Genetic Divergence Analysis in Wheat (*Triticum aestivum* L.)

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Abstract

Genetic divergence using D^2 statistics of 27 genotypes of wheat (*Triticum aestivum* L.) of different geographic origins revealed existence of considerable diversity. The genotypes were grouped into 6 clusters. The cluster I was the largest containing 7 genotypes followed by cluster II with 6 genotypes, cluster V with 5 genotypes, cluster III and IV had 4 genotypes each and cluster VI had only 1 genotype. The diversity among the genotypes measured by intercluster distance was adequate for improvement of wheat by hybridization and selection. The genotype included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better sergeants in wheat.

Wheat (*Triticum aestivum* L.) has been the prime and staple food crop of many human civilizations in the world. It is the second staple food in India after rice. It is cultivated for dual purpose grain and straw in India, Pakistan, Burma and Thailand. In India, Major wheat grown state *viz.,* U.P., Punjab, Haryana, Rajasthan and Madhya Pradesh. In India, it is cultivated on 28.89 mh area and 88.31 mt production in 2011-12. The average productivity of wheat is estimated to be 30.57 q ha^{-1} in 2011-12, which is lower than the china, USA and russia.

To evolve high yielding varieties plant breeder has to generate genetic variability i.e. the genotypes of diverse nature. Genetic divergence analysis is performed to identify the diverse genotype for hybridization purpose. Clustering by D^2 statistics is useful. The genotypes grouped together are less divergent that the ones which fall into different cluster. After having known diversity the genetic amelioration in a crop is possible by crossing superior types with respect to characters of economic value and important breeding programme could be followed to improve the yield attributes of the crop.

Materials and methods

The experimental material consisting of 27 genotypes *viz.,* Rajasthan –Raj-6560, Raj-1555, Raj-3765, Raj-3777, Raj-4037, Raj-3077, Raj-1482, Lok-1 and Durgapura-65, U.P. –UP-2338, UP-2425, A-9-30-1, CNN-RV-1, Kharachiya-65, Kalyan Sona, Kundan (DL-788-2) and Bijara, Punjab- PWB- 435, PWB-373 and PWB-343, Haryana-HD-2687, HD-2329, HD-4672, HD-2285, WH-542, WH-896 and HW-2004 of wheat (*Triticum aestivum* L.) collected from different parts of the country which were maintained in the previously received from Department of plant breeding and Genetics, R.B.S. college, Bichpuri, Agra, (U.P.).

The genotypes were sown in a randomized block design with three replications at Agricultural Research Farm R.B.S. College, Bichpuri, Agra (U.P.) in Rabi season 2007-08. In each replication consisted of three rows of each genotype with a 3.5 meter row length. Row to row and plant to plant distance was 25 x 10 cm. All the recommended agronomic cultural practices and plant protection measure were followed as and when required.

The following quantitative data were recorded on five randomly selected plants from each genotype in each replications for ten characters *viz.,* number of effective tillers per plant, initiation of spike (days), days to maturity (days), plant height at maturity (cm), number of spikelets per spike, 1000-grain weight (gm), number of grain per spike, grain yield per plant (gm) and grain yield per hectare (quintal). Except initation of spike (days), days to maturity (days) and grain yield per hectare (quintal) recorded on the plot basis. Replication wise data for each character were subjected for analysis of variance **(Panse and Sukhatme, 1985)** and then multivariate analysis of D^2 statistic **(Murti and Aurnachalam, 1967)**. The genotypes were grouped into different clusters following the Tocher's method **(Rao, C.R. 1952)**. The relative contributions of different characters towards genetic divergence were also worked out.

Results and Discussion

The significant treatment mean square indicated adequate variability among the genotype for all characters except number of effective tillers per plant and spike length in Table -1. On the basis of D^2 values for all possible 351 pairs of population. The 27 genotype were grouped into six clusters (Table-2).

Table : 1 Analysis of variance for different characters in wheat

Source of variance	D.F.	Number of effective tillers per plant	Initiation of spike (days)	Days to maturity (days)	Plant height at maturity (cm)	Spike length (cm)	Number of spikelet's per spike	1000 grain weight (g)	Number of grain per spike	Grain yi per pla (g)
Replication (r)	2	1.3459	3.1875	4.9375	3.06250	0.3425	1.1230	2.1210	4.0078	3.814
Treatment (t)	26	12.0379	21.9783**	67.1666**	324.4807**	2.5854	9.5536*	52.5222**	287.36**	26.1880
Error (e)	52	0.64054	2.2235	2.3613	4.03605	0.6438	1.2260	2.2645	3.6535	1.148
S.Em±		0.6534	1.2175	1.2546	1.6403	0.6551	0.9040	1.2287	1.5606	0.874
C.D. at 5%		0.6659	2.4478	2.5225	3.2978	0.7604	1.8176	2.4702	3.1377	1.758

Table 2: Clustering patterns of 27 genotypes on the basis of D² statistic in wheat

Cluster	No of genotypes	Genotype included
I	7	Raj-6560, Raj-1555, WH-896, A-9-30-1, CCN-RV-1, Raj-3077 and Kharachiya-65
II	6	PBW-435, Lok-1, HD-2687, UP-2425, PBW-373 and Raj-4037
III	4	HD-2285, HW-2004, Raj-3777 and PBW-343
IV	4	HD-2329, HD-4672, Raj-1482 and Kundan, (DL-788-2)
V	5	UP-2338, Raj-3765, Durgapura-65, Bijara and Kalyan Sona
VI	1	WH-542

The result revealed that different genotypes from different source and state were included in different clusters, indicating that genetic diversity and geographic diversity are not related. At least one genotype of Haryana and Rajasthan was present in mostly all the clusters.

The inter and intra cluster D² values and distance D are presented in Table -3.

Table 3: Inter and intra cluster arranged D² values and distance (D) among 27 genotype of wheat

Cluster		I	II	III	IV	V	VI
I	D	0.000					
	D²	(0.000)					
II	D	2.605	0.000				
	D²	(6.786)	(0.000)				
III	D	3.456	2.730	0.000			
	D²	(11.943)	(7.452)	(0.000)			
IV	D	3.921	3.268	3.181	0.000		
	D²	(15.374)	(10.679)	(10.118)	(0.000)		
V	D	3.358	3.804	3.647	3.192	0.000	
	D²	(11.276)	(14.470)	(13.300)	(10.188)	(0.000)	
VI	D	6.017	4.795	6.018	4.255	5.898	0.000
	D²	(36.204)	(22.992)	(36.216)	(18.105)	(34.786)	(0.000)

Inter and intra cluster D² values and distance(D) ranged from (0.000 to 36.216) and (0.000 to 6.018) respectively. The distance (D) and inter cluster D² values were maximum between cluster III and VI (6.018 and 36.216) followed by between cluster I and VI (6.017 and 36.204) and while minimum value were related between cluster I and II (2.605 and 6.786). Similar results were found **Singh and Diwivedi (2005). Sharma et al, (2006)** had grouped twenty four wheat genotypes into six clusters. The presence considerable genetic divergence among the genotype for most of the traits studied maximum

and minimum generalized distance were observed between clusters II and IV and between I and V, respectively.

The traits contributing maximum to divergence are given greater emphasis while deciding about the cluster to be used for the purpose of further selection and choice of parents for hybridization. The highest contributors in this regards were number of effective tillers per plant, number of spikelets per spike, number of grain per spike and spike length (Table-4).

Table 4: Cluster mean value of different character in wheat

S.No.	Characters	I	II	III	IV	V	VI
1	No of effective tillers per plant	11.19	11.11	8.33	9.25	8.20	13.33
2	Initiation of spike (days)	94.05	95.61	96.08	99.92	96.80	97.67
3	Days to maturity (days)	116.48	116.50	114.42	125.17	122.47	127.67
4	Plant height at maturity (cm)	88.62	88.06	90.83	88.75	112.73	88.00
5	Spike length (cm)	7.75	8.58	9.71	8.33	8.23	8.67
6	Number of spikelets per spike	16.67	18.83	18.25	18.75	17.40	23.67
7	1000-grain weight (g)	39.76	42.00	38.75	38.83	39.87	35.33
8	Number of grain per spike	39.29	57.22	47.33	49.67	40.27	63.33
9	Grain yield per plant (g)	14.48	15.00	11.50	10.33	13.33	11.67
10	Grain yield per hectare (quintal)	39.58	43.21	51.86	38.46	35.55	21.27

On considering cluster mean in respect of these six cluster. Cluster VI high mean value for number of effective tillers per plant, number of grain per spike, number of spikelets per spike and days to maturity and low mean value for 1000 grain weight, cluster III high mean value for spike length and grain yield per hectare and low mean value for grain yield per plant, cluster V high mean value for plant height at maturity and low mean value for number of effective tillers per plant, cluster IV high mean value for initiation of spike and low mean value for grain yield per plant, cluster II high mean value for 1000 grain weight and grain yield per plant and cluster I low mean value for spike length .

Conclusion

The crosses involving parents from the most divergent clusters are expected to manifest maximum heterosis and generate wide variability in genetic architecture. Thus crosses between the genotypes of cluster Ist with VIth and IIIrd with VIth would exhibit high heterosis and produce was recombination's with desired traits in wheat.

References

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