

Full Length Research Paper

Study of genetic variability and correlation among various traits of F₅ wheat (*Triticum aestivum* L.) populations

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Accepted 09 August, 2011

In order to study genetic variability and correlation among various wheat genotypes, an experiment was conducted comprising twenty five F₅ populations during 2008-09 at the Malakandher Research Farm Peshawar. Data were recorded on grains spike⁻¹, grain weight spike⁻¹, 1000 grain weight, biological yield, harvest index and yield ha⁻¹. Analysis of variance revealed highly significant differences for grains spike⁻¹, grain weight spike⁻¹, biological yield and grain yield ha⁻¹ while non significant differences were observed for 1000 grain weight and harvest index among all the populations. Phenotypic correlation coefficient of grain yield with grains spike⁻¹ and grain weight spike⁻¹ were significantly positive. Based on these results we concluded that the populations of Tak x Inq and G-98 x Tat could yield potential segregates.

Keywords: Wheat, F₅ population, traits, genetic variability, correlation.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal crop of the world. Among the food crops, wheat is one of the most abundant sources of energy and protein for the world population (Salem *et al.*, 2007). The importance of bread wheat being as a staple food in our economy cannot be ignored. Wheat is the leading grain crop and ranks first among the cereal crops in Pakistan. Several high yielding and tolerant varieties have been developed through the breeders' efforts and are being extensively grown throughout the country. Pakistan is the 7th largest wheat producer, accounting for 2.73 % of the world's wheat production from an area of 3.57 % of the world under wheat cultivation. Pakistan has a geographical area of 79.6 million hectares of which 19.3 million hectares (25%) are currently under cultivation (PDA, 2009). The annual area under wheat crop during 2009-10 was 9,105.4 ha with production of 23,916.5 tons and

average yield of 2,626 kg ha⁻¹ (MINFAL, 2009-10).

Characterization of genetic variability and estimating of the phenotypic and genetic relationship among varieties are essential to any breeding program, because segregation and combination of different favorable alleles in artificial crosses among parents are less similar (Bered *et al.*, 2002). Development of cultivars is based on the genotypic variability present for traits in a population. During the early stage of crop improvement, a plant breeder strives to know whether there is sufficient evidence of genetic variation in the material being tested and which are the characters that can be improved provided with particular selection intensity. Another important aspect to know is related to which improvement procedure would be more effective. Such questions may be partially answered by estimation of the genetic variability in a population. Variation in any character in a segregating population is due to genetic and environmental factors. The genetic factor is more important in plant breeding since it can be used to improve the population.

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Table 1. List of F₅ population with their abbreviated form as appear in the text

| S.NO | Abbreviation | Name | S.NO | Abbreviation | Name |
|------|--------------|-----------------------|------|--------------|--------------------------|
| 1 | Waf xTak | Wafaq x Takbeer | 14 | Tat x Inb | Tatara x Iqbal |
| 2 | Waf x Iqb | Wafaq x Iqbal | 15 | Tat x Mar | Tatara x Margalla |
| 3 | Waf x Mar | Wafaq x Margalla | 16 | Tat x G-98 | Tatara x Ghaznavi 98 |
| 4 | Waf x G-98 | Wafaq x Ghaznavi 98 | 17 | Tat x Inq | Tatara x Inqilab |
| 5 | Waf x K-wal | Wafaq x Khattakwal | 18 | Inb x Mar | Inqilab x Margalla |
| 6 | Waf x Inq | Wafaq x Inqilab | 19 | Inb x K-wal | Inqilab x Khattakwal |
| 7 | Tak x Inb | Takbeer x Iqbal | 20 | Mar x G-98 | Margalla x Ghaznavi 98 |
| 8 | Tak x Mar | Takbeer x Margalla | 21 | Mar x K-wal | Margalla x Khattakwal |
| 9 | Tak x G-98 | Takbeer x Ghaznavi 98 | 22 | Mar x Inq | Margalla x Inqilab |
| 10 | Tak x K-wal | Takbeer x Khattakwal | 23 | G-98 x K-wal | Ghaznavi 98 x Khattakwal |
| 11 | Tak x Inb | Takbeer x Inqilab | 24 | G-98 x Inq | Ghaznavi 98 x Inqilab |
| 12 | Tat x waf | Tatara x Wafaq | 25 | K-wal x Inq | Khattakwal x Inqilab |
| 13 | Tat x Tak | Tatara x Takbeer | | | |

Table 2. Mean square values for different traits of wheat genotypes during 2009.

| Source of variance | Df | Grains spike ⁻¹ | Grn. wt. spike ⁻¹ | 1000-grn wt. | Biologic al Yield | Harvest Index | Yield ha ⁻¹ |
|--------------------|----|----------------------------|------------------------------|--------------------|-------------------|--------------------|------------------------|
| Replication | 2 | 241.0 | 0.49 | 26.5 | 105.1 | 97.1 | 43510.5 |
| Genotype | 24 | 156.0** | 0.32** | 15.8 ^{NS} | 79.5 [*] | 70.5 ^{NS} | 180676.7** |
| Error | 48 | 32.4 | 0.12 | 14.5 | 32.3 | 68.3 | 36621.2 |
| CV% | | 15.4 | 14.6 | 21.7 | 14.8 | 17.1 | 10.8 |

**,* = Significant at 1 and 5% probability level, respectively. NS = Non-significant

The main objectives of this study were to study genetic variability at various important traits associated to crop yield and their correlation, and to identify potential populations for improvement in different traits.

MATERIALS AND METHODS

In order to study the genetic variability and correlation for various traits in F₅ bulked wheat populations developed from different wheat genotypes, an experiment was conducted during 2008-09 at Malakandher Research Farm, KP Agricultural University Peshawar, Pakistan. Breeding material comprised twenty-five different wheat populations (Table 1). The wheat genotypes were sown during mid of November, 2008 with inter-row spacing of 30 cm, in a randomized complete block (RCB) design in three replicates. Each plot of a genotype had six rows of five meter length. Land preparation, sowing and hoeing were applied same for all the entries to minimize the environmental variations.

RESULTS

Grains spike⁻¹

Analysis of variance revealed highly significant differences among all genotypes for grains spike⁻¹ (Table 2). The values for grains spike⁻¹ ranged from 50.2 to 75.3 with a mean value of 62.3. The population of Tak x G-98 exhibited maximum grains spike⁻¹ 75.3 while the population of Waf x K-wal showed minimum grains spike⁻¹ 50.2 (Table 3). Highly significant phenotypic correlation was observed for grains spike⁻¹ with grains weight spike⁻¹, yield ha⁻¹ while grains spike⁻¹ non-significant correlated with 1000 grain weight, biological yield and harvest index (Table 4).

Grains weight spike⁻¹ (g)

Genotypes had highly significant differences for grains weight spike⁻¹ (Table 2). The values for this parameter

Table 3. Mean performance for Grains spike⁻¹, Grain weight spike⁻¹, 1000 kernel weight, Biological Yield, Harvest Index and yield hectare⁻¹ of wheat genotypes during 2009.

| Genotypes | Grains spike ⁻¹ | Grn.Wt. spike ⁻¹ (g) | 1000-grain weight | Biological Yield | Harvest Index | Yield ha ⁻¹ |
|-----------------------|----------------------------|---------------------------------|-------------------|------------------|---------------|------------------------|
| Waf xTak | 67.37 | 2.23 | 33.20 | 57.87 | 39.03 | 1777.67 |
| Waf x lqb | 71.00 | 2.75 | 38.72 | 67.74 | 40.76 | 1657.33 |
| Waf x Mar | 74.98 | 2.74 | 36.47 | 66.56 | 41.52 | 1722.00 |
| Waf x G-98 | 63.57 | 2.41 | 37.88 | 58.60 | 41.45 | 1592.67 |
| Waf x K-wal | 50.23 | 1.85 | 37.11 | 52.07 | 35.73 | 1407.67 |
| Waf x Inq | 61.10 | 2.24 | 36.60 | 55.42 | 40.39 | 1648.33 |
| Tak x Inb | 72.27 | 2.90 | 40.03 | 65.46 | 44.37 | 2111.00 |
| Tak x Mar | 59.33 | 1.91 | 32.51 | 51.13 | 37.93 | 1722.33 |
| Tak x G-98 | 75.33 | 2.92 | 38.79 | 64.08 | 45.84 | 2018.67 |
| Tak x K-wal | 52.37 | 1.91 | 36.38 | 51.50 | 37.12 | 1314.67 |
| Tak x Inb | 57.30 | 2.13 | 37.42 | 53.57 | 39.93 | 1556.00 |
| Tat x waf | 68.90 | 2.38 | 34.57 | 62.24 | 38.51 | 1203.67 |
| Tat x Tak | 61.10 | 2.34 | 38.32 | 53.25 | 43.89 | 1963.00 |
| Tat x Inb | 63.50 | 2.01 | 31.73 | 51.13 | 39.41 | 1564.67 |
| Tat x Mar | 61.77 | 2.41 | 39.26 | 54.67 | 44.21 | 1704.00 |
| Tat x G-98 | 67.03 | 2.56 | 38.18 | 55.17 | 46.56 | 1657.67 |
| Tat x Inq | 62.50 | 2.47 | 39.46 | 59.67 | 41.44 | 1481.33 |
| Inb x Mar | 56.60 | 2.01 | 35.43 | 51.13 | 39.54 | 1694.67 |
| Inb x K-wal | 50.33 | 1.93 | 38.18 | 55.08 | 34.80 | 1324.00 |
| Mar x G-98 | 61.53 | 2.04 | 32.92 | 49.43 | 40.85 | 1583.33 |
| Mar x K-wal | 54.37 | 1.86 | 34.64 | 53.31 | 45.56 | 1185.00 |
| Mar x Inq | 54.97 | 2.00 | 36.23 | 48.61 | 40.87 | 1574.33 |
| G-98 x K-wal | 67.50 | 2.52 | 37.44 | 59.60 | 42.68 | 1296.00 |
| G-98 x Inq | 65.47 | 2.39 | 36.48 | 55.40 | 43.11 | 1639.00 |
| K-wal x Inq | 56.23 | 2.034 | 34.53 | 56.40 | 34.82 | 1203.33 |
| LSD _(0.05) | 9.35 | 0.56 | N.S | 10.57 | N.S | 314.20 |

Table 4. Pearson phenotypic correlation coefficient among various traits measured in different F₅ wheat populations

| Traits | Grains spike ⁻¹ | Grain wt. spike ⁻¹ | 1000 Grn wt. | Bio. Yield | Harvest Index | Yield ha ⁻¹ |
|----------------------------|----------------------------|-------------------------------|---------------------|---------------------|---------------------|------------------------|
| Grains spike ⁻¹ | - | 0.840** | 0.194 ^{NS} | 0.261 ^{NS} | 0.047 ^{NS} | 0.343** |
| Grn Wt spike ⁻¹ | | - | 0.687** | 0.727** | 0.690** | 0.362** |
| 1000-Grn Wt. | | | - | 0.314 ^{NS} | 0.046 ^{NS} | 0.174 ^{NS} |
| Bio.Yield | | | | - | 0.036 ^{NS} | 0.193 ^{NS} |
| Harvest Index | | | | | - | 0.246** |
| Yield ha ⁻¹ | | | | | | - |

** , * = Significant at 1 and 5% probability level, respectively. NS = Non-significant

ranged from 1.8 to 2.9g with a mean value of 2.8. Among twenty five F₅ wheat populations Tak x G-98 exhibited maximum 2.9 g while the population of Waf x K-wal gave minimum 1.8 g grains weight spike⁻¹(Table 3). Phenotypic correlation of grains weight spike⁻¹ with grains spike⁻¹, 1000 grain weight and yield ha⁻¹ were highly significant (Table 4).

1000-grain weight (g)

Analysis of variance revealed non-significant differences among the genotypes for 1000-grain weight (Table 2). The population of Tak x Inq exhibited maximum 1000-grains weight 40.0 g while population of Tat x Inq minimum 1000-grain weight 31.7 g (Table 3). Phenotypic

correlation of 1000-grain weight with grains weight spike⁻¹ was highly significant and non-significant with grains spike⁻¹, biological yield, harvest index and grain yield ha⁻¹ (Table 4)

Biological yield (g)

Genotypes had highly significant differences for biological yield (Table 2). The values for this parameter ranged from 67.7 to 48.6 g with a mean value of 58.2 g. Among twenty five F₅ wheat populations cross of Waf x Iqb exhibited maximum 67.7g while the cross of Mar x Inq displayed minimum 48.6 g grains weight spike⁻¹ (Table 3). Phenotypic correlation of biological yield with grains weight spike⁻¹ was highly significant and non significant with grains spike⁻¹, 1000 grain weight, harvest index, and yield ha⁻¹ (Table 4).

Harvest index (%)

Analysis of variance revealed non-significant differences among the genotypes for harvest index (Table 2). The cross of Tat x G-98 exhibited maximum harvest index 46.6 g while cross of Inq x K-wal minimum harvest index 34.8 g (Table 3). Phenotypic correlation of harvest index with grains weight spike⁻¹ and grain yield ha⁻¹ were highly significant and non-significant with grains spike⁻¹, 1000 grain weight and biological yield (Table 4).

Grain yield ha⁻¹(kg)

Genotypes showed highly significant differences for grain yield ha⁻¹ (Table 2). Mean data showed that grain yield ha⁻¹ ranged from 1185 kg to 2111 kg (Table 3). The population of Tak x Inq exhibited maximum grain yield ha⁻¹ 2111 kg while population of Mar x K-wal minimum grain yield ha⁻¹ 1185 kg (Table 2). Phenotypic correlation of grain yield ha⁻¹ with grains spike⁻¹, weight spike⁻¹ and harvest index were highly significant and non-significant with 1000-grain weight and biological yield (Table 4).

DISCUSSION

Significant differences were observed among genotypes for number of grains spike⁻¹. Similar results were also reported by Khan *et al* (2001). The population of Tak x G-98 gave maximum mean value for grains spike⁻¹. Significantly positive phenotypic correlations were observed for grains spike⁻¹ with grains weight spike⁻¹ and yield ha⁻¹. This indicated that increase in grains spike⁻¹ increased grains weight spike⁻¹ and yield ha⁻¹. The population of Tak x G-98 could yield potential segregants for grains spike⁻¹ and high grain yield. Genotypes dis-

played highly significant differences for grains weight spike⁻¹. Munir *et al* (1999), Ihsanullah and Muhammad (2000) also reported significant differences for grains weight spike⁻¹. However, the findings of Arif *et al* (2002) are contrary to our findings. The difference may be due to the difference in materials. Maximum grains weight spike⁻¹ for the population of Tak x G-98 infers that this population could give superior lines for grain weight spike⁻¹ and grain yield. Phenotypic correlation coefficients of grain weight sipke⁻¹ with grains spike⁻¹, 1000 grain weight and yield hectare⁻¹ were highly significantly positive, indicating that increase in these traits increased the grain weight spike⁻¹. Analysis of variance revealed non-significant differences among the genotypes for 1000-grain weight which are contrary to the results of Ahmad *et al* (2003). The reason for non-significant variation could be the result of the parent cultivars with narrow differences for 1000-grain weight. Highly significant positive phenotypic correlation was observed for 1000-grain weight with grain weight sipke⁻¹, means increase in grain weight sipke⁻¹ increased in 1000-grain weight. Genotypes had highly significant differences for biological yield. Kirshnawat and Sharma (1998) also reported similar results. Phenotypic correlation of biological yield with grains weight was highly significant and non significant with Harvest Index and yield hectare⁻¹ which are contrary to the results of Donmenz *et al*. (2001). Analysis of variance revealed non-significant differences among the genotypes for harvest index. Malik and Hussan (2001) also reported non-significant differences for harvest index in wheat lines. Phenotypic correlation of harvest index with grain yield hectare⁻¹ were highly significant and positive which are supported by the findings of Kumar *et al*. (1998). Highly significant differences were observed among the genotypes for grain yield hectare⁻¹. Possible reason for the highly significant differences among the genotypes could be due to dissimilar genetic background of the material. The results of grain yield are corroborating with the finding of Ahmad *et al*. (2001). The population of Takbeer x Inqilab exhibited maximum mean value for grain yield hectare⁻¹. Phenotypic correlation of grain yield hectare⁻¹ with grains spike⁻¹ and weight spike⁻¹ were highly significant and higher grain yield is a character of prime importance to the breeder as he is always keen to select the high yielding plants because it leads to enhance yield and thus accelerate the mission of achieving prosperity.

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