

Full Length Research Paper

Multivariate analysis of germination ability and tolerance to salinity in *Agropyron desertorum* genotypes in greenhouse condition

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Salinity stress is one of the major problems for crop production in arid and semiarid regions of the world. Hence, 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% 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% of the total variation among the traits. This component is entitled as the seed germination ability. Hierarchical cluster analysis classified the genotypes in three groups. In conclusion, selection for the higher amount of the traits roots length, plumule length, seedling length and seed vigor can improve the seed germination ability and salinity tolerance in *A. desertorum* genotypes at the seedling stage in greenhouse condition. Furthermore, crosses between the genotypes classified in the clusters 1 and 3 can cause the broadening of genetic variation and possibility of the efficient selection among the progenies obtained from these crosses.

Key words: *Agropyron desertorum*, salt stress, biplot analysis, hierarchical cluster, probit analysis, seedling stage.

INTRODUCTION

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 (Ashraf, 2004; Munns, 2005). 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 (Munns et al., 2006). 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.) (Kingsbury and Epstein, 1984), sorghum (*Sorghum bicolor* (L.) Moench) (Azhar and McNeilly, 1988), *Agrostis stolonifera* and *Festuca rubra* (Ashraf et al., 1986). Similarly, while evaluating 25 and 60 strains of *Agropyron desertorum* for salt tolerance, Dewey (1960, 1962) found a few strains tolerant to salt stress. Likewise, Ulfat et al. (2007) screened 32 lines of canola and they were able to identify five highly tolerant lines.

Since seed germination and seedling growth under saline conditions are critical for establishment of plant population (Noreen et al., 2007; Sabir and Ashraf, 2007), screening of different accessions/cultivars of a species at the germination stage in greenhouse condition may lead to find out salt tolerant genotypes at seedling stage.

A. 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 *A. desertorum* growing in different areas with different climatic conditions might have evolved some obligatory adaptational characters, including that of salt tolerance.

Therefore, this study was achieved to evaluate genetic variation for germination attributes under salinity stress condition by screening ten different accessions of *A. 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.

MATERIALS AND METHODS

Ten *A. desertorum* accessions (213-p11, 341-mix, 341-p11, 3477-p4, 3974-p11, 3965-p1, 3477-mix, 3974-p7 and 742-mix) used in the study were obtained from the Kradj Agricultural Research Center, Karadj, Iran. Before sowing, seeds were surface sterilized in 5% sodium hypochlorite solution for 5 min. 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, Khorasgan University, 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 ppm of available phosphorus, 504 ppm of available potassium, pH=7.37, acidity of 7.8 and 3.5 mmohs/cm electrical conductivity in 0 to 30 cm depth.

50 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.

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

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 *A. desertorum* genotypes by using the SAS₉ and Minitab₁₅ statistical softwares.

RESULTS AND DISCUSSION

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.

Principal component analysis revealed that the first and second principal components accounted for 62.3 and 35.3% of the variation that existed among the traits, respectively. The first component comprised of 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 *A. desertorum* genotypes. The second component involved fresh and dry weight of seedling. Biplot graphical display (Figure 1) classified the genotypes into three main groups that designated considerable genetic diversity for salinity tolerance and germination traits in *A. desertorum*.

Hierarchical cluster analysis based on unweighted pair-group method analysis (UPGMA) (Figure 2) also classified the genotypes into three distinct clusters similar to biplot analysis. Cluster 1 comprised of 213-p11, 341-mix, 341-p11 and 3477-p4. On the other hand, cluster 2 involved 3974-p7 and 742-mix genotypes. Clusters 1 and 3 had the highest genetic distance. Therefore, crosses between the genotypes that belong to these clusters have promising genetic efficacy to improve germination ability and tolerance to salinity stress in *A. 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 indicate different reaction of genotypes to salt stress. These dictate on the necessity of selection among these genotypes for different salinity levels. Arab (2006) reported reduction in seed vigor index with increase in salinity stress intensity among *Agropyron* and *Atriplex* accessions. This result is consistent with the findings of this study.

Probit analysis (Figure 3) showed that 341-mix was the most salinity stress tolerant and 3974-p11 was the most sensitive *Agropyron* genotypes. The genotype 341-mix showed LD₅₀ higher than the other genotypes. The highest amount of seedling length was observed in 341-mix and 3974-p7 genotypes. Arab (2006) and Jafari (1994) also reported significant difference between *Agropyron* genotypes for this trait. Lauchi and Epstein (1990) found sever reduction in plumule length more than root length which is the same with the findings in *A. desertorum* in this study.

Estimation of broad-sense heritability (Table 1) for the studied traits in *A. desertorum* indicates that seed vigor rate and germination rate had the highest heritability. Therefore, selection for these traits has proper efficiency in the breeding of these traits. Sabir and Ashraf (2007) and Munns et al. (2006) reported similar results.

In conclusion, selection for the higher amounts of the traits roots length, plumule length, seedling length and seed vigor will increase the seed germination ability in *A. desertorum* genotypes. Crosses between the genotypes

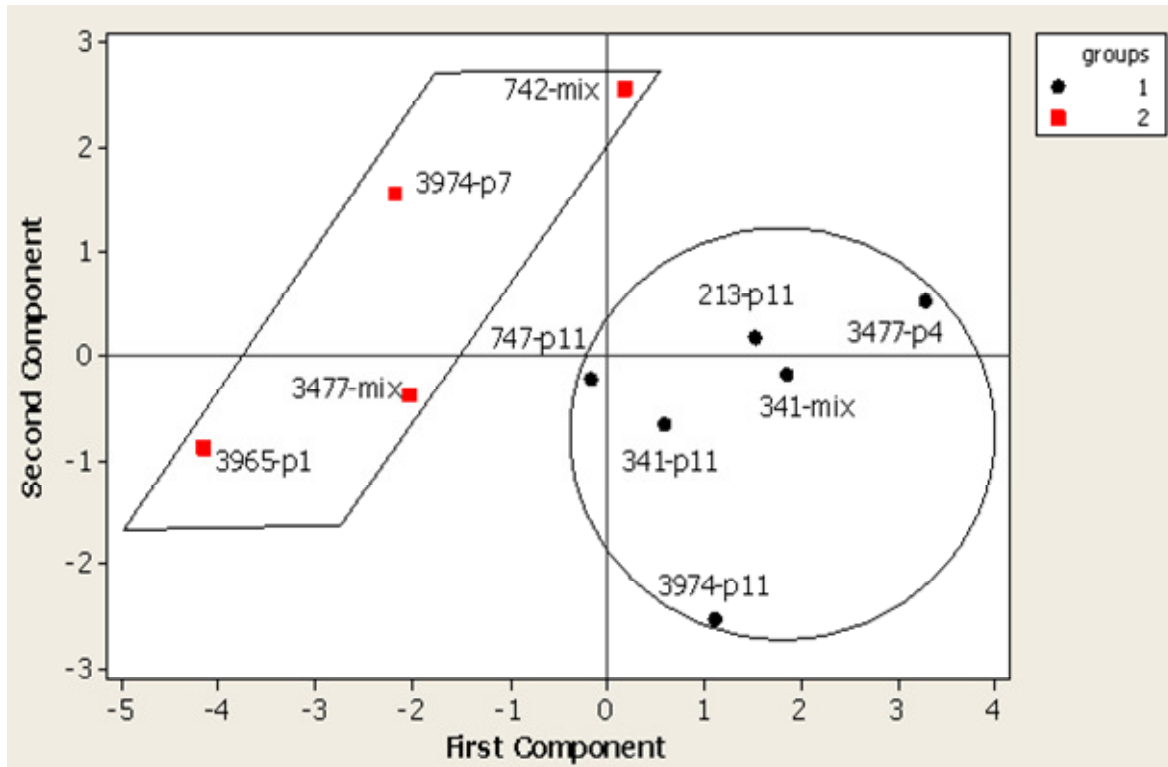


Figure 1. Biplot graphical display of *Agropyron desertorum* genotypes in greenhouse condition.

Similarity

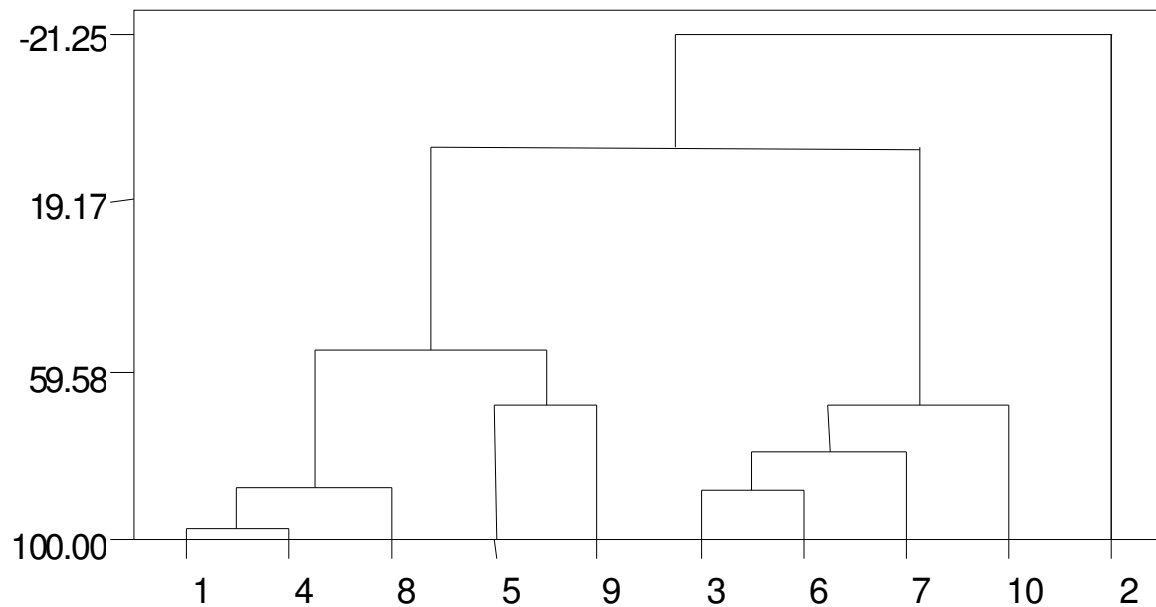


Figure 2. Cluster analysis of *Agropyron desertorum* genotypes in greenhouse condition based on UPGMA method.

classified in the clusters 1 and 4 can cause the broadening of genetic variation, transgressive segregation and possi-

bility of the efficient selection among progenies from these crosses.

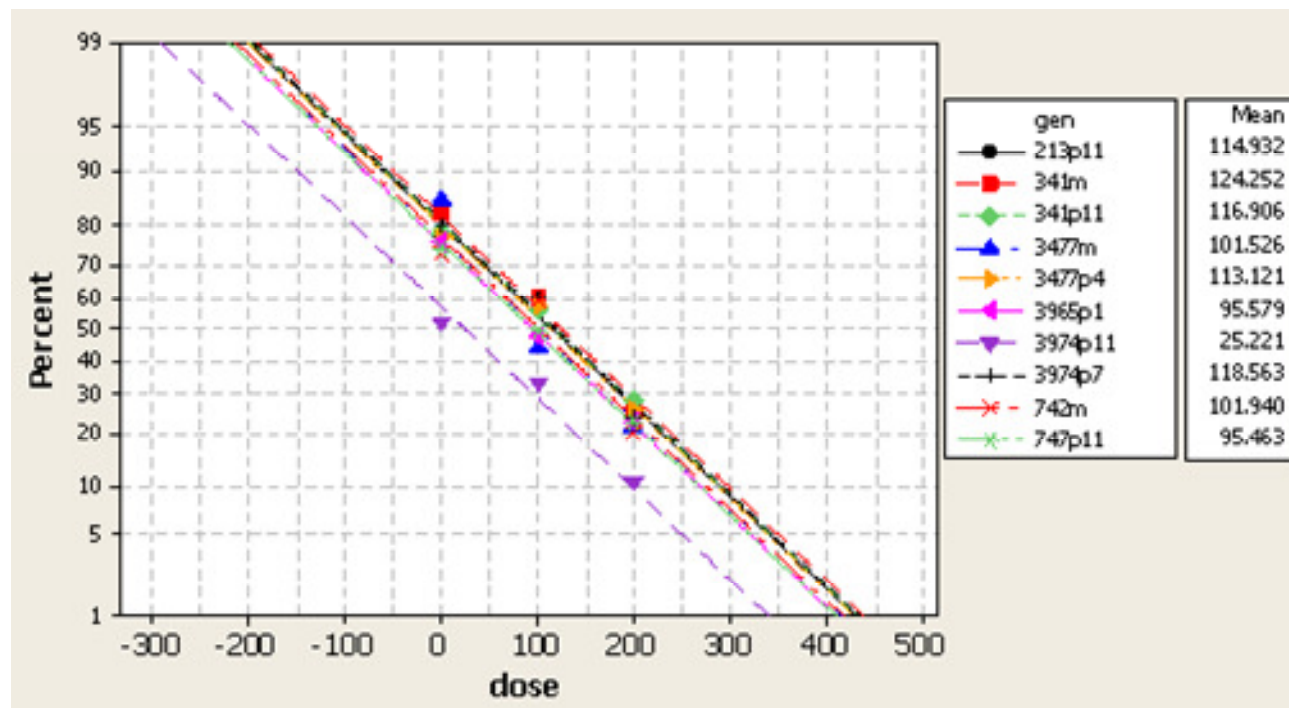


Figure 3. Probit analysis of *Agropyron desertorum* genotypes in greenhouse condition.

Table 1. Estimation of broad-sense heritability for the traits in *Agropyron desertorum* in greenhouse condition.

Parameter	Value
Germination percentage	0.62
Germination rate	0.68
Seed vigor index	0.63
Root length (cm)	0.39
Plumule length (cm)	0.21
Seedling length (cm)	0.29
Root/ colerhize	0.32
Seedling fresh weight	0.45
Seedling dry weight	0.32
Dry weight/fresh weight	0.24

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