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 mea-
sures for rendering salt affected soils fit for crop 
production are usually expensive and generally considered 
temporary solutions.

Alternatively, selection and breeding of cultivars toler-
ant 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
Poaceae 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, 3974-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 silt-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 mmols/cm electrical conductivity in 0 to 30 cm depth.

50 seeds of each accession were allowed to germinate in a pot at greenhouse with sufficient 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 SAS, 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 LD_{50} 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...
classified in the clusters 1 and 4 can cause the broadening of genetic variation, transgressive segregation and possibility 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.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
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<tbody>
<tr>
<td>Germination percentage</td>
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<tr>
<td>Germination rate</td>
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<tr>
<td>Seed vigor index</td>
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<tr>
<td>Root length (cm)</td>
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<tr>
<td>Plumule length (cm)</td>
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<td>Seedling length (cm)</td>
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<tr>
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</tr>
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<td>Seedling fresh weight</td>
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<tr>
<td>Seedling dry weight</td>
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</tr>
<tr>
<td>Dry weight/fresh weight</td>
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</tbody>
</table>

REFERENCES


