Pure Appl. Biol., 5(4): 913-920, December, 2016
http://dx.doi.org/10.19045/bspab.2016.50115

Research Article

Inheritance studies in F_2 segregating populations of bread Wheat genotypes

Naila Gandahi[1], Abdul Wahid Baloch[1], Munaiza Baloch[1], Tanweer Fatah Abro[1], Saleem Maseeh Bhatti[2], Aijaz Ahmed Soomro[3], Qamaruddin Jogi[3], Asad Marri[4] and Muharam Ali[5]
1. Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam-Pakistan
2 .Department of Soil Science, Sindh Agriculture University, Tandojam-Pakistan
3. Department of Agronomy, Sindh Agriculture University, Tandojam Pakistan
4. Institute of Food Sciences and Technology, Sindh Agriculture University, Tandojam Pakistan
5. Department of Biotechnology, Sindh Agriculture University, Tandojam-Pakistan
**Corresponding author's email*: balochbreeders@yahoo.com

Citation
Naila Gandahi, Abdul Wahid Baloch, Munaiza Baloch, Tanweer Fateh Abro, Saleem Maseeh Bhatti, Aijaz Ahmed Soomro, Qamaruddin Jogi, Asad Marri and Muharam Ali . Inheritance studies in F_2 segregating populations of bread Wheat genotypes. Pure and Applied Biology. Vol. 5, Issue 4, pp913-920.
http://dx.doi.org/10.19045/bspab.2016.50115

Received: 23/07/2016 Revised: 01/08/2016 Accepted: 16/08/2016 Online First: 25/08/2016

Abstract

This study was carried out to determine the inheritance pattern of various agronomic traits in six F_2 segregating populations of spring wheat. In this context, an experiment was conducted at the experimental field of Southern Wheat Research Station, Tandojam during Rabi 2014-2015. The experiment was laid out in randomized complete block design with three replications. The experimental material was consisted of nine parents, including Khirman, Imdad-05, Noori, Soughat, Mexipak, Moomal, Marvi, Kiran-95 and Anmol-91 and their six F2 progenies. The analysis of variance of the genotypes (including nine parents and their six F_2 progenies) showed that all the defined characters were differed significantly ($P<0.05$), offering the higher genetic variability among the genotypes which can further be exploited for various breeding programs to improve bread genotypes. On the basis of mean performance, among the parental lines, the parent Khirman exhibited outstanding performance for a range of characters (tillers plant^{-1}, spike length, spikelets spike^{-1}, grains spike^{-1} and grain yield plant^{-1}). Considering the F_2 hybrids, the progeny Khirman × Imdad-05 showed promising results for tillers plant^{-1}, spike length and spikelets spike^{-1}, whereas Anmol × Marvi gave desirable results for grain yield plant^{-1} and seed index, indicating that above mentioned genotypes may be proved reliable genetic resources. With regards to heritability percentage in broad sense, the F_2 progeny Khirman x Imdad-05 expressed high heritability for almost all studied traits, with the exception of grain yield plant^{-1}. This study suggests that most of the yield associated traits have been successfully transmitted. The information generated will be helpful for better understanding and selection of desirable material especially in advance generations.

Keywords: Bread wheat; F_2 population; Heritability; Inheritance

Introduction

Wheat (*Triticum aestivum* L.) is the most vital and major consumable food cereal of the world, including Pakistan. It is a staple food in many countries, including Pakistan [1]. The prime objective of wheat breeders is to evolve the wheat cultivars that show stability at genetic level, produce more grain yield and adapt well to a wide range of climatic conditions. Wheat requirement is increasing day by day due to ever increasing human population of the world. Competition among existing cultivars and advance lines of wheat has also shown up. Wheat cultivars with promising yield contributing characters need to be assessed and selected for further breeding **[2]**. Heritability estimates offer information concerning the extent to which particular crop trait, such as days to maturity, plant height, tillers plant^{-1}, spike length, grains spike^{-1}, grain weight spike^{-1}, 1000-grain weight and grain yield plant^{-1} are transferred to the following generations **[3]**. Selection would be easier, if the heritability is higher; consequently, greater will be the response to selection **[4]**. Heritability measures the phenotypic variance which is attributable to the genetic cause. The knowledge of heritability helps the plant breeders in anticipating the behavior of the succeeding generation and provides a major component of response to the selection for a successful breeding program **[5]**. Therefore, the current research was conducted to evaluate F_2 wheat population and assess various yield traits for available variation and to study heritability and genetic advance for the traits. This information will be helpful for improving the wheat yield through reliable selection.

Materials and methods

The present experiment was conducted at the experimental field of Southern Wheat Research Station, Tandojam during Rabi 2014-2015.The experiment was laid out in randomized complete block design with three replications. In a total, nine parental varieties lines (Khirman, Imdad-05, Mexipak, Noori, Soughat, Moomal, Marvi, Kiran-95 and Anmol-91) and six intervarietial F_2 hybrids (Khirman x Imdad-05, Noori x Imdad-05, Imdad-05 x Soughat, Mexipak x Moomal, Anmol-91 x Marvi and Kiran-95 x Imdad-05) were studied. The sowing was done by dibbling, keeping 20 cm space between plants and 30 cm between rows. The experimental site is situated at latitude 25o 25’ 28” N, and longitude 68o 32’ 25” E and is at an elevation of about 26 m above the mean sea level. The soil type was clay loam with pH 7.5. The recommended dose of fertilizer (134N: 67 P2O5 kg/ha) was applied to the experiment. The N fertilizer was used in three splits whereas P fertilizer was applied before the cultivation. The experiment was irrigated six times during entire cropping season, such as; first irrigation was applied at crown stage, second at tillering stage, third at booting stage, fourth at flowering stage, fifth at milky stage, and sixth at dough stage. The weedicide Loughran (160 grams/acre) was used to remove weeds from the experiment. The traits studied were tillers plant^{-1}, spike length (cm), spikelets spike^{-1}, grains spike^{-1}, grain yield plant^{-1} (g) and seed index (1000-grain weight, g). The entire data was statistically analyzed using analysis of variance (ANOVA) as suggested by Gomez and Gomez **[6]** and the means were compared by least significance difference test (LSD). The heritability of different traits was calculated as proposed by Falconer **[7]**.

Results and discussion

The combined analysis of variance including nine parents and their six F_2 populations showed that parents and segregating populations differed significantly ($P \leq 0.05$) for all defined traits (Table 1). The mean squares for parental lines and F_2 hybrids were also significantly different for majority of the studied traits, designating a high amount of genetic variability among the genotypes.

Table 1. Mean squares for various quantitative traits of bread wheat genotype

Source of variation	D.F.	Tillers plant^{-1}	Spike length	Spikelets spike^{-1}	Grains spike^{-1}	Grain yield plant^{-1}	Seed index
Replications	2	0.14	0.66	2.54	9.43	0.23	8.07
Genotypes	14	0.30**	1.67**	7.98**	48.19**	6.69**	63.78*
Parents	8	0.16^{NS}	0.93*	8.87**	75.18*	2.65*	28.13^{NS}
Crosses	5	0.14**	0.49*	1.49^{NS}	14.59*	7.05^{NS}	27.44^{NS}
Error	28	0.09	0.24	0.54	14.41	1.51	23.91

* = indicates 5% probability level; NS = indicates non-significant; ** = indicates 1% probability level

Mean performance and heritability estimates

The mean performance of parents and their F_2 progenies are reported in Table 2, while heritability and genetic advance for all the traits are summarized in Table 3 and 4. The results of each character is discussed below:

Tillers plant^{-1}

Among yield components, number of tillers plant^{-1} is an important attribute which increase grain yield in wheat. To evolve high yielding varieties, not only grain yield but yield related traits like number of tillers plant^{-1} also required a special attention. The mean performance for tillers plant^{-1} is presented in Table 2. Among parental lines, Khirman produced the maximum tillers plant^{-1} (5.20), whereas Moomal produced minimum tillers plant^{-1} (4.80). Maximum number of tillers (5.63) among F_2 generation was recorded in Khirman × Imdad-05, while Maxipak × Moomal produced minimum number of tillers plant^{-1} (4.96). Heritability percentage for tillers plant^{-1} in F_2 generations was ranged from 6.38 to 55.34%, whereas genetic advance was ranged from 0.09 to 2.00 (Table 3). Among the crosses, higher heritability (h^2=55.34%) was observed in Khirman × Imdad-05 with low genetic advance (GA= 2.00), indicating that high heritability is due to low environmental variance and high genetic variance for this cross. The rest of the crosses revealed low heritability. This suggests the effectiveness of Khirman x Imdad-05 for selection among current pool of genotypes for number of tillers plant^{-1}. Kumar and Shekhar [8] reported high heritability for tillers plant^{-1}, while on contrasting Ahmed *et al*. [9] and Kalimullah *et al*. [10] informed moderate heritability for tillers plant^{-1} in bread wheat genotypes.

Spike length (cm)

Among the parents, maximum spike length (9.53 cm) was found in Khirman, while minimum spike length (7.86 cm) was recorded in Noori. The longest spike (10.16 cm) among the F_2 progenies was observed in Khirman × Imdad-05 and the shortest (9.10 cm) was recorded in Imdad-05 × Soughat (Table 2). The heritability percentage (h^2) for the character spike length varied from 5.38 to 36.58%, while genetic advance varied from 0.04 to 0.57 (Table 3). The cross Khirman × Imdad-05 expressed moderate heritability (h^2 = 36.58) with low genetic advance (GA= 0.57). The moderate heritability is due to similar environmental variance and genetic variance for spike length in this cross, while rest of the F_2 progenies displayed low heritability. Previous workers like Ayciek and Yildirn [11] and Eid [12] also reported low heritability for spike length.

Spikelets spike^{-1}

The wheat breeding studies have reported that spikelets spike^{-1} may directly contribute towards grain yield. Among the genotypes, the maximum (19.46) number of spikelets spike^{-1}was noticed as maximum in Khirman, while minimum (13.2) was reported in Kiran-95. In case of F_2 hybrids, the maximum (18.53) spikelets spike^{-1} noticed in Khirman × Imdad-05 and the minimum (17.00) number of spikelets spike^{-1} was noticed in Imdad-05 × Soughat in F_2 progeny. The heritability percentage (h^2) for spikelets spike^{-1} varied from 7.39 to 51.32% (Table 3), while genetic advance varied from 0.27 to 5.32 (Table 3). The cross Khirman × Imdad-05 showed high heritability (h^2=51.32) with low genetic advance (GA=5.30), indicating that this trait could be improved by direct selection to enhance the grain yield in wheat cultivars. Earlier scientists like Ahmed *et al*. [9] and Jan *et al.* [13] reported low heritability for spike length, while Cheema *et al*. [14] and Erkul *et al.* [15] acquired high and moderate heritability, respectively, for spikelets spike^{-1}.

Table 2. Mean performance for grain yield and its components of nine wheat varieties and their six F_2 population

Genotypes	Tillers plant^{-1}	Spike length (cm)	Spikelets spike^{-1}	Grains spike^{-1}	Grain yield plant^{-1} (g)	Seed index (1000-grain weight, g)
Khirman	5.20	9.53	19.46	60.43	10.76	49.05
Imdad-05	4.96	9.06	15.96	51.50	9.31	48.72
Noori	4.63	7.86	16.46	47.60	7.99	40.71
Soughat	4.86	8.50	16.86	50.56	9.76	49.35
Maxipak	5.10	8.00	15.66	52.63	9.96	44.76
Moomal	4.80	8.06	15.26	48.73	8.93	48.01
Marvi	5.03	8.93	15.40	48.30	10.59	50.73
Kiran-95	4.73	8.40	13.20	46.56	10.17	47.70
Anmol-91	4.46	8.23	14.60	42.23	8.51	49.37
Khirman × Imdad-05	5.63	10.16	18.53	49.23	11.46	41.39
Noori × Imdad-05	5.23	9.20	16.66	54.43	10.32	42.04
Imdad-05 × Soughat	5.30	9.10	17.00	48.76	10.83	41.40
Maxipak × Moomal	4.96	9.86	18.13	49.66	9.97	37.37
Anmol-91 × Marvi	5.36	9.73	17.53	49.23	14.26	44.68
Kiran-95 × Imdad-05	5.43	9.70	17.93	48.63	11.61	36.68
LSD (5%)	0.50	0.82	1.23	6.35	2.05	8.17

Table 3. Genetic variance (σ^2g), phenotypic variance (σ^2p), heritability percentage in broad sense (h^2 b.s) and genetic advance (GA) for tillers plant^{-1}, spike length and spikelets spike^{-1} in six F_2 generations of bread wheat

Characters	F_2 progenies	Genetic variance (σ^2g)	Phenotypic variance (σ^2p)	Heritability (h^2%) broad sense	Genetic advance (GA)
Tillers plant^{-1}	Khirman × Imdad-05	0.97	1.75	55.34	2.00
	Noori × Imdad-05	0.06	0.94	6.38	0.12
	Imdad-05 × Soughat	0.04	0.67	7.11	0.09
	Mexipak × Moomal	0.11	0.92	11.94	0.22
	Anmol-91 × Marvi	0.06	0.68	9.86	0.13
	Kiran-95 × Imdad-05	0.08	0.59	13.93	0.16
Spike length	Khirman × Imdad-05	0.27	0.75	36.58	0.57
	Noori × Imdad-05	0.02	0.41	5.38	0.04
	Imdad-05 × Soughat	0.05	0.67	7.79	0.10
	Mexipak × Moomal	0.06	0.45	14.46	0.13
	Anmol-91 × Marvi	0.07	0.56	13.00	0.15
	Kiran-95 × Imdad-05	0.06	0.65	10.24	0.13
Spikelets spike^{-1}	Khirman × Imdad-05	2.57	5.012	51.32	5.30
	Noori × Imdad-05	0.34	1.54	22.14	0.70
	Imdad-05 × Soughat	0.13	1.78	7.39	0.27
	Mexipak × Moomal	0.20	1.74	11.94	0.43
	Anmol-91 × Marvi	0.21	1.76	12.29	0.44
	Kiran-95 × Imdad-05	0.66	3.26	20.25	1.36

Grains spike^1

The mean performance for grains spike^{-1} is given in Table 2. Among the parental genotypes, maximum (60.43) grains spike^{-1} was found in Khirman, while minimum (42.23) grains spike^{-1} was recorded in Anmol-91. Among the F_2 progenies, the maximum (54.43) number of grains spike^{-1} were set in Noori × Imdad-05, whereas minimum (48.63) were set in Kiran-95 × Imdad-05. The heritability percentage (h^2) for the character grains spike^{-1} was ranged from 8.98 to 31.95%, while genetic advance was ranged from 6.39 to 28.27 (Table 4). The higher heritability percentage (h^2=31.95%) among the F_2 progenies was recorded in Khirman × Imdad-05 coupled with high genetic advance of 28.27. Similar results were also found by Sial *et al.* **[16]**. These results shows that grains spike^{-1} could be used in direct selection criteria for grain yield improvement.

Grain yield plant^{-1}(g)

High grain yield is very crucial for development of crop varieties for farmer's point of view. Yield is a kind of trait which is controlled by polygenes and is the result of interplay between many genetic and non-genetic components **[17]**. The main objective of wheat breeding is to increase wheat production by exploiting the potential of existing genetic materials available to them. Considering the parents, the maximum (10.76 g) grain yield plant^{-1} was Observed in Khirman, while minimum (8.50 g) grain yield plant^{-1} was observed in Anmol-91 (Table-2) Among the F_2 population, the maximal (14.26 g) grain yield plant^{-1} was achieved in Anmol-91 × Marvi, while the minimal (9.976 g) grain yield plant^{-1} was recorded in Kiran-95 × Imdad-05. The extent of heritability percentage (h^2) and genetic advance for grain yield plant^{-1} was ranged from 2.99 to 79.51% and 0.11 to 12.48, respectively

(Table 4). High heritability for trait grain yield plant^{-1} was displayed by cross Anmol-91 × Marvi. The high heritability is due to low environmental variance and high genetic variance for this cross, while rest of the crosses displayed low heritability. Selection will be suitable for the improvement of grain yield. Similar results were also reported by Iftikhar *et al*. [18] Ijaz *et al*. [19] and Kumar *et al*. [20] however, Ashour *et al*. [21] found the results against this research for the trait yield plant^{-1}.

Seed index (1000-grain weight, g)

In respect to seed index, among the parents, Marvi stands first with the maximum 1000-grain weight of 50.73 g and Noori stands at the bottom with minimum 1000-grain weight (40.05 g). The highest 1000-grain weight (44.68 g) in F_2 population was recorded in Anmol-91 × Marvi, while the cross Kiran-95 × Imdad-05 showed the lowest 1000-grain weight (36.68 g) (Table 2). The heritability percentage (h^2) for 1000-grain weight varied from 15.77 to 51.37%, while genetic advance varied from 0.95 to 5.28, and the progeny Khirman × Imdad-05 showed high heritability (h^2=51.37%) with low genetic advance (GA=4.62) among the crosses (Table 4). This suggests that effective and proper selection is possible for the improvement of this trait.

Table 4. Genetic variance (σ^2g), phenotypic variance (σ^2p), heritability percentage in broad sense (h^2 b.s) and genetic advance (GA) for grains spike^{-1}, grain yield plant^{-1} and seed index in six F_2 generations of bread wheat.

Characters	F_2 progenies	Genetic variance (σ^2g)	Phenotypic variance (σ^2p)	Heritability (h^2%) broad sense	Genetic advance (GA)
Grains spike^{-1}	Khirman × Imdad-05	13.72	42.94	31.95	28.27
	Noori × Imdad-05	4.51	42.30	10.66	9.29
	Imdad-05 × Soughat	3.10	32.64	9.51	6.39
	Mexipak × Moomal	3.77	41.99	8.98	7.77
	Anmol-91 × Marvi	7.57	64.77	11.69	15.60
	Kiran-95 × Imdad-05	3.83	25.26	15.17	7.897
Grain yield plant^{-1}	Khirman × Imdad-05	2.25	4.88	46.91	4.63
	Noori × Imdad-05	0.05	1.88	2.99	0.11
	Imdad-05 × Soughat	0.21	2.74	7.73	0.43
	Mexipak × Moomal	0.46	3.08	14.93	0.95
	Anmol-91 × Marvi	6.06	7.62	79.51	12.48
	Kiran-95 × Imdad-05	0.15	2.24	6.94	0.32
Seed index	Khirman × Imdad-05	2.24	4.36	51.37	4.62
	Noori × Imdad-05	0.59	3.46	17.06	1.21
	Imdad-05 × Soughat	1.67	4.74	35.24	3.44
	Mexipak × Moomal	1.09	4.37	25.01	2.25
	Anmol-91 × Marvi	0.46	2.93	15.77	0.95
	Kiran-95 × Imdad-05	2.56	5.84	43.88	5.28

Conclusions

It was concluded that F2 progeny Khirman x Imdad-05 expressed high heritability for almost all studied traits. Thus, this combination may be utilized in coming breeding programs to improve the various quantitative traits, especially in advance generations.

Authors' contributions

Conceived and designed the experiments: N Gandahi, AW Baloch & TF Abro. Performed the experiments: N Gandahi. Analyzed the data: MS Bhatti, AW Baloch & A Marri. Contributed reagents/ materials/ analysis tools: AA Soomro. Wrote the paper: M Baloch, AW Baloch, N Gandahi & M Ali.

References

1. Baloch M, Baloch AW, Baloch MJ, Kandhro RA, Kandhro MN, Mandan DK, Baloch GM, Gandahi N, Baloch AM & Baloch NA (2016). Analysis of genetic divergence in exotic bread wheat genotypes. *Pure App Bio* 5(1): 26-30.
2. Khan OU, Ijaz F & Shahzad MT (2015). Heritability analysis for yield associated traits in wheat (*Triticum aestivum* L) *Sci Tech Develop* 34(4): 260-264.
3. Waqas M, Faheem M, Khan AS, Shehzad M & Ansari MAA (2014). Estimation of heritability and genetic advance for some yield traits in eight F2 populations of wheat (*Triticum aestivum* L). *Sci Letter* 2(2): 43-47.
4. Khan AS, Salim I & Ali Z (2003). Heritability of various morphological traits in wheat. *Int J Agri Bio* 5(2): 138-140.
5. Ijaz S & Khan IA (2009). Molecular characterization of wheat germplasm using microsatellite markers. *Genet Mol Res* 8(3): 809-815.
6. Gomez KA & Gomez AA (1984). Statistical procedures for agricultural research. John Wiley & Sons Inc. 2nd (ed.) New York U.S.A.
7. Falconer, DS (1989). Introduction to quantitative genetics 3rd (ed.) Longman Scientifical Techniqual.UK.
8. Kumar A & Shekhar R (2015). Genetic variability in relation to qualitative and quantitative traits in wheat (*Triticum aestivum* L) *Agrica* 3(1-2): 23-28.
9. Ahmed N, Chowdhry MA, Khaliq I & Maekawa M (2013). The inheritance of yield and yield components of five wheat hybrid populations under drought conditions. *Indonesian J Agri Sci* 8(2): 176-180.
10. Kalimullah SJ, Khan MI & Rahman HU (2012). Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. *J Anim Plant Sci* 22: 330-333.
11. Aycicek M & Yildirim T (2006). Heritability of yield and some yield components in bread wheat (*Triticum aestivum* L.) genotypes. *Bangladash J Bot* 35(1): 17-22.
12. Eid MH (2009). Estimation of heritability and genetic advance of yield traits in wheat (*Triticum aestivum* L.) under drought conditions. *Int J Gent Mol Bio* 1(7): 115-120.
13. Jan S, Mohammad F & Khan UF (2015). Genetic potential and heritability estimates of yield traits in F_3 segregating populations of bread wheat. *Int J Envir* 4(2): 106-115.
14. Cheema NM, Mian MA, Ihsan M, Rabbani G & Mahmood A (2006). Studies on variability and some genetic parameters in spring wheat. *Pak J Agri Sci* 43(1-2):32-35.
15. Erkul A, Aydin UN & Konak C (2010). Inheritance of yield and yield components in a bread wheat (*Triticum aestivum* L.) cross. *Turkish J Field Crops* 15(2): 137-140.
16. Sial MA, Dahot MU, Mangrio SM, Mangan BN, Arain MA, Naqvi MH & Memon S (2007). Genotype x environment interaction for grain yield of wheat genotypes tested under water stress conditions. *Sci Inter* 19(2): 133-137.
17. Sowmya HC, Shadakshari YG, Pranesh KJ, Srivastava A & Nandini B (2010). Character association and path analysis

in sunflower (*Helianthus annuus* L.). *Elect J Plant Breed* 1: 828-831.

18. Iftikhar R, Hussain SB & Khaliq I (2013). Study of inheritance for grain yield and related traits in bread wheat (*Triticum aestivum* L.). *SABRAO J Breed Genet* 45(2): 283-290.
19. Ijaz F, Khaliq I, Shahzad MT & Saleem B (2013). Computation of heritability of yield and some morphological traits in F_2 populations of spring wheat (*Triticum aestivum* L). *Int J Mod Agri* 2: 102-107.
20. Kumar B, Yadav HK, Singh BN & Vishwakarma SR (2014). Variability analysis for yield and yield attributes of bread wheat (*Triticum aestivum* L.) under sodic soil condition. *Trends Biosci* 7(14): 1748-1751.
21. Ashour BM, Arzani A, Rezaei A & Maibody SM (2006). Study of inheritance of yield and related traits in five crosses of bread wheat (*Triticum aestivum* L). *J Isfahan Uni Techno* 9(4): 123-136.