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STUDY OF GENETIC DIVERSITY OF QUANTITATIVE TRAITS WITH GRAIN YIELD IN BREAD WHEAT (*Tritivum aestivum* L.)

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ABSTRACT

Wheat is the most important food crop in India after rice. Total production of wheat worldwide during 2017 was 754.31 million tonnes whereas India contributed 97.4 million tonnes. The field experiment under present investigation was conducted during *rabi* season 2017-18 at Agricultural Research Farm of B.R.D.P.G. College (Campus), Deoria (U.P.). The experiment was conducted to evaluate 72 wheat germplasm line in normal soil under timely sown and irrigated condition with Augmented Block Design. 72 wheat genotypes were investigated to understand the extend of genetic diversity through 14 quantitative traits. Mahalanobis D2 analysis established the presence of wide genetic diversity among these genotypes by the formation of I different non-over lapping clusters. Cluster I had highest number of genotype 15, followed by cluster VI with 14 entries, cluster III with 11 entries, cluster II with 10 entries, cluster VII with 9 entries cluster iv with 6 entries, cluster VI with 5 entries, cluster V had 4 entries and cluster IX represented by only one entry. Higher inter cluster distance indicated greater genetic divergence between the genotypes of those clusters while lower inter-clusters were not much genetically diverse from each other. The inter and intra cluster group mean show that cluster mean for different traits indicated considerable differences between cluster.

Key word : *Wheat, genetic divergence, cluster analysis.*

Improvement of existing varieties is a continuous process in plant breeding. The selection of plants with high genetic variability is basic requirement in any successful hybridization programme. The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (1). The more the genetic diverse parents, the greater the chances of obtaining higher heterotic expression in F_1s and broad spectrum of variability in segregating population (2). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (3). The study of genetic divergence can assist in the choice of genotypes to be used in breeding programs for the development of new populations as it estimate the extent of diversity existed among selected genotypes (4). Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (2, 5). The present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among bread wheat genotypes for utilization in wheat breeding programme. According to (6) the study of phenotypic and genotypic diversity to identify groups with similar genotypes is important for conserving, evaluating and utilizing genetic resources; for studying the diversity of pre-breeding and breeding germplasm; and for determing the uniqueness and distinctness of the phenotypic and genetic constitutions of genotypes with the purpose of protecting a breeders intellectual property rights.

MATERIALS AND METHODS

The field experiment under present investigation was conducted during Rabi 2016-17 at Agriculture Research form of B.R.D.P.G College (Campus), Deoria UP. The experimental materials of studies comprised of 72 wheat genotypes form exotic and indigenous excluding 3 check varieties viz., DBW- 2967, PBW-502 and PBW-343 these genotypes were procured from Genetic stock available in wheat section, Department of Genetics and Plant Breeding, B.H.U. Varanasi" UP India These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters the check used in experiment are well adopted varieties of the region. The experiment was conducted to evaluate 72 wheat germplasm lines in normal soil under timely soon and irrigated conditions following augmented block design the entire experiment field was divided in 8 blocks of equal size and each the 3 checks, namely, HD-2967, PBW-502 and PBW-343 were randomly allocated each block .the remaining a plots of a block were used for accommodating the test genotypes which were not replicated. A test genotype was present only one block while the three checks were replicated in all the 8 blocks. Each plot consisted of two rows 2.5 meters length with spacing of five cm in the row and 23 cm .between the rows.

Table-1 : Clustring pattern of 72 genotype on the basis of mahalanobis D^2 statistics of wheat germ plasm.

Cluster number	Number of genotype	Genotypes
1	15	QUAIU#2, F-2004, SR-93, WH-1105, SR-165, SR-91, HUITES, BRAMBLING, RAJ-1482, KURUKU, YOUDA, PASTOR, ATTILA, HD-2723.
2	10	WBLL, AMSEL, DABU, SR-179, PIFED, KUNA, PBW-343, LOK-1, SITE, AKURI.
3	14	PBW-234, TECUPITO-83, PBW-621, CROC-4, TRCH, PUSA-2733,C-306, SR-90, CHAPIO, CR-100, SR-181, SR-164, TRAP-84, KINGBIRD#1.
4	6	KFA#1, HEILO, HD-2967, PBW-502, HD-2643.
5	4	PVN, KAV-2, SPARK, KBIRD.
6	5	HARUEST PLUS, HD-2329, PBW-220, AJEET-102, PBW-343#2
7	9	MURGA, SR-43, UP-2425, SR-29, RAJ-3077, SR-299, SONALIKA, SR-169, GANGA KAUERI.
8	11	PRINIA, MEGHDUT, NW-80, S-152, SR-177, HUW-468, SR-174, SRTU, SR-231, SRW-41, AMSEL.
9	1	HALANA.

Table-2 : Estimate of average Inter & Intra Cluster Distances for 9 clusters in wheat germplasm.

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster	9 Cluster
1 Cluster	391.632	619.942	490.226	710.151	1115.340	1339.939	1478.719	1571.967	1633.890
2 Cluster		583.530	952.668	1087.009	943.529	1107.033	1758.313	1750.799	1531.795
3 Cluster			0.000	671.715	2074.932	1695.585	1657.520	1996.520	1878.435
4 Cluster				658.564	1731.652	1885.659	1556.841	2080.178	2033.184
5 Cluster					0.000	1521.311	2864.708	1802.480	2759.039
6 Cluster						0.000	1774.373	4132.586	1266.436
7 Cluster							0.000	4203.866	1708.446
8 Cluster								0.000	3427.421
9 Cluster									0.000

RESULTS AND DISCUSSION

The study of genetic diversity among the 72 genotype of wheat germplasm was carried out by using 'MAHALANOBIS' D^2 statistics or described by 'Rao 1953'. The clustering pattern of the 72 genotype were grouped in to 9 different non-overlapping clusters (Table-1) cluster I had highest number of genotype 15, followed by cluster III with 14 entries, the cluster VIII with 11 entries, Cluster II with 10 entries, Cluster VII with 9 entries, Cluster IV with 6 entries, Cluster VI with 5 entries, Cluster V had 4 entries, Cluster IX represented byonly one entry. The estimate of Intra and Inter cluster distances represented by D^2 value have been given in (Table 2) the inter cluster distances range from 0.00 (Cluster VIII, V, IV, III and VII,) the maximum inter cluster distance was observed, between cluster V and I (1633.890) which suggested that member of these two cluster are genetically very divert to each other .

The inter cluster values between cluster VII (4203.866), Cluster IX (3427.421), Cluster VII (2864.708) and Cluster V (2074.432) were also very high, The minimum inter cluster D^2 value (1266.436) was recorded in case of cluster VI (3427.421) higher inter cluster distances indicated greater genetic divergence between the genotypes of those clusters while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other.

The inter and intra cluster group mean for 14 characters are given in (Table-3) perusal of table showed that cluster mean for different traits indicated considerable differences between the clusters. All the cluster from, cluster I to cluster VIII had in general medium mean performance for most of the characters exhibiting extreme cluster mean for non of the characters under study cluster IX and I having medium cluster mean for most of the characters exhibited lowest and highest mean for number of Grain yield per plant (g) respectively cluster III and VII showed low or high mean performance for certain characters.

Cluster IX is showed lowest mean performance and Cluster IV showed high mean performance for grain yield per spike (g) and Harvest index in per-cent. Cluster V and Cluster VI showed high to low mean performance for length of spike (cm). Cluster IX and Cluster V is showed low to high mean performance for Days to 50% flowering and Days to maturity.

Table-3 : Inter Cluster group means for 14 characters among wheat genotype.

Number of Cluster	Days to 50% Flowering	Days to Maturiety	Plant Height (cm)	Peduncle Lenght (cm)	Flag"s Leaf Area (cm²)	Ear Lenght (cm)	Tillers/ Plant
1 Cluster	78.500	117.176	90.026	46.634	31.248	9.758	7.984
2 Cluster	75.476	115.714	89.973	46.418	30.994	9.757	7.657
3 Cluster	79.000	116.000	90.651	42.059	23.782	9.861	6.685
4 Cluster	76.714	117.286	89.788	47.056	32.420	10.027	8.063
5 Cluster	84.000	124.000	90.647	51.346	44.045	12.774	8.525
6 Cluster	67.000	110.000	70.364	41.746	24.289	8.167	10.825
7 Cluster	66.000	109.000	70.391	40.746	28.649	9.654	10.765
8 Cluster	82.000	122.000	123.554	54.899	35.832	9.794	7.372
9 Cluster	55.000	89.000	84.931	48.446	31.622	9.341	8.392

Table-3 : Contd.......

Number of Cluster	Spiklets/ Spike	Biological Yield/Plant (g)	Yield/Spike (g)	Grains/ Spike	Grain Yield/ Plant (g)	1000 Grain's Weight (g)	harvest Index %
1 Cluster	23.407	33.382	1.968	50.183	16.008	42.335	47.895
2 Cluster	21.111	34.493	1.865	43.767	15.391	36.314	44.966
3 Cluster	26.603	28.800	1.801	56.185	13.222	54.200	45.900
4 Cluster	24.488	34.393	2.078	51.897	17.510	49.989	52.666
5 Cluster	14.176	38.400	1.801	30.785	16.542	30.400	43.070
6 Cluster	16.249	40.600	1.728	34.758	14.848	37.200	36.600
7 Cluster	24.683	30.200	1.895	50.998	21.742	40.000	71.980
8 Cluster	24.202	30.400	1.888	51.418	14.662	31.400	48.220
9 Cluster	22.702	33.800	1.578	49.791	14.682	35.600	43.440

Cluster VI and Cluster VIII showed mean for plant height (cm) Peduncle length (cm), low to high. Cluster III and Cluster VI showed low to high mean for Tillers per plant and Biological yield. Cluster III and V showed high to low mean for spikelet's per spike and No. of Grains per spike and 1000 Grains weight. Cluster VI and Cluster V showed low to high mean performance for Flag leaf area.

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REFERENCES

1. Kahrizi, D.; Maniee, M.; Mohammadi, R.; Cheghamirza, K. (2010b). Estimation of genetic parameters related to morpho-agronomic traits of Durum wheat (*Triticum turgidum* var. durum). *Biharean Biologist. 4(2):* 93-97.
2. Shekhawat, U.S.; Vijay, P.; Singhania, D.L. (2001). Genetic divergence in barley (*Hordeum vulgare* L.). *Indian J. Agric. Res. 35(2):* 121-123.
3. Samsuddin, A.K.M. (1985). Genetic diversity in relation to heterosis and combining ability analysis in spring wheat. *Theor. Appl. Genet. 70:* 306-308.
4. Mondal, M.A.A. (2003). Improvement of Potato (*Solanum tuberosum* L.) through hybridization and in-vitro culture technoique. *Ph.D. Thesis. Rajshahi University, Rajshahi,* Bangladesh.
5. Daniel, H.; Mebrahtom, M. and Tsige, G. (2011). Genetic Divergence Analysis on some Bread Wheat Genotypes Grown in Ethiopia. *J. Central Eur. Agric. 12(2):* 344-352.
6. Franco, J.; Crossa, J.; Raibut, J.M.; Warburton, M.L. and Dkarallah, M. (2001). A method for combining molecular markers and phenotypic attributes for classifying plant genotypes. *Thero. Appl. Genet., 103(6-7) :* 944-952.

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