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Phenotypic Characterization and Genetic Divergence of some Pearl Millet Genotypes Based on Cluster and Principal Component Analysis

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ABSTRACT

The presence of divergence in germplasm and its efficient utilization is essential for successful improvement of any fodder crop. During 2020-2021 summer seasons at Sids ARS. A total of ten pearl millet genotypes were grown with RCB design in three replicates to determine genetic variability, genotypic and phenotypic coefficients of variations, heritability, genetic advance and degree of linkage among various traits based on yield component, forage yield, and quality traits using cluster and principal components analysis (PCA). Results of combined analysis revealed significant differences among two years, genotypes and interaction of year x gen. for most traits. The genotypes (G2, G5 and G7) are promising and can be recommended in breeding programs due to revealing the highest yield components, forage yield, and quality values. The largest estimates of genotypic and phenotypic coefficients, high value of heritability connected with high value of genetic advance percent as mean were observed for most traits, indicating to existence of genetic variation beside efficient possibility selection for these traits. Results of cluster dendrogram analysis exposed a great genetic divergence among the tested genotypes, classifying them into 4 sub-clusters. The study detected six principal components (PCs) with Eigen values higher than 1.00 which, accounted for 90.027 % of the total variation for discriminating the 10- millet genotypes based on the studied traits. Therefore, these traits can be applied to selection criteria for yield improvement and determined appropriate genetic resource for efficient in pearl millet breeding program.

Keywords: Genetic divergence; millet; heritability

INTRODUCTION

Feed shortage during the summer season is a main defiance to increase for livestock product to cover the rising request for dairy and meat products; so, there are various options to fulfill the gap among supply and demand for feed, among them is the improvement to high forage yield cultivars (Eeswaran *et al.* 2022). Millet is gaining particular popularity due to its adaptability to acceptable yield, climate change impacts and nutritional quality (Jukanti *et al.* 2016).

There are many options to cover the gap between forage demand and supply, one of which is the adoption of high-yielding crop varieties (Hassan *et al.*, 2014; Babiker *et al.*, 2015).

Pearl millet (*Pennisetum glaucum* L.) considers the major cereal crops that the greatest production and is the main product of food and feed in arid as well as semi-arid regions. Typically, it is grown with unfavorable agro- climatic. Besides, millet has remarkable capacity to respond for propitious environments due to its rapid growth and capacity to achieve high growth rate and it has excellent nutritional qualities, good source of carbohydrates, vitamins and minerals (Ziki *et al.* 2019).

To success the improvement of crop depends on the reach of characterized germplasm for diverse traits available for desired cultivars in program of breeding where fodder millet has wide genetic diversity which is of little value unless it is characterized, estimated and classification properly to enhance its exploitation in crop improvement. To exploit effectively the available genetic diversity, the material must be properly characterized and catalogued (Singh *et al.* 2018).

Also, the improvement of crop at first search at the amount of genetic variation existent in population to can be benefited more from either by simple selection or through other breeding methods (Kumar *et al.* 2020). The degree and nature to which yield is related with other traits allows breeders to foresee the relative impact of different traits on yield improvement that allowing them to choose the traits that are desirable and crucial to achieving improvement.

Berwal and Khairwal (1997) and Ghazy *et al.* (2015) studied the genetic variation for forty genotypes of pearl millet and observed a significance difference in height of plant, no. of tillers, stem diameter, fresh, dry leaf/stem ratio and total fresh and dry forage yield across three cuts and over two seasons.

Likewise, the genetic variation for various growth and forage yield characteristics in millet was observed by many researchers such as Narasimhulu and Veeraghavaiah (2019) and Salama *et al.* (2020). Although millet has sufficient nutritional qualities but the increase in quality is necessary to meet the nutritional qualities standards of forage for livestock. The nutritional qualities of livestock forages stuff are estimated by its crude protein (CP), crude fiber (CF), carbohydrates, ether extract and ash contents. Although millet has sufficient nutritional value but the increase in quality is necessary to meet the nutritional standards of forage for livestock.

Hassan *et al.* (2014) studied the quality performance of eight varieties in pearl millet and found high significantly varied regarding crude protein% and crude fiber%. But non-significant differences were recorded among varieties

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regarding ash contents. Salma *et al.* (2020) found highly significant differences variations in the nutritional components among the five genotypes of pearl millet.

The efficiency of any selection depends on the genetic variance of the traits with a rise coefficient of variance and rise heritability conjunction with rise genetic advance. Estimating of heritability and genetic advance for different targeted traits helps the breeder to apply appropriate breeding methodology in the crop improvement program, where heritability is affected by the environment (Abubakar *et al.* 2019). In addition, Kumar *et al.* (2020) displayed the values coefficients of phenotype and genotype of variation for plant height and green forage yield and recorded comparative variation between 48 diverse pearl millet genotypes which were less influenced by the environment.

The useful multivariate statistical methods are related to the relationship between related genotypes, as cluster dendrogram analysis that is an efficient tool that aimed to detecting the amount of genetic variance among genotypes under study based on their contributing traits and performance (Govindaraj *et al.* 2020) and principal components analysis (PCsA), those have been widely used in variance study in germplasm groups of numerous species (Kumar *et al.* 2020).

Hence, the objectives of this investigation were as follows: (i) to evaluate ten pearl millet genotypes with focusing on genetic divergence and heritability for yield components yield, and quality traits; (ii) using cluster analysis and principal component analysis among tested genotypes to achieve genetic relationships.

MATERIALS AND METHODS

Plant material and experimental design

Two field experiments were achieved in clay soil at Sids Agricultural Research Station Farm in Beni- Suif Governorate, Egypt during successful summer seasons of 2020 and 2021. Soil physical and chemical analysis and available nutrients of the experimental site is shown in Table 1. The genetic materials for this study were consisted of 10 pearl millet genotypes where (G1- G8) were selected from commercial varieties during the two successive seasons of (2018 and 2019) beside two check varieties (local variety Shandaweel-1 (G9) and commercial variety Saudian millet (G10)). The previous crop in both seasons was Egyptian clover. On 9th and 6th June in the two seasons, respectively, the genotypes of pearl millet had planted in a Randomized Complete Blocks Design (RCBD) with three replicates and the rate of seeds for each genotype was 20 kg/fed. Genotypes of pearl millet were planted in a plot size of 6 m² where each plot was consisted of five rows with 2 m long, 0.6 m wide and hills spaced at 20 cm among plants. During seed bed preparation, 150 kg P₂O₅ fed⁻¹ (15.5% P₂O₅) was integrated in the soil surface. Nitrogen fertilizer 90 kg /fed⁻¹ (ammonium nitrate 33.5% N) was applied in three times; 15, 48 and 80 days after planting. In each season 3-cuts were picked at 45, 75, and 110 days from planted in both seasons.

Phenotypic data collecting and statistical analysis:

- 1- Plant Height "P.H." (cm): was detecting at harvest in every cut to average 5 plants from soil surface to the tip of the tallest tiller.
- 2- Leaf /Stem ratio "L/S" ratio: was determined by divided weight of leaf on weight of stem.

- 3- Stem diameter "SD" (cm): was detected at third internodes above soil surface.
- 4- Total fresh yield "TFY" (kg/ plot): the sum of cuts yield
- 5- Total dry yield "TDY" (kg/ plot): dry matter % was estimated dried the fresh sample at 70 °C to constant weight and multiplied fresh yield.

Table 1. Soil particle size distribution, chemical properties and available nutrients of the experimental site (Mean values for the two seasons)

Soil characteristics	Means of both seasons
Particle size distribution %	
Coarse Sand	6.76
Fine Sand	12.54
Silt	34.83
Clay	45.87
Textural Class	Clay
Chemical properties	
pH (suspension 1:2.5)	7.52
EC dS m ⁻¹ (saturated paste extract)	1.65
Organic Matter (%)	0.96
CaCO ₃ %	5.34
Available macronutrients (mg L ⁻¹)	
N	46.81
P	5.12
K	175

Chemical Composition:

Chemical composition *i.e.* crude fiber (CF %), crude protein (CP %), carbohydrates % and ash % followed the traditional method recommended by the Association of Official Agricultural Chemists (A.O.A.C. 2012) on the dried samples at 70°C for each cut of the second season only

Statistical analysis:

In each season, differences among genotypes were detected for the data. When the errors were homogeneous, pooled analysis was executed. The homogeneity of variances was checked using Bartlett (1937) test in two seasons, and then the combined across two seasons between the tested genotypes to test the significant difference, the standard statistical method according to Steel and Torrie (1987). The genotypic (G.C.V. %) and phenotypic (P.C.V. %) coefficients of variations were assessed using the pertinent mean square expectations according to the method suggested by Johnson *et al.* (1955) and broad sense heritability (h_b²) and genetic advance% as mean (GA %) were assessed as explained by Al-Jibouri *et al.* (1958). Cluster hierarchical analysis was performing on standardized data utilizing a measurement of Euclidean distance and Ward minimum variance method as outlined by Ward (1963). While principal components analysis (PCsA) was carried out as explained by Rao (1964).

RESULTS AND DISCUSSION

The combined analysis of variance for plant height, leaf/stem ratio, stem diameter and total fresh and dry yields (kg/ plot) of genotypes are demonstrated in Table (2). The results indicated that a highly significant difference exists between seasons for all studied traits except stem diameter (cm) and the genotypes showed highly significant differences for all studied traits in both years suggesting that there was wide variation among genotypes under study. In addition, the interaction effect between year and genotypes showed significant differences for the same traits. Our results are confirmed by Anuradha *et al.* (2018) who revealed presence

the highly significant difference among 130 lines of pearl millet for thirteen phenotypic characters were recorded in both years. Also, Narasimhulu *et al.* (2021) recorded that significant difference between 41 hybrids of millet for the

yield and its attributing traits. Therefore, these results help the breeder to select the best germplasm of pearl millet collections that are used in the programs of breeding

Table 2. Combined analysis of yield components and yield of 10- pearl millet genotypes over the two years of 2020 and 2021

S.O.V.	D. f.	Mean square				
		P.H. (cm)	L/S ratio	SD (cm)	TFY (kg/ plot)	TDY (kg/ plot)
Year (Y)	1	128.331**	0.529*	0.472	65.428**	2.426**
Rep/year	4	19.17	0.109	0.151	9.846	0.373
Genotypes (G)	9	96.583**	0.298**	0.256**	50.065**	1.952**
Y X G	9	8.021**	0.015*	0.038*	4.929**	0.256*
Error	36	2.841	0.006	0.013	2.547	0.062

* Significant at level of probability 5%, ** Significant at level of probability 1%.

The performance of mean for all the genetic materials in this study revealed a great deal of variation for all the traits under study Table 3. Data illustrated that, there were some selected genotypes significant exceeded the check variety G9 in plant height where G6 revealed the highest plant height of 138.4 cm followed by G2 (135.8 cm), G5 (133.9 cm) and G7 (133.5 cm) while the check variety G9 recorded 131.7 cm for plant height. With concerning to leaf /stem ratio, results distinguished that, G2 ranked first for leaf/stem ratio (0.839) followed by G5 (0.689), G7 (0.639) and G3 (0.608) compared to the check variety G10 that revealed (0.593). The increases in stem diameters were noticed with five genotypes but three only genotypes significantly overcome the check variety G9 where the highest mean values were (1.021, 0.985 and 0.912 cm) for G7, G2 and G5, respectively whereas the check variety G9 that recorded 0.849. With respect to total fresh yield, results from the same table showed clearly that, genotypes (G2, G5 and G7) significantly suppressed the check variety G9 which revealed (98.45, 95.58 and 92.67 kg/plot) respectively, while the check variety G9 recorded 87.32 kg/plot. In spite of, three selected genotypes G2 (14.26 kg/plot), G7 (13.91 kg/plot) and G5 (13.78 kg/plot) were higher than the check variety G9 (13.64 kg/plot) for total dry yield but two only genotypes were significantly observed. This agrees with Singh *et al.* (2018) who found significant difference among seven hybrids and their seventeen parents of pearl millet for 28 morphological and yield characters.

Further, the values for traits under study except plant height ranked the lowest for G8 genotype, where recorded (0.414) for leaf/stem ratio, (0.669 cm) for stem diameter, (79.75 kg/ plot) for total fresh yield and (10.65 kg/ plot) for total dry yield. Beside that G3 ranked the minimum value for plant height (122.9). These results agree with previous finding of Ramya *et al.* (2018) who noted highest response to selection in plant height, stem diameter and single plant yield for a set of 376 germplasm of millet. In the same direction

Kumer *et al.* (2020) stated that a large difference in mean values for plant height, leaf/ stem ratio and fodder dry yield illustrate sufficient divergence existed between the genotypes and traits. Mean performance for morphological traits is among affect steps toward the choice of appropriate superior genetic material that used for future millet crop improvement programs.

Table 3. Combined mean performances of the yield and its components of 10- pearl millet genotypes over the two years of 2020 and 2021

Genotypes	P.H. (cm)	L/S ratio	SD (cm)	TFY (kg/ plot)	TDY (kg/ plot)
G1	130.7	0.538	0.861	86.91	12.98
G2	135.8	0.839	0.985	98.45	14.26
G3	122.9	0.608	0.881	87.17	13.29
G4	130.7	0.479	0.778	84.32	11.06
G5	133.9	0.689	0.912	95.58	13.78
G6	138.4	0.566	0.878	89.16	13.23
G7	133.5	0.639	1.021	92.67	13.91
G8	125.3	0.414	0.669	79.75	10.65
G9	131.7	0.526	0.849	87.32	13.64
G10	127.9	0.593	0.811	84.17	13.42
L.S.D _{0.05}	2.16	0.024	0.053	1.931	0.236
L.S.D _{0.01}	3.02	0.048	0.071	2.687	0.359

Chemical Composition:

The analysis of variance showed a large significant difference in the chemical composition of crude fiber %, crude protein %, carbohydrates % and ash% in 2021 growing seasons among the 10 pearl millet genotypes (Table 4) indicating a high level of genetic variation. Comparable results were recorded by earlier researchers such as Muhammad *et al.* (1994), Amodu *et al.* (2007) and Noor *et al.* (2018) who found vary significantly regarding for crude protein, crude fiber and ash % between three varieties of pearl millet.

Table 4. Mean squares of chemical composition of 10- pearl millet genotypes (The second season only)

S.O.V.	D.f.	Mean squares			
		Crude fiber (CF%)	Crude protein (CP%)	Carbohydrates%	Ash %
Rep.	2	6.081	12.674	16.954	3.321
Genotypes	9	25.871**	36.917**	33.876*	14.456**
Error	18	1.562	3.761	2.78	0.987

* Significant at level of probability 5%, ** Significant at level of probability 1%.

Mean performances for four quality traits are illustrated in Table (5). Wide range of variations was observed among the 10- pearl millet genotypes under comparison. The maximum value for the crude fiber 31.73 % was detected for

G5 followed by 30.43% for G7 and 30.05 % for G2 compared with the check variety G9. For the crude protein %, the results cleared that the highest value was 12.18 % for G2 followed by 11.88% for G5 whereas the check variety G10 recorded

11.50 %. In connection with carbohydrates, results showed that, G2 and G7 recorded (36.65 and 36.35%) significant values with the check variety G9 (34.45%). The mean values of ash ranged from 5.46% for G4 to 8.42% for G2 whereas the check variety G9 recorded that 6.19 %. Similarly, Singh et al. (2003) and Makarana et al. (2017) also found some variation for these traits.

Table 5. Mean performances of the chemical composition of 10- pearl millet genotypes (The second season only)

Genotypes	Crude fiber (CF%)	Crude protein (CP%)	Carbohydrates %	Ash %
G1	29.13	10.58	35.04	6.82
G2	30.05	12.18	36.65	8.42
G3	29.30	10.75	35.21	6.99
G4	26.47	9.22	34.17	5.46
G5	31.73	11.88	35.97	7.74
G6	29.55	10.06	35.47	7.25
G7	30.43	11.01	36.35	8.12
G8	27.70	9.65	33.69	5.89
G9	28.39	9.95	34.45	6.19
G10	28.80	11.50	34.52	6.30
L.S.D _{0.05}	1.47	1.04	1.82	0.13
L.S.D _{0.01}	2.03	1.97	2.75	0.34

On the other hand, G4 had the lowest values for crude fiber (26.47%), crude protein (9.22%) and ash (5.46%) but G8 the lowest values for carbohydrates (33.69 %). Current findings were also supported by Yusuf et al. (2012) who found a highly significant in all pearl millet varieties under study for quality traits, Hassan et al. (2014) who observed highly differences in mean values for crude protein and crude fiber percentage of nine millet varieties and Sayed et al. (2022) who stated high statistically significant differences for crude fiber and crude protein% among the 5- genotypes of millet under salt stress.

Genetic parameters:

Highly significant differences were distinguished of all traits under study for the genotypic variance (δ^2g), the phenotypic variance (δ^2p), the genotypic coefficient of variance (G.C.V.), the phenotypic coefficient of variance (P.C.V.%), the broad sense heritability (h_b^2) and the genetic advance (G.A.) as a percent of mean, Table 6. G.C.V. percentage ranged from low to high. P.C.V. percentage was greater than G.C.V. percentage in all the traits Figure 1, indicated to the evident variation is not only to genetics but also to influences of environmental. Similar findings of G.C.V. and P.C.V. percentage were observed by Anuradha et al. (2018) and Annamalai et al. (2020).

Table 6. Variability coefficient, heritability and expected genetic advance of 10- pearl millet genotypes on traits under study

Traits	Mean	δ^2g	δ^2p	G.C.V %	P.C.V %	(h_b^2) %	GA
P.H.(cm)	131.08	14.76	16.10	2.93	3.06	91.70	5.78
L/S ratio	0.589	0.047	0.050	36.81	37.96	94.00	74.26
SD (cm)	0.865	0.036	0.043	21.93	23.97	85.16	45.35
TFY (kg/ plot)	88.55	7.52	8.34	3.10	3.26	90.15	6.06
TDY (kg/ plot)	13.02	0.283	0.325	4.06	4.41	87.08	7.85
CF %	29.23	8.10	9.67	9.74	10.64	83.76	18.36
CP %	10.68	11.05	14.81	31.13	36.04	74.61	55.38
Carbohydrates %	35.15	10.37	13.15	9.16	10.32	78.86	16.76
Ash%	6.92	4.49	5.48	30.62	33.83	81.93	57.09

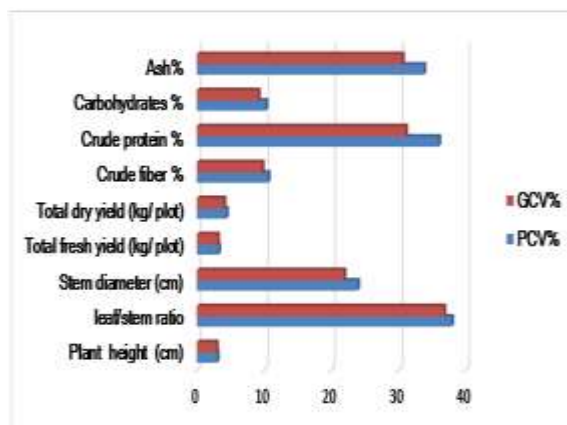


Figure 1. The genotypic coefficient and the phenotypic coefficient of variations for traits under study of 10- pearl millet genotypes

The estimates of genotypic coefficient of variability (G.C.V. % and P.C.V. %) were recorded for ph (2.93 and 3.06 %), l/s ratio (36.81 and 37.96%), SD (21.93 and 23.97 %), TFY (3.10 and 3.26%), TDY (4.06 and 4.41 %), CF (9.74 and 10.64 %), CP (31.13 and 36.04%), carbohydrates (9.16 and 10.32%) and ash (30.62 and 33.83%), respectively. The extend of the phenotypic and genotypic coefficients of variation indicates that there is a greater scope of selection of eminent germplasm entries for these traits and their efficient use in program of breeding (Kumar et al. 2020).

The heritability of broad sense (h_b^2) and the genetic advance (GA %) per mean were demonstrated graphically in Figure 2. Estimates of h_b^2 for differences among genotypes were a generally high for all traits under study and revealed values ranged from 74.61 % for crude protein to 94.00 % for leaf/stem ratio. Generally, the traits had higher genetic variance. Hence, it can be assumed that the genotypes of almost all traits are determined primarily by their phenotypes. Results were in concordance with Sumathi et al. (2010) and Bhasker et al. (2017). The estimates of genetic advance ranged from low to high for all studied investigate, where the genetic advance (GA) values revealed ranged from 5.78 for plant height to 74.26 for leaf/stem ratio. So, it is a more reliable indicator of trait selection.

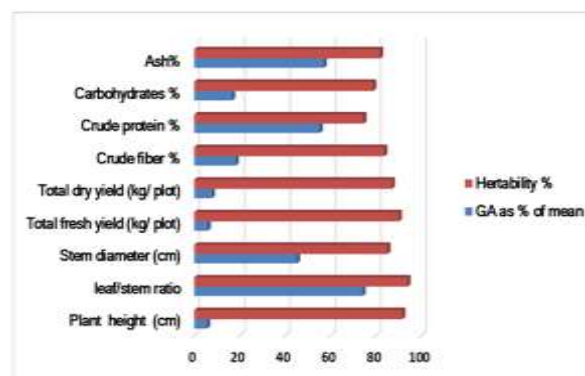


Figure 2. The heritability and the genetic advance % per mean for traits under study of 10- pearl millet genotypes.

These results are in conformity with Abubakar et al. (2019) who stated high genetic values for the traits. Furthermore, this suggests that the phenotypes were representatives true of their genotypes for these traits, and that phenotypic value selection could be reliable. According to the

findings, these traits are controlled by an additive type of gene action and can be improved through selection (Singh *et al.* 2018). Furthermore, based on these traits, selection can aid in the successful isolation of the desired genotype (Kalagare *et al.* 2022).

Cluster analysis:

Cluster analysis can be used to identify significant relationships among genotypes under study and gives a hierarchical distribution for them were considered as a preliminary stage in selecting the best parents which will use in breeding programs to produce better hybrids (Shashibhushan *et al.* 2022). The 10- pearl millet genotypes in this study were grouped in to four groups based on phenotypic trait and quality trait by Euclidean distance utilizing the UPGMA and the distance was realized as detect in the dendrogram graph (Figure 3).

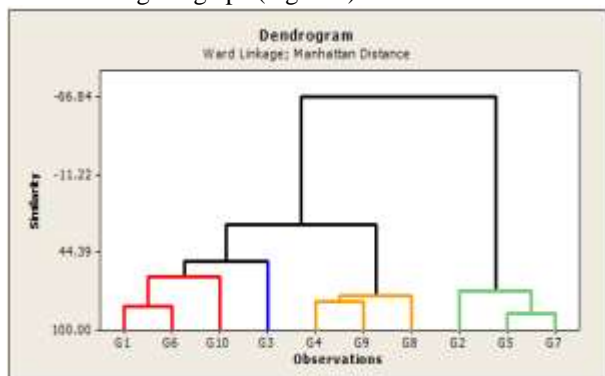


Figure 3. The dendrogram detecting the distance among 10- pearl millet genotypes based on traits under study

Tested ten genotypes of pearl millet grouped as two main clusters i.e. A and B. The first prime one divided into three sub clusters e.g., 1, 2 and 3. The first subcluster included (G1, G6 and G10). The 2nd sub cluster included only one genotype (G3). Also, the 3rd sub cluster included three genotypes (G4, G9 and G8). The 2nd main cluster consisted of one sub-cluster (4), that is; the 4th subcluster, it comprised of three genotypes (G2, G5 and G7). Our results agree with Ramya *et al.* (2018) who stated that the cluster hierarchical analysis of 60 parental strains of fodder millet was assigned into 8- clusters, revealed the presence of variability among these strains for 11- quantitative traits and (Kumar *et al.* 2020) reported that 48- genotypes of fodder millet grouped into 5- main clusters with a different number indicating the obvious differentiation between them with some exceptions

Principal components analysis (PCsA):

PCsA is a multivariate data used in studies of variance and numeral classification to examine relationships between different quantitative traits (Narasimhulu *et al.* 2022). The study gave six principal components (PCs) with Eigen value more than one that accounted for 90.027% of the total variation for discriminating the 10- Pearl millet genotypes based on yield components, yield and quality traits (Table 7& Figure 4). Singh *et al.* (2018) that assesse the genetic divergence for 40 genotypes of pearl millet and stated that first six PCs donated 78.29 % of the total variability for thirteen different quantitative traits for pooled data.

All studied characters contributed a positive direction in first component (PC1) except SD (cm) and CF (%). All remaining traits i.e. P. H., L/S ratio, TFY, TDY, CP %, carbohydrates % and ash % are the most important

component accounted for 3.492 of Eigen value and 43.159 of total variability and different traits. The high yielding lines were varied on the basis of these characters.

Table 7. The principal component analysis for measured traits under study of 10- pearl millet genotypes

Traits	PC1	PC2	PC3	PC4	PC5	PC6
P. H. (cm)	0.108	-0.980	0.057	-0.005	0.016	0.010
L/S ratio	0.255	0.124	-0.333	-0.178	-0.146	0.302
SD (cm)	-0.343	0.016	-0.293	0.684	0.453	-0.281
TFY (kg/ plot)	0.359	-0.079	-0.143	0.036	-0.386	0.355
TDY (kg/ plot)	0.148	-0.008	-0.465	-0.402	-0.183	-0.547
CF %	-0.247	0.038	0.298	-0.496	0.563	-0.103
CP %	0.340	0.083	0.589	0.220	-0.491	-0.428
Carbohydrates %	0.162	0.052	-0.016	0.201	0.012	0.360
Ash%	0.357	0.075	0.358	-0.054	0.181	0.285
Eigen value	3.492	1.945	1.263	0.952	0.827	0.645
Proportion %	43.159	17.683	13.711	11.983	10.413	10.005
Cumulative %	43.159	51.936	75.98	82.980	85.193	90.027

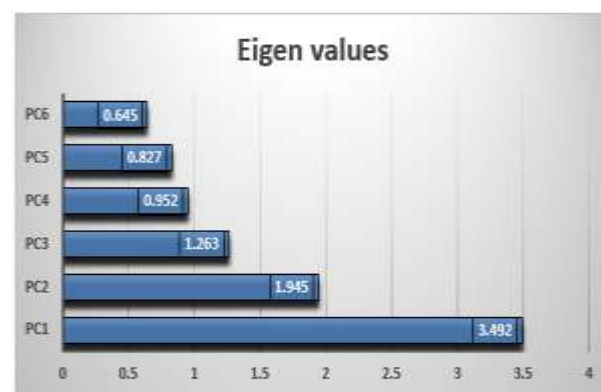


Figure 4. The Eigen values variation for traits under study of 10- pearl millet genotypes

Total fresh yield (TFY) had the greatest contribution followed by ash % in the first PC. Gupta and Khandlwal *et al.* (2022) studied genetic diversity of 31 hybrid pearl millet and the PC1 of total variability was 37.44% for green yield and its associating characters. The PC2 of an Eigen value of 1.945 and a variance contribution rate was 17.683%, plant height, total fresh and dry yields gave negatively but other traits gave positively for variation of PC2. In the third PC accounted for 13.711 % in total variation, crude protein % significant positive contributor while total dry yield is a negative contributor for PC3. Bhanupriya *et al.* (2014) reported that the traits that pregnancy high a positively or a negatively contributed more to the diversity. The PC4, accounting for 11.983 % of total variability and traits like stem diameter, crude protein and carbohydrates contributed in positive way. The PC5 had high loadings for crude fiber, stem diameter and ash % accounting for 10.413 % of the total variability. The sixth PC with Eigen value of 0.645 and variance contribution rate of 10.005% and traits like carbohydrates, total fresh yield, leaf/stem ratio and ash were the variables responsible for variation. These findings were supported by reports of Karunya *et al.* (2021) who evaluated the twenty– five genotypes of pearl millet for 9-phenotypic traits by PC analysis and found the third PC of the nine PCs had greater than one an Eigen values, indicating a 68.71 % of the total variability. Like that, Narasimhulu *et al.* (2022) who stated that, the PC analysis separated the plurality 68- pearl millet germplasm accessions among the yield and yield contributing

traits into the first eight PCs and the PC1 recorded 25.27 % of total variability.

CONCLUSION

The presence of variance is crucial of any genetic character to successful improvement and thus insight into the nature of variation is essential to deduce the genetic prospect of a given set of germplasm. Data appeared a wide significant variation among the studied genotypes for many of the assessed traits. Estimates of genetic parameters like phenotypic and genotypic coefficients, the heritability and the genetic advance revealed greatly significant differences. The dendrogram of cluster analysis divided into two main clusters and the PC analysis detached the plurality genotypes into the first six principal components. Overall, it can be concluded from our results, the selection is good to improve these traits in the genotypes under study and the genotypes G2, G5 and G7 available new promising materials can be used to generate potential breeding material to improve specific trait materials in pearl millet to enhance productivity.

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التوصيف المظهري والاختلاف الجيني لبعض التراكيب الوراثية من الدخن بناءً على تحليل المكونات الرئيسية والتحليل العنقودي

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المخلص

يعد وجود الاختلاف في الأصول الوراثية واستخدامها الفعال أمرًا ضروريًا لتحسين الناجح لأي محصول علفي. خلال موسمي الصيف 2020-2021 بمحطة بحوث الزراعة بسنس. تم زراعة عشرة تراكيب وراثية من الدخن في تصميم قطاعات كاملة العشوائية في ثلاثة مكررات لتحديد التباين الجيني والاختلاف الوراثي والظاهر ودرجة التوريث والتحسين الوراثي ودرجة الارتباط بين الصفات المختلفة بناءً على أداء محصول العلف ومكوناته و صفات الجودة باستخدام التحليل العنقودي وتحليل المكونات الرئيسية (PCA). كشفت نتائج التحليل التجمي عن وجود فروق معنوية كبيرة بين العامين والتراكيب الوراثية، والتفاعل لمعظم الصفات قيد الدراسة، أظهرت الملاحظة ان التراكيب الوراثية G2 و G5 و G7 سجلت أعلى قيم محصول العلف ومكوناته و صفات الجودة، مما يشير إلى أن هذه التراكيب الوراثية واعدة ويمكن التوصية باستخدامها في برامج التربية. لوحظ ان التقديرات العالية لمعامل الاختلاف المظهري والوراثي ودرجة التوريث مرتبطة بالنسبة العالية من التحسين الوراثي لمعظم الصفات، وهذا يشير إلى وجود التباين الجيني وبالتالي فاعلية الانتخاب لهذه الصفات. أظهرت نتائج التحليل العنقودي قدرًا كبيرًا من التباين بين التراكيب الوراثية وقسمت التراكيب الوراثية العشرة إلى 4 مجموعات فرعية. حددت الدراسة ست مكونات رئيسية (PCs) ل Eigen values أكبر من 1.00 والتي تمثل 90.027% من التباين الكلي لتمييز العشرة تراكيب وراثية للدخن بناءً على مكونات المحصول والمحصول وخصائص الجودة. لذلك، يمكن استخدام هذه الصفات في الانتخاب لتحسين المحصول وتحديد الموارد الوراثية الواعدة لبرنامج تربية فعال في الدخن.