Research Article

Estimates of heritability, genetic advance and correlation in F₃ populations of Wheat

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Abstract

Development of new high yielding wheat varieties is the main objectives of the wheat improvement programs. Knowledge about the genetic variability, heritability, genetic advance and correlation analysis for various parameters is indispensable to propose effective wheat breeding. This Research was carried out at Malakander research farm The University of Agriculture Peshawar, Pakistan during cropping season 2014-15. Nineteen wheat genotypes including 7 parents and their 12 F₃ segregating populations of wheat were evaluated in a RCB design replicated thrice. Analyzed data revealed significant genotypic variability among the genotypes for the studied parameters. The main purpose of the study was to estimate heritability, genetic advance and correlation. High heritability value was observed for grains per spike (0.95), grain yield plant⁻¹ (0.99), fertile tillers per plant (0.98), plant height (0.89), and leaf area (0.88). High genetic advance was observed for grain yield (14.16), flag leaf area (3.12) and grains per spike (2.49). Grains per spike and leaf area revealed significant and positive correlation with grain yield. Among the parents AUP (5008), JBZ and TATARA while, in segregating F₃ wheat populations JBZ × WTN, JBZ × F. Sarhad, AUP (5008) × WTN were found better performing for yield and its contributing traits. Therefore these parental lines and F₃ segregating populations could be used in future wheat improvement programs for economically important traits.

Keywords: Heritability; Genetic advance; Genotypes; Fertile tillers; Flag leaf area

Introduction

Wheat (*Triticum aestivum* L.) is considered one of the most important and main cereal

crop in world. It contains 20 percent calories and supply 36 percent food to accomplish basic food need of growing population.

Wheat was grown on area of about 9.03 million hectares and estimated yield of 25.286 m tonnes, while in Khyber Pakhtunkhwa wheat was cultivated on area of 0.68 m ha⁻¹ with yield of 1.25 m tonnes [1]. Pakistan is far below in the international ranking of wheat crop production it can be improved through the appropriate steps. There is dire need for valuable research to made better and high yielding genotypes and available to farmers. Heritability is an index for transmission of a character from one generation to next generation. The selection ability of wheat population mainly depends on the extent of heritable difference [2]. Inherited variation revealed primary role for wheat breeders to evaluate wheat in term of variability [3]. The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection [4]. High heritability along with high genetic advance is an indexing point for suitable selection [5]. Heritability, selection response and correlation analysis are imperative apparatus for the uplift of cultivated crops.

Materials and methods

This research was carried out at research farm of Plant Breeding and Genetics Department, The University of Agriculture Peshawar at 34°01'N and 71°35'E during winter 2014-15. Nineteen genotypes, including 7 parents i.e. JBZ, AUP(5008), Salim(2000), TATARA, WTN, F. Sarhad, Barsat, WTN and their 12 F₃ populations JBZ × Barsat, JBZ × F.Sarhad, JBZ × WTN, Salim(2000) × Barsat, Salim(2000) × F.Sarhad, Salim(2000) × WTN, TATARA × Barsat, TATARA × F.Sarhad, TATARA × WTN, AUP(5008) × Barsat, AUP(5008) × F.Sarhad, AUP(5008) × WTN were

evaluated in a randomized complete block design (RCBD) with 3 replications. Each genotype was grown in 4 rows of 4 m length with row to row distance was kept 30 cm. Normal recommended cultural practices were followed throughout the growing session.

Statistical analysis

The collected data was statistically analysed by using Statistic 8.1 package and Least Significant Difference (LSD) test was determined for the comparison of means of wheat genotypes (Parent and their F₃ segregating populations).

Heritability

Broad sense heritability was calculated (%) by the following formula explain by [6].

$$h^2 = \frac{VF_3 - \sqrt{VP_1 \times VP_2}}{VF_3} \times 100$$

Where,

h^2 = heritability broad based,

VF_3 = Var. F₃ wheat segregating population,

VP_1 = Var. parent 1,

VP_2 = Var. parent 2.

Genetic advance (GA)

Genetic advance (GA) was find out by mentioned formula described by [7].

$$\text{Genetic Advance} = i\sigma_p h^2$$

where,

i is the selection intensity and its value is 1.75 at 10

σ_p is the phenotypic std. deviation

$h^2_{(B.S)}$ = heritability broad based.

Results and discussion

Days to 50 % heading

Days to heading of parents and F₃ population are showed in (Figure 1). Parents JBZ, Sal-2000 and F₃ wheat population Sal-2000 × F.Sarhad initiate heading earlier as compared to other genotypes. While parent F. Sarhad and F₃ population TATARA × WTN were found late in heading. Low heritability for heading was observed (0.26) along with low genetic advance (1.35 days) (Table 1). Significant and positive correlation effect of heading with plant

height were observed ($r = 0.52$) (Table 2). [8] Reported also significant and positive

correlation of heading with plant height and grains spike⁻¹ in bread wheat.

Figure 1. Days to 50% heading of parents and F₃ populations of wheat genotypes

Table 1. Genotypic variance (V_g), environmental variance (V_e), phenotypic variance (V_p), heritability (h²) and genetic advance (GA) for days to 50% heading

Trait	V _g	V _e	V _p	h ²	GA
Days to 50 percent heading	0.48	1.35	1.83	0.26	1.35

Table 2. Correlation of various parameters of 19 wheat genotypes

	Days to heading	Plant height	Flag leaf	Fertile tiller	Grain spike ⁻¹	Grain yield
Days to heading		0.52*	-0.13	-0.16	0.39	0.09
Plant height	----	----	0.20	0.24	0.72**	0.50
Flag leaf	----	----	----	-0.70	0.36	0.62**
Fertile tiller	----	----	----	----	0.34	0.10
Grain spike ⁻¹	----	----	----	----	----	0.47*

Plant height

The F₃ population AUP5008×F.Sarhad showed maximum plant height while Sal-2000 had low plant height (Figure 2). Moderate to high heritability were observed for plant height, it's varied from 0.58 to 0.89 (Table 3). The genotype Sal-2000×Barsat had high heritability (0.89) while the F₃ population AUP (5008)×WTN had moderate heritability (0.58). Genetic advance ranged from 0.21 to 1.15 (Table 3). Significant and

positive correlation of plant height with grains spike⁻¹ ($r = 0.72$) were observed, whereas non-significant correlation with grain yield ($r = 0.5$) and tillers ($r = 0.24$) (Table 2). Similar results were reported [9, 10], Rashid *et al.* [10] who also reported highly significant genetic variation among genotypes evaluated under normal irrigation. Similarly, it has also been reported that plant height revealed significantly positive correlation with 1000 grains weight [11].

Figure 2. Plant height of parents and F₃ populations of wheat genotypes

Table 3. Heritability and genetic advance for plant height and flag leaf area of different populations of wheat genotypes

Genotypes	Plant height			Flag leaf area		
	Var.	h ²	GA	Var.	h ²	GA
Parents						
JBZ	0.21			1.17		
AUP(5008)	0.03			0.95		
Salim(2000)	0.01			36.99		
TATARA	0.13			0.48		
WTN	0.02			0.14		
F.Sarhad	0.07			1.88		
Barsat	0.13			0.49		
F₃ Populations						
JBZ x Barsat	0.97	0.83	1.15	6.39	0.88	3.12
JBZ x F.Sarhad	0.89	0.86	1.15	1.59	0.07	0.13
JBZ x WTN	0.29	0.76	0.57	0.57	0.29	0.31
Salim(2000) x Barsat	0.32	0.89	0.71	6.55	0.35	1.25
Salim(2000) x F.Sarhad	0.14	0.81	0.43	9.09	0.08	0.35
Salim(2000) x WTN	0.09	0.83	0.35	6.50	0.65	2.31
TATARA x Barsat	0.50	0.74	0.74	1.03	0.53	0.75
TATARA x F.Sarhad	0.45	0.73	0.60	1.96	0.51	1.01
TATARA x WTN	0.39	0.86	0.75	1.09	0.76	1.11
AUP-5008 x Barsaat	0.40	0.84	0.75	2.20	0.69	1.43
AUP-5008 x F.Sarhad	0.33	0.86	0.70	6.70	0.80	2.90
AUP-5008 x WTN	0.06	0.58	0.21	0.49	0.25	0.25

Flag leaf area

Genotypes had highly difference for flag leaf area the maximum flag leaf area was recorded by genotypes TATARA, while minimum was observed in salim (2000) × WTN (Figure 3). The results of our

experiment are supported by khan *et al.* [12] who reported the differences for flag leaf area among wheat genotypes. Low (0.07) to high (0.88) range of h² was observed for leaf area (Table 4). High broad sense heritability of 0.88 was showed by segregating

population JBZ $\times$ Barsat, while low heritability of 0.07 was showed by JBZ $\times$ F.Sarhad. Similarly, selection response for flag leaf area ranged from 0.13 to 3.12 cm² (Table 3). Significant and positive correlation of leaf area with grain yield ($r = 0.62$) were observed however and non-

significant with grains spike⁻¹ ($r = 0.36$) (Table 2). Results were reported by [10], who also observed significant genetic variation between spring wheat genotypes. [13]. Singh *et al.* [14] also elaborated the importance of correlation of flag leaf area with grains per spike⁻¹ and kernel weight.

Figure 3. Flag leaf area of parents and F₃ populations of wheat genotypes

Table 4. Heritability and genetic advance for fertile tillers plant⁻¹, grain spike⁻¹ and grain yield of different populations of wheat genotypes

Genotypes	Fertile tillers plant ⁻¹			Grains spike ⁻¹			Grain yield		
	Var.	h ²	GA	Var.	h ²	GA	Var.	h ²	GA
Parents									
JBZ	1.33			0.04			3.56		
AUP(5008)	1.89			0.33			7.23		
Salim(2000)	0.05			1.16			2.80		
TATARA	0.03			3.04			0.81		
WTN	0.41			0.89			1.38		
F.Sarhad	0.04			0.01			2.05		
Barsat	0.16			5.33			6.90		
F₃ Populations									
JBZ $\times$ Barsat	1.24	0.62	0.97	0.56	0.18	0.19	5.35	0.07	0.24
JBZ $\times$ F.Sarhad	1.44	0.83	1.40	0.49	0.95	0.94	3.53	0.23	0.61
JBZ $\times$ WTN	1.26	0.41	0.65	0.52	0.64	0.65	12.05	0.82	3.97
Salim(2000) $\times$ Barsat	0.65	0.86	0.97	3.61	0.31	0.82	24.46	0.82	5.68
Salim(2000) $\times$ F.Sarhad	0.20	0.76	0.48	0.21	0.41	0.26	47.49	0.95	9.16
Salim(2000) $\times$ WTN	0.51	0.71	0.72	5.00	0.80	2.49	47.07	0.96	9.20
TATARA $\times$ Barsat	1.32	0.98	1.58	4.44	0.09	0.28	54.84	0.96	9.92
TATARA $\times$ F.Sarhad	0.08	0.86	0.35	1.40	0.86	1.42	89.02	0.99	13.02
TATARA $\times$ WTN	0.21	0.83	0.54	2.64	0.38	0.86	100.06	0.99	13.86
AUP(5008) $\times$ Barsat	1.77	0.69	1.28	1.74	0.24	0.43	46.80	0.85	8.13
AUP(5008) $\times$ F.Sarhad	0.44	0.35	0.33	1.27	0.95	1.49	109.90	0.96	14.16
AUP(5008) $\times$ WTN	1.02	0.13	0.19	1.20	0.55	0.84	97.49	0.97	13.38

Fertile tillers plant⁻¹

Statistical analysis of the data revealed that significant differences were found among wheat genotypes for fertile tillers plant⁻¹. More number of fertile tillers (21.8) was of wheat genotype TATARA, whereas minimum fertile tillers were observed in genotype F.Sarhad (Figure 4). Low to high range of heritability was observed (0.13 to 0.98) (Table 4). Genetic advance was 0.19 to 1.58 (Table 4). Non-significant and positive

correlation of fertile tillers plant⁻¹ with grains spike⁻¹ ($r = 0.34$) and grain yield ($r = 0.10$) (Table 2). [9, 10] also reported moderate heritability for fertile tillers plant⁻¹ while studying 14 diverse bread wheat genotypes under irrigated environment. [14] Also reported that yield contributing components like productive tillers revealed significantly contributed towards grain yield.

Figure 4. Fertile tillers of parents and F₃ populations of wheat genotypes

Grains spike⁻¹

Statistical analysis of recorded data showed that best performing genotype in parents was AUP (5008) and in F₃ population was AUP (5008) × WTN while lowest grains spike⁻¹ were recorded in Salim (2000) and Salim (2000) × WTN (Figure 5). The present results are supported by Khan *et al.* [15] who recorded the differences in wheat genotypes for grains spike⁻¹. Among diverse F₃ wheat populations mean ranged from 56.4 to 69.3 however, parental wheat genotypes had range from 51.6 to 67.3. Very low to high levels of heritability for grains spike⁻¹ were observed (Table 4). High heritability was observed for F₃ wheat

population JBZ × F.Sarhad and AUP (5008) × F.Sarhad. Whereas, low heritability was observed for population TATARA × Barsat. Response to selection was 0.19 to 1.49 (Table 4). [16, 12] also reported medium to low selection response in 14 bread wheat genotypes under irrigated environment. However, genetic variations among wheat genotypes were enough. In-addition Significant and positive correlation were observed for grain spike⁻¹ with grain yield per plant ($r = 0.47$) (Table 2). [8] Also observed significantly positive correlation of grain yield plant⁻¹ with grains spike⁻¹, maturity and grain weight while studying 15 bread wheat advance lines.

Figure 5. Grains spike⁻¹ of parents and F₃ populations of wheat genotypes

Grain yield plant⁻¹

Data indicated significant differences among the genotypes for grain yield. Maximum grain yield were observed in F₃ genotypes JBZ × WTN (46.1 g) and in parental genotype AUP-5008 (46.1 g), whereas minimum grain yield was observed in F₃ segregating wheat population Salim (2000) × Barsat (23.9 g) (Figure 6). High heritability was observed in most of F₃ wheat population except JBZ × Barsat and JBZ × F.Sarhad (Table 4). The genotypes

TATARA × F.Sarhad was found best with highest heritability of 0.99 whereas, the F₃ population JBZ × Barsat was found low heritability of 0.07). Genetic advance for grain yield ranged from 0.24 to 14.16 (Table 4). Likewise, grain yield revealed positive and significant correlation with grains per spike ($r = 0.47$) (Table 2). The current results are accordance with the results of [17]. The current results are supported by [18], [19] who reported positive correlation of yield and harvest index in bread wheat.

Figure 6. Grains yield plant⁻¹ of parents and F₃ populations of wheat genotypes

Conclusion

Analyzed data revealed highly significant different differences among the parental lines and their F₃ segregating populations. High heritability along with better genetic advance for grain yield, biological yield, spike length, flag leaf area and harvest index suggests effectiveness of selection process for such traits. F₃ wheat populations like JBZ × WTN, JBZ × F. Sarhad, AUP(5008) × WTN were found superior for yield, however, AUP (5008), JBZ and TATARA were best among parents, therefore these parental genotypes and their segregating populations could be use in future wheat breeding programs to extract potential lines. Grains per plant and flag leaf area had significant positive correlation with grain yield, spike length; biological yield and harvest index indicated optimum opportunity for selection for these important traits.

Authors' contributions

Conceived and designed the experiments: W Ahmad & G Hassan, Performed the experiments: M Ali & M Ishaq, Analyzed the data: M Adnan, R Tajudin & K Afridi, Contributed reagents/ materials/ analysis tools: AU Rehman & N Khan, Wrote the paper: B Hussain & L Ullah & IA Shah.

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