

## Genetic diversity of germination attributes in *Agropyron desertorum* genotypes under salinity stress condition

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**Abstract.** Ten *Agropyron desertorum* genotypes originally collected from different areas of Iran with varying environmental conditions along with five different concentrations of NaCl solution were used to assess the genetic variation of germination attributes in this rangeland species. The set of accessions examined in this study showed considerable variation in all the germination attributes such as germination percentage and rate as well as seedling fresh and dry weights under salt stress. Principal component analysis revealed that four important principal components accounted for about 98.2 percent of the total variation among the traits studied. The first component comprises root length, plumule length, seedling length and seed vigor and accounted for 52.2 percent of the total variation among the traits. This component entitled as the seed germination ability. Cluster analysis classified the genotypes in four clusters. 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 in *Agropyron desertorum* genotypes. More over, crosses between the genotypes classified in the clusters 1 and 4 causes to broadening genetic variation and possibility of the efficient selection among the progenies exhausted from these crosses.

**Keywords:** *Agropyron desertorum*, Principal component analysis, cluster analysis, germination ability

### 1. Introduction

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 (Kingsbury & Epstein, 1984), sorghum (Azhar & 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 5 highly tolerant lines.

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

*Agropyron desertorum* is one of the important species of the Gramineae family. This plant naturally grows in most rangelands where high salt content is the characteristic of most soils.

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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

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 a growth room of the Department of Plant Breeding, Khorasgan University, Isfahan, Iran. Fifteen seeds of each accession were allowed to germinate in a Petri plate double lined with filter paper moistened with 10 mL 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  $\geq 5$  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.

The data obtained from the experimentation were subjected to a two-way analysis of variance, principal component analysis and cluster analysis to determine the best selection criteria, crosses and the most tolerant *Agropyron desertorum* genotypes by using the SAS<sub>9</sub> and SPSS statistical softwares.

## 3. Results and Discussion

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

Principal component analysis revealed that the principal components one to four accounted for 52.2, 18, 16 and 12 percent of the variation exist amount the traits.

The first component comprises plumule length, root 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 components involved fresh and dry weight of seedling. Biplot graphical display (figure 1) classified the genotypes in four groups that designated considerable genetic diversity for salinity tolerance and germination traits in *Agropyron desertorum*.

Cluster analysis (Figure 2) also classified the genotypes in four distinct clusters similar to biplot analysis. Cluster1 comprises 213-p11, 341-mix, 341-p11 and 3477-p4. On the other hand, cluster 4 involves 3974-p7 and 742-mix genotypes. Clusters 1 and 4 have the highest genetic distance. Therefore, crosses between the genotypes belong to these clusters have promising genetic efficacy to improve germination attributes and salt stress tolerance 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 (2006) 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.

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. Lauchli and Epstein (1990) found sever reduction in plumule length more than root length that is same with my findings in *Agropyron desertorum*.

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.

#### 4. Acknowledgements

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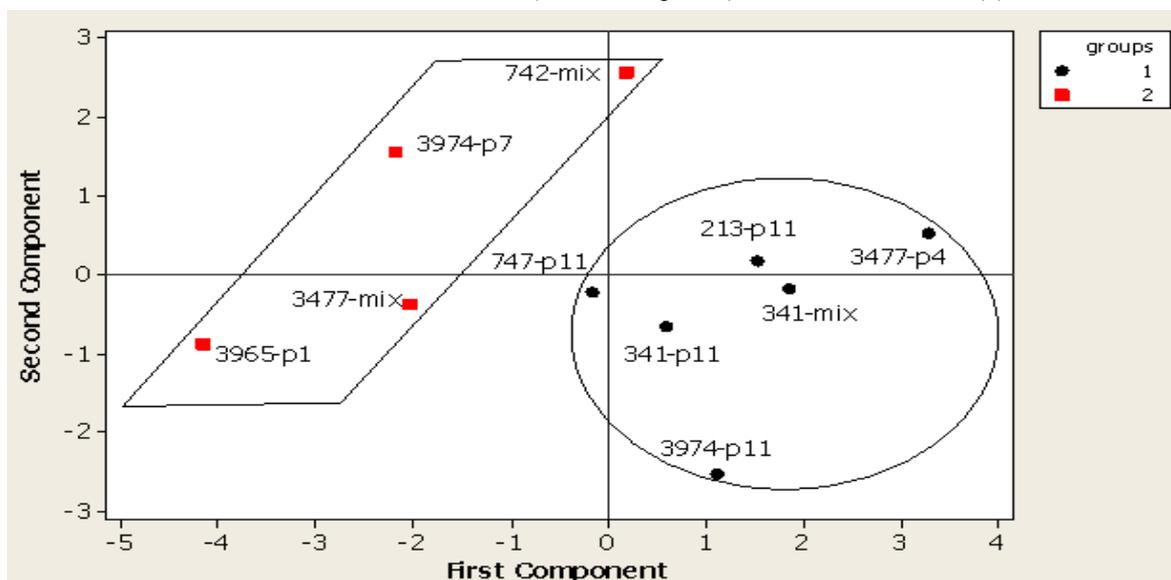


Figure1. Biplot graphical display for the *Agropyron desertorum* genotypes based on principal component analysis

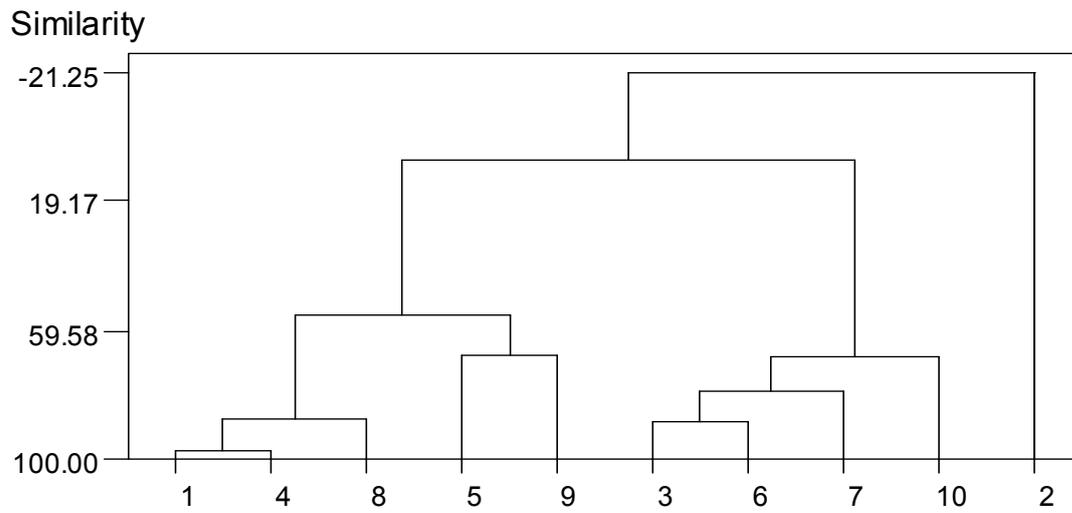


Figure2. Cluster analysis of *Agropyron desertorum* genotypes based on UPGMA method