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Classification of Phalaris aquatica Genotypes based on Morphological Traits

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Abstract: *Despite the importance of forage plants in animal husbandry, not much attention has been paid to the category of breeding and introduction of suitable forage plants in comparison with other crops at Iran. Therefore, the main objective of this study was to investigate Phalaris aquatica as a forage species in order to identify the desired genotypes for use in breeding projects. For this purpose, a study was implemented using 26 selected Ph. aquatica genotypes in a randomized complete block design with three replications in the research field of the Agricultural Biotechnology Research Institute of northwest and west region of the country in Tabriz at 2019-2020. The Ph. aquatica genotypes were examined in terms of morphological traits, seed and forage yield. The results of analysis of variance showed the existence of genetic diversity among selected genotypes. Cluster analysis classified the studied genotypes into two clusters. Considering traits such as yield and yield components, genotypes in the third sub-cluster can be a good choice for cultivation. Also, based on results of genetic distances study of the Ph. aquatica genotypes, the maximum genetic distance was obtained between the third sub-cluster and the fifth sub-cluster, which, if necessary, the genotypes of these two sub-clusters can be used in breeding programs in order to exploit their desirable genes. In the principal components analysis, four components were identified, which in total explained 84.3% of the total variance. In the first component, traits such as dry forage yield, crown diameter and canopy diameter, in the second component, only the leaf length and in the third component, traits such as number of days to flowering and number of days to pollination had the highest coefficients.*

Keywords: *Cluster analysis, Forage yield, Principal components analysis*

1. Introduction

Phalaris aquatica L. (Poaceae) is a perennial grass native to the Mediterranean and northwest Africa [1]. *Ph. aquatica* passes summer drought as buds at the base of reproductive tillers attached to the deep root system. *Ph. aquatica* is the most widespread perennial grass grown in southeastern Australia's temperate regions, combining high productivity and drought resistance to provide persistent pastures that can maintain high rates, especially for sheep and beef cattle [2].

Evaluation of genetic variation based on agronomic and morphological traits can be useful for organizing germplasm, parents' selection for hybridization, and producing segregating populations. With

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the ascending interest in using *P. aquatica* as forage, knowledge on the breeding behavior of germplasm is necessary. This study, assayed twenty-six Iranian *P. aquatica* genotypes.

2. Materials and Methods

The twenty-six *P. aquatica* genotypes were selected from a large replicated nursery established in 2019, mainly consisting of natural ecotypes of *P. aquatica* from broad geographical areas of Iran. The genotypes were planted in the field, with 60-cm spacing within and between the rows, according to a randomized complete block design with four replications. Eleven agro-morphological characteristics were measured (number of days to flowering, number of days to pollination, plant height, spike length, grain yield, number of stems, dry forage yield, crown diameter, canopy diameter, flag leaf length, flag leaf width). The experiment was conducted on research farm of the Agricultural Biotechnology Research Institute of northwest and west region of the country.

Analysis of variance and mean comparisons with Duncan's multiple range test were performed. Pearson correlation coefficients were computed. Cluster analysis by Euclidean distance coefficient and Ward's algorithm were used for grouping twenty-six Iranian *P. aquatica* genotypes. Principal components analysis (PCA) is used to confirm cluster analysis results. Statistical analysis was done by SPSS and NTSYS software's.

3. Results and Discussion

The results of analysis of variance showed the existence of genetic diversity among selected genotypes. Some genotypes with high production capacity can be used in breeding programs [3]. However, the studied genotypes will deliver valuable germplasm to employ in *P. aquatica* breeding programs for forage cultivar production [4]. This progress is essential in introducing these selected genotypes to develop a core collection of *P. aquatica* germplasm in Iran. Cluster analysis classified the studied genotypes into two clusters (Figure 1). Considering traits such as yield and yield components, genotypes in the third sub-cluster can be a good choice for cultivation. Also, based on results of genetic distances study of the *Ph. aquatica* genotypes, the maximum genetic distance was obtained between the third sub-cluster and the fifth sub-cluster, which, if necessary, the genotypes of these two sub-clusters can be used in breeding programs in order to exploit their desirable genes. Principal components analysis three-dimensional scatter plot of genotypes confirmed the results of cluster analysis (Figure 2). In the principal components analysis, four components were identified, which in total explained 84.3% of the total variance. In the first component, traits such as dry forage yield, crown diameter and canopy diameter, in the second component, only the leaf length and in the third component, traits such as number of days to flowering and number of days to pollination had the highest coefficients.

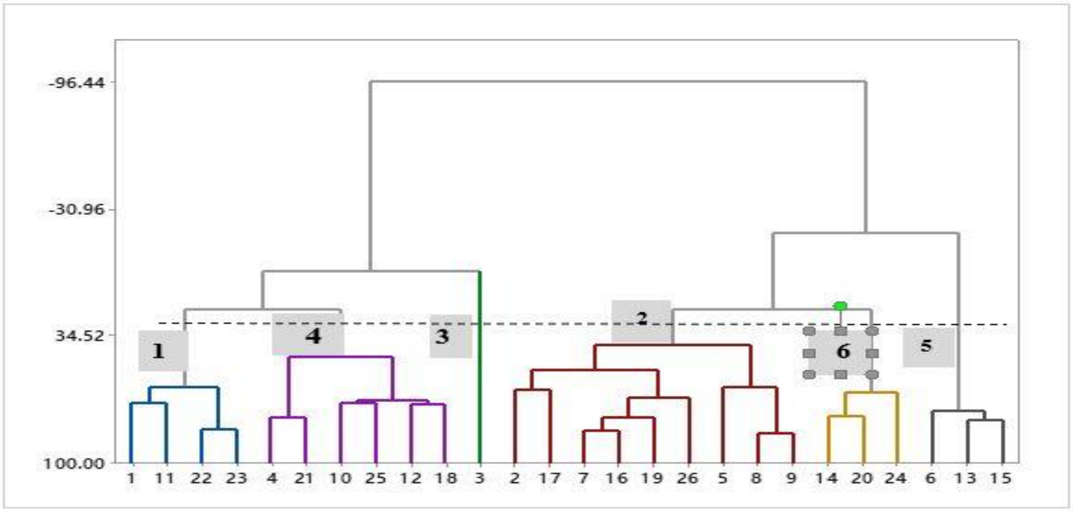

Fig. 1. Dendrogram of cluster analysis of *Phalaris aquatica* genotypes based on the measured traits means by Ward's algorithm

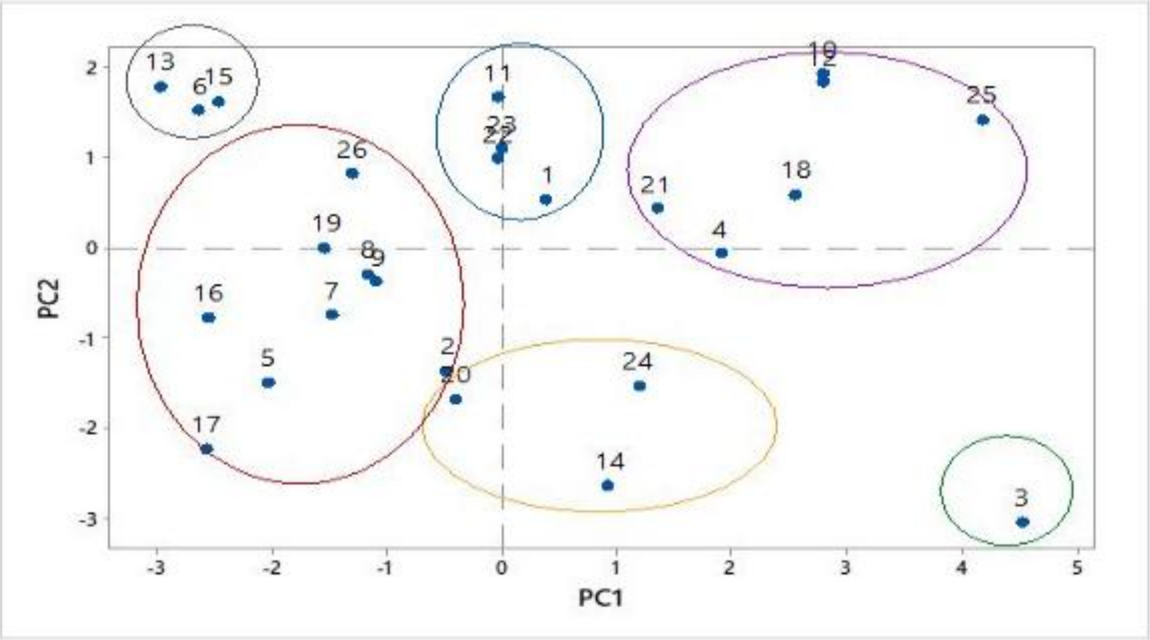

Fig. 2. Principal components analysis (PCA) scatter plot of different *Phalaris aquatica* genotypes based on the first two components

4. References

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