



IJABBR- 2014- eISSN: 2322-4827

International Journal of Advanced Biological and Biomedical Research

Journal homepage: www.ijabbr.com



Original Article

Genetic Diversity and Relationships of Agronomic Characters in Wheat Recombinant Inbred Lines

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ARTICLE INFO

Article history:

Received: 09 Sep, 2014

Revised: 28 Oct, 2014

Accepted: 22 Nov, 2014

ePublished: 30 Dec, 2014

Key words:

Agronomic traits

Genetic diversity

Grain yield

Recombinant inbred line

ABSTRACT

Objective: Wheat is the most important crop in Iran. Self sufficiency in wheat production is one of the economic and food safety policies in the country. In spite of the efforts which have been made in this area, the mean of wheat yield in Iran is less than its world average. **Methods:** In order to identifying of the high yielding wheat lines with optimal characteristics and to determine the traits which could be used as the selection index for increasing of grain yield, 40 recombinant inbred lines derived from a cross between Norstar and Zagros cultivars were evaluated in a randomized complete block design with three replications. **Results:** Significant differences were observed among the lines for all of studied traits, except the spike weight, flag leaf area and the straw yield. Higher genetic diversity was observed among the inbred lines with respect to the kernel per spike, the number of spikes, the biomass and the straw yield. The Peduncle weight, second internode weight, number of kernels per spike per spike, number of the spikes and 1000 kernel weight traits showed a high degree of heritability. The highest genetic gain was estimated for the peduncle weight, the second internode weight and number of kernel per spike. Correlation, stepwise regression and path analyses revealed the number of kernels per spike and the number of spikes in plot had highest direct effects on grain yield. The analyses were carried out using WARD algorithm and standardized data. Cluster analysis based on all traits assigned the lines into groups.

1.INTRODUCTION

Wheat (*Triticum aestivum* L.) has been a staple food of the major civilizations for 8000 years. It is the most widely grown cereal crop in the world, occupying 17% of the cultivated area worldwide, feeding about 40% of the world's population and providing 20% of the total food calories and protein in human nutrition (Gupta et al., 2005). The objective of plant breeding is development of cultivars combining high stability and productivity with good quality (Fasoula, 2008). A great success of

developing high yielding wheat genotypes has been achieved through breeding. Improvement of the grain yield is a major objective of most breeding programs. Recently, scientist have associated the progress in plant breeding with the presence of diverse source material with new germplasm, including such created by breeders as published by Mangova and Ra-chovska (2004). The use of multivariate statistical algorithms is an important strategy for classification of the inbred lines and analysis of the genetic relationships among the breeding material (Mohammadi & Prasanna, 2003). Yield is a complex trait

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and its value depends on yield components; the number of spikelet's per spike, the number of grain per spike, the grain weight per spike and other parameters, and also is influenced by the genotype and the agro ecological conditions (Drezner *et al.*, 2007).

2. MATERIALS AND METHODS

The experiment was carried out at the fields of Research Station in University of Tabriz, Iran, over one year (2013). The station is located at 38°52N latitude, 46°17E longitude and at altitude of 1360 m above the sea level. To identify high yielding wheat lines with optimal characteristics and to determine the traits which could be used as the selection index for increasing of grain yield, 40 recombinant inbred lines (RILs) derived from a cross between Norstar (winter wheat) and Zagros (spring wheat) cultivars (Table 1) were evaluated in a randomized complete block design with three

replications. Each plot of each RIL consisted of three 2m long rows with spacing of 20cm between rows. RILs evaluated for peduncle weight, second internode weight, spike weight, number of kernels per spike, biomass, grain yield, 1000 kernel weight, plant height, peduncle length, second internode length, spike length, harvest index, flag leaf area and straw yield traits. The data was analyzed using the SPSS V.20 and the Minitab software. In addition, the comparisons of the means were tested at the 1% and 5% levels using LSD and Duncan's method. The effects of the agronomic and morpho-physiological traits on yield were determined by simple correlation, stepwise regression. In path analysis, grain yield used as dependent variable, and the other studied traits were used as predictor variables.

Table 1.

The RILs numbers derived from crossing between Norstar and Zagros cultivars

Line	No.	Line	No.	Line	No.	Line	No.
RIL-206	32	RIL-95	21	RIL-45	11	(1) Zagros	1
RIL-225	33	RIL-102	22	RIL-46	12	(2) Norstar	2
RIL-239	34	RIL-143	23	RIL-51	13	RIL-8	3
RIL-265	35	RIL-145	24	RIL-58	14	RIL-15	4
RIL-281	36	RIL-159	25	RIL-62	15	RIL-23	5
RIL-293	37	RIL-163	26	RIL-63	16	RIL-26	6
RIL-296	38	RIL-182	27	RIL-68	17	RIL-27	7
RIL-298	39	RIL-183	28	RIL-86	18	RIL-28	8
RIL-300	40	RIL-184	29	RIL-93	19	RIL-31	9
RIL-328	32	RIL-195	30	RIL-94	20	RIL-32	10

3. RESULTS AND DISCUSSION

Being aware of the heritability of traits is one the essential information in determining the rate of success in plant selection, because response selection depends on additive genetic variance. Considering the fact that the genetic variance among the recombinant inbred lines is an estimation of double the additive genetic variance of the initial population (Carter *et al.*, 2005), therefore all of the genetic variances among the studied lines are additive and heritability is kind of narrow sense heritability.

The degree of studied traits heritability displayed in table 2. The highest degree of heritability was observed for number of kernels per spike, number of spike in plot and 1000 kernel weight traits (respectively 0.38, 0.35 and 0.34). A high heritability for the spike length (Manie *et al.*, 2009) and weight of 1000 kernels (Ahmad *et al.*, 2009) were observed in other researches.

The weight of the Peduncle showed highest genetic gain (20.35%) than other traits (Table 2), also had the highest genetic coefficient of variation (20.51%). The number of kernels per spike and weight of the second internode with 19.60% and 17.77% respectively, had the second and third highest values in genetic gain. The lowest genetic gain belonged to number of kernels per plot.

Correlation of the grain yield with biomass, number of spike, number of kernel per spike, Peduncle weight, spike weight, second internode weight, plant height, length of second internode and length of spike was positive and significant at 1% level of probability (Table 3). Among of grain yield components (the number of the spikes per plot, the number of kernels per spike and the weight of 1000 kernels) only 1000 kernels' weight did not show significant correlation with grain yield.

The biomass and the yield of straw showed the highest correlation ($r=0.954$). Considering the fact that biomass consists of the straw yield plus the grain yield, presence of such strong association between these two traits can

be logical. The biomass showed a positive and very significant correlation with number of spikes per plot and plant height. However, it had a positive but very low significant correlation with length of the peduncle, length of second internode, weight of peduncle and grain yield. In addition, it displayed a negative significant correlation with the harvest index Mohsin et al (2009) reported presence of a positive and significant correlation between the grain yield and the number of the spikes in wheat. Therefore, based on the correlation between this trait and the grain yield, selection of spikes with a higher number of spikes could be effective in increasing the yield of wheat.

Stepwise regression analysis, with 3 degrees of freedom, was significant at 1% level of probability. In this analysis, those variables which had a significant impact and remained in the equation were as followed: number of the kernel per spike, number of spike per plot, and weight of 1000 kernels. The adjusted coefficient of determination (R^2_{adj}) was 0.878, which means that about 88% of the changes in the yield were explained with remained traits in regression model.

Path analysis identified the number of spikes in plot as the variable with the most important direct effect (0.59) on grain yield (Table 4). The highest indirect effect of on grain yield was displayed by the number of kernels in spike via number of spike in plot. Despite the insignificance of the correlation between weight of 1000 kernels and grain yield, this trait had a positive and direct impact on the grain yield. It worth mentioning that the indirect effect of this trait on grain yield was positive via the number of kernels, but it was negative via the number of the spikes. Many researchers have reported the direct positive effect of the number of kernels (Kotal et al., 2010, Mohsin et al., 2009) on grain yield. In the many studies, number of kernels in spike has been reported as the most important factor affecting the grain yield. Aly and EL-Bana (1994) also with performing of path analysis for yield components of wheat genotypes grown at different levels of Nitrogen

fertilizer, showed that the number of spikes, number of kernels per spike, and weight of 1000 kernels justified 98.9% of the grain yield variations. Moreover, they associated the maximum number of direct effects with the number of spike per square meter. Cluster analysis based on squared Euclidean distance and ward's method, categorized the RILs into four groups (Figure 1). This classification was verified by discriminate analysis. The first group consisted of 13 RILs. The Zagros and Norstar parents were nested in this group and its members had the highest values for weight of spike, number of kernels, and grain yield in compared to others. The RILs in this group could be used to increase the grain yield in breeding projects. Four RILs were placed in the second group. The lines in this group had a lower mean values with regard to all of the traits in this study than other RILs and the other groups. The third group consisted of eight RILs and had the highest harvest index. In the fourth group, 15 lines were placed, which had intermediate values for studied traits.

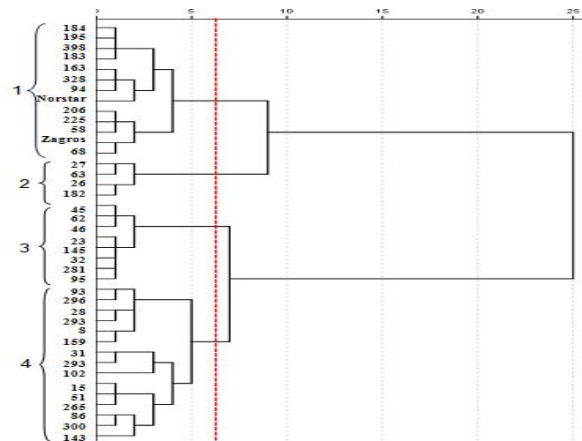


Figure 1. Dendrogram obtained by cluster analysis (Ward's method) of 40 RILs based on all traits

Table 2.

Variance components, genetic and phenotypic coefficients of variation and heritability for the measured characters

	flag leaf area	biomass	number of spike in plot	Number of kernels per spike	spike weight	second internode weight	peduncle weight
genetic variance	0.14	7967.52	1693.52	14.38	0.01	0.001	16×10 ⁻⁴
Genetic coefficient of variation (%)	5.36	11.32	11.63	16.01	8.5	17.43	20.51
variance phenotypic	0.82	17294.29	2242.39	18.67	0.05	16×10 ⁻⁴	26×10 ⁻⁴
narrow sense heritability	0.09	0.23	0.35	0.38	0.13	0.31	0.30
standard error of heritability	0.22	0.15	0.07	0.06	0.2	0.11	0.10
genetic gain	0.27	106.03	0.62	5.82	0.10	0.04	0.05
Percentage of genetic gain	3.88	13.31	0.18	19.60	6.10	17.77	20.35

	straw yield	harvest index	spike length	second internode length	peduncle length	plant height	1000 kernel weight	grain yield
genetic variance	4519.45	6.6×10 ⁻⁴	0.42	0.97	7.19	24.4	3.30	788.63
Genetic coefficient of variation (%)	13.14	7.26	9.10	6.17	8.24	7.54	5.40	9.79
variance phenotypic	12652.74	39×10 ⁻⁴	1.01	1.72	13.49	42.84	4.87	1993.86
narrow sense heritability	0.18	0.08	0.20	0.28	0.26	0.28	0.34	0.20
standard error of heritability	0.17	0.24	0.16	0.12	0.13	0.12	0.09	0.16
Genetic gain	70.3	0.02	0.73	1.29	3.42	6.52	2.59	30.9
Percentage of genetic gain	14.69	4.85	8.82	7.61	10.52	9.14	8.24	9.70

Table 3.

Correlations among studied characters in recombinant inbred lines of wheat

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1.peduncle weight	1														
2.second internode weight	0.62**	1													
3. spike weight	0.59**	0.70**	1												
4.Kernels per spike	0.59**	0.53**	0.81**	1											
5.Number of spike per plot	0.23 ^{ns}	0.12 ^{ns}	0.07 ^{ns}	0.24 ^{ns}	1										
6.Biomass	0.40**	0.19 ^{ns}	0.21 ^{ns}	0.24 ^{ns}	0.66**	1									
7.Grain yield	0.58**	0.45**	0.55**	0.74**	0.71**	0.56**	1								
8.1000 kernel weight	0.24 ^{ns}	0.22 ^{ns}	0.38*	0.06 ^{ns}	-0.12 ^{ns}	0.00 ^{ns}	0.14 ^{ns}	1							
9.plant height	0.78**	0.54**	0.48**	0.43**	-0.18 ^{ns}	0.60**	0.43**	0.11 ^{ns}	1						
10.peduncle length	0.64**	0.20 ^{ns}	0.18 ^{ns}	0.16 ^{ns}	-0.03 ^{ns}	0.43**	0.18 ^{ns}	0.14 ^{ns}	0.82**	1					
11.second internode length	0.63**	0.64**	0.43**	0.45**	0.24 ^{ns}	0.49**	0.46**	0.03 ^{ns}	0.77**	0.56**	1				
12.spike length	0.62**	0.70**	0.69**	0.53**	0.25 ^{ns}	0.31*	0.52**	0.31*	0.50**	0.22 ^{ns}	0.48**	1			
13.harvest index	0.03 ^{ns}	0.21 ^{ns}	0.27 ^{ns}	0.35*	-0.27 ^{ns}	-0.63**	0.22 ^{ns}	0.13 ^{ns}	-0.27 ^{ns}	-0.30 ^{ns}	-0.09 ^{ns}	0.18 ^{ns}	1		
14.flag leaf area	0.39*	0.50**	0.51**	-0.33*	-0.04 ^{ns}	0.02 ^{ns}	0.27 ^{ns}	0.50**	0.11 ^{ns}	0.01 ^{ns}	0.27 ^{ns}	0.58**	0.21 ^{ns}	1	
15.straw yield	0.24 ^{ns}	0.04 ^{ns}	0.02 ^{ns}	-0.00 ^{ns}	0.49**	0.99**	0.26 ^{ns}	-0.07 ^{ns}	0.53**	0.58**	0.40*	0.15 ^{ns}	-0.83**	0.07 ^{ns}	1

Table 4.

Path analysis of the grain yield with the associated traits in recombinant inbred lines of wheat

Variables added to the model	Indirect effect via			Direct	Simple correlation with grain yield
	1000 kernels weight	Number of spike per plot	Number of kernel per spike		
Number of kernel per spike	0.01	0.17	—	0.58	0.74**
Number of spike per plot	0.02	—	0.17	0.59	0.71**
1000 kernels weight	—	-0.07	0.03	0.18	0.14 ^{ns}

CONCLUSION

The weight of Peduncle, weight of 1000 kernels, number of spikes per plot, length of second internode and number of the kernels in spike benefited from a narrow sense heritability over 0.6; whereas, flag leaf area and harvest index traits had a lower heritability compared to the other traits. The weight of Peduncle, weight of second internode and number of kernels in the spike showed the highest genetic gain and the number of spikes per plot demonstrated the lowest. In the stepwise regression analysis, number of kernels, number of spikes, and the weight of 1000 kernels entered the model as the variables affecting the grain yield. These traits, together, determined 88% of variation in the grain yield. The cluster analysis based on all traits classified RILs into four clusters. The RILs placed in the first group could be used to increase the grain yield in breeding programs.

RECOMMENDATIONS

It is recommended to repeat the experiment longitudinally in multiple locations and years in order to study of genotypes and the environment interactions. Moreover, it is suggested to use the molecular markers as a complimentary method to study genetic variation.

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