b). Multivariate Analysis for Quantitative Traits in Finger Millet *(Eleusine coracana* subsp. *coracana)* Population Collected from Eastern and Southeastern Africa: Detection for Patterns of Genetic Diversity. *Int. J. Agric. Res.* 7 (6): 303-314.

Dida MM, Srinivasachary S, Ramakrishnan JL, Bennetzen MD, Devos KM (2007). The genetic map of finger millet, Eleusine *coracana. Theor. Applied Genet.* 114: 321-332.

Directorate of Economics and Statistics, Government of India, 2010-11.

Federer WT, Raghavarao D (1975). On Augmented Designs. *Biometrics.* 31: 29-35.

Gana AS, Shaba SZ, Tsado EK (2013). Principal component analysis of morphological traits in thirty-nine accessions of rice (*Oryza sativa* L.) grown in a rainfed lowland ecology of Nigeria. *J. Plant Breed. Crop Sci.* Vol. 5, pp. 120-126.

IBPGR-International Board for Plant Genetic Resources (1985). Descriptors for Finger Millet. IBPGR Secretariat, Rome, pp: 20.

Johnson HW, Robinson GF, Comstock RE (1955). Genotypic and phenotypic correlation in soyabean and their implications in selection. *Agron J.* 47: 477 - 485.

Johnson RA, Wichern DW (1988). Applied Multivariate Statistical Analysis. Prentice-Hall, Englewood Cliffs, NJ.

Kadam DD, Kulkarni SR, Jadhav BS (2009). Genetic variability, correlation and path analysis in finger millet. *J. Maharashtra Agric. Univ.* 34(2): 131-134.

Kebede Y, Menkir A (1986). Improvement of finger millet in Ethiopia, pp. 173-176. In Seetheram A, Rilley KW, Harinaryyana G (eds.). Small Millet in Global Agriculture: Proceeding of the First International Small Millet Workshop. October 29-November 2, 1986. Bangalore, India.

Khavari Khorasani S, Mostafavi KH, Zandipour E, Heidarian A (2011). Multivariate analysis of agronomic traits of new corn hybrids (*Zea maize* L.). *Int. J. Agric. Sci.* 1(6): 314-322.

Levesque R (2007). SPSS. Statistical package for the social sciences, version 16.0. SPSS Programming and data management. A guide for SPSS and SAS users, fourth edition, SPSS inc., Chicago III.

Mohammadi SA, Prasanna BM (2003). Analysis of genetic diversity in crop plants-salient statistical tools and considerations. *Crop Sci.* 43: 1235-1248.

Naik BJ, Shankare Gounda BT, Seetharam A (1994). Pattern of variability in relation to domestication of finger millet in Africa and India. In K.E. Riley: pp.347-363.

Narasamha Rao DV, Parathasarathi AV (1968). Studies on genetic variability of certain phenotypic variations, genetic advance and heritability of certain quantitative characters. *Madras Agri. J.* 55: 392-397.

Negash W, Asfaw Z, Yibra H (2005). Variation and association analysis on morphological characters of Linseed *(Linum usitatissimum* (L.) in Ethiopia. Ethiop. J. Sci., 28: 129-140.

Nirmalakumari A, Salini K, Veerabadhiran P (2010). Morphological Characterization and Evaluation of Little millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz.) Germplasm. *Elect. J. Plant Breed.* 1(2): 148-155.

Panse VG, Sukhatme PV (1964) Statistical methods for agricultural workers, 2nd Ed. ICAR, New Delhi.

Prasado Rao KE, De Wet JMJ, Gopal Reddy V, Mengesha MH (1994). Diversity in the small millets collection at ICRISAT. In K.E. Riley pp.331-345.

Rohlf FJ (1998). NTSYS-pc. Numerical taxonomy and multivariate analysis system, version 2.02. Exeter Software, Setauket, NY.

Salini KA, Nirmalakumari A, Muthiah R, Senthil N (2010). Evaluation of proso millet (*Panicum miliaceum* L.) germplasm collections. *Elect. J. Plant Breed.* 1(4): 489-499.

Upadhyaya HD, Gowda CLL, Pundir RPS, Reddy VG, Singh S (2006). Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Gen. Res. Crop Evo.* 53: 679-685.