







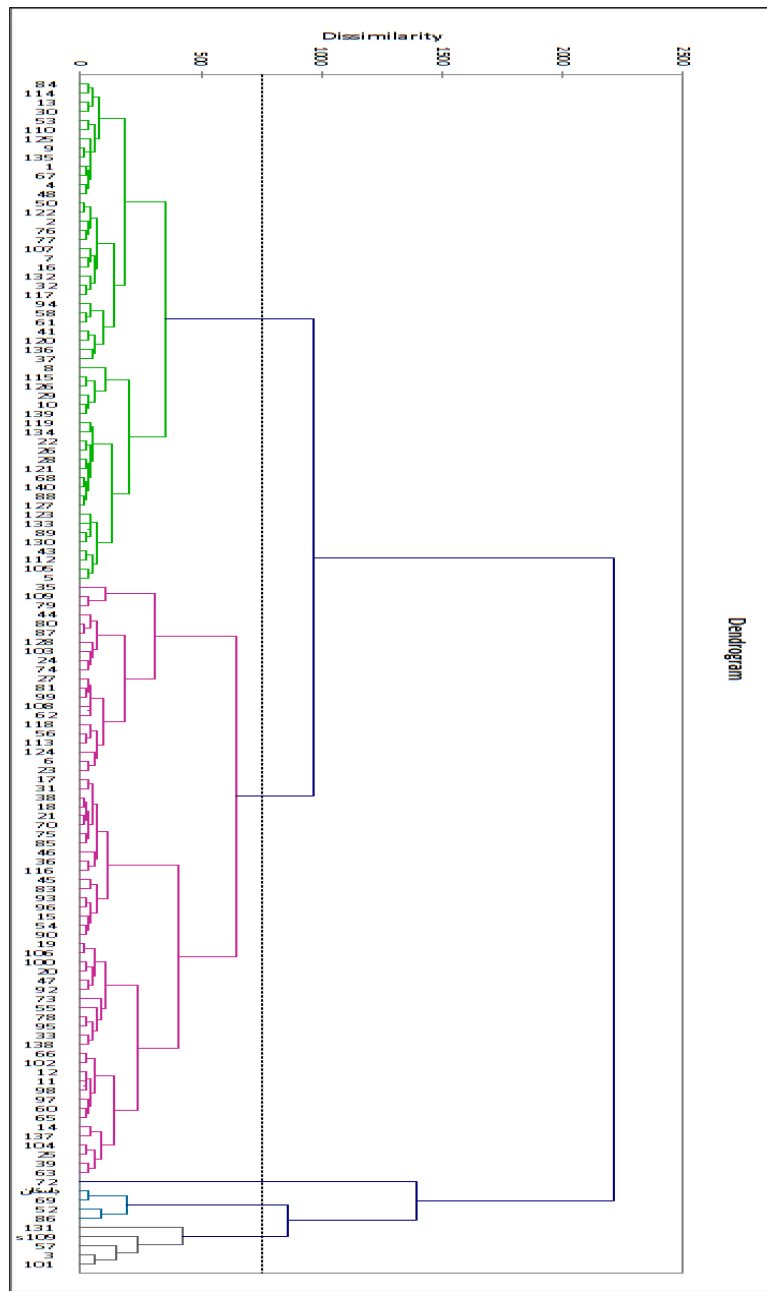






In order to cluster the genotypes under question, cluster analysis was used through UPGMA applying a Euclidean distance matrix. The tree diagram obtained from cluster analysis (**Figure 1**) shows five genotype groups containing 65, 55, 4, 5 and 1 genotypes. The genotypes in group 1 were almost average in most of their traits. Comparison of the characteristics of the genotypes of these groups showed that the mean of the most of the traits related to group 2 genotypes was lower than the total mean and the mean of the traits related to group 3 was higher than that of the total. The genotypes of the group 3 have a great potential regarding their grain yield, biological yield and height. The Bastan

cultivar with high grain and biological yields also belong this group. This is while the genotypes belonging to this group are somehow weak regarding these traits. Therefore, if programs are about to improve grain and biological yields, selecting from group 3 may be a proper choice. Group 4 genotypes are very close to those of group 3 considering most of their traits and had the highest rates regarding 1000-seed weight and harvest index traits. Group 5 contained only 1 genotype, which had a high rate regarding most of the traits. It was reported that cluster analysis using Ward method put the different barley genotypes in 4 groups at normal conditions and 3 at drought stress.



**Figure 1.** Cluster analysis in foxtail millet genotypes with using UPGMA method.

## CONCLUSION

The results of the cluster analysis showed that there is a high genetic diversity in the germplasm under study. Based on the clustering and the estimated means of the traits for the genotypes in each cluster, proper parents can be selected in the improvement programs to carry out purposeful crossings. Since there is closer affinity between the genotypes of these clusters compared to other clusters, crossings between clusters which have more differences can create a higher genetic diversity and heterosis.

To put everything in a nutshell, the present study showed that there was a sufficient diversity in the germplasm considering all the traits investigated. According to the results of the stepwise regression model for grain yield as a dependent variable in Foxtail millet genotypes, the number of grains per panicle, number of panicles, 1000-seed weight, height and number of tillers as indexing traits in selecting genotypes had the highest efficiency in selecting genotypes. Also, the present study revealed genotypes (S27 and S7) that had a higher rate of yield compared to the only Iranian cultivar, namely Bastan. These genotypes can be used in breeding and improving studies to produce superior cultivars.

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