HERITABILITY ESTIMATES IN F₂ SEGREGATING POPULATION IN HEXAPLOID WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

An investigation was undertaken to evaluate heritability and variability estimates among F₂ populations of bread wheat (*Triticum aestivum* L.). Twenty-two wheat genotypes including twelve parents and ten F₂ crosses were grown in the field according to Randomized Complete Block Design (RCBD) with three replications. The outcomes from the analysis of variance depicted that the genotypes, parents, crosses, and parents *versus* crosses were highly significant for flag leaf area, peduncle length, plant height, tillers plant⁻¹ and grain yield plant⁻¹. The mean performances of the parents and F₂ populations for the traits studied revealed that the parent genotype Tufan performed best regarding flag leaf area⁻¹, spikelets spike⁻¹ and grain yield plant⁻¹. Kiran-95 showed maximum peduncle length. and maximum tillers plant⁻¹ were produced by TD-1. The cross-combination NARC-2011 x Tufan gave maximum values for flag leaf area, peduncle length, plant height. The overall performances of the F₂ crosses for all the traits were way better than their parent genotypes. This suggests that these traits should be considered in selection program for breeding purposes. The results from the components of variance, i.e. phenotypic variance and genotypic variance revealed significant differences among the genotypes for all the traits. The phenotypic variance values were greater than the genotypic variance values indicating the much environmental impact on the expression of the traits studied. High heritability and genetic advance estimates were recorded in majority cases for flag leaf area, peduncle length, plant height, tillers plant⁻¹, grains spike⁻¹, seed index, and grain yield plant⁻¹ Therefore, the cross combinations with high genetic variability and heritability must be considered in future breeding programs.

Keywords: Bread wheat, F₂ population, heritability, phenotypic variance, grain yield

INTRODUCTION

Wheat (*Triticum aestivum* L.) is grown widely across almost all around the world, representing about 30% of the cereal cultivation area, providing 20% of the calories for the human population (Khan *et al.,* 2015). Since the advent of Green solution, wheat yields have increased in many regions of the world (Fang *et al*., 2017). It has been predicted that till 2050 research attentions towards wheat will be fast as to face the challenge of feeding a population of 9 billion (Rajaram and Braun, 2008). Moreover, several environmental constraints especially high-temperature effects and water deficit are responsible for serious threat in wheat production (Flexas *et al*., 2004; Prasad *et al*., 2009). Pakistan positions among the top countries that produce wheat (Agriculture Corner, 2010). However, our average yield is still less than the potential yield (Khan and Hassan 2017). In Pakistan, during 2016-17 Wheat production was estimated as 25.750 million tones witnessing an increase of 0.5 percent over the last year's production of 25.633 million tones (GOP, 2017).

Bread wheat is taken into consideration as a staple meal supply for a massive population of the entire world and gives quite some varied baked food products. Therefore, whole wheat and its production are the chief meals assets for human food regimen (Kumar *et al*., 2013). To meet the requirement of developing a population of Pakistan, wheat genotypes must be genetically improved to produce a high yield. For this reason, the utiliza-

tion of maximum genetic potential from given genetic resources of wheat is required. Segregating populations are usually demonstrated by F_2 hybrids, which are spotted in all crop species, showing an increasing amount of variation among the genotypes. The F_2 and succeeding generations developed through selfing are not desirable because of reduced yields and developmental characters (Wang *et al*., 2017).

An effective selection depends on the presence of genetic variability (Khan *et al*., 2015). Heritability plays a great role in plant breeding which predicts the performance of the subsequent generations and makes alluring choices. If the heritability is higher, the selection procedure becomes easy, and the response to selection becomes greater and drives towards genotypic variances that are influenced by phenotypic variances (Saleem *et al.*, 2016). Many different crop species are being studied in terms of genetic diversity considering qualitative and quantitative characters for selecting parents with greater genetic distance for hybridization (Shekhawat *et al*., 2001; Arega *et al*., 2007; Haydar *et al*., 2007; Ahmadi zadeh *et al*., 2011; Daniel *et al*., 2011). Information of a trait and its heritability thus directs a breeder to speculate the performance of succeeding generations and to estimate their selection response (Larik *et al*., 1989). Hence, the present research was conducted to measure the extent of genetic variability and heritability magnitude of different traits.

MATERIALS AND METHODS

The present study was conducted to evaluate F_2 populations of wheat genotypes along with their parents for genetic variability and heritability in Experimental Field (wheat section) of the Nuclear Institute of Agriculture (NIA), Tandojam. The experimental material comprised of 22 wheat genotypes including 12 parents (NIA-Sundar, Benazir, NARC-2011, TD-1, SD-888, Sarsabz, TJ-83, Tufan, Marvi-2000, NIA-Saarang, Kiran-95 and NIA-

Amber and their 10 F_2 crosses (Benazir × TD-1, Benazir × SD-888, NARC-2011 × Sarsabz, NARC-2011 × TD-1, NARC-2011 × Tufan, NIA-Sundar × NARC-2011, TJ-83 × Marvi-2000, NIA-Amber × Marvi-2000, NIA-Sarang × Marvi-2000 and Kiran-95 × Marvi-2000). All the tested wheat genotypes were grown according to randomized complete block design. The data were collected for flag leaf area (cm^2), peduncle length (cm), plant height (cm), tillers plant^{-1} and grain yield plant^{-1} (g).

Statistical analysis: The date for analysis of variance was done according to the statistical technique outlined by Gomez and Gomez (1984) through Statistics 8.1 computer software. The means of genotypes for all the traits were compared by using the least significant difference (LSD) at 5% probability level. The genetic, environmental and phenotypic variances, broad sense heritability (h^2) and expected response to selection was estimated according to Mahmud and Kramer (1951).

RESULTS AND DISCUSSION

The genetic variability studies in F_2 for all the traits indicated that sufficient amount of genetic variability is present in the population.

Flag leaf area (cm^2): Flag leaf area is one of the most important determinants of grain yield in cereals. The results of the flag leaf area revealed that the parents and their F_2 populations were significantly ($p < 0.01$) different (Table 1). The results revealed that the parent genotype Tufan had the highest flag leaf area (44.89 cm^2), followed by Kiran-95, NIA-Sarang, NARC-2011, Marvi-2000, NIA-Sundar, TD-1, NIA-Amber, SD-888, TJ-83, Benazir and Sursabz with 36.12, 30.13, 29.56, 28.73, 25.94, 25.48, 24.59, 22.87, 20.85, 20.40 and 20.15 respectively. Whereas in F_2 populations the cross-combination NARC-2011 x Tufan showed highest flag leaf area (49.98) while the lowest value of flag leaf area was shown by Benazir x TD-1 (25.91) (Table 2).

Table 1: Mean squares from analysis of variance for yield and its related traits in different wheat varieties and F$_2$ population

Characters	Replication D.F. = 2	Genotypes D.F. = 21	Parents (P) D.F. = 11	Hybrids (H) D.F. = 9	P x H D.F. = 1	Error D.F. = 42
Flag leaf area	0.82	189.73**	156.64**	119.96**	3341.07**	0.24
Peduncle length	0.18	107.76**	143.20**	76.32**	1374.57**	0.37
Plant height	0.46	728.42**	1110.62**	336.64**	6109.79**	0.52
Tillers plant^{-1}	0.04	12.20**	8.49**	16.55**	311.79**	0.31
Grain yield^{-1}	0.13	61.28**	28.14**	50.08**	526.69**	0.57

**= Significant at P<0.01 and *=P<0.05probability level, ns. = Non-significant

Table 2: Mean performance of parents and F$_2$ hybrids for yield and its related traits of bread wheat (*Triticum aestivum* L.)

Genotypes	Flag leaf area (cm^2)	Peduncle length (cm)	Plant height (cm)	Tillers plant^{-1}	Grain yield^{-1} (g)
Parents					
NIA-Sundar	25.94	40.56	117.00	8.56	32.11
Benazir	20.40	28.67	91.67	9.44	25.00
NARC-2011	29.56	41.58	94.78	8.44	23.89
TD-1	25.48	27.94	67.56	11.22	22.89
SD-888	22.87	21.78	50.22	6.56	22.89
Sarsabz	20.15	38.44	111.67	8.00	21.56
TJ-83	20.85	41.78	98.89	6.78	21.00
Tufan	44.89	40.72	110.00	6.44	26.44
Marvi-2000	28.73	41.89	97.56	6.67	22.67
NIA-Saarang	30.13	34.44	102.33	9.78	22.22
Kiran-95	36.12	43.44	109.44	11.00	21.89
NIA-Amber	24.59	37.22	101.78	7.78	25.89
Average	**27.48**	**36.54**	**96.07**	**8.39**	**24.04**
F$_2$ populations					
Benazir x TD-1	25.91	27.92	79.90	13.50	32.07
Benazir x SD-888	37.92	28.87	81.67	11.43	28.63
NARC-2011 x Sarsabz	29.97	37.30	103.73	9.13	29.00
NARC-2011 x TD-1	34.87	33.53	89.73	8.40	32.13
NARC-2011 x Tufan	49.98	41.60	112.50	6.30	25.67
NIA-Sundar x NARC-2011	33.17	39.70	103.80	9.13	33.63
TJ-83 x Marvi-2000	34.49	40.13	98.70	6.67	22.53
NIA-Amber x Marvi-2000	37.72	40.80	101.60	10.70	28.73
NIA-Saarang x Marvi-2000	38.66	36.77	102.70	6.87	27.93
Kiran-95 x Marvi-2000	37.06	41.00	103.93	10.97	36.77
Average	**35.97**	**36.76**	**97.83**	**9.31**	**29.71**
LSD (5%)	**0.801**	**1.01**	**1.19**	**1.13**	**1.56**

Table 3 shows the values for a phenotypic variance, genotypic variance, heritability and genetic advance for flag leaf area. The values for phenotypic variance and genotypic variance were low to high ranging from 6.50-65.93 and 5.58-61.13. The highest phenotypic variance (65.93) and genotypic

variance (61.13) values were observed in Benazir x SD-888 whereas the lowest phenotypic variance (6.50) and genotypic variance (5.58) values were shown by NARC-2011 x TD-1. The heritability & genetic advance estimates were moderate to high ranging from 55.40-92.72 and 5.69-19.57 respectively. The highest values for both these parameters were obtained from Benazir x SD-888 while

the lowest values were obtained from NARC-2011 x Tufan. These results indicated that this trait could be improved through selection as the additive component is highly involved (Table 3). Firouzian et $al.$, (2003), Katiyar (2003) and Riaz and Chowdhry (2003) also observed more flag leaf area in hybrids as compared to parents.

Table 3: Heritability estimates and genetic advance for different yield and metric traits in bread wheat (*Triticum aestivum* L.)

	Flag leaf area (cm^2)					Peduncle length				
F$_2$ populations	δ^2 p	δ^2 e	δ^2 g	h^2 %	G.A.	δ^2 p	δ^2 e	δ^2 g	h^2 %	G.A.
Benazir x TD-1	10.74	3.55	7.19	66.95	5.71	20.60	1.48	19.12	92.80	10.95
Benazir x SD-888	65.93	4.80	61.13	92.72	19.57	21.15	2.47	18.68	88.31	10.56
NARC-2011 x Sarsabz	10.28	2.62	7.66	74.51	6.21	5.25	2.13	3.12	59.42	3.54
NARC-2011 x TD-1	6.50	0.92	5.58	85.88	5.69	23.64	0.76	22.88	96.80	12.24
NARC-2011 x Tufan	29.51	13.16	16.35	55.40	7.82	10.11	2.15	7.96	78.72	6.51
NIA-Sundar x NARC-2011	27.08	9.09	17.99	66.44	8.99	8.56	3.01	5.56	64.89	4.94
TJ-83 x Marvi-2000	22.43	7.40	15.03	67.00	8.25	13.09	4.15	8.93	68.26	6.42
NIA-Amber x Marvi-2000	24.81	5.22	19.59	78.96	10.22	5.75	5.53	0.22	3.89	0.24
NIA-Saarang x Marvi-2000	57.61	7.38	50.22	87.18	17.20	7.63	5.07	2.56	33.59	2.41
Kiran-95 x Marvi-2000	18.36	5.23	13.14	71.53	7.97	17.79	5.57	12.22	68.70	7.53

Peduncle length: For peduncle length, the results showed that the genotypes were significant at p <0.01 (Table 1) for this trait. The mean performance results revealed that the genotype Kiran-95 exhibited highest peduncle length (43.44), followed by Marvi-2000 (41.89) while lowest peduncle length was observed in SD-888 (21.78). The cross-combination NARC-2011 x Tufan in F$_2$ population had the highest peduncle length of 41.60. The phenotypic variance and genotypic variance values for this trait were averages ranging from 5.25-23.64 and 0.22-22.88. The highest value for peduncle length for phenotypic variance (23.64) and genotypic variance (22.88) was obtained from NARC-2011 x TD-1 while the lowest value for this trait was shown by NARC-2011 x Sarsabz and NIA-Amber x Marvi-2000 (Table 2). The heritability and genetic advance values for this trait were moderate to high ranging from 33.59-96.80 and 3.54-12.24. The highest values were obtained from NARC-2011 x TD-1, and the lowest value of 3.89 and 0.24 was obtained from NIA-Amber x

Marvi-2000 (Table 3). The findings are similar to the results of Subhani et $al.$, (2000), Laghari et $al.$, (2010) and Ijaz et $al.$, (2013).

Plant height: Plant height is a quantitative trait as stated by Raut et $al.$ (1996) and Chowdhry et $al.$ (1997). This trait showed that this trait was also significant at p<0.01. The results revealed that genotypes possessed maximum height for NIA-Sundar (117.0). While the lowest height was exhibited in SD-888 (50.22). While among the cross combinations the cross NARC-2011 x Tufan showed the highest plant height (112.50) and the lowest value for plant height was recorded for Benazir x TD-1 (79.90). Table 4 results represent the phenotypic, genotypic, heritability and genetic advance estimates for plant height. Among the F$_2$ population, the phenotypic variance and genotypic variance values were usually high for plant height. The highest value for phenotypic and genotypic variance of 105.34 and 94.70 was obtained by the cross combination of Benazir x TD-1. While the lowest value among plant height was shown by

NARC-2011 x Sarsabz. The heritability and genetic advance estimates were high for plant height. The highest value of 91.17 and 24.05 for which was obtained by Benazir x SD-888 while the lowest value for these two parameters was given by NIA-Amber x Marvi-2000 (69.73-13.39) (Table

4). Thus, this result indicates that the given trait can also be improved through selection and the cross combination must be considered in a breeding program. Similar findings were reported by Dwivedi *et al*., (2002), Yousaf *et al*., (2008) and Yadawad *et al*., (2015).

Table 4: Heritability estimates and genetic advance for different yield and metric traits in bread wheat (*Triticum aestivum* L.)

F₂ populations	Plant height (cm)					Tillers plant[-1]				
	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	$h^2 \%$	G.A.	$\delta^2 p$	$\delta^2 e$	$\delta^2 g$	$h^2 \%$	G.A.
Benazir x TD-1	105.34	10.64	94.70	89.90	23.99	23.03	1.24	21.79	94.63	11.81
Benazir x SD-888	102.99	9.10	93.89	91.17	24.05	7.96	0.78	7.19	90.23	6.62
NARC-2011 x Sarsabz	41.37	4.72	36.65	88.59	14.82	2.62	0.51	2.11	80.39	3.38
NARC-2011 x TD-1	99.93	12.11	87.82	87.88	22.84	13.97	0.74	13.24	94.73	9.21
NARC-2011 x Tufan	54.81	11.22	43.59	79.53	15.31	5.87	0.28	5.59	95.27	6.00
NIA-Sundar x NARC- 2011	48.86	8.10	40.76	83.43	15.16	12.53	0.28	12.26	97.78	9.00
TJ-83 x Marvi-2000	72.36	14.07	58.29	80.56	17.82	9.26	0.60	8.67	93.55	7.40
NIA-Amber x Marvi- 2000	54.59	16.53	38.07	69.73	13.39	35.67	0.47	35.19	98.68	15.32
NIA-Saarang x Marvi- 2000	53.60	15.14	38.46	71.75	13.66	5.36	0.97	4.39	81.86	4.93
Kiran-95 x Marvi- 2000	63.31	16.28	47.03	74.29	15.37	12.52	0.75	11.77	94.01	8.65

Tillers plant[-1]: This trait showed that the numbers of tillers plant[-1] were significantly different at p< 0.01 (Table 1). The mean performance results exhibited that the variety TD-1 showed a maximum number of tillers plant[-1] (11.22) followed by Kiran-95 (11.0). In F₂ populations the number of tillers plant[-1] was maximum in cross combination Benazir x TD-1 (13.50) and minimum in NARC-2011 x Tufan (6.30) (Table 2). The phenotypic variance and genotypic variance values for a number of tillers plant[-1] ranged from 2.62-35.67 and 2.11-35.19. The highest phenotypic variance and genotypic variance value were observed for NIA-Amber x Marvi-2000 (35.67 and 35.19) and the lowest value was given by NARC-2011 x Sarsabz (2.62 and 2.11). All cross combinations usually exhibited high values for heritability and moderate to high for genetic advance except for NARC-2011 x Sarsabz (3.38). The highest value for heritability and the genetic advance was observed for NIA-Amber x Marvi-2000 (98.68 and 15.32). These high values for heritability and genetic advance indicate that no. of tillers plant[-1] could be improved through selection (Table 4). The current findings are similar to the results of Awaad (1996)

and Singh *et al.*, (1999) who reported high values for heritability in tillers plant[-1].

Grain yield plant[-1]: The analysis of variance results showed that the parents and the F₂ segregating population were significant at p<0.01 (Table 1). The data for mean performance revealed that the average grain yield was 24.04 for the parent genotypes. The highest grain yield was observed for NIA-Sundar (32.11) and the lowest (21.00) amount of grain yield was produced by TJ-83. Within the cross combination the cross Kiran-95 x Marvi-2000 showed the highest value for grain yield (36.77) and NARC-2011 x Tufan showed the lowest grain yield value (25.67) (Table 2). The phenotypic variance and genotypic variance values for grain yield plant[-1] were low to high as shown in (Table 5.) The highest phenotypic variance and genotypic variance value was obtained for Kiran-95 x Marvi-2000 (111.43 and 108.00), while the lowest value of 24.92 and 23.18 was obtained for NIA-Sundar x NARC-2011. The heritability and genetic advance estimates were high for grain yield plant[-1.] The highest heritability and genetic advance value were recorded for Benazir x TD-1 (98.58 and 26.81), closely followed by NARC-

2011 x Sarsabz (98.34 x 26.76). The wheat combinations NARC-2011 x Tufan and NIA-Sundar x NARC-2011 were observed for the lowest value of heritability and genetic advance (92.84 and

12.08) (Table 1). The outcomes are similar to Mangi *et al.*, (2010), Chowdhry *et al.*, (1997), Salim *et al.*, (2003) and Haq *et al.*, (2008).

Table 5: Heritability estimates and genetic advance for grain yield plant^{-1} in bread wheat (*Triticum aestivum* L.)

Grain yield plant^{-1}					
F$_2$ populations	δ^2 p	δ^2 e	δ^2 g	h^2 %	G.A.
Benazir x TD-1	109.43	1.56	107.87	98.58	26.81
Benazir x SD-888	41.51	1.18	40.33	97.16	16.28
NARC-2011 x Sarsabz	109.51	1.82	107.69	98.34	26.76
NARC-2011 x TD-1	25.94	1.74	24.20	93.31	12.35
NARC-2011 x Tufan	46.37	3.32	43.05	92.84	16.44
NIA-Sundar x NARC-2011	24.92	1.74	23.18	93.03	12.08
TJ-83 x Marvi-2000	63.79	1.38	62.42	97.84	20.32
NIA-Amber x Marvi-2000	96.02	2.18	93.84	97.73	24.90
NIA-Saarang x Marvi-2000	29.22	1.97	27.25	93.25	13.11
Kiran-95 x Marvi-2000	111.43	3.43	108.00	96.92	26.60

Conclusion

The analysis of variance revealed significant differences among the genotypes of parents and all F$_2$ cross of the traits studied. Based on mean performance it may be concluded that the parent variety Tufan exhibited maximum flag leaf area. NIA-Sundar had maximum plant height and grain yield plant^{-1}. Among the F$_2$ crosses NARC-2011 x Tufan performed well for flag leaf area, peduncle length and plant height. Kiran-95 x Marvi-2000 showed maximum grain yield plant^{-1}. Heritability estimates were high for plant height, tillers plant^{-1} and grain yield plant^{-1}. Moderate values of heritability were obtained for peduncle length and flag leaf area.

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