

Study of genetic parameters and genetic divergence for yield and yield components of bread wheat (*Triticum aestivum* L.)

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Abstract

Thirty wheat genotypes were evaluated for eleven variability parameters. Significant genotypic differences were observed for all the traits studied indicating considerable amount of variation among genotypes for each character. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield per plant, harvest index, number of grains per spike, number of tiller per plant and weight per ear. The remaining traits exhibit moderate to low PCV and GCV estimates. High heritability estimates were recorded for all the traits studied. These all traits also indicate high expected genetic advance except harvest index and number of grains per spike. Based on Euclidian dissimilarity distance, the cluster analysis separated the 30 wheat genotypes into eight different clusters. Genetic diversity among 30 lines of bread wheat was studied for yield and its component traits using Mahalanobis D² analysis. The distribution pattern of genotypes in different clusters was random. The highest numbers of genotypes were founded in cluster III whereas, cluster II and VIII were presented minimum number of genotypes. The highest intra cluster distance was observed within cluster VIII indicate that genotype in this cluster were genetically more divergent the intra cluster distance with in cluster VIII and IV were observed. Highest inter cluster value observed between cluster VII and III and the lowest inter cluster value observed in cluster between V and I.

Keywords: Genetic variation, heritability, genetic advance, genetic diversity and *T. aestivum*

Introduction

India is one of the main wheat producing and consuming country of the world. After the Green Revolution, the production of wheat has shown a huge increase. The major states involved Uttar Pradesh, Punjab and Haryana. They account for nearly 70 per cent of the total wheat produced in the country. Punjab and Haryana yield the highest amount of wheat because of the availability of better irrigation facilities. In traditional agricultural systems wheat populations often consist of landraces, informal farmer-maintained populations that often maintain high levels of morphological diversity. Although landraces of wheat are no longer grown in Europe and North America, they continue to be important elsewhere. Modern wheat breeding developed in the first years of the twentieth century and was closely linked to the development of Mendelian genetics. Modern wheat varieties have short stems, the result of *Rht* dwarfing genes that reduce the plant's sensitivity to gibberellic acid, a plant hormone that lengthens cells. For short plant height *rht* genes were introduced to modern wheat varieties from Norin 10 cultivars of wheat grown in Japan. During 2011-2012, in India, area under wheat was 29.90 m ha⁻¹ with the production 93.90 million tons productivity 3140 kg ha⁻¹ and share on world level 13.53 per cent. Haryana state on the whole has achieved a productivity level of 5.03 tonnes/ha on 2.5 million hectares (Anonymous, 2012). The most simple and convenient methods for working

out the genetic diversity among the genotype are available (Mahalanobis, 1936) in the form of D² analysis for grouping or clustering of wheat genotypes. Likewise, non-hierarchical Euclidean Cluster, Metroglyph and Canonical approaches are also available. The heritability estimate of a trait was computed as the ratio between estimate of genetic variance and phenotypic variance. Coefficient of variability (CV), heritability (broad sense) and genetic advance estimate was also worked out under present study.

Materials and methods

The present investigation was conducted to examine the genetic variability for several morphological traits in bread wheat (*Triticum aestivum* L.). The experiment was conducted at the Research Farm of Department of Genetics and Plant Breeding, Chaudhary Charan Singh University, Meerut during 2008 - 09. The experimental materials consist of thirty cultivars of bread wheat were grown in the randomized block design (RBD) with three replications. Seeds were shown in a single row plot of 2.5 meter length with 25 centimetres with an appropriate plant to plant distance of 5 centimetres. All the agronomical packages and practices were applied to raise healthy crop. At the time of maturity, five competitive plants of each genotype from each replication were randomly selected. The data was recorded for various quantitative characters *viz.*, plant height, number of tillers per plant, number of spikelets per spike, spike length (cm), weight per ear (g), number of grains per spike, number of grains per plant, biological yield per plant, grain yield per plant,

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test weight and harvest index. The Analysis of variance was carried out for each of the characters studied as per Panse and Sukhatme (1985). For computation of genotypic and phenotypic coefficient of variations (GCV & PCV) (Burton, 1952); for heritability and genetic advance (Allard, 1960) and the genetic advance in per cent of mean (Johnson *et al.*, 1955) were followed.

Results and discussion

The analysis of variance showed highly significant differences among the genotypes for all the characters studied (Table-1), thereby suggesting the presence of considerable amount of variability among the thirty cultivars of wheat evaluated in present study, similar findings were also reported by Narwal *et al.*, (1999) and Tazeen *et al.*, (2009). The phenotypic and genotypic coefficient of variation (PCV and GCV) estimates of the component of variance, heritability and genetic advance are shown in Table 2. The PCV was generally higher than the GCV for all the characters. The highest values were shown by number of grains per plant components namely grain yield per plant, number of grains per spike, number of tillers per plant, weight per ear and harvest index. Most of the correlation coefficients obtained in the present study are broadly in conformity with previous reports in wheat (Kumar *et al.*, 2002 and Kumar *et al.*, 2003).

High heritability estimates were associated with high genetic advance for number of grains per spike, biological yield per plant and grain yield per plant for reflected the involvement of additive gene action. Similar results have been reported by Atta *et al.* (2008), Bhoite *et al.* (2008), Ajmal *et al.* (2009) and Bharat *et al.* (2013). Such estimates of genetic advance indicated that moderate gains could be achieved with strengthening the selection. High heritability with high genetic advance (GA) for plant height (cm) and number of grains per spike demonstrate the presence of additive genes.

Genetic divergence (D^2) is the basis of variability and helps to craft the designed genotypes as per the requirement. The present study aims analyzing the genetic divergence of 30 genotypes of indigenous and exotic origin (Table 3 & 4). The method proposed by Tocher as reported by Rao (1952) was used to confirm the clusters groups. The maximum number of seven genotypes were in cluster III, four genotypes in cluster I, IV, VI, and VII respectively, while three genotypes in cluster V and two genotypes in cluster II and VIII respectively. The highest intra cluster distance observed in cluster VIII indicated that genotype in this cluster were genetically more divergent. Highest intra cluster value observed between cluster VII and III and the lowest in cluster between V and I. Ihsanullah and Mohammad (2001) found the same results.

Table 1. Analysis of variance among eleven characters in wheat

| Source of variation | df | Plant height | Tillers/ plant | Spike weight | Spike length | Spikelets/ spike | Grains/ spike | Grains / plant | Biological yield | Grain yield | Test weight | Harvest index |
|---------------------|----|--------------|----------------|--------------|--------------|------------------|---------------|----------------|------------------|-------------|-------------|---------------|
| Replication | 2 | 42.875 | 6.041 | 5.76 | 0.288 | 5.065 | 41.941 | 13834.00 | 22.988 | 14.835 | 19.21 | 123.531 |
| Treatment | 29 | 134.045** | 18.692** | 3.00* | 4.276** | 5.786** | 260.745** | 98405.379** | 73.590** | 60.419** | 47.173** | 685.487** |
| Error | 58 | 17.331 | 2.527 | 4.875 | 0.797 | 1.166 | 18.524 | 22489.793 | 15.656 | 8.695 | 11.469 | 116.110 |

* , ** significant at 5 and 1 per cent respectively.

Table 2. Estimates of variability for 11 traits in wheat

| Character | GCV | PCV | Heritability | Genetic Advance |
|------------------|-------|-------|--------------|-----------------|
| Plant height | 7.78 | 9.35 | 89.72 | 10.69 |
| Tillers/plant | 14.97 | 18.07 | 68.34 | 3.94 |
| Grain weight/ear | 14.06 | 17.67 | 63.63 | 0.47 |
| Spike length | 11.31 | 14.70 | 59.54 | 1.71 |
| Spikelets/spike | 6.54 | 8.67 | 56.18 | 1.93 |
| Grains/spike | 18.56 | 20.58 | 81.00 | 16.69 |
| Grains/plant | 21.49 | 29.53 | 52.25 | 2.38 |
| Biological yield | 13.02 | 17.52 | 55.34 | 6.73 |
| Grain yield | 21.24 | 26.05 | 66.17 | 6.97 |
| Test weight | 8.73 | 12.23 | 50.20 | 5.07 |
| Harvest index | 23.10 | 29.33 | 62.28 | 22.35 |

Table 3. Distribution of 30 genotypes indifferent clusters in wheat

| Cluster | Genotype | Number of genotype |
|---------|--|--------------------|
| I | UP 2338, PBW 502, HD 2932, HD 2687 | 4 |
| II | HD 1981, HD 2620, | 2 |
| III | HD 2402, HD 2380, HD 2770, HD 2428, CPAN 1964, HUW 107, WH 196 | 7 |
| IV | HD 2281, HD 2733, DH 2307, CPAN 1910 | 4 |
| V | PBW 543, HD 2329, HD 2643 | 3 |
| VI | UP 2425, HD 2285, HD 2189, WH 556 | 4 |
| VII | PBW 226, HUW 44, CDWR 9526, CPAN 4062 | 4 |
| VIII | WH 711, PBW 154 | 2 |

Table 4. Mean performance of clusters for eleven characters in wheat

| Character | I | II | III | IV | V | VI | VII | VIII |
|-------------------------|--------|--------|--------|--------|--------|--------|--------|-------|
| Plant height | 72.88 | 87.23 | 82.97 | 79.95 | 74.21 | 85.24 | 79.08 | 79.9 |
| Tillers/ plant | 13 | 10.13 | 10.47 | 13.13 | 12.81 | 12.83 | 10.07 | 11.28 |
| Grain weight | 2.11 | 1.88 | 1.85 | 1.69 | 2.2 | 2.2 | 2.37 | 2.52 |
| Spike length | 8.26 | 11.39 | 8.96 | 10.04 | 8.24 | 9.87 | 10.67 | 10.13 |
| Spikelets/ spike | 20.86 | 17.92 | 19.56 | 18.66 | 17.92 | 15.57 | 18.8 | 19.66 |
| Grains/ spike | 60.65 | 31.4 | 48.01 | 44.85 | 43.72 | 46.77 | 48.55 | 59.64 |
| Grains/ plant | 780.16 | 311.48 | 479.35 | 562.57 | 526.97 | 552.28 | 490.24 | 654.2 |
| Biological yield/ plant | 37.3 | 37.6 | 33.66 | 26.15 | 33.72 | 32.96 | 36.07 | 35.18 |
| Grain yield/ plant | 18.19 | 17.58 | 19.17 | 13.17 | 15.11 | 17.95 | 19.41 | 18.05 |
| Test weight | 37.82 | 45.3 | 37.04 | 41.83 | 44.11 | 35.91 | 42.46 | 35.65 |
| Harvest index | 51.45 | 47.28 | 60.28 | 74.37 | 46.67 | 55.29 | 54.93 | 94.17 |

The cluster I had the highest number of spikelets per spike (20.87), number of grains per plant (780.16) and number of grains per spike (69.05) and lowest cluster mean for the plant height (72.88). The cluster II had highest mean for plant height (87.23), spike length (11.39), biological yield per plant (37.6) and test weight (45.3) and lowest

cluster mean for number of grains per spike (31.40) and harvest index (47.28). The cluster III had highest mean for grain yield per plant (19.73). The cluster IV had the highest number of tillers per plant (13.13) and lowest cluster mean for grain weight per ear (1.69), biological yield per plant (26.15) and grain yield per plant (13.17).

Cluster V had lowest mean for spike length per plant (8.24). Lowest mean in cluster VI for number of spike lets per spike (15.57) and cluster VII had number of tillers per plant (10.07) and number of grain per plant (490.24). The cluster VIII had the highest grain weight per ear (2.52) and harvest index (94.17) and lowest cluster mean test weight (35.65). Similar findings have been reported by Singh & Dwivedi (2002), Arega *et al.* (2007) Daniel *et al.* (2011). Therefore, in view of considerable genetic diversity found in the present study, showed sufficient scope for genotypic improvement through hybridization between the genotypes from divergent clusters.

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