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Grouping of wheat recombinant inbred lines (RILs) in terms of yield and yield component at two years

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Abstract

To study genetic diversity and grouping of wheat recombinant inbred lines (RILs) in terms of yield and yield component, 38 RILs derived from across between Zagros (facultative type, early maturing and drought resistant) and Norstar (winter type, late maturing and cold resistant) along with parental lines were evaluated in randomized complete block design (RCBD) with three replications during 2010-2011 and 2011-2012 years. Based on combined analysis of variance, significant differences were observed between lines for grain yield and 1000 grain weight. Line × year interaction was significant for number of grain per spike, number of spike per square meter and 1000 grain weight. Based on two years mean for number of grain per spike lines of 51, 32, 296, 15 and 58, number of spike per square meter lines numbers 183, 145, 293, 328, 195 and 184, 1000 grain weight lines 145, 93, 159, 46 and Zagros and grain yield lines 28, 31, 145, 281, 15, 93, 328, 296, 239, 195, 293 and 23 were identified as the superior lines. The maximum genetic and phenotypic coefficient of variation and genetic gain were estimated for grain yield and the highest heritability was observed for1000 grain weight. Cluster analysis using Ward's method and based on yield and yield component data assigned the lines into three groups. Based on deviation from total average, second group lines were superior than other two groups.

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Introduction

For any planned breeding programs to improve grain yield potentials of crops it is necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability for example, is used to indicate the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates also suggests the extent to which improvement is possible through selection (Singh, 2009; Valizadeh and Moghaddam, 2003).

Wheat is the most important crop that widely cultivated in many countries, including Iran. Bread wheat was domesticated 1,200 years ago in the fertile areas (Salamini *et al*., 2002). Cultivated area and amount of wheat production in world and Iran during 2012 were 216 and 7 million hectares and 675 and 13.5 million tones, respectively (FAO, 2012). According to the increase of wheat yield is main goal of wheat breeding, so genetic diversity of lines for yield and yield components as well as the inheritance of them helps to successful breeding program. On the other hand the importance yield components in increasing of yield and their relatively high heritability, so choosing based on the characters is the fast and confident way to screen plant communities and improve the performance (Yap and Harvey, 1972). Breeders classify different varieties of plants to discover the genetic distance and diversity between them for use in breeding programs. Using analysis of genetic relationships among breeding materials is necessary (Mohammadi and Prasanna, 2003).

One way of producing desirable varieties is production parental with completive specification and use of recombination between their genome to achieve the desired traits. Recombinant inbred lines that during several generations from selfing of progeny from crosses between two parents, due to different recombination of parental genes, are considered as desirable genetic resources for the production of new varieties (Esch *et al*., 2007). The results obtained from Eqbal *et al.* (2007) on spring wheat, general heritability for grain yield had reported low. Aharizad *et al.* (2012) with study of 79 wheat bread recombinant inbred lines estimated highest heritability for 1000 grain weight and lowest heritability for number of grain per spike. Also were reported highest genotypic and phenotypic coefficient of variation for grain yield, number of grain per spike and number of spike per square.

The main objective of this study was to evaluate genetic diversity of bread wheat recombinant inbred lines in terms of yield and yield component and classify lines by using cluster analysis to identify lines that have significant role in performance improvement.

Materials and methods

Measure of traits

Plant materials consisted of 38 bread wheat recombinant inbred lines derived from a across between Zagros (a spring variety, resistant to terminal drought and heat) and Norstar (a winter variety, cold resistant and tall) varieties along with parental lines (Kindly provided by Center of Excellence in Cereal Molecular Breeding, University of Tabriz, Iran). The genotypes were evaluated in a randomized complete block design (RCBD) with three replications during 2010-2011 and 2011-2012 cropping seasons at Agricultural Research station of University of Tabriz. The measured traits included yield, number of grain per spike, number of spike per square meter and 1000 grain weight. Combined analysis of variance was performed based on two years data. Before analysis of variance, assumptions of analysis of variance were assessed and all the traits except number of grain per spike fulfilled the assumptions. Logarithmic transformation was used for number of grain per spike. For evaluation of yield component, ten plants per plot were collected and the mean data points were used for statistical analysis and about yield, all of plants per plot were measured.

Evaluation methods of genetic parameters

Genetic parameters were estimated based on grain yield and yield components. For estimate of heritability (h^2) and genetic gain (Gc) with selection intensity of 10%, the following formula was used:

$$h^2 = \frac{\sigma_g^2}{\sigma_{ph}^2}$$

σ_g^2: genetic variance, σ_{ph}^2: phenotypic variance

$$Gc = 1.75 \times h^2 \times \sqrt{\sigma_{ph}^2}$$

Genetic variance (σ_g^2) and phenotypic variance (σ_{ph}^2) is calculated due to the expected MS and according to the following formula:

$$\sigma_g^2 = \frac{MSG - MSGY}{ry}$$

$$\sigma_{ph}^2 = \sigma_g^2 + \frac{\sigma_e^2}{ry} + \frac{\sigma_{gy}^2}{y}$$

MSG: mean square genetic, MSGY: mean square interaction effect of genetic and year, σ_{gy}^2: interaction effect of genetic and year variance, r and y represent number of repeats and year, respectively.

In order to better compare the progress of genetic traits, genetic gain as a percentage of the average lines in two years was estimated based on the following formula:

$$Gy = \frac{Gc}{\bar{x}_{..}} \times 100$$

Standard error heritability calculated using Kempthorne (1973) formula as fallow:

$$SE_{h^2} = \sqrt{\frac{2MS_e^2 \times \left[\frac{1}{(df_e+2)} + \frac{1}{(df_t+2)}\right]}{MST^2}}$$

In the mentioned formula, MSe and MST are respectively the averages of square mean error and line. df_e and df_t represent degree of freedom related to mean error and line, respectively.

To grouping of studied lines, standardized date was used for cluster analysis and discriminant function was used to determine where to cut the dendrogram. For statistical calculations were used from MSTAT-C, SPSS and Excel software.

Results and discussion

Combined analysis of variance

Combined analysis of variance (Table 1) revealed significant differences between years for number of grain per spike, number of spike per square meter and 1000 grain weight. Differences among lines were significant for grain yield and 1000 grain weight. Significant of line effect, indicating the existence of genetic diversity between lines were tested. Line × year interaction was significant for number of grain per spike, number of spike per square meter and 1000 grain weight.

Mean comparison based on average of two years

For the selection of superior lines in terms of yield and yield component lines mean comparison done in average two years (Table 2). Between recombinant inbred lines, Line 51 had the highest number of grain per spike and lines of 32, 296, 15 and 58 had not significantly different with line of 51. Based on the mean number of spike per square meter, Line 183 had the highest number of spike also lines 145, 293, 328, 195 and 184 had not significant differences in the number of spike per square meter with line 183. By evaluation of studied lines was determined that Zagros, 93 and 145 had the highest 1000 grain weight. The mean comparison of grain yield in evaluated lines showed that line 28 has the highest grain yield. It is noteworthy that lines 31, 145, 281, 15, 93, 328, 296, 239, 293, 195 and 23 had not significantly different from line 28. The results of the mean comparison studied lines in terms of evaluated traits showed that Line 15 has the highest grain yield and number of grain per spike. Highest number of spike and 1000 grain weight was belonged to line 145 and also this line was superior in terms of grain yield.

Heritability

Amounts of genetic and phenotypic coefficient of variation, heritability and genetic gain for each of the traits were estimated in average of two years are presented in Table 3. The highest and lowest phenotypic coefficient of variation was belonged to grain yield (11.45) and 1000 grain weight (6.90), respectively**.** Number of grain per spike had lowest genetic coefficients of variation (3.11) and grain yield had the highest genetic coefficients of variation (9). Aharizad *et al.* (2012) also were reported high genotypic and phenotypic coefficient of variation for grain yield and number of spike per square meter. In general high levels of genetic coefficient of variation indicate high genetic diversity among the studied lines for these traits. It is clear that more genetic diversity between the lines in terms of studied traits, can be made better selection (Valizadeh and Moghaddam, 2003).

Table 1. Combined analysis of variance grain yield and yield component of bread wheat recombinant inbred lines.

		Mean Square			
Source of variation	DF	No. of grain per spike	No. of spike per square meter	1000 grain weight	Grain yield
Year	1	2204.022^{*}	1158704.07^{**}	2484.97^{**}	115573.78^{ns}
Yea/Repeatr	4	311.50	61991.07	21.97	145288.59
Line	39	73.45^{ns}	11991.28^{ns}	34.27^{**}	9090.69^{**}
Line×Year	39	51.53^{**}	10969.47^{**}	11.58^{**}	3093.67^{ns}
Error	156	21.96	5428.92	6.65	3579.91

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

Table 2. Mean of studied recombinant inbred lines in terms of evaluated traits in average two years.

No. of lines	No. of grain per spike	No. of spike per square meter	1000 grain weight (gr)	Grain yield (g/m^{2})
Zagros	25.33	322.80	38.16	289.70
Norstar	31.43	384.20	30.69	272.70
8	34.33	401.20	35.20	332.20
15	37.95	426.50	33.73	394.00
23	35.82	371.30	36.65	365.70
26	31.83	321.70	36.89	292.80
27	26.13	420.30	33.87	334.20
28	32.02	423.30	34.15	418.90
31	36.30	398.80	34.20	401.30
32	38.00	399.30	34.63	349.20
45	35.15	439.30	33.20	350.80
46	31.60	391.30	37.90	310.10
51	41.63	391.30	32.86	316.50
58	37.85	410.20	31.72	327.00
62	30.28	401.80	36.53	336.00
63	28.00	378.60	30.62	280.80
68	29.20	385.00	33.56	257.00
86	34.00	356.50	30.90	308.60
93	33.68	431.10	39.15	388.40
94	34.05	364.30	33.82	319.70
95	32.37	427.20	37.32	362.40
102	29.05	403.00	32.86	353.20
143	31.18	430.00	35.54	302.80
145	33.87	483.00	40.35	400.30
159	32.85	374.30	38.06	346.00
163	29.40	410.30	35.25	318.30
182	35.63	332.00	33.65	321.50
183	31.87	505.50	32.46	344.80
184	33.92	462.80	32.27	352.60
195	29.52	464.70	32.13	366.20
206	28.85	436.30	34.38	339.20
225	28.60	334.50	33.14	280.40
239	32.47	440.30	35.61	372.00
265	35.18	342.10	34.96	337.60
281	34.12	393.30	37.64	397.30
293	31.27	477.20	32.22	368.20
296	37.95	408.00	36.09	377.90
298	31.72	433.20	32.14	317.10
300	35.17	372.00	36.24	313.40
328	29.15	474.50	33.91	377.90
LSD	4.67	57.95	2.25	53.25

Amount of heritability for measured traits in evaluated lines was fluctuating from 0.09 for number of spike per square meter until 0.66 for 1000 grain weight. Low levels of heritability for number of spike per square meter were indicative of the great influence of environmental factors on this trait. The highest heritability was for 1000 grain weight (0.66) and grain yield per square meter (0.63). Before Subhashchandra *et al.* (2009) as well as reported a high percentage of heritability for grain yield and 1000 grain weight. Also Aharizad *et al.* (2012) with study of 79 wheat recombinant inbred lines expressed highest heritability for 1000 grain weight. Due to the genetic variance among recombinant inbred lines is only additive variance (Valizadeh and Moghaddam, 2003), so the estimated heritability for the traits can be as narrow sense heritability. It is clear that traits with high narrow sense heritability are more under control of additive gene effects.

Table 3. Phenotypic and genetic coefficient of variation and variance, heritability, standard error of heritability and genetic gain for yield and yield component in wheat recombinant inbred lines.

	No. of grain per spike	No. of spike per square meter	1000 grain weight	Grain yield
Phenotypic coefficient of variation	10.69	10.99	6.90	11.45
Genetic coefficient of variation	5.84	3.11	5.62	9.00
Genetic variance	3.65	158.64	3.78	934.67
Phenotypic variance	12.24	1986.88	5.71	1515.12
Heritability	0.30	0.09	0.66	0.63
Standard error of heritability	0.07	0.11	0.05	0.1
Genetic gain	1.83	6.23	2.77	42.02
Genetic gain (% of mean)	5.58	1.54	8.00	12.36

Table 4. Canonical discriminant function analysis based on groups from cluster analysis.

No. of group	Wilk's Lambda	Chi-square	Prob.
2	0.05	106.58	0.000
3	0.32	39.92	0.000
4	0.99	0.50	0.78

Genetic gain for the evaluated traits was estimated as a percentage of total average. Selection for grain yield per square meter was more efficient than selection for other traits. The high rate of genetic gain for grain yield per square meter shows selection progress between the lines in terms of this trait. To this cause efficiency selection is high and due to grain yield per square meter can be better detection the desirable and undesirable lines.

Cluster analysis based on yield and yield component

For grouping studied lines cluster analysis using Ward's method of with standardized data based on two years average yield and yield component (Fig. 1). Discrimination function analysis showed the best discrimination in the three groups (Table 4). Mean and the percent of deviation from total average of each group are presented in Table 5. Based on the evaluated traits in average two years, the first group consists of 13 lines had mean higher in terms of number of spike per square meter than the other two groups and in terms of grain yield than third group. Second group with 11 lines, due to percent of deviation from total average, had highest number of grain per spike, 1000 grain weight and grain yield per square meter than the other two groups. Third group compared to the other two groups had the most number of lines (16 lines), despite was superior in terms of number of grain per spike and 1000 grain weight than lines of first group but in terms of number of spike per square meter and grain yield had less value than mean of total lines. Considering all evaluated traits, can be use from lines of second group to achieving the goals of breeding and raising rates of yield on wheat bread.

Table 5. Mean and percent of deviation from the mean of each group compared to the total average in bread wheat recombinant inbred lines.

			Means of traits			
Group	Line	Statistical indexes	No. of grain per spike	No. of spike per square meter	1000 grain weight (gr)	Grain yield (gr/m^2)
1	27, 45, 62, 102, 143, 163, 183, 184, 195, 206, 293, 298, 328	Mean	30.58	443.00	33.60	343.17
		Deviation from total average (%)	-6.55	9.23	-2.94	0.97
2	15, 23, 28, 31, 32, 93, 95, 145, 239, 281, 296	Mean	34.96	418.38	36.32	384.30
		Deviation from total average (%)	6.85	3.16	4.92	13.08
3	Zagros, Norstar, 8, 26, 46, 51, 58, 63, 68, 86, 94, 159, 182, 225, 265, 300	Mean	32.92	366.36	34.27	306.63
		Deviation from total average (%)	0.61	-9.67	-0.99	-9.78
-	All of lines	Total mean	32.72	405.57	34.62	339.86

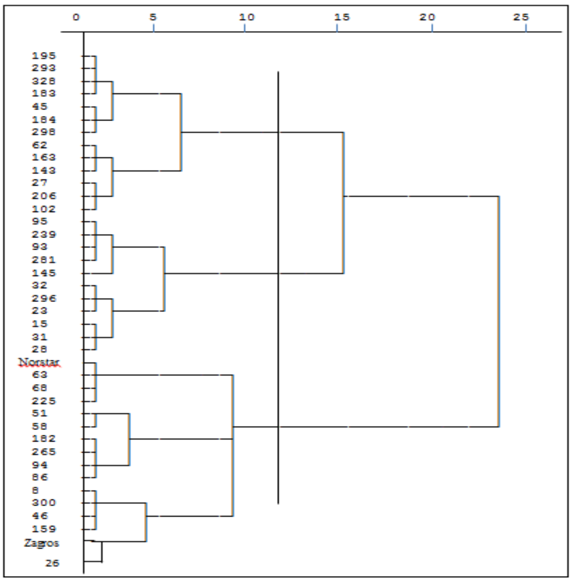

Fig. 1. Dendrogram of studied recombinant inbred lines using cluster analysis with Ward's method and standardized data based on yield and component yield in average of two years.

In general, these results indicated that among of studied recombinant inbred lines there are considerable genetic diversity in terms of important economic and agronomic traits. So depending on the goals of breeding programs the studied lines provide suitable genetic background to select superior genotypes. On the other hand selecting superior lines only through grain yield may not have a good selection result. But given the high heritability of some yield components and its influential role on grain yield can be used them as selection index for improving grain yield. In this regard, second group had high priority on average of two years.

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