RESEARCH ARTICLE

Genetic divergence analysis in bread wheat (*Triticum aestivum* L.)

■ MANISHA SAINI, SHWETA AND SUNIL KUMAR PASWAN

SUMMARY

Fifty genotype of wheat were evaluated to access the genetic divergence for eleven quantitative traits. The D^2 cluster analysis grouped 50 genotypes in to eight clusters. This indicates existence of high degree of genetic diversity in the genotypes evaluated. Analysis of variance show significant difference among all the genotype under study. Maximum inter-cluster distance was observed between cluster VII with all. Cluster VIII holds first rank in yield per plant, test weight and plant height, cluster VII holds first rank in plant height, number of reproductive tillers per plant, number of spikelet per spike. Therefore, crosses between member of cluster separated by high inter-cluster distance are likely to throw desirable segregants. Thus, crosses between promising lines belonging to clusters pairs having high inter-cluster distance may be attempted for isolating desirable recombinants for grain yield.

Key Words : Cluster, D^2 analysis, Genetic variation, Inter cluster distance, Transgressive segregants

Wheat with scientific name *Triticum aestivum* L. em. Thell, is the first cereal and most important crop in the world. It is a member of *Graminae* family (Sub-family *Poaceae*) and genus *Triticum*, and the world leading cereal grain. Wheat is one of the most important food crop as it has abundant sources of protein and energy. The importance of wheat at global level can be realized from the fact that the FAO's symbol has a bread wheat spike with the Latin motto 'Flat pains' meaning 'let there be bread'. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. Wheat provides 20 per cent dietary calories of the world. Wheat is the most important source of carbohydrate in majority of countries. Wheat contains minerals, vitamins and fats and with a small amount of nutrition's. It contains 70 per cent carbohydrates, 22 per cent crude fibres, 12 per cent protein, 12 per cent water 2 per cent fat, and 1.8 per cent minerals. A predominately wheat-based diet

———● MEMBERS OF THE RESEARCH FORUM ●———

Author to be contacted :
MANISHA SAINI, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, KANPUR (U.P.) INDIA

Address of the Co-authors:
SHWETA AND SUNIL KUMAR PASWAN, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, KANPUR (U.P.) INDIA

is higher in fibre than a meat-based diet.

India is the largest wheat producing country in the world after China and account for more than 13.06 per cent of the world's wheat production. During the crop year 2014-15, India harvested 95.85 million tonnes of wheat in an area of 31 million hectares with productivity of 2800 kg/ha (Anonymous, 2012).

Knowledge of genetic diversity in a crop species is a fundamental study for its improvement. In crop improvement programme to increase productivity breeders need to maintain a pool of diverse desirable donor parent. D^2 analysis is the most important statistical tool to identify diverse genotypes for hybridization programme in order to exploit the heterosis and to isolate desirable segregants (Singh and Salgotra, 2014). Thus, suitable genotypes from diverse cluster can be used in breeding programme for improvement of yield.

MATERIAL AND METHODS

The experimental materials comprised of 50 wheat genotypes from Indian origin was carried out during *Rabi* 2015-16 at Research Farm Nawabganj of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P). All the genotypes were sown in Randomized Complete Block Design with three replications. Each genotype was sown in two lines in 5.0 m long and 1.38 m broad plots and space planted at 23 x 5 cm between row to row and plant to plant distance, respectively. Recommended cultural practices were practiced to raise a good crop. Data were recorded from five randomly plants except days to 50 per cent flowering which was recorded on the plot basis. The data were recorded for days to 50 per cent flowering, days to reproductive phase, days to maturity, plant height (cm), number of reproductive tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike,

grain weight per spike (g), test weight (g) and grain yield per plant (g). The quantitative diversity of genotypes was grouped into different clusters following D^2 cluster analysis (Rao, 1952).

RESULTS AND DISCUSSION

The D^2 values were computed in each possible combination of wheat (*Triticum aestivum*) genotypes. All the 50 genotypes were group into eight different clusters according to closeness of genotypes in respect of their D^2 values (Table 1). The composition of different clusters varied from 1 to 21 genotypes. Cluster IV consist of 21 genotypes followed by cluster II having 12 genotypes, III having 6 genotypes, I having 4 genotypes, VIII having 3 genotypes, VII having 2 genotypes and cluster V and VI were represented by 1 entries each. The discrimination of lines into so many discrete clusters suggested presence of high degree of genetic diversity in the material evaluated.

Average intra and inter cluster distances were calculated and presented in Table 2. Maximum intra-cluster distance was observed in cluster VIII (348.03), followed by cluster IV (195.82) indicating wide genetic variability within the genotypes of these two clusters. The inter-cluster distance varied from 1957.97 to 101.61. the maximum inter-cluster distance was observed between clusters VII and VIII (1957.97) followed by clusters VI and VII (1209.25) and clusters III and VII (1174.57) which indicated maximum diversity between the genotypes of these clusters. The minimum inter-cluster distance between clusters I and V (101.61), indicated that the genotypes of these clusters were genetically least diverse and almost of the same genetic architecture (Jeena and Singh, 2002). Therefore, it is suggested that the genotypes of these clusters were genetically least diverse. Such genotypes can also be

Table 1 : Grouping of fifty genotypes of bread wheat into eight clusters based on D^2 analysis

Sr. No.	Genotypes	No of genotype per cluster
1.	KA1510, KA1515, KA1502, KA1526	4
2.	KA1520, KA1530, KA1525, KA1539, KA1516, KA1531, KA1503, KA1504, KA1538, KA1535, KA1505, KA1540	12
3.	KA1517, KA1532, KA1522, KA1537, KA1523, KA1508	6
4.	KA1527, KA1529, KA1501, KA1534, KA1544, KA1541, KA1528, KA1506, KA1533, KA1512, KA1547, KA1545, KA1524, KA1542, KA1519, KA1521, KA1550, KA1509, KA1511, KA1518, KA1549	21
5.	KA1546	1
6.	KA1548	1
7.	KA1536, KA1543	2
8.	KA1513, KA1514, KA1507	3

Table 2 : Inter and intra cluster distances (D²) among eight clusters for fifty genotype in bread wheat

Cluster	I	II	III	IV	V	VI	VII	VIII
I	47.17	131.02	167.29	261.40	101.61	308.55	650.03	577.96
II		87.47	281.63	200.06	226.91	319.35	538.55	830.54
III			129.73	500.28	232.68	662.80	1174.57	373.14
IV				195.82	362.75	312.82	443.27	1105.01
V					0.00	239.64	643.33	571.01
VI						0.00	185.93	1209.25
VII							84.62	1957.97
VIII								348.03

Table 3 : Cluster mean among eight clusters for eleven characters of fifty genotypes in bread wheat

Cluster No.	Days to 50% flowering	Days to reproductive phase	Days to maturity	Plant height (cm)	Spike length (cm)	Number of reproductive tillers per plant	Number of spikelets per spike	Number of grains per spike	Grain weight per spike (g)	Test weight (g)	Yield per plant (g)
I	61.05	49.89	110.10	82.59	10.75	6.85	16.67	46.03	0.75	36.93	9.31
II	65.18	49.66	114.58	79.56	9.73	7.38	18.95	46.31	0.84	39.55	9.38
III	64.35	48.17	112.41	88.99	9.44	7.58	19.47	46.71	0.88	39.28	8.67
IV	62.88	49.65	112.37	76.08	10.01	7.38	18.22	51.00	1.09	39.67	8.97
V	62.42	43.37	106.13	81.30	11.22	7.83	20.22	42.27	0.63	42.11	8.03
VI	61.74	43.15	104.47	71.67	9.80	6.13	16.63	44.33	1.82	36.84	8.58
VII	68.20	49.04	107.02	64.30	10.60	8.03	20.30	43.77	1.78	39.38	8.42
VIII	63.04	45.72	108.46	95.39	9.54	7.68	16.65	46.56	1.44	42.91	9.54

used in breeding programmes for developing biparental crosses between the most diverse and closest groups to break the undesirable linkages. Similar findings were also reported by Singh and Dwivedi (2002); Verma *et al.* (2006); Lal *et al.* (2009) and Ali and Bhardwaj (2015).

To exploit genetic diversity through hybridization programme inter-cluster distance must be taken into consideration. The cluster with lower intra-cluster distance indicates the compactness of the group. Genetic diversity is directly proportional to the inter-cluster distance. Higher the distance between cluster greater the diversity between them and *vice-versa*.

The cluster means for different characters are presented in Table 3. Cluster VIII exhibited the highest mean value for yield per plant, test weight, plant height and days to maturity. Highest mean value for number of reproductive tillers per plant and number of spikelets per spike was observed in cluster VII. Highest mean value for flag leaf area and 1000seed weight observed in cluster VI while, it exhibited least mean values for spikelets fertility. Highest mean value for Spike length was observed in cluster V. The low mean value for days to 50% flowering was observed in cluster I and days to maturity, were found in cluster VI. These results indicated

that none of the clusters contained genotypes with all desirable traits, which could be directly selected and utilized. Therefore, the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes.

Based on divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of cluster V, VII and VIII in varietal improvement programme.

REFERENCES

Ali, Tabinda and Bhardwaj, Dinesh Narayan (2015). Study of genetic divergence in wheat (*Triticum aestivum* L.) *Central Agriculture Communication*, **3**(2) : 1-6.

Anonymous (2012). FAOSTAT database. www.faostat.com

Jeena, A.S. and Singh, I.S. (2002). Genetic divergence analysis in wild lentils. *Legume Res.*, **25** (3):175-179.

Lal, B.K., Ruchig. M. and Upadhyay, A. (2009). Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). *Asian J. Agric. Sci.*, **1** (1): 4-6.

Rao, C.R. (1952). *Advance statistical methods in biometrics*

research. Hanfner Pub. Co. Darion. pp. 371-378.

Singh, Praveen and Salgotra, S.K. (2014). Genetic divergence study in improved bread wheat varieties (Triticum aestivum). *African J. Agric. Res.,* **9**(4) : 507-512.

Singh, S.P. and Dwivedi, V.K. (2002). Genetic divergence in wheat (*Triticum aestivum* L.). *New Agriculturist*, **13** (1/2): 5-7.

Verma, A.K., Singh, P.K., Vishwakarma, S.R. and Tripathi, R.M. (2006). Genetic divergence in wheat (*T. aestivum* L.). *Farm Sci. J.*, **15** (1) : 32-34.

12th Year
★ ★ ★ ★ ★ of Excellence ★ ★ ★ ★ ★