Study of Genetic Divergence among Genotypes of Hexaploid Wheat (*Triticum aestivum*) (L.) em. Thell)

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Abstract: **One hundred and fifty-two genotypes of national and international origin used to analysed genetic diversity and found clustered in six groups. Cluster IV was superior for flag leaf area while cluster V had members with more spikelets\spike and protein content. High yield and high hectolitre weight were observed in cluster VI but were tall. Hybrids coming out of cross combinations obtained between clusters V and VI may be more useful and promising.**

Keywords: **diversity, wheat, hybrid, genetic diversity, clusters, D^2.**

1. Introduction

Selection of parents is the first step in plant breeding program through hybridization. In order to get better seggregants, genetic divergence between parents is of prime importance. (Joshi et.al.2004) Genetic divergence is dependent on geographical diversity as well as phenotypic components of varieties, and its quantitative assessment could provide a rational basis for the selection of parents for any breeding programme. Joshi and Dhawan (1966), Anand and Murrty, (1968), Benadeki, (1992), Singh (2006) suggested that the chances of higher heterosis is directly proportional with genetic distance of parents. The hybrid wheat program initiated in 1995 with an emphasis on diversity of genotypes used to identify harnessable commercial heterosis. Since then a number of genotypes were selected from various national and international sources. These were evaluated for various morphological characters, which can be useful in hybrid wheat programme for hybrid seed production and standard heterosis. Non-hierarchical Euclidean cluster analysis helps in separating out genotypes in clusters. This assists in identifying probable male and female lines\groups that will result in to standard heterosis. The aim of the present investigation is to develop clusters of genotypes for various yield-contributing characters.

2. Materials and Methods

One hundred and fifty two genotypes of spring wheat (*Triticum aestivum* L.) of national and international origin were evaluated at Agriculture Research Farm, Narain P.G. College, Shikohabad, UP during 2017-18 rabi season. The genotypes were grown in paired rows of two-meter length. The distance between rows was 0.23m while distance between plants was 0.02m. Five competitive plants from each plot was randomly taken for recording observations on flag leaf area, plant height, spike length and spike lets/spike. The flag leaf area was computed by using the product of flag leaf length, breadth and a factor 0.80. The observation on days to 50% heading was taken on plot basis. A random sample of seeds from plot was used for measurement on protein content (%) and hectolitre weight (kg\hl). The protein content (%) was estimated using Near Infrared Reflectance Analyser (NIR) Model Infratec-1255 Food and Feed Analyser. The hectolitre weight was estimated using "new DWR hectolitre instrument". The genetic divergence and related statistics were estimated by using D2 statistics as suggested by Mahalanobis (1936) and Rao (1952).

3. Results and Discussion

One hundred fifty-two genotypes collected from various national and international sources were grouped into different clusters based upon the method as applied in non–hierarchical Euclidean cluster analysis (Beale 1969, Spark 1973). The method is used to form a range of clusters from 2-15 so as to see if the genotypes could be grouped into lesser number of clusters without any loss of information. No major differences in variance of genotypes in each cluster was observed between 6-clusters and 15-clusters, as 6 clusters were as effective as 15 clusters in providing useful information on diversity (Table 1). However, as we drop one more cluster from 6-clusters the value of variance become just more than double which suggests inconsistency in grouping the genotypes in to 5- clusters or below. Hence, it is judicious to group 152 genotypes in to 6-clusters without loosing any information. Suri and Sharma (1999) had divided 200 genotypes of wheat into 10 clusters and found that grain yield and tiller number were major contributors towards genetic divergence with moderate contribution from 1000-grainweight, grains/ear and harvest index.

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Table 1
% Distribution of genotypes in each cluster based on grouping into different number of clusters ranging from 2-15

Cluster Number	15	14	13	12	11	10	09	08	07	06	05	04	03	02
I	15	15	15	16	16	18	22	21	28	28	43	57	64	95
II	11	12	12	12	13	14	14	15	17	18	23	34	38	57
III	15	16	17	22	23	26	25	28	28	26	40	32	50	
IV	13	11	11	13	14	14	17	17	17	24	30	29		
V	6	6	16	6	6	12	11	14	14	18	16			
VI	13	14	14	19	19	23	23	29	31	38				
VII	9	12	12	12	12	12	13	15	17					
VII	8	8	12	11	11	11	12	13						
IX	11	11	11	12	12	19	15							
X	3	3	3	3	3	3								
XI	21	22	22	21	23									
XII	5	5	5	5										
XII	10	10	12											
XIV	7	7												
XV	5													
Variance	22	24	23	37	39	43	26	40	48	55	128	164	169	722

Table 2
Estimates of average Intra- and Inter- cluster distances for six clusters

Cluster Number	I	II	III	IV	V	VI
I	1.942	3.346	1.933	2.181	3.211	2.814
II		2.270	2.892	2.822	2.447	3.134
III			1.975	2.391	3.050	2.682
IV				2.263	2.845	2.521
V					2.401	2.926
VI						2.362

`____´ Intra cluster distance

Table 3
Cluster means, Standard deviation and Coefficient of variation of 6 clusters for 8 characters

Characters		I	II	III	IV	V	VI
Days to 50% heading	X	99.8	107.8##	99.1#	101.5	103.0	101.3
	SD	1.66	4.23	2.94	3.78	3.97	4.75
	CV	1.663	3.92	2.96	3.72	3.85	4.68
Flag leaf area (sq. cm)	X	43.5	43.3	42.4#	59.3##	44.3	46.6
	SD	5.46	7.54	4.77	8.85	6.60	9.53
	CV	12.5	17.4	11.25	14.9	14.8	20.4
Plant height (cm)	X	99.5	99.9	97.4#	101.4	101.7	113.7##
	SD	7.0	5.40	4.79	4.94	8.99	6.53
	CV	7.03	5.40	4.91	4.87	8.83	5.74
Spike length (cm)	X	8.56	10.1##	8.50#	8.9	9.7	9.68
	SD	0.97	1.31	0.76	0.96	0.69	0.96
	CV	11.3	12.9	8.94	10.7	7.11	9.91
Spike lets per spike	X	15.93*	20.3	19.0	18.3	21.0**	19.3
	SD	1.02	1.68	1.44	1.27	0.97	1.44
	CV	6.40	8.27	7.57	6.93	4.61	7.46
Protein (%)	X	12.63	12.4	11.8#	12.6	13.4##	12.4
	SD	0.51	0.45	0.46	0.57	0.68	0.55
	CV	4.03	3.62	3.89	4.52	5.07	4.37
Hectolitre weight (kg/hl)	X	73.8	73.5	73.5	74.7	70.2#	76.4##
	SD	2.53	2.98	3.04	2.82	4.16	2.37
	CV	3.42	4.05	4.13	3.77	5.92	3.10
Yield (kg/plot)	X	0.70	0.48#	0.69	0.63	0.73	0.86##
	SD	0.15	0.09	0.17	0.18	0.15	0.15
	CV	21.4	18.75	24.6	28.5	20.5	17.4

\#   = Least X value
\#\# = Highest value

The intra-and inter-cluster distance for 6-clusters have been discussed in Table 2. It is desirable to have high inter-cluster distance and low intra-cluster distance. The inter-cluster distances range from 1.933 to 3.346. The maximum inter-cluster distance (3.346) was observed between clusters II and I. The intra-cluster distance was lowest in cluster I (1.942) and highest in cluster II (2.270). Hence, desirable segregates as well as single cross hybrids can be obtained by crossing between 28 and 18 genotypes spread in cluster I and cluster II, respectively

in various characters. The cluster superior in different characters like yield (Cluster VI), protein (Cluster V), spikelets\spike (Cluster V), spike length (Cluster II), flag leaf area (Cluster IV) and dwarf plants (Cluster III). The members of cluster VI have highest value for yield and hectolitre weight but were tall (Table 3). On the other hand members of cluster V had highest value for protein % and spike lets\spike but it was poor in hectolitre weight. A combination of both yield and protein can be attempted in hybrids by selecting parents from

Table 4
Pedigree details of Cluster V and VI that may be used as parental lines in hybrid programme

Cluster V	Cluster VI
Female	Male
AMSEL/CAZO	CATBIRD
Chirya4=CS/AC//GLEN/3/ALD/PVN/4/NING MA76/YAIGAAM	OPATA/KILL'S
FASAN	F 10S-1
KAUZ/CMH77.308//BAU	SN64//SKI/2*ANI/3/SX/4/BEZI
HE1/3*CNO79/12*SERI/3/ATTILA	PRINIA
VEE#5//DOVE/BUC/3/STAR/4/HE1/3*CNO79*SERI	URES/BOW//OPATA
ATTILLA*2/LOTUS 5	LIRA/SHA5
K134(60)/VEE//BOW/PVN	(KASYON)/PVN/SPRW
BUC'S'/PVN'S'=PAPAO M86	SW89.5422-51
STAR//TAN/VEE	SHENGHI 7-49
VS965.AGA/2*CMH74A.582//CMH76A.912/3/CMH79.681/4/BOW	CUPE/ATTILA
URES/BOW/OPATA	KAUZ/KAUZ/PVN
ND//VG1999//KAL/BB/3/YACO/4/VEE'S'	KAUZ*2//DOVE/BUC/3/KAUZ
BSP93-21-OZAF	CATBIRD
MAYA/NAC	NANJING/82149/KAUZ
FIRETAIL	SERI82/CPAN2010
IRENA	TONI/LIRA'S'//PRL'S'/HUW318-5
BJY/COC//PRL/BOW	SITE//CNO79/PRL
PRL/VEE#6/VORONA/3/2*PRL/VEE#6	BUC/FLK//MYNA/VUL
MRL/BUC/3/CNDR/ANA//CNDR/IMVS/4/PRL/VEE#6	CNO/PRL/CHIL
KAUZ*2/4/CAR//KAL/BB/3/NAC/5/KAUZ	WL711/HD2160//HD2204
NL838-41	BOW//BUC/BUL/3/WH576
BH1146*3/TUI/CARC//CHEN/CHTO/4/ATTILA	
URU84 (92027)	
URU87 (92054)	
ATTILA/3/TUI/CARC//CHEN/CHTO/4/ATTILA	
URES/BOW/BAU	
CM//79A.95513*/CNO79	
PAT10/ALD//PAT72300/3/PVN/4/URES/5/PFAU	

cluster V and VI. The genotypes of cluster II had long spike and more spikelets/spike coupled with long vegetative phase expressed as delayed heading. Longer flag leaf was a characteristic of members of cluster IV. Members of cluster III exhibited early heading with dwarf plant type but poorer in protein, spike length and flag leaf size.

Looking at the strengths of each cluster depending upon the out performance of a cluster for a character or group of characters indicate that cluster I, II and III are close to each other while cluster V and VI are close and complimented for yield and protein character(Table-2). The overlapping between clusters indicates commonality in superiority for specific characters under study. Hence, the cumulative effect of desirable characters in wheat hybrids can be felt by attempting a number of cross combinations between members of the clusters like V and VI with desirable characteristics. Cross combinations between members of cluster V and VI may combine high yield as well high protein content. It will be desirable to use members of cluster VI as male which may be superior for yield and yield components, hectolitre weight and tall while members of cluster V were superior for protein content, yield components and dwarf as females. Singh and Chatrath (1993) opined that grain yield, ear-bearing tillers and plant height were the potent variables which could be used as parameters in selecting genetically divergent parents in crossing programme for breeding high yielding wheat varieties for salt-affected soils. The inter- and intra- cluster distances among cluster III and I was lowest and had genotypes with early heading. On the other hand on the basis of overall diversity among clusters, members of cluster I and II are diverse.

To search some commonality in genetic background of genotypes in each cluster it was not possible to find any commonness in pedigree of genotypes especially in cluster V and VI. Our observation was in accordance with Singh and Chatrath (1993), Suri and Sharma (1999), Yousuf Ali et.al 2008, who observed that genetic divergence was independent of pedigree as well as place/origin.

4. Conclusion

This paper presented a study on genetic divergence among genotypes of hexaploid wheat.

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