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Annals of Biological Research, 2012, 3 (12):5744-5747
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Evaluation of Bread Wheat Recombinant Inbred Lines under drought conditions

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ABSTRACT

To analyze genetic diversity and to estimate heritability and genetic gain of bread wheat recombinant inbred lines (RILs), 79 RILs derived from a cross between a commercial variety Yecoro Rojo and NO.49 an Iranian local genotype were assessed using square lattice design under normal and water deficit conditions. Combined analysis of variance revealed significant differences among lines for all the studied traits, whereas line and the irrigation interaction was not significant. Among the measured traits, grain yield, number of spikes per square meter, number of grain per spike, plant height and harvest index showed higher phenotypic and genotypic coefficient of variation. Narrow-sense heritability ranged from 38.04 for number of grain per spike to 86.25 for 1000-grain weight. Expected genetic gain was varied from 7.10% (day to heading) to 29.83% (harvest index).

Key words: Bread wheat, Genetic gain, Genetic variability, Narrow-sense heritability, Recombinant inbred line

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the most important cultivated agricultural plant that not only allocating approximately one sixth of arable soil to itself, but also constituting a major part of human's food [1]. Cultivated land and crop yield of wheat are respectively 6.6 million hectares and 13.4 million tonnes in Iran and 225.4 million hectares and 681.9 million tonnes in the planet Earth [2]. drought stress is a limitation on successfully producing the wheat. According to Pfeiffer et al. [3] regularly around 50% or 230 million ha wheat cropland is annually affected by drought conditions. Therefore, genotypes of wheat which are tolerable to drought stress can be selected to increase the productivity in some regions [4]. In order to produce and select productive strains, genetic resources and the information on major traits' genetic parameters should be available. Heritability is regarded as one of the genetic parameters used to determine the breeding methods, which is also indicative of phenotype and genotype adaptation degree [5]. The additive genetic variance portion is important for genotype selection; as in successful selection, it is essential for the additive variance portion to be high enough in genetic variance (narrow-sense heritability) [6]. Simple phenotypic selection can be used in traits showing high heritability [7]. However, high heritability is not sufficient for selection in generations unless it is accompanied by an increase in genetic gain [8]. Manal [9] found rather high heritability in "day to heading", "spike length" and "1000 grain weight". Soylo [10] reported low heritability for narrow-sense heritability of "number of spikes per square meter" and "number of grains per spike". By evaluating wheat doubled haploid lines, Heidari et al. [11] showed high narrow-sense heritability and genetic gain of selection for plant height, 1000 grain weight, and harvest index. The purpose of this research is to investigate

genetic variability, to estimate trait's heritability and to determine genetic gain of recombinant inbred lines under drought conditions.

MATERIALS AND METHODS

Current research was undertaken in Tabriz university research station (1360m above mean sea level, longitude: 46°, 17' E and latitude: 38°, 5' N). The population studied consisted of 79 F₇ recombinant inbred lines (RILs) obtained by single seed descent from a cross between No.49 genotype as maternal parent (Tall, drought-resistant, Iranian origin) to Yecora Rojo cultivar as paternal parent (dwarf, semi-resistant to drought, American origin) and the parents. The assessment carried out in the form of dual square lattice pattern under both normal irrigation and lack of irrigation conditions. Each test unit was comprised of three rows of two-meter length placed at 15cm intervals for each genotype. Grains were placed on rows at 2cm intervals. Under normal condition, irrigation was conducted after 70mm evaporation from class A pan. Under drought condition, irrigation carried out based on 70mm evaporation until heading stage and on 120mm evaporation between heading stage and maturity stage. Apart from evaluating grain yield and harvest index for which all test unit plants were assessed, in order to study other traits we have used 10 plants in each test unit as a sample. Combined analysis of variance was used based on randomized complete blocks of adjusted averages of genotypes. In this analysis, the mean error degrees of freedom were calculated from total degrees of freedom of error in the analysis of variance. Mean error's degrees of freedom calculated for grain yield, numbers of grain per spike and thousand-grain weight respectively as follows: 160, 128 and 128. For other traits, it was calculated as 144. Regarding that for all traits analyzed in combined analysis, the interaction effect of line × conditions was not significant; genetic parameters was determined based on mean irrigation conditions. Genetic variance of traits calculated on the basis of $\sigma_g^2 = (MS_L - MS_{L \times C}) / (r \times p)$ formula in which MS_L and MS_{L×C} respectively indicates mean square line and interaction effect of line in condition. r and p represent number of repeats and environment, respectively. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variability (PCV) of traits respectively calculated by genetic variance square root and phenotype variance square root divided by mean of each trait (in percentage) [12]. Due to the fact that lines were inbred; narrow-sense heritability was estimated by dividing genetic variance by phenotype variance [13]. Standard error of heritability calculated using Kempthorne [14] formula as follows:

$$SE_{h_N} = \sqrt{\frac{2MSE^2 \times \left(\frac{1}{(df_e + 2)} + \frac{1}{(df_l + 2)} \right)}{MST^2}}$$

In the mentioned formula, MS_E and MS_L are respectively the averages of square mean error and line. df_e and df_l represent degree of freedom related to mean error and line, respectively. In order to calculate genetic gain (R) we

used $R = \frac{KC\sigma_g^2}{\sigma_g^2 + \frac{\sigma_e^2}{2}}$ formula in which K indicates selection intensity (equivalent to 1.5) and C indicates parents

control coefficient (equivalent to 1). The calculated genetic gain (R) determined as a percentage of whole genotypes' average (μ) for each trait in the following formula: Genetic gain = $\frac{R}{\mu} \times 100$

RESULTS AND DISCUSSION

Combined analysis results showed that there is 1% significant difference between lines with respect to all studied traits and probability levels, which suggests that there is a high genetic variation among lines with respect to such traits. Regarding all studied traits, the interaction effect of line × conditions were not significant, which in turn indicates that the effect of lines were similar under both normal irrigation and drought stress (table1). Genetic and phenotype parameters were evaluated on the basis of data obtained from combined analysis (table 2). Phenotypic Coefficient of Variability of all traits had higher amounts than genotypic coefficient of variation. This suggests that environmental factors have significant effect on expression of such traits. Similar result was observed by Shivkumar [15]. The highest value of phenotypic coefficient of variability related to grain yield, harvest index and number of grains per spike; while day to heading and plant height contained the lowest value. The highest and lowest amount of genotypic coefficient of variation was related to grain yield and day to heading, respectively. Concerning standard errors, the heritability of all studied traits were significant. The highest estimations of narrow-sense heritability belonged to 1000 grain weight and harvest index; while lowest estimation was related to number of grains per spike. Plant height, spike length, 1000 grain weight and harvest index had moderate to high narrow-sense heritability. There were also high amounts of genetic gain estimated for such traits, which suggests the additive nature of gene function in the expression of such traits. Results of the present study agreed with Prasad et al., [16] Grain yield had rather low narrow-sense heritability whereas its genetic gain evaluated was high (23.70%). This indicates that

environmental factors play more important role in the expression of this trait. Liu et al. [17] results were similar to our data. Low value of heritability, moderate genetic efficiency and relatively high amount of phenotype coefficient of variation for number of grains per spike and number of spikes per square meter indicate non-additive nature of gene function and higher effect of environment on such traits. Therefore, these traits doesn't have the capability to be exploited in genetic improvement programs. Nayeem et al. [18], obtained same results while studying on Durum Wheat genotypes.

Table 1- Combined analysis of variance for all traits in recombinant inbred lines under normal and drought stress conditions

source	DF	Plant Height	Spike Length	Day to Heading	Mean Square				
					No. spikes	1000-grain weight	No. grains/spike	Grain yield	Harvest Index
condition	1	181/40**	0/465**	25/282**	366795/472**	19/144**	90/788**	129775/42**	49/346**
lines	80	110/892**	1/01**	43/662**	8115/361**	55/394**	40/132**	4861/35**	180/072
Lines×Condition	80	21/595 ^{ns}	0/218	5/281 ^{ns}	2574/77 ^{ns}	2/29 ^{ns}	9/611 ^{ns}	792/73 ^{ns}	6/600 ^{ns}
Mean Errors	144	18/465	0/159	4/290	1964/541	2/122	11/611	1302/47	7/632

*, ** Significant at 5% and 1% probability levels, respectively; ns, not significant.

Table 2- Estimation of phenotypic, genetic and environmental variances; phenotypic and genetic coefficient of variability, heritability, Standard error of heritability and genetic gain (% of mean) for all traits in 81 RILs under mean normal and drought stress conditions.

	Plant Height	Spike Length	Day to Heading	No. spikes	1000-grain weight	No. grains/spike	Grain yield	Harvest Index
Genetic variance	23/106	0/212	9/543	1537/705	13/318	7/13	889/72	43/11
Phenotypic variance	41/57	0/371	14/133	3502/246	15/44	18/74	2192/19	50/74
environmental variance	18/465	0/159	4/290	1964/54	2/122	11/611	1302/47	7/632
phenotypic Coefficient of variation	13/93	9/68	6/31	17/12	15/03	18/39	29/70	22/50
Genotypic Coefficient of Variation	10/38	7/32	5/26	11/34	13/96	11/34	18/92	20/75
heritability	55/56	57/22	69/64	43/90	86/25	38/04	41/78	84/95
Genetic gain (% of mean)	13/18	9/38	7/10	13/29	20/16	6/70	21/57	29/83
Standard error of heritability	0/032	0/030	0/019	0/057	0/022	0/057	0/077	0/036

CONCLUSION

Concerning calculated values of genotype coefficient of variation for traits in studied recombinant inbred lines, we found that grain yield, number of grains per spike, 1000 grain weight, number of spikes per square meter, plant height and harvest index compared to other traits, had higher capacity to be selected in genetic improvement programs. Evaluation of genetic gain related to selection of traits showed that in addition to sufficient genetic variation, high amount of heritability is required to increase genetic gain. Furthermore, the results showed that although genetic variation and genetic gain for grain yield was high; due to low amount of heritability, this trait cannot be used as a selection index for the next generation. Among studied lines some traits showed favorable values of genetic variation, heritability and genetic efficiency including: 1000 grain weight, harvest index and plant height. As a result, by selecting better lines with respect to such factors, selection efficiency could be improved in order to increase grain yield.

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