

Evaluation of genetic diversity in Mexican wheat (*Triticum aestivum* L.) genotypes for qualitative and quantitative traits

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ABSTRACT

Genetic diversity of the thirty Mexican wheat (*Triticum aestivum* L.) genotypes were evaluated on the basis of ten different traits in Randomized Block Design during *Rabi* season, 2007 – 2008. These genotypes were grouped into six different clusters by using Mahalanobis D² analysis. Cluster V had maximum number of (12) genotypes while, cluster I had only one genotypes. Distribution pattern of all the genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits studied. Maximum generalized distances were observed between clusters I and VI. Yield per plant, gluten content (%) and plant height showed maximum contribution to the total genetic divergence. The genotypes present in cluster I and VI may be used as parents in hybridization programmes to develop high yielding wheat varieties.

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INTRODUCTION

Wheat is one of the most important and widely cultivated crops in the world and nearly 95 per cent of wheat grown today is hexaploid, used for the preparation of bread and other baked products (Debasis and Khurana, 2001). India is the second largest wheat producing nation in the world. It has been considered that wheat is an integral component of the food security system of several nations for human consumption and support nearly 35 per cent of the world population. Globally, wheat is being grown in 122 countries and occupies an area of 215 m ha producing nearly 630 m tonnes of wheat (FAO, 2010).

Selection is usually practiced for pooling favourable

genes while hybridization is predominantly utilized to accumulate favourable genes in a variety for obtaining better performance. Genetic diversity is created by nature and genetic recombination added by plant breeders for the varietal improvement, the selection of parents for varietal improvement programmes depends on the knowledge of available diversity (Singh *et al.*, 2006). Knowledge of genetic diversity in a crop species is fundamental to its improvement. Mahalanobis (1936) D² statistics has been recognized as a powerful tool in the hands of the breeders to quantify the degree of divergence between genotypes. An assessment of the nature and magnitude of diversity between genotypes will help to choose better parents for hybridization. Therefore, the present study

has been under taken to ascertain the nature and magnitude of genetic diversity among thirty Mexican wheat genotypes.

MATERIAL AND METHODS

The experimental material comprised of thirty genotypes of Mexican wheat. The experiment were conducted at experimental research center of Department of Genetics and Plant Breeding, Allahabad Agricultural Institute-Deemed University, Allahabad, U.P. during *Rabi* season, 2007 and 2008. These genotypes were grown in Randomized Block Design (RBD) with three replications. Each plot consisted of three rows of 3 meter length with spaced at 20 cm and plants within rows at 5cm. The observations were recorded on various qualitative and quantitative characters on the basis of five randomly selected plants. The pooled data were subjected to analyze by using Mahalanobis (1936) D^2 statistics and genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance exhibited significant differences among the genotypes for all the characters studied, this indicated the existence of significant amount of variability present in the genotypes. Based on Mahalanobis diversity (D^2 values) analysis, the thirty genotypes were grouped into six different clusters (Table 1) following by Tocher's method (Rao, 1952). Majority of genotypes (12) had been included in clusters V and the remaining are found in cluster I, II, III, IV and VI. The criterion used for clustering was that any two genotypes belonging to the same clusters should at least on

an average, show a smaller D^2 value than those belonging to different clusters.

The average intra and inter cluster distance (D^2 values) were presented in Table 2. The intra cluster distance were observed in cluster I, II, III, IV and V while it was not observed in cluster VI because in this cluster had single genotype. Similar findings were also recorded by Singh and Dwivedi (2002). Inter cluster distance is the main criterion for selection of genotypes using D^2 analysis. Genotypes belonging to those clusters having maximum inter cluster distance are genetically more divergent and hybridization between these genotypes of different clusters is likely to produce wide variability with desirable sergeants (Gartnar *et al.*, 1989 and Singh *et al.*, 2006). The maximum generalized inter cluster distance (D^2) was recorded between cluster I and VI (225.37), while it was minimum between clusters III and V (33.4). The relative divergence of each cluster from other clusters (intercluster distance) indicated high order of divergence between cluster I and VI followed by II and VI, IV and V. Thus, hybridization between genotypes from these clusters should result in maximum hybrid vigour and highest number of useful segregates (Shwi *et al.*, 1972). Hybridization between genotypes from highly divergent groups could even produce new gene combinations. The minimum distance between cluster III and V indicated that the genotypes in these two clusters were relatively close to each other.

The average cluster means for different qualitative and quantitative characters are shown in Table 3. It revealed that the genotypes included in cluster II, I and IV were early flowering and the genotypes included in cluster IV were early maturing. Maximum spike length was recorded in cluster I.

| Table 1 : Grouping of thirty Mexican wheat genotypes into different clusters | | |
|--|---------------------|--|
| Clusters | Number of genotypes | Name of Genotype present in the clusters |
| Cluster I | 5 | IBWSN-1003, IBWSN-1025, IBWSN-1010, IBWSN-1016, IBWSN-1036 |
| Cluster II | 2 | IBWSN-1008, IBWSN-1014 |
| Cluster III | 6 | IBWSN-1005, IBWSN-1038, IBWSN-1030, IBWSN-1046, IBWSN-1029, IBWSN-1050 |
| Cluster IV | 4 | IBWSN-1032, IBWSN-1035, IBWSN-1017, IBWSN-1033 |
| Cluster V | 12 | IBWSN-1009, IBWSN-1011, IBWSN-1017, IBWSN-1033, IBWSN-1034, IBWSN-1031, IBWSN-1026, IBWSN-1018, IBWSN-1019 |
| Cluster VI | 1 | IBWSN-1015 |

IBWSN – International Bread Wheat Screening Nursery

| Table 2 : Inter and Intra (bold) cluster distance for different Mexican wheat genotypes | | | | | | |
|---|-----------|------------|-------------|------------|-----------|------------|
| Cluster | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI |
| Cluster I | 34.389 | 64.094 | 67.455 | 65.740 | 102.257 | 225.370 |
| Cluster II | | 16.412 | 54.803 | 66.142 | 64.979 | 119.359 |
| Cluster III | | | 19.186 | 35.969 | 33.405 | 88.323 |
| Cluster IV | | | | 13.613 | 74.852 | 102.808 |
| Cluster V | | | | | 22.879 | 73.089 |
| Cluster VI | | | | | | 0.000 |

Table 3 : Cluster means for various qualitative and quantitative traits in Mexican wheat

| Cluster | Days to 50 % flowering | Plant height (cm) | Tillers per plant | Days to maturity | Spike length (cm) | Grains per spike | Harvest index (%) | Gluten content (%) | Test weight (g) | Yield per plant (g) |
|-------------|------------------------|-------------------|-------------------|------------------|-------------------|------------------|-------------------|--------------------|-----------------|---------------------|
| Cluster I | 86.533 | 111.899 | 11.201 | 122.533 | 11.682 | 48.842 | 40.095 | 9.575 | 46.889 | 47.074 |
| Cluster II | 81.333 | 95.675 | 9.425 | 120.500 | 10.433 | 43.695 | 36.977 | 9.683 | 46.057 | 40.848 |
| Cluster III | 88.611 | 108.617 | 9.939 | 120.944 | 10.689 | 42.214 | 33.566 | 10.552 | 41.880 | 37.466 |
| Cluster IV | 87.333 | 104.467 | 11.016 | 119.500 | 11.363 | 45.736 | 33.502 | 12.589 | 40.357 | 41.976 |
| Cluster V | 88.917 | 101.018 | 9.211 | 121.417 | 10.547 | 40.848 | 35.287 | 8.267 | 40.593 | 33.999 |
| Cluster VI | 88.000 | 84.940 | 8.557 | 120.00 | 10.410 | 42.250 | 31.187 | 11.547 | 34.967 | 26.393 |
| G. Mean | 87.711 | 103.919 | 9.921 | 121.144 | 10.862 | 43.342 | 35.482 | 9.722 | 46.722 | 38.138 |

Table 4 : Per cent contribution of different characters to total genetic divergence

| Sr. No. | Source | Times ranked 1 st | Contribution (%) |
|---------|---------------------|------------------------------|------------------|
| 1. | Days to flowering | 5 | 1.15 |
| 2. | Plant height (cm) | 56 | 12.87 |
| 3. | Tillers per plant | 6 | 1.38 |
| 4. | Days to maturity | 20 | 4.68 |
| 5. | Spike length (cm) | 3 | 0.69 |
| 6. | Grains per spike | 0 | 0.00 |
| 7. | Harvest index (%) | 16 | 3.68 |
| 8. | Gluten content (%) | 108 | 24.83 |
| 9. | Test weight (g) | 36 | 8.28 |
| 10. | Yield per plant (g) | 185 | 42.53 |

The genotypes of cluster I had maximum number of tiller per plant, grains per spike, harvest index, test weight and yield per plant however, the genotypes of cluster VI had high Gluten content (%) but low cluster mean for yield per plant, test weight, harvest index and spike length. Thus, the genotypes of cluster I and cluster VI had great potential as a parent to obtain promising hybrids and to create further variability for these characters. These finding are in agreement with the finding of Singh *et al.* (2006) and Mostafa *et al.* (2011).

In addition to the general features of variation and divergence, this study also indicated that all the characters contributed differently to the total genetic divergence among genotypes (Table 4). The most important trait that causing maximum genetic divergence was yield per plant and it was responsible for differentiating the genotypes studied. Gluten content (%), plant height and test weight were important traits that is also contributed more in the genetic divergence studied. Similar findings were also reported by Salavati *et al.* (2008) and Jishan and Zhu (2008). Grains per spike and spike length contributed minimum contribution to the genetic divergence among the genotypes studied.

From the present study, it is concluded that crosses involving genotypes I and VI, II and VI, IV and VI and I and V should be attempted as these crosses are expected to generate combinations of desirable characters for high yield.

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