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CORRELATION AND FACTOR ANALYSIS OF GRAIN YIELD AND SOME IMPORTANT COMPONENT CHARACTERS IN SPRING BREAD WHEAT GENOTYPES

S. EBRAHIMNEJAD[1], V. RAMEEH[1,*]

* E-mail: v.rameeh@aero.ir

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ABSTRACT. In order to evaluate several agro-morphological traits in 21 spring bread wheat genotypes, an experiment based on randomized complete block design with three replications was carried out in two locations during three years (2008-2011).The traits including grain yield(GY), biological yield (BY), spike weight (SW), grain weight per spike(GWS), harvest index (HI), spike length (SL), spikelet per spike (SPS), number of grain per spike (NGS), number of spike per square meter (SPM), 1000-grain weight (GW), plant height (PH), stem straw weight (SSW), spike straw weight (SRW) were evaluated. The result of combined analysis of variance revealed that years, genotypes and their interaction effects were significant for all the traits. Location had significant difference for all the traits except SL and SPS. GY was significant correlated with BY (0.72**), SW (0.75**), GWS (0.69**), NGS (0.59**), SSW (0.62**) and SRW (0.66**). Factor analysis was used for understanding the data structure and trait relations. The factor analysis divided the thirteen traits into three factors. The cumulative variation for these factors was 0.76 and also it's portions for factor one to three were 0.59, 0.16 and 0.06, respectively. In the first factor, the traits including GY, BY, SW, GWS, SPS, NGS and SSW had high factor loadings. The traits compromise HI, SSW and SRW had high factor loadings in second factor and also SPM, GW and PH had high values of factor loadings in third factor. The genotypes including Morvarid, N-80-19 and N-85-14 had high mean values of grain yield. The genotypes had high genetic coefficient variation for SRW, BY, SW and GY, therefore the efficiency of selection of the genotypes for improving these traits will be high.

Key words: Factor analysis; Morphological traits; Grain yield.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the world's most important crop that excels all other cereal crops both in area and production (Schulthess *et al.*,

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[1] Agronomic and Horticulture Crops Research Department, Mazandaran Agricultural and Natural Resources Research and Education Center, AREEO, Sari, Iran

2000; Stipesevic *et al.,* 2009; Deyong, 2011), thereby providing about 20 per cent of total food calories for the people of the world (FAOSTAT, 2012). The extent of genetic variability has been considered as an important factor which is an essential pre-requisite for a successful hybridization aimed at producing high yielding progenies (Singh and Chowdhury, 1985; Akhtar and Chowdhary, 2006; Dehghani and *et al.,* 2008). The selection of parents becomes more difficult if the improvement is made for a polygenetically controlled complex character like grain yield. Since, efficient selection of genetically superior individuals requires adequate phenotypic variance in the base population and sufficient high heritability (Sabo *et al.,* 2002; Hailegiorgis *et al.,* 2011). Breeding high yielding wheat cultivars which are an important strategy to sustain yield production draws the plant breeders' attention. Indirect selection through traits related to grain yield is one of the most important strategies in wheat breeding (Garcia *et al.,* 2003; Golabady and Arzani, 2003). While researching crops grown for grain yield, their yield components are marked and these are: spike density, number of grains per spike, and 1000-seed weight. Grain yield of wheat is the integration of many traits that affect plant growth throughout the growing period (Mohammadi and Prasanna, 2003; Leilah and Al-Khateeb, 2005; Protic *et al.,* 2009). Each trait changes to a different extent and direction under the influence of environmental factors. The studied traits are usually correlated, and therefore it may be interesting to find general regularities in the interrelations that occur among them (Sadegh Ghol Moqadam *et al.,* 2011; Rymuza *et al.,* 2012). The know-how regarding the nature and magnitude of association among plant traits is essential to improve crops yields. Singh and Dewivedi (2002) have reported significant positive association of grain yield plant^{-1} with number of spikes bearing tillers plant^{-1} both at genotypic and phenotypic levels. Tammam *et al.* (2000) reported that grain yield plant^{-1} had a positive genetic correlation with number of spikes plant^{-1} and 1000-kernel weight. Khaliq *et al.* (2004) observed that spike length had significant positive genotypic correlation with grain yield. Hosseinpor *et al.* (2003) reported that grain yield exhibited highly significant and positive correlation with tillering capacity, spikelets spike^{-1} at both the genotypic and phenotypic levels. Kashif and Khaliq (2004) reported that plant height, spike length, spikelets spike^{-1} and 1000-grain weight were positively and significantly correlated with grain yield at genotypic level. Therefore, the objective of this study was to assertion the genetic and phenotypic correlations among yield traits of the direct and reciprocal crosses derived from two diverse wheat cultivars under normal and late planting conditions. Statistical analysis of agronomic traits could be informative in wheat breeding program, because agronomic traits are a reflection of gene effects. Different statistical procedures have been used in modeling crop yield, including principal component analysis and factor analysis (Westerlund *et al.,* 1991). Factor analysis is a multivariate statistical method for exploring and simplifying complex data sets. Each factor is a linear combination of the original variables, and so it is often possible to ascribe the meaning to what the components represent (Leilah and Al-Khateeb, 2005). Leilah and Al-Khateeb (2005) illustrated that number of tillers and 1000-seed weight positively improved yield potential. The 1000-seed weight was reported by many researchers as the variable most closely related to grain yield and was often used in selecting high yielding wheat cultivars (Deyong, 2011; Rymuza *et al.,* 2012). Mohamed (1999) found that two factors (grain yield and spike density) accounted for 80.8% of variation among traits in some bread wheat genotypes. Leilah and Al-Khateeb (2005) studied bread wheat genotypes and they showed that three factors including yield factor, biomass factor and harvest index factor accounted for 74.4% of total variation.

The objective of this investigation was to evaluate genetic diversity of bread wheat clarify the association among some agronomic traits of bread wheat using correlation and factor analysis, which provide valuable information for breeding new high yielding wheat cultivars.

MATERIAL AND METHODS

Twenty one genotypes of spring bread wheat were assessed using a randomized complete block design with three replications during three years (2008-2011) at two locations including: Baykola Agriculture Research Station, located in Neka, Iran (53°, 13′ E longitude and 36° 43′ N latitude, 15 m above sea level) and Qarakheil Agronomy Research Station, located in Qaemshar, Iran (52°, 46′ E longitude and 36° 26′ N latitude, 14.7 m above sea level). Minimum and maximum temperatures at the first Research Station were -2°C and 35°C, respectively, and the climate is characterized by mean annual precipitation of 610 mm and also in the second Research Station minimum and maximum temperatures were 1.8°C and 32°C, respectively, and the annual precipitation was 745 mm. In each Research Station during three years, sowing was done by hand in plots with six rows 5 m long and 25 cm wide. Tillage of all field plots was performed prior to sowing date and fertility was constrained by low organic matter and phosphorus contents. The fertilizer application was performed before sowing, 60 kg ha^{-1} of N, 30 kg ha^{-1} of P_2O_5 and 20 kg ha^{-1} of K_2O were broadcast on the surface and tilled into the soil and the weeds were controlled chemically. The traits including grain yield (GY), biological yield (BY), spike weight (SW), grain weight per spike (GWS), harvest index (HI), spike length (SL), spikelet per spike (SPS), number of grain per spike (NGS), number of spike per square meter (SPM), 1000-grain weight (GW), plant height (PH), stem straw weight (SSW), spike straw weight (SRW) were evaluated. Variance components were estimated from the mean squares in the analysis of variance (Singh *et al.,* 1993). The component of variance including error variance (VE), genotypic variance (VG) and phenotypic variance (VP) were estimated according to the following formula:

VE= MSE
VG= (MSG-MSE)/r
VP= VG+VE

The coefficient of variation was estimated as $CV = (\sqrt{VG})/\mu$, in which μ is the mean of genotypes for each trait. The correlation coefficients between the traits were estimated and then factor analysis on the base of major factors analysis and varimax rotations was done on the data. Principal components method analysis was used to extract factorial load of matrix and also to estimate the number of factors (Sharma, 1996). Therefore, the factors which had a root bigger than one were selected and were used to form factorial coefficients matrix. By means of varimax rotation, rotation was done on the major factorial loads matrix and the matrix of rotated factorial loads was obtained. All the analyses were performed using MS-Excel and SAS software version 9 (SAS INSTITUTE INC, 2004).

RESULTS AND DISCUSSION

Combined analysis of variance

Mean squares due to genotypes were significant for grain yield(GY), biological yield (BY), spike weight (SW), grain weight per spike (GWS), harvest index (HI), spike length (SL), spikelet per spike (SPS), number of grain per spike (NGS), number of spike per square meter (SPM), 1000-grain weight (GW), plant height (PH), stem straw weight (SSW), spike straw weight (SRW) (*Table 1*) as revealed by ANOVA. This provides evidence of sufficient genetic variability for the genotypes. Three years had significant difference for the traits of the genotypes. Location had significant difference for all the traits except SL and SPS. Significant mean squares of interaction effects of years × locations, years × genotypes and locations × genotypes were also significant for all the traits. These results are in confirmation with (Deyong, 2011; Hailegiorgis *et al.,* 2011) showing strong variation of the wheat genotypes for yield and yield components.

Statistical parameters of yield components and correlation analysis

Statistical parameters of the traits are presented in *Table 2*. Grain yield (GY) was varied from 4.46 to 5.91 ton/ha and Morvarid, N-80-19 and N-85-14 were three top genotypes for improving this trait. The genotypes had 7.2 of genetic coefficient of variation for GY, indicating that gain from selection for improving this trait will be high. BY ranged from 4.45 to 6.09 ton/ha and its average mean was 5.23 ton/ha. The genotypes including Darya, Morvarid and Moghan3 had high mean values of this trait. The genotypes with 7.9 genetic coefficient of variation for BY had more genetic diversity than GY.

Table 1 - Combined analysis of variance (ANOVA) for yield components of spring bread wheat

S.O.V	Years (Y)	Location (L)	Y×L	E1	Genotypes (G)	Y×G	L×G	Y×L×G	E2
df	2	1	2	18	20	40	20	40	360
GY	34.6**	262.3**	6.10**	0.17	3.43**	0.81**	0.75**	0.63**	0.09
BY	52.7**	24.7**	3.42**	0.13	3.96**	0.66**	0.60**	0.52**	0.08
SW	16.3**	17.9**	2.06**	0.05	1.33**	0.28**	0.35**	0.21**	0.04
GWS	10.1**	20.7**	0.77**	0.02	0.54**	0.11**	0.16**	0.09**	0.02
HI	1174.9**	1995.1**	69.31**	2.27	56.65**	19.63**	26.96**	21.84**	3.76
SL	185.9**	0.76^{ns}	24.79**	0.29	10.11**	1.03**	1.14**	0.56**	0.24
SPS	490.1**	0.16^{ns}	73.68**	0.99	23.57**	2.44**	1.68**	1.76**	0.42
NGS	7452.3**	2408.7**	1189.4**	18.88	337.76**	48.73**	51.06**	41.16**	11.55
SPM	162925**	119436**	84012**	649.6	5643.3**	3935**	2043**	1826**	352.4
GW	393.2**	551.2**	127.2**	1.97	60.07**	11.56**	6.08**	5.92**	1.31
PH	1663.4**	1177.2**	216.3**	3.96	341.23**	27.28**	15.96**	20.4**	3.05
SSW	10.6**	0.55**	0.44**	0.03	0.86**	0.17**	0.10**	0.14**	0.02
SRW	4.6**	0.10*	0.32**	0.02	0.28**	0.13**	0.12**	0.12**	0.02

1-GY: grain yield; 2-BY: biological yield; 3-SW: spike weight; 4-GWS: grain weight per spike; 5-HI: harvest index; 6-SL: spike length; 7-SPS: spikelet per spike; 8-NGS: number of grain per spike; 9-SPM: number of spike per square meter; 10-GW: 1000-grain weight; 11-PH: plant height; 12-SSW:stem straw weight; 13-SRW: spike straw weight.

Table 2 - Statistical parameters for yield components of spring bread wheat

Variable	Mean	Standard deviation	Minimum	Maximum	Genetic coefficient variation (%)	Three top genotypes
GY(Ton/ha)	5.28	0.38	4.46	5.91	7.2	Morvarid, N-80-19, N-85-14
BY(Ton/ha)	5.23	0.41	4.45	6.09	7.9	Darya, Morvarid, Moghan3
SW(g)	3.02	0.23	2.59	3.53	7.8	N-86-7- Darya, N-85-14
GWS(g)	2.25	0.15	2.00	2.56	6.8	Moghan3, N-86-7, N-86-8
HI	43.18	1.54	40.57	45.77	3.6	N-86-8, Nai60, N-86-7
SL(cm)	10.23	0.65	9.31	11.69	6.2	N-86-8, N-85-14, N-84-14
SPS	20.13	0.99	18.20	21.85	5	N-86-3, N-85-12, Milan
NGS	52.83	3.75	45.08	59.53	7	Nai60, Shanghi, N-86-7
SPM	452.07	15.33	424.54	492.13	3.4	Tajan, N-80-19, Morvarid
GW(g)	41.63	1.58	39.24	43.74	3.8	Nai60, Tajan, N-85-12
PH(cm)	98.82	3.77	92.72	106.00	3.7	N-86-3, N-86-8, N-85-10
SSW(g)	2.21	0.19	1.86	2.56	8.7	N-86-6, Shanghi, N-86-3
SRW(g)	0.77	0.11	0.56	1.02	14.5	N-86-12, N-86-6, N-86-7

1-GY: grain yield; 2-BY: biological yield; 3-SW: spike weight; 4- GWS: grain weight per spike; 5-HI: harvest index; 6-SL: spike length; 7-SPS: spikelet per spike; 8-NGS: number of grain per spike; 9-SPM: number of spike per square meter; 10-GW: 1000-grain weight; 11-PH: plant height; 12-SSW:stem straw weight; 13- SRW: spike straw weight.

Table 3 - Correlation analysis of yield components of spring bread wheat

Traits	GY	BY	SW	GWS	HI	SL	SPS	NGS	SPM	GW	PH	SSW	SRW
GY	1												
BY	0.72**	1											
SW	0.75**	0.97**	1										
GWS	0.69**	0.88**	0.93**	1									
HI	-0.30	-0.55**	-0.38	-0.09	1								
SL	0.23	0.46*	0.52*	0.41	-0.19	1							
SPS	0.41	0.51*	0.56**	0.50*	-0.14	0.52*	1						
NGS	0.59**	0.68**	0.72**	0.77**	-0.08	0.42*	0.61**	1					
SPM	0.37	-0.11	-0.07	-0.13	0.02	0.02	0.26	0.15	1				
GW	0.14	0.29	0.28	0.29	-0.14	-0.03	-0.15	-0.32	-0.36				
PH	0.03	0.35	0.28	0.33	-0.19	-0.17	0.24	0.13	-0.34	0.33	1		
SSW	0.62**	0.95**	0.84**	0.74**	-0.70**	0.35	0.40	0.58**	-0.13	0.29	0.41	1	
SRW	0.66**	0.85**	0.85**	0.60**	-0.70**	0.53*	0.49*	0.47*	-0.01	0.18	0.15	0.78**	1

1-GY: grain yield; 2-BY: biological yield; 3-SW: spike weight; 4-GWS: grain weight per spike; 5-HI: harvest index; 6-SL: spike length; 7-SPS: spikelet per spike; 8-NGS: number of grain per spike; 9-SPM: number of spike per square meter; 10-GW: 1000-grain weight; 11-PH: plant height; 12-SSW:stem straw weight; 13- SRW: spike straw weight.

Correlations coefficients between studied traits are shown in *Table 3*. Significant positive correlation was detected between GY and BY (0.72**), therefore BY can be used as indirect selection criterion for improving GY. SW was significant correlated with GY and the genotypes including N-86-7- Darya and N-85-14 had high mean values of this trait. GWS was significant correlated with GY (0.69**), BY (0.88**) and SW (0.93**). Present findings are in confirmation with (Akhtar and Chowdhary, 2006; Singh *et al.,* 2012) showing strong association of yield with component traits viz. tillers m^{-1}, grain weight spike^{-1} and grains spike^{-1} suggested that grain yield potential can be effectively improved by obtaining maximum expression of spike length, spikes plant^{-1}, grains spike^{-1} and grain weight spike^{-1} etc. Significant negative correlation was detected between HI and BY and high mean values of HI were related to N-86-8, Nai60 and N-86-7. SL was varied from 9.31 to 11.69 cm and the genotypes including N-86-8, N-85-14 and N-84-14 exhibited high mean values of this trait. SPS ranged from 18.2 to 21.85 and N-86-3, N-85-12 and Milan were three top genotypes for improving this trait. Average mean of GW was 41.63 g with 1.58 standard error. The genotypes had low genetic coefficient variation for GW. GW ranged from 39.24 to 43.74 g and high mean values of this trait were detected in Nai60, Tajan and N-85-12. PH had not significant correlation with GY, therefore selection based on low mean values of PH will not have considerable effects on GY). Leilah and Al-Khateeb (2005) illustrated that number of tillers and 1000-seed weight positively improved yield potential. The 1000-seed weight was reported by many researchers as the variable most closely related to grain yield and was often used in selecting high yielding wheat cultivars (Deyong, 2011; Rymuza *et al.,* 2012). Due to low mean values selection of PH have increasing effects on tolerance to lodging, the genotypes including N-86-3, N-86-8 and N-85-10 will be preferable. SSW was varied from 1.86 to 2.56g and the genotypes including N-86-6, Shanghi, and N-86-3 had high mean values of this trait. SSW was significant positive correlated with GY, BY, SW and also it was significant negative correlated with HI. SRW had significant correlation with GY, BY, SW and GWS and also it had negative correlation with HI. The genotypes including N-86-12, N-86-6 and N-86-7 with high mean values of SRW will be favorable for improving this trait.

Factor analysis

The factor analysis divided the thirteen traits into three groups or factors (*Table 4*) and the varimax orthogonal rotation was subjected to the matrix of factor loadings after the first extraction of factor loadings. This rotation accentuated the larger loadings in the extracted factors and suppressed the minor loadings thus improving the opportunity of achieving meaningful interpretation of factors. The factor which made the largest contribution accounted for 50% of the total variation and was composed of the some components of grain yield including GY, BY, SW, GWS, SPS, NGS and SSW (*Table 4*). Increasing BY, SW, GWS, SPS and NGS would be the most effective way of increasing GY. The second factor, which accounted for 16% of the total variation, was composed of some of morphological traits and indicated the importance of the HI, SSW and SRW. It is clear that both of the first two factors, which would express the combined effect of BY, SW, GWS, SPS, NGS, HI, SSW and SRW were most closely associated with grain yield. Grain yield of bread wheat may be regarded as being composed of the components such as heads per plant, spikelets per spike, grains per spike and the 1000-seed weight (Leilah and Al-Khateeb, 2005; Protic *et al.,* 2009). The third factor, which accounted for 9% of the total variation, was composed of SPM, GW and PH (*Table 4*). Variations of factor analysis and factor rotation are explained in details by Leilah and Al-Khateeb (2005) and in making comparison, consideration should be given to costs involved in estimating genetic parameters of various crops (Dehghani *et al.,* 2008; Hailegiorgis *et al.,* 2011).

Table 4 - Factor analysis for yield components of spring bread wheat

Traits	Factor loadings		
	1	2	3
GY	0.68	0.42	-0.10
BY	0.77	0.55	0.32
SW	0.84	0.43	0.27
GWS	0.88	0.12	0.38
HI	-0.04	-0.94	-0.04
SL	0.56	0.23	-0.19
SPS	0.76	0.04	-0.15
NGS	0.93	-0.02	-0.10
SPM	0.15	0.06	-0.78
GW	-0.10	0.31	0.71
PH	0.20	0.01	0.72
SSW	0.61	0.65	0.34
SRW	0.58	0.74	0.07
Eigen value	6.15	2.09	1.26
Portion	0.50	0.06	0.09
Cumulative	0.50	0.66	0.76

1-GY: grain yield; 2-BY: biological yield; 3-SW: spike weight; 4-GWS: grain weight per spike; 5-HI: harvest index; 6-SL: spike length; 7-SPS: spikelet per spike; 8-NGS: number of grain per spike; 9-SPM: number of spike per square meter; 10-GW: 1000-grain weight; 11-PH: plant height; 12-SSW:stem straw weight; 13- SRW: spike straw weight.

Communality values of factor analysis for the measured traits of bread wheat are given in *Table 4* and results indicated that GY, BY, SW, GWS, SPS, NGS and SSW raits had the highest communality and consequently the high relative contribution in wheat grain yield.

CONCLUSIONS

In this investigation, the increased traits including BY, SW, GWS and, NGS together were the main components of yield. Under these circumstances, selection should be made for increased BY, SW, GWS, NGS, SSW and SRW. Similarly, a considerable SSW and SRW were important to obtaining higher grain yield. The factor analysis is statistical techniques that is useful for the description of the relations that occur among bread wheat characteristics. The obtained non-correlated traits may be used for further analysis, where the assumption of having no co-linearity problem of variables is needed. Reduction of several analyzed wheat characteristics to some PCAs and factors makes it possible to explain about 76% of the total input data variability. The genotypes had high genetic coefficient variation for SRW, BY, SW and GY, therefore the efficiency of selection of the genotypes for improving these traits will be high.

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