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# Evaluation of genetic diversity of 22 rice (*Oryza sativa*) landraces native to northern Iran in terms of some germination components and growth indices

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ABSTRACT

Increasing population and limited arable lands has perpetuated the efforts to improve yield per unit area through various methods such as sophisticated agronomical operations, selection of productive and tolerant genotypes and improving germination components. In order to study genetic diversity of 22 rice (*Oryza sativa* L.) landraces native to northern part of the country in terms of germination components and of some growth indices, an experiment was conducted at laboratory of agriculture faculty of Islamic Azad University, Ardabil branch, as randomized complete blocks design with three replications, in year 2011. Estimation of phenotypic and genotypic coefficients for various traits revealed that genotypes being studied were more genetically diverse in terms of FGP, GI, GRI, Rs, VI, seedling length, radicle length and total fresh weight of sample than in terms of other traits. Study genotypes were classified into four groups using cluster analysis. Mean squares between the groups were significant for all the traits except for ratio of radicle length to seedling length. Germination indices were more heritable than traits associated with growth indices. Results from cluster analysis showed that group 2 including genotypes numbered 2, 16, 5, 14, 22 and 6, had the highest values for all the traits and was in average status in terms of traits such as MGT, Rs, MDG and ratio of radicle length to seedling length and consequently was recognized as the best group.

**Key words:** Cluster analysis, Genetic diversity, Germination component, Growth indices, Rice landrace

High germination power and strong components for germination are among the most important traits determining the better establishment of rice (*Oryza sativa* L.) seedling in direct sowing systems. Since, high germination power of a genotype also contribute a lot in preventing weed growth, using varieties with high germination power in tropic regions, which are inherently subject to drought stress, has proved useful. As a result, currently high germination power is regarded as one of the useful traits in developing varieties for bred rice (Peterson *et al.* 1978, Miura *et al*. 2002 and Zhang *et al*. 2005). In spite of genetic diversity for germination power and traits associated with germination in rice (Mgonja *et al*. 1993, Redona and Mackill 1996, Wan *et al*. 2006, Zeng *et al*. 2006 and Zhang *et al*. 2005), rice breeders not were so successful in improving this trait through classic ways (McKenzie *et al*. 1980).

Based on forgoing discussion, it is highly important to conduct studies on genetic diversity of various cultivars of this plant for breeding program. Heydari *et al*. (2006) in their study to investigate genetic diversity of various traits in 157 double haploid bread wheat lines found that the lines were genetically more diverse in terms of length of final internode, number of fertile spike per unit area, plant height, grain number and grain yield per main spike than in terms of other traits including volumetric grain weight, day number to ripening, day number to heading and anthesis. Golababady and Arzani (2003) after studying genetic diversity of 300 Durum wheat genotypes reported that the variation of the genotypes for traits such as grain yield, harvest index and spike number per unit area was significantly high. Garavandi and Kahrizi (2010) in their study on genetic variation of 20 bread wheat genotypes reported that the genotypes were of higher genetic diversity in terms of grain yield, spike number/$m^2$, grain number/spike, spike concentration and awn length than in terms of other traits. They maintained that grain yield had a positively significant correlation with harvest index, biological yield, days to ripening, grain number per spike and grain weight per spike. Mahfoozi *et al*. (2004) reported that genetic diversity among genotypes might contribute to increasing grain yield under drought area, after they examined breeding methods for increasing wheat yield under cold and dry regions of Iran.

Shahryari *et al*. (2011) in their study on genetic diversity of 18 bread wheat genotypes with respect to phenological and morphological traits demonstrated that the genotypes were genetically more diverse in terms of plant height, weight of 1 000 grains, grain number per spike, spike length, spike weight, peduncle length, peduncle weight and

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Table 1 Name of improved rice landraces being studied

| Number | Genotype | Number | Genotype |
|---|---|---|---|
| 1 | Hashemi | 12 | Salari |
| 2 | Noksiah | 13 | Ghasro-dashti |
| 3 | Shahpasand | 14 | Mosajo |
| 4 | Anbarboe-Ilam | 15 | Sangjoe-tarum |
| 5 | Amrollahi | 16 | Hashemi-zodras |
| 6 | Binam | 17 | Hassansaraei |
| 7 | Hassani | 18 | Sangjo |
| 8 | Domzard | 19 | Mosatarum |
| 9 | Hassansaraei-atashghah | 20 | Gharibsiah-ryhani |
| 10 | Anbarbo | 21 | Gharib |
| 11 | domsefid | 22 | Alikazemi |

grain yield than in terms of other traits.

Mollasadeghi (2010) in his study on 12 bread wheat genotypes argued that the genotypes exhibited more genetic diversity in terms of plant height, spike length, grain number per spike, grain weight per spike, weight of 1000 grains and date of heading than in terms of other traits. In addition, cluster analysis in this study classified the study genotypes into two groups. Mean squares between the groups were significant for all traits other than grain yield, spike length and date of heading. Yield components produced more heritability than grain yield.

The present study was conducted in order to investigate the genetic diversity in terms of germination components and some growth indices of rice genotypes being studied, so to identify their close and far groups to use the obtained results for appropriate intersections.

## MATERIALS AND METHODS

The experiment was conducted in laboratory of Islamic Azad University, Ardabil branch, in 2011. Plant materials included 22 improved rice landraces, which were provided by National Rice Research Institute based in Rasht (Table 1). The design used for experiment was randomized complete blocks with three replications. Five seeds were cultured in each Peteri dish. Germination test was done in the germinator under such conditions as 25 ÚC, 70% relative humidity under 16 hr light and 8 hr dark. In order to measure germination indices, the germinated seeds were counted daily, whereas at the end of last day, indices for germination and seedling growth such as final germination percentage (FGP), coefficient of velocity of germination (CVG), germination index (GI), germination rate index (GRI), mean germination time (MGT), velocity of germination (Rs) and mean daily germination (MDG), vigor index (VI), leaf number, root number, seedling length, radicle length, total fresh weight of sample, and ratio of radicle length to seedling length were measured. The calculations were done using the following equations:

Coefficient of velocity of germination (CVG):

$$CVG = 100 \times \sum Ni/\sum NiTi$$

where, Ni is the number of germinated seeds for each day, Ti is number of days as of the start of experiment, Germination index (GI):

$$GI = (13 \times N1) + (12 \times N2) + \ldots. + (1 \times N13)$$

where, N1 and N2 and … are the number of germinated seeds in first and second days, respectively, and so forth; numbers 10, 9 and … are weights applied on the number of germinated seeds at first and second days and so forth.

Germination rate index (GRI):

$$GRI = G1/1 + G2/2 + \ldots + Gx/x$$

where germination percentage at first day;

G2, germination percentage at second day and so forth.

Mean germination time (MGT): (Andalibi *et al*. 2005)

$$MGT = \sum NiTi/\sum Ni = 100/CVG$$

where, Ni is number of germinated seeds for each day, Ti is number of days as of the start of experiment, Final germination percentage (FGP): (Al-Mudaris 1998, Gharineh *et al*. 2004)

$$FGP = Ng/Nt \times 100$$

Table 2 Variance analysis of the measured traits in 22 genotypes rice landraces of northern Iran

| SOV | df | MS | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | Final germination percent | Coefficient of velocity of germination | Germination index | Germination rate index | Mean germination term | Germination rate | Mean daily germination |
| Replication | 2 | 90.48 | 0.887 | 200.05 | 245576.19 | 6.694 | 0.045 | 1.67 |
| Genotypes | 21 | 1 589.9** | 4.219 | 2 652.85** | 4 392 989.78** | 3.768 | 2.287** | 30.957** |
| Error | 42 | 283.07 | 2.720 | 351.07 | 613 986.07 | 6.302 | 0.276 | 6.256 |
| CV (%) | 22.73 | 16.47 | 27.65 | 29.38 | 23.95 | 24.15 | 30.1 | |
| Replication | 2 | 3.661 | 3.3** | 4.473* | 2.505 | 2.762 | 0.154** | 0.877** |
| Genotypes | 21 | 4 8.582** | 0.614* | 2.058* | 14.28* | 8.92** | 0.144** | 0.386** |
| Error | 42 | 5.889 | 0.335 | 1.147 | 2.335 | 1.647 | 0.026 | 0.041 |
| CV (%) | 28.86 | 27.77 | 28.9 | 26.43 | 27.87 | 28.3 | 29.5 | |

* and ** Significantly at $p < 0.05$ and $< 0.01$, respectively.

Table 3 Mean of traits, diversities extent, diversity coefficients and general heritability of traits in 22 genotypes rice landraces of northern Iran

| | Final germination percent | Coefficient of velocity of germination | Germination index | Germination rate index | Mean germination term | Germination rate | Mean daily germination |
|---|---|---|---|---|---|---|---|
| Mean | 81.52 | 10.68 | 76.028 | 2 999.18 | 11.02 | 2.43 | 9.197 |
| Rang | 80 | 4.02 | 116.80 | 4680 | 10.96 | 3.23 | 12.80 |
| δ2e | 188.46 | 0.421 | 404.57 | 722 994.23 | 2.369 | 0.288 | 6.727 |
| δ2g | 309.38 | 0.11 | 500.24 | 821 787.88 | 0.28 | 0.44 | 4.64 |
| δ2ph | 497.84 | 0.531 | 904.83 | 1 844 872.11 | 2.65 | 0.73 | 11.37 |
| PCV | 27.37 | 6.82 | 39.56 | 41.45 | 14.77 | 35.21 | 36.66 |
| GCV | 21.58 | 3.10 | 29.42 | 30.23 | 4.80 | 27.33 | 23.42 |
| h² | 62.14 | 20.71 | 55.28 | 53.20 | 10.57 | 60.49 | 40.81 |
| Mean | 9.604 | 2.273 | 4.065 | 6.644 | 5.087 | 0.368 | 0.8318 |
| Rang | 17.84 | 2 | 4.33 | 9.45 | 8.40 | 1 | 3.80 |
| δ2e | 5.12 | 0.101 | 0.43 | 1.714 | 0.869 | 0.025 | 0.109 |
| δ2g | 10.84 | 0.06 | 0.282 | 2.52 | 2.4 | 0.04 | 0.11 |
| δ2ph | 15.96 | 0.17 | 0.71 | 4.23 | 3.26 | 0.06 | 0.23 |
| PCV | 41.59 | 18.14 | 13.06 | 30.95 | 35.49 | 66.51 | 83.07 |
| GCV | 34.28 | 10.78 | 20.73 | 23.9 | 30.45 | 54.30 | 39.87 |
| h² | 67.92 | 35.37 | 39.75 | 59.50 | 73.49 | 64.52 | 48.24 |

where, Ng is total number of germinated seeds, Nt is total number of evaluated seeds, germination speed (Rs): was estimated based on Magour method and by using the following equation (Rajabi and Poustini 2005)

$$Rs = \sum Si/Di$$

where, Si is the number of germinated seeds in $i^{th}$ day, Di is day number to $n^{th}$ counting Mean daily germination (MDG), which is an index of daily germination and is calculated using the following equation:

$$MDG = FGP/d$$

where, FGP is final germination percentage (viability), d is day number to reach final germination (Kafi and Goldani 2001) Vigor Index:

$$VI = (FGP \times L)/100$$

where, FGP is final germination percentage (viability), L is sum of radicle and seedling lengths. The study genotypes were classified using cluster analysis based on all the traits and data standardized using WARD. Statistical calculations were done using MSTAT-C and Minitab-15, SPSS-16 software. Diagrams and statistical tables were drawn using Excel and Word programs.

## RESULTS AND DISCUSSION

Results from analysis of variance (Table 2) showed that mean squares of the genotypes were significant for all the traits, which represent a significant difference between the genotypes in terms of all the traits. The estimated phenotypic and genotypic coefficients (Table 3) suggest that there was a high genetic diversity among the genotypes in terms of FGP, GI, GRI, Rs, VI, seedling length, radicle length and total fresh weight of sample. In contrast, coefficient of velocity of germination (CVG), mean germination time (MGT), mean daily germination (MDG), leaf number, root number and ratio of radicle length to seedling length produced a low genetic diversity. Results from this study are consistent with findings by (Sabouri 2010). Sabouri (2010) reported that genetic diversity in terms of most of the traits associated with germination was high in rice.

Sabouri (2010) showed that the highest value of general heritability belonged to peduncle length and peduncle weight (87% and 81%, respectively), whereas the lowest value of heritability belonged to plant weight (31%) and harvest index. Furthermore, value of general heritability for grain yield was 65% in their experiment.

The genotypes being studied were classified, using cluster analysis, in terms of traits such as final germination percent (FGP), coefficient of velocity of germination (CVG), germination index (GI), germination rate index (GRI), mean germination time (MGT), germination speed (Rs) and mean daily germination (MDG), vigor index (VI), leaf number, root number, seedling length, radicle length, total fresh weight of sample and ratio of radicle length to seedling length (Fig 1). The genotypes were classified into four groups based on these traits. This classification was verified 100% by analysis of discriminant function (Fig 1). Mean squares obtained from cluster analysis were significant for FGP, CVG, GI, GRI, MGT, Rs MDG, VI, root number, seedling length and total fresh weight of sample at 1% probability level; whereas they were significant for leaf number, radicle length at 5% probability level. Traits of ratio of radicle length to seedling length did not produce a significant variation (Table 4).

Genotypes numbered 1, 3, 18, 11, 21, 4 and 9 were classified as group 1. These genotypes were in a poor status for all the traits. Genotypes numbered 2. 16, 5, 14,

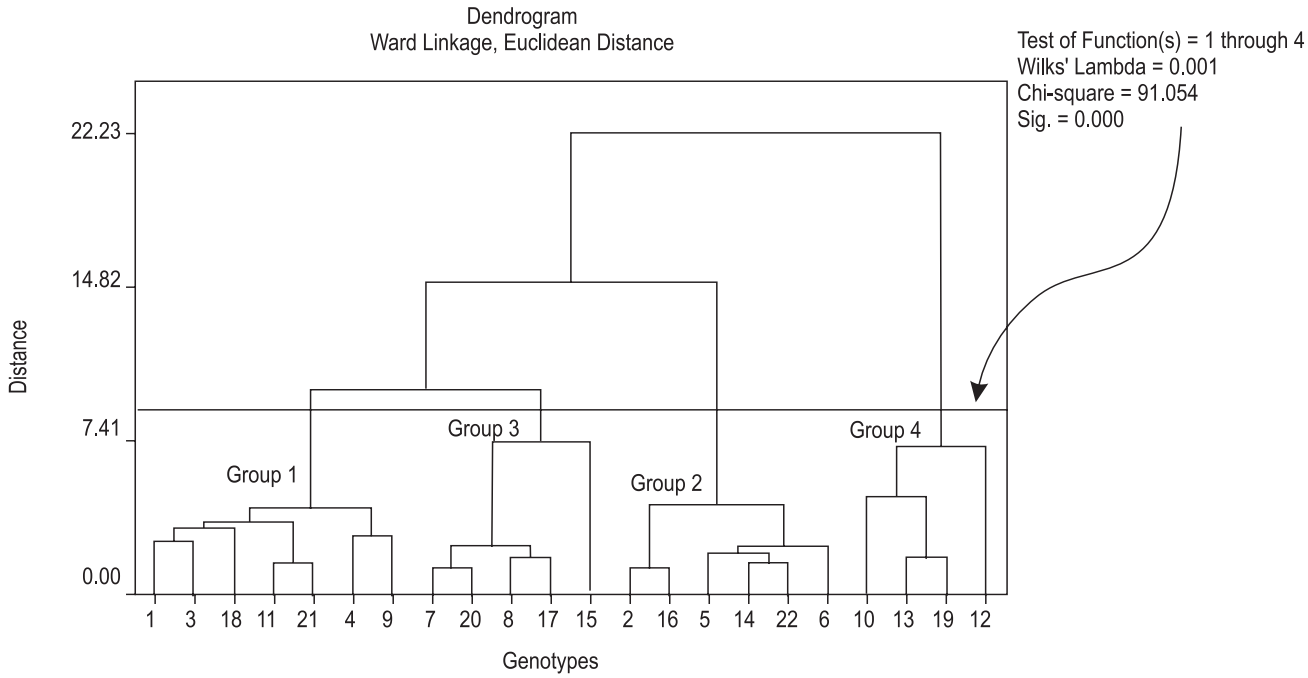


Fig 1 Dendrogram from cluster analysis based on traits significant in analysis of variance of 22 rice landraces native to northern Iran using WARD

Table 4 Comparison of groups given from cluster analysis for different traits

| Traits | Means | | | | |
|---|---|---|---|---|---|
| | Group 1 | Group 2 | Group 3 | Group 4 | Oneway Anova |
| Final germination percent | 80.95c | 94.44a | 92 b | 50 d | ** |
| Coefficient of velocity of germination | 10.72c | 10.99a | 10.92b | 9.84d | ** |
| Germination index | 71.37c | 95.53a | 93.85b | 32.67d | ** |
| Germination rate index | 2 788.57c | 3790a | 3 753.33b | 1 233.33d | ** |
| Mean germination term | 10.87b | 10.43c | 10.41d | 12.91a | ** |
| Germination rate | 2.32c | 2.95b | 2.97a | 1.16d | ** |
| Mean daily germination | 8.55b | 10.54b | 11.81a | 5.05d | ** |
| Vigor index | 9.23 b | 14.06a | 8.22c | 5.31d | ** |
| leaf number | 2.368b | 2.476a | 1.991d | 2.153c | * |
| Root number | 4.31b | 4.61a | 3.47d | 3.57c | ** |
| Seedling length | 7.07b | 8.19a | 4.84d | 5.83c | ** |
| Rootlet length | 4.39c | 6.75a | 4.11d | 5.04b | * |
| Total fresh weight of sample | 0.319b | 0.661a | 0.227c | 0.192d | ** |
| Ratio of rootlet length to seedling length | 0.614d | 0.825c | 1.08a | 0.869b | ns |

Differences between averages of each column which have common characters are not significant at probability level of 5%.

22 and 6 were classified as group 2. In contrast, these genotypes had the highest values for all the traits, while they had an average status in terms of traits such as MGT, Rs, MDG and ratio of radicle length to seedling length. Genotypes numbered 7, 20, 8, 17 and 15 were classified as group 3. These genotypes had the highest values for Rs, MDG and ratio of radicle length to seedling length, whereas for the remaining traits they were in an average status. Genotypes numbered 10, 13, 19 and 12 were classified as group 4. They had the highest values for MGT, whereas for the remaining traits they had an average to low status (Table 4).

Based on results from this study one can do appropriate intersections between the genotypes of 4 groups, particularly far genotypes for developing one or more productive varieties and improving germination power and traits associated to germination for rice native to northern Iran.

## REFERENCES

Al-Mudaris M A. 1998. Notes on various parameters recording the speed of seed germination. *Der Tropenlandwirt* **99**: 147–54.

Andalibi B Zangani E and Haghnazari A 2005. Effects of water stress on germination indices in six repeseed cultivars (*Brassica napus* L.). *Iran Journal of Agricultural Sciences* **36**: 457–63.

Garavandi M and Kahrizi D 2010. Evaluation of genetic diversity of bread wheat genotypes for henologic and morphologic traits. *Proceedings of the 11th Crop Science and Plant Breeding Congress*, (CSPBC'10), Iran, pp 537–41.

Gharineh M H. Bakhshandeh A and Ghasemi-Golezani K 2004. Vigor and seed germination of wheat cultivar in Khuzestan environmental condition. *Science Journal of Agricultural* **27**:

65–76.

Golababady M and Arzani A. 2003. Study of genetic variation and factor analysis of agronomic traits in durum wheat. *Journal of Science and Technology Agricultural and Natural Resources* **7**: 115–27.

Heydari B, Saeedi S G, Seyyed Tabatabaei B A and Soenaga K 2006. Evaluation of genetic diversity and estimation of heritability of some quantity traits in double haploid lines of wheat. *Iranian Journal of Agricultural Sciences* **37**(2): 347–56.

Kafi M and Goldani M. 2001. Effect potential water and material causing the on germination three crops wheat, sugar beet and peas. *Journal of Agricultural Industries* **15**: 121–35.

Mahfoozi S, Roustaii M, Jasemi S H, Ketata H and David Flower B 2004. Breeding for increasing wheat yield in the cold dryland regions of Iran. *Proceeding of the 4th International/Crop Science Congress*, Brisbane, September 26- October 1, 2004, Australia.

McKenzie K S, Rutger J N and Peterson M L 1980. Relation of seedling vigor to semidwarfism, early maturity and pubescence in closely related rice lines. *Crop Science* **20**: 169–72.

Mahabub H, 2005. Dose rice research redues poverty in Asia? Rice Today. **5**(1): 37.

Mgonja M A, Ladeinde T A O and Aken'Ova M E 1993. Genetic analysis of mesocotyl length and its relationship with other agronomic characters in rice (*Oryza sativa* L.). *Euphytica* **72**: 189–95.

Miura K, Lin S, Yano M and Nagamine T. 2002. Mapping quantitative trait loci controlling seed longevity in rice (*Oryza sativa* L.). *Theoretical and Applied Genetics* **104**: 981–6.

Mollasadeghi V. 2010. Effect of potassium humate on yield and yield components of wheat genotypes under end seasonal drought stress condition. MSc thesis, Islamic Azad University, Ardabil branch, Iran.

Peterson M L, Jones D B and Rutger J N. 1978. Cool temperature screening of rice lines for seedling vigour. *ILRiso* **27**: 269–74.

Rajabi R and Poustini K 2005. Effects of NaCl salinity on seed germination of 30 Wheat (*Triticum aestivum* L.) cultivars. *Science Journal of Agricultural* **28**: 29–44.

Redona E D and Mackill D J. 1996. Mapping quantitative trait loci associated with cold tolerance at the post-germination stage in rice. *Biotechnology Equipment* **22**: 536–40.

Sabouri, H. 2010. Positioning of QTLs for germination characters in rice genotypes using micro markers of satellite under salinity condition. *Iranian Journal of Biology* **23**: 333–42.

Shahryari R, Mahfoozi B, Mollasadeghi V and Khayatnezhad M. 2011. Genetic diversity in bread wheat for phenological and morphological traits under terminal drought stress condition. *Advances in Environmental Biology* **5**(1): 169–72.

Wan J M, Liang L, Tang J Y, Wang C M, Hou M Y, Jing W and Zhang L X 2006. Genetic dissection if the seed dormancy traits in cultivated rice (Oryza sativa L.). *Plant Sciences* **170**: 786–92.

Zeng D L, Guo L B, Xu Y B, Yasukumi K, Zhu L H and Qian Q. 2006. QTL analysis of seed storability in rice. *Plant Breeding* **125**: 57–60. doi: 10.1111/j.1439-0523.2006.01169.x

Zhang Z.H, Yu S B, Yu T, Huang Z and Zhu Y G, 2005. Mapping Quantitative Trait Loci (QTLs) for seedling vigour using recombinant inbred lines of rice (*Oryza sativa* L.). *Field Crop Research* **91**: 161–70.