

Assessment of Genetic variability and Diversity for Yield and its Contributing Traits among CIMMYT Based Wheat Germplasm

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Abstract

Present experiment was carried out with fifty international bread wheat screening nursery (IBWSN) genotypes procured from CIMMYT, Mexico to study nature and magnitude of genetic variability and diversity for utilization in development of superior varieties. Genotypes were evaluated using a randomized complete block design with three replications. Days to 50 % flowering, days to maturity, plant height, tillers per meter, spike length, grains per spike, test weight, grain yield per plant were recorded. Analysis of variance showed sufficient amount of variability was found in the entire gene pool for all traits studied. Grain yield per plant showed highest genotypic and phenotypic coefficient of variation. High heritability coupled with high genetic advance was recorded for grains per spike and grain yield per plant. Based on D² value the genotypes were grouped into eight different non-overlapping clusters. Highest inter-cluster distance was observed between cluster III and VIII followed by cluster (II & VIII) and (III & VII). This indicates that the genotypes included in these clusters have wide genetic diversity. Grain yield per plant (79.84 %) had highest contribution towards genetic divergence; hence, this trait was major determinants of genetic diversity.

Keywords: Wheat, genetic parameters, D² statistics, clustering pattern, quantitative traits.

1. Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops of the world. Due to its wide adaptability, it can be grown under various agro-climatic conditions. International bread wheat screening nursery (IBWSN) genotypes that were emanated from CIMMYT bred, which is internationally distributed as wheat breeding programme in the form of international screening nursery. IBWSN served as vehicle for dissemination of improved and genetically diverse bread wheat genotypes. The material can be used in crossing programme or tested for direct release to farmers.

The world acreage under wheat crop is 225.53 million ha with production of 713 million tonnes (WASDE; Bloomberg Jan. 2013). In India, wheat is the second most important crop after rice occupying 29.69 million ha,

with production of 92.4 million tonnes with an average productivity of 3118 kg per hectare (Anonymous, 2012). Uttar Pradesh, Madhya Pradesh and Punjab are important states from the point of both area and production.

The variability present among different genotypes of a species is known as genetic diversity. Genetic diversity in crops arises due to changes in the environment, mutation, recombination in chromosomes, genes, DNA. Variability differs from diversity in the sense that the former has observable phenotypic differences whereas the later may or may not have such an expression. Magnitude of genetic diversity among parental stocks largely determines inherent capacity of a cross, as it influences the chances of desirable recombinants (Bhatt, 1973). The important approaches to wheat breeding are hybridization and

subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to get transgressive segregation, genetic distance between parents is necessary (Joshi *et al.* 2004). Through higher genetic distance between parents, the higher heterosis in progeny can be observed (Joshi and Dhawan, 1966; Anand and Murty, 1968). Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004).

Keeping these things in the view, an effort has been made in the present study to evaluate a set of wheat genotypes with the objectives, to estimate the variability, heritability and genetic advance for yield, yield components traits and divergence among biological populations by D² statistics developed by Mahalanobis (1936).

2. Materials and methods

2.1 Experimental detail: The fifty international bread wheat screening nursery (IBWSN) genotypes procured from International Maize and Wheat Improvement Center (CIMMYT), Mexico, were grown at Field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad Agriculture Institute-Deemed University, Allahabad. The experiment was laid out in a randomized complete block design with three replications during 2009-2010. The entries were sown in three rows each of 3 m length with row to row spacing 25 cm and plant to plant 5 cm, ten randomly selected plants from each replication was taken for observations.

Data collection: Data of characters *viz.*, days to 50 % flowering, days to maturity, plant height (cm), tillers per meter, spike length (cm), grains per spike, test weight (g), grain yield per plant (g) in each genotypes and replication.

Statistical analysis: Mean values were subjected to analysis of variance following the procedure of Panse and Sukhatme (1962). Genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance as percentage of mean were calculated as followed by Singh and Chaudhary (1977).

$$PCV = \frac{\sqrt{VP}}{\bar{X}} \times 100 \quad VP = \text{Phenotypic variance, } \bar{X} = \text{Grand mean} \\ PCV = \text{Phenotypic coefficient of variation}$$

$$GCV = \frac{\sqrt{VG}}{\bar{X}} \times 100 \quad VG = \text{Genotypic variance} \\ GCV = \text{Phenotypic coefficient of variation}$$

$$h^2_{(BS)} = \frac{VG}{VP} \times 100 \quad h^2_{(BS)} = \text{Heritability in Broad sense}$$

$$GA = K \cdot \sigma_p \cdot h^2$$

Where,

K = Constant selection differential at 5% level intensity (= 2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

Genetic diversity among genotypes was carried out following D² cluster analysis given by Mahalanobis (1936).

D² values were calculated by using the formula

$$D^2 = W_{ij} (X_i^1 - X_i^2) (X_j^1 - X_j^2)$$

Where, W_{ij} = Inverse of estimated variance, co-variance matrix.

$(\bar{X}_i^1 - \bar{X}_i^2)$ and $(\bar{X}_j^1 - \bar{X}_j^2)$ = Differences in the mean of the two populations.

Clustering of genotypes was done by Tochers's method as detailed by Rao (1952).

3. Results and discussion

The analysis of variance revealed significant variation among the 50 genotypes for all the traits indicating sufficient amount variability present for further improvement. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes.

The character possessing high genotypic coefficient of variation (GCV) value has better scope of improvement through selection. Since, the extent of variability is measured by genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) which provides information about relative amount of variation in different characters. The influence of environment on each trait could be determined on the basis of difference between phenotypic coefficient of variation and genotypic coefficient of variation. A perusal of coefficient of variation revealed that the highest estimate of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed in case of grain yield per plant (33.91%, 33.95%). Similar findings has been also reported by Jagashoran (1995). Moderate estimate of GCV and PCV were recorded for tillers per meter (13.55%, 14.96%), grains per spike (13.40%, 14.17%) and test weight (12.59%, 13.17%). Report of Jagashoran (1995) for number of grains per spike, Singh *et al.* (1996) and Sharma *et al.* (1998) for test weight support our results for GCV and PCV in wheat population. Days to 50% flowering (4.83, 5.33), days to maturity (2.35, 2.65), plant height (4.07, 6.83) and spike length (7.27, 9.48) exhibited low estimates of GCV and PCV. This indicated low variability for such traits among genotypes.

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush 1949). In this context, the high estimates of heritability were recorded for days to 50 % flowering, days to maturity, tillers per meter, grains per spike, test weight, and grain

yield per plant while moderate for plant height and spike length (Table 1). Bijendrapal and Garg (1992), Kamboj *et al.* (2000) also reported high heritability values for grains per spike, test weight and grain yield per plant which in fact demonstrated the presence of additive genes effect indicating effectiveness of selection for the improvement of these traits. The characters which exhibited high

heritability, suggested that the selection will be more effective because these traits are governed predominantly by additive gene action and could be improved through individual plant selection. Whereas, low heritability indicated that the characters were highly influenced by environmental effect and genetic improvement through selection will be difficult due to effect of environment.

Table 1. Estimation of mean, range and different genetic parameters for different traits

Characters	Range	Mean	GCV (%)	PCV (%)	CV	h^2 (bs)	GA %
Days to 50 % flowering	72-96	82.08	4.83	5.33	2.27	81.9	9.00
Days to maturity	116-134	121.24	2.35	2.65	1.20	79.2	4.32
Plant Height (cm)	81-109	91.07	4.07	6.83	5.48	35.5	4.99
Tiller per meter	92-176	135.53	13.55	14.96	6.32	82.1	25.31
Spike length (cm)	9.7-13.5	11.34	7.27	9.48	6.08	58.8	11.49
Grain per Spike	34-62	49.03	13.40	14.17	4.59	89.5	26.12
Test Weight (gm)	37-59	49.79	12.59	13.17	3.87	91.4	24.80
Grain yield per plant (gm)	13-53	37.98	33.91	33.95	1.6	99.8	69.77

GCV=Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2 (bs) =Heritability (broad sense), GA = Genetic advance

Johnson *et al.* (1955) have showed that a character exhibiting high heritability may not necessarily give high genetic advance. It can be find out with greater degree of accuracy when heritability in conjunction with genetic advance is studied (Dudley and Moll, 1969). Thus a character possessing high heritability along with high genetic advance will be valuable in the selection programme. High heritability coupled with high genetic advance as percent mean were observed for tillers per meter, grains per spike, test weight, and grain yield per plant similar kind of result was also reported by Atta *et al.* (2008) for grains per spike, Thakur *et al.* (1999) for tillers per meter and Pawar *et al.* (2002) for test weight. It indicated predominance of additive gene action. Therefore, direct selection for such trait would be effective. The traits days to 50 percent flowering, days to maturity, plant height, and spike length showed high heritability in conjunction with low genetic advance suggested predominance of non-additive gene action hence; direct selection for such traits would mislead the expected result. With phenotypic differences, wide range of genetic distance in the available cultivars is of immense importance for selecting the parents to be used in hybridization programme for obtaining desirable genetic recombination.

Genetic diversity is the basic for genetic improvement. It is widely accepted that information on germplasm diversity and genetic relatedness among elite breeding materials are fundamental elements in plant breeding (Mukhtar *et al.* 2002). Based on Mahalanobis D^2 statistics values the genotypes were grouped into eight non-hierarchical

clusters (Table 2). The discrimination of genotypes in to discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregants for seed yield and other important characters.

The clusters VIII and VII formed the biggest cluster (12 genotypes each) followed by cluster I (8 genotypes), cluster II, V and VI (5 genotypes each), clusters III (2 genotypes) and VI had single genotype. The genotypes belonging to diverse ecological regions clustered together, while those of same region entered separate groups. These findings were similar to the reports of Das (2000). Average highest intra-cluster distance was observed by cluster IV (119.75) is characterized by highest mean performance for days to 50 percent flowering (96.50 days), days to maturity (134.50 days), tillers per meter (168.50), spike length (12.38 cm) and lowest for plant height (81.00 cm) followed by cluster I (82.15) with cluster mean values highest for plant height (95.90 cm), cluster VIII (61.79) with highest cluster mean values for test weight (56.58 g), while cluster VI had minimum intra-cluster distance (0.00) with highest cluster mean values for grains per spike (56.70) and remaining cluster VII (64.76), cluster II (47.16) cluster V (45.54), cluster III (44.23) were characterised average mean values for all traits presented in (Table 3). This suggested that the genotypes in clusters IV were relatively more diverse among themselves with more desirable characteristics.

Table 2. Distribution of 50 genotypes into different clusters

Cluster No.	No. of Genotypes	Name of the Genotypes
I	8	IBWSN 1001,IBWSN 1014,IBWSN 1012,IBWSN 1003,IBWSN 1009, IBWSN 1010, IBWSN 1006
II	5	IBWSN 1004, IBWSN 1016, IBWSN 1015,PBW-343,HD-2009
III	2	IBWSN 1005, IBWSN 1008
IV	5	IBWSN 1011, IBWSN 1033, IBWSN 1007, IBWSN 1024, IBWSN 1035
V	5	IBWSN 1017, IBWSN 1048, IBWSN 1019, IBWSN 1018, IBWSN 1049
VI	1	IBWSN 1013
VII	12	IBWSN 1021, IBWSN 1031, IBWSN 1039, IBWSN 1022, IBWSN 1030, IBWSN 1037, IBWSN 1032, IBWSN 1025, IBWSN 1026, IBWSN 1027, IBWSN 1044, IBWSN 1050
VIII	12	IBWSN 1028, IBWSN 1045, IBWSN 1036, IBWSN 1038, IBWSN 1041, IBWSN 1042, IBWSN 1043, IBWSN 1046, IBWSN 1023, IBWSN 1029, IBWSN 1034, IBWSN 1047

IBWSN: International bread wheat screening nursery

Table 3. Average intra and inter cluster D^2 value of 50 wheat genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII
I	82.15	173.59	212.25	680.93	753.51	807.82	1663.23	2338.24
II		47.16	161.07	1011.81	1115.31	1261.64	2303.13	3180.41
III			44.23	1414.08	1487.42	1470.07	2771.95	3593.22
IV				119.75	147.47	407.80	397.17	813.82
V					45.54	284.73	306.83	644.08
VI						0.00	583.59	823.80
VII							64.76	158.54
VIII								61.79

Since, high or optimum genetic divergence is desired between the parents of hybridization plan for obtaining higher frequency of desirable recombinants, the chances of obtaining good segregants by crossing the little diverse genotypes belonging same cluster are very low. In order to increase the possibility of isolating good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. In this context, highest inter-cluster distance occurred between cluster III and VIII (3593.22) followed by clusters II and VIII (3180.41), cluster III and VII (2771.95), cluster I and VIII (2338.24), cluster II and VII (2303.13).

The utility of D^2 -statistics is enhanced by its applicability to estimate the relative contribution of the various characters to genetic divergence. The selection and choice of parents mainly depends upon contribution of characters towards divergence. Grain yield per plant (79.84%) was contributed to maximum divergence, followed by test weight (8.98), grains per spike (6.20%) However, in all cases the inter cluster distances were greater than the intra-cluster distances implying presence of greater degree of

genetic diversity between the genotypes of two clusters than the genotypes present within the cluster. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement.

It could be concluded from experiment, the genotype IBWSN 1023, IBWSN 1028, IBWSN 1034, IBWSN 1042, IBWSN 1045 from cluster VIII and genotypes IBWSN 1005, IBWSN 1008 from cluster III would be best in improvement for test weight, grain yield per plant and days to 50 percent flowering followed by the genotypes IBWSN 1007, IBWSN 1024 were identified as the best grains per spike at Allahabad region. The characters grain yield per plant, tillers per meter, grain per spike and test weight with high to moderate GCV, heritability, genetic advance, and percent contribution should be given top priority during selection. The cluster III and VIII was most diverse to each other. Therefore, crosses could be planned between genotypes of cluster III and VIII with those of cluster VIII and II, which may yield wide spectrum of variability for these characters.

Table 4. The mean values of twelve characters in 8 clusters in wheat genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	Contribution %
Days to 50 % flowering	76.62	79.70	76.00	81.60	85.40	96.50	83.04	84.30	0.41
Days to maturity	119.80	120.40	118.70	121.00	123.00	134.50	120.40	122.00	1.47
Plant Height (cm)	95.90	93.07	89.85	87.90	89.38	81.00	90.60	90.40	0.00
Tiller per meter	126.50	146.30	111.25	129.10	148.70	168.50	142.00	129.08	2.69
Spike length (cm)	12.06	10.77	11.47	10.79	11.26	12.38	10.98	11.67	0.41
Grain per Spike	48.68	46.90	41.25	56.70	40.30	53.00	51.75	48.83	6.20
Test Weight (gm)	51.65	41.50	52.07	44.03	41.14	54.80	50.44	56.58	8.98
Grain yield per plant (gm)	22.97	18.29	15.65	36.93	37.63	35.70	47.07	51.61	79.84

References

- Anand IJ and BR Murty. 1968. Genetic divergence and hybrid performance in linseed. *Indian Journal of Genetics and plant Breeding* **28**:178-185.
- Anonymous. 2013. The World Agricultural Supply & Demand Estimates (WASDE), Bloomberg and Syngenta analysis. www.nxtbook.com/nxteu/Syngenta/ourindustry_2013/index.php?startid.
- Anonymous. 2012. Reports on Agricultural Statistics, Agricultural Situation in India, Directorate of Economics and Statistics, Government of India.
- Atta YA, BMJ Akhter and PZ Lateef. 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pakistan Journal of Botany* **40**(5): 2087-2097.
- Bhatt GM. 1973. Comparison of various methods of selecting parents for hybridization in common bread wheat (*Triticum aestivum* L.). *Australian Journal of agricultural Research* **24**:21-27
- Bijendra P and DK Garg. 1992. Estimation of genetic parameters in three wheat crosses. *Crop Improvement* **19**: 149-151.
- Das PN. 2000. Genetic divergence and selection of genotypes in soybean. *Journal of Maharashtra Agricultural University* **25**(3): 250-252.
- Dudley JW and RH Moll. 1969. Interpretation and uses of estimates of heritability and genetic variance in plant breeding. *Crop Science* **9**:257-262.
- Eshghi R, F Abrahimpour, J Ojaghi, S Salayeva, M Baraty and M Rahimi. 2012. Evaluation of genetic variability in naked barley (*Hordeum vulgare* L.). *International Journal of Agriculture and Crop Sciences* **4**:1166-1179.
- Islam MR. 2004. Genetic diversity in irrigated rice. *Pakistan Journal of Biological Science* **2**: 226-229.
- Jagshoran. 1995. Estimation of variability parameters and path coefficient for some quantitative characters in hill wheat. *Madras Agricultural Journal* **82**: 441-444.
- Johnson RE, HW Robinson and HF Comstock. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* **47**: 314-318.
- Joshi AB and NL Dhawan. 1966. Genetic improvement of yield with special reference to self-fertilizing crops. *Indian Journal of Genetics and Plant Breeding* **26**: 101-113.
- Joshi BK, A Mudwari, MR Bhatta and GO Ferrara. 2004. Genetic diversity in Nepalese wheat cultivars based on agro-morphological traits and coefficients of parentage. *Nepal Agricultural Research Journal* **5**: 7-17.
- Kamboj MC, C Naveen, S Yadav and N Chaundra. 2000. Genetic analysis of yield and its components in bread wheat (*Triticum aestivum* L.). *Atlas of Agri-Bio-Research* **5**(1): 41-43.
- Lush JL. 1949. Heritability of quantitative characters in farm animals. *Proceedings of 8th Congress of Genetics and Heriditas* **35**: 356-375.
- Mahalanobis PC. 1936. On the generalized distance in statistics. in: *Proceedings of National Academy of Science (Indian)* **2**: 49-55.
- Mukhtar MS, M Rahman and Y Zafar. 2002. Assessment of genetic diversity among wheat (*Triticum aestivum* L.) cultivars from a range of localities across Pakistan using random amplified polymorphic DNA (RAPD) analysis. *Euphytica* **128**: 417-425.
- Panse VG and PV Sukhatme. 1962. Statistical Method for Agri. Workers. *Indian Council of Agricultural Research New Delhi* 381.
- Pawar SV, SC Patil, RM Naik and VM Jambhale. 2002. Genetic variability and heritability in wheat. *Journal of Maharashtra Agricultural University* **27**(3): 324-325.

21. Rao CR. 1952. Advanced Statistical Methods in Biometrical Res. John Wiley And Sons, *New York* 357-369.
22. Sharma PK, PK Gupta and HS Balyan. 1998. Genetic diversity in a large collection of wheats (*Triticum* spp.). *Indian Journal of Genetics and Plant Breeding* **58**(3): 271-278.
23. Singh RK and BD Chaudhary. 1977. Biometrical Methods in Quantitative Genetic Analysis, p 266. *Kalyani Publishers*, New Delhi.
24. Singh NK, LP Tiwari and AK Joshi. 1996. Genetic variability and characters association in common wheat. *Madras Agricultural Journal* **83**: 589-590.
25. Thakur SK, RL Pandey and US Kandarlikar. 1999. Genetic association and variability of grain yield and other quantitative characters in F₂ population of wheat crosses. *Advances in Plant Sciences* **12**: 237-239.