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Probit Analysis and Heritability of Salinity Tolerance in *Agropyron desertorum* Genotypes

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Abstract

Germination ability and salt stress tolerance of *Agropyron desertorum* were evaluated using ten genotypes originally collected from different areas of Iran in greenhouse condition. Five different concentrations of NaCl solution were used in this experiment. Analysis of variance showed considerable variation in all the germination attributes under salinity stress. Principal component analysis revealed that first and second components accounted for about 97.6 percent of the total variation among the traits studied. The first component included root length, plumule length, seedling length and seed vigor and accounted for 62.3 percent of the total variation among the traits. This component entitled as the seed germination ability. Hierarchical cluster analysis classified the genotypes in three groups. In conclusion, selection for the higher amounts of the traits root length, plumule length, seedling length and seed vigor can improve the seed germination ability and salinity tolerance in *Agropyron desertorum* genotypes at the seedling stage in greenhouse condition. Furthermore, crosses between the genotypes classified in the clusters 1 and 3 causes to broadening genetic variation and possibility of the efficient selection among the progenies obtained from these crosses.

Keywords: Agropyron desertorum, heritability, cluster analysis, probit analysis, PCA.

1. Introduction

A-biotic stress such as salinity whether from soil or water affects plant growth and development due to salt-induced water deficit, low uptake and accumulation of essential nutrients, and high accumulation of toxic ions such as Na+ and Cl-. All these factors cause changes in a wide variety of physiological and biochemical processes such as photosynthesis, protein synthesis and nucleic acid metabolism [1,2]. Reclamative and preventive measures for rendering salt affected soils fit for crop production are usually expensive and generally considered temporary solutions.

Alternatively, selection and breeding of cultivars tolerant to salinity is a feasible and economical approach for utilizing salt affected soils [3]. However, the success of this approach depends on the presence of genetic variation in the gene pool of a species. For example, variability for salt tolerance, within and between species, has been found in cultivated and wild species such as wheat (Triticum aestivum L.) [4], sorghum (*Sorghum bicolor* (L.) Moench.) [5], Agrostis stolonifera and Festuca rubra [6]. Similarly, while evaluating 25 and 60 strains of Agropyron desertorum for salt tolerance, Dewey DR [7,8] found a few strains tolerant to salt stress. Likewise, Ulfat M et al [9] screened 32 lines of canola and they were able to identify 5 highly tolerant lines. Since seed germination and seedling growth under saline conditions are critical for establishment of plant population [10,11],screening of different accessions or cultivars of a species at the germination stage in greenhouse condition may lead to find out salt tolerant genotypes at seedling stage. *Agropyron desertorum* is one of the important species of the Poacea family. This plant naturally grows in most rangelands where high salt content is the characteristic of most soils. In view of this information, it was hypothesized that different accessions of *Agropyron desertorum* growing in different areas with different climatic conditions might have evolved some obligatory adaptational characters, including that of salt tolerance. Therefore, the present study was achieved to evaluate genetic variation for germination attributes under salinity stress condition by screening ten different accessions of *Agropyron desertorum* at the germination stage. The intra-specific variation so explored for salt tolerance could be exploited in future breeding programs for the improvement of salt tolerance trait, the best crosses between *Agropyron* genotypes and selection of the genotypes tolerant to salinity stress.

2. Materials and Methods

2.1 Plant material

Ten *Agropyron desertorum* accessions (213-p11, 341-mix, 341-p11, 3477-p4, 3974-p11, 3965-p1, 3477-mix, 3974-p7 and 742-mix) used in the present study were obtained from the Kradj Agricultural Research Center, Karadj, Iran. Before sowing, seeds were surface sterilized in 5% Sodium hypochlorite solution for 5 minutes. Five different concentrations of NaCl (0, 100, 200, 300 and 400 mM) in Hoagland's nutrient solution were used. The experiment was setup in a completely randomized (CRD) factorial design with four replicates in greenhouse of the Department of Plant Breeding, Islamic Azad University, Khorasgan Branch, Isfahan, Iran. The research station is located in east of Isfahan (32◦ 38'N 51◦47'E) with 1550 m elevation. Region climate was dry or cold dry according to Demartin and ambergay methods, respectively. Mean annual precipitation is 114.5 mm and mean temperature of region is 15.1◦c. Maximum temperature in July was 42.6◦c and minimum in January was 17.25◦c. Evapotranspiration of this region is 1723.25 mm per year. Soil texture was silty-loam with 1.5% of organic carbon, 0.02% of nitrogen, 20 p.p.m of available phosphorus, 504 p.p.m of available potassium, pH=7.37, acidity of 7.8 and 3.5 mmohs/cm electrical conductivity in 0 to 30 cm depth. Fifty seeds of each accession were allowed to germinate in a pot at greenhouse with efficient amounts of NaCl solution. Salt levels were maintained daily by dripping out and applying fresh salt solution twice (Figure 1).

Figure 1. Seeds of *Agropyron desertorum* genotypes.

2.2 Data collection

Germination was recorded daily and a seed was considered germinated when the radicle attained length ≥5 mm. After 7 days of sowing, germinated seeds were collected, their plumules and roots carefully separated and fresh and dry weights recorded. Germination percentage, germination rate, plumule length and root length also recorded for each experimental unit (Figure 2).

2.3 Statistical analysis

The data obtained from the experimentation were subjected to a two-way analysis of variance, principal component analysis, cluster and probit analysis to determine the best selection criteria, crosses and the most tolerant *Agropyron desertorum* genotypes by using the SAS_9 and $SPSS_{18}$ statistical softwares.

Figure 2. Germination of *Agropyron desertorum* genotypes.

3. Results and Discussion

3.1 Simple anova

Analysis of variance showed the significant differences for seed vigor index, germination percentage, plumule length, root length, germination rate and seedling dry weight between genotypes, salinity stress levels and their interactions (Table 1).

Table 1. Analysis of variance of the measured traits in *Agropyron desertorum* genotypes.

S.V	df	y1	y2	y3	y4	y5	y6
Salinity	4	3.2^{**}	12.9^{**}	8.6^{**}	1.4^{**}	5.7^{**}	2.3^{**}
Genotypes	9	10.7^{**}	15.4^{**}	24.1^{**}	2.5^{**}	6.3^{**}	6.5^{**}
S*G	36	23.1^{**}	36.4^{**}	45.2^{**}	3.6^{**}	10.1^{**}	1.7^{**}
Error	150	0.05	1.2	3.2	0.1	2.1	0.1

**: significant at 1% probability level.

3.2 PCA

Principal component analysis revealed that the first and second principal components accounted for 62.3 and 35.3 percent of the variation exist amount the traits, respectively. The first component comprises root length, plumule length, seedling length and seed vigor. Therefore, this component was entitled as seed germination ability mean while selection for the higher amounts of these traits can improve the seed germination ability in *Agropyron desertorum* genotypes. The second component involved fresh and dry weight of seedling. Biplot graphical display (Figure 3) classified the genotypes in three main groups that designated considerable genetic diversity for salinity tolerance and germination traits in *Agropyron desertorum*.

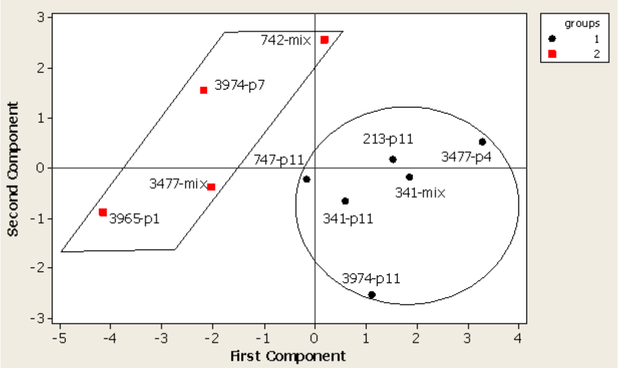

Figure 3. Graphical display of Agropyron desertorum genotypes in greenhouse condition Based on biplot analysis.

3.3 Cluster analysis

Cluster analysis based on UPGMA method also classified the genotypes in three distinct clusters similar to biplot analysis (Figure 4). Cluster1 comprises 213-p11, 341-mix, 341-p11 and 3477-p4. On the other hand, cluster 2 involves 3974-p7 and 742-mix genotypes. Clusters 1 and 3 have the highest genetic distance. Therefore, crosses between the genotypes belong to these clusters have promising genetic efficacy to improve germination ability and tolerance to salinity stress in *Agropyron desertorum* genotypes. Genotypes 341-mix and 3974-p11 showed the highest and lowest germination percentage and germination rate, respectively. Significant interaction effect between genotypes and salinity stress levels for germination percentage indicated different reaction of genotypes to salt stress. These dictate on the necessary of selection among these genotypes for different salinity levels. Arab F [12] reported reduction in seed vigor index with increase in salinity stress intensity among *Agropyron* and Atriplex accessions. This result is in consistent with my findings.

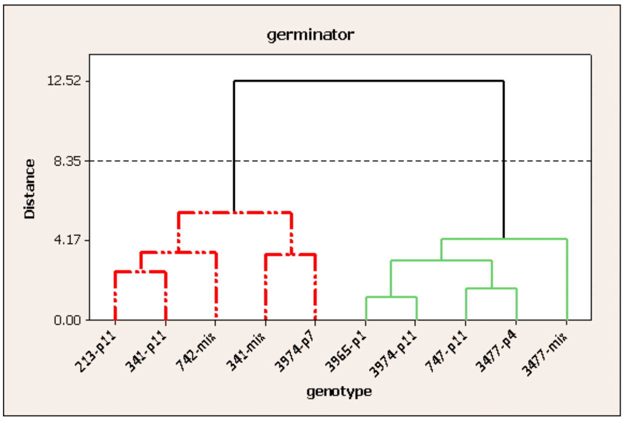

Figure 4. Hierarchical cluster analysis of *Agropyron desertorum* genotypes in greenhouse condition based on UPGMA method

3.4 Probit analysis

Probit analysis (Figure 5) showed that 341-mix was the most salinity stress tolerant and 3974-p11 the most sensitive *Agropyron* genotypes. The genotype 341-mix showed LD50 higher than other genotypes. The highest amount of seedling length was observed in 341-mix and 3974-p7 genotypes. Arab F [12] and Jafari M [13] also reported significant difference between *Agropyron* genotypes for this trait. Other researchers found sever reduction in plumule length more than root length that is same with my findings in *Agropyron desertorum* and *Panicum turgidum* Forssk [14, 15].

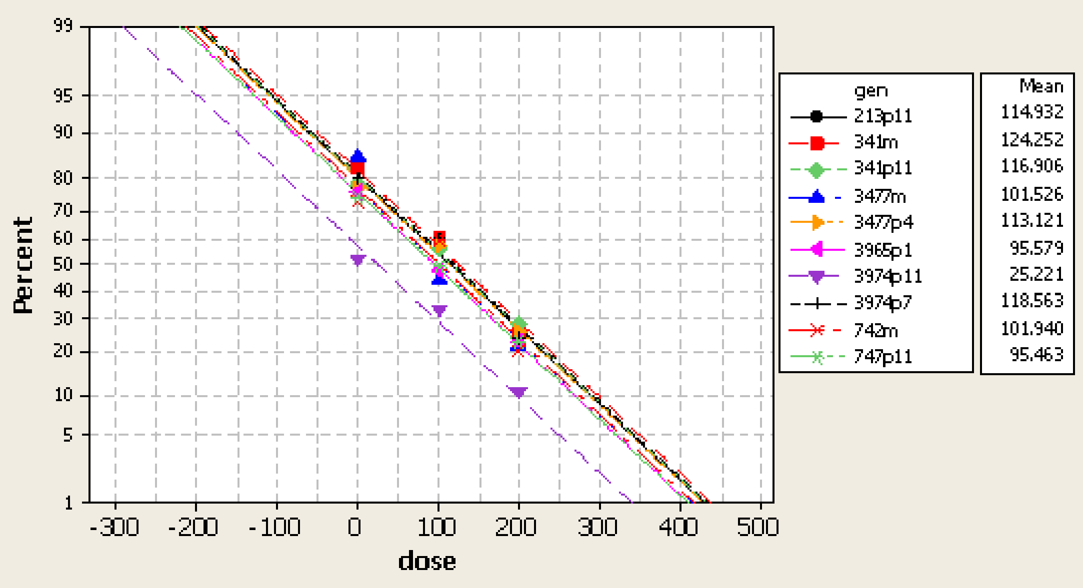

Figure 5. Determination of the LD50 for Agropyron desertorum genotypes using probit analysis

3.5 Heritability estimation

Estimation of broad-sence heritability for the studied traits in *Agropyron desertorum* indicated that seed vigor rate and germination rate having 63 and 68 percent showed the highest heritability. Therefore, selection for these traits has proper efficiency in breeding of these traits. Sabir P and Ashraf M [11] and Munns R et al. [3] reported the similar results.

4. Conclusion

In conclusion, selection for the higher amounts of the traits root length, plumule length, seedling length and seed vigor will increase the seed germination ability in *Agropyron desertorum* genotypes. Crosses between the genotypes classified in the clusters 1 and 4 causes to broadening genetic variation, transgressive segregation and possibility of the efficient selection among progenies exhausted from these crosses.

Acknowledgements

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