Indian Journal of Fundamental and Applied Life Sciences ISSN: 2231-6345 (Online)
An Open Access, Online International Journal Available at http://www.cibtech.org/jls.htm
2015 Vol. 5 (3) July-September, pp.19-23/Haghdoost
Research Article

GROUPING GERMINATION TRAITS OF PEAS LINES UNDER THE IMPACT OF HYDRO AND HUMIC-PRIMING USING CLUSTER ANALYSIS

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ABSTRACT
To group germination traits of some pea lines, a test was conducted in the laboratory of Islamic Azad University of Ardebil in season year 2013. In this study, 7 pea's lines were cultivated in a factorial experiment based on completely random block plan with three replications. After standardizing data, cluster analysis was performed using WARD method and the Euclidean squared distance factor, and genotypes in both hydro-priming and humic-priming treatments were placed in 2 groups. Under hydro-priming, the first cluster had five lines. The deviation of the mean percent of the cluster was negative for all traits. All lines of the cluster had lower middle positive deviations of the mean in terms of traits. The second cluster included two lines. Therefore, superior lines of this cluster can be used in future studies. In the humic-priming treatment, the first cluster consisted of three lines, and all traits had positive deviation from the mean. Thus, the superior lines of the cluster can be used in future studies. In the second cluster, which included four lines, the deviation from the mean for all traits of the cluster was negative, and all lines of the cluster had lower middle traits.

Keywords: *Pea Line, Humic Priming, Cluster Analysis, Germination Traits*

INTRODUCTION
Pea is called with scientific name of *Cicer arietinum* for its nitrogen fixation. Pea is an annual, herbaceous, confervoid and a long day plant, and has short shrub with thin branches and small leaves with white flowers (Kanouni *et al.,* 2008). Pea has the first rank in terms of grain crop production and cultivation in Iran. Among 45 pea producing countries in the world, Iran has the last rank in terms of yield. According to FAO statistics, the world area under cultivation of grain crops in 2004 was 63.8 million hectares and its production is71 million tons (Asanjou news magazine, 2013). The area under cultivation of pea in Ardabil province in the 2010-2011 season year was 4089 hectares. In this area, 2765 tons of pea was obtained, where the yield production was 676.27 kg/ha. Of the area under cultivation, 62011 hectares included dryland farming, and 3540 included irrigated farming. Germination is the first stage of plant development. It is one of the critical stages in the life cycle of plants and a key process in the emergence of plants (De Villiers, 1994). The root is considered as part of the plant which causes the establishment of the plant and plays an important role in the absorption of water and nutrients, especially in the stressful conditions (rain fed cultivation) (Ganjali, 2005). Root growth is affected by factors such as humidity, temperature, and soil nutrients (Miasaka and Grunes, 1988). One of the techniques that improve the seedling power and establishment and thus the efficiency of the plant is seed priming. Priming refers to a number of different methods to improve seed (Faroog *et al.,* 2006). The seed is allowed to absorb a little water in the priming; So that the early stages of germination (including activation of enzymes) to be performed; but the radical does not get out. Seeds is dried, stored and can be grown after priming (MacDonald, 1999). Recently, the use of humic acid has raised for seed priming before planting. Humic acid and folic acid are extracted from various sources such as soil, peat, oxidized lignite, coal, etc. They are different in terms of chemical structure and molecular size (Sebahattin and Necdet, 2005). Humic acids have beneficial effects on alkaline soil and with chelation essential elements, increase its absorption and soil fertility and crop yield (Liu & Cooper, 2000). Khodabakhsh *et al.,* (2010) tested hydro-priming and osmopriming effect on germination, growth factors, and the number of root nodules in terms of salinity tension for two commercial types of peas. They observed that osmoprimed plants have higher

number of nodules compared to hydroprimed and control plants. It was also found that in salinity tension, seedlings from osmoprimed and hydroprimed seeds have better germination, root fresh weight and dry weight compared to non-primed seeds (control group). Results of a study by Fateh *et al.*, (2010) showed that the pea hydro-priming under irrigation increases performance from 2602 to 3533 kilograms. Results of another study by Musa (2001) showed that seed priming is associate with early flowering and pod formation in pea plants. When specialist of plant breeding wants to categorize varieties and cultivars, in order to figure out the genetic distance and their diversity, he uses cluster analysis methods via mathematical formulas (Farshadfar, 1999 and Bryan and Manly, 2004). Since the varieties in a group have less genetic distance in comparison to the varieties of the other groups, therefore in hybridization, according to the varieties in different groups and amount of mean value of each group in order to achieve a better yield, phenomena such as Heterosis and transgressive segregation can be used.

MATERIALS AND METHODS

Experiment Location

The plot was a factorial experiment based on completely random block plan with three replications, and seedlings length was measured at three different times on the seventh, tenth and thirteenth days, and preparation of the seeds (Table 1) based on a prepared plan of the Agriculture and Natural Resources Research Center of Ardabil province included:

1. Zero hour of soaking in distilled water immediately before sowing
2. Zero hour of humic-priming of the seed
3. Soaking seeds in water for 8 hours (hydro-priming)
4. Humic-priming of seed for 8 hours
5. Hydro-priming of seeds for 10 hours
6. Humic-priming of seeds for 10 hours
7. Hydro-priming of seeds for 12 hours
8. Humic-priming of seeds for 12 hours.

Experiment Plot

The first factor was the type of priming and included priming with the humic and soaking in distilled water, and the second factor was the time of priming and included priming time (zero, 8, 10, and 12 hours), and he third factor was the pea varieties. For humic priming, liquid humic fertilizer produced in the country with 12%humic acid and folic acid content of two per thousand rate was used. For the treatment application, 50 seeds were randomly selected from each line for each treatment, and after completion of the primings, primed seeds were washed with distilled water. All seeds were dried at room temperature and dark place to reach the initial weight.

Table 1: Names the studied genotypes

Number	Line	Number	Line
1	Adap2 R4-1	5	Adap2 R4-11
2	Adap2 R-4	6	Adap2 R4-8
3	Adap2 R4-9	7	Adap2 R3-5
4	Adap2 R3-2		

Statistical Analysis

To determine the genetic affinity of genotypes and grouping them, cluster analysis using WARD method and Euclidean distance square distance coefficient was performed (Hoque and Rahman, 2006). For statistical analysis SPSS and Minitab software were used.

RESULTS AND DISCUSSION

In this study, in order to classify genotype cluster analysis based on standard data and WARD methods was used. In a breeding program as the parents are genetically distant from each other; transgressive

segregation of their offspring will be increased. The main goal of cluster analysis is to determine genetic distance of hybrids from each other, so the researcher instead of spending time on a huge number of randomized genotype to obtain a good result accidentally, first categorizes the studied genotypes according to cluster analysis and then by choosing some hybrids from spurious from the distant clusters and based on their traits takes some blocks of hybridizations. Thus in hybridization among distant genotypes, which has been chosen from distance clusters, the possibility of achieving optimum results increases.

Grouping Pea Lines Using Cluster Analysis for in Vitro Hydro-Priming

To distinguish the traits of each group in terms of the traits under study, the mean and the deviation of the mean of each cluster out of the total mean were calculated (Table 2). A cluster that has higher than the average traits is considered as the superior line. The first cluster consisted of five lines. The deviation of the mean percent of the cluster was negative for all traits. All lines of the cluster had lower middle positive deviations of the mean in terms of traits. The second cluster included two lines. Therefore, superior lines of this cluster can be used in future studies.

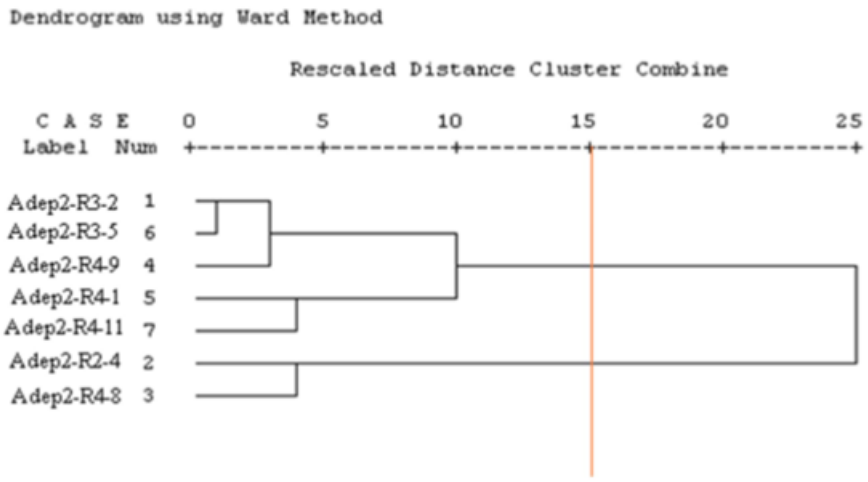

Figure 1: Dendrogram of cluster analysis method on WARD all traits treated hydro-priming

Table 2: Grouping pea lines using cluster analysis for in vitro hydro-priming

Diameter hypocotyl	Length of coleoptile	Root length	Stem length	Seedling length	Cluster			
1.26	1.16	7.22	20.95	28.22	$\overline{X}$	Cluster genotypes: 1, 6, 4, 5, 7	1	contains
-1.01	-0.07	-0.47	-1.02	-1.91	$\overline{X}_h - \overline{X}_{..}$			
1.28	1.42	8.88	24.52	34.89	$\overline{X}$	Cluster genotypes: 2 and 3	1	contains
0.01	0.19	1.19	2.55	4.76	$\overline{X}_h - \overline{X}_{..}$			
1.27	1.23	7.69	21.97	30.13	Mean			

Grouping Pea Lines using Cluster Analysis for in Vitro Humic Priming

To distinguish the traits of each group in terms of the traits under study, the mean and the deviation of the mean of each cluster out of the total mean were calculated (Table 3). A cluster that has higher than the average traits is considered as the superior line. The first cluster consisted of three lines, and all traits had positive deviation from the mean. Thus, the superior lines of the cluster can be used in future studies. In the second cluster, which included four lines, the deviation from the mean for all traits of the cluster was negative, and all lines of the cluster had lower middle traits.

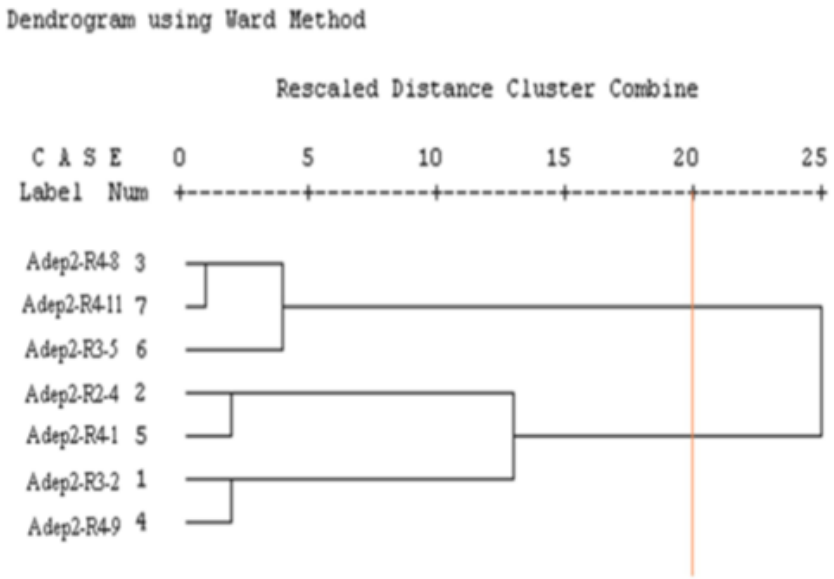

Figure 2: Dendrogram of cluster analysis method on WARD all traits treated Humic-priming

Table 3: Grouping pea lines using cluster analysis for in vitro humic-priming

Diameter hypocotyl	Length of coleoptile	Root length	Stem length	Seedling length	Cluster			
1.18	0.998	10.49	18.85	30.57	$\overline{X}$	Cluster genotypes: 3, 6 and 7	1	contains
0.01	0.075	1.6	2.59	4.24	$\overline{X}_h - \overline{X}_{..}$			
1.17	0.876	7.69	14.32	22.99	$\overline{X}$	Cluster genotypes: 1, 2, 4 and 5	2	contains
0	-0.047	-1.2	-2.03	-3.24	$\overline{X}_h - \overline{X}_{..}$			
1.17	0.9228	8.89	16.26	26.23	Mean			

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