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Original Article

# Genetic diversity analysis in Pakistani commercial and landrace genotypes of bread wheat

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## Abstract

In this analysis, the genetic diversity in 50 (25 commercial and 25 landraces) bread wheat genotypes were examined for phenotype, with a goal of revealing correlations between yield and 12 other common agro-morphological characters. An experiment was conducted in a randomized complete block design with three replicates. The mean squares values from analysis of variance revealed highly significant differences for all 13 character among the tested genotypes, indicating that these materials can be evaluated in further experiments. Based on mean performance, the commercial wheat variety NIA-Sundar and landrace T-23 produced the maximum grain yield per plot when compared to the other genotypes, demonstrating the importance of these two genotypes in wheat breeding programs. High heritability estimates (h2) were detected for all character, signifying that the variation observed was mainly under genetic control and was less influenced by the environment. Hence, the improvement of this character can be made through direct phenotypic selection. The results also showed that spike length, grains spike$^{-1}$, grain weight spike$^{-1}$, tillers/m$^{2}$, seed index, and biological yield plot$^{-1}$ had positive and significant associations with grain yield plot$^{-1}$, demonstrating that genotypes having more of this character may be preferred in selection for generating high yielding bread wheat genotypes. Comparing the genetic variability between commercial and landraces of bread wheat through PCA, traditional wheat genotypes tended to possess more genetic variance in the first three components of PCA than its counterpart. That indicates that old wheat genotypes possess precious genetic resources; thus, these genetic resources should be cultivated in future breeding programs. Via cluster analysis, diverse parents have also been identified, signifying their importance for upcoming hybridization programs.

**Keywords**: Bread wheat, Genetic diversity, Commercial and Landraces Genotypes

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## Introduction

Bread wheat comprises the primary food in Pakistan and possesses a focal position in horticulture. Many foodstuffs, such as chapatis, bread, noodles, wafers, cakes, breakfast items, treat rolls, and various confectionaries are made from wheat (Laghari et al., 2012). Wheat is generally bred to succeed in a wide range of climatic conditions. To obtain high yield and potential resistance to the biotic and abiotic threats, numerous breeding programs have resulted in promising cultivars. Wheat has a unique position among grain crops, as grains retain protein with excellent biochemical and biophysical properties useful both in further processing and in preserving a high nutritive value (Ali et al., 2013). For continued improvement, the very best genotypes need to be identified and chosen for future development. An efficient hybridization program might be a sensible approach to doing just that. The accomplishment of such rearing projects mainly relies upon the appraisal of the principal characters and genetic stability of the current germplasm (Sanghera et al., 2014).

Assessing many different wheat genotypes is critical. Current popular cultivars with unmistakable agro-morphological and economic characteristics are accessible as rearing materials (Zalewski, 2001), as are old landraces. Wheat breeders are now aiming for varieties with improved yields as to adapt to the expanding population (Memon et al., 2007).

The success of a breeding program relies upon numerous factors. For example, breeders must identify key attributes, the degree of quality activity, hereditary frameworks controlling legacy varieties, and ecological variables that impact the outflow of genes (Rashidi, 2011). Such plants can be distinguished by a few strategies; for example, through morphological screening of qualities that improve nutritive value (Akcura, 2011). As per (Mollasadeghi et al., 2012), the number of spikes per plot area, plant height and grain number show more hereditary variety in germplasm studies.

Heritability refers to the proportion of phenotypes in a population that can be transmitted to progeny. Varieties found at a phenotypic level can either be attributed to hereditary or environmental factors. Heritable qualities can then be used to further develop improved crops (Degewione et al., 2013). In breeding programs, the legacy of the hereditary factors and expected genetic improvements are fundamental to choosing varieties that can succeed in various ecological conditions, which in turn allows for continued selection (Khan et al., 2008) An examination of heritability can reveal the hereditary and non-hereditary factors that generate phenotype (Memon et al., 2007). Correlation coefficients between character, notably yield and any other phenotypic characters, are also vital measures that can help plant breeders select the highest-yielding genotypes (Mohammadi and Prasanna, 2003). The present investigation examined 50 wheat varieties (25 commercial and 25 landraces) to ascertain which produced the most useful and heritable qualities, which in turn revealed which varieties can be used in future breeding programs. Additionally, the genetic variability of commercial and landraces were compared using multivariate statistical analyses.

## Material and Methods

Fifty genotypes including 25 commercial wheat varieties and 25 landraces were grown in the experimental area of the Nuclear Institute of Agriculture (NIA) Tandojam during the growing season of 2015-16. The experiment was carried out in a randomized complete block design (RCBD) with three replications. Four rows of each genotype with a row length of 2.5 meters and row to row distance of 30 cm was used. At maturity, ten plants per genotype per replication were randomly selected, and phenotypic assessment was done.

**Parameters to be recorded:**

**Days to 75% flowering:** It was counted in days from sowing to the emergence of 75% spikes from flag leaf.

**Days to 75% maturity:** Days to 75% maturity was taken when 75% of plants showed yellow peduncle, thus reached to 75% physiological maturity.

**Plant height(cm):** Plant height (excluding awns) was measured from soil surface to the tip of the spike at about half grain filling stage.

**Peduncle length(cm):** Peduncle length was measured in centimeters from the base of the spike to the first node of the stem.

**Spike length(cm):** Length of the spike of the main tiller was measured in centimeters from the base of the spike to the uppermost spikelets, excluding awns.

**Spikelet's spike$^{-1}$:** The quantities of spikelets in the essential tiller of each selected plant were counted and the information was recorded as no of spikelets spike$^{1}$.

**Grains spike$^{-1}$**: The total number of seeds of randomly selected spikes were counted and an average number of seeds per spike was recorded.

**Grain weight spike$^{-1}$:** Grain weight spike$^{-1}$ was taken by threshing each spike separately and weighed in grams with electric balance.

**Tillers/m$^2$:** The number of tillers in each selected plot per replication per genotype were counted at the time of crop harvest and was recorded as a number of tillers per meter square.

**Seed index (weight of 1000 grains in gram):** One thousand grains were randomly taken from each selected sample and weighed in grams on electric balance.

**Grain yield plot$^{-1}$ (g)**: After harvesting, each plot was threshed separately with single plant wheat thresher and clean seeds were obtained for laboratory studies. The grains were weighed on an electric balance and yield per plot/m$^2$ in grams was recorded.

**Biological yield plot$^{-1}$ (g):** After harvesting, each plot was weighed on an electric digital balance and weight of each plot/ m$^2$ was recorded in grams.

**Harvest index (%):** The harvest index (%) was determined as the ratio of the grain yield per plot/m$^2$ to the biological yield per plot/m$^2$.

$$\text{Harvest index (\%)} = \frac{\text{Grain yield per plot/m2}}{\text{Biological yield per plot/m2}} \times 100$$

**Statistical analysis:** The analysis of variance (ANOVA), mean comparisons, correlation, and principal components analysis (PCA) was derived through Statistix v. 8.1 computer software. Genetic distance and cluster analysis were obtained with the help of SPSS v. 17 computer software. Heritability analysis was carried out as suggested by Allard (1960).

## Results

### Analysis of variance

The ANOVA for all the characters is given in Table-1. The obtained results revealed that genotypes all differed significantly from each other (P <01) for all character studied.

### Mean performance

Mean values of the character measured in fifty genotypes are presented in Table-2 (a & b). Considering Daysto75%flowering, landrace T-4 had the maximum number of days to heading (106.76), while SKD-1 exhibited the minimum number (59.67). While landrace T-2 took the longest time to mature (135.33 days), TD-1 took the shortest time (121.00 days). For plant height, T-21 produced the tallest plants (144.73 cm), while TD-1 produced the shortest (76.60 cm). Peduncles were longest in T-21 (54.47 cm) and shortest in T-3 (30.47 cm). The genotype Bhittai grew the most extended spike (14.97 cm), while genotype T-7 produced the shortest (5.53 cm).

**Table 1. Mean square values from ANOVA for thirteen quantitative characters in wheat genotypes**

| Character | Replications D.F.= 2 | Genotypes D.F. = 49 | Error D.F. = 98 |
|---|---|---|---|
| **Days to 75% flowering** | 162.85 | 390.23** | 1.29 |
| **Days to 75% maturity** | 2.67 | 37.04** | 0.88 |
| **Plant height** | 7.43 | 825.15** | 13.55 |
| **Peduncle length** | 0.39 | 105.48** | 4.49 |
| **Spike length** | 0.40 | 14.88** | 0.21 |
| **Spikelets spike$^{-1}$** | 0.49 | 16.22** | 0.72 |
| **Grains spike$^{-1}$** | 1.79 | 316.14** | 15.09 |
| **Grain weight spike$^{-1}$** | 0.008 | 0.922** | 0.009 |
| **Tillers/m$^2$** | 1.00 | 126718** | 4413 |
| **Seed index** | 3.34 | 137.79** | 1.23 |
| **Grain yield plot$^{-1}$** | 12400.30 | 48343.70** | 5299.90 |
| **Biological yield plot$^{-1}$** | 85475 | 224699.00** | 42366.00 |
| **Harvest index** | 26.93 | 81.51** | 16.58 |

** = Significant at the 1% probability level.

**Table 2a. Mean performance of wheat genotypes for daysto75%flowering, daysto75%maturity, plant height (cm), peduncle length(cm), spike length(cm) and spikelets spike-$^{1}$**

| Genotype | Daysto75%flowering | Daysto75%maturity | Plant height(cm) | Peduncle length(cm) | Spike length (cm) | Spikelets spike$^{-1}$ |
|---|---|---|---|---|---|---|
| T-1 | 106.00 | 134.00 | 124.13 | 47.60 | 9.43 | 25.27 |
| T-2 | 105.33 | 135.33 | 130.13 | 51.40 | 9.83 | 26.67 |
| T-3 | 90.33 | 128.33 | 102.93 | 30.47 | 5.63 | 20.60 |
| T-4 | 106.67 | 134.33 | 140.33 | 51.73 | 8.90 | 23.40 |
| T-5 | 92.00 | 126.67 | 117.93 | 42.93 | 5.73 | 20.13 |
| T-6 | 91.67 | 124.33 | 120.93 | 43.53 | 5.57 | 18.87 |
| T-7 | 91.33 | 126.67 | 122.00 | 42.27 | 5.53 | 18.53 |
| T-8 | 90.00 | 127.67 | 125.40 | 36.53 | 9.53 | 19.87 |
| T-9 | 92.67 | 129.33 | 125.13 | 33.33 | 9.23 | 20.20 |
| T-10 | 89.00 | 127.33 | 129.53 | 45.00 | 10.03 | 18.80 |
| T-11 | 85.33 | 124.33 | 128.33 | 52.27 | 9.27 | 18.53 |
| T-12 | 87.33 | 125.00 | 129.40 | 43.27 | 9.37 | 18.33 |
| T-13 | 86.00 | 126.67 | 128.27 | 42.13 | 10.57 | 20.13 |
| T-14 | 94.33 | 128.67 | 127.00 | 34.53 | 9.67 | 23.00 |
| T-15 | 96.67 | 130.33 | 126.07 | 33.67 | 10.58 | 20.93 |
| T-16 | 92.33 | 128.00 | 128.13 | 44.00 | 12.00 | 24.73 |
| T-17 | 89.00 | 129.67 | 137.00 | 49.73 | 9.53 | 20.20 |
| T-18 | 95.00 | 129.00 | 128.80 | 47.20 | 10.40 | 21.47 |
| T-19 | 86.67 | 127.33 | 134.80 | 46.73 | 9.97 | 21.73 |
| T-20 | 89.00 | 126.33 | 125.07 | 43.47 | 10.10 | 20.60 |
| T-21 | 80.67 | 124.67 | 144.73 | 54.47 | 10.60 | 21.33 |
| T-22 | 80.67 | 125.67 | 124.27 | 49.87 | 9.83 | 19.60 |
| T-23 | 83.00 | 126.67 | 120.07 | 53.67 | 9.77 | 18.60 |
| T-24 | 85.67 | 128.00 | 127.73 | 46.20 | 8.77 | 20.33 |
| T-25 | 87.00 | 126.33 | 127.00 | 44.27 | 8.87 | 21.40 |
| Kiran-95 | 72.00 | 125.33 | 99.27 | 49.40 | 13.23 | 19.67 |
| Marvi-2000 | 68.00 | 121.33 | 89.13 | 47.47 | 13.77 | 21.20 |
| Bhittai | 90.67 | 124.00 | 111.07 | 40.53 | 14.97 | 28.60 |
| Sassui | 88.33 | 123.00 | 102.87 | 39.80 | 14.87 | 23.60 |
| Khirman | 70.33 | 125.33 | 103.53 | 46.87 | 12.13 | 22.40 |
| NIA-Sunder | 62.67 | 121.22 | 104.00 | 48.47 | 10.93 | 17.60 |
| Sarsabz | 70.67 | 122.67 | 104.47 | 44.53 | 13.60 | 21.93 |
| Soghat-90 | 81.00 | 123.67 | 104.40 | 44.40 | 11.50 | 21.73 |
| TD-1 | 63.00 | 121.00 | 76.60 | 33.13 | 11.10 | 17.07 |
| Imdad-05 | 72.00 | 124.00 | 99.20 | 40.60 | 12.17 | 21.00 |
| NIA-Sarang | 70.00 | 122.67 | 99.10 | 39.88 | 11.13 | 21.18 |
| TJ-83 | 74.67 | 120.67 | 94.73 | 42.00 | 13.17 | 20.60 |
| Inqilab-91 | 68.00 | 121.33 | 90.48 | 41.67 | 12.82 | 19.53 |
| Bakhar-2000 | 66.67 | 122.67 | 86.93 | 40.53 | 11.83 | 16.80 |
| Aas-2011 | 69.67 | 123.33 | 100.47 | 40.67 | 13.87 | 23.07 |
| NARC-2011 | 90.00 | 119.67 | 102.87 | 36.07 | 12.03 | 21.67 |
| NIA-Amber | 88.00 | 124.67 | 97.07 | 35.47 | 11.50 | 22.20 |
| Benazir | 73.33 | 125.67 | 101.00 | 34.20 | 11.57 | 19.87 |
| Zardana | 87.67 | 123.33 | 94.87 | 36.33 | 13.63 | 22.80 |
| NIA-Sunheri | 83.00 | 122.00 | 98.93 | 41.67 | 11.07 | 21.73 |
| Hamal | 86.33 | 122.67 | 100.60 | 35.07 | 11.53 | 22.33 |
| SKD-1 | 59.67 | 121.67 | 84.67 | 38.40 | 11.07 | 18.27 |
| Johar-78 | 78.33 | 123.33 | 107.53 | 46.33 | 13.40 | 22.07 |
| NIFA-Barsat | 85.33 | 125.33 | 102.20 | 36.67 | 13.10 | 23.07 |
| Seher-2006 | 66.67 | 121.33 | 92.80 | 38.37 | 10.63 | 19.27 |
| LSD (5%) | 1.84 | 1.52 | 5.96 | 3.43 | 0.74 | 1.37 |

Table 2b. Mean performance of wheat genotypes for grains spike$^{-1}$, grain weight spike$^{-1}$, Tillers/m$^{2}$, seed index (g), biological yield plot$^{-1}$ (g), grain yield plot$^{-1}$ (g) and harvest index (%)

| Genotype | Grainsspike$^{-1}$ | Grainweightspike$^{-1}$ | Tillers/m$^{2}$ | Seedindex (1000-grain weight,g) | Biological yield plot$^{-1}$ (g) | Grain yield plot$^{-1}$(g) | Harvest index (%) |
|---|---|---|---|---|---|---|---|
| T-1 | 50.67 | 2.47 | 437.91 | 44.92 | 822.80 | 236.50 | 28.82 |
| T-2 | 58.07 | 2.82 | 548.28 | 42.52 | 649.00 | 271.70 | 41.90 |
| T-3 | 46.87 | 1.48 | 858.70 | 27.97 | 809.60 | 288.20 | 35.37 |
| T-4 | 55.13 | 2.71 | 659.13 | 44.62 | 1067.00 | 291.50 | 27.23 |
| T-5 | 38.33 | 1.33 | 916.09 | 32.75 | 1298.00 | 312.40 | 24.15 |
| T-6 | 44.87 | 1.52 | 1243.45 | 30.57 | 764.50 | 278.30 | 36.54 |
| T-7 | 42.80 | 1.62 | 1014.36 | 28.10 | 1127.50 | 305.80 | 27.34 |
| T-8 | 40.93 | 1.67 | 1119.33 | 33.18 | 1103.30 | 294.80 | 26.81 |
| T-9 | 39.33 | 1.62 | 878.37 | 32.30 | 1023.00 | 355.30 | 35.09 |
| T-10 | 42.80 | 1.74 | 1154.10 | 34.05 | 1173.70 | 336.60 | 28.66 |
| T-11 | 49.47 | 1.99 | 997.27 | 38.80 | 1008.70 | 312.40 | 31.03 |
| T-12 | 44.60 | 1.57 | 624.81 | 33.93 | 1027.40 | 354.20 | 34.54 |
| T-13 | 48.73 | 1.51 | 883.13 | 30.57 | 1206.70 | 401.50 | 33.03 |
| T-14 | 44.20 | 1.42 | 874.36 | 26.47 | 1021.90 | 321.20 | 31.55 |
| T-15 | 51.07 | 1.70 | 1244.80 | 28.63 | 1389.30 | 288.20 | 20.99 |
| T-16 | 40.93 | 1.99 | 848.61 | 40.02 | 1364.00 | 372.90 | 27.56 |
| T-17 | 51.73 | 1.55 | 964.10 | 25.25 | 1226.50 | 322.30 | 26.48 |
| T-18 | 45.07 | 1.53 | 1297.56 | 26.67 | 1280.40 | 324.50 | 25.45 |
| T-19 | 54.67 | 1.69 | 650.93 | 27.83 | 1026.30 | 313.50 | 30.65 |
| T-20 | 37.27 | 1.69 | 771.91 | 37.03 | 1097.80 | 312.40 | 28.38 |
| T-21 | 46.33 | 1.34 | 1222.30 | 22.80 | 1402.50 | 407.00 | 29.02 |
| T-22 | 44.07 | 1.22 | 1157.07 | 23.95 | 1474.00 | 412.50 | 28.07 |
| T-23 | 39.33 | 1.91 | 774.68 | 27.63 | 1503.70 | 514.80 | 34.68 |
| T-24 | 47.33 | 1.47 | 1203.60 | 23.05 | 1279.30 | 364.10 | 28.84 |
| T-25 | 47.60 | 1.65 | 1101.14 | 30.52 | 1006.50 | 298.10 | 30.09 |
| Kiran-95 | 65.67 | 2.58 | 782.07 | 38.92 | 1515.80 | 535.70 | 35.72 |
| Marvi-2000 | 64.00 | 2.83 | 600.33 | 43.45 | 1258.40 | 465.30 | 36.89 |
| Bhittai | 83.93 | 3.52 | 685.51 | 39.58 | 1718.20 | 504.90 | 29.85 |
| Sassui | 65.20 | 2.66 | 632.44 | 39.28 | 1540.00 | 504.90 | 33.05 |
| Khirman | 67.20 | 2.67 | 663.76 | 39.02 | 1637.90 | 535.70 | 32.97 |
| NIA-Sunder | 51.27 | 2.21 | 568.36 | 39.25 | 1537.80 | 642.40 | 42.00 |
| Sarsabz | 65.73 | 2.76 | 645.16 | 37.53 | 1835.90 | 628.10 | 34.08 |
| Soghat-90 | 59.00 | 1.93 | 768.25 | 35.08 | 1509.20 | 545.60 | 36.07 |
| TD-1 | 51.53 | 2.48 | 975.93 | 37.52 | 1389.30 | 563.20 | 40.63 |
| Imdad-05 | 59.20 | 2.96 | 772.83 | 52.30 | 1466.30 | 534.60 | 36.56 |
| NIA-Sarang | 63.18 | 2.53 | 542.81 | 42.22 | 1458.60 | 524.70 | 36.05 |
| TJ-83 | 66.13 | 2.63 | 939.96 | 30.58 | 1582.90 | 592.90 | 37.83 |
| Inqilab-91 | 63.52 | 2.45 | 1013.32 | 37.12 | 1655.50 | 550.00 | 33.18 |
| Bakhar-2000 | 53.87 | 2.00 | 849.44 | 37.32 | 1463.00 | 486.20 | 34.23 |
| Aas-2011 | 73.00 | 3.35 | 714.43 | 42.98 | 1467.40 | 542.30 | 37.09 |
| NARC-2011 | 58.20 | 2.36 | 814.86 | 36.70 | 1426.70 | 437.80 | 30.75 |
| NIA-Amber | 55.73 | 1.60 | 829.21 | 33.70 | 1397.00 | 553.30 | 40.00 |
| Benazir | 54.93 | 2.15 | 810.00 | 40.57 | 1480.60 | 565.40 | 38.03 |
| Zardana | 61.07 | 2.37 | 894.95 | 39.95 | 1466.30 | 614.90 | 42.69 |
| NIA-Sunheri | 47.73 | 1.77 | 766.65 | 41.03 | 1465.20 | 603.90 | 41.00 |
| Hamal | 68.73 | 2.09 | 873.69 | 30.50 | 1602.70 | 621.50 | 39.17 |
| SKD-1 | 45.87 | 1.86 | 843.75 | 37.52 | 1493.80 | 621.50 | 41.58 |
| Johar-78 | 56.07 | 2.22 | 723.30 | 43.07 | 1780.90 | 588.50 | 32.86 |
| NIFA-Barsat | 66.00 | 2.79 | 799.90 | 40.32 | 1722.60 | 632.50 | 36.58 |
| Seher-2006 | 53.07 | 2.37 | 897.78 | 48.02 | 1415.70 | 547.80 | 38.86 |
| LSD (5%) | 6.29 | 0.15 | 107.63 | 1.798 | 333.51 | 117.96 | 6.598 |

Bhittaialso set the highest number of spikelets spike$^{-1}$ (28.60), while Bakhar-2000 set the lowest number of spikelets spike$^{-1}$ (16.80). For the character grains spike$^{-1}$, the Bhittai set maximum (83.93), whereas accession T-20 set the minimum (37.27). Considering grain weight spike$^{-1}$, the genotype Bhittai weighed the most (3.52 g), whereas NIA-Sunder weighed the least (1.22 g). Accession T-18 produced the maximum number of tillers/m$^2$ (1297.56), whereas accession T-1 produced the fewest (437.91). The maximum seed index (52.30 g) was reported for Imdad-05, and the minimum seed index was observed in T-21 (22.80). Considering grain yield plot$^{-1}$, NIA-Sunder demonstrated the maximum (642.40 g), while genotype T-1produced the minimum (236.50 g). Sarsabz produced the maximum biological yield plot$^{-1}$ (1835.90 g), whereas genotype T-2 produced the minimum (649.00 g). Finally, regarding the harvest index, the NIA-Sunder had the highest percentage (42.00 %), whereas T-15 had the lowest (20.99 %).

**Broad-sense heritability estimates:** The broad-sense heritability estimates (h$^2$), genetic variance ($\delta^2$ g) and phenotypic variance ($\delta^2$ p) from variance components for various character studied are depicted in Table-3. Genetic variance ($\delta^2$g ) for all 13 characters studied were lower than phenotypic variance ($\delta^2$p), resulting in high heritability estimates (h$^2$) ranging from (Harvest index =79.85% to Grain weight spike$^{-1}$= 99.94%). All phenotypes were correspondingly less influenced by the environment than genetic.

**Correlation analyses between each pair of characters:** Correlation coefficients between each pair of characters is shown in Table 4. Specifically, the correlation coefficients between yield and the other 12 characters are described below.

**Days to heading v/s grain yield plot$^{-1}$:** The correlation between days to heading and grain yield plot$^{-1}$ was negatively and highly significant (r= -0.65**). That shows an increase in days to headings associated with a significant decrease in grain yield plot$^{-1}$.

**Days to maturity v/s grain yield plot$^{-1}$:** The association between days to maturity and grain yield plot$^{-1}$ was negative and highly significant (r= -0.65**). This relationship also indicates that as days to maturity increases, the yield decreases to a great extent.

**Plant height v/s grain yield plot$^{-1}$:** The association between plant height and grain yield plot$^{-1}$ was negative and highly significant (r= -0.69**). This interrelationship reveals that taller plants have considerably reduced yields.

**Table 3. Broad-sense heritability estimates for 13 quantitative character of landraces and commercial bread wheat genotypes**

| Characters | Genotypic variance ($\delta^2$g) | Phenotypic variance ($\delta^2$p) | Heritability % (Broad sense) |
|---|---|---|---|
| **Days to 75% flowering** | 2.39 | 2.40 | 99.58 |
| **Days to 75% maturity** | 13.54 | 13.87 | 97.62 |
| **Plant height** | 109.23 | 111.06 | 98.35 |
| **Peduncle length** | 258.95 | 270.46 | 95.74 |
| **Spike length** | 36.68 | 37.20 | 98.60 |
| **Spikelet's spike$^{-1}$** | 31.63 | 33.10 | 95.55 |
| **Grains spike$^{-1}$** | 168.18 | 176.61 | 95.23 |
| **Grain weight spike$^{-1}$** | 4401.68 | 4404.27 | 99.94 |
| **Tillers/m$^2$** | 122305.00 | 126718.00 | 96.51 |
| **Seed index** | 40.89 | 41.25 | 98.13 |
| **Biological yield plot$^{-1}$** | 2.13 | 2.63 | 80.99 |
| **Grain yield plot$^{-1}$** | 3.47 | 3.90 | 88.97 |
| **Harvest index** | 2.41 | 3.03 | 79.85 |

**Peduncle length v/s grain yield plot$^{-1}$:** The correlation result showed negative and significant association (r= -0.17*) between peduncle length and grain yield plot$^{-1}$, indicating that as peduncle length increases, yield decreases significantly.

**Spike length v/s grain yield plot$^{-1}$:** The association between spike length and grain yield plot$^{-1}$ was positively and highly significant (r= 0.64**), revealing that plants with longer spikes will have a substantial improvement in grain yield.

**Spikelets spike$^{-1}$ v/s grain yield plot$^{-1}$:** The spikelets spike$^{-1}$ and grain yield plot$^{-1}$ revealed a positive but non-significant correlation with each other (r= 0.06$^{ns}$), reflecting that an increase in spikelets spike$^{-1}$ will not be associated with a significant increase in grain yield.

**Grains spike$^{-1}$ v/s grain yield plot$^{-1}$:** The result about the interrelationship between grains spike$^{-1}$ and grain yield plot$^{-1}$ indicated a positive and highly significant correlation (r= 0.49**); this suggests that with an increase in the grains spike$^{-1}$, the grain yield plot$^{-1}$ will also increase substantially.

**Grain weight spike$^{-1}$ v/s grain yield plot$^{-1}$:** The data revealed that grain weight spike$^{-1}$ and grain yield plot$^{-1}$ are positively and profoundly significantly correlated with each other (r= 0.48**), indicating that improvements in grain weight spike$^{-1}$are associated with simultaneous improvements in grain yield plot$^{-1}$.

**Tillers/m$^2$ v/s grain yield plot$^{-1}$:** Table-4 indicates the interrelationship between tillers/m$^2$ and grain yield plot$^{-1}$, which was negative and highly significant (r= 0.27**), showing that as tillers/m$^2$ increases, the grain yield also increases significantly.

**Seed index v/s grain yield plot$^{-1}$:** The correlation results indicate a significant and positive correlation between seed index and grain yield plot-$^{1}$ (r= 0.34**); this association shows that as seed index increases, the grain yield also increases considerably.

**Biological yield plot$^{-1}$(g) v/s grain yield plot$^{-1}$:** The data revealed that biological yield plot$^{-1}$are positively and highly significantly correlated with each other (r= 0.81**), representing that an increase in biological yield plot$^{-1}$ indicates an increase in grain yield plot$^{-1}$.

**Grain yield plot$^{-1}$ v/s harvest index:** The harvested index is positively and highly significantly correlated with grain yield plot$^{-1}$ (r= 0.61**), indicating that increase in harvest index is related to significant improvements in grain yield.

**Principal components analysis**

PCAs were carried out by correlation for all studied character. The contribution of the first three principal component axes ("components") for commercial cultivars was61.5%, for landraces was72.0%, and for both landraces and commercial cultivars was72.2% (Table 5). Regarding landraces genotypes, the first component was highly correlated with the number of days to 75% flowering, spikelets spike-$^{1}$, grains spike-$^{1}$ and grain weight spike-$^{1}$; the second component with spike length and seed index; and the third component with biological yield plot$^{-1}$. Considering the commercial cultivars, the landrace coefficients of the first components associated with peduncle length, grain yield plot$^{-1,}$ and biological yield plot$^{-1}$; the second component with plant height, spike length and grains spike$^{-1}$; and the third component with biological yield plot$^{-1}$. Consider combined PCAs of commercial and landraces genotypes the first component was correlated with grain yield plot$^{-1}$ and biological yield plot$^{-1}$; the second component with plant height, peduncle length and spikelets spike$^{-1}$; and third component with peduncle length and harvest index.

A dendrogram was obtained from a cluster analysis of all 50 genotypes by 13 characters (Fig. 1). Wheat genotypes grouped into two major clusters, group one and group two. Group one (Fig. 1) possessed all commercial cultivars, except two landraces (T-23 and T-26), whereas group two consisted of all landraces.

Furthermore, group one further partitioned into five sub-cluster one comprised six commercial cultivars: Kiran-95, Soghat-90, T-23, Imdad-05, NIA-Sunheri, and Aas-2011. Sub-cluster two consisted of six bread wheat genotypes: NIA-Amber, Benazir, SKD-1, Bhakar-2000, NARC-2011, and T-16. The third sub-cluster also was composed of six commercial wheat genotypes: TJ-83, Hamal, Zardana, Sehar-2006, TD-1 and Inqilab-91, while the fourth sub-cluster possessed only three commercial wheat genotypes: NIA-Sundar, NIA-Sarang, and Marvi-2000. The last sub-cluster of group one (fifth sub-cluster) possessed six commercial cultivars: Johar-78, NIFA-Barsat, Bhittai, Khiram, Sassui, and Sarsabz.

Group two, composed of all landrace genotypes and is further divided into four sub-clusters. The first sub-cluster had seven landraces: T-5, T-17, T-13, T-9, T-14, T-3 and T-20, while second sub-cluster comprised five landrace genotypes: T-4, T-19, T-12, T-1 and T-2. The third sub-cluster was composed of six landrace genotypes: T-15, T-21, T-18, T-10, T-24 and T-22, whereas the last sub-cluster (fourth sub-cluster) contained only five landrace genotypes: T-8, T-25, T-7, T-11, and T-6.

## Discussion

Introduction, evaluation, and identification of potentially useful germplasm is the first and foremost step in a crop improvement program. The high yielding genotypes with good adaptation and agronomically desirable attributes could be directly utilized for general cultivation. However, an effective and massive hybridization program would be a viable approach and for such hybridization program to be successful, the characterization and variability pattern of the available germplasm holds a promise. To sustain the high productivity level of wheat, genetic variability existing in nature or created through crop breeding is of immense value. Genetic uniformity within a crop is readily brought about by using the same gene or gene complexes during breeding programs. When uniformity becomes the cause of genetic vulnerability, genetic diversity is the only insurance against it. To overcome the menace of this uniformity, it is essential that genetic variability, present in both the cultivated and wild species, is systematically exploited and used to generate new gene complexes for higher grain yield and tolerance to biotic and abiotic stresses. The effectiveness of selection depends upon the range of genetic variability already existing in the population in respect of important economic characters. The progress of breeding is conditioned, primarily by the magnitude, nature and inters relationship of genetic variation for various plant characters in such a population (Sanghera et al., 2014).

**Table 4. Correlation coefficients for each pair of characters examined in wheat genotypes**

| **Character** | **Days to 75% maturity** | **Plant height** | **Peduncle length** | **Spike length** | **Spikelets spike$^{-1}$** | **Grains spike$^{-1}$** | **Grain weight spike$^{-1}$** | **Tillers/m$^2$** | **Seed index** | **Biological yield plot$^{-1}$** | **Grain yield plot$^{-1}$** | **Harvest index(%)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to75%flowering | 0.75$^{**}$ | 0.70$^{**}$ | 0.07$^{ns}$ | -0.43$^{**}$ | 0.47$^{**}$ | -0.29$^{**}$ | -0.33$^{**}$ | 0.11$^{ns}$ | -0.26$^{**}$ | -0.51$^{**}$ | -0.65$^{**}$ | -0.42$^{**}$ |
| Daysto75%maturity | - | 0.69$^{**}$ | 0.23$^{**}$ | -0.45$^{**}$ | 0.33$^{**}$ | -0.33$^{**}$ | -0.28$^{**}$ | 0.03$^{ns}$ | -0.18$^{*}$ | -0.53$^{**}$ | -0.65$^{**}$ | -0.38$^{**}$ |
| Plant height | | - | 0.46$^{**}$ | -0.49$^{**}$ | 0.18$^{*}$ | -0.46$^{**}$ | -0.54$^{**}$ | 0.27$^{**}$ | -0.47$^{**}$ | -0.46$^{**}$ | -0.69$^{**}$ | -0.56$^{**}$ |
| Peduncle length | | | - | -0.07$^{ns}$ | 0.01$^{ns}$ | -0.08$^{ns}$ | 0.08$^{ns}$ | 0.07$^{ns}$ | -0.06$^{ns}$ | -0.07$^{ns}$ | -0.17$^{*}$ | -0.19$^{*}$ |
| Spike length | | | | - | 0.35$^{**}$ | 0.72 $^{**}$ | 0.73$^{**}$ | 0.34$^{**}$ | 0.46$^{**}$ | 0.62$^{**}$ | 0.64$^{**}$ | 0.28$^{**}$ |
| Spikelets spike$^{-1}$ | | | | | - | 0.46$^{**}$ | 0.39$^{**}$ | -0.35$^{**}$ | 0.26$^{**}$ | 0.02$^{ns}$ | 0.06$^{ns}$ | -0.08$^{ns}$ |
| Grains spike$^{-1}$ | | | | | | - | 0.81$^{**}$ | -0.39$^{**}$ | 0.41$^{**}$ | 0.44$^{**}$ | 0.49$^{**}$ | 0.28$^{**}$ |
| Grain weight pike$^{-1}$ | | | | | | | - | -0.52$^{**}$ | 0.67$^{**}$ | 0.39$^{**}$ | 0.48$^{**}$ | 0.33$^{**}$ |
| Tillers/m$^2$ | | | | | | | | - | -0.60$^{**}$ | -0.08$^{ns}$ | 0.27$^{**}$ | 0.35$^{**}$ |
| Seed index | | | | | | | | | - | 0.18$^{*}$ | 0.34$^{**}$ | 0.34$^{**}$ |
| Biological yield | | | | | | | | | | - | 0.81$^{**}$ | 0.04$^{ns}$ |
| Grain yield plot$^{-1}$ | | | | | | | | | | | - | 0.61$^{**}$ |

**Table 5. A character with their contribution to the first three principal components of commercial, landraces and all genotypes**

| **Variables** | **Commercial wheat genotypes** | | | **Landraces wheat genotypes** | | | **Commercial and landrace wheat genotypes** | | |
|---|---|---|---|---|---|---|---|---|---|
| | **PC1** | **PC2** | **PC3** | **PC1** | **PC2** | **PC3** | **PC1** | **PC2** | **PC3** |
| **Days to 75% flowering** | 0.310 | -0.403 | 0.157 | -0.384 | -0.097 | 0.258 | -0.384 | -0.097 | 0.258 |
| **Days to 75% maturity** | 0.218 | -0.068 | -0.209 | -0.370 | 0.054 | 0.210 | -0.370 | 0.054 | 0.210 |
| **Plant height** | 0.389 | 0.004 | -0.252 | -0.071 | 0.495 | 0.063 | -0.071 | 0.495 | 0.062 |
| **Peduncle length** | -0.223 | -0.439 | -0.223 | 0.295 | 0.017 | 0.355 | 0.295 | 0.017 | 0.355 |
| **Spike length** | -0.132 | 0.489 | -0.301 | -0.053 | 0.430 | -0.302 | -0.053 | 0.430 | -0.302 |
| **Spikelets spike$^{-1}$** | 0.359 | 0.024 | 0.150 | -0.045 | 0.487 | 0.029 | -0.045 | 0.487 | 0.028 |
| **Grains spike$^{-1}$** | 0.418 | -0.171 | 0.056 | -0.348 | 0.133 | 0.114 | -0.347 | 0.133 | 0.133 |
| **Grain weight spike$^{-1}$** | 0.388 | -0.048 | 0.161 | -0.274 | 0.149 | 0.012 | -0.274 | 0.149 | 0.012 |
| **Tillers/m$^2$** | 0.045 | -0.015 | 0.194 | -0.375 | 0.158 | -0.09 | -0.575 | 0.158 | -0.094 |
| **Seed index** | 0.011 | 0.442 | -0.053 | -0.347 | -0.009 | -0.084 | -0.347 | -0.009 | -0.084 |
| **Grain yield plot$^{-1}$** | 0.274 | -0.176 | -0.371 | 0.264 | 0.300 | -0.359 | 0.264 | 0.300 | -0.359 |
| **Biological yield plot$^{-1}$** | 0.095 | 0.329 | 0.639 | 0.264 | 0.300 | -0.359 | 0.280 | 0.362 | 0.212 |
| **Harvest index** | -0.332 | -0.18 | 0.298 | -0.112 | -0.177 | 0.680 | -0.112 | -0.177 | 0.454 |
| **Percent of variance** | 34.0 | 14.7 | 12.8 | 40.3 | 20.2 | 11.5 | 43.9 | 18.2 | 10.0 |
| **Cumulative percent of variance** | 34.00 | 48.71 | 61.50 | 40.30 | 60.50 | 72.00 | 43.90 | 62.20 | 72.20 |

The analysis of variance revealed that all the varieties performed significantly different ($P \leq 0.01$) for days to 75% flowering, days to 75% maturity, plant height, peduncle length, spike length, spikelets spike$^{-1}$, grains spike$^{-1}$, grain weight spike$^{-1}$, tillers/m$^2$, seed index, biological yield plot$^{-1}$, grain yield plot$^{-1}$ and harvest index, suggesting that studied materials possess useful genetic resources for a variety of traits thus can extensively be used for upcoming breeding programs. Almost similar results have also been reported by Baloch et al. (2014a). These researchers also found a significant genetic variance for the number of quantitative traits in their studies.

Mean values of the traits measured in fifty genotypes are presented in Table-2 (a & b). Considering days to heading, the maximum days to heading were taken by landrace T-4, while minimum days to heading were taken by SKD-1. While maximum days to maturity were taken by landrace T-2 and TD-1 took minimum days to maturity; consequently, this genotype may be preferred for breeding early maturing genotype in wheat breeding programs. While for the trait of plant height, the T-21 produced the tallest plants, whereas TD-1 was the shortest genotype, it is well-established fact that dwarf wheat verities are the choice breeding materials in turn to achieve maximum grain yield, thus TD-1 may be used for breeding the dwarf stature wheat genotype. The peduncle length was maximum and minimum in T-21 and T-23, respectively; studies have confirmed that longer peduncle retains green part of the plants for a longer time, as a resultant, more photosynthesis takes place which is benefitted for plants. Spike length character is more important because the larger spike is considered to produce more grain higher yield. Consider the spike length; the genotype Bhittai grew the longest spike, this genotype may be referred to in a future breeding program. Spikelets Spike$^{-1}$ is also an important trait in wheat, as more number of the spikelets spike$^{-1}$, consequently higher grain yield plant$^{-1}$. With regards to spikelets spike$^{-1}$, the Bhittai set a maximum number of spikelets spike$^{-1}$ and also produced maximum grains spike$^{-1}$; however, the minimum grains spike$^{-1}$ were produced by the accession T-20. Considering the grain weight spike$^{-1}$, the genotype Bhittai weighted maximum and minimum was weighted in NIA-Sunder. The T-18 produced maximum tillers/m$^2$, whereas the accession T-1 produced a minimum number of tillers/m$^2$. The maximum seed index was reported in Imdad-05 and minimum seed index was observed in T-21. Considering the grain yield plot$^1$, the NIA-Sunder demonstrated maximum grain yield plot$^{-1}$. While minimum grain yields plot$^{-1}$ was produced by genotype T-1. The Sarsabz produced maximum biological yield plot$^{-1}$, and minimum biological yield plot$^{-1}$ was found in genotype T-2. Taking the harvest index, the NIA-Sunder produced maximum harvest index, whereas the genotype T-15 produced minimum harvest index. All in all, SKD-1, TD-1, T-21, Bhittai, T-18, Imdad-05, NIA-Sundar, and Sarsabz showed promising performance for different quantitative traits, indicating that these genotypes possess potential genetic resources, hence may be utilized in upcoming breeding programs.

Heritability estimates are helpful in deciding the characters to be considered while making a selection. High heritability estimates (h2 b.s.) were observed for days to 75% flowering, days to 75% maturity, plant height, peduncle length, spike length, spikelets spike$^{-1}$, grains spike$^{-1}$, grain weight spike$^{-1}$, tillers/m$^{2}$, seed index, biological yield plot$^{-1}$, grain yield plot$^{-1}$, and harvest index. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment, indicating the influence of additive gene action for these traits. Hence, the improvement of these traits can be made through direct phenotypic selection. These findings are in accordance with previous reports of Khodadadi et al. (2011) and Baloch et al. (2014a).

The correlation coefficient is an important statistical technique which can assist wheat breeder in selection crop plants for higher yields. The present study showed that various yield-related traits established positive and significant ($P<0.05$) correlation with grain yield plot$^{-1}$. The characters spike length, grains spike$^{-1}$, grain weight spike$^{-1}$, tillers/m$^{2}$, seed index, and biological yield plot$^{-1}$ made positive and significant ($P<0.05$) associations with grain yield plot$^{-1}$. This indicates that an intensive selection of above-mentioned traits will significantly enhance grain yield in bread wheat genotypes, therefore, a thorough selection of these yield-related traits may be preferred in any breeding program. (Fellahi et al. 2013) who calculated the genotypic and phenotypic correlations in 29 bread wheat cultivars and concluded spike length and number of tillers plant-1 exhibited positive and were highly and significantly correlated with grain yield. Al-Tabbal and (Al-Fraihat, 2012) determined inter-relationship in 29 promising wheat genotypes and reported that grain yield plant-1 showed highly significant positive genetic and phenotypic correlation with seed index, number of kernels per main spike and number of spikelets per the main spike. Baloch et al. (2014b) also studied 20 advance bread wheat genotypes and reported that traits like ear head length, spikelets spike$^{-1}$, grains spike$^{-1}$, seed index, and harvest index established positive and significant correlations with grain yield plant$^{-1}$. Nevertheless, significant negative relations were noted between days to 75% heading and grain yield plot$^{-1}$, days to 75% maturity and grain yield plot$^{-1}$ and between plant height and grain yield plot$^{-1}$. It is interesting to note that a thorough selection for earlier, taller and high yielder varieties is somewhat a tedious task in wheat breeding.

The preservation and utilization of genetic resources could be made by partitioning the total variance into its components. It also provides a chance for the exploitation of suitable germplasm in crop improvement for particular plant traits (Pecetti et al., 1996). PCA is an influential tool to obtain parental lines for successful breeding programs (Nazir et al., 2013). In the current study, principal component analysis (PCA) was carried out on the basis of correlation for various quantitative traits in bread wheat genotypes. The contribution of the first three components for commercial cultivars were 61.5%, for landraces were 72.0% and the contribution of the first three components for both landraces and commercial cultivars was 72.2%. As landraces genotype is concerned, in the first PCA grains spike-1 contributed more to variations followed by plant height, grain weight spike$^{-1}$, spikelets spike$^{-1}$, days to heading, grain yield plot$^{-1}$ and days to maturity, while little contribution to the variation was achieved from biological yield plot$^{-1}$, seed index and tillers/m$^{-2}$, indicating the importance of these traits to the total variation. While, only two characters, including spikelets spike$^{-1}$ and biological yield plot$^{-1}$, contributed more towards the variation across the first three components in landraces wheat genotypes. Considering the commercial cultivars, the coefficients of first PCA were associated with peduncle length, grain yield plot$^{-1,}$ and biological yield plot$^{-1}$; second PCA with plant height and spike length and grains spike$^{-1}$, while biological yield plot$^{-1}$ was correlated with third PCA; these characters contributed substantially towards genetic divergence in commercial varieties. Considering combined PCAs of commercial and landraces genotypes, the first PCA was correlated with grain yield plot$^{-1}$ and biological yield plot$^{-1}$; the second PCA correlated with plant height, peduncle length and spikelets spike$^{-1}$ and third PCA were correlated with peduncle length and harvest index. It indicates that these characters may be preferred to exploited genetic variation in bread wheat genotypes. Our results are in agreement with those of (Khodadadi et al, 2011), (Syed et al. 2014) and (Singh et al. 2014).

Cluster analysis is one of the most important statistical analysis, which helps to do a grouping of genotypes in different groups based on genetic variability which is existed for various traits. The weighted pair group method using the arithmetic average (UPGMA) in classifying the 50 genotypes into two major groups, while further dividing into total eight sub-groups. This indicates the presence of wide genetic diversity among the tested genotypes. According to grouping under study, wheat genotypes divided into two major clusters. Group one (Fig. 1) possessed all commercial cultivars, with the exception of two landraces (T-23 and T-26), whereas group two consisted of all landraces. Furthermore, group one divided into five sub-groups, sub-cluster one comprised of six commercial cultivars, such as Kiran-95, Soghat-90, T-23, Imdad-05, NIA-Sunheri, and Aas-2011, while sub-cluster two consisted of six bread wheat genotypes, namely NIA-Amber, Benazir, SKD-1, Bhakar-2000, NARC-2011 and T-16. The third sub-cluster also composed of six commercial wheat genotypes, such as TJ-83, Hamal, Zardana, Sehar-2006, TD-1 and Inqilab-91, whereas fourth sub-cluster possessed only three commercial wheat genotypes (NIA-Sundar, NIA-Sarang, and Marvi-2000). The last sub-cluster of major cluster one, possessed six commercial cultivars, including Johar-78, NIFA-Barsat, Bhittai, Khiram, Sassu, and Sarsabz. Considering the second major group/cluster, which is composed of all landrace genotypes and is further divided into four sub-groups/clusters. The first sub-cluster made of seven landraces, including T-5, T-17, T-13, T-9, T-14, T-3, and T-20, while second sub-cluster composed of five landrace genotypes, such as T-4, T-19, T-12, T-1, and T-2. The third sub-cluster composed of six landrace genotypes, namely T-15, T-21, T-18, T-10, T-24 and T-22, whereas the last sub-cluster (fourth sub-cluster) contained only five landrace genotypes, including T-8, T-25, T-7, T-11, and T-6. Clustering patterns designated that bread wheat genotypes divided into two major groups, group one possesses only commercial wheat bread genotypes, with the exception few from landraces, while group two contains only landraces. Though, it appears that both the group of genotypes possess different morphological features, which indicates great genetic divergence. Genotypes belonging to sub-clusters one and sub-cluster eight could have greater genetic divergence and intermating between the genotypes belonging to them would give more transgressive segregates in advanced generations.

## Conclusion

The mean squares from analysis of variance revealed highly significant for all the character among the tested genotypes, indicating that used materials can be evaluated for further experiments. The genetic variability between commercial and landraces of bread wheat, it was noticed that traditional wheat genotypes tend to possess more genetic variance in the first three components of PCA than its counterpart. That exhibits that old wheat genotypes also possess precious genetic resources; thus, these genetic resources may be exploited in upcoming breeding programs. The cluster analysis, diverse parents have also been identified, signifying their importance for forthcoming hybridization programs in wheat crops.

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## Contribution of Authors

Rind RA: Conceived Idea, Designed Research Methodology, Literature Search, Data Collection, Literature Review, Data Interpretation, Statistical Analysis, Manuscript Writing, Manuscript final reading and approval

Baloch AW: Conceived Idea, Designed Research Methodology, Statistical Analysis

Jatoi WA: Conceived Idea, Designed Research Methodology, Statistical Analysis

Asad MA: Conceived Idea, Designed Research Methodology

Khokhar AA: Literature Search, Data Collection, Literature Review

Nizamani FG: Literature Search, Data Collection, Literature Review

Rind MR: Literature Search, Data Collection, Literature Review

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Nizamani MM: Literature Search, Data Collection, Literature Review, Manuscript Writing, Manuscript final reading and approval

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