

Research Article

Heritability estimates and correlation analysis in bread wheat (*Triticum aestivum* L.) under normal and late plantings

Muhammad Adnan^{1*}, Fida Muhammad¹, Quaid Hussain^{1,2}, Iqbal Hussain¹ and Fawad Ali¹

1. Department of Plant Breeding and Genetics, The University of Agriculture Peshawar-Pakistan

2. Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences, Key Laboratory of Biology and Genetic Improvement of Oil Crops, Ministry of Agriculture, Wuhan, Hubei Province, 430062-China

*Corresponding author's email: adnanswat121@gmail.com

Citation

Muhammad Adnan, Fida Mohammad, Quaid Hussain, Iqbal Hussain and Fawad Ali. Heritability estimates and correlation analysis in bread wheat (*Triticum aestivum* L.) under normal and late plantings. Pure and Applied Biology. Vol. 6, Issue 4, pp1151-1160. <http://dx.doi.org/10.19045/bspab.2017.600123>

Received: 22/04/2017

Revised: 28/08/2017

Accepted: 11/09/2017

Online First: 14/09/2017

Abstract

To estimate heritability and correlation coefficients in bread wheat under normal and late plantings, an experiment was carried out at the research farm of Plant Breeding and genetics, The University of Agriculture Peshawar, Pakistan during 2013. Forty wheat genotypes (39 Advance lines and 1 local check) were tested under normal and late sowing in 5×8 alpha lattice design with three replicates. Combined analysis of variance exhibited significant genotype by environment interactions for spikes m⁻², grains spike⁻¹, 1000-grain weight, bio-mass yield, grain yield and harvest index. Under normal planting assessments of broad-sense heritability for days to heading were (84%), grains spike⁻¹ (88%), 1000-grain weight (95%), bio-mass yield (89%), grain yield (96%) and harvest index (86%) under late planting estimates of broad-sense heritability for days to heading was (63%), grains spike⁻¹ (93%), 1000-grain weight (94%), bio-mass yield (88%), grain yield (93%) and harvest index (77%) were calculated. Grain yield showed positive and significant genotypic and phenotypic correlations with spikes m⁻², 1000-grain weight, bio-mass yield and harvest index under both planting conditions. Genotype SRN 19111 was identified to be best for 1000-grain weight, bio-mass yield and grain yield under normal planting while genotype PR-107 exhibited higher grain yield under late planting. Genotype SRN 19111 and PR-107 are recommended for further extensive testing.

Keywords: Heritability; Correlation; Variation; Wheat; Yields

Introduction

Wheat (*Triticum aestivum* L.) is one of the world's crucial cereal crop and is used as staple food in many regions of the world. It is grown under both irrigated and rain-fed

conditions. It belongs to family Gramineae [1]. As wheat is used as staple food crop in many regions of the world it is known as “king” of cereal crops [2]. The cereal crop in the world which has been first domesticated

in the world was wheat. Different sowing methods i.e., varietal potential, irrigation systems and seed rates etc. are the major factors which is responsible for low yield. However, the most important factors are variety and genetic diversity [3]. The cause of low yield of wheat crop in Pakistan is because of availability of less genetic diversity using in the breeding program for varietal development of wheat [1]. Due to exponential increase in population, the demand of wheat for human consumption is increasing day by day. So, it is required that those wheat genotypes which having desired wheat characters are should be selected and used in wheat breeding programs. According to USDA, 2013 wheat crop was cultivated worldwide on an area of 219.5 million hectares, which gives a production of 712.8 million metric tons with an average yield of 3.25 metric tons ha⁻¹. Similarly, FBS, 2013 reported that in Pakistan the total acreage of wheat was 8693 thousand hectares and the total average yield was 2727 kg ha⁻¹. In KP, the wheat crop production was 1130.3 thousand tons. The total average yield of wheat was 1550 kg ha⁻¹ from approximately 730 thousand hectares. One hundred grams of spring wheat grains contains about 15.4% of protein, 1.9% fat, 68% carbohydrate, 12.2% dietary fiber, and 0.0036 mg of iron which is approximately 20% of daily iron requirements [4].

The achievement of a crop depends on the availability of genetic variability in available germplasm. To bring genetic improvement in economic traits through a process of selection and other breeding methods genetics parameters must be estimated before starting of any breeding program.

Heritability of character is the ratio between genotypic variance and phenotypic variance which tells that to what extent the character is transferred to the next generation. Heritability estimates are determined as the extent of phenotype which is determined by

genetic makeup or genotypic response is called heritability in broad sense. Selection among genotypes for yield and attributing traits would be fruitful if the values of heritability and genetic advance are high [5]. High values of heritability and genetic response discloses strong role of additive gene action for traits appearance and selection based on these plays significant role in the upsurge of final yield [6].

Correlation (genotypic and phenotypic) analysis is commonly practiced to determine the relationship of grain yield with its component traits. Grain yield is a quantitative trait, which is a function of many parameters which have associations among themselves and can affect the grain yield directly or indirectly. For this reason, determining the relationship between grain yield and other traits is necessary when indirect selection is made for higher grain yield. It is reasonable to know whether a yield component has a direct or indirect effect on grain yield while making selection for higher yield [7].

Materials and methods

The current research was conducted at Plant Breeding and Genetics research farm, The University of Agriculture, Peshawar. Experimental material consisted of 40 genotypes (39 Advance lines and 1 local check) were planted under normal and late planting dates to study the effects of planting time on different genotypes and to estimate heritability for various yield related traits. Genotypes were received from the National Agriculture Research Center (NARC) Islamabad as National Uniform Yield Trial (NUYT) 2013-14. Experiment was laid out in 5×8 alpha lattice design with 3 replicates. Every genotype was planted in a 6-row plot, having row to row and plant to plant distance of 0.25 m and 5 m, respectively. Normal planting was done on November 20, 2013, while late planting was done on December 21, 2013. All other

cultural practices were applied uniformly to the experiments planted under normal and late planting dates. Three to four irrigations were applied.

Statistical analysis

Analyses were carried and the significant means for various traits were separated with the application of least significant differences (LSD) test. Data analysis was done through IBM-SPSS20 and Microsoft excel.

Heritability

Genotypic variance, environmental variance, heritability percentage in broad sense, was calculated as described by [8] as follows:

Phenotypic and genotypic correlations

Phenotypic and genotypic correlations among various traits were assessed using genotypic, phenotypic and environmental covariance's as outlined by [9].

Results and discussion

Spikes m⁻²

Analysis of variance observed highly significant differences among genotypes for spikes m⁻² and interaction of genotype was significant with planting date (Table 1). These significant differences are pointing towards the presence of sufficient genetic variations among the genotypes. The results are in accordance with the findings of [10]. Genotype Guard-C showed maximum (199) spikes m⁻² while genotype SAWSN-02-102

showed minimum (99) spikes m⁻² under normal planting condition. Under late planting condition genotype CIM-04-10 showed minimum (57) number of spikes m⁻² whereas genotype PR-107 showed maximum (145) number of spikes m⁻² (Table 2). The interaction mean value for number of spikes m⁻² for normal and late planting ranged from 166 for genotypes Guard-C to 81 for genotype CIM-04-10. Heritability estimates for spikes m⁻² were 63 and 90 % under normal and late planting respectively (Table 3 and 4). [11] also found similar result which was related to my result. Genotypic and phenotypic correlations of spikes m⁻² recorded with biomass, grain yield and harvest index were significant under both normal and late plantings. Similarly, under late planting the association of the said trait was significant with 1000-grain weight for both genotypic and phenotypic level whereas spikes m⁻² showed significant and negative phenotypic correlations with plant height, spike length and grain spike⁻¹ under both normal and late plantings while the genetic association was negative and significant for normal planting whereas the genetic association was negative and significant for grain spike⁻¹ only (Table 5 and 6). These results are in conformity with results of [12].

Table 1. Mean square for spike m⁻², spike length, grain spike⁻¹, 1000-grain weight, bio-mass yield, grain yield and harvest index of 40 wheat genotypes under normal and late plantings

SOV	DF	Spike m ⁻²	Spike Length	Grains Spike ⁻¹	1000-grain Weight	Bio-mass Yield	Grain Yield	Harvest Index
Environments (E)	1	99358.01**	180.32	2681.81**	3700.89**	2134000000.00**	136500000.0**	922.93**
Rep(E)	4	43.28	1.00	5.8	3.76	233524.76	3983.19	0.86
S-block(E × R)	24	21.80	0.54	2.71	2.95	163630.03	3829.54	3.60
Genotypes (G)	39	2421.93**	2.51**	142.60**	295.19**	6060921.29**	949291.98**	79.54**
E × G	39	1126.25**	0.53 ^{ns}	117.36**	132.12**	2787899.65**	357907.17**	49.12**
Residuals	132	34.99	0.41	2.62	3.67	144780.40	4007.55	4.75

Table 2. Mean performance of wheat genotypes for spikes m⁻², spike length, grain spike⁻¹, 1000 grain weight, bio-mass yield kg ha⁻¹, grain yield kg ha⁻¹ and harvest index for wheat genotypes under normal and late plantings

Traits	Normal				Late			
	Ranges	Means	Best genotype	LSD (0.05)	Ranges	Means	Best genotype	LSD (0.05)
Spike m ⁻²	99-199	140	Guard-C	7	56-145	100	CIM-04-10	7
Spike length (cm)	9.7-13.2	11.63	109384	0.7	8.31-11.56	9.92	Aas-11	0.6
Grains spike ⁻¹	27-59	39	CM-04-10	2	22-53	32	Janbaz	2
1000- grain weight	51.74-87.59	70	SRN 09111	1.9	36.27-75.46	50.24	V07096	2
Bio-mass yield kg ha ⁻¹	8533-13667	11089	SRN 09111	403	2400-7933.3	4895	NR-421	390
Grain yield kg ha ⁻¹	1869-5336	3127	SRN 09111	51	540-27389	1548.21	PR-107	68
Harvest index	21-35	28	RCA-1	1.4	20.4-41.6	32.4	V-9082	2.7

Table 3. Genetic variance (V_G), environmental variance (V_E), broad-sense heritability (h²) for various traits of 40 wheat genotypes under normal planting

Traits	V _G	V _E	V _P	h ² (%)
Spike m ⁻²	497.13	57.44	554.57	90
Spike length	0.37	0.50	0.87	43
Grain spike ⁻¹	39.83	5.53	45.36	88
1000-grain weight	85.03	4.05	89.08	95
Bio-mass yield	1542734.20	183429.51	1726164	89
Grain yield	137500.71	5934.79	143435.50	96
Harvest index	11.61	1.92	13.52	86

Table 4. Genetic variance (V_G), environmental variance (V_E), broad-sense heritability (h²) for various traits of 40 wheat genotypes under late planting

Traits	V _G	V _E	V _P	h ² (%)
Spike m ⁻²	641.27	48.67	689.94	93
Spike length	0.34	0.35	0.694	49
Grain spike ⁻¹	42.30	3.17	45.47	93
1000-grain weight	54.98	3.44	58.42	94
Bio-mass yield	1249984.72	172064.64	1422049	88
Grain yield	96184.74	7142.73	103327.5	93
Harvest index	27.61	8.38	35.99	77

Table 5. Phenotypic (above) and genotypic (below) correlation coefficients, spike m⁻², spike length, grain spike⁻¹, 1000-grain weight, bio-mass yield kg ha⁻¹, grain yield kg ha⁻¹ and harvest index for wheat genotypes under normal planting

Traits	Spike m ⁻²	SPKL	Gspike ⁻¹	TGW	BY	GY	HI
Spike m ⁻²	--	-0.33**	0.44**	0.02	0.31**	0.57**	0.40**
Spike length	-0.46**	--	0.41**	-0.17	0.01	-0.09	-0.10
Grains spike ⁻¹	-0.38**	0.47**	--	-0.60**	0.02	-0.06	-0.07
1000- grain weight	-0.06	0.14	-0.15	--	0.24**	0.42**	0.31**
Bio-mass yield kg ha ⁻¹	0.47**	0.04	0.01	0.28	---	0.64**	-0.15
Grain yield kg ha ⁻¹	0.57**	-0.13	-0.05	0.46**	0.69**	---	0.64**
Harvest index	0.38*	-0.17	-0.05	0.19	0.04	0.64**	--

**=Highly significant at (p ≤ 0.01), *=Significant at (p ≤ 0.05), ns = Non-significant

Table 6. Phenotypic (above) and genotypic (below) correlation coefficients for spikes m⁻², spike length, grain spike⁻¹, 1000 grain weight, bio-mass yield kg ha⁻¹, grain yield kg ha⁻¹ and harvest index for wheat genotypes under late planting

Traits	Spike m ⁻²	SPKL	Gspike ⁻¹	TGW	BY	GY	HI
Spike m ⁻²	--	-0.22*	-0.38**	0.39**	0.66**	0.83**	0.38**
Spike length	-0.24	--	0.10	0.15	0.01	-0.04	-0.15
Grains spike ⁻¹	-0.373*	0.05	--	-0.54**	-0.02	-0.01	0.03
1000- grain weight	0.367*	0.13	-0.23	--	0.41**	0.50**	0.21**
Bio-mass yield kg ha ⁻¹	0.676**	0.01	-0.01	.514**	--	0.78**	-0.16
Grain yield kg ha ⁻¹	0.821**	-0.08	0.04	.424**	.765**	--	0.46**
Harvest index	0.427**	-0.18	0.03	0.20	-0.08	.475**	--

**=Highly significant at (p ≤ 0.01), *=Significant at (p ≤ 0.05), ns =Non-significant

Spike length (cm)

Analysis of variance exhibited highly significant differences ($P \leq 0.01$) for spike length (Table 1). Variation was also significant among the genotypes. This shows that wide range of genetic variability existed among 40 genotypes of wheat. The genotype × environment interaction for spike length was non-significant ($P \geq 0.05$). Difference in spike lengths of the genotypes was also reported by Kakar *et al.* [13]. Under normal planting genotype Guard-C showed minimum (10 cm) spike length while genotype 109384 showed maximum (13 cm) spike length. In contrast, genotype CT 09137 showed minimum (8 cm) spike length under late planting condition. While genotype Aas-11 showed maximum (12 cm) spike length (Table 2). Mean over the two planting environments genotype Aas-11 produced plants with maximum spike length

13 cm while genotype CT 09137 produced plants with minimum spike length 9 cm. Mean for 40 wheat genotypes under normal and late planting were 12 and 10 cm respectively. Spike length showed moderate heritability of 43 and 49 % under normal and late planting respectively. (Table 3 and 4)

These results are in the accordance with the findings of [14].

Spike length showed significant and positive genetic and phenotypic correlation with grains spike⁻¹ under normal planting while the genetic association was significant with grains spike⁻¹. Whereas the spike length showed non-significant genotypic and phenotypic correlation with 1000-grain weight, bio-mass yield kg ha⁻¹, grain yield kg ha⁻¹ and harvest index under both normal and late planting (Table 5 and 6). [15] have

also reported positive association between spike length and grains spike⁻¹.

Number of grains spike⁻¹

Genotypes had significant ($P \leq 0.01$) differences for grains spike⁻¹ with significant genotype by date of planting interaction (Table 1). In wheat, grains per spike is one of the important primary yield contributing character. Similar result was also recorded by Ahmed *et al.* [16].

Minimum number of grains spike⁻¹ (32) were observed in late sowing as average across 40 wheat genotype while normal sowing showed maximum (39) number of grains spike⁻¹ (Table 2). Under late planting condition minimum (22) number of grains spike⁻¹ was observed for genotype CT 09137, while genotype Janbaz showed maximum (52) number of grains spike⁻¹. In contrast genotype CIM-04-10 produce maximum (59) number of grains spike⁻¹ while genotype Guard-C produce minimum (27) numbers of grain spike under normal planting (Table 2). Planting dates showed significant variation in number of grains spike⁻¹ in wheat genotypes. The significant $G \times E$ interaction can be confirmed from the mean values for number of grains spike⁻¹ as the genotype showing maximum number of grains spike⁻¹ in normal sowing did not produce plants with maximum number of grains spike⁻¹ in late sowing which means that the ranking of genotype in changed on the basis for their performance for number of grains spike⁻¹ under normal and late planting. While based on heritability analysis number of grains spike⁻¹ showed high heritability value for both normal and late planting which is 88 and 93 % respectively (Table 3 and 4). These findings have already been reported by Ali *et al.* [14] and Ahmed *et al.* [16]. Grains spike⁻¹ showed significant genetic association with spike length under normal planting. While with rest of the traits grains spike⁻¹ showed non-significant correlation at both genotypic

and phenotypic level whereas genetic association was significant and negative with spike m⁻² under late planting similarly grains spike⁻¹ showed non-significant phenotypic and genotypic correlation with the remaining traits (Table 5 and 6).

1000-grain weight (g)

Analysis of variance revealed highly significant differences among genotypes for 1000-grain weight with significant ($P \leq 0.01$) genotype by date of planting interaction (Table 1). [13] also found significant variation in wheat genotypes for 1000-grain weight.

Minimum (52g) 1000-grain weight was recorded for genotypes SD-998 and NIA-MN-08 and maximum (88 g) for genotype SRN 09111 at normal planting while at late planting (36 g) and (75 g) for genotypes NIA-MN-08 and V 07096 respectively (Table 2). Minimum 1000-grain weight was recorded by genotype NIA-MN-08 under normal and late plantings (Table 2). In overall interaction value for 1000 grain-weight ranged from (36 g) for genotype NIA-MN-08 to (88 g) for genotype SRN09111. The average value calculated for 40 wheat genotype was 70 and 50g for normal and late planting respectively. The averaged 1000-grain weight of wheat genotypes was 20 g more than the wheat genotypes sown at late planting condition. On basis of heritability estimation, the value calculated for 1000-grain weight were 95 and 94 % for normal and late planting respectively (Table 3 and 4). These findings of our research are similar with the research findings of [17].

The data recorded for 1000-grain weight exhibited positive and significant phenotypic correlation with bio-mass yield kg ha⁻¹, grain yield kg ha⁻¹ and harvest index under both normal and late planting. Whereas the genetic association was positive and significant with grain yield kg ha⁻¹ while the said trait showed non-significant genetic

association with the rest of the traits under normal planting while under late planting it showed significant and positive genetic association with spike m^{-2} . (Table 5 and 6). [18] also found significant and negative correlation between 1000-grain weight grains spike $^{-1}$.

Bio-mass yield (kg/ha)

Analysis of variance showed highly significant differences for biomass among genotypes with significant genotype by date of planting interaction (Table 1). The significant differences show that the selection of superior genotype will be easy from the varied population or genotypes. Differences in bio-mass yields of the genotypes might be attributed to the genetic characteristic of each genotype as reported by Kakar *et al.* [13]. The interaction for bio-mass yield ranged from 2400 kg ha $^{-1}$ for genotype SD-998 to 13667 for genotype SRN 09111 (Table 2). Minimum (8533) biomass was recorded for genotype TD-1 and maximum (13667) biomass for genotype SRN 09111 at normal planting condition while at late planting minimum (2400 kg) and maximum (7933kg) biomass for genotype SD-998 and NR-421 respectively. Averaged over normal and late planting minimum (5767 kg ha $^{-1}$) biomass was observed for genotype TD-1 while maximum (9700 kg ha $^{-1}$) for genotype NR-421. The 40 wheat genotypes produce an average 10885 kg ha $^{-1}$ at normal plantings while the same genotypes sown late produce an average yield of 5990 kg ha $^{-1}$. It is obvious from the result that the wheat genotypes sown at their normal sowing period produce biomass yield of 4895 kg ha $^{-1}$ than the wheat genotypes sown at late condition. Heritability estimates for biomass were 89 and 88% for normal and late planting respectively (Table 3 and 4). [19] also estimated high heritability value for bio-mass yield kg ha $^{-1}$.

Biomass showed positive and significant phenotypic correlations with number of spikes m^{-2} , 1000-grain weight and grain yield kg ha $^{-1}$ under both normal and late plantings. Similarly, genotypic correlation was also positive and significant with spikes m^{-2} and grain yield kg ha $^{-1}$ under both planting conditions while under late planting the genetic association of biomass was also positive and significant with 1000-grain weight whereas significant and negative genetic correlation was observed with days to emergence under late planting while to the rest of the traits it showed non-significant correlation at genetic level. Negative but Significant phenotypic correlation was recorded for bio-mass yield kg ha $^{-1}$ and days to emergence under both planting conditions. Biomass showed positive and significant correlation with plant height under late planting (Table 5 and 6). The positive association of biological yield with grain yield was earlier reported by Akhtar and Chowdhary [20].

Grain yield (kg/ha)

Analysis of variance revealed significant differences among genotypes for grain yield and the genotype by date of planting was also significant ($P \leq 0.01$) (Table 1). [21] conducted a research and confirmed that the performance of wheat genotypes related to yield is changed at different environmental conditions wheat genotypes are sowing.

Mean value for grain yield ranged from 540 kg ha $^{-1}$ for genotype NIA-MN-08 to 5336 for genotype SRN 09111 (Table 2). Minimum (1869 kg ha $^{-1}$) grain yield was recorded for genotype NIA-MN-08 and maximum (5336 kg ha $^{-1}$) for genotype SRN 09111 under normal planting while at late planting genotype NIA-MN-08 showed minimum (540 kg ha $^{-1}$) and genotype PR-107 showed maximum (2739 kg ha $^{-1}$) grain yield. Across normal and late plantings minimum (1205 kg ha $^{-1}$) grain yield kg ha $^{-1}$ was recorded for genotype NIA-MN-08 and

maximum (3329 kg ha⁻¹) for genotype V-11005 (Table 2). The 40 genotypes which were included in the study produce grain yield 3127 kg ha⁻¹ under normal planting condition while the same 40 genotypes which were sown late produce grain yield of 1548 kg ha⁻¹. Hence a reduction of 1579 kg ha⁻¹ occurred in grain yield due to late planting. Because in late sowing condition not available all facilities to crop such as time, food etc. High heritability value was recorded for grain yield which is 96 % for normal planting and 93 % for late planting (Table 3 and 4). Similarly, high heritability for grain yield was noted by Chowdhry *et al.* [22].

Grain yield showed significant and positive genotypic and phenotypic correlations with spikes m⁻², 1000-grain weight, biomass and harvest index under normal and late planting. [18] also reported significant correlations between harvest index and grain yield. With other traits, it showed non-significant genotypic and phenotypic correlations under both normal and late planting (Table 5 and 6). [23] also found similar results.

Harvest index

Analysis of variance for harvest index displayed highly significant differences ($P \leq 0.01$) between normal and late plantings (Table 1). At normal planting condition harvest index varies from 21 to 35 %, while at late planting the harvest index of same wheat genotypes varied from 20 to 42 % (Table 2). Genotype RCA-1 gave maximum harvest index of 35 percent whereas genotype SD-998 shows minimum harvest index of 21 percent under normal planting. Under late planting condition genotypes V-09082 and 32 gave maximum harvest index of 42 percent while genotype UAF-9452 gave minimum harvest index of 20 percent. Averaged over normal and late planting genotype TW96010 gave minimum harvest index of 23 percent while genotypes V-

09082 and Gauard-C maximum harvest index of 37 percent. Mean value averaged for 40 genotype harvest index were 28 percent under normal and 32 percent under late planting. Heritability estimation showed high heritability value of harvest index 96 and 93 % under normal and late plantings respectively (Table 3 and 4). [24] also estimated high heritability for harvest index. Harvest index exhibited significant and positive phenotypic correlations with spikes m⁻² 1000-grain weight and grain yield under normal and late planting similarly the association was positive and significant with spikes m⁻² and grain yield under normal and late plantings at genotypic level (Table 5 and 6). Significant association of harvest index was also observed with grains spike⁻¹ and grain yield in the research study of [25, 26].

Conclusions

Genotype SRN 19111 was identified to be best for 1000-grain weight, bio-mass yield and grain yield under normal planting while genotype PR-107 exhibited higher grain yield under late planting. Therefore, these genotypes are recommended for further extensive testing. Genotype SRN 19111 and PR-107 would be the appropriate selection criteria for better seed yield in wheat.

Authors' contribution

Conceived and designed the experiments: M Adnan, Performed the experiments: M Adnan & Q Hussain, Analyzed the data: Q Hussain, I Hussain & F Ali, Contributed reagents/ materials/ analysis tools: F Mohammad, Wrote the paper: M Adnan.

References

1. Ijaz S & Khan IA (2009). Molecular characterization of wheat germplasm using microsatellite markers. *Genet Mol Res* 8(3): 809-815.
2. Anonymous (2007). Pakistan Economic Survey (2007-08). Government of Pakistan, Finance Division Economic Adviser's Wing, Islamabad, 24.

3. Alam SM & Shereen A (2003). Effect of different levels of zinc and phosphorus on growth and chlorophyll content of wheat. *Asian J Plant Sci* 1(4): 364-366.
4. USDA (2013). United States Department of Agriculture. *Nutrient data laboratory*.
5. Ghandorah MO & El-Shawaf IIS (1993). Genetic variability, heritability estimates and predicted genetic advance for some character in Faba bean. *Journal of King Saud University Wheat J Agric Res* 28(3): 193-200.
6. Iqbal MZ & Khan SA (2003). Genetic variability, partial regression, co heritability studies and their implications in selection in selection of high yielding potato genotype. *Pak J Sci and Ind Res* 46: 123-125.
7. Meyari S, Nouri F, Sasani S, Najafian G & Aghayari F (2013). Correlation and path analysis of grain yield and its components of some bread wheat (*Triticum aestivum* L.) under normal and source restriction conditions. *IJFAS Journal-2013-2-23/1065*.
8. Larik AS, Hafiz HMI & Khushk AM (1989). Estimation of genetic parameters in wheat populations derived from intercultural hybridization. *Pakphyton* 1: 51-56.
9. Singh KN, Singh SP & Singh GS (1995). Relationship of physiological attributes with yield components in bread wheat under rain fed condition. *Agric Sci Digest* 15(1-2): 11-14.
10. Munir I, Swati MS, Muhammad F, Ahmad R & Imtiaz M (1999). Heterosis in different crosses of wheat. *Sarhad J Agric* 15: 299-303.
11. Khalid M, Khalil IH, Ullah F, Tahir M, Ali S, Anwar S, Ali A, Bari A & Ismail M (2011). Assessment of heritability estimates for some yield traits in winter wheat (*Triticum aestivum* L.) *Pak J Bot* 43(6): 2733-2736.
12. Shah Z, Shah SMA, Hassnain A, Ali S, Khalil IH & Munir I (2007). Genotypic variation for yield and yield related traits and their correlation studies in wheat. *Sarhad J Agric* 23(3):
13. Kakar KM, Ullah S, Kakar Z & Shawani MI (2003). Varietal dynamics of yield stability in wheat. *J Biol Sci* 3(2): 137-140.
14. Ali Y, Atta BM, Akhter J, Moneveux P & Lateef Z (2008). Genetic variability, association and diversity studies in wheat germplasm. *Pak J Bot* 40(5): 2087-2097.
15. Bashir A, Khalil IU, Iqbal U & Rahman H (2010). Genotypic and Phenotypic Correlation among yield components in bread wheat under normal and late plantings. *Sarhad J Agric* 26(2):
16. Ahmed N, Chowdhry MA, Khaliq I & Maekaw M (2007). The inheritance of yield and yield components of five wheat hybrid populations under drought conditions. *Indo J Agri Sci* 8(2): 53-59.
17. Ashraf M, Ghafoor A, Khan NA & Yousaf A (2002). Path coefficient in wheat under rainfed conditions. *Pak J Agric Res* 17(1): 1-6.
18. Degewione A, Dejene T & Sharif M (2013). Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. *International Research Journal of Agricultural Sciences* 1(2): 19-29.
19. Haq W, Malik MF, Rashid M, Munir M & Akram Z (2008). Evaluation and estimation of heritability and genetic advancement for yield related attributes in wheat lines. *Pak J Bot* 40(4): 1699-1702.
20. Akhtar N & Chowdhary MA (2006). Estimation of genetic and phenotypic correlation coefficients among grain yield and its components in bread wheat. *Int'l J Agric Biol* 8(4): 516-522.

21. Inamullah N, Shah Z, Haq Z & Khan F (2007). An analysis of the planting dates effect on yield and yield attributes of spring wheat (*Triticum aestivum* L.) *Sarhad J Agri* 23: 269-271.
22. Chowdhry MA, Iqbal S, Subhani GM & Khaliq I (1997). Heritability of some quantitative character in bread wheat. *JAPS* 7: 27-28.
23. Amin M, Mohammad T, Khan AJ, Irfaq M, Ali A & Tahir GR (2005). Yield stability of spring wheat (*Triticum aestivum* L.) in the North-West Frontier Province, Pakistan. *Song J Sci Technol* 27(6): 1147-1150.
24. Baloch MJ, Baloch E, Jatoti WA & Veesar NF (2013). Correlation and heritability estimates and yield attributing traits in wheat. *Pak J Agri Agril Engg Vet Sci* 29(2): 96-105.
25. Ali A, Shah SMA, Hassnain A, Shah Z & Munir I (2007). Genotypic variation for yield and morphological traits in wheat. *Sarhad J Agric* 23(4):124-128.
26. Khan MA, Malik T, Abbas SJ, Abbas Z, Khan A, Malik M & Asghar S (2011). Study of genetic variability and correlation among various traits of F₅ wheat (*Triticum aestivum* L.) populations. *Int Res J Agric Sci and Soil Sci* 1(8): 344-348.