



Evaluation of Selected Forage Pearl Millet Germplasm for Yield and Yield Component Traits

**Tamer G. El-Gaafarey ^{a*}, Safwat Hussein Hatab ^a
and S. A. Arab ^b**

^a Forage Crops Research Department, Field Crops Research Institute, Agricultural Research Center, Egypt.

^b National Gene Bank, ARC, Giza, Egypt.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/AJAAR/2023/v21i4425

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/97726>

Original Research Article

Received: 25/01/2023

Accepted: 29/03/2023

Published: 12/04/2023

ABSTRACT

The present study aimed to evaluate the productivity of pearl millet (*Pennisetum glaucum L.*) genotypes to select the promising genotypes for fresh and dry forage yields and its traits of thirteen selected genotypes of pearl millet from forty eight genotypes. The experiments grown in a randomized complete blocks design with three replications at Sids Agricultural Research Stations, in 2021 and 2022 summer seasons.

Studied traits showed highly significant different of mean squares for genotypes. Analysis of variance for 13 Pearl millet genotypes revealed highly significant variation for total fresh and dry forage yield whereas the highest one was millet6 followed by population Shandawal 1 and population millet Sids 3 which had 85.5, 80.8 and 74.9 kg/plot, respectively. While, the lowest one were millet10 followed by millet12 and millet11 which had 44.9,45.0 and 46.5 kg/plot, respectively. Also, the highest mean values for total dry yield were millet 6 followed by population shandawal

*Corresponding author: Email: tamerelgafarey@gmail.com;

1and population millet Sids 3 which had 12.2,11.1 and 9.6 kg/plot, respectively. Variance components of total fresh forage yield for combined showed that grand mean 58.6, (δ^2p 385.9) and(δ^2g 383.1) and genetic advance 40.3. Also, total dry yield had 7.37,11.25,11.16 and 6.88 for grand mean, δ^2p , δ^2g and genetic advance, respectively. The most discriminating environment for millet genotype which is due to the differences between δ^2g and δ^2p . Also, the effects of the difference between genotypes were high. Heritability values were high for total fresh and dry yield which had 99.64 and 99.59, respectively. Heritability estimates increased when the differences between (G.C.V. %) and P.C.V. % values were the least values. The results cleared that were variations between all studied genotypes had possibility used these genotypes to improve the studied traits during breeding program. The results indicated that millet 6, population Shandawal 1 and population Sids 3 had the best genotypes and could be used in breeding program for fresh and dry yield, plant height, fresh and dry leaf stem percent.

Keywords: Pearl millet; genotypes; forage yield; *Pennisetum*; different geographic origin.

1. INTRODUCTION

Pear millet (*Pennisetum americanum* L.) was originated in Africa and it's commonly grown in the arid and semi-arid regions .It is particularly adapted to nutrient poor soil and low rainfall conditions, yet it is capable of rapid and vigorous growth under favorable conditions [1]. In Egypt, pearl millet is not the staple food of rural populations as in the other countries of Africa, but using as summer fodder crop. South Sinai, as arid region with low rainfall and high evapo-transpiration (ET), brackish or saline ground water is the main source of water for both domestic and agriculture use [2] and [3].

Studying variability is very important for breeders to select the genotypes that possess the high level of variability and high performances for yield and its component traits. Also, the choice of high genetic stable parents in the beginning of the breeding program is very important step for the success of such program. So understanding the nature of genotypes is very important to breeders to test and select the more efficient genotypes. Breeding genotypes with wide adaptability has long been a universal goal among plant breeders. Genotypes have a significant impact in multi-environmental trials. Selection of genotypes for high and low yielding environment could severely be limited in the presence of genotype environment interaction. Therefore, it is necessary to assess the environmental sensitivity of genotypes in terms of higher yields.

The environments where crops grow include several elements in each season. Weather conditions and the other factors are important to determine yield potential of a genotype. The yielding ability of most cultivars varied according

to environmental conditions. Plant breeders noticed that different genotypes do not react in similar way to the changes of environment; therefore, they have the interest to examine their genotypes for stability under several different [4]. Plant breeders refer to produce varieties or hybrids of as near universal adaptation as possible. The information on adaptability and performance of genotypes across years and locations is very important for national policy in crop production. characterize among breeding materials in various stages of germplasm development, have been primarily of two types, the measurement of response of to environmental changes of that response. To be useful in a breeding program these measures (yield response and stability) must be heritable, repeatable and provide information useful to the breeder over and above yield *per se* [5].

Several methods have been proposed to describe and interpret the response of genotypes to environmental variation. Some of them are based on the analysis of variance and others use regression analysis. Developed and modified this method [6]. Developed the analysis of variance approach to estimate genotype x environment interaction. Pearl millet is one of the most important staple cereals for subsistence farmers living in semiarid tropics of Africa [7 and 8]. In contrast, millet is the major source of energy and protein for millions of people in Africa. It has been reported that millet has many nutritious and medical functions [9].

Landraces are traditional crop varieties developed by farmers through years of natural and human selection and are adapted to the local conditions. As distinct plant populations, landraces are named and maintained by traditional farmers to meet their social, economic,

cultural, and ecological needs [10]. A successful breeding program for yield improvement using phenotypic selection is mainly dependent on the nature and magnitude of variation in the available material and role played by the environment in the expression of plant characters.

Principal component analysis is one of the most important analysis for reducing the multiple dimensions of the observed variables to a smaller intrinsic dimensionality of independent variables [11].

This study aimed to determine the productivity of thirteen pearl millet genotypes, genetic parameters and study the variation performance parameters of yield and its components to could be used for the crop improvement.

2. MATERIALS AND METHODS

Forty eight landraces of pearl millet of different geographic origin were collected and planting from 2013 to 2017 and select the best depend on high yield. Thirteen landraces were selected of pearl millet and evaluated in this study (Table 1). This study was carried out at the experimental field at Sids Agricultural Research Station, BaniSweif Governorate during the two summer seasons 2021 and 2022. Soil analysis of the experimental field in the two seasons (Table 2). The field trial was arranged in a randomized complete block design with three replications. The plot area was 3.6m^2 (2 row*0.6 *3 m) and the seeds were sown at the rate of 20 kg/ha (20 cm between hills). Planting dates in the first and second seasons were 20/5/2021 and 27/5/2022, respectively. Three cuts were performed during the first growing season 2021 (20/7/2021, 23/8/2021 and 5/10/2021) as well as three cuts during 2022 season (27/7/2022, 24/8/2022 and 25/9/2022).

Nitrogen fertilizer in the form of urea 46.5 %N was applied in three equal doses of 20 unit of nitrogen for each cut. Normal cultural practices for millet growing were done in each seasons, and studies traits were as follow:

- 1- Plant height (cm.). (PH)
- 2- Stem diameter (cm.). (SD)
- 3- Fresh forage yield (kg/ plot) for every cut and total yield, (FY) and (TFY).
- 4- Dry forage yield (kg/ plot) for every cut and total yield, (DY) and (TDY).
- 5- Fresh and dry leaf stem%. (F.L/SP) and (D.L/S.P)

Statistical analysis was subjected to proper statistical analysis of Randomized complete block design with three replications. Means were compared at 0.05 level of significance by least significant different (L.S.D) test using [12]. The combined analysis for the experiment was done when the homogeneity test was not significant, computed by [13]. Genetic parameters were estimated according the formula given by [14,15].

3. RESULTS AND DISCUSSION

Analysis of variance of millet genotypes for fresh and dry forage yield and its traits are presented in Table 3. Results revealed highly significant differences of genotypes for fresh and dry forage yields in the three cuts and total yields. Highly significant differences were detect among years, for both fresh and dry forage yields in the three cuts and their total similar results obtained [16-18]. The results in Table 3 showed that plant height, stem diameter, fresh and dry leaf stem percent for thirteen genotypes were highly significant different. The interactions between genotypes and years were in significant different over two years for all traits, except the third cut of plant height [19-26]. Years with genotypes interaction were insignificant effect of fresh yield but significant at the first cut and highly significant for third cut and total dry yield. Years had effects on yields it's may be due to unpredictable environments variability were more effective. Also, the yield of these genotypes was different between them, and all genotypes don't similarly respond [1,27,28]. But several researchers showed that genotype x years were more important for sorghum yield [29 - 33].

Selection should be based on both genotypes and genotypes x environment interaction rather than on one of them, also, the benefit selection depend on combined data. The effect of years on forage yield and its components is due to the long period of the first season 138 days and 121days for the second season.

Mean performance for fresh and dry forage yields, plant height (cm), stem diameter (cm), green and dry leaf/stem percent on three cuts over two seasons were calculated and presented in Table 4. Total fresh yield ranged from 44.9 kg/plot (Millet 10) to 85.5 kg/plot (millet 6) within average yield 65.2 kg/plot. Yield of genotype millet 6 gave the highest green yield and significant exceed the lowest genotype by 68.86%. Total dry yield ranged from 5.1 kg/plot

Table 1. List name collection site of pearl millet and their origin

No.	Name	Origin	No.	Name	Origin
1	Millet 1	Introduction from Burkina Faso-Africa	8	Millet 13	SOHAG
2	Shandawal 1	population Shandawal 1	9	Millet 15	SOHAG
3	Millet 6	SOHAG	10	Millet 16	SOHAG
4	Millet 9	SOHAG	11	population Millet Sids 1	Selection from breeding program
5	Millet 10	SOHAG	12	population Millet Sids 2	Selection from breeding program
6	Millet 11	SOHAG	13	population Millet Sids 3	Selection from breeding program
7	Millet 12	SOHAG	-	-	-

Table 2. Mechanical and chemical soil analysis of the experimental field in the two seasons

2021						
A-Mechanical analysis						
Sand%	Silt %	Clay %	Texture			
18.25	33.8	47.95	Clay			
B-Chemical analysis						
pH	EC(ds/m)	OM%	Total N%	Available (N) ppm	Available (p) ppm	Available (K) ppm
8.1	0.56	2.04	0.13	28	17.3	435
2022						
A-Mechanical analysis						
Sand%	Silt %	Clay %	Texture			
16.4	32.38	51.2	Clay			
B-Chemical analysis						
pH	EC(ds/m)	OM%	Total N%	Available (N) ppm	Available (p) ppm	Available (K) ppm
7.9	0.60	2.20	0.14	30	19.1	446

Table 3. Combined analysis of variance of the yield and yield components of thirteen genotypes of pear millet over two years

S.O.V	df	Fresh yield kg / plot			Tfy	Dry yield kg /plot			TDy
		cut1	cut2	cut3		cut1	cut2	cut3	
year	1	183.08**	140.54**	76.81**	1166.2**	9.22**	7.86**	5.82**	68.11**
Error	4	1.02	0.092	0.53	0.802	0.011	0.015	0.003	0.015
Genotypes	12	136.33**	66.79**	204.99**	1154.82**	3.5**	2.34**	6.027**	33.67**
Y.*G.	12	0.56Ns	0.256Ns	0.83Ns	4.622Ns	0.058*	0.04Ns	0.098**	0.54**
Error	48	1.88	0.68	0.64	2.778	0.029	0.023	0.027	0.092
Total	77								
		Plant height cm			Stem diameter cm				
S.O.V	df	cut1	cut2	cut3	cut1	cut2	cut3		
year	1	6770.422**	8343.1**	8896**	0.446**	0.374**	0.29**		
Error	4	2.916	4.922	3.089	0.001	0.003	0.002		
Genotypes	12	2577.703**	2415.6**	2237.5**	0.143**	0.119**	0.132**		
Y.*G.	12	11.371 Ns	9.816 Ns	9.131 **	0.002Ns	0.002Ns	0.001Ns		
Error	48	3.509	6.113	7.152	0.005	0.006	0.006		
Total	77								
		fresh leaf/ stem percent			dry leaf/ stem percent				
S.O.V	df	cut1	cut2	cut3	cut1	cut2	cut3		
year	1	413.08**	480.52**	531.97**	618.9**	694.2**	741.1**		
Error	4	4.289	0.709	0.099	0.703	1.464	0.046		
Genotypes	12	41.97**	18.36**	23.709**	103.1**	83.77**	51.36**		
Y.*G.	12	0.177 Ns	0.087Ns	0.098Ns	0.421Ns	0.342Ns	0.209Ns		
Error	48	1.86	1.425	1.564	0.612	0.457	0.516		
Total	77								

Table 4. Mean performance of the fresh and dry yields and its components at three cuts and total yields of thirteen genotypes of pearl millet over two seasons

Genotypes	FyC1	FyC2	FyC3	TFY	DYC1	DYC2	DYC3	TDY	PHC1	PHC2	PHC3
Millet 1	24.0	21.8	15.7	61.4	2.6	2.5	2.0	7.1	168.3	163.6	145.1
Population Shandawal 1	31.7	24.9	24.1	80.8	4.0	3.4	3.7	11.1	195.5	191.8	170.8
Millet 6	32	27.9	25.7	85.5	4.3	3.9	4.0	12.2	199.9	196.5	178.3
Millet 9	27.6	23.2	20.4	71.1	3.1	2.9	2.9	8.9	181.7	178	163.6
Millet 10	18.6	17.4	8.9	44.9	2.1	2.1	1.2	5.4	144.8	138.8	122.2
Millet 11	19.1	17.7	9.7	46.5	2.0	1.9	1.2	5.1	147.0	140.7	123.5
Millet 12	18.8	16.9	9.3	45.0	2.3	1.8	1.2	5.3	146.3	139.4	122.2
Millet 13	23.1	21.2	14.7	59.0	2.4	2.3	1.9	6.6	162.9	159.2	141.9
Millet 15	20.5	17.8	10.7	48.9	2.1	1.9	1.3	5.3	151.7	145.4	128.2
Millet 16	20.7	19.1	11.3	51.1	2.1	2.1	1.3	5.5	155.1	150.1	132.5
Population Millet sids 1	22.3	20.2	12.7	55.2	2.4	2.2	1.6	6.1	158.9	153.9	135.7
Population Millet sids 2	24.6	22.6	17.7	64.9	2.4	2.7	2.4	7.5	172.0	168.4	151.4
Population Millet sids 3	29.4	23.9	21.6	74.9	3.5	3	3.2	9.6	190.5	183.6	176.0
Grand Mean	24.02	21.44	17.25	58.55	2.71	2.51	2.15	7.37	167.27	162.25	145.48
F.Test	**	**	**	**	**	**	**	**	**	**	**
L.S.D(0.05)	1.59	0.96	0.93	1.94	1.198	0.176	0.19	0.35	3.104	2.87	2.17
Range	19.1 -32.0	19.1-27.9	8.9 -25.7	44.9 - 85.5	2.1 - 4.3	1.8 - 3.9	1.2- 4.0	5.1 -12.2	144.8 - 199.9	138.8 -196.5	122.2 -178.3
Genotypes	SD C1	SD C2	SD C3	F.L/s.p C1	F.L/s.p C2	F.L/s.p C3	D.L/s.p C1	D.L/s.p C2	D.L/s.p C3		
Millet 1	1.20	1.20	1.10	36.3	38.2	40.3	43.2	45.7	47.3		
Population Shandawal	1.30	1.30	1.20	32.9	37.6	38.2	38.5	42.0	44.5		
Millet 6	1.40	1.30	1.30	31.0	36.7	39.5	37.6	41.4	43.9		
Millet 9	1.30	1.20	1.80	33.5	37.0	39.2	41.2	43.4	46.3		
Millet 10	1.00	0.90	0.80	40.1	42.3	44.2	50.1	52.3	53.0		
Millet 11	1.00	0.90	0.90	38.2	40.4	42.9	47.9	50.6	51.4		
Millet 12	1.00	0.90	0.80	38.5	41.4	43.9	49.5	51.1	52.3		
Millet 13	1.20	1.10	1.00	36.8	38.7	41.2	44.2	46.9	48.8		
Millet 15	1.10	1.00	0.90	38.1	40.3	42.3	47.4	49.9	50.3		

Genotypes	FyC1	FyC2	FyC3	TFY	DYC1	DYC2	DYC3	TDY	PHC1	PHC2	PHC3
Millet 16	1.10	1.10	1.00	37.5	39.8	41.8	46.8	49.3	49.2		
Population	1.10	1.10	1.00	37.1	39.6	41.5	45.6	47.6	48.8		
Millet sids 1											
Population	1.20	1.20	1.10	34.5	37.1	39.3	41.8	44.7	46.8		
Millet sids 2											
Population	1.30	1.20	1.20	33.8	39.2	38.6	39.8	42.6	45.2		
Millet sids 3											
Grand Mean	1.16	1.09	1.01	36.22	39.09	40.99	44.60	46.74	48.29		
F.Test	**	**	**	**	**	**	**	**	**	**	**
L.S.D(0.05)	0.082	0.100	0.090	1.58	1.386	1.45	0.908	0.785	0.834		
Range	1.0 -1.4	0.90 -1.3	0.80 -1.3	31.0 -40.1	36.7-42.3	38.2 -44.2	37.6 -50.1	41.4 -52.3	43.9 -53.0		

Where:C: Cut; PH: Plant height; FY: Fresh yield; SD: Stem diameter; TFY: Total fresh yield; F.L/SP: Fresh leaf stem percent; DY: Dry yield; D.L/S.P: Dry leaf stem percent and TDY: Total dry yield.

Table 5. Phenotypic ($\delta^2 p$) genotypic ($\delta^2 g$), variance, phenotypic (P.C.V.%) and genotypic (G.C.V.%) coefficient of variability heritability (h^2) and genetic advance as unit(GA unit)and as percentage (GA %) for all studied traits over two seasons

Traits	FyC1	FyC2	FyC3	TFY	DYC1	DYC2	DYC3	TDY	PHC1	PHC2	PHC3
Phenotypic $\delta^2 p$	46.07	22.49	68.54	385.87	1.18	0.79	2.02	11.25	748.22	807.24	863.02
genotypic $\delta^2 g$	44.19	21.81	67.90	383.09	1.15	0.76	1.99	11.16	741.07	801.12	851.65
P.C.V.%	28.26	22.12	48.01	33.55	40.05	35.36	66.13	45.54	16.35	17.51	20.19
G.C.V.%	27.68	21.79	47.78	33.43	39.55	34.84	65.69	45.36	16.27	17.45	20.06
Heritability % h^2	97.94	98.48	99.53	99.64	98.76	98.53	99.33	99.59	99.52	99.62	99.34
Ga unit	13.69	9.62	16.98	40.32	2.21	1.80	2.91	6.88	56.08	58.31	60.12
Ga %	57.02	44.88	98.44	68.86	81.48	71.77	135.32	93.43	33.53	35.94	41.32
Traits	SDC1	SDC2	SDC3	F.L/s.p C1	F.L/s.p C2	F.L/s.p C3	D.L/s.p C1	D.L/s.p C2	D.L/s.p C3		
Phenotypic $\delta^2 p$	0.05	0.04	0.05	14.61	6.60	8.42	34.57	28.08	17.29		
genotypic $\delta^2 g$	0.04	0.04	0.04	12.75	5.17	6.86	33.96	27.62	16.78		
P.C.V.%	19.16	18.73	21.28	10.55	6.57	7.08	13.18	11.34	8.61		
G.C.V.%	17.97	17.33	19.84	9.86	5.82	6.39	13.07	11.24	8.48		
Heritability % h^2	93.77	92.52	93.25	93.42	88.54	90.24	99.11	99.18	98.50		
Ga unit	0.43	0.39	0.41	7.36	4.68	5.40	12.00	10.83	8.44		
Ga %	37.01	35.69	40.87	20.31	11.98	13.16	26.92	23.16	17.47		

Where:C: Cut; PH: Plant height; FY: Fresh yield; SD: Stem diameter; TFY: Total fresh yield; F.L/SP: Fresh leaf stem percent; DY: Dry yield; D.L/S.P: Dry leaf stem percent and TDY: Total dry yield; PCV :Phenotypic coefficients of variation ; GCV: Genotypic coefficients of variation

(genotype millet 11) to 12.2 kg/plot (millet6) within average yield 8.65 kg/plot. Yield of millet 6 gave the highest dry yield and significant exceeded by 52.5% than millet 10 for total fresh forage yield. The results indicated that the selected genotype Millet 6 produced the highest mean values for total fresh yield 85.5 kg/plot and total dry yield 12.2kg/plot, followed by population Shandawal 1, whereas had 80.8 and 11.1 kg/plot for total fresh and total dry yield over the two seasons respectively. While, the lowest one were millet 10,11 and 12 whears, had (44.9,45.0, 46.5 kg/plot)for fresh yield and millet 11,12 and 10 for total dry forage yield, whereas had (5.4,5.1and 5.3 kg/plot)for dry yield, respectively, The lowest fresh and dry yield may be due to had the lowest plant height and stem diameter [20, 26,34].

Plant height cm ranged from 144.8 cm (millet10) to 199.9 cm (millet6), 138.8(millet 10) to 196.5 cm (millet 6) and 122.2 cm (millet 10) to 178.3 cm (millet 6) for the three cuts, respectively. The millet 6 had the highest plant height and significant exceeded by 72.43%, 69.43% and 61.13 % from millet 10 for first, second and third cut, respectively than the lowest one [35 - 38].

Millet 6 and Shandawal 1 had highest mean values for plant height which had (199.9,196.5 and 178.3 cm) and (195.5,191.8 and 170.8 cm)for first, second and third cut, respectively. Meanwhile, the lowest one was millet 10 which had (144.8, 138.8 and 122.2cm),followed by millet 12 which had (146.3,139.4 and 122.2cm), for first, second and third cut, respectively.

Stem diameter ranged from 1.0 cm (millet 10,11and 12) to 1.4 cm. (millet 6) for first cut, 0.9 cm (millet 10,11and 12)to 1.3 (millet6)for second cut and 0.8cm (millet 10 and 12) to 1.3 (millet6) for third cut. The millet 6 gave the highest stem diameter and significant exceed than millet 10 by 28.58%, 30.77% and 38.46 % for first, second and third cut, respectively for the lowest one. The same trend for stem diameter where as,millet6 had highest mean values which had 1.40,1.30 and 1.30 cm followed by Shandawal 1 which had 1.30,1.30 and 1.20cm for first, second and third cut, respectively. Also, the lowest mean values were millt10, millet11 and millet 12 with insignificant between them over two seasons.

Fresh leaf/stem percent ranged from 31.0% to 40.1%, 36.7% to 42.3% and 38.2% to 44.2% for first, second and third cut, respectively. The highest mean values was millet 10 which had

40.1,42.3 and 44.2 for first, second and third cut, respectively, but the lowest one was millet 6 which had 31.0,36.7 for first and second cuts, respectively. While, Shandawal 1 had the lowest mean value 38.2 for the third cut. The genotype millet 10 gave the highest fresh leaf/stem percent and significant exceeded than millet 6 by 22.70 %, 13.24 % and 10.84 % for first, second and third cut, respectively for the lowest one.

Meanwhile dry leaf/stem percent ranged from 37.6% to 50.1 %, 41.4% to 52.3% and 43.9% to 53.0% for first, second and third cut, respectively. The genotype millet 10 gave the highest dry leaf/stem percent and significant exceeded than millet 6 by 24.06%, 20.85% and 17.16% for first, second and third cut, respectively than the lowest one. The results for dry leaf stem percent cleared that highest mean value was at millet 10 which had 50.1%,52.3 % and 53.0%. On the other hand the lowest mean values for dry leaf/stem percent was found at millet 6 which it were 37.6, 41.4 and 43.9%, for first, second and third cut ,respectively over two years [39-41].

Phenotypic ($\delta^2 p$) genotypic ($\delta^2 g$), variance, phenotypic (P.C.V.) and genotypic (G.C.V.) coefficient of variability, heritability (h^2), genetic advance as unit (Ga unit) and as percentage (Ga%) for all studied charters across two years for studied traits are presented in Table 5.

In general data showed that the phenotypic and genotypic variance and genotypic coefficient of variability were narrow. Considerable consistency of values was observed between (P.C.V.) and (G.C.V.) percentage for all the other studied traits as the same ($\delta^2 p$) and ($\delta^2 g$) values were narrow at the most traits and cuts. The differences among (G.C.V.) and (P.C.V.) were narrow suggesting the presence of effects for environments appeared in the genotypes x year's interaction which was small effect in most traits and cuts were insignificant [42, 43].

Generally, high estimates of heritability (h^2)were found for all studied traits. High heritability (h^2) ($\delta^2 p$) and ($\delta^2 g$) values were narrow for fresh yield at the three cuts and total yield, which it were 385.87 and 383.09 and the same trend for (G.C.V.) and (P.C.V.), which it were 33.55 and 33.43% over two years. The environmental variation ($\delta^2 p - \delta^2 g$) / ($\delta^2 p$) x 100 were 0.72 for total fresh yield over two years, indicated that this trait is relatively less effected by environment and largely influenced by the additive effect of genes and the improvement in these traits may be

achieved through the phenotypic selection [44, 45].

Heritability (h^2) were ranged from 88.54 % to 99.62 % indicated that a largely influenced by the additive effect of genes and phenotypic selection will be beneficial [15, 46].

The estimates of expected genetic advance (Ga unit) express that if plant breeder select among these genotypes for the studied traits, the average of selection would increase by 13.69 kg(57.02%), 9.62 kg(44.88%), 16.98kg(98.44%) and 40.32 kg(68.86%) for first, second, third cut and total fresh yield, respectively [47-50].

Also, dry yield, had the same direction which had phenotypic ($\delta^2 p$) variance had 1.18, 0.79, 2.02, and 11.25 while, genotypic ($\delta^2 g$) variance had 1.15, 0.76, 1.99 and 11.16 for first, second, third cut and total dry yield, respectively. The environmental variation $(\delta^2 p - \delta^2 g) / (\delta^2 p) \times 100$ were 0.80 for total dry yield over two years, indicated that this trait is relatively less effected by environment and largely influenced by the additive effect of genes and the improvement in these traits may be achieved through the phenotypic selection. On the other hand, P.C.V.% had 40.05, 35.36, 66.13 and 45.54 while G.C.V. % had P.C.V. % which had 39.55, 34.84, 65.69, and 45.36 for first, second, third cut and total dry yield, respectively. Heritability (h^2) were 98.76, 98.53, 99.33 and 99.59 for first, second, third cut and total dry yield, respectively. The estimates of expected genetic advance (Ga unit) were 2.21kg (81.86%), 1.80kg (71.77%), 2.91 kg(135.32%) and 6.88kg (93.43%) for first, second, third cut and total dry yield, respectively [6, 51-53].

Meanwhile, The environmental variation for plant height were $(\delta^2 p - \delta^2 g) / (\delta^2 p) \times 100$ which had 0.96, 0.76 and 1.32 for first, second, third cut over two years, indicated that this trait is relatively less effected by environment and largely influenced by the additive effect of genes and the improvement in these traits may be achieved through the phenotypic selection especially in first and second cut.

Plant height were had phenotypic ($\delta^2 p$) variance had values 748.22, 807.24 and 863.02 While, genotypic ($\delta^2 g$) variance had 741.07, 801.12 and 851.65 for first, second, third cut, respectively. Meanwhile, P.C.V.% had 16.35, 17.51 and 20.19 while G.C.V. % had less values than P.C.V. % which had 16.27, 17.45, and 20.06 for first,

second and third cut, respectively. Heritability (h^2) had highest values which had 99.52, 99.62 and 99.34 for first, second and third cut, respectively. The estimates of expected genetic advance (Ga unit) were 56.08cm (33.53%), 58.31cm (35.94%) and 60.12cm (41.32%) for first, second and third cut, respectively [54-56]. The results indicated that The environmental variation for stem diameter were $(\delta^2 p - \delta^2 g) / (\delta^2 p) \times 100$ which had 0.20, 0.000 and 20 for first, second, third cut over two years. indicated that this trait is relatively affected by environment and less influenced by the additive effect of genes these may be due to small values which affected by environment.

For stem diameter phenotypic ($\delta^2 p$) variance had values 0.05, 0.04 and 0.05, also, genotypic ($\delta^2 g$) variance had 0.04, 0.04 and 0.04 for first, second and third cut, respectively [15, 46]. P.C.V.% had 19.16, 18.73 and 21.28 meanwhile G.C.V. % had less values than P.C.V. % which had 17.97, 17.33, and 19.84 for first, second and third cut, respectively. Heritability (h^2) had highest values which had 93.77, 92.52 and 93.42 for first, second and third cut, respectively. The estimates of expected genetic advance (Ga unit) were 0.43 cm (37.01%), 0.39 cm(35.69%) and 0.41 cm(40.87%) for first, second and third cut, respectively [52-57].

For fresh and dry leaf percent The environmental variation were $(\delta^2 p - \delta^2 g) / (\delta^2 p) \times 100$ which had 12.73, 21.67 and 18.53 for first, second, third cut over two years for fresh leaf percent, 1.76, 1.64, 2.95 for first, second, third cut over two years for dry leaf percent, indicated that this trait is relatively affected by environment and less influenced by the additive effect of genes. While, phenotypic ($\delta^2 p$) variance had values 14.61, 6.60, 8.42, 34.57, 28.08 and 17.29, also, genotypic ($\delta^2 g$) variance had 12.75, 5.17, 6.86, 33.96, 27.62 and 16.78 for first, second, third cut, respectively. Meanwhile, values P.C.V.% had 10.55, 6.57, 7.08, 13.18, 11.34 and 8.61 also, G.C.V. % had less than P.C.V. % which had 9.86, 5.82, 6.39, 13.07, 11.24 and 8.48 for first, second and third cut, respectively. Heritability (h^2) had highest values which had 93.42, 88.54, 90.24, 99.11, 99.18 and 98.50 for first, second and third cut, respectively. Genetic advance (Ga unit) and as percentage (Ga %) were 7.36 (20.31%), 4.68(11.98%), 5.40(13.16%), 12.0(26.92%), 10.83(23.16) and 8.44(17.47%) for first, second and third cut, respectively [51, 54, 56]. High heritability indicated that traits were less affected

Table 6. The matrix of simple correlation for yield and yield components of all genotypes of pearl millet over two years

	Total fresh yield (TFY)	Total dry yield (TDY)	Plant height (PH)	Stem diameter (SD)	Fresh leaf stem percent (F.L/s.p)	Dry stem percent (D.L/s.p)
(TFY)	1.000					
(TDY)	0.983**	1.000				
(PH)	0.996**	0.975**	1.000			
(SD)	0.905**	0.847**	0.910**	1.000		
(F.L/s.p)	-0.957**	-0.898**	-0.953**	-0.942**	1.000	
(D.L/s.p)	-0.982**	-0.932**	-0.983**	-0.926**	0.986**	1.000

Table 7. Path Analysis for total fresh yield and yield components of all genotypes of pearl millet over two years

	Total dry yield (TDY)	Plant height (PH)	Stem diameter (SD)	Fresh leaf stem Percent (F.L/s.p)	Dry leaf stem percent (D.L/s.p)
TFY x TDY	(0.551)	-0.100	0.0445	-0.0934	0.580
TFY x PH	0.538	(-0.103)	0.047	-0.991	0.612
TFY x SD	0.467	-0.0938	(0.052)	-0.098	0.576
TFY x FSR	-0.495	0.982	-0.0495	(0.104)	-0.614
TFY x DSR	-0.622	-0.514	-0.048	0.102	(-0.622)

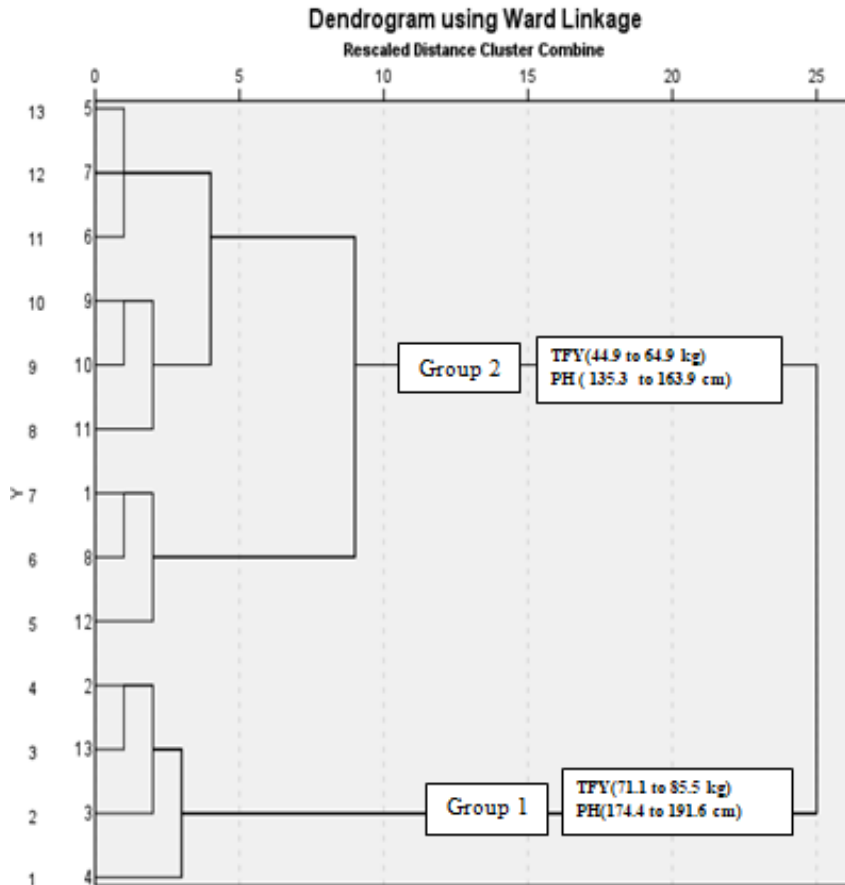


Fig. 1. Phonogram showing the relationships between 13 genotypes of Pearl millet, using distance metric of 1- Euclidean correlation coefficient and average linkage method

by environment and largely influenced by the additive effect of genes and the improvement in these traits may be achieved through the phenotypic selection [15,46].

The correlation matrix for all traits over two years calculated and the results are presented in Table 6. The results cleared that significant positive correlation was obtained between total fresh yield (TFY), plant height (pH) and stem diameter (SD) with values 0.996 and 0.905, respectively. Also, the results cleared that significant and positive correlation between total dry yield (TDY) and each of plant height (PH) and stem diameter with the values 0.975 and 0.847, respectively, but fresh and dry leaf stem percent had highly significant negative correlation with the other traits [46]. On the other hand between plant height and stem diameter significant and positive correlation with value 0.910, leaf stem percent and dry leaf stem percent with value 0.986. The traits, plant height,

stem diameter and leaf stem percent may be useful tools for selecting high yielding genotypes [58].

Path analysis is statistical methodology used to separate overall effect in to (direct) and in direct effect, which mean path analysis partitions the total correlation co-efficient in to (direct) and in direct effects and measures the relative importance of causal factor individually [59,60]. The values regarding the path analysis are given in Table 7. In the present study, total fresh yield was considered as dependent character and other characters were taken as independent characters. Total dry yield contributed maximum positive (direct) effect (0.551) followed by fresh leaf stem percent (0.104), while plant height had maximum negative effect (-0.103) to total fresh yield. Hence, selection for either one of the components will have an adverse effect on the other hand lead to decrease in yield. All studied traits had negative indirect effect via by or

through by means of dry leaf stem percent on fresh forage yield, while the direct and indirect effects of total dry yield and plant height were positive. Thus improvement response of any of these traits would simultaneously improve total fresh forage yield because of correlated response of yield by applying strong, selection on these traits [58,61,62].

3.1 Cluster Analysis

Cluster analysis can be used to identify significant relationships among genotypes and provides a hierarchical classification of them where considered as a preliminary stage in selecting the best parents which will use in breeding programs to produce better genotypes [63]. Cluster analysis is used to investigate and interpret data Fig. 1. The results of the cluster analysis showed that all accessions are divided into two major clusters. Fresh forage yield and plant height were valuable in splitting the studied accessions into two groups. The first group contains accessions of 2, 3,4 and 13. The value of fresh forage yield and plant height were between (71.1 to 85.5 kg) and (174.4 to 191.6 cm), respectively. The second group contains others accessions the value of Plant height were between (44.9 to 64.9 kg) and (135.3 to 163.9 cm), respectively. The second group was divided into two subgroups. Fresh forage yield and Plant height trait were valuable in splitting the studied genotypes into two sub groups. The first sub group contains accessions of 1, 8 and 12, values of fresh forage yield and plant height were (59 to 64.9kg), (154.7 to 163.9 cm), respectively. The second group contains others accessions the values of fresh forage yield and plant height were (44.9 to 552 kg), (135.3 to 149.5 cm), respectively.

4. CONCLUSION

The results cleared that were variations between all studied genotypes and possibility used these genotypes to improve the studied traits during breeding program, millet 6, population shandawal 1 and population Sids 3 had the best genotypes and could be used in breeding program for fresh and dry yield, plant height, fresh and dry leaf stem percent.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Abd Allah Ahmed M, Hend HM. Hassan, Awad MM. Forage productivity, competition indices and economics of forage millet and guar as affected by intercropping pattern and nitrogen fertilizer under sandy soil conditions. Journal of Plant Production Sciences; Suez Canal University. 2020;9(1):47-59.
2. Reiad M. Sh, Maha MA. Hamada, Abd ELMaaboud M. Sh, Khalil MH. Forage growth and productivity of pearl millet as affected by soil mulching, planting date under salinity conditions. Egypt. J. Agron. 2014;36(1):75-94.
3. Ghazy M. F. Mona, Sakr HO, Magda N. Rajab. Estimation of genetic variability and divergence in some selected lines of pearl millet. Agric. Chem.and Biotechn., Mansoura Univ. 2015;6(12): 615- 626.
4. Mungra KD, Jadhav BD, Khandelwal V. Genetic analysis for yield and quality traits in forage sorghum (*Sorghum bicolor* (L.) Moench). Indian Journal of Genetics and Plant Breeding. 2011;71(3):223-230.
5. Casler MD, Hovin AW. Genotype x environment interaction for need Canary grass for yield. Crop Sci. 1984;24:633-636.
6. Carlos TSD, Koranowski WJ. Model selection of cross validation in additive main effect and multiplication interaction models. Crop Sci. 2003;43:865-873.
7. Comstock RE, Moll RH. Genotypic environment interaction. Symp. On Stat. Genetics and Plant Breeding. NAS-NRC Pup. 1963;982:164-196.
8. Ramanatha Rao, Toby Hodgkin. Genetic diversity and conservation and utilization of plant genetic resources. Plant Cell, Tissue and Organ Culture. 2002;68:1-19.
9. Yang X, Wan Z, Perry L, Lu H, Wang Q, Hao C, Li J, Xie F, Yu J, Cui T, Wang T, Li M, Ge QH. Early millet use in northern China. Proc. Nat. Acad. Sci. USA. 2012;1-5.
10. Worede M, Tesemma T, Feyissa R. Keeping diversity alive: An Ethiopian perspective.' In S. B. Brush (ed.), Genes in the Field: On-farm Conservation of Crop Diversity. Boca Raton, Florida: Lewis Publishers with IDRC and IPGRI. 2000;143-161.
11. Johnson RA, Wichern DW. Applied multivariate statistical analysis. 6th Edition, Pearson Prentice Hall, Upper Saddle River; 2007.

12. Mstat C. Amicro computer program for the design experiment Michigan State Univ, USA; 1986.
13. Bartlett MS. Properties of sufficiency and statistical test. Proc. Roy. Soc., 1937;A160:268-282.bioRxiv preprint first posted online Feb. 3.
DOI: <https://doi.org/10.1101/105940>.
14. Robinson HV, Comstock, Harvey H. Genotypic and phenotypic correlations in corn and their implications in selection. Agron. J. 1951;43:282-285.
15. Johanson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron. J. 1955;47:314- 318.
16. Kana Ram Kumawat NK, Sharma, Nemichand Sharma. Genetic variability and character association analysis in pearl millet single cross hybrids under dry conditions of Rajasthan. Electronic Journal of Plant Breeding. 2019;10(3):1067 - 1070.
17. Tarrad MM, Rizk RM, Aly RSH, Zayed EM. Evaluation of some teosinte Genotypes under Egyptian conditions. Egypt. J. Agric. Res. 2010;88(1):265- 281.
18. Sayed Mervat RI, Zayed EM, Morsi Nahid AA. Identification of molecular genetic markers associated with salt tolerance in pearl millet. Middle East Journal of Agriculture Research. 2022;11(2):451-465.
19. Heba S.A. Salama, Ahmed M. Shaalan, Mohamed EA. Nasser. Forage performance of pearl millet (*Pennisetum glaucum* [L.] R. Br.) in arid regions: Yield and quality assessment of new genotypes on different sowing dates. Chilean journal of Agricultural Research. 2020;80(4):572-584.
20. Ghazy, Mona, MF, Ali FM, El-Diasty ZM, Hamada MS. Estimation of some genetic parameters of economic traits in sorghum : Gene action and heritability. The second field crops Conference 47- 58, FCRI, Giza, Egypt, 14-16 Oct; 2008.
21. Ghanbarian AT, Hurst LD. Neighboring genes show correlated evolution in gene expression. Mol. Biol. Evol. 2015;32:1748-1766.
22. Tania Brunette. Evaluation of forage millet cultivars on the performance of dairy cows. A thesis submitted to McGill University in partial fulfillment of the requirements of the degree of Master of Science. Department of Animal Science McGill University, Montreal. 2014;1-108.
23. Allard RW, Bradshaw AD. Implications of genotype x environment interactions in applied plant breeding. Crop Sci. 1964;4:503-507.
24. Rakesh G, Shashibhushan D, Dayakar Reddy T, Uma Nagesh J. Evaluation of bajra [*Pennisetum glaucum* (L.) R.Br.] Germplasm lines for yield and yield related traits using principal component analysis. Agriculture and Technology. INDIA. 2015;10 (Special-VII) :3885-3887 Meerut (U.P.)
25. Reza Ataei, Mohammad Reza Shiri. Multi-environment evaluation of foxtail millet advanced lines for forage yield stability. Genetika. 2020;52(3):835-850.
26. Jyoti Kaushik, Dev Vart, Mukesh Kumar, Mamta Nehra, Ramesh Kumar. Genetic diversity assessment of pearl millet maintainer lines. Journal of Pharmacognosy and Phytochemistry. 2018;7(5):2428-2432.
27. Abd El-Maksoud MM, El-Adl AM, Rammah A, Sakr HO. Diallal analysis over Two Locations for fodder yield components in teosinte. Proceeding of the 26th Annual Meeting of Genetic, Alex. 1998;29-30 Spt.317-329.
28. Abdel-Twab FM, Rashed. Esterase, peroxidase and Catalase Isozyme Polymorphism in zea,teosinte and sorghum form different origins. Egypt. Genet, Cytol. 1985;14:274-281.
29. Obilana AB, El-Rouby MM. Recurrent mass selection for yield in two random mating populations of sorghum (*Sorghum bicolor*). Madica. 1980;25:127-133.
30. Saeed M, Francis CA, Rajewski JF. Maturity effects on genotype x environment interactions in grain sorghum. Agron. J. 1984;76:55-58.
31. Ali MA. Heterosis, combining ability and stability studies in grain sorghum. Ph.D Thesis, Faculty of Agriculture, Essiut University, Egypt; 2000.
32. Ezzat EM, Ali MA, Mahmoud AM. Agronomic performance, genotype x environment interaction and stability analysis of grain sorghum (*Sorghum bicolor* L. Monech). Asian Journal of Crop Science. 2010;2(4):250-260.
33. Yan W, Hunt A. Biplot analysis of diallel data. Crop Sci. 2000;42:21-30.
34. Pucher A, Angarawai OSI, Gondah J, Zangre RG, Ouedraogo M, Sanogo MD, Boureima S, Hash CT, Haussmann BIG. Diversity and agro morphological characterization of West Central African

- pearl millet accessions. *Crop Science*. 2015;55:737–748.
35. Anne Lorant, Sarah Pedersen, Irene Holst, Matthew B. Hufford, Klaus Winter, Dolores Piperno, Jeffrey Ross-Ibarra. The potential role of genetic assimilation during maize domestication; 2017.
 36. Kumari J, Bag MK, Pandey S, Jha SK, Chauhan SS, Jha GK, Dutta M. Assessment of phenotypic diversity in pearl millet [*Pennisetum glaucum* (L.) R. Br.] germplasm of Indian origin and identification of trait-specific germplasm. *Crop Pasture Science*. 2016;67:1223–1234.
 37. Allison L. Weber, William H. Briggs, Jesse Rucker, Baltazar M. Baltazar, José de Jesús Sánchez-Gonzalez, Ping Feng, Edward S. Buckler, John Doebley. The genetic architecture of complex traits in teosinte (*Zea mays* ssp. *parviglumis*): New evidence from association mapping. 2008;180(2):1221–1232.
 38. Mithlesh Kumar, Kirti Rani, Ajay BC, Patel MS, Mungra KD, Patel MP. Study of genetic variability, heritability and path analysis for grain micronutrients concentration, yield and component traits in pearl millet (*Pennisetum glaucum* (L.) R. Br.). *Journal of Pharmacognosy and Phytochemistry*. 2020;9(2):1402-1409.
 39. Sheng Nan Wei, Eun Chan Jeong, Yan Fen Li, Hak Jin Kim, Farhad Ahmadi, Jong Geun Kim Sheng Nan Wei. Evaluation of forage production, feed value, and ensilability of proso millet (*Panicum miliaceum* L.). *J Anim Sci Technol*. 2022;64(1):38-51.
 40. Reddy PRR, Sankar GRM, Das ND. Genotype x environment interactions in rabi sorghum. *Journal of Maharashtra Agricultural Universities*. 2004;29(1):21-24.
 41. Dov Pasternak, Ali Ibrahim, Ayantunde Augustine. Evaluation of five pearl millet varieties for yield and forage quality under two planting densities in the Sahel. *African Journal of Agricultural Research*. 2012;(32):4526-4535, 21.
 42. Samuel JL. Ziki EMI, Zeidan AYA. El-Banna, Omar AEA. Growth and forage yield of pearl millet as influenced by cutting date and nitrogen fertilization. *Zagazig J. Agric. Res*. 2019;46(5):1351- 1361.
 43. Annamalai R, Aananthi N, Arumugam Pillai M, Leninraja D. Assessment of variability and character association in pearl millet [*Pennisetum glaucum* (L.) R.Br.]. *Int. J. Curr. Microbiol. App. Sci*. 2020;9(6):3247-3259.
 44. Sathya M, Kumari Vinodhana N, Sumathi P. Hierarchical clustering of pearl millet (*Pennisetum glaucum* (L.) R.Br) inbreds for morpho-physiological traits. *Int. J. Curr. Microbiol. App. Sci*. 2013;2(12):647-652.
 45. Assaeed AM. Evaluation of some forage sorghum varieties under the condition of central region, Saudi Arabia. *Annals Agric, Sci., Ain shams Univ., Cairo*. 1994;39(2):649-654.
 46. Bakheit BR. Genetic variability, genotypic and phenotypic correlations and path – coefficient analysis in Egyptian clover (*Trifolium alexandrinum* L.) *Crops Sci*. 1986;157:58-63.
 47. Tariq AS, Akram Z, Sabbir G, Khan KS, Mohamood T, Iqbal MS. Heterosis and combining ability evaluation for quality traits in forage sorghum SABRAO *Journal of Breeding and Genetics*. 2014;46(2):174-182.
 48. Manal MH, Metwali EMR, Mohamed AI. Assessment of genetic diversity of sorghum (*Sorghum bicolor* L. Moench) genotypes under saline irrigation water based on some selection indices. *Australian Journal of Crop Science*. 2013;7(12):1935:1945.
 49. Aruna C, Swarnalatha M, Kumar PP, Devender V, Suguna M, Blummel M, Patil JV. Genetic options for improving fodder yield and quality in forage sorghum. *Tropical Grass Lands-Fortrajes Tropicales*. 2015;3:49-58.
 50. Narasimhulu R, Satyavathi CT, Reddy BS, Ajay BC. Principal of components of genetic diversity and association studies for yield related traits in pearl millet. *Electronic Journal of Plant Breeding*. 2022;13(1):175-181.
 51. Sumathi P, Sumamth M, Vearabadharam P. Genetic variability for different biometrical traits in pear millet genotypes (*Pennisotum glucum* L.R.Br.). *Electronic Journal of Plant Breeding*. 2010;1(4):347-440.
 52. Yadav OP, Weltzien RE, Bhandari DC. Genetic variation and trait relationship with pearl millet landraces from Rajasthan. *Indian J. Gen. Plant Breeding*. 2001;61(4):322-326.
 53. Lakshmana D, Biradan BD, Ravikumar RL. Genetic variability studies for quantitative traits in a pool of restorers and maintainers lines of pearl millet (*Pennisetum glaucum*

- (L.). Karnataka J. Agric. Sci. 2009;22(4):881-882.
54. Govindaraj MS, Selvi B, Rajarathinam S, Sumathi P. Genetic variability and heritability of grain yield components and grain mineral concentration in India's pear millet (*Pennisotum glaucum* (L.) R.Br.), accessions. African J. Food, Agric. Nutr. Dev. 2011;11:4758-4771.
55. Subi MIM, Idris AE. Genetic variability, heritability and genetic advance in pearl millet (*Penisetum glaucum* (L.) R.B.D. Genotypes. British Biotechnology Journal. 2013;3(1):564-65.
56. Salih AIS, Ismail MI, Abdalla E, Osman KA, Ali AM. Genetic variation among pearl millet genotypes for yield and its components in semi-arid zone Sudan. Inter. J. of Agric. and Crop Sci. 2014;7(11):822-826.
57. Vetriventhan M, Nirmalakumar A. Studies on variability parameters in pearl millet (*Pennisetum glaucum* (L.) R.Br.). Madras Agric. J. 2007;94:118-120.
58. Sharma B, Kumar L, Kumar C, Sheoran R, Vivek K Singh, Sood M. Study on genetic variability, heritability and correlation in pearl millets germplasm. Journal of Pharmacognosy and Phytochemistry. 2018;7(6):1983-1987.
59. Nakawuka Ck, Adipala E. Path coefficient analysis of some yield component interaction in cowpea African Crop Science Journal. 1999;71327- 331.
60. Dewey DR, Lue KH. A correlation and path –coefficient analysis of components of crested wheatgrass seed production. Argon. J. 1959;51:515-518.
61. Iyanar K, Vijayakumar G, Khan AK. Fazlullah. Correlation and Path Analysis in Multicut Fodder Sorghum. Electronic Journal of Plant Breeding. 2010;1:1006-1009.
62. Awan ZK, Naseem SA, Massood, Nasir B, Sarwar F, Amin E, Ali Q. How to improve *Sorghum bicolor*(L.) Monch production : An Over view. Life Sci. 2015;1(1)44-57.
63. Shashibhushan D, Kumar CVS, Kon RKR. Genetic analysis of pearl millet germplasm by cluster analysis. Emer Life Sci Res. 2022;8(1):70-74.

© 2023 El-Gaafarey et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/97726>