***Pak. J. Bot.*, 45(5): 1841-1846, 2013.**

GENETIC STUDIES OF SOME YIELD CONTRIBUTING TRAITS OF F_2 SEGREGATING GENERATION OF BREAD WHEAT

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Abstract

Studies on heritability estimates were carried out in 30 F_2 segregating population originated through cross combinations of six different parental lines/varieties of bread wheat. Genetic parameters such as environmental variance (Ve), genetic variance (Vg), heritability percentage in broad sense (h^2 b.s.) and genetic advance (G.A) were calculated for two important yield contributing traits viz., number of grains per spike and grain yield per spike. The highest mean number of grains per spike (80-100.8) and main spike yield (4.0 to 4.58 g) were recorded in 23 progenies. Eighteen progenies showed the highest heritability (81.2 to 94.3%) in broad sense (h^2) coupled with higher genetic advance (1.69-30.58%) for number of grains per spike; indicating more effective selection which could be possible from segregating progenies for this particular trait. Twenty six progenies showed the highest heritability (59.4 to 97.1%) for main spike grain yield character. The results depicted that most of the segregating progenies showed genetic improvement in both quantitative traits in terms of more heritability (h^2 b.s.) and genetic advance. Identification of superior plants possesses desirable traits with high heritability estimates provide basic understanding of breeding material in early segregating generations. The better progenies could be effectively used to select the superior hybrid plants with desirable genes in successive generations.

Introduction

World cereal production recorded during 2007 was 2146.4 million tones which estimated to reach 2283.2 million tones in 2008, while world wheat production recorded was 625.6 million tones in 2007 which estimated 681.4 million tones in 2008 (Anonymous, 2010). Asia contributes major share in world cereal production including wheat. Wheat provides food for 36% of world population, about 40% (278.6 million tones) of the total world wheat production (681.4 million tones) has been produced from the Asia (Anon., 2010). Wheat is a major staple food crop of Pakistan grown over 9.046 million hectares with annual production of 24.032 million tones (Anon., 2009). The area and production of wheat crop during 2008-09 has increased by 5.8 and 14.7% respectively as compared to 2007-08. The possible reason for substantial increase in wheat yield could be the better management practices adapted by the growers and the introduction of new high yielding varieties which possesses tolerance to biotic and abiotic stresses (Aycicek & Yildirim, 2006; Sial *et al.,* 2009; Bux *et al*., 2013; Sial *et al.,* 2012a).

Wheat grain yield is determined by the environmental factors and the several yield components such as productive tillers per unit area, number of grains per spike, grain weight per spike, semi-dwarf type plant height and the high 1000-grain weight (Ahmedi & Bajelan, 2008; Mohsin *et al*., 2009; Sial *et al.,* 2010). Heritability and combining ability play a major role in predicting the performance of further generations (Cooper *et al.*, 2013). The increase in yield is attributed to increase in any one of these major factors, while understanding the mechanism of genetic control of these economic traits allows effective selection for improved traits (Mangi *et al.,* 2008). The studies have shown that there is a strong correlation between grain yield and the number of grains per spike (Sayre *et al*., 1997; Savin & Slafer, 1991; Fischer, 1993). Therefore, increase in number of grains per spike which lead to increase in final yield is a new breeding strategy to enhance the wheat crop productivity (Reynolds *et al.,* 2004). Heritability studies provide valuable genetic information to the breeders to predict the interaction of genes in segregating generations (Ansari *et al.,* 1991; Korkut *et al*., 2001; Sial *et al.,* 2012b; Degewione *et al.,* 2013). It has been observed that in breeding programs, magnitude of genetic inheritance and expected genetic gains are very essential to predict response to selection in diverse environments and provide the basis for effective selection for particular traits in segregating populations. Khan *et al.,* (2008) suggested that the higher the heritability and genetic advance, simple the selection procedure. The present studies were therefore undertaken to investigate the heritability of two important yield components (number of grains per spike and main spike yield) in F_2 cross progenies and to know that how much of the phenotype has been passed on to the successive generation. The information generated will be helpful for the breeders while making selection of the appropriate parental lines for effective cross combinations to get more yields from wheat.

Materials and Methods

F_2 segregating population consisting of six parental lines (Sarsabz, Bhittai, NR-234, Nesser, PFAU/VEE #9//URES and Sitta) and thirty cross combinations of bread wheat (*Triticum aestivum* L.) viz., C-31 (NR-234 x Nesser), C-32 (NR-234 x Sarsabz), C-33 (NR-234 x Bhittai), C-34 (NR-234 x PFAU/VEE #9//URES), C-35 (NR-234 x Sitta), C-36 (Nesser x NR-234), C-37 (Nesser x Sarsabz), C-38 (Nesser X Bhittai), C-39 (Nesser x PFAU/VEE #9//URES), C-40 (Nesser x Sitta), C-41 (Sarsabz x NR-234), C-42 (Sarsabz x Nesser), C-43 (Sarsabz x Bhittai), C-44 (Sarsabz x PFAU/VEE #9//URES), C-45 (Sarsabz x Sitta), C-46 (Bhittai x NR-

234), C-47 (Bhittai x Nesser), C-48 (Bhittai x Sarsabz), C-49 (Bhittai x PFAU/VEE #9//URES), C-50 (Bhittai x Sitta), C-51 (PFAU/VEE #9//URES x NR-234), C-52 (PFAU/VEE #9//URES x Nesser), C-53 (PFAU/ VEE #9//URES x Sarsabz), C-54 (PFAU/VEE #9//URES x BHITTAI), C-55 (PFAU/VEE#9//URES x sitta), C-56 (Sitta x NR-234), C-57 (Sitta x Nesser), C-58 (Sitta x Sarsabz), C-59 (Sitta x Bhittai) and C-60 (Sitta x PFAU/VEE#9//URES) were evaluated under field conditions at Nuclear Institute of Agriculture and Biology (NIAB), Faisalabad during rabi season 2008-09. The experiment was laid out in RCBD with 3 replications. The parental lines and F_2 progeny were sown through single seed dibbling method at the distance of 20 cm between plants and 30 cm between rows. The soil where the experiment was sown had highly fertile and clay loam in nature having pH. 7.5. The fertilizer dose applied to the experiment was (100N: 50 P_2O_5 kg/ha). Five irrigations were applied to the experiment during various growth stages. All other related practices such as removal of weeds and any mixture were performed manually. At maturity, single spike selection was made from each five randomly selected plants of each parental line and segregating hybrid progeny. Two important yield contributing traits viz., number of grains per spike and main spike yield were studied. Genetic parameters viz., heritability percentage in broad sense (h^2 b.s), environmental variance (Ve), genetic variance (Vg) and genetic advance (G.A) were calculated as suggested by Falconer (1977) and Singh & Chaudhry (1985). Means were compared using standard error of each hybrid progeny with its each respective parent.

Results and Discussion

Overall performance of F_2 hybrid progenies was outstanding as compared to their respective parents. Hybrid progenies indicated different response for the number of grains per spike and main spike grain yield (Table 1). Twenty two segregating progenies (viz., C-33, C-35, C-39, C-40, C-42, C-43, C-44, C-46, C-47, C-48, C-49, C-50, C-51, C-52, C-53, C-54, C-55, C-56, C-57, C-58, C-59, C-60) originated from different cross combinations revealed the highest average number of grains per spike ranged from 80-100.8 as compared to their parental lines. Standard error for the mean number of grains per spike of hybrid progenies was also higher as compared to their both female and male parents. Hybrid progenies C-56 (Sitta x NR-234) and C-54 (PFAU/VEE#9//URES x Bhittai) produced the highest average number of grains per spike (100.8 and 98.2 grains respectively) with high standard error (4.25 and 6.51 respectively) than their respective parental lines and other cross combinations. The cross progeny C-34 (NR-234 x Bhittai) produced less number of grains per spike (70.2) than other cross progenies. The parental lines Nesser could produce minimum number of grains (52.0), while Sitta and Bhittai produced the highest number of grains (82.4 and 79.6 respectively). It was also observed that the nine hybrid progenies viz., C-56, C-57, C-58, C-59, C-60, C-46, C-47, C-48 and C-49 originated from cross combination where the Sitta and Bhittai were used as female parents gave the highest number of grains per spike (>80 grains per spike). These findings suggested that these parental lines could be used to produce hybrid plants with more number of grains per spike. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value between generations (Shukla *et al.,* 2006; Laghari *et al.,* 2010; Al-Tabbal *et al.,* 2012; Zaazaa *et al*., 2012).

Eight hybrid progenies viz., C-31, C-34, C-35, C-59, C-38, C-41, C-45 and C-50 did not show any genetic improvement in mean number of grains per spike as compared to their respective parental lines. Seventeen hybrid progenies (C-33, C-37, C-39, C-42, C-43, C-44, C-46, C-47, C-48, C-49, C-52, C-53, C-54, C-56, C-58, C-59 and C-60) revealed improvement in main spike grain yield than their parents. The highest grain yield per spike was recorded from these progenies. Their average main spike grain yield ranged from 3.08 to 4.58 g, which showed significant increase over both parental lines. Parental lines NR-234, Bhittai & Sitta gave higher grain yield per spike (4.17, 3.83 and 3.72 g respectively), while Nesser parent could produce low main spike yield (1.73 g) as compared to other parental lines (Table 1).

Genetic parameters viz., genetic variance (V.g), phenotypic variance (V.p), heritability percentage (h^2) in broad sense and genetic advance (G.A) for number of grains per spike and main spike yield calculated from each F_2 cross combination are presented in Table 2. Wide variations in genetic parameters were estimated in hybrid progenies for both characters; indicating the transfer of desirable genes from the parents to their offspring. The heritability percentage (h^2) in broad sense for the number of grains per spike ranged from the lowest (-891%) in C-34 to the highest (94.28%) in C-43, indicated that the genetic variability has been successfully created in F_2 progenies (Table 2). Eighteen F_2 progenies (C-31, C-32, C-33, C-36, C-37, C-43, C-44, C-45, C-49, C-50, C-52, C-53, C-54, C-55, C-56, C-57, C-58 and C-60) showed the highest (81.2 to 94.38%) heritability percentage in broad sense (h^2) coupled with higher genetic advance (G.A.). These findings suggested the more effective selection chances from these segregating progenies for the particular trait originated from these combinations. These parental lines could be use more effectively to transfer the desirable important trait to hybrid progenies to achieve genetic improvement. Riaz-Ud-Din *et al.,* (2010) have also reported the high heritability estimates for grain yield and various yield components such as plant height, tillers per plant, seeds/spike, spikelets/ spike and the 100-seed weight. It has been well-documented that higher the heritability, more effective would be the selection, whereas the high estimates are attributed to fixable component of genetic variation (Larik, 1999). The variation in genetic advance was also estimated for number of grains per spike ranged from -5.39 to 30.63 in F_2 segregating population. Twenty six cross progenies except C-34 and C-35, C-37 and C-41 showed the highest heritability % in broad sense for grain yield per spike ranged from 59.4 to 97.1% and the high genetic advance. Rajper *et al.,* (1998) have also reported the high heritability for different characters in hybrids offers the scope of selection in segregating generations, however, high coefficient of variability and genetic variance reflects the amount of variation. The high heritability associated with low genetic advance is probably due to non additive gene (dominance and epistasis) effects (Sharma & Tyagi, 1991).

Table 1. Mean and standard error (s.e) of number of grains per spike and main spike yield (g) of F_2 segregating population and their parental lines of wheat genotypes.

Cross/parents	Parents/ crosses	Number of grains/spike	Main spike yield (g)
		Mean ± standard error (s.e)	Mean ± standard error (s.e)
C-31 (NR-234 x NESSER)	♀	77.0 ± 2.03	4.17 ± 0.121
	♂	52.0 ± 2.00	1.73 ± 0.063
	x	75.0 ± 7.22	3.33 ± 0.295
C-32 (NR-234 x SARSABZ)	♀	77.0 ± 2.03	4.17 ± 0.121
	♂	59.8 ± 1.72	2.43 ± 0.093
	x	77.6 ± 5.32	3.84 ± 0.210
C-33 (NR-234 x BHITTAI)	♀	77.0 ± 2.03	4.17 ± 0.121
	♂	79.6 ± 1.51	3.83 ± 0.125
	x	83.2 ± 17.06	4.42 ± 0.456
C-34(NR-234x PFAU/VEE#9//URES)	♀	77.0 ± 2.03	4.17 ± 0.121
	♂	59.0 ± 2.17	2.67 ± 0.071
	x	70.2 ± 2.01	3.65 ± 0.098
C-35 (NR-234 x SITTA)	♀	77.0 ± 2.03	4.17 ± 0.121
	♂	82.4 ± 0.93	3.72 ± 0.076
	x	71.8 ± 1.86	3.44 ± 0.049
C-36 (NESSER x NR-234)	♀	52.0 ± 2.00	1.73 ± 0.063
	♂	77.0 ± 2.02	4.17 ± 0.121
	x	77.8 ± 6.14	3.63 ± 0.183
C-37 (NESSER x SARSABZ)	♀	52.0 ± 2.00	1.73 ± 0.063
	♂	59.8 ± 1.72	2.43 ± 0.094
	x	79.4 ± 4.30	3.08 ± 0.098
C-38 (NESSER x BHITTAI)	♀	52.0 ± 2.00	1.73 ± 0.063
	♂	79.6 ± 1.51	3.83 ± 0.125
	x	72.0 ± 4.65	3.32 ± 0.161
C-39 (NESSER x PFAU/VEE#9//URES)	♀	52.0 ± 2.00	1.73 ± 0.063
	♂	59.0 ± 2.17	2.67 ± 0.072
	x	85.0 ± 1.58	3.66 ± 0.148
C-40 (NESSER x SITTA)	♀	52.0 ± 2.00	1.73 ± 0.063
	♂	82.4 ± 0.93	3.72 ± 0.076
	x	84.6 ± 2.70	3.44 ± 0.206
C-41 (SARSABZ x NR-234)	♀	59.8 ± 1.72	2.43 ± 0.094
	♂	77.0 ± 2.03	4.17 ± 0.121
	x	76.0 ± 2.33	3.43 ± 0.103
C-42 (SARSABZ x NESSER)	♀	59.8 ± 1.72	2.43 ± 0.094
	♂	52.0 ± 2.00	1.73 ± 0.063
	x	83.2 ± 2.58	3.75 ± 0.165
C-43 (SARSABZ x BHITTAI)	♀	59.8 ± 1.72	2.43 ± 0.094
	♂	79.6 ± 1.51	3.83 ± 0.125
	x	83.0 ± 6.74	4.02 ± 0.349
C-44 (SARSABZ x PFAU/VEE#9//URES)	♀	59.8 ± 1.72	2.4 ± 0.094
	♂	59.0 ± 2.17	2.67 ± 0.072
	x	82.2 ± 6.32	3.42 ± 0.483
C-45 (SARSABZ x SITTA)	♀	59.8 ± 1.72	2.43 ± 0.094
	♂	82.4 ± 0.93	3.72 ± 0.076
	x	79.4 ± 4.11	3.57 ± 0.385

Table 1. (Cont'd.).

Cross/parents	Parents/ crosses	Number of grains/spike	Main spike yield (g)
		Mean ± standard error (s.e)	Mean ± standard error (s.e)
C-46 (BHITTAI x NR-234)	♀	79.6 ± 1.51	3.83 ± 0.125
	♂	77.0 ± 2.03	4.17 ± 0.121
	x	85.6 ± 2.54	4.43 ± 0.237
C-47 (BHITTAI x NESSER)	♀	79.6 ± 1.51	3.83 ± 0.125
	♂	52.0 ± 2.00	1.73 ± 0.063
	x	87.8 ± 3.26	3.88 ± 0.215
C-48 (BHITTAI x SARSABZ)	♀	79.6 ± 1.51	3.83 ± 0.125
	♂	59.8 ± 1.72	2.43 ± 0.094
	x	87.8 ± 2.35	4.02 ± 0.219
C-49 (BHITTAI x PFAU/VEE#9//URES)	♀	79.6 ± 1.51	3.83 ± 0.125
	♂	59.0 ± 2.17	2.67 ± 0.072
	x	81.4 ± 7.14	4.10 ± 0.380
C-50 (BHITTAI x SITTA)	♀	79.6 ± 1.51	3.83 ± 0.125
	♂	82.4 ± 0.93	3.72 ± 0.076
	x	78.2 ± 4.33	3.42 ± 0.264
C-51(PFAU/VEE#9//URES x NR-234)	♀	59.0 ± 2.17	2.67 ± 0.072
	♂	77.0 ± 2.03	4.17 ± 0.121
	x	82.8 ± 2.34	3.76 ± 0.246
C-52 (PFAU/VEE#9//URES x NESSER)	♀	59.0 ± 2.17	2.67 ± 0.072
	♂	52.0 ± 2.00	1.73 ± 0.063
	x	86.4 ± 6.30	3.29 ± 0.363
C-53 (PFAU/VEE#9//URES x SARSABZ)	♀	59.0 ± 2.17	2.67 ± 0.072
	♂	59.8 ± 1.72	2.43 ± 0.094
	x	88.6 ± 6.75	3.33 ± 0.264
C-54 (PFAU/VEE#9//URES x BHITTAI)	♀	59.0 ± 2.17	2.67 ± 0.072
	♂	79.6 ± 1.51	3.83 ± 0.126
	x	98.2 ± 6.51	4.19 ± 0.260
C-55 (PFAU/VEE#9//URES x SITTA)	♀	59.0 ± 2.17	2.67 ± 0.072
	♂	82.4 ± 0.93	3.72 ± 0.076
	x	87.4 ± 4.79	3.47 ± 0.206
C-56 (SITTA x NR-234)	♀	82.4 ± 0.93	3.72 ± 0.076
	♂	77.0 ± 2.03	4.17 ± 0.121
	x	100.8 ± 4.25	4.58 ± 0.367
C-57 (SITTA x NESSER)	♀	82.4 ± 0.93	3.72 ± 0.076
	♂	52.0 ± 2.00	1.73 ± 0.063
	x	83.0 ± 4.78	3.71 ± 0.184
C-58 (SITTA x SARSABZ)	♀	82.4 ± 0.93	3.72 ± 0.076
	♂	60.2 ± 1.91	2.43 ± 0.094
	x	90.4 ± 5.94	3.87 ± 0.282
C-59 (SITTA x BHITTAI)	♀	82.4 ± 0.93	3.72 ± 0.076
	♂	79.6 ± 1.51	3.83 ± 0.126
	x	86.4 ± 4.28	4.05 ± 0.309
C-60 (SITTA x PFAU/VEE#9//URES)	♀	82.4 ± 0.93	3.72 ± 0.076
	♂	59.0 ± 2.17	2.67 ± 0.072
	x	87.2 ± 2.54	3.86 ± 0.174

Table 2. Values of genetic variance (Vg), heritability percentage in broad sense (h^2 b.s), and genetic advance (G.A) for grains per spike and main spike yield of F_2 hybrids of wheat.

Crosses	Grains per spike			Main spike yield (g)		
	Genetic	Heritability	Genetic	Genetic	Heritability	Genetic

	variance (V.g)	**percent in broad sense (h^2 b.s)**	**advance (G.A)**	**variance (V.g)**	**percent in broad sense (h^2 b.s)**	**advance (G.A)**
C-31 (NR-234 x NESSER)	240.25	92.22	30.58	0.391	89.6	1.21
C-32 (NR-234 x SARSABZ)	123.7	87.54	21.42	0.1656	74.51	0.723
C-33 (NR-234 x BHITTAI)	233.3	93.61	30.43	0.963	92.82	1.947
C-34 (NR-234 x PFAU/VEE#9//URES)	-1.8	-891	-0.824	-0.033	-65.95	-0.305
C-35 (NR-234 x SITTA)	5.875	34.15	2.917	-0.036	-297.5	-0.682
C-36 (NESSER x NR-234)	167.95	89.24	25.208	0.1125	67.34	0.564
C-37 (NESSER x SARSABZ)	74.95	81.202	16.07	-0.172	-352.6	-0.016
C-38 (NESSER x BHITTAI)	48.53	75.54	12.449	0.0831	63.13	0.472
C-39 (NESSER x PFAU/VEE#9//URES)	-9.25	-74.0	-5.389	0.084	79.039	0.531
C-40 (NESSER x SITTA)	23.8	65.56	8.137	0.184	88.75	0.833
C-41(SARSABZ x NR-234)	9.4	34.81	3.725	-0.028	-54.48	-0.257
C-42 (SARSABZ x NESSER)	15.85	47.74	5.66	0.0851	62.14	0.047
C-43 (SARSABZ x BHITTAI)	214.5	94.28	29.29	0.549	90.13	1.45
C-44 (SARSABZ x PFAU/VEE#9//URES)	180.6	90.43	26.32	1.137	97.102	2.165
C-45 (SARSABZ x SITTA)	74.8	88.73	16.78	0.703	95.26	1.685
C-46 (BHITTAI x NR-234)	16.55	51.23	0.599	0.166	59.48	0.648
C-47 (BHITTAI x NESSER)	37.58	70.64	1.062	0.1783	78.59	0.077
C-48 (BHITTAI x SARSABZ)	14.7	53.068	0.575	0.1832	75.284	0.0765
C-49 (BHITTAI x PFAU/VEE#9//URES)	237.4	93.171	30.63	0.676	92.88	1.633
C-50 (BHITTAI x SITTA)	85.9	91.67	18.28	0.314	91.93	1.108
C-51 (PFAU/VEE#9//URES x NR-234)	5.2	19.11	0.205	0.242	79.88	0.0905
C-52 (PFAU/VEE#9//URES x NESSER)	176.55	89.03	2.58	0.6380	96.59	0.161
C-53 (PFAU/VEE#9//URES x SARSABZ)	208.7	91.62	2.849	0.310	90.15	0.109
C-54 (PFAU/VEE#9//URES x BHITTAI)	194.3	91.78	2.75	0.2813	84.45	0.1004
C-55 (PFAU/VEE#9//URES x SITTA)	100.9	87.89	12.52	0.182	87.26	0.821
C-56 (SITTA x NR-234)	77.8	86.25	1.694	0.617	92.68	0.1557
C-57 (SITTA x NESSER)	101.85	89.34	1.966	0.1425	85.91	0.0720
C-58 (SITTA x SARSABZ)	165.02	93.61	2.561	0.3637	91.228	0.1156
C-59 (SITTA x BHITTAI)	83.5	91.45	3.77	0.4232	88.91	0.1263
C-60 (SITTA x PFAU/VEE#9//URES)	18.6	56.83	0.664	0.1262	82.59	0.0665

Taking both yield parameters (grains per spike and main spike grain yield) in to consideration, it was observed that 17 progenies (C-31, C-32, C-33, C-36, C-43, C-44, C-45, C-49, C-50, C-52, C-53, C-54, C-55, C-56, C-57, C-58 and C-60) had high heritability percentage in broad sense (h^2) and high genetic advance (G.A) for both important yield contributing traits. These results depicted that these progenies showed genetic improvement in terms of more heritability percentage in broad sense (h^2) and genetic advance possess better potential to transfer the heritable traits; therefore could be effectively used to select the superior hybrid plants with desirable genes in successive generations. The information generated through this study will be obviously useful to breeders for future breeding keeping in view the selection of promising lines endowed with better yield potential, good quality and tolerance/ resistance to biotic and abiotic stresses.

Acknowledgements

The main author sincerely acknowledge the coordination of Dr. Javed Akhtar, Director, Nuclear Institute for Agriculture& Biology (NIAB), Faisalabad for providing the breeding material for this study.

References

Ahmedi, H and B. Bajelan. 2008. Heritability of drought tolerance in wheat. *American-Eurasian J. Agric.& Environ. Sci*., 3(4):632-635.

Al-Tabbal, J.A. and A.H. Al-Fraihat. 2012. Heritability studies of yield and yield associated traits in wheat genotypes**.** *Journal of Agricultural Science,* 4(4): 11-22.

Anonymous. 2010. Global wheat supply and demand brief crop prospectus and food situation. *FAO Global Information and early warning system on food and agriculture*, Vol. 1 p.7.

Anonymous. 2009. *Agricultural Statistics of Pakistan*-2008-09. Government of Pakistan, Ministry of Food and Agriculture (Economic Wing), Islamabad, Pakistan, pp. 3-4.

Ansari, B.A., M.M. Rajper, A.J. Malik and A.G. Magsi. 1991. Heritability estimates of plant height, yield and yield components in *Triticum aestivum* L. *Pak. J. Agric. Engg. Vet. Sci*., 7: 35-40.

Aycicek M. and T. Yildirim. 2006. Heritability of yield and some yield components in bread wheat (*Triticum aestivum* L.) genotypes. *Bangladesh J. Bot*., 35(1): 17-22.

Bux, H., A. Rasheed, M.A. Sial, Kazi, A.G. Kazi, A.Z. Napir and A. Mujeeb Kazi. 2013. An overview of stripe rust of wheat (*Puccinia striiformis* f. sp. *tritici*) in Pakistan. *Archives of Phyto pathology and Plant Protection (UK).* 45(19): 2278-2289.

Cooper, J.K., A.M.H. Ibrahim, J. Rudd, D. Hays, S. Malla and J. Baker. 2013. Increasing hard winter wheat yield potential via synthetic hexaploid wheat: II. Heritability and combining ability of yield and its components. *Crop Sci*., 53: 67-73.

Degewione, A., T. Dejene and M. Sharif. 2013. Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. *International Research Journal of Agricultural Sciences,* 1(2): 19-29.

Falconer, D.S. 1977. *Introduction to Quantitative Genetics*. Richard Clay Ltd. Bungay Suffolk, Great Britain, pp. 129-185.

Fischer, R.A. 1993. Irrigated spring wheat and timing and amount of nitrogen fertilizer. II. Physiology of grain yield response. *Field Crops Res*., 33: 57-80.

Khan, H., H. Rahman, H. Ahmed and H. Ali. 2008. Magnitude of heterosis and heritability in sunflower over environments. *Pak. J. Bot*., 1: 301-308.

Korkut, K., I. Baser and O. Bilgin. 2001. Genotypic and phenotypic variability, heritability and phenotypic correlation for yield and yield components in bread wheat varieties. *Acta-Agronomica*, 43: 237-242.

Laghari, K.A., M.A. Sial, M.A. Arain, A.A. Mirbahar, A.J. Pirzada, M.U. Dahot and S.M. Mangrio. 2010. Heritability studies of yield and yield associated traits in bread wheat. *Pak. J. Bot*., 42(1): 111-115.

Larik, A.S., A.A. Kakar, M.A. Naz and M.A. Shaikh. 1999. Estimation of genetic parameters in bread wheat (*Triticum aestivum* L.) crosses. *Sarhad J. Agri*., 15(1): 203-204.

Mohsin, T., N. Khan and F.N. Naqvi. 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *J. Food, Agri. Envi*., 7(3&4): 278-282. 2009.

Mangi, S.A., M.A. Sial, M.A. Arain and B. A. Ansari. 2008. Study of genetic parameters in segregating populations of spring wheat. *Pak. J. Bot*., (Special Issue) 39(7): 2407-2413.

Rajper, A.A., B.A. Ansari, A.S. Larik and Z.A. Soomro. 1998. Magnitude of heterosis and heritability in F2 populations of bread wheat. *Pak. J. Agri. Agril. Engg. Vet. Sc.,* 14(2): 55-57.

Riaz-ud-Din, G.M. Subhani, N. Ahmad, M. Hussain and Abdur-Rehman. 2010. Effect of temperature on development and grain formation in spring wheat. *Pak. J. Bot*., 42(2): 899-906.

Reynolds, M., A.J. Condon, G.J. Rebetzke and R.A. Richards. 2004. Evidence for excess photosynthetic capacity and sink-limitation to yield and biomass in elite spring wheat. In: *Proceedings of the 4th International Crop Science Congress*, Brisbane.

Savin, R. and G.A. Slafer. 1991. Shading effects on the yield of an Argentinian wheat cultivar. *J. Agric. Sci., Camb*., 116: 1-7.

Sayre, K.D., S. Rajaram and R.A. Fischer. 1997. Yield potential progress in short bread wheat in northwest Mexico. *Crop Sci*., 37: 36-42.

Sharma, S. and B.R. Tyagi. 1991. Character correlation, Path coefficient and heritability analysis of essential oil and quality components in Japanese mint. *J. Genet. and Pl. Breed*., 45: 257-262.

Shukla, S., A. Bhargava, A. Chatterjee, A. Srivastava and S.P. Singh. 2006. Genotypic variability in vegetable amaranth (*Amaranthus tricolor* L.) for foliage yield and its contributing traits over successive cuttings and years. *Euphytica*., 151: 103-110.

Sial, M.A., M.U. Dahot, M.A. Arain, G.S. Markhand, S.M. Mangrio, M.H. Naqvi, K.A. Laghari and A.A. Mirbahar. 2009. Effect of Water Stress on yield and yield components of semi-dwarf bread wheat (*Triticum aestivum* L.). *Pak. J. Bot*., 41(4): 1715-1728.

Sial, M.A., M.A. Arain, M.U. Dahot, G.S. Markhand, K.A. Laghari, S.M. Mangrio, A.A. Mirbahar and M.H. Naqvi. 2010. Effect of sowing dates on yield and yield components of bread wheat. *Pak. J. Bot*., 42 (1): 269-277.

Sial, M.A., K.A. Laghari, N.A. Panhawar, M.A. Arain and G.M. Balouch. 2012. Genetic improvement of drought tolerance in semi-dwarf wheat. Science, *Technology and Development,* 31(4): 335-340.

Sial, M.A, M.A. Arain and K.A. Laghari. 2012. Evolution of New wheat variety NIA-Amber for the general cultivation in sindh province-a case study 2012. *Pak. J. Bot*., 44(1): 301-306.

Singh, R.K. and B.D. Chaudhary. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, N. Delhi, India.

Zaazaa, E.I., M.A. Hager and E.F. El-Hashash. 2012. Genetical analysis of some quantitative traits in wheat using six parameters genetic model. *American-Eurasian J. Agric. & Environ. Sci*., 12 (4): 456-462.

(Received for publication 15 April 2012)