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GENETIC DIVERGENCE IN F4:6WHEAT LINES FOR YIELD AND ITS CONTRIBUTING TRAITS

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A B S T R A C T

Studying genetic divergence of quantitative traits and their contribution towards yield is essential for developing high yielding varieties. To study genetic divergence of $F_{4:6}$ wheat lines for yield contributing traits, an experiment was conducted comprising 48 advance wheat lines and a check cultivar Janbaz at the University of Agricultural Peshawar, Pakistan during 2010-11. The research was laid out in alpha lattice design with 2 replications. Analysis of variance revealed highly significant differences among wheat lines for yield and related traits. Moderate to high magnitude of heritability estimates (0.53-0.93) were observed for days to heading, flag leaf area, plant height (cm), spikes plot^{-1}, grain weight spike^{-1}, grain yield and harvest index, while low to moderate heritability estimates (0.23-0.48) for spike length, grains spike^{-1}, 1000-grain weight and biological yield. The selection response were 6.40 days for heading, 9.57 cm^2 for flag leaf area, 11.74 cm for plant height, 0.83 cm for spike length, 185.11 spikes for spikes plot^{-1}, 7.49 for grains spike^{-1}, 0.67 g for grain weight spike^{-1}, 5.07 g for 1000 grain weight, 628.50 kg ha^{-1} for biological yield, 855.92 kg ha^{-1} for grain yield and 5.56 % for harvest index, respectively. Selection differentials were 208.4 spikes for spikes plot^{-1}, 1.9 cm for spike length, 13.4 for grains spike^{-1}, 0.7 g for grain weight spike^{-1}, 8.1 g for 1000 grain weight and 795.4 kg ha^{-1} for grain yield, respectively. Spikes plot^{-1}, grains spike^{-1}, grain weight spike^{-1}, 1000-grain weight and harvest index had high correlations with grain yield. The crossings of Tatara, Ghaznavi-98 and Wafaq performed better than the check cultivar for most of the yield based desirable traits.

Keywords: Genetic divergence, $F_{4:6}$ Lines, heritability, selection response, selection differential.

INTRODUCTION

Wheat is the most important food crop of the world including Pakistan and ranks first among cereals. In Pakistan total area under food crops (wheat, rice, jowar, maize, bajra and barley) cultivation is 34305 thousand hectares. Wheat is cultivated on 73.5% area of total food crop area and an average yield is 2833 Kg per hectare. In gross value addition wheat worth 575570 million Pak Rupees to Pakistan economy (Pakistan, 2010-2011). It fulfills nutritional requirement of people in the form of protein and carbohydrates. Wheat yields of the country are much lower as compared to many other countries of the world. To improve wheat yield per hectare in Pakistan, wheat breeders are concentrating their efforts to improve the yield potential by developing new varieties with desirable genetic makeup. This can be achieve by development of improved cultivars by using genetic potential and genetic variability present for traits in a breeding population (Iqbal and Khan, 2006). High heritability associated with high genetic advance for quantitative traits in wheat offer better scope of selection of genotypes in early segregating generations (Memon *et al*., 2005). Heritability plays an important role for planning the breeding strategy (Sial, 2007). Correlation study is an essential positive tool for identifying traits for selection. The association among yield and its components has successfully exploited for identifying high yielding genotypes. Major objectives of this research were to; i) study genetic divergence of some newly developed lines for yield and related traits, and ii) determine correlation among various traits.

MATERIALS AND METHODS

A set of 48 $F_{4:6}$ wheat lines along with a check cultivar

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Janbaz (Table 1) was evaluated in alpha lattice design with two replicates during 2010-11 at Agricultural University Peshawar, Pakistan. These lines were collected from germplasm collection of department of plant breeding and genetics, Khyber pakhtunkhwa, Agricultural University Peshawar, Pakistan. Each genotype was planted in 2 rows of 4 meter length with a row to row space of 30 cm. Urea and DAP fertilizers were applied @ 120 and 60 kg ha^{-1}, respectively. Half dose of urea and full dose of DAP were applied at the time of seed bed preparation while the remaining half dose of urea was applied at the time of first irrigation. All other cultural practices were applied time to time as and when required.

Table 1. List of F4:6 wheat lines evaluated at Agricultural University Peshawar during 2010-11.

Line	I.D No*	Line	I.D No*
Wafa /Takbeer	4	Ghaznavi-98/Khattakwal	4
Marqalla/Inqalab	2	Wafaq/Ghaznavi-98	3
Inqalab/Khattakwal	1	Takbeer/Marqalla	1
Tatara/Ghaznavi-98	1	Tatara/Inqalab	8
Tatara/Inqalab	2	Khattakwal/Inqalab	6
Marqalla/Khattakwal	1	Tatara/Ghaznavi-98	4
Takbeer/Inqalab	5	Wafaq/Khattakwal	3
Takbeer/Ghaznavi-98	3	Wafaq/Takbeer	3
Wafaq/Ghaznavi-98	1	Inqalab/Marqalla	2
Takbeer/Khattakwal	9	Tatara/Ghaznavi-98	6
Marqalla/Khattakwal	2	Takbeer/Marqalla	9
Wafaq/Ghaznavi-98	4	Wafaq/Takbeer	5
Wafaq/Ghaznavi-98	7	Wafaq/Inqalab	4
Tatara/Ghaznavi-98	7	Takbeer/Khattakwal	5
Wafaq/Takbeer	2	Wafaq/Ghaznavi-98	8
Khattakwal/Inqalab	2	Wafaq/Ghaznavi-98	5
Khattakwal/Inqalab	5	Takbeer/Ghaznavi-98	9
Takbeer/Marqalla	7	Tatara/Takbeer	1
Inqalab/Khattakwal	2	Takbeer/Inqalab	2
Tatara/Inqalab	7	Marqalla/Ghaznavi-98	3
Tatara/Ghaznavi-98	7	Wafaq/Takbeer	1
Tatara/Inqalab	4	Tatara/Inqalab	1
Takbeer/Inqalab	7	Tatara/Wafaq	2
Ghaznavi-98/Khattakwal	1	Ghaznavi-98/Khattakwal	3
Janbaz	Check		

* Progenies of the same parents (sister lines).

Traits measurement: Days to heading were the number of days from planting to 50 % spike emergence. Flag leaf area was measured from the base of the lamina to the extreme tip, while the width was measured at its broadest place (Francis *et al*., 1969). Plant height (cm) was measured from ground level to the tip of the last spikelet, excluding awns. Spike length (cm) was measured from the base of first spikelet to the tip of the spike excluding awns. Spikes $plot^{-1}$ was counted in each plot as the total number of spikes in two rows. Spike of each randomly selected plant was threshed and the total number of grains were counted and recorded as number of grains $spike^{-1}$. Grains from each of the randomly selected spike were weighed individually to determine grain weight $spike^{-1}$. Thousand kernel weight was recorded by weighing 1000 kernels. Biological yield and grain yield were obtained from each plot and converted to kg ha^{-1}. The harvest index was determined

as the ratio of grain yield plot^{-1} to the biological yield plot^{-1}.

Statistical Analysis: Data was subjected to analysis of variance (ANOVA) according to Steel and Torrie (1980) to test the null hypothesis of no differences among various $F_{4:6}$ lines. The least significant difference (LSD) test was also used for means separation and comparison after significance. Heritability (broad sense) was calculated according to Singh and Chaudhary (1985). Expected response to selection (Re) was determined using 20% selection intensity according to the procedure outlined by Falconer and Mackay (1996). The simple correlation coefficients (r) of grain yield with other yield components were also worked out according to Kwon and Torrie (1964).

RESULTS AND DISCUSSION

Days to heading: Analysis of variance for days to heading revealed significant differences in genotypes (Table 2). Days to heading varied from 105.5 to 134.0 days among wheat genotypes (Table 3). Maximum days to heading (134.0 days) were observed for Wafaq/Ghaznavi-98 (Waf/G-98-1) while Takbeer/Inqalab-2 (Tak/Inq-2) revealed minimum days to heading (105.5 days). The check cultivar had 120 days for heading (Table 3). Heritability estimate for days to heading was 0.53 with expected selection response of 6.4 days (Table 3). Early heading provides sufficient time for grain formation. If heading is delayed, duration of grain filling is squeezed resulting in modest grain weight, therefore early heading is desirable in wheat. Wider range in mean values of days to heading in this study validates the genotypic differences (Ahmad *et al.,* 2011).

Table 2. Mean squares for various traits in F4:6 wheat lines 2010-2011, AUP.

Source of variation	Df	Days to heading	Flag leaf area	Spike length	Plant height	Spikes plot-1	Grains spike-1	Grs. Wt spike-1	1000-Grs.Wt.	Biological yield	Grain yield	Harvest index
Replication	1	587.8	3.2	29.3	59.1	2997.6	13.2	0.01	118.4	22222254.1	58369.7	177.9
Block	12	28.3**	1.9**	1.1*	24.4**	938.4*	22.5**	0.03**	18.5**	948693.1*	17461.2**	5.8**
Treatments	48	98.9**	125.8**	3.1*	245.2**	39639.2**	195.7**	0.67**	74.6**	4583356.5*	837364.8**	77.5**
Error	36	47.8	12.2	1.7	43.5	1648.5	72.2	0.09	37.9	3141526.6	31460.04	21.5
CV%		5.6	8.8	10.9	6.0	7.6	15.4	14.6	15.7	14.8	6.4	17.1

**,* = Significant at 1 and 5% probability level, respectively

Flag leaf area (cm^2): Genotypes expressed significant differences for flag leaf area (Table 2). Means for flag leaf area ranged from 17.4 to 55.6 cm^2 (Table 3). Genotype Tak/Inq-8 exhibited maximum flag leaf area (55.6 cm^2) while minimum flag leaf area (17.4 cm^2) was recorded for Tat/Inq-1 (Table 3). Broad sense heritability estimate and expected response to selection for flag leaf area were 0.82 and 9.5 cm^2, respectively (Table 3). Flag leaf area contributes significantly to grain filling (Khan *et al*., 2003). Bigger flag leaf area has higher photosynthesis and thus more photosynthates are partitioned to grains. Broad sense heritability estimate and expected response were 0.82 and 9.6 cm^2 respectively for flag leaf area.

Plant height (cm): Genotypes for plant height had significant differences (Table 2). Data for plant height ranged from 83.7 to 134.5 cm with a mean value of 103.1 cm (Table 3). Maximum value for plant height was recorded for genotype K-wal/Inq-2 (134.5 cm) while minimum plant height was observed for Waf/G-98-3. Heritability estimate for plant height was 0.70 and the expected selection response was 11.74 cm at 20% selection intensity (Table 3). Plant height was significantly negative correlated with grain yield (Table 5). Short stature and uniform wheat plants are preferred by plant breeders because of their lodging resistance and positive response to fertilizers and irrigation (Khan and Khalil, 2006). The reduction in yield was associated with the increased plant height thus plant height is one of the most important traits determining the yield and a major selection parameter in wheat breeding programs (Yagdi and Sozen, 2009).

Spikes plot^{-1}: Genotypes expressed significant differences for spikes plot^{-1} (Table 2). Spikes plot^{-1} varied from 303.0 to 805.5 spikes among wheat genotypes (Table 3). Genotype Tak/G-98-3 had maximum spikes plot^{-1} (805.5) while minimum spikes plot^{-1} was observed for Tak/Inq-7 (303.0).

For check spikes plot^{-1} was (547.0). Heritability estimate for spike plot^{-1} was 0.92 and expected selection response was 185.1 spikes at 20% selection intensity (Table 3). Selection differential for spikes plot^{-1} were 208.4 spikes (Table 4). Spikes plot^{-1} showed significantly positive phenotypic correlation with grain yield (Table 5). Spikes plot^{-1} is one of the most important yield component and leads to an increase in grain yield. High heritability estimate for spikes plot^{-1}, indicating less influence of environment on this trait. Spikes plot^{-1} was significantly positive correlated with grain yield. Tammam *et al*. (2000) noticed that spikes plot^{-1} was the most important components in determining grain yield.

Table 3. Ranges, mean, heritability and selection response for various traits in F4:6 wheat lines 2010-11, AUP.

Traits	Range		Mean	Mean (Check)	h2	Re
	Minimum	Maximum				
Days to heading	105.5	134.0	117.0	107.0	0.53	6.4
Flag leaf area (cm2)	17.4	55.6	35.2	40.7	0.82	9.5
Plant height (cm)	83.7	134.5	103.1	88.5	0.70	11.7
Spike length (cm)	8.6	14.7	11.4	11.9	0.38	0.83
Spikes plot-1	303.0	805.5	501.7	547.0	0.92	185.1
Grains spike-1	31.5	71.7	50.5	53.2	0.46	7.5
Grs. Wt spike-1 (g)	1.06	3.11	1.90	2.07	0.76	0.66
1000-Grs.Wt. (g)	25.4	54.1	36.4	38.7	0.48	5.1
Biological yield (Kg ha-1)	8541.7	16458.4	10977.9	9375.0	0.23	628.5
Grain yield (Kg ha-1)	1012.5	4181.3	2632.7	2968.7	0.93	855.9
Harvest index (%)	11.4	42.6	24.2	31.7	0.57	5.6

Spike length (cm): Genotypes exhibited significant differences for spike length (Table 2). Spike length of 48 wheat genotypes ranged from 8.6 cm to 14.7 cm (Table 3). Genotype Tak/Inq-8 had maximum spike length (14.7 cm) while Tak/K-wal-5 showed minimum spike length (8.6 cm). For check cultivar spike length was 11.9 cm. Heritability for spike length was 0.38 with expected selection response for spike length was 0.83 cm (Table 3). The difference between the mean of a population and the mean of the individuals selected to be parents of the next generation (selection differential) for spike length was 1.9 cm (Table 4). Spike length is a trait of considerable importance which has significant relationship with grains spike^{-1} and finally to grain yield, as larger spike tends to have greater photosynthetic area which accommodates more number of spikelets. Significant differences were observed for spike length among wheat genotypes. Muhammad *et al*. (2006) also found significant variation for spike length. The wider range in mean value of wheat genotypes for spike length validates the genotypic differences.

Grains spike^{-1}: Analysis of variance revealed significant differences among wheat genotypes for grains spike^{-1}(Table 2). Data for grains spike^{-1} ranged from 31.5 to 71.7 with a mean value of 50.5. Among the 48 wheat genotypes maximum number of grains spike^{-1} were recorded for genotype Waf/G-98-4 (71.7) while minimum number of grains spike^{-1} was observed for Tak/Inq-2 (31.5). For check cultivar grains spike^{-1} was 53.2 (Table 3). Broad-sense heritability estimates for number of grains spike^{-1} was 0.46 with expected selection response of 7.49 at 20% selection intensity (Table 3). Selection differential for grains spike^{-1} was 13.4 (Table 4). Grains spike^{-1} had significantly positive correlation with grain yield (Table 5). In yield contributing traits grains spike^{-1} is an important trait which has direct effect on grain yield (Ashfaq *et al*., 2003). Genotypes showed highly significant differences for grains spike^{-1} which are similar to the findings of Memon *et al*. (2007). Heritability estimates for grains spike^{-1} was moderate which infers that selection needs to be delayed for this trait. The present result is supported by Eid (2009), who also reported low heritability for grains spike^{-1}. Grains spike^{-1} had significantly positive correlation with grain yield. Ajmal *et al*. (2009) also reported positive association of grains spike^{-1} with grain yield.

Grain weight spike^{-1} (g): Genotypes showed significant differences for grain weight spike^{-1} (Table 2). Aliu and Fetahu (2010) also observed genetic differences among

wheat lines for grain weight spike^{-1}. Grain weight spike^{-1} varied from 1.06 to 3.11 g for wheat genotypes. Genotype Tat/G-98-7 had maximum grain weight spike^{-1} among all wheat genotype. For check cultivar grain weight spike^{-1} was 2.07 g (Table 3). Broad-sense heritability estimate was 0.76 for grain weight spike^{-1} with 0.66 g expected selection response at 20% selection intensity (Table 3). High heritability is in lined with the findings of Asif *et al*. (2004) who also found high heritability for grain weight spike^{-1}. Selection differential for grain weight spike^{-1} was 0.7 g (Table 4). Grain weight spike^{-1} was significantly positive correlated with grain yield (Table 4). Grain weight spike^{-1} is a vital and prominent yield enhancing trait and selection for this trait would boost up the grain yield.

1000-grain weight (g): Significant differences were observed among genotypes for 1000-grain weight (Table 2). Ahmad *et al*. (2011) also found considerable variation among wheat genotypes for 1000-grain weight. Maximum value of 1000-grain weight was recorded for genotype Tat/G-98-7 (54.1 g) while Tak/K-wal-5 exhibited minimum value for 1000-grain weight (25.4 g). For check cultivar 1000-grain weight was 38.7 g (Table 3). For 1000-grain weight broad-sense heritability estimate was 0.48 with 5.07 g expected selection response using 20% selection intensity (Table 3). Selection differential for 1000-grain weight was 8.1 g (Table 4). The grain weight of wheat generally expressed as 1000-grain weight and it is one of the most imperative yield components and could be used as potential selection criteria for grain yield. Phenotypic correlation of 1000-grain weight with grain yield was significantly positive (Table 5).

Biological yield (kg ha^{-1}): Genotypes for biological yield had significant differences (Table 2). Similarly, Rashidi (2011) also observed significant differences in biomass of wheat genotypes. Biological yield ranged from 8541.7 to 16458.4 kg ha^{-1} (Table 3). Genotype Tat/Inq-8 showed maximum value (16458.4 kg ha^{-1}) for biological yield while minimum value was recorded for genotype Tak/Mar-7 (8541.7 kg ha^{-1}). Broad-sense heritability estimate for biological yield was 0.23 and expected selection response for biological yield was 628.50 kg ha^{-1} (Table 3). Low broad-sense heritability estimate 0.23 was observed for biological yield which is in contrast to the finding of Gupta and Verma (2000) who reported moderate to high heritability for biological yield.

Table 4. Mean of top 20% selected lines (S), and mean of all 49 genotypes ( ) and selection differential (S) of yield and yield components in F4:6 wheat lines 2010-11, AUP.

Traits	$\overline{X}$ S	$\overline{X}$	S
Spikes plot-1	710.1	501.7	208.4
Spike length (cm)	13.3	11.4	1.9
Grains spike-1	63.9	50.5	13.4
Grain weight spike-1(g)	2.60	1.9	0.7
1000-grain weight(g)	44.5	36.4	8.1
Grain yield (kg ha-1)	3428.1	2632.7	795.4

Table 5. Significant phenotypic correlations of grain yield with other traits.

Traits	Correlation with grain yield
Plant height (cm)	-0.308*
Spikes plot-1	0.692**
Grains spike-1	0.389*
Grs. Wt spike-1 (g)	0.473**
1000-Grs.Wt. (g)	0.351*
Harvest index (%)	0.784**

Grain yield (kg ha^{-1}): Analysis of variance showed significant differences among wheat lines for grain yield (Table 2). Farooq *et al*. (2010) also reported considerable variation among wheat lines for grain yield. Grain yield ranged from 1012.5 to 4181.3 kg ha^{-1}. Genotype Tat/G-98-7 showed maximum grain yield (4181.3 kg ha^{-1}) while minimum grain yield was recorded for genotype Tak/K-wal-9 (1012.5 kg ha^{-1}). For check cultivar grain yield was 2968.7 kg ha^{-1} (Table 3). For grain yield broad-sense heritability estimate was 0.93 with expected selection response of 855.92 kg ha^{-1} at 20% selection intensity (Table 3). Selection differential for grain yield was 795.4 kg ha^{-1} (Table 4). Grain yield is a complex quantitative trait and it is directly or indirectly influence by other plant traits. Grain yield had significantly positive correlations with spikes plot^{-1}, grains spike^{-1}, grain weight spike^{-1}, 1000-grain weight and harvest index. However, grain yield negative significantly correlated with plant height (Table 5). Akram *et al*. (2008) also reported significant and positive association of grain yield with yield related traits and negative association of grain yield with plant height.

Harvest index (%): Genotypes exhibited significant differences for harvest index (Table 2). Harvest index ranged from 11.4 to 42.6 % for wheat genotypes (Table 3). Maximum value for harvest index was recorded for genotype Tat/G-98-7 (42.6 %) while genotype Tak/K-wal-9 exhibited minimum harvest index (11.4 %). Heritability for harvest index was 0.57 with expected selection advance of 5.56 % at 20 % selection intensity (Table 3). Moderately high heritability value for harvest index validates the findings of Farshadfar *et al*. (2005) who also found high to medium heritability for harvest index. Harvest index has direct contact with grain yield. Enhancing in harvest index will boost the share of grain yield to the total yield. Harvest index showed significant correlation with grain yield (Table 5).

CONCLUSIONS

Significant genetic differences were observed among 48 wheat genotypes for yield and yield associated traits. From statistical calculation e.g means square, heritability and selection response it was concluded that grain yield had significant correlations with spikes plot^{-1}, grains spike^{-1}, grain weight spike^{-1}, 1000-grain weight and harvest index. Based on the results of this study, the $F_{4:6}$ lines Tat/G-98-7, Tat/G-98-6, Tak/G-98-3, Waf/G-98-3 and Waf/G-98-7 performed better than the check cultivar and therefore, these are recommended for extensive testing.

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