ISSN: 1023-1072 (Print), ISSN: 2663-7863 (Online)

Pak. J. Agri., Agril. Engg., Vet. Sci., 2019, 35 (2): 86-92

ASSESSING GENETIC ANALYSES AND PERFORMANCE OF F2 WHEAT (*TRITICUM AESTIVUM* L.) SEGREGATING POPULATION FOR VARIOUS YIELD AND ITS ASSOCIATED TRAITS

S. Nazir[*1], Z. A. Soomro[1], J. Mangi[2], G. M. Balouch[1] and K. A. Laghari[3]

[1]Sindh Agriculture University, Tandojam, Pakistan
[2]Institute of Plant Sciences, University of Sindh, Jamshoro, Pakistan
[3]Nuclear Institute of Agriculture, Tandojam

ABSTRACT

The research work was carried out to determine the heritability, genetic advance and performance for grain yield and various associated traits of six F_2 bread wheat segregating population which include NIA Sunhari x Marvi, Marvi x CIM 24/87, NIA Amber x Marvi, NIA-10/8 x NIA Amber, TD-1 x Khirman, and CIM 24/87 x Bhittai. These crosses were originated from eight parental lines viz NIA Sunhari, Marvi, CIM 24/87, NIA Amber, NIA 10/8, T.D-1, Khirman and Bhittai. The trial was organized in three replications under Randomized Complete Block Design (RCB). The results regarding mean squares depicted that genotypes and parents were highly significant at P<0.01 for days to spike emergence, days to maturity, plant height, spike length, spikelets spike^{-1}, spike yield, 100-grains weight, yield plant^{-1} and biological yield which showed that higher variation exist in both parents and F_2 population for these traits. The non-significant differences were observed for grain spike^{-1} among genotypes and parents that indicated existence of narrow variability among parents and hybrid for this trait. Cross combinations of F_2 population were strongly significant at P<0.01 for plant height, spikelets spike^{-1}, 100- grain weight, grain yield and biological yield. Days to maturity, spike length and grains spike^{-1} showed significant differences at 0.05 probability level in hybrids. Days to 75% spike emergence and main spike yield showed non-significant effects. Grain yield results indicated that cross NIA Amber x Marvi produced higher yield (23.90 g), while minimum grain yield plant^{-1} was noted in parent TD-1 (15.54 g). The higher 100-grain weight plant^{-1} (4.79 g) was recorded in CIM 24/87, followed by variety TD-1 (4.77 g). The heritability estimates indicated that cross NIA-Sunhari x Marvi had highest heritability (91.68%), followed by cross NIA-Amber x Marvi (84.16%) for grain yield plant^{-1}. Crosses Marvi x CIM 24/87 and CIM 24/87 x Bhittai showed highest heritability values for 100-grain weight (92.36, 61.53, respectively). Cross NIA-Amber x Marvi proved to be most effective cross combination for most of the traits.

Keywords: cross combinations, genetic advance, heritability, mean performance, parents

INTRODUCTION

Wheat is one of the major food stuffs and is main crop of the globe and Pakistan. It is planted in all over the world over an area of 221 million hectares with production of 744 million tons (FAO, 2018). Pakistan ranked 8th in wheat area and production (FAO, 2013). World population has increased many folds and is expected to reach 9 billion people by 2050 (Rosegrant and Agcaoili, 2010). Current wheat consumption and production is at par or some year produce is less (Grain Report, 2017). Climate change, increasing abiotic stress (heat, drought, salinity) or biotic stresses such as rust and many foliar diseases and even insect pests have become greater constraints for wheat potential production (IPCC, 2007). So, continuous improvement in wheat is needed for higher grain yield and for various stresses. Crossing programme had long success history in developing high yielding, disease resistant, drought, high temperature and salinity tolerant cultivars in large number of countries. First of all, successful breeding programme look for allelic variation for desirable traits to be crossed or incorporated. Secondly, to select parents or plants which have such heritable variation. Thirdly, phenotypic protocol to evaluate gene expression in targeted environments is implemented. Genetic knowledge of traits of interest and its selection based on presence and

[*]Corresponding author: sajidagaddi@gmail.com

absence of gene and its inheritance are some of the key features to successfully develop desirable plants, progenies and genotypes (Allard, 1960). In order to successfully breed for desirable traits, genetic variation is a key to success and breeder must know about gene involved for regulating the required traits and its inheritance mechanisms in its population (Henderson and Salt, 2017). Genetic variability and heritability estimates in early generation are important to identify and select superior families which can be utilized for the enhancement of grain yield and yield contributors (Shamayrira *et al*., 2019). Heritability analysis is important tool for selection and improvement of desirable traits including yield (Saleem *et al*., 2016). Secondly, variation is the key to select for desirable traits and produce sustainable crop yield (Din *et al*., 2018). Breeders usually select desirable plants/ progenies in early generations. Hence, present study was conducted to assess performance of parental lines and segregating population and workout genetic analysis for grain yield and its related traits.

MATERIALS AND METHODS

The trial was conducted at Nuclear Institute of Agriculture (NIA), Tandojam in Rabi season 2012-13. The experiment was sown in mid of November 2012. The soil was non-saline and clay loam in texture. The sowing was done in RCB (Randomized Complete Block) design in three replications. One row of each female and male parents was sown along with 6 rows of respective cross combination in each replication. The row length was 05 meter and row to row distance was 30 cm. The normal five irrigations were provided in the experiment. First irrigation was provided at seedling stage, second at tillering stage, third at booting stage, fourth at milky stage and fifth at dough stage of crop. Nitrogen (N) and phosphorous (P) were applied @ ratio of 4:3. Phosphate and N fertilizer DAP was applied as basal dose at the time of sowing, while remaining nitrogen was applied in splits during cropping period. First dose of Urea was applied at seedling stage, second at tillering and last at booting stage of crop. Weeding was done by hand. Cropping season usually remained favorable throughout growing season, except heat waved occurred in the month of April. The eight parental lines along their six cross combinations in F_2 generation were used for heritability assessment and for various yield and yield contributing traits. Parental lines include NIA Sunhari, Marvi, CIM 24/87, NIA Amber, NIA 10/8, TD-1, Khirman and Bhittai. The parental lines NIA-Sunhari and Marvi are disease resistant parents while Khirman, NIA-Amber and TD-1 are high yielding and widely adaptable cultivars of the province. CIM-24/87 is early maturing and NIA-10/8 is late maturing genotype. Hence these parents were selected to combine disease resistance, high yield, early maturity, short height into cross combination to select desirable plants/progenies. Six cross combinations viz NIA Sunhari x Marvi, Marvi x CIM 24/87, NIA Amber x Marvi, NIA-10/8 x NIA Amber, TD-1 x Khirman and CIM 24/87 x Bhittai were made by using these parents.

Crop was harvested in mid April 2013. At the time of crop maturity, 20 plants from each replication and each parental line and cross combinations were randomly selected and data were recorded. Data were recorded on days to 75% spike emergence, days to maturity, plant height, spike length, spikelets spike^{-1}, grains spike^{-1}, main spike yield, 100-grain weight, grain yield plant^{-1} and biological yield plant^{-1}. Days to spike emergence was recorded from the time of sowing up to emergence of 75% spikes of genotype. Days to maturity was noted from sowing till genotype become physiologically mature and turned its stem to yellowish color and spikes turned to side. Plant height was recorded when genotype attained its full growth and become mature. It was measured by meter scale from the earth surface to the upper most spikelets. Spike length was scaled in centimeters from bottom spikelet upto topper spikelet excluding awns. The number of spikelets spike^{-1} was noted by counting from basal spikelet to upper spikelet. To count grains spike^{-1}, selected spike was threshed singly and all the grains obtained from threshing of single spike were added. 100-grains were manually counted to record 100-grain weight on electronic balance. Single plant yield in grams was recorded by harvesting and threshing of selected individual plants which was later on weighed on electronic balance to obtain per plant yield data. Biological yield data or biomass of a genotype was weighed at the time of harvesting. The total produce including grains and straw were collectively weighed to record biological yield.

Statistical and genetic analyses

Analysis of variance (ANOVA) and Duncan multiple range test (DMRT) were obtained using software Statistix 8.1. Heritability estimates in broad sense (h^2 b.s), environmental variance

(Ve) and genetic variance (Vg) were computed as suggested by Falconer (1977), while genetic advance (G.A) with a selection intensity of 5% was also calculated as suggested by Larik *et al*. (1989). Following equations were used for calculating various parameters of genetic analyses:

Sum of Square (S.S)	=	$\sum (x)^2 - \sum (x)^2/N$
Variance (S^2)	=	S.S / n-1
Standard Deviation (SD)	=	$\sqrt{s^2}$
Genetic Variance (Vg)	=	VF_2 - Ve
Environmental variance (Ve)	=	$(VP_1 + VP_2)/2$
Heritability percentage in broad sense (h^2 b.s%)	=	Vg / VF_2 x 100
Genetic advance (G.A)	=	K x (H) x SD
Where, V	=	variance F_2 generation, and p = parent
S.D	=	Phenotypic standard deviation
K	=	constant (2.06) for selection difference at 5% selection intensity

RESULTS AND DISCUSSION

We present the analysis of variance for all the studied traits in Table 1a and 1b. Statistical analyses revealed that genotypes and parents were strongly significant at P<0.01 for spike emergence, days to maturity, plant height, spike length, spikelets spike^{-1}, spike yield, 100-grain weight, grain yield plant^{-1}, biological yield plant^{-1}, whereas grains spike^{-1} was non-significant in both genotypes and parental lines. It showed that larger variation exist for all other traits except grains spike$^{-1.}$ In case of hybrids, plant height, spikelets spike^{-1}, 100-grain weight, grain yield plant^{-1}, biological yield plant^{-1} were strongly significant at P<0.01 level. In hybrids days to maturity, spike length and grains spike^{-1} were significant at P<0.05 level, while days to spike emergence and spike yield was non-significant in hybrids. Hence in segregating populations, no any statistically significant difference existed for days to spike emergence and spike yield. Amein and Atta (2016) evaluated relative response of selection for grain produce and its contributors in a bread wheat cross. Statistical analyses pointed out significant differences among genotypes, families and parents for yield, plant height, spike length, spikelets spike^{-1} grains spike^{-1} across F_2, F_3 and F_4 generations. Therefore, greater responses to selection were expected.

Mean performance of different traits of wheat

The mean performance of parental lines and their crosses (hybrid) are described in Table 2. Results indicated that more number of days to spike emergence (58.93) was taken by parental line NIA 10/8, followed by cross NIA Amber x Marvi (56.78 days), whereas the parent CIM-24/87 produced its spike earlier in 52.4 days. Days to maturity data showed that the higher number of days to maturity (136.93) were used by parents NIA-10/8 and Khirman (132.53). The parent cultivar NIA-Sunhari matured earlier (123.53 days). Taller plant of 109.90 cm was noted in parent Bhittai and NIA-108 (105.27 cm). The shortest plant of 68.10 cm was measured in parent TD-1. The longer spike of 14.31 cm was produced by cross combination NIA 10/8 x NIA Amber and the shortest spike (9.60 cm) was produced by variety TD-1. The highest spikelets spike^{-1} (25.26) was recorded in variety Bhittai and NIA 10/8 (24.76), while lower spikelets spike^{-1} (15.93) was counted in variety TD-1. We noted higher grain spike^{-1} (75.73, 72.93) in Marvi and Bhittai, whereas, the lowest number of grains spike^{-1} (51.0) were found in variety Khirman. We noted highest spike yield of 3.38 g in Marvi, followed by variety Bhittai (3.08 g) and the lowest spike yield of 1.91 g in variety Sunhari. Highest 100-grain weight of 4.79 g was recorded in parent CIM-24/87 and TD-1 (4.79, 4.77 g, respectively) whereas, the smallest, 100-grain weight, (3.55 g) was produced by variety NIA-Amber. Highest per plant grain yield (23.90 g) was recorded in cross NIA-Amber x Marvi, followed by cross NIA-Sunhari x Marvi (22.74 g) and the lowest grain yield plant^{-1} (15.54 g) was produced by variety TD-1. The maximum biological yield 62.76 g plant^{-1} were produced by cross Marvi x CIM-24/87 and the lowest biological yield plant^{-1} (35.20 g) was produced by variety TD-1. Jan *et al*. (2015) evaluated 5 parental lines and their 19 F_3 populations; Cross Ghazanavi-98 x Pirsabak-05 produced higher 1000-grain weight (47.75 g). Highest harvest index and grain yield were recorded in cross Pirsabak-05 x AUP-4006 while among parents Pirsabak produced more grains per spike.

Heritability estimates for different cross combinations and genetic advance results regarding days to spike emergence are described in Table 3. Cross NIA- Sunahri x Marvi exhibited highest heritability (99.51%), followed by cross TD-1 x Khirman (92.35%). Genetic advance showed that cross NIA-Sunahri x Marvi also showed highest genetic advance (34.34). Days to 75% maturity data revealed that cross CIM 24/87 x Bhittai and NIA-Amber x Marvi had higher heritability (94.63 and 89.96%, respectively). Results for genetic advance estimated that crosses CIM24/87 x Bhittai and NIA- Amber x Marvi had higher genetic advance 10.39 and 7.79%, respectively. The results regarding plant height for different cross combinations and their heritability estimates showed that crosses TD-1 x Khirman and CIM 24/87 x Bhittai showed highest heritability (91.55, and 90.71%) and cross NIA-Sunhari x Marvi with heritability 70.71% went on third in rank in lieu of heritability. Result observed for genetic advance indicated that crosses TD-1 x Khirman and CIM 24/87 x Bhittai showed highest genetic advance (24.53, and 22.19%, respectively). Spike length data showed the highest heritability in crosses NIA-Amber x Marvi (76.35%) and Marvi x CIM24/87 (72.47%). Genetic advance results showed that cross NIA-Amber x Marvi had greater genetic advance (3.09).

Table 1a. Mean squares for various phenotypic traits of parents and hybrid of F_2 bread wheat populations

Source of Variation	D.F	Mean Square				
		Days to 75% heading	Days to 75% maturity	Plant (height)	Spike length	Spikelets (spike^{-1})
Replications	02	02.88	01.55	08.49	2.38	00.26
Genotypes	13	09.04**	36.78**	568.47**	6.26**	14.13**
Parents	07	12.90**	60.51**	899.72**	7.85**	24.42**
Hybrid	05	00.94$^{N.S}$	10.00*	134.81**	4.18*	02.36**
Error	26	01.03	01.00	17.02	0.50	00.67
Total	41					

** =Significant at $P\leq$ 0.01 level * =Significant at $P\leq$0.05 level N.S= Non Significant.

Table 1b. Mean squares for various phenotypic traits of parents and hybrid of F_2 bread wheat populations

Source of Variation	D.F	Mean Square				
		Grains (spike^{-1})	Main spike yield	100-grain (weight)	Grain yield (plant^{-1})	Biological yield (plant^{-1})
Replications	02	352.46	0.75	0.17	08.85	10.53
Genotypes	13	222.71$^{N.S}$	0.42**	0.41**	20.83**	148.34**
Parents	07	343.62$^{N.S}$	0.72**	0.48**	20.29**	179.80**
Hybrid	05	091.55*	0.09 $^{N.S}$	0.38**	15.42**	112.04**
Error	26	107.43	0.03	0.02	02.03	05.65
Total	41					

** =Significant at $P\leq$ 0.01 probability level * =Significant at $P\leq$0.05 probability level N.S= Non Significant.

Table 2. Mean performance of parents and different F_2 cross combinations for yield and its associated traits in bread wheat

Genotypes	Days to 75% heading	Days to 75% maturity	Plant height	Spike length (cm)	Spikelets (spike^{-1})	Grains (spike^{-1})	Main spike yield (g)	100-grain weight (g)	Grain yield (g plant^{-1})	Biological yield (g plant^{-1})
NIA Sunhari	54.53 cd	123.53 i	92.87 efg	10.16 ef	20.60 de	48.60 d	1.91 h	4.52abcd	22.19 ab	55.93 b
Marvi	54.60 cd	125.60 h	81.13 i	13.87 a	22.13 bc	75.73 a	3.38 a	4.70 abc	18.15 ef	46.26 ef
CIM 24/87	52.40 e	132.40 b	104.91 a	10.59 def	21.73 bcd	54.20 cd	2.60 def	4.79 a	22.10 abc	56.93 b
Bhittai	54.26 cd	132.27 b	109.90 b	13.17 ab	25.26 a	72.93 ab	3.08 ab	4.61 abcd	20.86 bcd	55.93 b
TD-1	55.20 bc	126.20 gh	68.10 j	9.60 f	15.93 f	52.26 cd	2.20 gh	4.77 a	15.54 g	35.20 g
NIA Amber	53.33 de	129.40 de	96.43 def	11.04 de	20.60 de	57.46 bcd	2.37 fg	3.55 e	17.85 efg	48.46 de
Khirman	52.46 e	132.53 b	102.47 cd	11.76 cd	22.76 b	51.00 d	3.00 bc	4.65 abc	15.90 fg	44.46 f
NIA 10/8	58.93 a	136.93 a	105.27 bc	13.43 ab	24.40 a	68.73 abc	2.48 efg	4.45 cd	19.72 cde	55.93 b
NIA Sunhari x Marvi	56.33 b	127.82 efg	84.76 hi	11.20 cde	20.60 de	57.38 bcd	2.37 fg	4.49 bcd	22.74 ab	45.78 ef
Marvi x CIM 24/87	55.91 bc	127.42 fg	88.54 gh	13.17 ab	22.18 bc	63.26abcd	2.70 cde	3.79 e	22.58 ab	62.76 a
NIA Amber x Marvi	56.78 b	129.47 de	90.11 fgh	12.33 bc	20.91cde	68.71 abc	2.79 bcde	4.69 abc	23.90 a	56.80 b
NIA 10/8 x NIA Amber	55.51 bc	132.07 bc	98.38 cde	14.31 a	22.10 bc	64.13abcd	2.55 def	4.35 d	18.23 ef	54.20 bc
TD-1 x Khirman	55.21 bc	130.48 cd	84.83 hi	11.27 cde	20.23 e	64.41abcd	2.80 bcd	4.70 abc	21.34 bc	50.60 cd
CIM 24/87 x Bhittai	55.91 bc	127.92 ef	100.30 cd	12.34 bc	22.18 bc	53.38 cd	2.48 defg	4.74 ab	18.88 be	48.78 de

Note: Parents/ crosses having letter representing similar alphabets are statistically non significant from each other

Table 3. Heritability and genetic advance of various cross combinations for growth and yield contributors

Crosses	Days to heading		Days to maturity		Plant height (cm)		Spike length (cm)		Spikelet spike^{-1}	
	h^2 (B.S) (Broad Sense heritability)	GA (Genetic advance)	h^2 (B.S) (Broad Sense heritability)	GA (Genetic advance)	h^2 (B.S) (Broad sense heritability)	GA (Genetic advance)	h^2 (B.S) (Broad sense heritability)	GA (Genetic advance)	h^2 (B.S) (Broad sense eritability)	GA (Genetic dvance)
NIA-Sunhari x Marvi	99.51	34.34	36.18	2.43	70.71	15.58	61.35	1.55	66.46	2.82
NIA-Amber x Marvi	67.15	4.77	89.96	7.79	69.90	9.82	76.35	3.09	91.33	9.69
NIA 10/8 x NIA Amber	59.43	2.09	86.93	6.04	45.36	8.75	52.34	1.51	42.23	1.91
TD-1 x Khirman	92.35	7.12	87.95	6.32	91.55	24.53	67.93	2.18	67.76	3.69
Marvi x CIM24/87	90.46	7.60	84.76	5.43	70.31	13.13	72.47	2.28	59.71	2.83
CIM24/87 x Bhittai	81.75	4.32	94.63	10.39	90.71	22.19	61.89	1.78	77.18	5.48

Table 4. Heritability and genetic advance of various cross combinations for yield and yield contributors

Crosses	Grains (spike^{-1})		Main spike yield (g)		100- grain weight		Grain yield (g plot^{-1})		Biological yield (g plot^{-1})	
	h^2 (B.S) (Broad sense heritability)	GA (Genetic advance)	h^2 (B.S) (Broad sense heritability)	GA (Genetic advance)	h^2 (B.S) (Broad sense heritability)	GA (Genetic advance)	h^2 (B.S) (Broad sense heritability)	GA (Genetic advance)	h^2 (B.S) (Broad sense heritability)	GA (Genetic advance)
NIA-Sunhari x Marvi	50.46	11.09	42.10	0.42	57.69	0.46	91.68	20.60	55.41	10.97
NIA-Amber x Marvi	77.67	33.75	68.90	1.26	33.33	0.26	84.16	11.24	71.73	17.82
NIA 10/8 x NIA Amber	59.19	18.75	53.12	0.63	48.64	0.42	36.18	2.19	39.77	6.37
TD-1 x Khirman	71.79	26.16	57.44	0.86	50.00	0.28	64.07	5.27	57.03	11.01
Marvi x CIM 24/87	56.17	16.80	49.46	0.68	92.36	2.08	72.96	8.21	73.03	18.40
CIM 24/87 x Bhittai	65.91	22.12	53.52	0.94	61.53	0.36	59.12	6.44	70.96	14.52

This cross combination of NIA-Amber x Marvi showed higher contribution for the trait spike length. Cross NIA- Amber x Marvi with heritability 91.33%, followed by cross CIM 24/87 x Bhittai 77.18% heritability for spikelets spike^{-1} proved good combination for spikelets spike^{-1}. Highest genetic advance (9.69) of cross NIA-Amber x Marvi also indicates that this cross combination can be effective selection in improving spikelet spike^{-1}. Shah *et al*. (2018) found genetic advance, heritability of various traits of F_3 population. Eight cross combinations and their parents were evaluated. According to their study the high heritability, high genetic advance were recorded for fertile tillers plant^{-1}, plant height, grain spike^{-1}, spike length, 100-grain weight, grain yield, etc. Hence, effective selection and improvements can be made for these traits. The combinations, Barsat x NR395, Marvi-2000 x NRL1107, NRL1107 x Lalma, NR0707 x Barsat and RIL085 x Barsat were found promising and had better mean performance and genetic values.

Results of heritability assessment and genetic advance of various cross combinations for grains spike^{-1}, spike yield, biological yield and grain yield are presented in Table 4. Highest heritability for grains spike^{-1} was calculated for cross NIA-Amber x Marvi (77.67%), followed by cross TD-1 x Khirman (71.79%). Results for genetic advance also indicated that crosses NIA- Amber x Marvi and TD-1 x Khirman had highest genetic advance (33.75, and 26.16%, respectively). Hence selection for these traits can be effective among these cross populations. Iqbal *et al*. (2017) recorded high heritability for days to ripening, length of spike, number of spike, grain weight and other yield related traits. Heritability estimates for main spike yield depicted that cross NIA- Amber x Marvi had highest heritability (68.90%), followed by cross TD-1 x Khirman (57.44%). Genetic advance also indicated that cross NIA- Amber x Marvi showed highest genetic advance (1.26%). Results regarding heritability estimates for 100-grain weight showed that cross Marvi x CIM 24/87 and CIM-24/87 x Bhittai with high heritability 92.36% 61.53%, respectively can be effective selection for bold grain. Results observed for genetic advance indicated that cross Marvi x CIM 24/87 showed highest genetic advance (2.08%). Saleem *et al*. (2016) published that grain weight had high heritability as compared with other traits. In their study, cross combination 9436 x Iqbal 2000 and 9436 x Lasani 2009 possesses higher heritability for majority of yield components and yield also. In another study conducted by Adhiena *et al*. (2016) estimated 4.51% heritability for number of tiller and 96.86% for grain weight. The high genetic advance 19.745 was also found for plant biomass. The results of heritability estimates for grain yield plant^{-1} showed that cross NIA- Sunahri x Marvi had highest heritability (91.68%), followed by NIA-Amber x Marvi (84.16%) and cross Marvi x CIM 24/87 (72.96%). Results for genetic advance indicated that cross NIA- Sunahri x Marvi also had highest genetic advance (20.60%) for grain yield plant^{-1}. Hence selection for higher grain yield can be fruitful among these cross combinations. Ijaz *et al*. (2013) had reported the higher heritability and genetic advance for yield, grain weight, height, tillers and leaf area. The results for biological yield plant^{-1} of different cross combinations and their heritability estimates showed that cross Marvi x CIM 24/87 exhibits highest heritability (73.03%), followed by cross NIA- Amber x Marvi (71.73%). Results for genetic advance showed that crosses Marvi x CIM 24/87 and NIA- Amber x Marvi also indicated higher genetic advance (18.40, and 17.82%, respectively.

CONCLUSION

Cross NIA Amber x Marvi produced the highest grain yield (23.90g). It could be better selection for improving grain yield. The heritability estimates indicated that cross NIA- Sunhari x Marvi had highest heritability (91.68%) followed by cross NIA-Amber x Marvi (84.16%) for grain yield plant^{-1}. Crosses Marvi x CIM 24/87 and CIM 24/87 x Bhittai showed highest heritability values for 100-grain weight (92.36, 61.53, respectively). The CIM 24/87 x Bhittai and NIA-Amber x Marvi had higher heritability percentage for days to maturity (94.63, 89.96, respectively). These cross combination can be effectively used to improve respective traits. Overall, cross NIA-Amber x Marvi proved to be most effective cross combination for most of the traits.

AUTHOR'S CONTRIBUTION

S. Nazir: Research Scholar.
Z. A. Soomro: Supervisor.
J. Mangi: Data analyses.
G. M. Baloch: Data interpretation.
K. A. Laghari: Technical support.

REFERENCES

Allard, R. W. 1960. Principle of plant breeding, John Wiley and Sons. Inc. New York , USA.

Amein, M. M. M and M. M. M. Atta. 2016. Relative response of selection for grain yield and its components on one bread cross (*Triticum aestivum* L.). Journal of Agriculture Food and Applied Sciences, 4 (1): 13-19.

Adhiena, M., W. Mohammed and T. Dessalegn. 2016. Estimation of heritability and genetic advance of yield and yield related traits in bread wheat (*Triticum aestivum* L.) Genotypes at Ofla district, Northern Ethiopia. International Journal of Plant Breeding and Genetics, 10: 31-37.

Din, I., F. Munsif, I. A. Shah, H. Khan, F. U. Khan, I. Brarullah, S. Uddin and T. Islam. 2018. Genetic variability and heritability for yield and yield associated traits of wheat genotypes in Nowshera Valley, Pakistan. Pakistan Journal of Agricultural Research, 31 (3): 216-222.

Falconer, D. S. 1977. Introduction to quantitative genetics. Richard Clay Ltd. Bungay Suffolk, Great Britain, pp. 129-185.

FAO, 2013. Cereal supply and demand brief and USDA.

FAO, 2018. Crop Prospectus and food situations, GIEWS, Global Information and early warning system on Food and Agriculture.

Grain Report. 2017. Global Agriculture Information Network, USDA, Foreign Agricultural Services, March, 2017.

Henderson, I. R. and D. E Salt. 2017. Natural genetic variation and Hybridization in plants. Journal of Experimental Botany, 68 (20): 5415-5417.

Ijaz, F., I. Khaliq, M. T. Shahzad and B. Saleem. 2013. Computation of heritability of yield and some morphological traits in F_2 populations of bread wheat. International Journal of Modern Agriculture, 2 (3): 102-107.

IPCC. 2007. Climate change: impacts, adaptation and vulnerability. *In:* Contribution of working Group II to Fourth Assessment Report of the Inter governmental Panel on Climate Change, M. L. Parry; O.F.

Iqbal, A., I. H. Khalil, S. M. A. Shah and M. S. Kakar. 2017. Estimation of heritability, genetic advance and correlation for morphological traits in spring wheat. Sarhad Journal of Agriculture, 33 (4): 674-679.

Jan, S., F. Mohammad and F. Khan. 2015. Genetic potential and heritability estimates of yield traits in F_3 segregating populations of bread wheat. International Journal of Environment, 4 (2): 106-115.

Larik, A. S., H. M. I. Hafiz and A. M. Khushik. 1989. Estimation of genetic parameters in wheat populations derived from intercultural hybridization. Pakphyton, 1: 51-56.

Rosegrant, M. W. and M. Agcaoili. 2010. Global food demand, supply and price prospects to International Food Policy Research Institute, Washington, DC.USA.

Saleem, B., A. S. Khan, M. T. Shahzad and F. Ijaz. 2016. Estimation of heritability and genetic advance for various metric traits in seven F_2 populations of bread wheat (*Triticum aestivum* L.). Journal of Agricultural Sciences, 61 (1): 1-9.

Shah. A., G. Hassan, F. I. Azam, J. Amin, A. Ahmed and F. Ghani. 2018. Estimation of genetic parmeters and interrelationship among important traits in bread wheat. International Journal of Farm and Applied Sciences, 7 (3): 93-99.

Shamayarira, K. W., H. S. T. Tapera and T. J. Tsilo. 2019. Genetic advancement of newly developed wheat population under drought stressed and non-stressed conditions. Journal of Crop Science and Biotechnology, 22 (2): 169-176.

(Received: September 23, 2019; Accepted: December 31, 2019; Published: January, 2020)