Pak. J. Bot., 49(SI): 163-170, 2017.

GENETIC ANALYSIS OF SOME YIELD ASSOCIATED TRAITS AND LEAF RUST RESISTANCE OF F_2 SEGREGATING POPULATION OF WHEAT

ABDUL WAJID CHANNA[1*], MAHBOOB ALI SIAL[2], HADI BUX[1], SADAF TABASSUM QURESHI[1] AND RABIA ASMA MEMON[1]

[1]*Institute of Plant Sciences, University of Sindh, Jamshoro, Pakistan*
[2]*Plant Genetics Division, Nuclear Institute of Agriculture (NIA), Tandojam, Pakistan*
[*]*Corresponding author's email: awabdulwajid440@gmail.com*

Abstracts

Genetic analysis of some yield contributing traits of four F_2 segregating populations (NIA-Amber x Marvi-2000, TD-1 x Khirman, NIA-10/8 x NIA-Amber and Marvi-2000 x NIA-Sunehri) originated from cross combinations of six parental wheat varieties was conducted. Experiment was carried out at Experimental Farm of Nuclear Institute of Agriculture, Tandojam, Pakistan during wheat season, 2013-14. Genetic parameters viz. genetic variance (Vg), environmental variance (Ve), heritability in broad sense (h^2b.s) and genetic advance (G.A) were studied for days to booting, days to heading, days to maturity, grain filling period, plant height, spike length, spikelets per spike, grains per spike, thousand grains weight, grain yield per plant, grain yield per plot, biological yield per plot, harvest index and leaf rust resistance. Results revealed that F_2 progenies Marvi-2000 x NIA-Sunehri and NIA-10/8 x NIA-Amber were found best combiner progenies with potential to transfer highest heritability with genetic advance for traits viz. days to booting, days to heading, days to maturity, grain filling period, plant height, grains per spike, grain yield per plant and harvest index. For leaf rust resistance, NIA-10/8 x NIA-Amber showed highest heritability along with genetic advance, indicating selection improvement and greater effectiveness. Highest heritability (h^2b.s) was recorded for plant height (80.1%), 1000-grain weight (90.7%), grain yield per plant (95.9%), grain yield per plot (95.7%), harvest index (95.8%) and leaf rust resistance (85.2%). Our findings provided valid information regarding genetic architecture of various yield associated traits and leaf rust resistance of above segregating progenies which could be utilized in future breeding programmes.

Keywords: Segregating population, genetic variability, heritability, genetic advance.

Introduction

Wheat is considered the most important cereal crop, due to fact it provides more calories in diet than any other crop (Adams *et al*., 2002; Shewry, 2009). The available genetic resources are being utilized by wheat breeders to modify the cultivated varieties for fulfilment of demand of ever increasing population and ever changing requirements (Mba *et al*., 2012; Sial *et al*., 2013). Wheat yields in this region are highly affected due to diseases, pests and the abiotic factors like water and heat stresses (Sial *et al.,*2010; Channa *et al;* 2016). To meet the challenges of low grain yields and other environmental stresses the fast and effective selection of wheat advance lines containing required traits in wheat breeding programs is pre-requisite (Piepho *et al.,*2016). The segregating population studies are important in determining the performance of newly evolved breeding material through evaluating their genetic parameters (Laghari *et al*., 2010). Breeders could generate significant genetic knowledge through heritability studies to predict interaction of genes involved in segregating populations (Ansari *et al.,* 1991; Sial *et al.,* 2012b; Degewione *et al.,* 2013).

Genetic potential and relationship of parents and progeny can also be determined by evaluating heritability values (Azam *et al*., 2013). However heritability estimates alone do not provide sufficient idea regarding expected positive gain in future generations until it should be associated with genetic advance (Al-Tabbal and Al-Fraihat, 2012; Zaazaa *et al*., 2012). Cooper *et al*., (2013) suggested that combining ability and heritability estimates enable to make prediction regarding the possible gain by which selection procedures become simpler. For the crop improvement, breeders use best genetic stock by making selection through heritability percentage and genetic advance (Arati *et al*., 2015). The success of selection program is based on heritability which determines the reliability of phenotypic variation (Hamdi, 1992).

Various wheat breeders studied broad sense heritability to evaluate hybrid population (Pawar *et al*., 1988; Larik *et al*., 1999; Ansari *et al*., 2002; Sial *et al.,* 2013). Heritability in broad sense (h^2b.s), genetic advance (G.A), phenotypic and genotypic variance were used to evaluate the variance magnitude in breeding material of wheat (Khan, 1990). Plant height is considered the most important character (Kashif & Khaliq, 2004) and selection parameter in wheat breeding programs which determines the yield because the decreased lodging has been related with increased crop yields (Rebetzke *et al.,* 2012). Plant breeders often prefer the uniform and short stature plants having lodging resistance and positive response to fertilizers (Ikramullah *et al*., 2011). Spike length is significantly important trait which has considerable relationship with grains per spike and ultimately to grain yield. Grains per spike is an important yield contributing trait that has direct influence on wheat grain yield (Ashfaq *et al*., 2003). 1000-grain weight is one of most imperative yield component which may be used as an important selection criteria for increased grain yield.

Leaf rust caused by (*Puccinia triticina*) is serious and most common disease of Wheat crop (Huerta-Espino *et al*., 2011) causing reduction in grains per spike and lower seed weight (Kolmer et al., 2005). Genetic variability for leaf rust in wheat segregating populations is recorded by Vijaykumar *et al*., (2013). Present study was carried out to analyse yield and yield associated traits; to evaluate the variability of desired traits and to investigate new sources of resistance among the segregating populations.

Material and Methods

The research study was carried out at the experimental field at Nuclear Institute of agriculture (NIA) Tandojam during wheat growing season (2013-14). The experimental material comprised of 6 varieties/parental lines of wheat viz., NIA-Amber, Marvi-2000, TD-1, Khirman, NIA-Sunehri, and NIA-10/8 along with four F_2 segregating population viz., NIA-Amber x Marvi-2000, TD-1 x Khirman, NIA-10/8 x NIA-Amber and Marvi-2000 x NIA-Sunehri. The experimental material was screened in the field using randomized complete block design (RCBD) with three replications. Two rows, two meter long of each genotype per replication were grown keeping 15cm space between plants and 30 cm between the rows. Data were recorded on days to booting, days to heading, days to maturity, grain filling period, plant height, spike length, spikelets per spike, 1000-grain weight, number of grains per spike, grain yield per plant, grain yield per plot, biological yield per plot, harvest index, leaf rust resistance and statistically analysed. The current experimental material was selected for creating the genetic variability and observing heritability in segregating populations of wheat and for obtaining the best individual genotype having high yielding qualities along with resistance against leaf rust disease. Data was analyzed using software Statistics 8.1 version. Broad sense heritability was calculated following Panse and Sukhatme, (1965). Each parameter was subjected to analysis of variance (ANOVA) according to (Gomez & Gomez., 1984) and the means were compared through LSD at 5 percent level of probability using Duncan's Multiple Range Test (DMRT) as suggested by Duncan (1955). Genetic parameters viz., heritability percentage in broad sense (h^2b.s), environmental variance (Ve), genetic variance (Vg) and genetic advance (G.A) were calculated for all the traits viz. days to booting, days to heading, days to maturity, grain filling period, plant height, spike length, spikelets per spike, 1000-grain weight, number of grains per spike, grain yield per plant, grain yield per plot, biological yield per plot, harvest index and leaf rust resistance as suggested by Falconer (1977) and Singh and Chaudhry, (1985). Means were compared using standard error of each hybrid progeny with its each respective parent.

Results

The mean square results from analysis of variance depicted the significant differences among genotypes for various traits. The highly significant difference ($P \leq 0.05$) observed for all traits except for days to booting, days to heading, days to maturity and grain filling period (Table 1a -1c).

Table 1a. Mean squares (MS) from analysis of variance (ANOVA) for different traits of F_2 population and parental lines of wheat evaluated for heritability studies

Source of variation	Mean squares (MS)				
	D.F	Days to booting	Days to heading	Days to 75 % maturity	Grain filling period
Replications	4	73.7	78.1	70.8	17.7
Genotype	9	150.1	128.2	48.8	24.3
Error	36	73.2	62.2	52.3	43.1
Total	49	--	--	--	--

* = Significant at $P \leq 0.05$, ** = Significant at $P \leq 0.01$, *** = Significant at $P \leq 0.001$ level of probability

Table 1b. Mean squares (MS) from analysis of variance (ANOVA) for different traits of F_2 population and parental lines of wheat

Source of variation	Mean squares (MS)					
	D.F	Plant height	Spike length	Spikelets per spike	Grains per spike	1000-grain width
Replications	4	76.5	3.33	7.78	328.6	8.02
Genotype	9	1087.8***	22.7***	52.3***	590.7***	208.3***
Error	36	125.0	2.48	3.3	115.4	9.7
Total	49	--	--	--	--	

* = Significant at $P \leq 0.05$, ** = Significant at $P \leq 0.01$, *** = Significant at $P \leq 0.$ 001 level of probability

Table 1c: Mean squares (MS) from analysis of variance (ANOVA) for different traits of F_2 population and parental lines of wheat

Source of variation	Mean squares (MS)				
	D.F	Grain yield per plant	Grain yield per plot	Biological yield per plot	Harvest index
Replications	4	1.4	3608.6	13567	91.9
Genotype	9	113.6***	10262.7***	136632***	569.2***
Error	36	4.3	1292.9	10904	58.6
Total	49	--	--	--	--

* = Significant at $P \leq 0.05$, ** = Significant at $P \leq 0.01$, *** = Significant at $P \leq 0.001$ level of probability

Days to booting: Non-significant difference was observed among genotypes for their days to booting trait (Table 1a). Days to booting ranged from (72.6 days) in parental line TD-1 to (87.6 days) in other parental line NIA-10/8. The parental line NIA-10/8 took long period (87.6 days) for booting followed by NIA-Sunehri (85.8 days) and Marvi-2000 (83.0 days). Progeny NIA-Amber x Marvi-2000 also took more time for days to booting (78.2 days) followed by NIA-10/8 x NIA Amber (74.0 days) (Table.2). Heritability estimates for days to booting ranged from 29.9 to73.0 for F_2 segregating populations of Marvi-2000 x NIA-Sunehri and NIA-Amber x Marvi-2000 respectively. Highest heritability was recorded in progenies NIA-10/8 x NIA-Amber (72.62%) and NIA-Amber x Marvi-2000 (73%) coupled with genetic advance (G.A 15.62 and 10.27) respectively (Table 4).

Days to heading: Among genotypes non-significant variability was recorded for days to heading (Table 1a). The highest days to heading were recorded in the parental variety NIA-10/8 which took (95.2 days) followed by two other parental lines NIA-Sunehri (92.6 days) and Marvi-2000 (88.6 days). Data revealed that minimum days for heading were taken by TD-1 (80.2 days). Maximum days for heading was recorded for offspring NIA-Amber x Marvi-2000 (86 days) while offspring TD-1 x Khirman took less (81.8 days) for heading (Table 2). Results revealed that cross progenies NIA-Amber x Marvi-2000 and NIA-10/8 x NIA-Amber had highest heritability (79.7 and 61.51%) along with genetic advance (GA 10.48 and 14.5) respectively while Marvi-2000 x NIA-Sunheri had low heritability estimates (7.48%) (Table 4).

Days to maturity: For days to maturity non-significant variation was recorded among the genotypes (Table 1a). The parental lines NIA-10/8, NIA-Sunehri and Marvi-2000 matured in long duration and took more (119.6, 116.6 and 116.2 days) to maturity respectively. Progeny NIA-Amber x Marvi 2000 took more time to maturation (113 days) as compared to others. Minimum days to maturity were recorded in parent TD-1 (109.8 days) and in progeny TD-1 x Khirman (111.6 days) (Table 2). Highest value of heritability estimates was obtained for cross combination Marvi-2000 x NIA-Sunheri (88.9%) and NIA-10/8 x NIA-Amber (78.5%) along with genetic advance (GA 48.94 and 20.39) respectively (Table 4).

Grain filling period: Non-significant differences were observed for grain filling period among genotypes (Table 1a). Parental line TD-1 took maximum (29.6 days) for grain filling duration followed by Khirman (28.2 days) and Marvi-2000 (27.6 days). Cross combination Marvi-2000 x NIA-Sunheri utilized more (30 days) for grain formation followed by NIA-10/8 x NIA-Amber (29.4 days). Minimum time was recorded in parental line NIA-Sunehri (23.6 days) for grain filling period (Table 2). Observations revealed that genotypes were non-significantly different among each other. Moderate heritability estimates were recorded for progenies NIA-10/8 x NIA-Amber (47.5%) to Marvi-2000 x NIA-Sunheri (61.6%) coupled with genetic advance (GA 5.66 and 12.27) respectively (Table 4). Heritability in broad sense showed no any genetic advancement for other two progenies (NIA-Amber x Marvi-2000 and TD-1 x Khirman). Observation revealed that genotypes were non-significantly different among each other.

Table 2. Overall mean comparison of yield and yield associated traits of F_2 segregating population and their parental varieties of wheat genotypes

Cross combination	Parents/ Crosses	Days to booting	Days heading	Days maturity	Grain filling period	Plant height (cm)	Spike length (cm)
NIA-Amber x Marvi-2000	♀	77.8AB	83.8BC	112.6AB	26.8A	91.2DE	9.2E
	♂	83.0AB	88.6ABC	116.2AB	27.6A	86.2E	9.4E
	⊕	78.2AB	86.0ABC	113.0AB	27.0A	96.4CDE	12.2CD
TD-1 x Khirman	♀	72.6B	80.2C	109.8B	29.6A	67.4F	14.0ABC
	♂	73.6B	81.8C	110.0B	28.2A	95.4CDE	10.6DE
	⊕	74.0B	81.8C	111.6AB	25.4A	118.4A	15.1A
NIA-10/8 x NIA-Amber	♀	87.6A	95.2A	119.6A	24.4A	103.8BCD	12.4BCD
	♂	77.8AB	83.8BC	112.6AB	26.8A	91.2DE	9.2E
	⊕	74.8B	82.8BC	112.2AB	29.4A	108.8ABC	14.3AB
Marvi-2000 x NIA-Sunehri	♀	83.0AB	88.6ABC	116.2AB	27.6A	86.2E	9.4E
	♂	85.8A	92.6AB	116.6AB	23.6A	100.2BCDE	10.0E
	⊕	73.8B	82.2C	112.2AB	30.0A	114.0AB	13.3ABC
Mean		78.5	85.6	113.5	27.2	96.6	11.5
LSD (0.05)		10.97	10.1	9.28	8.42	14.3	2.02
Standard Error		5.41	4.98	4.57	4.15	7.07	0.99

Table 3. Overall mean comparison of yield and yield associated traits of F_2 segregating population and their parental varieties of wheat genotypes.

Cross combination	Parents/ Crosses	Spikelets per spike	1000-grain weight (g)	Grains per spike	Grain yield per plant (g)	Grain yield per plot (g)	Biological yield per plant (g)	Harvest index %
NIA-Amber x Marvi-2000	♀	16.0E	42.2D	44.8FG	11.4D	226.4CD	841.0B	26.9B
	♂	13.2F	38.8D	51.8BCD	12.7D	236.4BC	908.0B	26.0B
	⊕	18.4D	45.8CD	52.2BC	24.7A	294.4A	1053.0A	27.9B
TD-1 x Khirman	♀	21.0BC	57.2BC	50.0CDE	12.2D	173.8E	701.0CD	24.6B
	♂	19.6CD	46.6CDE	48.0DEF	11.9D	181.6DE	640.0DE	28.5B
	⊕	23.0AB	62.6AB	65.4A	20.3B	215.8CDE	780.0BC	28.1B
NIA-10/8 x NIA-Amber	♀	21.4ABC	62.2AB	47.2EF	12.0D	276.8AB	600.0DE	46.4A
	♂	16.0E	42.2D	44.8FG	11.4D	226.4CD	841.0B	26.9B
	⊕	24.0A	73.2A	55.6B	20.3B	295.0A	600.0DE	52.1A
Marvi-2000 x NIA-Sunehri	♀	13.2G	38.8D	51.8BCD	12.7D	236.4BC	908.0B	26.0B
	♂	17.8DE	46.6CD	42.6G	12.3D	184.8DE	860.0B	21.7B
	⊕	19.2CD	56.0BC	54.4B	16.9C	222.0CD	530.0E	44.2A
Mean		18.6	51.1	50.7	14.9	230.8	771.8	31.6
LSD (0.05)		2.35	13.78	4.0	2.68	46.1	133.94	9.82
Standard Error		1.15	6.79	1.97	1.32	22.7	66.04	4.84

Table 4. Genetic parameters viz., Genetic variance (Vg), environmental variance (Ve), heritability percentage (h^2b.s) in broad sense and genetic advance (G.A) for traits, days to booting, days to heading, days to 75% maturity and grain filling period of four F_2 progenies of wheat.

F^2 Progenies	Days to booting				Days to heading				Days to maturity				Grain filling period			
	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A
NIA-Amber x Marvi-2000	12.6	34.1	73	10.27	10.24	40.26	79.7	10.48	23.0	0.5	2.12	0.20	32	-2	-6.6	-0.67
TD-1 x Khirman	128.8	80.2	38.3	11.3	89.85	85.85	48.8	13.10	62.35	12.95	17.19	3.03	61.2	-11	-21.9	-3.05
NIA-10/8 x NIA-Amber	31.05	82.65	72.62	15.62	51.45	82.25	61.51	14.5	37.4	137.05	78.5	20.39	18	16.3	47.5	5.66
Marvi-2000 x NIA-Sunehri	35.6	1.1	29.9	3.72	21	1.7	7.48	0.67	80.3	648.9	88.9	48.94	36.6	58.9	61.6	12.27

Table 5: Genetic parameters viz., genetic variance (Vg), heritability percentage (h^2b.s) and genetic advance (GA) for traits, plant height (cm), spike length (cm) and spikelets per spike of F_2 progenies of wheat.

F^2 Progenies	Plant height (cm)				Spike length (cm)				Spikelets per spike			
	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A
NIA-Amber x Marvi-2000	56.45	51.34	47.63	10.04	1.94	7.01	78.34	4.82	8.35	7.45	47.15	3.85
TD-1 x Khirman	162.8	16.0	8.94	2.19	0.59	-0.02	-4	-0.061	1.4	2.1	60.0	2.22
NIA-10/8 x NIA-Amber	40.5	13.2	24.5	3.6	0.7	0.1	12.5	0.19	2.0	2.5	55.0	2.16
Marvi-2000 x NIA-Sunehri	57.3	231.1	80.1	27.8	3.6	2.52	41.17	2.02	2.5	1.2	32.4	1.25

Plant height: Among the parental lines and progenies, significant ($P \leq 0.05$) variation was recorded for the trait plant height (Table1b). Maximum plant height was observed in the progenies i.e. TD-1 x Khirman (118.4cm), Marvi 2000 x NIA- Sunehri (114cm) followed by NIA-10/8 x NIA-Amber (108.8cm) while among parents NIA-10/8 obtained maximum height (103.8cm) followed by NIA- Sunehri (100.2cm). Minimum plant height was recorded for parent TD-1 (67cm) (Table 2). Highest heritability was observed in progenies Marvi-2000 x NIA-Sunehri (80.1) and NIA-Amber x Marvi-2000 (47.4) coupled with high genetic advance (G.A 27.8 and 10.04) respectively (Table 5). While lowest heritability percentage was observed in progeny TD-1 x Khirman (8.94).

Spike length: Various wheat breeders have suggested that the spike length is quantitatively inherited trait and has key role in segregating populations with maximum heritability. For spike length among genotypes significant ($P \leq 0.05$) difference was recorded (Table 1b). The progeny TD-1 x Khirman had long spike and maximum spike length (15.1cm) was significantly ($P \leq 0.05$) differentiated from all other genotypes followed by NIA-10/8 x NIA-Amber (14.3 cm). From parents, TD-1 obtained maximum spike length (14.0 cm) followed by NIA-10/8 (12.4 cm) (Table 2). Minimum length of spike was recorded in the parental line NIA-Amber (9.2cm). Heritability in broad sense showed that NIA-Amber x Marvi-2000 (78.34%) has highest heritability percentage for spike length trait followed by Marvi-2000 x NIA-Sunehri (41.17%) coupled with high genetic advance (G.A 4.82 and 2.02) respectively (Table 6).

Spikelets per spike: Among the genotypes significant ($P \leq 0.05$) variability was noted for spikelets per spike (Table 1b). Maximum spikelets per spike were observed in two progeny lines NIA-10/8 x NIA-Amber (24.0) and TD-1 x Khirman (23.0) spikelets followed by parental lines NIA-10/8 (21.4) spikelets and TD-1 has (21.0) spikelets (Table 3). Similarly other genotypes Khirman and NIA-Amber x Marvi-2000 have (19.5) and (19.2) spikelets per spike respectively. Minimum spikelets per spike were recorded in parental variety Marvi-2000 (13.2). Two cross progenies TD-1 x Khirman (60%) and NIA-10/8 x NIA-Amber (55%) showed highest heritability while lowest heritability was recorded in Marvi-2000 x NIA-Sunehri (32.4%) (Table 5).

1000-grain weight: For 1000-grain weight, significant ($P \leq 0.05$) variation was noted among the genotypes (Table1b). Results revealed that maximum 1000-grain weight was observed in offspring population i.e. TD-1 x Khirman (65.4g) and NIA-10/8 x NIA-Amber (55.6g) followed by Marvi-2000 x NIA-Sunehri (54.4g). Likewise Marvi-2000 has maximum 1000-grain weight (55g) followed by TD-1 (50.0g) and Khirman (48.0g). Minimum 1000-grain weight was observed in parental line NIA-Sunehri (42.6g) (Table 3). Highest heritability in broad sense was recorded for progenies TD-1 x Khirman (90.7%) followed by NIA-Amber x Marvi-2000 (82.5%) with genetic advance (G.A 11.38 and 5.26) respectively, while, moderate was observed in progeny NIA-10/8 x NIA-Amber (42.2%) (Table 6).

Number of grains per spike: Significant diversity was observed for number of grains per spike among the genotypes (Table1b). Observations revealed that genotypes were significantly ($P \leq 0.05$) different among each other. Variability for number of grains per spike ranged from (45.8 to 73.2) for progenies while it ranged from (38.8 to 62.2) for parental lines. Cross combination NIA-10/8 x NIA-Amber produced highest number of grains per spike (73.2) followed by TD-1 x Khirman (62.6) while lowest number of grains per spike was produced by NIA-Amber x Marvi-2000 (45.8) (Table 3). Parental line NIA-10/8 produced maximum (62.2) number of grains per spike followed by TD-1 (57.2). The minimum grains per spike were produced by Marvi-2000 (38.8). High heritability was recorded for cross progeny NIA-10/8 x NIA-Amber (59.5%) with genetic advance (GA-15.68) (Table 6).

Grain yield per plant: Grain yield per plant is an important yield associated trait considered to play a key role in enhancing the total grain yield. Among offspring, the cross NIA-Amber x Marvi-2000 produced highest grain yield per plant (24.7g) followed by NIA-10/8 x NIA-Amber (20.36g) and TD-1 x Khirman (20.34g) (Table 3). Maximum grain yield per plant was produced by parental line Marvi-2000 (12.7g) and minimum was recorded from NIA-Amber (11.4g). Significant ($P \leq 0.05$) variation among parental and offspring lines were recorded (Table 1c). For the grain yield per plant trait, the heritability percentage (h^2%) in broad sense ranged from the lowest (2.3%) in progeny NIA-10/8 x NIA-Amber to highest (95.9%) in TD-1 x Khirman followed by (86.49% and 35.9%) in NIA-Amber x Marvi-2000 and Marvi-2000 x NIA-Sunehri. Both the progenies TD-1 x Khirman and NIA-Amber x Marvi-2000 have highest heritability coupled with the high genetic advance (G.A 8.19 and 2.51) respectively (Table 6).

Grain yield per plot: Genotypes including parental lines and segregating population showed significant ($P \leq 0.05$) diversity for grain yield per plot (Table1c). Maximum grain yield per plot was recorded in progeny NIA-10/8 x NIA-Amber (295g) followed by NIA-Amber x Marvi-2000 (294.4g). Similarly, parental varieties NIA-10/8, Marvi-2000 and NIA-Amber produced higher grain yield per plant (276.8, 236.4 and 226.4g respectively). Analysed data showed that parental line TD-1 produced minimum (173.8g) grain yield per plot (Table 3). Moderate to highest heritability in broad sense was recorded in progenies NIA-Amber x Marvi-2000 (59.5%), NIA-10/8 x NIA-Amber (62.9%), and Marvi-2000 x NIA-Sunehri (95.7%) together with high advance (G.A 45.7, 69.08 and 51.4) respectively. TD-1 x Khirman showed lowest heritability percentage (8.61%) (Table 7).

Biological yield per plot: Biological yield per plot of genotypes showed significant ($P \leq 0.05$) variability for the trait biological yield per plot (Table 1c). The progeny NIA-Amber x Marvi-2000 has maximum biological yield per plot (1053g) followed by TD-1 x Khirman (780g) (Table1c). Similarly, results revealed that parental genotypes Marvi-2000 possess maximum (908g) biological yield per plot followed by NIA-Sunehri (860g), NIA-Amber (841g). Minimum biological yield per plot was recorded for both parental line NIA 10/8 (600g) and offspring Marvi-2000 x NIA-Sunehri (530g) (Table 3). The heritability percentage (h^2) in broad sense showed that the offspring line NIA-Amber x Marvi-2000 had highest heritability (79.7%) (Table 7).

Harvest index: Among parental genotypes and their progenies significant ($P \leq 0.05$) divergence was recorded for harvest index (Table1c). Among parents maximum harvest index was recorded for (46.4%) in NIA-10/8 followed by Khirman (28.5%) while the cross combination NIA-10/8 x NIA-Amber (52.1%) produced maximum harvest index (Table 3). Lowest harvest index percentage was observed for parent NIA-Sunheri (21.7%). High heritability in broad sense showed that offspring Marvi-2000 x NIA-Sunehri has maximum harvest index (95.8%) followed by NIA-10/8 x NIA-Amber (86.05%) coupled with the high genetic advance (G.A 28.12 and 28.18) respectively. While, TD-1 x Khirman showed moderate to low heritability estimates (4 4.85%) for harvest index trait (Table 7).

Leaf rust resistance

F^2 Progenies	Leaf rust resistance			
	v.e	v.g	h^2%	G.A
NIA-Amber x Marvi-2000	12.5	32.5	72.2	10.05
TD-1 x Khirman	65.0	265.0	80.3	29.9
NIA-10/8 x NIA-Amber	47.2	272.8	85.2	31.3
Marvi-2000 x NIA-Sunehri	33.75	8.75	20.58	2.74

Leaf rust resistance data showed the existence of wide range of genetic variability for leaf rust resistance in above cross progenies of bread wheat. The offspring line NIA-10/8 x NIA-Amber showed highest heritability (85.5%) coupled with high genetic advance (31.3) followed by cross progeny TD-1 x Khirman (80.3%). Similarly NIA-Amber x Marvi-2000 also performed better and showed improvement for leaf rust resistance having heritability (72.2%) along with moderate genetic advance (10.05). While cross combination Marvi-2000 x NIA-Sunehri showed lowest heritability (20.58%) along with low genetic advance (2.74).

Table 6. Genetic parameters viz., genetic variance (Vg), heritability percentage (h^2 b.s) and genetic advance (GA) for traits 1000- grain weight, number of grains per spike and grain yield per plant of F_2 progenies of wheat.

F_2 Progenies	1000- grain weight (g)				Number of grains per spike				Grain yield per plant (g)			
	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A
NIA-Amber x Marvi-2000	1.69	8.01	82.5	5.26	116.7	47	28.7	7.56	1.10	7.06	86.49	2.51
TD-1 x Khirman	3.5	34.3	90. 7	11.38	216.7	107.6	33.17	12.23	0.73	16.9	95.9	8.19
NIA-10/8 x NIA-Amber	2.6	1.9	42.2	1.83	67.3	98.9	59.5	15.68	8.4	0.2	2.3	0.11
Marvi x NIA-Sunehri	9	13.3	59.6	5.71	69.4	23.8	25.5	4.97	2.69	1.51	35.9	1.47

Table 7. Genetic parameters viz., genetic variance (Vg), heritability percentage (h^2 b.s) and genetic advance (GA) for traits grain yield per plot, biological yield per plot and harvest index % of F_2 progenies of wheat.

F^2 Progenies	Grain yield per plot (g)				Biological yield per plot (g)				Harvest index %			
	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A	v.e	v.g	h^2%	G.A
NIA-Amber x Marvi-2000	574.3	845	59.5	45.7	2350	11595	79.7	175.1	6.45	-2.78	-75.74	-2.95
TD-1 x Khirman	1936.2	182.45	8.611	8.15	14002.5	-2002.5	-16.68	-36.09	29.48	23.98	44.85	6.6
NIA-10/8 x NIA-Amber	1085.2	1840.6	62.9	69.08	13500	5250	28	78.9	35.3	217.88	86.05	28.18
Marvi-2000 x NIA-Sunehri	29.6	666.4	95.7	51.4	10000	3650	26.7	62.5	8.48	198.02	95.8	28.12

Discussion

The genetic constitution of parental lines of cross progenies has major contribution for genetic improvement and heritability estimates. To create genetic variability, hybridization is one of the fundamental tools. In any crop species the improvement and selection based on genetic variability is pre-requisite. Broader variability range makes it significant to choose a particular character with efficacy and simplicity. For a successful hybridization the amount of genetic variation has been considered as essential factor which provides the opportunity to evolve a vigorous genotype having the desirable traits (Santosh *et al*., 2013). To evolve the genetically diverse resistant genotypes against leaf rust is essential to cope with evolution of new races which overcome resistance genes causing break down of resistance. Creation of offsprings equipped with resistance against diseases and with superior performance for desired traits has remained the prime aim of wheat breeding strategies. Objective of current study was to evaluate the heritability among different yield contributing traits and the leaf rust disease resistance in four segregating populations of wheat.

Our finding showed that cross progeny Marvi-2000 x NIA-Sunehri performed better as compared to other cross combinations and produced highest heritability (h^2b.s) for traits days to maturity (88.9%), grain filling duration (61.6%), plant height (80.1%), grain yield per plot (95.7%) and harvest index (95.8%) coupled with high genetic advance (48.94, 12.27, 27.8, 51.4 and 28.12) respectively. The high heritability estimates for plant height and grain yield per plot were also recorded by (Riaz-Ud-Din *et al.,* 2010; Gulnaz *et al*., 2011 ; Yadav *et al*., 2011).

The offspring NIA-10/8 x NIA-Amber showed genetic improvement in terms of high heritability for number of grains per spike (59.5%) coupled with high genetic advance (15.68). Variability in number of grains per spike exhibited by different wheat cultivars may be due to their genetic potential (Shafi *et al*., 2015). Results revealed that on the basis of heritability estimates performance, the NIA-10/8 x NIA-Amber progeny occupied the second position in terms of transfer of characters after Marvi-2000 x NIA-Sunehri. This offspring also performed better for most of traits viz. days to booting, days to heading, days to maturity, grain formation duration, plant height, biological yield etc. High heritability along with genetic advance for days to heading and grains per spike was reported by (Abinasa *et al.,* 2011 and Jan *et al*., 2015).

Results depicted that TD-1 x Khirman progeny produced higher heritability percentage for spikelets per spike (60%), 1000-grain weight (90.7%) and grain yield per plant (95.9%) coupled with high genetic advance. The high heritability percentages for thousand grain weight, grain yield per plant and spikelets per spike has been reported (Rashidi, 2011 and Saleem *et al*., 2016) while Awale *et al.,* (2013) recorded moderate percentages. TD-1 x Khirman progeny should be critically examined further as most of its traits has low to moderate heritability and genetic advance which indicated that selection for desired traits in early segregating population seems difficult.

While the offspring NIA-Amber x Marvi-2000 had higher heritability magnitude for spike length (78.34%), biological yield per plot (79.7%) coupled with high genetic advance. Although NIA-Amber x Marvi-2000 has highest heritability for days to booting and days to heading (73% and 79.7%) but low genetic advance (10.27, 10.48) as compare to NIA-10/8 x NIA-Amber has (72.62% and 61.51%) but contain higher genetic advance (15.62, 14.5) showing the improvement for traits.

Field screening observations for leaf rust of parents and segregating populations revealed that parental varieties TD-1 and NIA-10/8 severely affected by leaf rust epidemic showed susceptibility, NIA-Amber and Khirman were found moderately susceptible, NIA-Sunehri was moderately resistant to moderately susceptible while parental variety Marvi-2000 showed resistance against the leaf rust disease under natural field conditions. Results of cross progenies revealed that highest heritability estimates were recorded for NIA-10/8 x NIA-Amber (85.5%) for leaf rust resistance followed by offspring TD-1 x Khirman and NIA-Amber x Marvi-2000 which has (80.3% and 72.2%) along with high genetic advance.

Observations showed that broad range was recorded for leaf rust resistance by F_2 segregating population, indicating ample selection scope of promising and superior genotypes existed for further yield improvement and resistance against leaf rust disease (Arati *et al*., 2015).

Results showed that different traits have a broad range of expression suggesting the enough existence of variability in these populations. Through sensible and attentive selection of different yield contributing traits among these cross combinations can be improved, keeping in mind that the promising genotypes endowed with greater potential of yield and resistance to leaf rust disease will be suitable for future breeding purpose.

Conclusion

From the estimates of heritability it is evident that cross progenies (Marvi-2000 x NIA-Sunehri and NIA-10/8 x NIA-Amber) possessed high heritability (h^2 b.s) along with genetic advance for the traits days to booting, days to heading, days to maturity, grain filling period, plant height, grains per spike, grain yield per plant and harvest index. For leaf rust resistance NIA-10/8 x NIA-Amber has highest (85.5%) heritability followed by other progenies. Thus, findings warrant that the crosses performed better should be given due importance while selecting promising plants in further breeding program. As these cross progenies have also maintained their superiority over both their parents in most of traits and have proven best combiner offsprings with great potential to transfer the yield related traits and leaf rust resistance with highest heritability and genetic advance. The current knowledge generated will be useful for future breeding strategies to wheat breeders.

References

Abinasa, M, Ayana, A., Bultosa, G. 2011. Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. *var. Durum*) genotypes. *Afr. J. Agric. Res*., 6(17): 3972-3979.

Adams, M.L., E. Lombi, F.J. Zhao and S.P. McGrath. 2002. Evidence of low selenium concentrations in UK bread-making wheat grain. *J. Sci. Food & Agri*., 82: 1160-1165.

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

Ansari, B.A., A.M. Khushik and K.A. Ansari. 2002. Heritability and genetic advance of yield traits in the hybrids of spring wheat. *Pak. J. Agri. Engg. Vet. Sc.,* 18(1-2): 5-9.

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.

Arati, Y., R.R. Hanchinal, H.L. Nadaf, S.A. Desai, S. Biradar and R.V. Naik. 2015. Genetic variability for yield parameters and rust resistance in F2 population of wheat (*Triticum aestivum* L.). *The Bioscan*., 10(2): 707-710.

Ashfaq, M., A.S. Khan and Z. Ali. 2003. Association of morphological traits with grain yield in wheat (*Triticum aestivum* L.). *Int. J. Agric. Bio*., 5: 262-264.

Awale, D., T. Dejene and M. Sharif. 2013. Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. International research *J. Agri. Sci*., 1(2): 19-29.

Azam, S. M., F. M, I. Ahmad, I. H. Khalil, S. A. Jadoon and A. Nasim. 2013. Divergence in f$_3$ segregating bread wheat populations. *IJBAS – IJENS*., 13(03): 94-99.

Channa, A.W., M.A. Sial, H. Bux and J.G.M. Sahito. 2016. Resistance to leaf rust in commercial wheat varieties of Sindh and their agronomic performance under different sowing regimes. *Pak. J. Phytopathol*., Vol.28 (01): 61-69.

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. *Int. Res. J. Agri. Sci*., 1(2): 19-29.

Duncan, D.B. 1955. Multiple Range and Multiple F-test. *Biometrics,* 11: 01-42.

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

Gomez, K.A. and A.A. Gomez 1984. Statistical procedures in agricultural research. John wiley & sons, New York.

Gulnaz, S., M. Sajjad, I. Khaliq, A.S. Khan and S.H. Khan. 2011. Relationship among coleoptiles length, plant height and tillering capacity for developing improved wheat varieties. *Int. J. Agri. & Biol*., 13:130-133.

Hamdi, A. 1992. Heritability and combining ability of root characters in lentil (*Lens culinaris* Medik) *Egyptian J. Agric. Res*., 70(1): 247-255.

Huerta-Espino, J., R.P. Singh, S. German, B.D. McCallum, R.F. Park, W.Q. Chen, S.C. Bhardwaj and H. Goyeau. 2011. Global status of wheat leaf rust caused by *Puccinia triticina*. *Euphytica*, 179: 143-160.

Ikramullah, I.H. Khalil, H.U. Rahman, F. Mohammad, H. Ullah and S.K. Khalil. 2011. Magnitude of heritability and selection response for yield traits in wheat under two different environments. *Pak. J. Bot*., 43(5): 2359-2363.

Jan, S., M. Fida and F.U. Khan. 2015. Genetic potential and heritability estimates of yield traits in f3 segregating populations of bread wheat. *Int. J. Environ*., 4(2): 106-115.

Kashif and Khaliq. 2004. Heritability, correlation and path coefficient analysis for some metric traits in wheat. *Int. J.Agri.& Biol*., 1: 138-142.

Khan, N.I. 1990. Variability and character association in wheat. *J. Agric. Res*., 28(3): 193-200.

Kolmer, J.A., D.L. Long and M.E. Hughes. 2005. Physiological specialization of *Puccinia triticina* on wheat in the United States in 2003. *Plant Dis*., 89: 1201-1206.

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.

Mba, Chikelu., E. P. Guimaraes and K. Ghosh. 2012. Re-orienting crop improvement for the changing climatic conditions of the 21st century. *Agri. & Food Security,* 1:7. http://www.agricultureandfoodsecurity.com/content/1/1/7.

Panse, V.G. and P.V. Sukhatme.1965. Statistical methods for agricultural workers. Indian Council. Agric. Res., New Dehli, p.381.

Pawar, I.S., R.S. Paroda and S. Singh. 1988. Study of heritability and genetic advance in three wheat populations. *Bang. J. Agir. Res*., 14(1): 24-26.

Piepho, H.P., M.F. Nazir, M. Qamar, A.R. Rattu, Riaz ud-Din, M. Hussain., G. Ahmad, Fazal-e-Subhane, J. Ahmad, Abdullah, K.B. Laghari., I.A. Vistro, M.S. Kakar, M.A. Rashidi. 2016. Stability analysis for a countrywide series of wheat trials in Pakistan. *Crop Sci.,* 56(5): 2465-2475.

Rashidi, V. 2011. Genetic parameters of some morphological and physiological traits in durum wheat genotypes (*Triticum aestivum* L.). *Afr. J. Agric. Res.,* 6:2285-2288.

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

Rebetzke, G.J. M.H. Ellis, D.G. Bonnett, B. Mickelson, A.G. Condon, R.A. Richards.2012. Height reduction and agronomic performance for selected gibberellin-responsive dwarfing genes in bread wheat (*Triticum aesitivum* L.). *Field Crops Research.,* 126. 87–96.

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.). *J. Agri. Sci*., 61(1): 1-9.

Saleem, S., M. Kashif, M. Hussain, A. S. Khan and M. F. Saleem. 2016. Genetic behavior of morpho-physiological traits and their role for breeding drought tolerant wheat. *Pak. J. Bot*., 48(3): 925-933.

Santosh, A., D.K. Mishra and S.S. Bornare. 2013. Screening genetic variability in advance lines for drought tolerance of bread wheat (*Triticum aestivum* L). *The Bioscan*., 8(4): 1193-1196.

Shafi M., R.Zaman, J. Bakht, Y. Hayat and Shaheenshah. 2015. Dry matter partitioning and grain yield of wheat as affected by Phosphorus and its applications. *Pak. J. Bot*., 47(SI): 281-287.

Sial, M.A., M.U. Dahot, S.M. Mangrio, M.A. Arain, K.A. Laghari and A.A. Simiar. 2010. Screening of wheat genotypes for water stress tolerance. *Pak. J. Biotech*., 7(1-2): 137-143.

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. *Pak. J. Bot*., 44(1): 301-306.

Sial, M.A., J. Akhter, A.A. Mirbahar, K.D. Jamali, N. Ahmed and H. Bux. 2013. Genetic studies of some yield contributing traits of F$_2$ segregating generation of bread wheat. *Pak. J. Bot*., 45(5): 1841-1846.

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

Shewry, P.R. 2009. The health grain programme opens new opportunities for improving wheat for nutrition and health. *Nutr. Bull*., 34(2): 225–231.

Vijaykumar, H., R. Naik, H.L. Nadaf, S.A. Desai, S.K. Deshpande, I.K. Kalappanavar and B.N. Patil. 2013. Genetic studies in free threshable advanced segregating population of tetraploid wheat (*Triticum dicoccum*). *Karnataka J. Agri. Sci*., 26(1): 10-13.

Yadav, A.K., R.K. Maan, S. Kumar and P. Kumar. 2011. Variability, heritability and genetic advance for quantitative characters in hexaploid wheat (*Triticum aestivum* L.). *Electronic J. Plant Breed*., 2: 405-408.

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 January 2016)