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Full Length Research Paper

Genetic analysis of some quantitative traits in bread wheat across environments

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Performance of eight bread wheat (*Triticum aestivum* L.) genotypes; namely, Wafaq-2001, Takbeer, Tatara, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqalab-91, were evaluated under three diverse environments (early, normal and late sown conditions) through an 8x8 diallel cross. Observations were recorded on days to heading, productive tillers plant^{-1}, number of grains spike^{-1}, 1000-grain weight and grain yield plant^{-1}. Highly significant differences were observed among the genotypes for all traits. Analysis of genetic components revealed significant additive (D) and dominant (H) genetic variations for days to heading, productive tillers plant^{-1}, number of grains spike^{-1}, 1000-grain weight and grain yield plant^{-1} under early planting. Under normal planting both additive (D) and dominant (H) genetic components were significant for days to heading, productive tillers plant^{-1}, grain yield plant^{-1} and 1000-grain weight. Similarly, under late planting significant additive (D) and dominant (H) genetic variations were observed for number of grains spike^{-1} and grain yield plant^{-1}, while for 1000-grain weight only additive (D) genetic component was found significant. Genetic analyses of the traits confirm the involvement of both additive and non-additive gene effects in governing the inheritance.

Key words: Genetic analysis, bread wheat, quantitative traits, environmental variations.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most widely cultivated crop among the cereals and is the principal food crop in most areas of the world. It is the leading grain crop of the temperate climates of the world, and is grown on 215.27 million hectares in the world (FAO, 1999). Global demand for wheat is growing at approximately 2% per year, twice the current rate of gain in genetic yield potential (Skovmand and Reynolds, 2000). Wheat is the major staple food of about 130 the area under this important crop is reported to be 8.057 million hectares (Anonymous, 2001-2002). Wheat production can be enhanced through the development of new cultivars having wider genetic base and better performance under various agro-climatic conditions. Genetic improvements in wheat have been taking place, both by slow processes of nature and by the selective processes of man, since the earliest time of wheat cultivation. It is known that phenotypic expression of quantitative traits is highly influenced by environmental fluctuations (Allard and Bradshaw, 1964). Therefore, it is necessary to study the genetic architecture of wheat genotypes in relation to the environment for which they have to be developed. Diallel mating design has been a useful tool for genetic analyze mating system in which a set of varieties are intercrossed in all possible combinations.

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Researchers (Griffing, 1956; Hayman, 1954 and Mather and Jinks,1982) developed techniques to analyze genotypes for all possible crosses. Genetic analysis of some economic characters showed different pattern of inheritance. Khan et al. (1992) reported that partial dominance with additive gene effects was important for plant height. Singh et al. (1988) revealed that, number of tillers per plant was conditioned by partial dominance type of gene action. Iqbal et al. (1991) studied the gene action for peduncle length and found that, it was of partial dominance with additive type.

Economic yield in wheat is a polygenic trait and is also influenced by a number of environmental factors including temperature at emergence, vegetative stage, grain filling period and grain formation. Sowing time is the most important in this respect. Timely sowing allows proper emergence, adequate vegetative growth and sufficient grain filling period which permits sufficient photosynthates to be stored in grains leading to healthy grain formation. Delayed sowing alter the germination and provide short period for grain filling causing poor grain formation and resulting in yield loss. Cultivation of wheat at proper sowing time, is thus of extreme importance to obtain high yields. The objectives of the present study were to:

(1) To study the effect of environment x genotype interaction of eight bread wheat genotypes and their hybrids by using three different sowing environments.

(2) To estimates components of genetic variance for yield and its components over three different planting dates.

MATERIALS AND METHODS

Eight cultivars of bread wheat, namely: Wafaq-2001, Takbeer, Tatara, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqalab-91 were crossed in an 8x8 diallel fashion during 2002 to 2003. Eight parental cultivars and their resulting 56 F1s were grown in a randomized complete block design with three replications under early, (E1 - October 17, 2003), normal (E2 -November 10, 2003) and late (E3 - December 4, 2003) sowing conditions at the experimental farm of NWFP Agricultural University, Peshawar during 2003 to 2004. Plant to plant and row to row spacing were kept 15 and 30 cm, respectively. One healthy seed was planted per site. Each treatment comprised a single row 3 m in length having 20 healthy plants. Data on the following parameters were recorded on five randomly selected plants at an adequate time from each date of sowing.

Days to heading

Data on days to heading were recorded from the date of sowing to the date of 50% heading. The stage when spikes emerged after the unfolding of the flag leaf was regarded as heading stage.

Genetic components of variations under normal planting revealed.

Productive tillers plant^{-1}

Five plants were randomly selected from each treatment to determine productive tillers plant^{-1}.

Grains spike^{-1}

Five spikes from five randomly selected plants were hand threshed to record the number of grains spike^{-1}. Average value for each treatment was then calculated.

Grain yield plant^{-1} (g)

Total produce of five plants from each treatment was weighed by using an electronic balance and average grain yield plant^{-1} was calculated in grams.

1000-grain weight (g)

Weight of 1000-grains were recorded using an electronic balance. For this purpose, five samples of 1000-grains from the final produce of the treatment were used and finally average 1000-grain weight was recorded. The mean of each treatment was used for statistical analysis. Data were analyzed statistically, using analysis of variance technique (Steel and Torrie, 1984) and significant differences among the genotypes were further analyzed using diallel analysis techniques (Hayman, 1954a, b; Mather and Jinks, 1982).

RESULTS AND DISCUSSION

Pooled analysis of variance showed significant differences among the genotypes (Table 1) for all the characters studied indicating that, material used had significant genetic diversity. Significant differences among environments also indicated the differential influence of environment on character expression. In view of the significant genotype x environment interaction for all the traits, analysis of variance in individual environments was conducted which yielded significant differences among genotypes for all traits in each environment (Table 2).

Two scaling tests were applied following Mather and Jinks (1982) for testing the validity of additive-dominance model. The first test was the joint regression coefficient test, followed by analysis of variance of Wr+Vr and Wr-Vr for the confirmation of absence of non-allelic interaction. Additive-dominance model was found adequate for days to heading and 1000-grain weight under early, normal and late plantings, for productive tillers plant^{-1} and grain yield plant^{-1} under normal planting and for number of grains spike^{-1} under late planting (Tables 3a, b and c). Therefore, further genetic analyses

Were carried out for days to heading and 1000-grain weight under early, normal and late plantings, for productive tillers plant^{-1} and grain yield plant^{-1} under

Table 1. Pooled analysis of variance for the characters studied under early, normal and late plantings (Mean squares).

Characters	Env. (df=2)	Reps. (Env) (df=6)	Genotypes (df=63)	Geno x Env (df=126)	Pooled error (df=378)
Days to heading	44345.42**	5.59	24.63**	5.70**	1.17
Productive tillers plant^{-1}	4053.13**	5.71	33.56**	22.52**	1.93
Grains spike^{-1}	4916.78**	21.74	379.69**	155.12**	14.47
Grain yield plant^{-1}	30442.70**	13.71	331.28**	224.32**	12.66
1000-grain weight	1662.59**	146.05	128.29**	40.26**	14.50

** P≤0.01

planting and for number of grains spike^{-1} under late planting (Table 4).

Days to heading

Presence of both additive and dominance gene action was indicated by the significant values of D and H components under early, normal and late plantings (Table 4) suggesting that, days to heading was under the control of both additive and dominance gene effects; however, the magnitude of additive gene effects was greater in early planting. In case of early planting, average degree of dominance indicated partial dominance, while it indicated over-dominance gene action in case of both normal and late planting. Unequal values of H1 and H2, indicated presence of positive and negative alleles in unequal frequencies. This was also supported by the ratio of H2/4H1, that was less than 0.25 under early, normal and late plantings. It was suggested that, when the genes are equally distributed among the parent cultivars, this value is equal to 0.25 (Singh and Choudhry, 1985). Under early and late planting, F was positive and significant indicating greater proportion of dominant genes. This was also supported by the ratio of dominant to recessive alleles (1.78 and 2.52) which was more than one, showing the importance of greater proportion of dominant genes. However, under normal planting F was positive but non-significant.

Similarly, ratio of dominant to recessive alleles was more than one (1.23) confirming the greater frequency of dominant genes for the trait. Value of h2 was non-significant under early and late planting, while it was significant under normal planting, displaying the presence of dominance due to heterogeneity at loci. Environmental effect (E) was non-significant under all three environments. Additive gene action for this trait has also been reported by Singh (2003), Taleei and Beigi (1996), Karam et al. (1996) and Dhayal and Sastry (2003), while Rajara and Maheshwari (1996) reported the importance of both additive and non-additive gene actions for days to heading.

High narrow sense heritability estimates (71.09 and 50.89%) under early and normal plantings indicated greater proportion of additive genetic variation in the total heritable genetic variation, while under late planting high broad sense heritability estimates indicated greater proportion of dominant genes in the total heritable genetic variation (Table 4). Productive tillers plant^{-1}. Genetic components of variations under normal planting revealed that, both additive (D) and dominance (H) variations were significant (Table 4). Unequal values of H1 and H2 suggested that, positive and negative alleles were unequal among parental cultivars. This was also supported by the ratio of H2/4H1 (0.16) which was less than 0.25. Significant and positive value of F (11.61), revealed the greater frequency of dominant genes for productive tillers plant^{-1}. This was also supported by the ratio of dominant to recessive genes (3.830). Average degree of dominance (1.42) suggested an over-dominant type of gene action. Value of h2 was non-significant. No environmental influence was indicated (non-significant E). These results are in accordance with those of Sangwan and Choudhry (1999), Rajara and Maheshwari (1996), Dhayal and Sastry (2003), Senapati et al. (2000) who also reported non-additive type of gene action for tillers plant^{-1} while Soylu and Sade (2003) estimated additive type of gene effects for tillers plant^{-1}. Broad sense heritability estimates were much greater than narrow sense, indicating the presence of very small additive but high dominant variation in total heritable genetic variation.

Number of grains spike-1 Significant (D) and (H) components under late planting, indicated presence of both additive and dominance gene actions (Table 4). Unequal values of H1 and H2 suggested that, positive and negative alleles were unequal among parental cultivars. This was also supported by the ratio of H2/4H1 (0.18) which was less

Table 2. Analysis of variance for the characters studied under early, normal and late plantings (Mean squares).

Characters	Early			Normal			Late		
	Reps. (df=2)	Genotypes (df=63)	Error (df=126)	Reps. (df=2)	Genotypes (df=63)	Error (df=126)	Reps. (df=2)	Genotypes (df=63)	Error (df=126)
Days to heading	1.94	20.03**	1.10	7.90**	12.03**	1.18	6.94*	3.97**	1.24
Productive tillers plant^{-1}	10.41*	56.06**	3.11	3.77	12.43**	1.98	2.95**	10.11**	0.70
Grains spike^{-1}	31.83	305.76**	23.68	21.29	271.16**	18.83	12.11	113.02**	11.97
Grain yield plant^{-1}	5.32	592.72**	20.72	4.81	109.89**	12.52	31.01**	77.32**	4.76
1000-grain weight	46.84*	61.41**	11.53	19.45	68.30**	12.18	371.85**	79.11**	19.79

** P≤0.01

Table 3a. Test of adequacy of additive-dominance model for 8x8 diallel cross of wheat sown under early planting.

Characters	Regression analysis		Analysis of array variance		Remarks
	b=0	b=1	wr+vr	wr-vr	
Days to heading	**	NS	**	**	Regression analysis indicated adequacy of the model but analysis of arrays invalidates the model, it was considered partially adequate.
Productive tillers plant^{-1}	NS	NS	**	**	Both tests suggested inadequacy of the model.
Number of grains spike^{-1}	NS	*	**	**	Both tests suggested inadequacy of the model.
1000-grain weight	**	NS	*	NS	Both tests suggested adequacy of the model.
Grain yield plant^{-1}	NS	*	**	**	Both tests suggested inadequacy of the model.

Table 3b. Test of adequacy of additive-dominance model for 8x8 diallel cross of wheat sown under normal planting.

Characters	Regression analysis		Analysis of array variance		Remarks
	b=0	b=1	wr+vr	wr-vr	
Days to heading	NS	**	NS	*	Regression analysis invalidates the model but analysis of arrays suggests the model to be adequate, it was considered partially adequate.
Productive tillers plant^{-1}	*	NS	**	NS	Both tests suggested adequacy of the model.
Number of grains spike^{-1}	NS	NS	**	**	Both tests suggested inadequacy of the model.
1000-grain weight	**	NS	**	NS	Both tests suggested adequacy of the model.
Grain yield plant^{-1}	*	NS	**	**	Regression analysis indicated adequacy of the model but analysis of arrays invalidates the model, it was considered partially adequate.

Table 3c. Test of adequacy of additive-dominance model for 8x8 diallel cross of wheat sown under late planting.

Characters	Regression analysis		Analysis of array variance		Remarks
	b=0	b=1	wr+vr	wr-vr	
Days to heading	NS	NS	*	NS	Regression analysis invalidates the model but analysis of arrays suggests the model to be adequate, it was considered partially adequate.
Productive tillers plant^{-1}	NS	NS	**	**	Both tests suggested inadequacy of the model.
Number of grains spike^{-1}	**	NS	**	NS	Both tests suggested adequacy of the model.
1000-grain weight	**	NS	NS	NS	Both tests suggested adequacy of the model.
Grain yield plant^{-1}	NS	**	*	**	Both tests suggested inadequacy of the model.

* = Significant ** = Highly significant NS = Non-significant.

Table 4. Estimates of genetic components of variation for various traits.

Components	Days to heading			Productive tillers plant^{-1}	Grains spike^{-1}	Grain yield	1000-grain weight		
	Early	Normal	Late	Normal	Late	Normal	Early	Normal	Late
D	10.64±0.92*	1.68±0.77*	1.54±0.32*	6.95±1.04*	64.17±3.15*	20.95±5.66*	32.45±3.89*	16.27±1.94*	34.83±3.41*
H1	8.79±2.13*	7.17±1.79*	1.79±0.75*	14.13±2.39*	51.34±7.28*	97.70±13.07*	27.38±8.99*	36.33±4.48*	13.28±7.88ns
H2	5.46±1.85*	4.77±1.56*	2.79±0.73*	8.84±2.08*	36.68±6.33*	60.39±11.37*	26.03±7.82*	33.89±3.90*	9.80±6.86ns
F	5.43±2.19*	0.72±1.84ns	1.91±0.64*	11.61±2.46*	45.05±7.48*	53.93±13.44*	16.43±9.24ns	1.60±4.60ns	6.26±8.10ns
h^2	1.70±1.24ns	3.61±1.04*	-0.01±0.43ns	0.65±1.39ns	5.36±4.24ns	5.94±7.61ns	38.53±5.23*	2.38±2.61ns	33.38±4.59*
E	0.37±0.31ns	0.43±0.26ns	0.44±0.12*	0.67±0.35ns	3.99±1.05*	4.13±1.89*	4.03±1.30*	4.10±0.65*	8.43±1.14*
(H1/D)½	0.91	2.06	1.35	1.42	0.89	2.16	0.92	1.49	0.62
H2/4H1	0.15	0.17	0.17	0.16	0.18	0.15	0.24	0.23	0.18
(4DH1)½+F / (4DH1)½-F	1.78	1.23	2.52	3.83	2.29	3.95	1.76	1.07	1.34
Heritability (ns)%	71.09	50.89	25.54	9.74	56.21	10.13	45.19	40.49	59.56
Heritability (bs)%	93.82	87.06	64.07	79.05	86.72	80.69	79.06	80.60	68.67

* Value is significant when it exceeds 1.96 when it is divided by its std. error, ns non-significant. D measures additive effect, H1 and H2 measures dominance effect, F determines frequencies of dominant to recessive alleles in parents, h^2 determines the overall dominance effect due to heterozygous loci, E shows environment effect, (H1/D)½ measures average degree of dominance, H2/4H1 determines proportion of genes with positive and negative effects in the parents, (4DH1)½+F/(4DH1)½-F measures proportion of dominant and recessive genes in the parents.

than 0.25. Average degree of dominance was less than one (0.89), suggesting partial dominance.

Significant and positive value of F (45.05) revealed the greater frequency and important role of dominant genes for number of grains spike^{-1}. This was also supported by the ratio of dominant

to recessive genes (2.29). Value of h2 was non-significant. Influence of environment (E) was indicated by its significant value. These results are in accordance with those of Jag et al. (2003), Sangwan and Choudhry (1999), Karam et al. (1996), Rajara and Maheshwari (1996) who also reported non-additive gene action for number of grains spike^{-1}, while Ali and Khan (1998) and Asad et al. (1992) reported the importance of additive type of gene action for this trait. Narrow sense heritability estimates under late planting was about 56.21% indicating that, more than half of the inherited variation was of additive nature.

Grain yield plant^{-1}

Under normal planting both additive (D) and dominant (H) variations were significant (Table 4). Unequal values of H1 and H2, supported by the ratio of H2/4H1 (0.15) indicated unequal distribution of positive and negative alleles among parent cultivars. The value of F was positive and significant, indicating the frequent distribution and important role of dominant genes for yield plant^{-1}. This was also supported by the ratio of dominant to recessive genes (3.95). Average degree of dominance (2.16) displayed an over dominant gene action. The value of h2 was non-significant. Significant value of E depicted the influence of environment on grain yield plant^{-1}.

These results are in accordance with those of Sangwan and Choudhry (1999), Dhayal and Sastry (2003), Karam et al. (1996), Kuruvadi (1991), Mishra et al. (1994), Larik et al. (1995), Mann et al. (1995) and El-Hennawy (1996) who also reported non-additive gene effects for grain yield plant^{-1}. Narrow sense heritability estimate under normal planting was very low (10.13%) as compared to broad sense heritability (80.69%), which also indicated the preponderance of dominant variation in the total inherited genetic variation.

1000-grain weight

Genetic components of variation revealed that, both additive (D) and dominance (H) gene effects were significant under early and normal plantings, while under late planting only additive (D) gene effects were significant (Table 4). Unequal values of H1 and H2 supported by the ratio of H2/4H1 (0.24, 0.23 and 0.18) suggested that, positive and negative alleles were unequal among parental cultivars under all three environments. Average degrees of dominance in case of early and late planting (0.92 and 0.62, respectively) indicated partial dominance, while in case of normal planting (1.49) over dominance gene action was observed. Under early, normal and late plantings, F was positive and non-significant.

However, ratio of dominant to recessive genes (1.76, 1.07 and 1.34), which were more than one displayed the greater proportion of dominant genes. Values of h2 were significant under early and late planting showing the presence of overall dominance effect due to heterozygous loci, while it was non-significant under normal planting. Significance of environment (E) was indicated in early, normal and late plantings. Asad et al. (1992) and Rajara and Maheshwari (1996) reported non-additive gene action for 1000-grains weight, while Dhayal and Sastry (2003), Karam et al. (1996), Singh et al. (2002) and Taleei and Beigi (1996) reported additive gene effects for the trait under study.

The values of narrow sense heritability estimates (45.19 and 40.49%) under early and normal planting indicated that, more than half of the total inherited genetic variation was of additive nature and less than half was of dominance nature. Narrow sense heritability under late planting was 59.56% indicating that, greater proportion of the inherited variation was of additive nature.

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