



EVALUATION OF GENETIC DIVERSITY OF 10 GENOTYPE ZEA MAYS IN TERMS OF SOME GERMINATION COMPONENTS

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ABSTRACT: In order to study genetic diversity of 10 genotype in terms of germination components an experiment was conducted at laboratory of agriculture faculty of Islamic Azad University, Dezful branch, as randomized complete blocks design with three replications, in year 2013. The traits measured during the study included 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) and vigor index (VI). 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 and VI of sample than in terms of other traits. Study genotypes were classified into 2 groups using cluster analysis. Mean squares between the groups were significant for all the traits. Genotypes numbered 1, 3, 4 and 9 were classified as group 1. These genotypes were in a poor status for all the traits. Genotypes numbered 2, 5, 6, 7, 8 and 10 were classified as group 2. In contrast, these genotypes had the highest values for all the traits.

Keywords: Zea mays, genetic diversity, germination components, cluster analysis

INTRODUCTION

Including grain maize temperate and tropical regions of the world is important and valuable in terms of variety, however, is of vital importance. Corn production in the world's third largest cereal crop after rice is important [1]. The old power plant due to high adaptation and adjustment is spread all over the world with different climates [2]. High germination power and strong components for germination are among the most important traits determining the better establishment of rice 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 [3]. In spite of genetic diversity for germination power and traits associated with germination in rice [3 and 4], rice breeders have not been so successful in improving this trait through classic ways [5]. Based on forgoing discussion, it is highly important to conduct studies on genetic diversity of various cultivars of this plant for breeding program. Golabadi [6] after studying genetic diversity of 300 Durum wheat genotype reported that the variation of the genotypes for traits such as grain yield harvest index and spike number per unit area was significantly high. Geravandi and Kahrizi [7] 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 per m², grain number per 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. Mahfouzi et al [8] 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. The present study was designed to investigate the genetic diversity of maize seed germination was carried out in terms of components.

MATERIALS AND METHODS

The experiment was conducted in laboratory of Islamic Azad University, Dezful branch, in 2012. The design used for experiment was randomized complete blocks with three replications. 10 seeds were cultured in each Peteri dish. Germination test was done in the germinator under such conditions as 25 °C, 70% relative humidity under 16 hours light and 8 hours 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) and vigor index (VI) were measured. The calculations were done using the following equations:

- 1) Coefficient of velocity of germination (CVG):

$$CVG = 100 \times \sum N_i / \sum N_i T_i$$

where, N_i is the number of germinated seeds for each day, T_i is number of days as of the start of experiment,

- 2) Germination index (GI):

$$GI = (13 \times N_1) + (12 \times N_2) + \dots + (1 \times N_{13})$$

where, N_1 and N_2 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.

- 3) Germination rate index (GRI):

$$GRI = G_1/1 + G_2/2 + \dots + G_x/x$$

G_1 = germination percentage at first day

G_2 = germination percentage at second day and so forth

- 4) Mean germination time (MGT): [9]

$$MGT = \sum N_i T_i / \sum N_i = 100 / CVG$$

where, N_i is number of germinated seeds for each day, T_i is number of days as of the start of experiment,

- 5) Final germination percentage (FGP): [10 and 11]:

$$FGP = N_g / N_t \times 100$$

where, N_g is total number of germinated seeds, N_t is total number of evaluated seeds,

- 6) Germination speed (Rs): was estimated based on Magour method and by using the following equation, [12]

$$R_s = \sum S_i / D_i$$

where, S_i is the number of germinated seeds in i th day, D_i is day number to n th counting

- 7) 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 [13]

- 8) 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.

Table 1 - genotypes in this study

Number	Genotypes
1	SC647
2	SC260
3	SC301
4	SC604
5	SC370
6	SC700
7	SC302
8	SC704
9	SC400
10	SC500

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 not included) suggest that there was a high genetic diversity among the genotypes in terms of FGP, GI, GRI, Rs and VI. Results from this study are consistent with findings by Sabouri [14]. Sabouri [14] reported that genetic diversity in terms of most of the traits associated with germination was high in rice. 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) and vigor index (VI). The genotypes were classified into four groups based on these traits. This classification was verified 100% by analysis of discriminant function. Mean squares obtained from cluster analysis were significant for FGP, CVG, GI, GRI, MGT, Rs and MDG, VI, at 1% probability level (Table 3). Genotypes numbered 1, 3, 4 and 9 were classified as group 1. These genotypes were in a poor status for all the traits. Genotypes numbered 2, 5, 6, 7, 8 and 10 were classified as group 2. In contrast, these genotypes had the highest values for all the traits. 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 3).

Table 2- Analysis of variance

S. O. V	df	MS							
		Final Germination Percent	Coefficient of Velocity of Germination	Germination Index	Germination Rate Index	Mean Germination Term	Germination rate	Mean daily germination	Vigor Index
Replication	2	80.48	0.987	260.05	298841.19	5.094	0.145	5.05	8.661
Genotypes	9	2089.9**	5.219	2962.85**	5458989.78**	4.08	5.287**	20.957**	52.582**
Error	20	383.07	3.720	381.07	614520.07	8.302	0.376	4.235	6.889
CV (%)		12.73	6.47	17.65	19.08	3.95	14.15	25.1	25.5

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

Table 3 - Comparison of groups given from cluster analysis for different traits

Traits	Means		
	The 1 group	The 2 group	Oneway Anova
Final Germination Percent	80.95 c	94.44 a	**
Coefficient of Velocity of Germination	10.72 c	10.99 a	**
Germination Index	71.37 c	95.53 a	**
Germination Rate Index	2788.57 c	3790 a	**
Mean Germination Term	10.87 b	10.43 c	**
Germination rate	2.32 c	2.95 b	**
Mean daily germination	8.55 b	10.54 b	**
Vigor Index	9.23 b	14.06 a	**

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

REFERENCES

- [1] Khavari khorasani, S. 2009. The Corn Handbook. Golami Publication, Tehran, Iran.
- [2] Mir-Hadi, M. 2002. Maize. Res. org. Agric. Eyten and Educate, 131p. (In Persian).
- [3] Zhang, Z.H., S.B. Yu, T. Yu, Z. Huang and Y.G. Zhu, 2005. Mapping Quantitative Trait Loci (QTLs) for seedling vigour using recombinant inbred lines of rice (*Oryza sativa* L.). *Field Crop Res.*, 91: 161-170.
- [4] Zeng, D.L., L.B. Guo, Y.B. Xu, K. Yasukumi, L.H. Zhu and Q. Qian, 2006. QTL analysis of seed storability in rice. *Plant Breeding*. 125: 57-60. doi: 10.1111/j.1439-0523.2006.01169.x
- [5] McKenzie, K.S., J.N. Rutger and M.L. Peterson, 1980. Relation of seedling vigor to semidwarfism, early maturity and pubescence in closely related rice lines. *Crop Sci.*, 20:169-172.

- [6] Golababady, M. and A. Arzani, 2003) Study of genetic variation and factor analysis of agronomic traits in durum wheat. *J. Sci and Technol. Agric and Natur. Resour.* 7: 115-127.
- [7] Garavandi, M. and D. Kahrizi, 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: 537-541.*
- [8] Mahfoozi, S., M. Roustaii, S.H. Jasemi, H. Ketata and B. David Flower, 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.*
- [9] Andalibi, B., E. Zangani and A. Haghazari, 2005. Effects of water stress on germination indices in six reseed cultivars (*Brassica napus L.*). *Iran J. Agric. Sci.*, 36: 457-463.
- [10] Al-Mudaris, M.A., 1998. Notes on various parameters recording the speed of seed germination. *Der Tropenlandwirt*, 99: 147-154.
- [11] Gharineh, M.H., A. Bakhshandeh and K. Ghasemi-Golezani, 2004. Vigor and seed germination of wheat cultivar in Khuzestan environmental condition. *Sci. J. Agric.*, 27: 65-76.
- [12] Rajabi, R. and K. Poustini, 2005. Effects of NaCl salinity on seed germination of 30 Wheat (*Triticum aestivum L.*) cultivars. *Sci. J. Agric.*, 28: 29-44.
- [13] Kafi, M. and M. Goldani, 2001. Effect potential water and material causing the on germination three crops wheat, sugar beet and peas. *J. Agric. Indus.*, 15: 121-135.
- [14] Sabouri, H., 2010. Positioning of QTLs for germination characters in rice genotypes using micro markers of satellite under salinity condition. *Iranian J. Biol.*, 23: 333-342.