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CHARACTERIZATION OF PEARL MILLET GERMPLASM FOR VARIOUS MORPHOLOGICAL AND FODDER YIELD PARAMETERS

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Abstract

This study was performed to evaluate and characterize 27 pearl millet accessions for various morphological and fodder yield parameters. The germplasm displayed considerable variability for days to 50 % flowering, leaf area, flag leaf area, plant height and green fodder yield. The genotypes, however, didn't exhibit any variation for ligule presence, auricle absence and leaf midrib color. Different genotypes displayed potential for selection of the desired traits. Sel.-2(8802) was the earliest accession in terms of 50% flowering while maximum leaf area was recorded for Sel.-1(No.8802) and Sel.-2(No.8802). Sel.-4(No.8781) had the maximum plant height while Sel-3(No.8781) produced the highest green fodder yield. Cluster analysis for quantitative traits depicted five clusters at a dissimilarity level of 4.8. The first cluster consisted of four genotypes while the second cluster contained nine genotypes. Ten genotypes comprised the third cluster while the fourth cluster constituted only four genotypes. The genetic potential of Sel.-2(8802), Sel.-1(No.8802), Sel.-2(No.8802) Sel.-3(No.8781) and Sel.-4(No.8781) can be exploited in future pearl millet breeding programs**.** Further, these genotypes are also recommended as such for commercial cultivation to meet the fodder needs of the country.

Introduction

Pearl millet (*Pennisetum glaucum*) is an indispensable source of fodder in many regions of the world (Bhatangar *et al.,* 1998). It is used for pasture, silage, hay and grazing in several countries like USA, Australia, South America, South Africa, Pakistan and India. Its green fodder is a valuable feed for livestock. It also makes an excellent annual pasture grass without prussic acid, a poisoning potential commonly found in sorghum and sundal grass (Sedivec & Schatz, 1991).

Pearl millet is an important fodder and grain crop of Pakistan. This crop is widely cultivated in Gujrat, Gujranwala, Chakwal, Mianwali, Bahawalnagar, Bahawalpur, Rawalpindi, Attock and Jhelum in Punjab province; Hyderabad, Khairpur, Dadu, Nawabshah and Sanghar in Sindh province; Lorali, Khuzdar and Sibbi in Balochistan; and Bunnu, Karak, D.I.Khan in North West Frontier Province (NWFP) (Chaudhry, 1979).

Livestock industry of Pakistan is expanding day by day. Lack of quality fodder is one of the major constrains to improve livestock production (Ullah *et al*., 2010). To meet its growing demand, high fodder yielding and nutritious varieties of fodder crops are needed. Pearl millet offers an excellent choice for this purpose. It is more tolerant to low soil fertility and drought, and often has higher protein concentrations than sorghum and corn (Pearson, 1985; Asgharipour & Heidari, 2011). Its green fodder is a valuable feed for livestock which warrants its utilization during all months of the year.

Characterization of pearl millet germplasm is imperative for categorization of germplasm and identification of the desirable genotypes for introgression into breeding programs. The present study was, therefore carried out to morphologically characterize pearl millet accessions for yield and quality parameters and to identify promising genotypes for the desired traits for future utilization in pearl millet breeding programs.

Materials and Methods

The present study was performed on 27 accessions of pearl millet at Plant Breeding and Genetics (PBG) Research Farm, NWFP Agricultural University, Peshawar during July-October 2007 and 2008. List of these pearl millet genotypes along with their origin is presented in Table 1. Each accession was planted in a four row plot with row length of 3 m long and row-row distance of 30 cm. Standard crop production technology as needed for pearl millet crop was used in the experiment. Data were recorded on 5 qualitative and 13 quantitative parameters. Qualitative traits taken into consideration were node type, leaf color, midrib color, the presence/absence of auricle and the presence/absence of ligules. Quantitative traits studied were days to 50% flowering, plant height, peduncle length, panicle length, number of tillers plant^{-1}, number of nodes plant^{-1}, internode length, leaf area, number of leaves plant^{-1}, flag leaf area, root lodging, green fodder yield at 50% maturity and green fodder yield at 100% maturity. Both qualitative and quantitative traits data were recorded on five randomly selected plants of each accession. Days to 50% flowering for each accession were recorded from the date of sowing till 50% panicle emergence on plot basis. Number of nodes and tillers per plant were counted for each accession. Number of leaves plant^{-1} was counted when the crop became ready for fodder purpose. Leaf area was determined by the formula previously used by Zaman *et al.,* (2004).

Leaf area = Maximum length (cm) x Maximum breadth (cm) x 0.75 (Correction factor)

Plant height was taken in centimeters from the base of the plant up to the flag leaf at 50% flowering. Internode length was measured using 7th internode as standard in all the accessions while peduncle length was the distance in

centimeters between last node and panicle base on the culm. Panicle was measured in centimeters from the base of panicle to the tip of the panicle. Data of root lodging was taken in percentage on plot basis. When the crop reached 50% maturity, two rows of each accession were harvested and yield was determined as follows:

$$\text{Yield (t ha}^{-1}) = \frac{\text{Green fresh weight row}^{-1}\text{(kg) x No. of harvested rows x 10000 m}^2\text{ x ton}}{3.6\ \text{m}^2\ \text{x ha x 1000kg}}$$

Table 1. List of pearl millet germplasm used in the study.

Pearl millet genotypes	Origin
Sel.-1(No.8778)	Selection from USA material Nigerian population
Acc.No.8802	Exb D_2 Bulk x BMR
Sel.-1(No.8802)	Selection from 3
Sel.-2(No.8802)	Selection from 3
NARC-Pop-1	Nigerian population imported from USA
Sel.-1(NARC-Pop-1)	Selection from USA material Nigerian population
Sel.-3(No.8781)	Selection from USA material Nigerian population
Sel.-4(No.8781)	Selection from USA material Nigerian population
Acc.No.8787	Selection from USA material Nigerian population
Acc.No.8789	Selection from USA material Nigerian population
Sel.-1(No.8789)	Selection from USA material Nigerian population
Acc.No.8794	American variety Tift-86
Sel.-1(No.8795)	Selection from USA material Purdue population
Sel.-2(No.8795)	Selection from USA material Purdue population
Acc.No.8796	Selection from USA material Nigerian population
Sel.-2(No.8796)	Selection from USA material Nigerian population
Acc.No.8798	Selection from USA material Purdue population
Sel.-1(No.8800)	Selection from USA material Nigerian population
Acc.No.8803	Selection from USA material Purdue population
Sel.-1(No.8803)	Selection from USA material Purdue population
Sel.-3(No.8803)	Selection from USA material Purdue population
Sel.-1(No.8805)	Selection from USA material Nigerian population
Sel.-2(No.8805)	Selection from USA material Nigerian population
Acc.No.8807	Selection from USA material Nigerian population
Sel.-1(No.8808)	Selection from USA material Nigerian population
Sel.-1(No.8809)	Selection from USA material Purdue population
Sel.-2(No.8781)	Selection from USA material Nigerian population

At 100% maturity, remaining two rows of each accession were harvested and yield was determined as previously determined at 50 % maturity.

Data analysis: Mean values were determined for all the studied quantitative traits. Pairwise Euclidean distance of genotypes was computed on qualitative, quantitative and both qualitative and quantitative traits taken together, and the resulting matrices were used to synthesize dendrograms by unweighted pair-group method with arithmetic means (UPGMA) cluster analysis using the SAHN (sequential, agglomerative, hierarchical, and nested) option of NTSYS-pc 2.02k version (Rohlf, 1994). Mean values per accession were used and standardized prior to analyses.

Results and Discussion

Qualitative traits: Variation was observed among the studied accessions of pearl millet for node type. Both pubescent and glabrous types of nodes were observed. Ten genotypes displayed pubescent nodes while 6 genotypes showed glabrous nodes. 11 genotypes manifested both types of nodes e.g. their lower nodes were glabrous while upper ones were pubescent. Variation was observed in the leaf colors. Most of the genotypes had light green leaves while some were green and others very dark green. No variation was observed among the genotypes for leaf midrib color and the presence/absence of ligules and auricles. All the genotypes displayed white color leaf midrib. Ligules were present while auricles were absent in all the studied accessions (Table 2).

Quantitative traits

The results of quantitative traits are presented in Table 3. The important results of these traits are as follows:

Days to 50% flowering: Days to 50% heading serve as a useful criterion determining the maturity range of the genotypes. Performance of the genotypes for this trait depicted considerable variation. Means for days to 50% flowering among the germplasm lines ranged from 67 to 77 days. Sel.-2(No.8802), Sel.-1(No.8802), Sel.-3(No.8781), Sel.-1(No.8795) and Sel.-1(No.8778) took minimum days (67) to reach 50 % flowering. On the other hand, Sel.-1(No.8803), Sel.-2(No.8781) and Sel.-1(No.8809) took maximum days (77) to reach 50% flowering, followed by Acc. No.8803 and Sel.-1(No.8800) with 76 days. Sharma *et al.*, (2003) also observed genetic variation among 115 germplasm of pearl millet for days to heading.

Table 2. Qualitative traits expression in the pearl millet genotypes.

Accessions	Node type	Presence/ absence of ligules	Presence/ absence of auricles	Leaf color	Midrib color
Sel.-1(No.8778)	Pub	Present	Absent	Light green	White
Acc.No.8802	Pub	Present	Absent	Green	White
Sel.-1(No.8802)	Pub	Present	Absent	Light green	White
Sel.-2(No.8802)	Pub	Present	Absent	Light green	White
NARC-Pop-1	Glab	Present	Absent	Light green	White
Se.l-1(NARC-Pop-1)	Glab	Present	Absent	Light green	White
Sel.-3(No.8781)	Glab	Present	Absent	Dark green	White
Sel.-4(No.8781)	Pub	Present	Absent	Green	White
Acc.No.8787	Glab	Present	Absent	Light green	White
Acc.No.8789	Pub	Present	Absent	Light green	White
Sel.-1(No.8789)	Pub	Present	Absent	Light green	White
Acc.No.8794	Pub	Present	Absent	Light green	White
Sel.-1(No.8795)	Glab	Present	Absent	Light green	White
Sel.-2(No.8795)	Glab	Present	Absent	Light green	White
Acc.No.8796	Pub	Present	Absent	Light green	White
Sel.-2(No.8796)	Pub	Present	Absent	Dark green	White
Acc.No.8798	Pub/Glab	Present	Absent	Dark green	White
Sel.-1(No.8800)	Pub/Glab	Present	Absent	Light green	White
Acc.No.8803	Pub/Glab	Present	Absent	Light green	White
Sel.-1(No.8803)	Pub/Glab	Present	Absent	Light green	White
Sel.-3(No.8803)	Pub/Glab	Present	Absent	Light green	White
Sel.-1(No.8805)	Pub/Glab	Present	Absent	Light green	White
Sel.-2(No.8805)	Pub/Glab	Present	Absent	Dark green	White
Acc.No.8807	Pub/Glab	Present	Absent	Light green	White
Sel.-1(No.8808)	Pub/Glab	Present	Absent	Light green	White
Sel.-1(No.8809)	Pub/Glab	Present	Absent	Light green	White
Sel.-2(No.8781)	Pub/Glab	Present	Absent	Light green	White

Table 3. Mean values for days to 50% flowering (DF), plant height (PH), tiller plant^{-1}, leaves plant^{-1} (LPP), internode length (IL), leaf area (LA), flag leaf area (FLA), peduncle length (PDL), panicle length (PAL), node plant^{-1} (NPP), root lodging, (RL), green fodder yield at 50% maturity (GFY1) and green fodder yield at 100% (GFY2) maturity of pearl millet genotypes.

Pearl millet genotypes	DF	PH (cm)	TPP	IL (cm)	LPP	LA (cm^2)	FLA (cm^2)	PDL (cm)	PAL (cm)	NPP	RL (%)	GFY1 (t ha^{-1})	GFY2 (t ha^{-1})
Sel.-1(No.8778)	67	207	2	18	12	214	35	32	29	12	0	35	61
Acc.No.8802	70	207	2	18	14	256	108	31	23	14	3	68	56
Sel.-1(No.8802)	67	210	2	17	14	256	109	29	25	14	2	50	44
Sel.-2(No.8802)	66	182	2	17	12	148	76	29	25	12	0	64	83
NARC-Pop-1	71	186	2	22	14	154	79	30	20	14	0	72	61
Se.l-1(NARC-Pop-1)	70	188	3	21	14	183	86	27	20	14	0	91	72
Sel.-3(No.8781)	67	215	2	19	12	241	105	27	28	12	2	130	56
Sel.-4(No.8781)	68	227	1	19	13	237	106	32	31	13	4	102	56
Acc.No.8787	71	170	3	16	14	140	72	24	25	14	5	58	33
Acc.No.8789	73	160	3	16	13	176	79	27	19	13	0	60	44
Sel.-1(No.8789)	75	182	1	19	14	190	86	25	20	14	4	56	50
Acc.No.8794	71	174	1	21	14	139	73	24	18	14	0	46	56
Sel.-1(No.8795)	67	191	2	18	12	200	90	27	25	12	10	57	67
Sel.-2(No.8795)	73	189	3	17	13	163	81	25	23	13	5	70	78
Acc.No.8796	71	190	2	19	13	150	78	21	22	13	0	56	60
Sel.-2(No.8796)	70	221	3	19	14	248	109	26	28	14	3	83	56
Acc.No.8798	69	205	2	21	14	210	96	28	25	14	0	84	67
Sel.-1(No.8800)	76	183	0	17	14	133	73	23	21	14	5	61	50
Acc.No.8803	76	155	2	15	13	110	61	25	17	13	0	66	50
Sel.-1(No.8803)	77	178	2	18	14	136	73	26	22	14	0	71	54
Sel.-3(No.8803)	72	157	1	15	12	128	66	26	19	12	9	71	56
Sel.-1(No.8805)	74	156	1	21	13	145	70	22	19	13	0	46	56
Sel.-2(No.8805)	74	203	2	14	14	214	97	28	25	14	20	51	50
Acc.No.8807	75	149	1	12	12	109	59	23	15	12	0	88	100
Sel.-1(No.8808)	75	143	1	16	11	108	58	20	16	11	5	62	56
Sel.-1(No.8809)	77	207	3	23	14	200	94	32	22	14	5	89	65
Sel.-2(No.8781)	77	191	1	22	15	215	94	29	22	15	10	98	64
Mean	72	186	1.8	18	13	178	82	26	22	13	3.4	70	59
Variance	12.3	518	0.6	7	1	2226	331	11	16	1	22	425	174

Number of nodes, leaves, tillers plant^{-1}: The means for number of nodes plant^{-1} varied between 11 and 15. Sel.-2(No.8781) displayed maximum number of nodes plant^{-1} (15) while Sel.-1(No.8808) had minimum number of nodes plant^{-1} (11). Khairwal *et al*., (2007) reported a range of 6 to 14 number of nodes plant^{-1} while evaluating 180 landraces of pearl millet.

Increase in that number of leaves is important for enhancing fodder yield and quality and ultimately increases production of pearl millet crop. Mitra *et al*., (2001) observed highest response to selection in number of leaves plant^{-1} when they observed genetic components of variance in a pearl millet population in respect for fodder yield. Variation was observed among the accessions for number of leaves plant^{-1}. Number of leaves per plant varied from 11 to 15. Sel.-2(No.8781) produced maximum number of leaves plant^{-1} (15) while minimum number of leaves plant^{-1} (11) was observed in Sel.-1(No.8808). Genetic variation for number of leaves was previously reported by Khan *et al*., (2004).

Increased tillers plant^{-1} can effectively increase the green fodder yield in millet. Number of tillers plant^{-1} among the available germplasm varied between 0 and 3. Sel.-1(NARC-Pop-1), Acc.No.8789, Sel.-2(No.8795), Sel.-2(No.8796) and Sel.-1(No.8809) had maximum numbers of tillers plant^{-1} while Sel.-1(8800) was the sole genotype with no tiller at all. These observations are also supported by Sharma *et al*., (2003) who evaluated 115 accessions of pearl millet germplasm for green fodder yield and observed considerable variation for this trait.

Leaf area and Flag leaf area (cm^2): Increased leaf area can play a crucial role in increasing fodder yield. Variation was more prominent for leaf area among the studied accessions. Sel.-1(No.8802) and Sel.-2(No.8802) produced maximum leaf area of 256.5 cm^2 while Sel-1(No.8808) produced the least leaf area of 108 cm^2. The results of our study are compatible with the findings of Chohan *et al*., (2006) who also observed considerable variation among pearl millet germplasm for this trait.

Flag leaf area among the accessions ranged from 109 cm^2 to 35 cm^2. Sel.-1(No.8802) and Sel.-2(No.8796) produced the maximum flag leaf area of 109 cm^2. On the other hand, Sel.-1(No.8778) had the minimum flag leaf area of 35 cm^2.

Plant height, internode, peduncle and panicle length (cm): Maximum plant height can effectively increase the green fodder yield. Considerable variation was observed among the studied germplasm lines for plant height. Plant height among the genotypes ranged between 143 cm and 227 cm. Sel.-4(No.8781) was the tallest accession (227 cm), closely followed by Sel.-2(No.8796) with plant height of 221 cm and Sel.-3(No8781) with 215 cm. Acc. No.8807 attained minimum plant height with a value of 143 cm. Sel.-4(No.8781) on account of maximum plant height offers as an excellent choice for utilization in pearl millet breeding programs. Naeem *et al*., (2002) had also reported significant differences for this plant height while evaluating nine varieties of pearl millet.

Internode length among the accessions of pearl millet varied between 12 and 23 cm. Sel.-1(No.8809) showed maximum internode length (23 cm) while Acc.No.8807 displayed minimum internode length (12 cm). Range of peduncle length among the accessions varied between 20 and 32 cm. Maximum peduncle length (32 cm) was recorded for the Sel.-1(No.8778), Sel.-4(No.8781) and Sel.-1(No.8809) while Sel.-1(No.8808) produced minimum peduncle length (20 cm).

Considerable variation among the pearl millet accessions was observed in panicle length. The values for this trait among the genotypes ranged between 15 and 31 cm. Sel.-4(No.8781) displayed maximum panicle length (31 cm) and was closely followed by Sel.-1(No.8778), Sel.-3(No.8781) and Sel.-2(No.8796) with values of 29, 28 and 28 cm, respectively. Acc. No.8807, however, produced smallest panicle of 15 cm. Kumar and Rao (1987) had also reported variation in panicle length of Oasis and Zongo forms of millet.

Root lodging (%age): Root lodging was not a serious problem in the most of the studied accessions of pearl millet, probably due to the deep root penetration of these genotypes. However, Sel.-2(No.8805) had 20% root lodging while both Sel.-1(No.8795) and Sel.-2(No.8781) showed 10% lodging.

Green fodder yield (t ha^{-1}): Considerable variation among the pearl millet accessions was depicted for green fodder yield at 50 and 100% maturity levels. Green fodder yield among the pearl millet accessions at 50 maturity level varied from 35 to 130 t ha^{-1}. Sel.-3(No.8781) was the outstanding genotype for this trait and displayed maximum green fodder yield of 130 t ha^{-1}, followed by Sel.-4(No.8781) and Sel.-2(No.8781) with 102 t ha^{-1} and 98 t ha^{-1}, respectively. Sel.-1(No.8778) manifested minimum green fodder yield of 35 t ha^{-1}. Green fodder yield at 100% maturity ranged from 33 to 100 t ha^{-1}. Acc.No.8787 had maximum fodder yield at 100 % maturity 100 t ha^{-1} followed by Sel.-2(No.8802) with 83 t ha^{-1}. Zaman *et al*., (2004) reported a range of 12.3 to 56.5 t ha^{-1} while evaluating 9 varieties of pearl millet. Muhammad *et al*., (2002) and Naeem *et al*., (2003) also observed significant differences among the pearl millet genotypes for green fodder yield. High fodder yield is closely associated with high values for plant height, number of leaves, number of tillers plant^{-1} and leaf area. Reddy *et al*., (1996) also observed positive association of green fodder yield with these parameters.

Cluster analysis: The qualitative traits dendrogram showed that 4 clusters were formed at dissimilarity coefficient of 1.1. The first cluster contained nine genotypes viz. Sel.-1 (No.8778), Sel.-1 (No.8802), Sel.-2 (No.8802), Acc. No. 8789, Sel.-1 (No.8789), Acc. No. 8794, Acc. No. 8796, Acc. No. 8802 and Sel.-4 (No.8781). The second cluster comprised fourteen genotypes which included NARC-Pop-1, Sel.-1 (NARC-Pop-1), Sel.-1 (No.8795), Sel.-2 (No.8795), Acc. No. 8787, Sel.-1 (No.8800), Sel.-2 (No.8781), Acc.No.8807, Sel.-1(No.8805), Sel.-1 (No.8803), Sel.-1 (No.8808), Sel.-1 (No.8809), Sel.-3 (No.8803) and Acc. No. 8803. The third cluster had only three genotypes viz. Sel.-3 (No.8781), Acc. No. 8798 and Sel.-2 (No.8805) genotypes whereas fourth cluster constituted only Sel.-2 (No.8796) (Fig. 1).

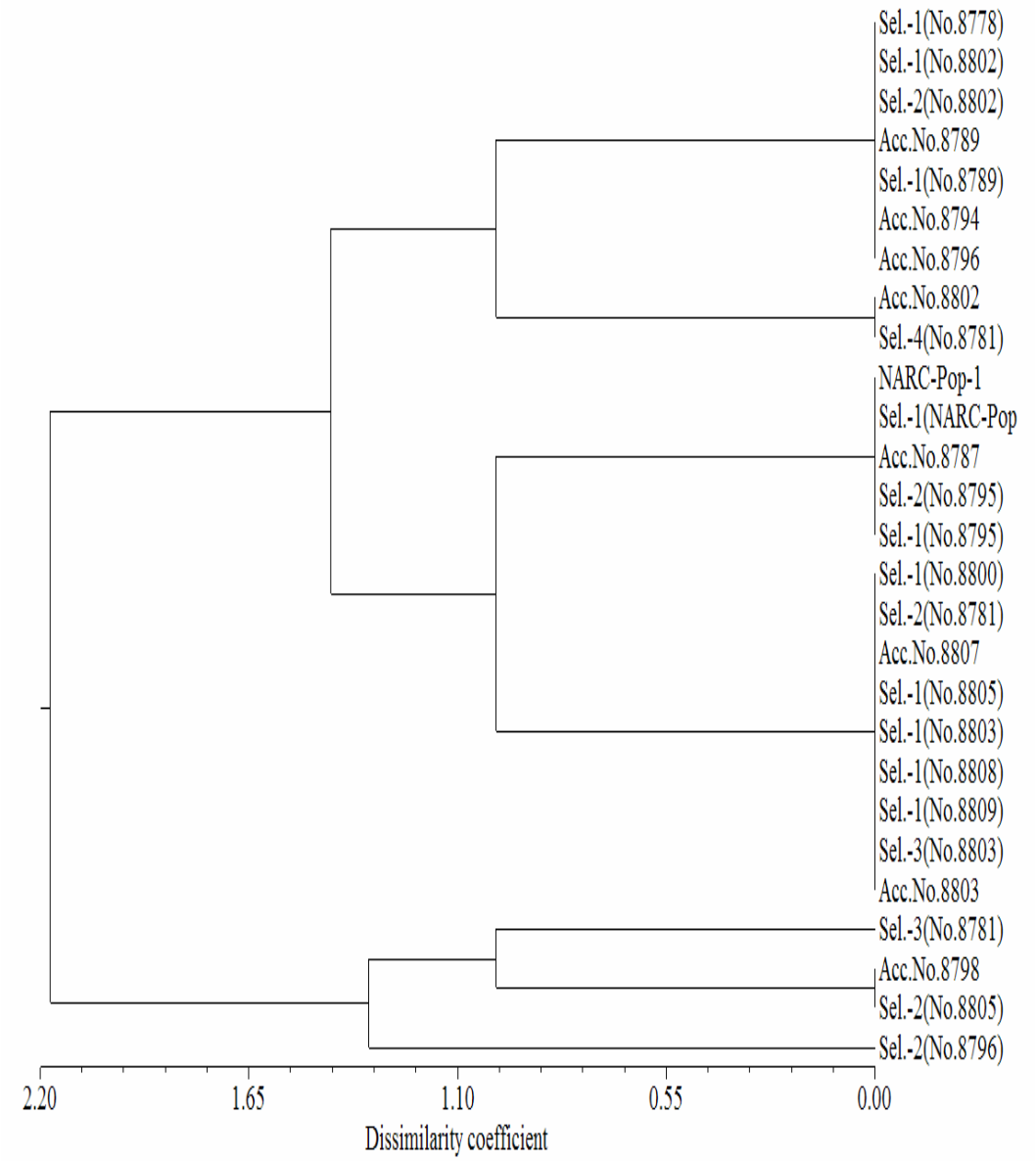

Fig. 1. Dendrogram of pearl millet germplasm based on dissimilarity matrix of Euclidean distances for qualitative traits.

On the basis of quantitative traits, 5 clusters can be identified at a dissimilarity level of 4.8. The first cluster comprised 4 genotypes viz. Sel.-1(No.8778), Sel.-2(No.8802), Sel.-1(No.8795) and Sel.-2(No.8795). The second cluster had 9 genotypes viz. Acc.No.8787, Acc.No.8789, Acc.No.8803, Sel.-1(No.8789), Sel.-1(No.8800), Sel.-1(No.8803), Acc.No.8794, Sel.-1(No.8805) and Acc.No.8796. Ten genotypes viz. Acc.No.8802, Sel.-1(No.8802), Sel.-2(No.8796), NARC-pop-1, Sel.-1(NARC-pop-1), Acc.No.8798, Sel.-1(No.8809), Sel.-2(No.8781), Sel.-3(No.8781) and Sel.-4(No.8781) constituted the third cluster. The fourth cluster had only 4 genotypes viz. Sel.-2(No.8805), Sel.-3(No.8803), Sel.-1(No.8808) and Acc.No.8807 (Fig. 2).

The dendrogram for combined qualitative and quantitative traits showed 5 clusters at dissimilarity level of 5.26. The first cluster comprised 2 genotypes viz. Sel.-1(No.878) and Sel.-2(No.8802). The second cluster consisted of 6 genotypes viz Acc.No.8802, Sel.-1(No.8802), Sel.-2(No.8796), Acc.No.8798, Sel.-4(No.8781) and Sel.-3(No.8781). The third cluster composed had NARC-Pop-1, Sel.-1(NARC-Pop-1), Sel.-1(No.8809), Sel.-2(No.8781), Sel.-1(No.8795), Sel.-2(No.8795), Acc.No.8787, Acc.No.8789, Acc.No.8803, Sel.-1(No.8803), Sel.-1(No.8789), Acc.No.8794, Sel.-1(No.8805), Acc.No.8796 and Sel.-1(No.8800). The fourth cluster comprised only Sel.-2(No.88050 while the fifth cluster comprised Sel.-3(No.8803), Sel.-1(No.8808) and Acc.No.8807 (Fig. 3)

The results of the present study revealed that sufficient genetic diversity existed among the studied accessions of pearl millet. Reddy *et al*., (1996) had also reported genetic diversity in the peal millet germplasm on the basis of cluster analysis.

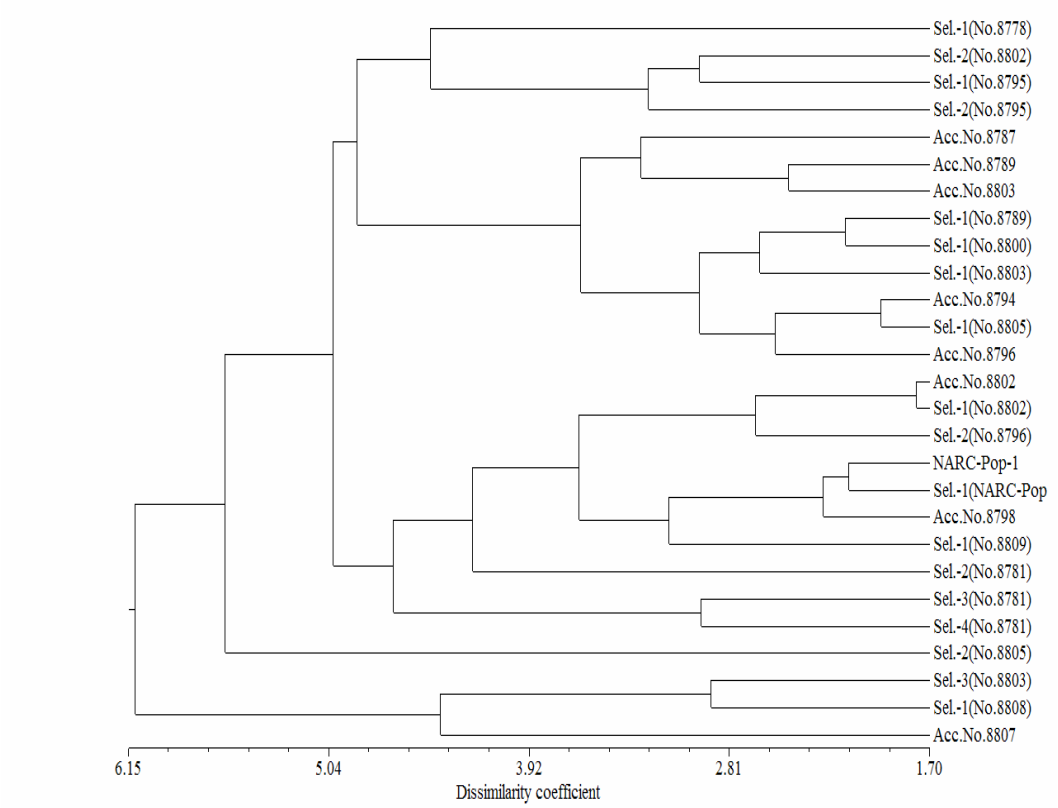

Fig. 2. Dendrogram of pearl millet germplasm based on dissimilarity matrix of Euclidean distances for quantitative traits.

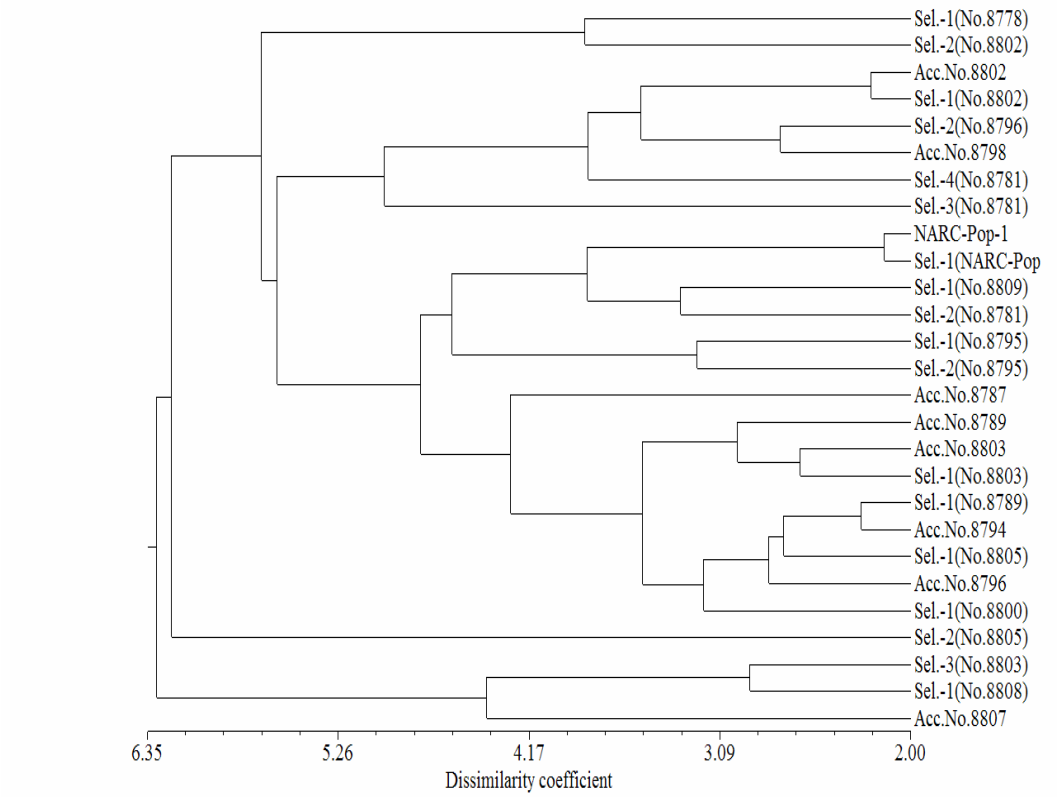

Fig. 3. Dendrogram of pearl millet germplasm based on dissimilarity matrix of Euclidean distances for both qualitative and quantitative traits.

Conclusion

The present study revealed sufficient genetic diversity in the available pearl millet germplasm for different traits. Different genotypes of pearl millet displayed potential for selection of the desired traits. Based on maturity traits, Sel.-2(No.8802), Sel.-1(No.8802), Sel.-3(No.8781) and Sel.-1(No.8795) were early maturing genotypes. Sel.-4(No.8781), Sel.-2(No.8796), Sel.-3(No.8781) and Sel.-1(No.8802) were the tallest genotypes among the studied accessions. On the basis of leaf area, Acc.No.8802, Sel.-1(No.8802), Sel.-2(No.8796) and Sel.-3(No.8781) performed well for this trait. Based on green fodder yield, it could be concluded that the Sel.-3(No.8781), Sel.-4(No.8781), Sel.-2(No.8781) and Sel.-1(NARC-Pop-1) were high yielding genotypes. The above mentioned genotypes can be recommended as such for commercial cultivation after multi-location trials and their genetic potential can also be exploited in pearl millet breeding programs.

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