# ESTIMATION OF GENETIC VARIABILITY AND DIVERGENCE IN SOME SELECTED LINES OF PEARL MILLET

**Mona M.F. Ghazy; H.O.Sakr and Magda N. Rajab**
**Forage Crops Res. Dept.; Field Crops Res. Inst., Agric. Res. Center. Egypt.**

## ABSTRACT

The objective of this study was to estimate the genetic variability , heritability , genotypic and phenotypic coefficients of variations , genetic advance , range , genotypic and phenotypic variances and to study the genetic divergence by using multivariate analysis for yield and yield components in forty selected lines of pearl millet during 2012 and 2013 summer seasons at Sakha Agriculture Research Station . Analysis of variance manifested highly significant differences among all selected lines for all the studied traits. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). Heritability in broad sense ranged from 11.12% for fresh leaf/ stem ratio to 86.87% for stem diameter. High estimates of bread sense heritability were found in all the studied traits, except dry matter and fresh leaf/stem ratio which, were medium and low, respectably.   The environmental variance ranged from 13.13% for stem diameter to 88.88% for fresh leaf / stem ratio. The results also cleared that the genetic advance ranged from 0.91% for fresh leaf / stem ratio to 24.72% for total fresh forage yield. The results cleared that the ascendant order of the importance of evaluated traits were, the first factor accounted 41.78% (number of tillers, plant height, total dry forage yield and total fresh forage yield) while, the second factor accounted 59.62% (dry matter, stem diameter and fresh leaf /stem ratio) of the multivariate variance.   The forty selected lines were grouped into eight clusters based on dissimilarity coefficients. Thus, the pearl millet breeder would use these selected lines from divergent cluster for hybridization in order to isolate useful recombinants in the segregating generations.

**Keywords:** Multivariate analysis, genetic divergence, genotypic and phenotypic coefficient of variation, genetic advance.

## INTRODUCTION

Pearl millet was originated in Africa and it is commonly grown in the arid and semi-arid regions. It is particularly adapted to nutrient poor soil and low rainfall condition. Pearl millet is one of the efficient crops for these types of regions because of its high utilization of soil moisture and level of heat tolerant than sorghum and pearl millet (Shah *et al.*, 2012). The green fodder of pear millet is more palatable because it does not have HCN content as that of sorghum.

In Egypt, pearl millet is considered an important summer forage crops. Genetic variability for agronomic traits is the key components of breeding program for broadening the gene pool of crops. However, the genetic variability for maize traits is limited in cultivated germplasm (Sumathet al., 2010). Genetic variation among selected lines is of vital importance to breeding programmes that aim to produce improved cultivars for marginal growing environments (Yadav *et al.*, 2001). In these studies, heritability

estimates of quantitative traits play an important role in expressing the reliability of variance value as a selection guideline to plant breeder during the succeeding generations. Heritability along with genetic advancement would be jointly considered an important tool to arrive to reliable conclusion (Johnson *et al.*, 1955). Therefore, it becomes necessary to partition the observed variability, into its heritable and non-heritable components to understand the genetic parameters such as genetic coefficient of variation, heritability and genetic advancement. Earlier studies by Chand *et al.* (2008), Larik *et al.* (2000), Vidya *et al.* (2002) indicated that genetic improvement of crops for quantitative traits requires reliable estimates of genetic variability, heritability and genetic advancement for traits such as grain yield, plant height, stem diameter. The success of any breeding method depends on the availability of genetic diversity in the accessions which would be utilized as parents in the hybridization programs to produce superior hybrids. Therefore, there is a need to evaluate the available genotypes for their genetic diversity. Hierarchical cluster analysis highlights the nature of relationship between any type of samples described by any type of descriptors. This could serve as a basis for selection of parental types which produce superior hybrids (Sathya *et al.*, 2013 and Ogumbayo *et al.*, 2005). The objectives were to: estimate variability, heritability, genetic advance, genotypic and phenotypic coefficient of variation and analyze the genetic diversity among pearl millet genotypes for yield and its components in a set of selected genotypes and popular cultivar in pear millet.

# MATERIALS AND METHODS

The genetic materials for this study were consisted of 40 selected genotypes of pear millet. They were selected from commercial cultivars during the four successive seasons of 2008, 2009, 2010 and 2011. The study was conducted at Sakha Agriculture Research Station during 2012 and 2013 summer seasons. A randomized complete block design was used with three replications. Genotype was grown in one row three m in length. The distance between rows and between hills were 0.60 and 0.30 m, respectively.

All recommended agriculture practices were applied at the optimum levels for maximum productivity. Three cuts were taken offer 50, 90 and 120 days from sowing in both seasons. The data were recorded on total fresh and dry forage yield in kg/plot, plant height in centimeter, stem diameter in centimeter, fresh leaf to stem ratio, number of tillers/plant and dry matter. The agronomic traits were calculated as average over all cuts per season. A combined analysis of variances over the two seasons were carried out according to Snedecor and Cochran (1989) using SPSS computer program (1995). Before combined analysis, homogeneity test of variance was computed by Bartlet's test 1937. Genoptypic and phenotypic ($\sigma^2 g$ and $\sigma^2 p$) variances according to Al-Jibouri *et al.* (1958). The phenotypic and genotypic coefficients of variability (PCV and GCV) were computed according to the method suggested by Burton (1952). Heritability in broad sense estimates ($h^2_b$) and genetic advance ($G_a$) as percent of means were categorized as

suggested by Johnson *et al.* (1955). A multivariate technique was conducted using the principal component analysis according to Hair *et al.* (1987). This analysis was calculated from a matrix based on correlation between the contributed traits for all genotypes. The principal components (PC) associated with all genotypes were expressed as Eigen value and manifested Eigen vector for all the studied traits in each PC axis. The array of communality, the amount of the variance of a variable accounted, by the common factor together, was estimated by the highest correlation coefficient in each array. The dissimilarity coefficients among pear millet genotypes were estimated according to Johnson and Wichern (1988). Hierarchical clustering was then carried out using word's minimum variance methods, which minimize within cluster sum of square across all partitions. Results from principal components analysis and cluster analysis were presented in graphical and dendrogram presentation. These computation were performed using SPSS procedure.

## RESULTS AND DISCUSSION

The combined analysis of variance for all the studied traits are presented in Table (1) years mean squares for all the studied traits were highly significant, except stem diameter and number of tillers /plant. Genotypes mean squares were highly significant for all the studied traits in both years indicating the wide diversity between the parental materials used in the present study. No significant interaction between G x Y was found, this indicates that the genotypes were not affected by years.

**Table 1: Combined analysis of variance over the tow year of 2012 and 2013 for the yield and its component traits.**

| S.O.V | d.f | T.F.F.Y (kg\plot) | S.D (cm) | No.T/ plant | Ph (cm) | Dm % | L./S % | T.D.F.Y (kg\plot) |
|---|---|---|---|---|---|---|---|---|
| Years | 1 | 9.0171** | 0.0584 | 10.317 | 16679.67** | 57.291** | 5.454** | 0.0075** |
| Reps(years) | 4 | 4.7746 | 0.0220 | 1.0652 | 70.8550 | 2.5481 | 61.1175 | 0.0455 |
| Genotypes | 39 | 14.372** | 0.0801** | 3.763** | 154.26** | 0.2699** | 1.950** | 0.2939** |
| Genotypes X Years | 39 | 0.0327 | 0.000663 | 0.2195 | 7.19 | 0.0036 | 0.154 | 0.00104 |
| Error | 156 | 0.573 | 0.002199 | 0.2114 | 12.54 | 0.09612 | 2.391 | 0.01513 |

Total fresh forage yield (TFFY), stem diameter (SD), number of tillers (No. T), plant height (PH), dry matter (DM), fresh leaf/stem ratio (L/S%) and total dry forage yield (TDFY) across three cuts and over two seasons were calculated and presented in Table (2).

**Table 2: The combined mean performances of the yield and its components of all genotypes over the two years of 2012 and 2013.**

| Genotype | TFFY(kg\plot) | SD(cm) | No.T/plant | PH(cm) | Dm% | FL./S % | TDFY(kg\plot) |
|---|---|---|---|---|---|---|---|
| 1 | 10.31 | 1.28 | 7.83 | 139.51 | 13.69 | 40.86 | 1.39 |
| 2 | 11.08 | 1.21 | 9.36 | 136.93 | 13.97 | 41.54 | 1.53 |
| 3 | 8.77 | 1.48 | 8.19 | 127.21 | 13.88 | 42.37 | 1.21 |
| 4 | 10.80 | 1.26 | 8.11 | 138.16 | 13.99 | 42.35 | 1.48 |
| 5 | 11.93 | 1.37 | 8.38 | 137.03 | 14.06 | 40.61 | 1.64 |
| 6 | 12.78 | 1.32 | 9.06 | 142.66 | 13.97 | 40.53 | 1.75 |
| 7 | 10.66 | 1.45 | 9.16 | 137.16 | 13.83 | 40.81 | 1.48 |
| 8 | 11.82 | 1.38 | 8.59 | 129.60 | 13.83 | 41.58 | 1.62 |
| 9 | 11.83 | 1.28 | 9.04 | 134.61 | 14.07 | 42.07 | 1.68 |
| 10 | 11.66 | 1.28 | 7.94 | 143.71 | 13.88 | 41.51 | 1.62 |
| 11 | 11.28 | 1.24 | 9.85 | 132.33 | 13.88 | 41.05 | 1.54 |
| 12 | 11.95 | 1.46 | 7.87 | 132.58 | 13.96 | 42.05 | 1.67 |
| 13 | 11.73 | 1.33 | 8.14 | 135.03 | 14.03 | 42.69 | 1.67 |
| 14 | 11.89 | 1.38 | 9.12 | 129.80 | 14.07 | 42.32 | 1.68 |
| 15 | 12.64 | 1.26 | 8.87 | 141.11 | 14.32 | 41.73 | 1.80 |
| 16 | 13.47 | 1.36 | 9.79 | 138.50 | 14.01 | 41.30 | 1.89 |
| 17 | 10.97 | 1.32 | 8.08 | 132.78 | 14.34 | 41.10 | 1.57 |
| 18 | 13.55 | 1.44 | 9.48 | 144.41 | 14.09 | 41.52 | 1.86 |
| 19 | 11.06 | 1.32 | 8.98 | 136.10 | 14.00 | 40.82 | 1.50 |
| 20 | 11.13 | 1.25 | 8.28 | 133.76 | 14.00 | 41.72 | 1.53 |
| 21 | 9.65 | 1.51 | 6.59 | 135.10 | 14.06 | 42.12 | 1.34 |
| 22 | 10.18 | 1.25 | 7.85 | 131.63 | 14.45 | 41.81 | 1.45 |
| 23 | 9.73 | 1.22 | 7.53 | 132.69 | 14.45 | 41.30 | 1.39 |
| 24 | 12.01 | 1.42 | 8.60 | 139.36 | 14.11 | 41.77 | 1.64 |
| 25 | 12.42 | 1.80 | 7.71 | 138.56 | 14.12 | 41.83 | 1.74 |
| 26 | 15.41 | 1.33 | 9.51 | 138.15 | 14.22 | 40.78 | 2.19 |
| 27 | 11.07 | 1.35 | 8.76 | 132.61 | 14.13 | 41.36 | 1.55 |
| 28 | 11.50 | 1.33 | 8.14 | 136.58 | 14.12 | 41.61 | 1.58 |
| 29 | 13.67 | 1.53 | 9.12 | 142.56 | 14.13 | 42.03 | 1.93 |
| 30 | 15.90 | 1.59 | 9.66 | 142.63 | 14.07 | 41.75 | 2.24 |
| 31 | 9.53 | 1.26 | 8.75 | 130.05 | 14.22 | 42.71 | 1.33 |
| 32 | 14.24 | 1.51 | 8.94 | 139.98 | 14.23 | 41.96 | 2.00 |
| 33 | 10.33 | 1.27 | 7.54 | 143.63 | 14.06 | 42.60 | 1.43 |
| 34 | 10.77 | 1.38 | 7.83 | 149.51 | 14.26 | 41.50 | 1.49 |
| 35 | 11.82 | 1.31 | 8.65 | 135.66 | 14.35 | 41.56 | 1.71 |
| 36 | 10.92 | 1.31 | 7.68 | 142.60 | 14.50 | 42.12 | 1.55 |
| 37 | 10.40 | 1.34 | 9.87 | 135.63 | 14.39 | 42.42 | 1.48 |
| 38 | 9.01 | 1.24 | 7.05 | 129.86 | 14.58 | 41.50 | 1.29 |
| 39 | 11.83 | 1.43 | 7.83 | 136.48 | 14.51 | 41.68 | 1.68 |
| 40 | 10.74 | 1.34 | 7.88 | 128.00 | 14.42 | 42.06 | 1.55 |
| LSD $_{0.05}$ | 1.02 | 0.06 | 0.62 | 4.78 | 1.32 | 2.09 | 0.06 |
| LSD $_{0.01}$ | 1.45 | 0.09 | 0.89 | 6.79 | 1.88 | 2.97 | 0.08 |

The results indicated that for total fresh forage yield the selected genotypes No.30 had the highest mean value and the genotypes. No. 3 had the lowest value with   mean values of 15.90 kg/plot and 8.77 kg/plot,

respectively. The highest mean for stem diameter was the selected genotype No.25 with the mean value of 1.80 cm and the lowest mean value was 1.21 cm of the selected genotype No. 23.

For number of tillers, the results cleared that the highest mean value was 9.87 for the selected genotype number 11 but, the lowest mean value was for the selected genotype number 38 with the mean value of 6.59. Also, the results illustrated that for plant height, the selected genotype No.34 had the highest mean value and the selected genotype No. 3 had the lowest mean value of 149.51 and 127.21 cm, respectively. For dry matter, the results cleared that, the highest mean value was 14.59 for the selected genotype Number 38 and the lowest mean value was 13.69 for the selected genotype Number 1.

For fresh leaf/stem ratio, the genotype Number 31 had the highest mean value while the lowest mean value was for the selected genotype Number 6 by 42.72 and 40.53, respectively. For total dry forage yield, the results indicated that the selected genotype Number 30 had the highest mean value 2.24 kg per plot but the selected genotype number 3 had the lowest mean value for this trait with the mean value 1.21 kg per plot.

Range, grand mean (X), , genotypic, phenotypic variance ($\sigma^2$g and $\sigma^2$P), genotypic and phenotypic coefficient of variations (GCV and PCV), heritability in broad sense ($h^2_b$), genetic advance as percentage of mean (G.a%) and environmental variation (En.V) over the two years for the studied traits were calculated and are presented in Table 3. Total fresh forage yield ranged from 8.77 kg/plot (genotype No. 3) to 15.90 kg/plot (genotype No. 30) with an a average value of 11.17 kg/plot; Stem diameter ranged from 1.21 cm for the genotype No. 23 to 1.80 cm for genotypes No. 25 with an average value 1.36 cm. For the number of tillers ranged from 6.59 for genotype No. 38 to 9.87 for the selected genotype No. 11 with an average value 8.49 tillers.

**Table 3: Range, grand mean (X), genotypic, phenotypic variance ($\sigma^2$g and $\sigma^2$p), genotypic and phenotypic coefficient of variations (GCV and PCV), heritability in broad sense ($h^2_{b.s}$), genetic advance (Ga%) and environmental variation (En.V.) of the yield and yield components of all genotypes of pearl millet over two years 2012 , 2013 .**

| traits | Range | X̄ | $\sigma^2$e | $\sigma^2$g | $\sigma^2$p | G.C.V. | P.C.V. | $H^2_{b.s}$ | Ga% | En.V. |
|---|---|---|---|---|---|---|---|---|---|---|
| TFFY | 8.77 : 15.90 | 11.17 | 0.57 | 2.39 | 2.96 | 13.36 | 14.88 | 80.66 | 24.72 | 19.34 |
| SD | 1.21 : 1.80 | 1.36 | 0.01 | 0.01 | 0.02 | 8.46 | 9.08 | 86.87 | 16.24 | 13.13 |
| No.T. | 6.59 : 9.87 | 8.49 | 0.21 | 0.59 | 0.805 | 9.05 | 10.57 | 73.39 | 15.97 | 26.61 |
| Ph. | 127.21 : 149.51 | 136.61 | 12.54 | 24.51 | 37.05 | 3.62 | 4.46 | 66.15 | 6.07 | 33.85 |
| DM. | 13.69 : 14.59 | 14.13 | 0.10 | 0.05 | 0.141 | 1.49 | 2.65 | 31.59 | 17.26 | 68.41 |
| L./S% | 40.53 : 42.72 | 41.68 | 2.39 | 0.30 | 2.69 | 1.31 | 3.49 | 11.12 | 0.91 | 88.88 |
| TDFY | 1.21: 2.24 | 1.62 | 0.02 | 0.05 | 0.07 | 13.64 | 15.61 | 76.34 | 24.54 | 23.66 |

For plant height, the values ranged from 127.21 cm for the genotype No. 3 to 149.51 cm for genotype No. 34 with an average value of 136.61 cm; dry matter ranged from 13.70 for genotype No.1 to 14.59 for genotype No.38 with a mean value of 14.13. Fresh leaf/stem ratio ranged from 40.53 for genotype

No. 6 to 42.72 for genotype No. 31 with an average value of 41.68. Also, total dry forage yield ranged from 1.21 kg/plot for genotype No. 3 to 2.24 kg/plot for genotype No. 30 with an average value of 1.62 kg/plot.

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). Considerable consistency of values was observed between PCV and GCV percentage for all the studied traits. The differences among GCV and PCV were narrow suggesting the presence of effects for environments appeared in the genotypes x year's interaction. These results are in agreement with many authors among them: Sumathi *et al.* (2010), Yadav *et al.* (2001), Lakshmana *et al.* (2009), Govindaraj *et al.* (2011), Subi and Idris (2013) and Salih *et al.* (2014).

The heritability in broad sense ranged from 11.12% for fresh leaf/stem ratio (L/S) to 86.87% for stem diameter. High heritability indicated that the traits were less affected by environments and largely influenced by the additive gene action or/and non-additive gene action it present. The improvement of these traits would be achieved through the phenotypic selection if the magnitude of additive effects were more important. Similar results were obtain of by: Johnson *et al.* (1955), and Subi and Idris. (2013). Yadav *et al.* (2001), Lakshmana *et al.* (2003), Galeta *et al.* (2005),Ganpathy *et al.* (2011).

The estimates of expected genetic advance (Ga%) indicated that the selection among these genotype, would be increased by 24.72% for total fresh forage yield (TFFY/P); 16.24% for stem diameter (SD); 15.95% for number of tillers; 6.07% for plant height; 17.26% for dry matter; 0.91% for fresh leaf/stem ratio (FL/S%) and 24.54% for total dry forage yield per plant (TDFY). These results were very close to those obtained indicated by Yadav *et al.* (2001), Vetriventhan and Nirmalakumar (2007),Lakshmana *et al.* (2009), Sumathi *et al.* (2010), Govindaraj *et al.* (2011) and Salih *et al.* (2014).

**Principal component analysis (PCA):**

Principle component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). This analysis seemed to elucidate patterns of variation in agronomic attributes which are of economic importance and obtain initial factor solution using eigen values. These values could measure the explained variance associated with each vector, trait.Two principal components of (PCs) whose eigen values were greater than one were significant and accounted for about 59.627% of total variation of all traits as presented in Table 4.

The first PC explained about 41.779% of total variation with highest eigen value of 2.925 and the second PC explained 59.627% with eigen value of 1.249 and these two PCs contributed more to the total variation.

According to Chahal and Gosal, 2002, traits with largest absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero.

In this study, differentiation of the association into different cluster was observed because of the cumulative effect of a large number of traits rather than the contribution of specific few traits. Traits having relatively higher value in the first principal component (PC1) like total fresh forage yield (TFFY),

number of tillers (No.T), plant height (Ph) and total dry forage yield (TDFY) showed more contribution to the total variation and they also differentiated the cluster. The second principal component was principally affected by stem diameter (SD), dry matter (Dm) and fresh leaf/stem ratio as seen in Table 4 and Figure 1.The present study confirmed that pear millet genotypes showed wide amount of variations for the studied traits and suggest ample opportunities for its genetic improvement.  . These traits would be used to screen different genotypes in breeding programs. In this was in agreement with these of  Shah *et al.* (2012), Ogumbayo *et al.* (2005) and Sathya *et al.* (2013)  presented similar results.

**Table 4: Principle component analysis of all traits associated with 40 pearl millet genotypes.**

| Traits | PC1 | PC2 |
|---|---|---|
| Total fresh forage yield | 0.962 | 0.119 |
| Stem diameter | 0.448 | 0.565 |
| Number of tillers | 0.664 | -0.381 |
| Plant height | 0.665 | 0.108 |
| Dry matter | -0.245 | 0.517 |
| Fresh leaf stem ratio | -0.320 | 0.678 |
| Total dry forage yield | 0.936 | 0.180 |
| Eigen value | 2.925 | 1.249 |
| Proportion | 41.779 | 17.847 |
| Cumulative% | 41.779 | 59.627 |

Loading Plot of F.F.Y-D.F.Y
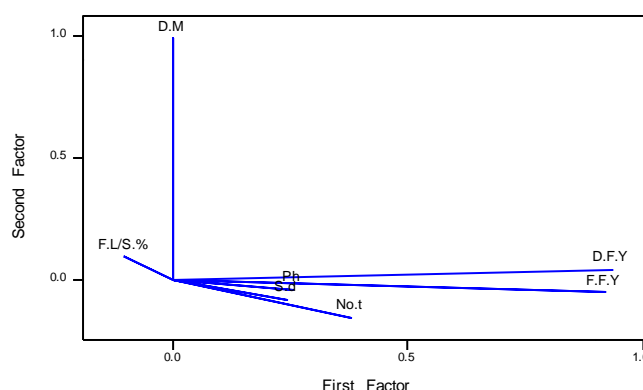


**Fig.1 :Loading of seven traits contributed in yield and yield components**

**Cluster analysis:**

The forty selected genotypes of pearl millet evaluated in this study were grouped in to eight clusters by using hierarchical cluster analysis on basis of dissimilarity among the genotypes and the contribution of the evaluated traits as seen in Table 5 and Figure 2. Table 5 cleared the Euclidean distances among the forty selected genotypes of pear millet while Figure 2 showed the shape of clustering.
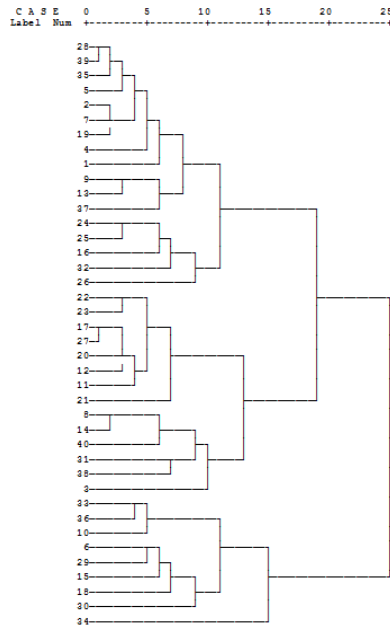
**Fig. 2:Dendrogram showing the grouping of forty pearl millet selected genotypes into different cluster**

Figure 2 cleared that the cluster No. 1 is consisted of 7 genotypes i.e. 1, 2, 4, 5, 7, 24 and genotypes No. 25; cluster No. 2 was the largest and consists of 9 selected genotypes i.e. genotypes No. 9, 13, 19, 20, 21, 28, 35, 37 and 39, while, the cluster No.3 contain 4 genotypes i.e. No. 3, 31, 38 and 40.

Three selected genotypes were in cluster No.4 and, i.e. No. 10, 33 and 36 in the cluster No. 4, but the cluster No.5 is consisting of 5 selected genotypes, which were No. 6, 15, 18, 29 and 30. The cluster No.6 contained only one genotype and it is No. 34.

The cluster No. 7 consisted of three selected genotypes of pear miller i.e. No. 16, 26, and No. 32. Finally, the cluster No. 8 contained seven selected genotypes of pear millet which were No. 8, 11, 12, 14, 17, 22, 23 and 27.

similer results were obtained by other authors among them Ogumbyo *et al.* (2005); Shah *et al.* (2012), and Sathya *et al.* (2013).

The inter cluster distances among eight cluster calculated and presented in Table 6. The results cleared that, the highest distance was between cluster No. 6 and cluster No. 3 with the mean distance of 20.784. Also, the distance between cluster No. 6 and No. 2, cluster No. 4 and No. 3 and cluster No. 8 and cluster No. 5 were 14.101, 14.609 and 17.779, respectively. On the other hand, the lowest, genetic distance was founed between cluster No. 2 and cluster No. 1 with the mean distance value of 2.716.

**Table 6 inter cluster distances among eight cluster**

| cluster | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
|---|---|---|---|---|---|---|---|
| 1 | 2.716 | 9.548 | 5.319 | 5.237 | 11.446 | 3.336 | 6.361 |
| 2 | | 6.896 | 7.910 | 7.720 | 14.101 | 4.828 | 3.699 |
| 3 | | | 14.609 | 14.599 | 20.784 | 11.347 | 3.468 |
| 4 | | | | 3.273 | 6.236 | 5.916 | 11.596 |
| 5 | | | | | 7.591 | 3.873 | 11.265 |
| 6 | | | | | | 11.365 | 17.779 |
| 7 | | | | | | | 7.910 |

# REFERENCES

Al-Jiouri, H.A.; P.a. Millerand and H.F. Robinson (1958). Genotypic and environmental variance and covariance's in an upland cotton cross of interspecific origin. Agron. J. 50: 633-636.

Barlett, M.S. (1937). Properties of sufficient and statistical tests. Proceedings of the Royal Statistical Society, Series A 160, 268-282.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. 6th Int. Grassland Congr., 1: 277-283.

Chahal, G. S. and S. S. Gosal (2002) Principal and procedures of plant breeding. Biot. Convention approaches, New Delhi.

Chand, N.; S.R. Vishwaama; O.P. Verma and K. Manoj (2008). Worth of genetic parameters to sort out new elite barley lines over heterogenous environments. Barley gen. Newsletti, 38: 10-13.

Galeta, N.; H.Mohamed and H. Zelleke (2005). Genetic variability and genetic advance in sorghum (*Sorghum bicolor* (L.) Moench) germplasm. Crop Res. 30: 439-445.

Ganapathy, S.; A. Nirmalakumari and A.R. Muthiah (2011). Gentic variability and interrelationship analysis for economic traits in finger millet germplasm. World Journal of Agricultural Science 7(2): 185-188.

Govindaraj, M.; P. Shanmugsund Aram and A.R. Muthiah (2010). Estimates of genetic parameters for yield and yield attributes in elite lines and popular cultivars of India's pearl millet. Afr. J. Agric. Res.., 5: 3060-3064.

Govindaraj, M.S.; B. Selvi; S. Rajarathinam and P. Sumathi (2011). 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. 11: 4758-4771.

Hair, J.F.; Jr. R.E. Anderson and R.L. Tatham (1987). Multivariate data analysis with reading Mac Millan Pub. Co. New York.

Johanson, H.W.; H.F. Robinson and R.E. Comstock (1955). Estimates of genetic and environmental variability in soybeans. Agron. J. 47: 314-318.

Johnson, R.A. and D.W. Wichern (1988). Applied multivariate statistical analysis 2nd ed. Prentice Hall, Englewood Cliffs, NJ, USA.

Lakshmana, D.; B.D.; Biradan and R.L. Ravikumar (2009). Genetic variability studies for quantitative traits in a pool of restorers and maintainers lines of pearl millet (*Pennisetum glaucum* (L.). Karanataka J. Agric. Sci. 2009; 22(4): 881-882.

Lakshmana, D.; P. Surendra and R. Gurumuthy (2003). Combining ability studies in pear millet. Res. Crops 4: 358-362.

Larik, A. S., S. I. Malik, A. A. Sakar and M. A. Naz. (2000). Assessment of heritability and genetic advance for yield components in G.hirsutum Sci. Ent. Khyber,13:39-44

Ogumbayo, A.S.; K.D.G. Oje; GR. Guei; O. Oyelakin and K.A. Sanni, (2005). Phylogenetic diversity and relationship among 40 rice accessions using morphological and RAPD techniques. African J. Biotechnol. 4(11): 1234-1244.

Salih, A.I.S.; M.I. Ismail; E. Abdalla; K.A. Osman and A.M. Ali (2014). Genetic variation among pearl millet genotypes for yield and its components in semi-arid zone Sudan. Inter. J. of Agric. and Crop Sci. 7(11): 822-826.

Sathya, M.; N. K. Vimodana and P. Sumathi (2013). Hierarchical clustering of pearl millet (*Pennisetum glaucum* (L.) R.Br.) inbreds for morpho-physiological traits. Int. J. Curr. Microbiol. Appl. Sci. 2(12): 647-652.

Shah, A.H.; H. Rahman; S.M.A. Shah; S. Rahman and M. Noor (2012). Characerization of pear millet germplasm for various morphological and fodder yield parameters. Pakistan. J. Bot. 44: 273-279.

Sharma J.R.(1998) Statistical and biometrical techniques in plant breeding. New Age. Int. Ltd, Puna, Inddia

Snedecor, G.W. and W.G. Cochran (1989). Statistical methods, 8th ed. Iowa State Univ. Press, Iowa, USA.

SPSS (1995). SPSS computer user's guide, USA.

Subi, MIM. and A.E. Idris (2013). Genetic variability, heritability and genetic advance in pearl millet (*Penisetum glaucum* (L.) R.B.D. Genotypes. British Biotechnology Journal 3(1): 564-65.

Sumathi, P.; M. Sumamth and P. Vearabadhiram (2010) Genetic variability for different biometrical traits in pear millet genotypes (*Pennisotum glucum* L.R.Br.). Electronic Journal of Plant Breeding, 1(4): 347-440.

Vetriventhan, M. and A. Nirmalakumar (2007). Studies on variability parameters in pearl millet (*Pennisetum glaucum* (L.) R.Br.). Madras Agric. J. 94: 118-120.

Vidya, C., S. K. Oommen and K. Vijayaraghava (2002). Genetic variability and heritability of yield and related character in yard. Long bean .J. Trop. Agric., 40:11-13.

Yadav, O.P.; R.E. Weltzien nd D.C. Bhandari (2001). Genetic variation and trait relationship with pearl millet landraces from Rajasthan. Indian J. Gen. Plant Breeding, 61(4): 322-326.

## تقدير الاختلافات الوراثية والتباعد الوراثي لبعض سلالات الدخن المنتخبة

### مني محمد فتحي غازي ، حسام الدين عثمان صقر و ماجدة نادي رجب
### قسم بحوث محاصيل العلف – مركز البحوث الزراعية – مصر

تهدف هذه الدراسة الي تقدير الاختلافات الوراثية و معامل التوريث بالمدي الواسع ومعامل الاختلاف الكلي والوراثي ومقدار التقدم الناتج عن الانتخاب والتباين الكلى والوراثي والتباعد الوراثي باستخدام التحليل العاملي لصفات المحصول ومكوناته في ٤٠ سلالة منتخبة من الدخن في الموسمين الزراعيين ٢٠١٢ و ٢٠١٣ بمحطة البحوث الزراعية بسخا . اظهرت قياسات تحليل التباين وجود اختلافات عالية المعنوية بين كل التراكيب الوراثية الداخلة في الدراسة كما اظهرت النتائج ايضا ان معامل الاختلاف الظاهرى كان اعلي من معامل الاختلاف الوراثي لكل الصفات الموجودة تحت الدراسة . اظهرت قياسات معامل التوريث بالمدي الواسع قيما مرتفعة لكل الصفات الموجودة تحت الدراسة فيما عدا صفتي المادة الجافة ونسبة الورق للسيقان اخضر وتراوحت قيم معامل التوريث من ١١.١٢% لنسبة الورق للسيقان اخضر الي ٨٦.٨٧% لصفة قطر الساق . كان مقدار التحسين الناتج عن الانتخاب يتراوح من ٠.٩١% لصفة نسبة الورق للسيقان اخضر الي ٢٤.٧٢% للمحصول الاخضر . اظهرت ايضا النتائج الخاصة بالتحليل العاملي ان صفات المحصول الاخضر وعدد الافرع وطول النبات والمحصول الجاف كانت في المحور الاول بمقدار ٤١.٧٨% من اجمالي التباين في حين ان صفات نسبة الورق للسيقان اخضر والمادة الجافة وقطر الساق كانت ممثلة بالمحور الثاني بنسبة ٥٩.٦٢% من اجمالي التباين . ايضا عن طريق تحليل التباعد الوراثي تم تقسيم المنتخبات الاربعون في الدخن الي ٨ مجاميع وراثية كبيرة ومن خلال هذا التقسيم فانه يمكن لمربي الدخن من اختيار السلالات في المجاميع المتباعدة وادخالها في برامج التربية والتهجين وذلك لعزل تراكيب وراثية جيدة ومفيدة في الاجيال الانعزالية وذلك لتحسين الصفات تحت الدراسة والحصول علي هجن وسلالات متفوقة محصوليا .

**Table 5 Euclidean distances among the 40 pearl millet genotypes over two years 2012 and 2013**

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 000 | 1010 | 197 | 161 | 608 | 094 | 740 | 251 | 696 | 465 | 472 | 263 | 723 | 452 | 292 | 439 | 790 | 117 | 335 | 368 | 562 | 484 | 274 | 277 | 462 | 436 | 136 | 625 | 752 | 719 | 447 | 707 | 1269 | 168 | 597 | 184 | 774 | 187 | 909 | 11615 |
| 2 | | 000 | 1115 | 1047 | 1610 | 1030 | 400 | 808 | 1678 | 609 | 627 | 837 | 419 | 1448 | 1240 | 614 | 1793 | 934 | 701 | 809 | 473 | 574 | 1261 | 1197 | 1300 | 600 | 979 | 1616 | 1709 | 304 | 1394 | 1650 | 2241 | 906 | 1556 | 875 | 311 | 982 | 227 | 9087 |
| 3 | | | 000 | 240 | 534 | 214 | 867 | 383 | 568 | 625 | 573 | 330 | 850 | 364 | 337 | 555 | 703 | 274 | 446 | 363 | 661 | 572 | 188 | 189 | 513 | 569 | 190 | 538 | 703 | 826 | 404 | 552 | 1139 | 290 | 449 | 315 | 862 | 219 | 1019 | 2388 |
| 4 | | | | 000 | 575 | 153 | 749 | 290 | 677 | 500 | 471 | 291 | 747 | 434 | 266 | 441 | 771 | 143 | 354 | 381 | 584 | 500 | 263 | 219 | 388 | 457 | 121 | 604 | 711 | 769 | 405 | 713 | 1259 | 171 | 592 | 316 | 792 | 140 | 924 | 10187 |
| 5 | | | | | 000 | 591 | 1315 | 825 | 215 | 1050 | 1031 | 807 | 1303 | 201 | 436 | 1013 | 221 | 680 | 917 | 872 | 1149 | 1059 | 365 | 455 | 528 | 1024 | 639 | 178 | 346 | 1323 | 340 | 369 | 732 | 716 | 288 | 773 | 1355 | 651 | 1495 | 9244 |
| 6 | | | | | | 000 | 771 | 310 | 678 | 494 | 510 | 323 | 763 | 456 | 324 | 457 | 786 | 118 | 367 | 370 | 584 | 492 | 283 | 291 | 493 | 463 | 169 | 632 | 769 | 748 | 474 | 691 | 1245 | 218 | 583 | 243 | 785 | 221 | 936 | 14946 |
| 7 | | | | | | | 000 | 506 | 1413 | 309 | 310 | 556 | 095 | 1156 | 913 | 340 | 1494 | 659 | 424 | 627 | 279 | 395 | 977 | 904 | 937 | 313 | 700 | 1312 | 1371 | 264 | 1068 | 1418 | 1996 | 608 | 1308 | 640 | 332 | 695 | 220 | 9364 |
| 8 | | | | | | | | 000 | 919 | 270 | 237 | 118 | 483 | 657 | 436 | 246 | 998 | 209 | 139 | 333 | 365 | 334 | 479 | 425 | 525 | 228 | 223 | 817 | 904 | 518 | 589 | 927 | 1500 | 126 | 816 | 201 | 593 | 230 | 682 | 2197 |
| 9 | | | | | | | | | 000 | 1157 | 1116 | 877 | 1400 | 298 | 584 | 1098 | 257 | 775 | 997 | 898 | 1220 | 1122 | 443 | 525 | 697 | 1115 | 715 | 270 | 478 | 1392 | 471 | 177 | 588 | 810 | 163 | 848 | 1415 | 727 | 1577 | 6817 |
| 10 | | | | | | | | | | 000 | 235 | 363 | 299 | 899 | 657 | 191 | 1233 | 389 | 224 | 471 | 256 | 288 | 723 | 677 | 719 | 122 | 465 | 1060 | 1134 | 352 | 833 | 1167 | 1733 | 366 | 1058 | 372 | 444 | 474 | 492 | 15766 |
| 11 | | | | | | | | | | | 000 | 256 | 306 | 864 | 646 | 147 | 1207 | 400 | 157 | 367 | 211 | 246 | 684 | 603 | 691 | 146 | 407 | 1022 | 1097 | 370 | 783 | 1119 | 1699 | 326 | 1009 | 401 | 419 | 396 | 476 | 4922 |
| 12 | | | | | | | | | | | | 000 | 534 | 628 | 445 | 288 | 973 | 242 | 172 | 268 | 388 | 347 | 447 | 377 | 541 | 291 | 191 | 788 | 888 | 549 | 567 | 874 | 1458 | 144 | 766 | 232 | 609 | 187 | 714 | 4762 |
| 13 | | | | | | | | | | | | | 000 | 1137 | 893 | 352 | 1474 | 653 | 418 | 630 | 289 | 411 | 960 | 892 | 922 | 311 | 690 | 1290 | 1348 | 246 | 1046 | 1401 | 1981 | 595 | 1293 | 608 | 369 | 685 | 251 | 7142 |
| 14 | | | | | | | | | | | | | | 000 | 295 | 857 | 350 | 536 | 754 | 713 | 986 | 903 | 191 | 287 | 425 | 866 | 475 | 185 | 374 | 1155 | 201 | 378 | 868 | 552 | 262 | 606 | 1198 | 483 | 1330 | 2506 |
| 15 | | | | | | | | | | | | | | | 000 | 650 | 593 | 355 | 552 | 612 | 790 | 730 | 215 | 244 | 209 | 645 | 324 | 420 | 483 | 951 | 200 | 657 | 1153 | 350 | 537 | 439 | 1013 | 332 | 1106 | 13300 |
| 16 | | | | | | | | | | | | | | | | 000 | 1202 | 347 | 124 | 324 | 158 | 139 | 673 | 605 | 716 | 078 | 388 | 1026 | 1118 | 355 | 802 | 1099 | 1675 | 310 | 988 | 366 | 370 | 386 | 489 | 11055 |
| 17 | | | | | | | | | | | | | | | | | 000 | 874 | 1100 | 1054 | 1334 | 1250 | 537 | 624 | 659 | 1209 | 822 | 196 | 300 | 1500 | 455 | 606 | 897 | 377 | 941 | 1546 | 830 | 1675 | 4885 |
| 18 | | | | | | | | | | | | | | | | | | 000 | 260 | 325 | 482 | 399 | 356 | 330 | 489 | 353 | 133 | 710 | 825 | 654 | 517 | 790 | 1349 | 125 | 678 | 205 | 690 | 176 | 829 | 16751 |
| 19 | | | | | | | | | | | | | | | | | | | 000 | 266 | 242 | 202 | 568 | 504 | 636 | 131 | 285 | 922 | 1019 | 421 | 701 | 996 | 1577 | 210 | 888 | 268 | 465 | 289 | 582 | 8286 |
| 20 | | | | | | | | | | | | | | | | | | | | 000 | 377 | 275 | 529 | 462 | 733 | 367 | 290 | 887 | 1031 | 553 | 714 | 863 | 1453 | 313 | 770 | 343 | 536 | 296 | 731 | 5823 |
| 21 | | | | | | | | | | | | | | | | | | | | | 000 | 131 | 800 | 733 | 862 | 171 | 515 | 1157 | 1257 | 215 | 937 | 1204 | 1790 | 445 | 1100 | 453 | 229 | 513 | 369 | 7311 |
| 22 | | | | | | | | | | | | | | | | | | | | | | 000 | 716 | 653 | 818 | 186 | 434 | 1079 | 1194 | 326 | 873 | 1103 | 1686 | 382 | 1001 | 397 | 297 | 437 | 489 | 3685 |
| 23 | | | | | | | | | | | | | | | | | | | | | | | 000 | 133 | 391 | 683 | 288 | 367 | 523 | 970 | 238 | 477 | 1026 | 372 | 357 | 433 | 1010 | 302 | 1147 | 4887 |
| 24 | | | | | | | | | | | | | | | | | | | | | | | | 000 | 373 | 623 | 230 | 444 | 572 | 913 | 264 | 556 | 1109 | 317 | 436 | 426 | 942 | 225 | 1072 | 11470 |
| 25 | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 713 | 455 | 495 | 462 | 1026 | 255 | 798 | 1244 | 455 | 677 | 591 | 1083 | 443 | 11139 | 10722 |
| 26 | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 404 | 1032 | 1119 | 330 | 805 | 1117 | 1693 | 316 | 1008 | 346 | 387 | 408 | 478 | 111386 |
| 27 | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 647 | 767 | 694 | 447 | 724 | 1297 | 112 | 610 | 241 | 727 | 062 | 863 | 4776 |
| 28 | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 234 | 1322 | 266 | 392 | 768 | 719 | 316 | 774 | 1372 | 652 | 1492 | 8634 |
| 29 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 1420 | 323 | 616 | 883 | 817 | 545 | 898 | 1479 | 764 | 1564 | 14921 |
| 30 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 1104 | 1366 | 1957 | 619 | 1269 | 577 | 218 | 699 | 263 | 15640 |
| 31 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 560 | 1024 | 498 | 446 | 592 | 1157 | 442 | 1254 | 2634 |
| 32 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 602 | 825 | 136 | 834 | 1389 | 739 | 1565 | 12535 |
| 33 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 1392 | 696 | 1408 | 1975 | 1309 | 2153 | 15652 |
| 34 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 708 | 208 | 666 | 118 | 780 | 21528 |
| 35 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 733 | 1291 | 621 | 1460 | 7801 |
| 36 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 663 | 275 | 790 | 14603 |
| 37 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 725 | 276 | 7902 |
| 38 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 856 | 2760 |
| 39 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 000 | 8561 |
| 40 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 0000 |