Genotypic divergence analysis for stay green characters in Wheat (*Triticum aestivum* L. em. Thell)

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ABSTRACT

An experiment was conducted to study the genotypic divergence for stay green traits along with different morphophysiological characters under normal and late sown conditions. Genotypic divergence was carried out according to Mahalanobis D^2 statistics. The 36 genotypes were grouped into 9 clusters under normal sown and 6 clusters under late sown conditions revealing the presence of wide range of genotypic variation. Inter cluster D^2 values ranged from 21.9 (between Clusters V and VI) to 56.1 (between clusters VII and IX) under normal sown conditions and from 26.5 (between clusters III and IV) and 73.34 (between clusters II and V) in late sown condition. Genotypes WH147M and MLU2 (Cluster IX, normal sown and Cluster II late sown) exhibited strong stay green character. These can be used to transfer this trait into fast growing, high yielding and widely adapted genotypes like Raj 3765 to develop wheat varieties for various agro ecological conditions.

1 INTRODUCTION

Wheat (*Triticum aestivum* L. em. Thell) 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. Wheat is normally grown under sub-tropical environment during mild winter, which warms up towards the grain-filling stage of the crop. Prolonged duration of preceding crop or untimely rain during sowing period compel farmers to postpone sowing of wheat. Therefore, the crop is exposed to sub-optimal temperature during grain filling stages which reduces the grain yield to a larger extent. In the tropics, a shorter grain-filling period is conducive to a quick change in the source: sink ratio after anthesis (Cruz-Aguado et al., 1999), which could be associated with changes in the physiological factors limiting grain filling. Under such conditions, high respiratory losses and low leaf area duration might lead to source limitation in biomass increment (Rawson, 1986). In many cereals relationships have been observed between grain yield and duration of grain filling as well as the area of total canopy and of specific leaves (Thomas, 1987, 1992). There is preliminary evidence that some stay green lines contain a high level of cytokinins than normal (Ambler et al., 1987) which reduce the rate of loss of both chlorophyll and photosynthesis in senescing wheat seedling (Wittenbach, 1977), producing a stay green phenotype. This specific character is not studied adequately so far in wheat. In lines exhibiting the stay green phenotype, many of the desirable characters associated with grain yield such as tiller number per plant, number of grains per spike and duration of grain filling are significantly enhanced and it is recognized that multiple benefit may accrue from building extended greenness. Delayed leaf senescence is an important character that is transmissible to the next generation as found by Crafts - Brandner and Poneleist (1987) in maize. This kind of approach looks quite promising. Different wheat genotypes interact differently with prevailing temperatures. This forms the basis for differences in expression of potential traits contributing to high temperature stress tolerance in wheat genotypes. In this context, genotypes showing delayed leaf senescence i.e. stay green would prove promising.

Before attempting diversity analysis, it is pertinent to understand some basic concepts. The variability present among different genotypes of a species is known as genetic diversity. Genetic diversity in crops arises due to mutation, recombination, geographical separation or due to genetic barriers to crossability. 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. Genetic divergence refers to degree of diversification with regard to component traits and determines the relative proportion of each such trait to the total divergence. Phenotypic variability is the observable variation present in a population .It includes both genotypic and environmental components of variation and, as a result its magnitude differs under different environmental conditions. Genotypic variation on the other hand is the component of variation which is due to the genotype differences among individuals within a population and is the main concern of the plant breeder. Phenotypic plasticity is the consequence of efficient physiological mechanisms which compensates for the disturbances due to environment. Genetic control of development of a line in such a manner that it is able to adjust to the recurrent fluctuations in the environment so that the vital functions of line continue unimpaired. It is responsible for genotypic variability by minimizing the effects of natural selection.

Magnitude of genetic diversity among parental stocks largely determines inherent capacity of a cross, as it influences the chances of desirable recombinants (Bhatt, 1973). Quantitative traits are highly influenced by the environment. Consequently it becomes difficult to determine heritable genetic differences on the basis of phenotype of a plant. Therefore, quantitative assessment of degree of divergence in parental varieties entering the crosses is essential. Hence, a technique which can provide direct and reliable estimates of diversity at genotypic level will be more useful. D^2 proposed by Mahalnobis (1936) based on multivariate analysis is most appropriate method for selecting the parents as it furnishes a measure of actual divergence between any pair of population(Rao,1952).

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Keeping the above facts in view, present study was conducted to determine genotypic divergence for stay green character in wheat genotypes.

2 MATERIAL AND METHODS

Eco-geographically and genetically divergent thirty six genotypes of bread wheat differing in pedigree, yield potential and levels of thermo tolerance comprised experimental plant material. These genotypes were developed in different countries/different research station within a country for example TD, TD-A, TD-B, TD-C, TD-D, TD-E (Australia) ,WH147, WH147 M, WH157, WH283, WH-416, WH423, WH542, WH711, Sonak, C306 (Plant Breeding , CCSHAU, Hisar) HT90, DI 8, DI 717,SG22 , SG150, SG 170, SG199, SG 215, SG8809, HD2009M ,(Genetics, CCSHAU, Hisar) MLU1, MLU2(Germany) ,HD2009, HD 2329,(IARI, New Delhi) , (UP2338 (U.P.,), PBW343(PAU, Ludhiana), Raj3765,(Rajasthan) ,SM 5, SM6, SM17(Mahrashtra) . These were grown in randomized block design with three replications under two different dates of sowing *viz.*, 23rd Nov 2004 (normal sown, NS) and 10th Jan 2005 (late sown, LS). Each plot consisted of single row of two meter length spaced 30 cm apart while keeping plant to plant distance of 10 cm in each row in each replication . Observations were recorded on 5 randomly selected competitive plants for 25 morpho-physiological traits related to adaptation and yield. These traits were days to 50% flowering (DF), days to 50% anthesis (DA), days to 50 % maturity (DM), days to 50% flag leaf senescence (FLS), spike length (SL), peduncle length (PL). plant height (PH) , number of spikelets per spike (S/S), thousand grain weight (TW), number of grains per spike (G/S), leaf area (LA), biological yield (BY), grain yield(GY), harvest index (HI), chlorophyll 'a' at anthesis : (CA-1), chlorophyll 'b' at anthesis (CB-1), chlorophyll 'a' at 28 DAA(days after an thesis , CA-2), chlorophyll 'b' at 28 DAA(CB-2), total chlorophyll at anthesis (TC-1), total chlorophyll at 28 DAA (TC-2), heat units (HU), photothermic quantum (PQ), grain growth rate at 14 days after anthesis (GR-1), grain growth rate at 21 days after anthesis (GR-2) and grain growth rate at 28 days after anthesis (GR-3).

2.1 GENETIC DIVERGENCE ANALYSIS

In order to quantify the genetic distance between any two genotypes, Mahalanalobis (1936) D^2 statistics as described by Rao (1952) was employed. The variance and covariances were subjected to multivariate analysis. The original intermated variables (x's) were first transformed into set of mutually uncorrelated variable (y's as linear function of x's) and the D^2 values were worked out. Pivotal condensation method was used to compute inverse matrix of the error dispersion matrix (Rao, 1952). The generalized distance function (D^2) between two genotypes is simply the sum of square of differences in y's i.e.

$$D^2 = \sum_{i=1}^{p} (Y_{1i} - Y_{2i})^2$$

The value between the variables on the basis of P character is:

$$DP^2 = \sum_{i=1}^{P} \sum_{j=1}^{P} (W_{ij}\, d_i d_j)$$

Where, DP^2 = D^2 value between the variables on the basis of P character.

W_{ij}= Inverse matrix of pooled common dispersion obtained from error matrix

'd'= Difference of mean value for the character of respective genotypes as indicated by i and j.

2.2 DETERMINATION OF GROUP CONSTELLATIONS

The D2 values for all combinations presented in the matrix form were arranged in increasing order of magnitude and clustering was according to method suggested by Tocher (Rao, 1952). At first, two most closely associated genotypes were chosen and then third genotype was located which had the smallest D^2 value with the 1st two genotypes. This procedure was continued. The new genotypes were added so long as increase in average D^2 value become abruptly high, then this genotype was not included in the former group. The genotypes of 1st cluster were omitted and rest were treated similarly for constructing new clusters. A few genotypes which had comparatively very high D^2 value from the others formed independent clusters.

2.3 INTRA AND INTER-CLUSTER DISTANCES

The intra cluster D^2 value was calculated as the sum of n (n-1)/2. D^2 values among the genotypes within a cluster divided by n (n-1)/2. Single Genotype always has zero intra cluster D^2 value. For calculating the inter cluster D^2 value all possible D^2 values between genotypes of the clusters were added and than divided by n_1 x n_2, where n_1 and n_2 are number of genotypes in first and second cluster, respectively. The intra and inter cluster distances were calculated by taking the squares root of respective D^2 value between genotypes of a particular cluster and between genotypes belonging to two clusters, respectively.

2.4 CLUSTER MEAN VALUE

The cluster mean of a particular character is the summation of mean value of genotypes included in a cluster, divided by number of genotypes in the same cluster.

3 RESULTS

Analysis of variance (data not given for brevity) revealed significant genetic variation among 36 wheat genotypes for all the 25 morphological and physiological traits and these were amenable to genetic improvement through recombination breeding.

Mean (Table 1) for most of the characters were higher in normal sown conditions as compared to the late sown conditions except chlorophyll related traits where it was slightly higher in late sown condition. Also, magnitude of phenotypic (PCV) and Genotypic(GCV) coefficients of

variation for most of the traits was almost similar over two sowing environments except for days to flowering , days to anthesis, leaf area, chlorophyll a(28 days after anthesis) , total Chlorophyll(28 days after anthesis), and Photothermic Quantum which also showed relatively higher differences in character expression. Thus environmental effects for these traits were more than the other traits.

Table 1: Mean, range, co-efficient of variation (phenotypic and genotypic) for different characters under normal and late sown conditions

Characters	Mean±SE	Range	Co-efficient of variations (%)	
			PCV	GCV
Days to Flowering	90.08±1.32	81-122	9.42	9.16
	72.18±1.42	65-115	17.65	17.32
Days to Anthesis	94.98±1.25	87-124	8.27	7.95
	75.28±1.42	67-118	16.73	16.41
Peduncle Length (cm)	38.68±0.80	23.8-48.3	15.84	15.43
	32.72±0.86	22.3-43.6	15.84	15.17
Days to Flag Leaf Senescence	114±0.94	102-144	7.92	7.79
	94±1.58	84-127	8.96	8.49
Days to 50% Maturity	121.92±0.85	108-147	7.13	7.02
	97.39±0.182	87-131	8.27	8.15
Spike Length (cm)	9.53±0.26	6.33-13.66	15.62	14.89
	9.17±0.38	7.33-13.50	16.17	14.49
No. of Spikelets /Spike	18.61±0.59	15.0-22.7	11.78	10.39
	18.01±0.56	15.6-22.5	10.12	8.60
1000 Grain Weight	38.84±1.43	30.4-52.6	14.81	13.37
	35.14±1.05	29.2-42.8	12.33	11.19
No. of Grains/Spike	40.92±1.28	12.7-54.2	21.37	20.67
	36.75±1.19	14.3-51.7	21.93	21.19
Leaf Area (cm^2)	38.64±0.91	22.4-56.9	27.53	27.22
	37.95±1.45	25.0-49.9	21.12	20.25
Biological Yield (g)	218±8.0	135.8-287.0	17.81	16.63
	193.3±7.9	116.6-258.3	20.09	18.79
Grain Yield (g)	87.64±2.28	48.8-158.4	26.50	26.05
	74.06±1.68	48.5-148.8	25.68	25.38
Harvest Index (%)	40.22±1.24	25.9-53.1	18.47	17.68
	38.61±1.43	25.5-57.3	17.96	16.77
Plant Height (cm)	104.2±2.2	71.2-136.5	17.37	16.98
	99.8±1.5	76.7-126.0	16.87	16.65
Chlorophyll a(anthesis) ,mg/g fresh weight	1.770±0.070	1.455-2.189	14.58	12.72
	1.893±0.020	1.520-2.320	13.79	13.72
Chlorophyll b(anthesis). mg/g fresh weight	0.257±0.007	0.163-0.312	15.87	15.07
	0.279±0.010	0.160-0.390	17.27	16.93
Chlorophyll a(28 days After Anthesis) ,mg/g fresh weight	0.938±0.061	0.656-1.638	25.82	23.25
	1.084±0.090	0.660-1.560	22.69	17.65
Chlorophyll b(28 days After Anthesis), mg/g fresh weight	0.181±0.003	0.136-0.283	18.62	18.34
	0.257±0.010	0.160-0.380	18.64	18.2

Table 1: continued

Characters	Mean±SE	Range	Co-efficient of variations (%)	
			PCV	GCV
Total Chlorophyll (at Anthesis) , mg/g fresh weight	2.025±0.075	1.618-2.498	13.81	12.23
	2.169±0.020	1.750-2.720	13.71	13.56
Total Chlorophyll(After 28 days of Anthesis), mg/g fresh weight	1.126±0.08	0.792-1.656	24.47	20.91
	1.346±0.07	0.910-1.920	17.68	15.29
Heat Units (0day)	780.3±12.57	704-1044	8.26	7.77
	609.0±20.76	566-798	9.97	8.03
Photothermic Quantum	8226±213	7303-10749	10.94	9.96
(0 day hr)	1944±609	1082-8361	103.77	88.42
Grain Growth Rate(14) (mg/day/grain)	0.298±0.021	0.081-0.471	25.24	22.11
	0.277±0.020	0.389-0.938	27.05	24.44
Grain Growth Rate(21) (mg/day/grain)	0.440±0.018	0.178-0.651	20.72	19.41
	0.414±0.020	0.178-0.597	21.57	20.06
Grain Growth Rate(28) (mg/day/grain)	0.423±0.018	0.241-0.631	18.61	16.91
	0.408±0.020	0.249-0.566	18.54	17.26

3.1 GENETIC DIVERGENCE

In order to select genetically divergent parents for hybridization , D^2 statistic was computed for clustering genotypes based on genotypic divergence following Tocher' s method (Rao, 1952) .The magnitude of genetic divergence among the 36 genotypes varied for two sowing environments due to differences in character expression.

3.2 CLUSTERING OF GENOTYPES

Thirty six wheat genotypes were classified (Table 2) into 9 clusters under normal sown and 6 clusters under the late sown crop. The cluster VI possessed the largest number of genotypes (9) in normal sown condition, followed by cluster I (6), cluster II (5) and cluster IV (5). Clusters III, V and IX included 2 genotypes each, followed by the cluster VII having only one genotype. In late sown conditions, cluster III possessed the maximum number of genotypes (14) followed by cluster V (9) and cluster I (6). Cluster VI, II and IV included 4, 2 and 1 genotypes, respectively.

3.3 INTRA AND INTERCLUSTER D^2 VALUES

Genotypes grouped in the same cluster (intra cluster) are expected to be genetically more similar to each other while genotypes grouped in different clusters (inter clusters) as genetically more divergent. The cluster which are separated by greatest statistical distance show maximum divergence. Intra cluster D^2 values amongst various clusters (Table 3) ranged from 13.60 (Cluster VIII) to 29.9 (Cluster IX) as compared to inter cluster D^2 values which ranged from 21.9 (between Clusters V and VI) to 56.1(between clusters VII and IX) under normal sown conditions. Likewise, intra cluster D^2 values ranged from 16.29 (cluster VI) to 32.8 (Cluster II) while inter cluster values ranged from 26.5(between clusters III and IV) and 73.34(between clusters II and V) under late sown condition. Cluster VII in normal sown (Sonak) and IV in late sown conditions (Raj 3765) contained only one genotype. These were unique in one or more characters that made them so divergent from rest of the genotypes.

Table 2 Clusters, genotypes and their genotypic divergence in wheat under normal sown conditions

NORMAL SOWN				LATE SOWN			
Cluster No.	**Number of genotypes**	**Name of genotypes**	**Genotypic divergence**	**Cluster No.**	**Number of genotypes**	**Name of genotypes**	**Genotypic divergence**
I	6	TD, C-306, MLU-1, SG 150, TD(E), SG 8809	20.23	I	6	TD, TD (E), WH 711, WH 542, HD 2009, SG 22	26.43
II	5	WH 711, WH 157, WH 542, WH 416, SG 22	19.74	II	2	WH 147M, MLU-2	32.87
III	2	DI-8, Raj3765	22.06	III	14	MLU-1, WH 283, WH 416, DI-8, HD 2329, SM 6, UP 2338, DI-717, SM 5, HT 90, C-306, SG 8809, HD 2009M, Sonak	21.06
IV	5	SM 5, DI 717, HD 2009M, WH 147, HT 90	20.30	IV	1	Raj 3765	0.00
V	2	SM 6, SG 199	20.28	V	9	SG 150, WH 47, PBW 343, SM 17, SG 170, WH 157, SG 215, SG 199, WH 423	21.85
VI	9	SG 170, WH 423, SG 215, UP 2338, PBW 343, SM 17, HD 2009, WH 283, HD 2329	16.32	VI	4	TD (D), TD (C), TD (B), TD (A)	16.29
VII	1	Sonak	0.00				
VIII	4	TD (D), TD (B), TD (C), TD (A)	13.6				
IX	2	WH 147M, MLU-2	29.90				

Table 3 Intra-clusters (diagonal) and inter-cluster genotypic divergence values in wheat under normal and late sown conditions.

	NORMAL SOWN									LATE SOWN					
Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**I**	**II**	**III**	**IV**	**V**	**VI**
I	20.2	23.5	30.9	26.9	29.5	22.3	34.3	25.2	44.7	26.4	43.7	44.7	64.3	33.0	36.1
II		19.7	32.5	28.9	29.7	23.9	41.4	31.7	44.1		32.8	53.0	73.3	46.8	45.1
III			22.0	31.5	31.2	28.8	40.2	43.9	54.0			21.0	41.3	26.5	30.2
IV				20.3	27.9	23.2	41.8	32.0	45.0				0.000	49.0	57.6
V					20.2	21.9	37.8	37.4	55.3					21.8	27.9
VI						18.3	29.9	28.0	46.1						16.2
VII							0.000	37.1	56.1						
VIII								13.6	46.6						
IX									29.9						

3.4 CLUSTER MEANS

Under normal sown conditions the lowest and highest cluster means (Table 4) respectively for different traits were observed *i.e.* for DF (VII and IX), DA, DM, FLS (V and IX), PL (IX and VIII), SL, S/S (IV and V), GW (IX and V), G/S (I and VIII), LA (II and IV), BY (IX and III), GY and HI (VIII and III), PH (IX and VIII), CA-1 (V and IX), CB-1 (I and II), CA-2 (II and IX), CB-2 (I and IX), TC-1 (V and IX), TC-2 (IV, V and IX), HU and PQ (VII and IX), GR-1, GR-2 and GR-3 (IX and V).

Table 4 Cluster mean of different characters under normal sown of wheat

Cluster	DF	DA	DM	FLS	PL	SL	S/S	GW	G/S	LA	BY	GY	HI
Cluster-1	92.0	96.0	125.7	118.1	41.0	9.4	19.5	38.4	31.0	31.1	215.0	93.5	44.0
Cluster-2	91.2	97.2	124.3	116.0	33.2	9.9	18.4	35.8	37.2	29.4	214.6	83.2	38.7
Cluster-3	85.5	91.6	119.0	112.8	39.1	9.3	19.2	45.3	41.3	42.9	278.0	155.0	55.6
Cluster-4	89.0	93.6	122.0	114.6	37.3	8.1	17.5	43.5	44.9	55.4	218.1	82.7	39.0
Cluster-5	88.8	88.5	108.3	102.0	42.4	13.0	20.5	36.2	50.7	44.3	222.5	90.0	42.0
Cluster-6	85.8	91.6	116.0	109.1	39.1	10.1	18.9	39.1	39.7	40.2	223.2	86.6	39.1
Cluster-7	81.3	88.6	109.6	102.6	43.6	10.6	17.6	46.7	40.3	29.7	275.0	115.1	41.6
Cluster-8	87.9	93.5	126.0	118.5	46.2	8.2	17.5	35.3	52.8	30.4	192.5	59.8	31.2
Cluster-9	117.6	120.3	144.8	141.1	24.6	8.2	17.5	33.5	45.7	45.1	169.1	69.2	40.1
GM	90.0	94.9	121.9	114.0	38.7	9.5	18.6	38.8	40.9	38.6	218.0	87.6	40.2
CD	3.7	3.5	2.4	2.6	2.2	0.7	1.6	4.0	3.5	2.5	22.5	6.4	3.5

Cluster	PH	CA-1	CB-1	CA-2	CB-2	TC-1	TC-2	HU	PQ	GR-1	GR-2	GR-3
Cluster-1	116.5	1.8	0.2	0.9	0.1	2.0	1.1	789.7	8343.2	0.3	0.4	0.4
Cluster-2	87.2	2.0	0.3	0.8	0.2	2.3	1.0	804.9	8520.2	0.28	0.42	0.40
Cluster-3	102.800	1.57	0.25	0.83	0.22	1.8	1.1	747.3	7783.5	0.30	0.45	0.43
Cluster-4	106.733	1.62	0.24	0.89	0.17	1.8	0.9	766.7	7993.9	0.28	0.45	0.42
Cluster-5	105.217	1.51	0.26	0.80	0.20	1.7	0.9	737.7	7675.5	0.33	0.50	0.48
Cluster-6	95.863	1.76	0.26	0.82	0.15	2.0	1.0	752.9	7846.1	0.34	0.49	0.47
Cluster-7	104.867	1.79	0.21	0.98	0.18	2.0	1.2	704.7	7303.9	0.30	0.36	0.34
Cluster-8	133.717	1.64	0.25	1.12	0.19	1.8	1.2	774.7	8309.5	0.30	0.43	0.40
Cluster-9	82.200	2.03	0.27	1.60	0.21	2.3	1.8	973.5	10720.7	0.11	0.21	0.29
GM	104.2	1.77	0.25	0.93	0.18	2.0	1.1	780.3	8226	0.29	0.44	0.42
CD	6.1	0.2	0.02	0.17	0.01	0.21	0.2	35.4	603	0.05	0.05	0.05

Under late sown conditions the lowest and highest cluster means (Table5), respectively, for different traits were observed *i.e.* DF and DA (III and II), DM and FLS (IV and II), PL (II and VI), SL and S/S (II and V), GW (I and IV), G/S (I and V), LA (VI and V), B, GY and HI (VI and IV), PH (II and VI), CA-1 (III, IV and I), CB-1 (III, IV and I, II), CA-2 (IV , V and II), CB-2 (II and III), TC-1 (III, IV and I),TC-2 (IV and I), HU and PQ (III and II), GR-1 and GR-2 (II and IV), GR-3 (II, III and IV).

Table 5 Cluster mean of different characters under late sown of wheat

Cluster	DF	DA	DM	FLS	PL	SL	S/S	GW	G/S	LA	BY	GY	HI
Cluster-1	72.1	75.0	100.1	97.1	32.9	8.5	18.1	31.6	26.6	32.9	180.3	66.4	37.2
Cluster-2	121.3	124.0	120.0	116.6	23.3	8.2	17.0	34.0	32.1	38.8	188.5	79.2	41.5
Cluster-3	67.7	70.9	93.8	90.9	31.3	9.0	17.7	36.8	30.0	40.1	212.5	79.7	38.1
Cluster-4	69.0	74.6	91.3	86.3	31.6	9.0	17.9	38.5	35.4	40.7	260.0	148.8	57.2
Cluster-5	68.8	71.8	95.2	91.1	33.9	10.1	19.0	36.1	36.9	41.7	174.2	69.9	40.7
Cluster-6	71.5	74.2	100.7	96.0	39.3	8.7	18.6	32.0	34.8	28.2	173.7	53.4	31.0
GM	72.2	75.3	97.4	94.0	32.7	9.2	18.0	35.1	36.8	38.0	193.3	74.0	38.6
CD	4.0	4.0	1.6	4.4	2.4	1.1	1.6	3.0	3.4	4.1	22.4	4.7	4.0

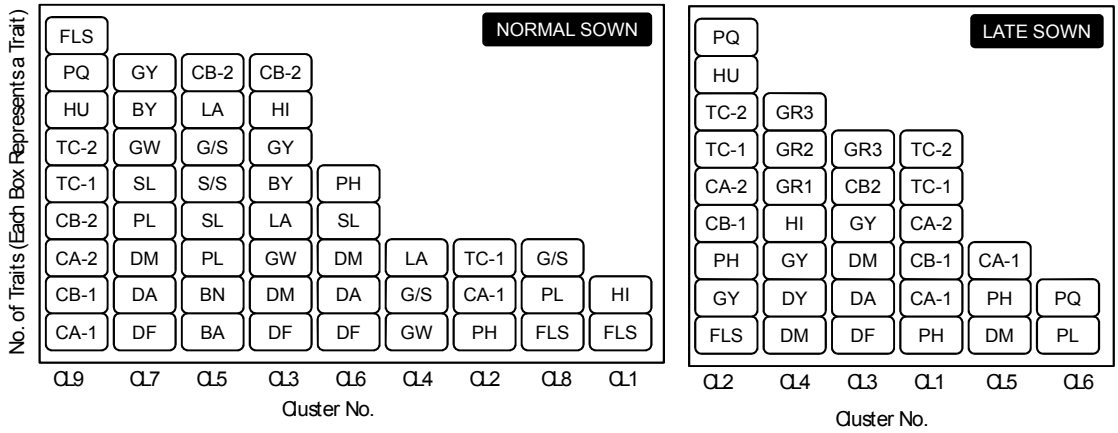
Cluster	PH	CA-1	CB-1	CA-2	CB-2	TC-1	TC-2	HU	PQ	GR-1	GR-2	GR-3
Cluster-1	94.4	2.3	0.33	1.34	0.25	2.6	1.6	633.7	1957.5	0.23	0.36	0.35
Cluster-2	86.6	1.9	0.34	1.37	0.18	2.2	1.5	778.7	3136.0	0.16	0.22	0.28
Cluster-3	98.2	1.6	0.25	0.98	0.29	1.9	1.2	584.6	1216.3	0.28	0.41	0.95
Cluster-4	100.5	1.6	0.24	0.84	0.21	1.9	1.0	591.2	1326.3	0.39	0.53	0.52
Cluster-5	89.2	1.9	0.28	0.84	0.28	2.2	1.3	593.9	1629.1	0.31	0.46	0.44
Cluster-6	120.7	1.8	0.26	1.11	0.23	2.0	1.2	610.6	2262.4	0.28	0.41	0.40
GM	99.8	1.8	0.28	1.1	0.26	2.1	1.3	609.0	1944	0.27	0.41	0.40
CD	4.3	0.04	0.01	0.25	0.02	0.07	0.19	58.6	171.9	0.05	0.05	0.06

The perusal of Fig 1 reveals that some cluster contained genotypes depicting significantly higher mean performance for 2 or more traits as compared to general means over all the 36 genotypes in normal as well as late sown conditions. In that context, Cluster IX (WH147M and MLU-2) figured important under normal sown conditions for traits related to senescence and adaptation like chlorophyll a and b and total chlorophyll at two different stages and heat units and photothermic quantum, flag leaf senescence. Similarly, Cluster VII, V and III contained genotypes depicting higher means for phenological traits, biological and grain yield and their attributes including harvest index (cluster III). Genotypes in cluster I showed higher means for delayed flag leaf senescence and harvest index.

Likewise under late sown conditions Cluster II (WH147 M and MLU-2) showed higher mean performance for traits such as chlorophyll a and b, total chlorophyll at two different stages, heat units and photothermic quantum, flag leaf senescence and grain yield. Also cluster I genotypes exhibited higher means for chlorophyll contents at different stages. Interestingly, Cluster III contained genotypes depicting higher means for phenological traits, and grain yield.

Similarly, cluster IV genotypes had higher means for post anthesis grain growth rate, biological and grain yield, and harvest index.

Figure 1 Clusters showing above average performance for various traits



Legends: Days to 50% flowering (DF), days to 50% anthesis (DA), days to 50 % maturity(DM), days to 50% flag leaf senescence(FLS), Spike length(SL) , Peduncle length(PL). Plant height (PH) , Number of spikelets per spike(S/S), Thousand grain weight(TW), Number of grains per spike (G/S),. Leaf area (LA), Biological yield(BY), Grain yield(GY), Harvest index (HI), Chlorophyll 'a' at anthesis : (CA-1), Chlorophyll 'b' at anthesisCB-1), Chlorophyll 'a' at 28 DAA (CA-2), Chlorophyll 'b' at 28 DAA(CB-2), Total chlorophyll at anthesis (TC-1),. Total chlorophyll at 28 DAA(TC-2), Heat units(HU), Photothermic quantum(PQ), Grain Growth Rate at 14 days after anthesis (GR-1), Grain Growth Rate at 21 days after anthesis (GR-2) and Grain Growth Rate at 28 days after anthesis (GR-3).

4 DISCUSSION

In breeding self pollinated crops like wheat, usually the concept of pure line and progeny selection is practiced. Unlike allogamous crops, this system of mating and breeding imposes a restriction on population for its genetic expansion as inbreeding leads to rapid fixation, precludes free exchange of favourable genes and greatly prevents emergence of desirable gene constellation (Joshi, and Singh, 1979). Moreover, the germplasm in self pollinated crops is available in the form of multitude of pure lines and the genes of interest are scattered over these lines. Assembling such gene constellations determining traits related to phenology, adaptation, biological and grain yield etc., followed by establishing the recombinants as pure lines is main strategy for the improvement of self pollinated crops. This situation warrants for critical choice of the parents in breeding programme, particularly if the aim is improvement of complex quantitative traits. Such work would be facilitated if breeder is able to broadly classify the germplasm on the basis of given set of characters and then to pick up parents for hybridization either to exploit heterosis or for transgressive segregants in subsequent generations (Chandra, 1977). Therefore choice

of parents for hybridization should be based not only on agronomic performance but also on genetic variances, genetic divergence (Bhatt, 1973) as it would help in understanding genetic potentiality of populations to yield desirable genotypes. Therefore , D^2 statistics proposed by based on multivariate analysis (Mahalnobis , 1936) being one of the most appropriate method for selecting the parents is used in present study to determine genetic divergence among 36 wheat genotypes for grouping them into different cluster using Tocher method Rao,1952).

In Indian subcontinent wheat is generally grown under subtropical and tropical climates where post anthesis increase in ambient temperature is a major constraint in the realization of potential yield of genotypes (Abrol *et. al.,* 1991). In late planting, the crop is exposed to sub-optimal temperature during grain filling stages which brings down the grain yield to a larger extent. The increase in yield under terminal heat stress is possible either through increase in grain number/m^2 or 1000-grain weight (Reynolds *et. al.*, 1996) or through a stay green phenotype. The balance between these two important yield parameters determines the yield potential of a genotype and its suitability to stress environment. Genotypes included in Cluster III (DI-8 and Raj 3765) under normal sown and cluster IV (Raj 365) under late sown condition had the highest cluster mean for grain yield and least for days to flag leaf senescence. On the other hand genotypes included in cluster IX (WH147 M and MLU-2) under normal sown and cluster II (WH147 M and MLU-2) under late sown condition had the highest cluster mean for days to flag leaf senescence and least for grain yield. Also, genotypes MLU-2 and WH147M expressed the strongest stay green trait. These two lines varied drastically, in certain morphological and productivity features, from the normal wheat cultivars. They showed higher values for the mean performance of days to flag leaf senescence, heat units and photothermic quantum. They also possessed higher chlorophyll content at 21 DAA as compared to the other genotypes. This indicates that, they were photosynthetically more active for a comparatively longer period. Contrary to this, the grains/spike, 1000 gain weight, spike length, biological yield and gain yield were minimum in these genotypes under normal as well as late sown conditions. The lower yields despite of comparatively higher GGRs at 21 and 28 DAA might be because of poor translocation of photosynthesis. Ahlawat *et al* (2007) observed that chlorophyll 'a' at anthesis had a direct positive effect on grain yield and chlorophyll 'a' at 20 days after anthesis displayed a positive direct effect on days to flag leaf senescence. Gashaw et al (2007) clustered indigenous durum wheat genotypes of diverse origin into homogenous groups based on estimates of genetic divergence (D^2) for the hybridization programme. They found that there was no correspondence between geographic and genetic distances i.e. germplasm collected from the same geographic area were placed into different cluster groups and those collected from different geographic regions were placed into the same cluster. This was also the situation in present study. For example genotypes developed in Australia (TD series), MLU-1, MLU-2 (Germany), CCSHAU, Hisar, India (WH and SG series) and at various institutes in India got clustered together .It was interesting to note that both the stay green genotypes(WH147M and MLU-2) grouped together in cluster IX in normal and cluster II in late sown conditions.

It has been emphasized that the grain filling rate is more temperature sensitive (Zhong Hu and Rajaram, 1994) than days to anthesis and duration of grain filling and the rate of grain growth (GGR) is more important than the duration as a selection criterion to improve kernal weight (Whan *et. al.,*1996) and ultimately, grain yield. Hui *et. al.,* (2007) reported that improved photosynthetic capacity and duration after anthesis are important physiological bases for enhancing grain yield from increased grain weight. Barma *et. al.,* (2002) observed that higher biomass at harvest, CHB retention at 28 days after anthesis, delayed leaf senescence and grain weight showed good correlation with yield under stress conditions. Rampino *et al.* (2006) studied the expression pattern of photosynthesis related genes. A mutant of durum wheat cultivar Trinakria (designated as 504), having delayed leaf senescence, on analysis showed that it was functionally stay green. Blanco *et al.* (2000) reported several synthetically derived lines showed higher photosynthetic rates than their recurrent parents. Also, WH147M and MLU 2 could be used as candidate 'plants' for isolating genes governing delayed monocarpic senescence. Ahlawat *et al.* (2008) identified four RAPD primers (OPB-18, OPC-01, OPH-16, OPQ-07) out of 20 primers tested which produced 7 unique bands that were present and/or absent in these two stay-green genotypes.

5 CONCLUSIONS

The objective of present investigation was to evaluate genotypic diversity for stay green and other traits related to yield. Also, an attempt was made to classify these genotypes using D^2 values as a measure of genetic distance among genotypes and identify stay green genotypes for wheat improvement for target environments. Wide range of mean performance was observed for peduncle length, number of grain per spike, leaf area, grain yield, total chlorophyll at 28 DAA and GGR at 21 DAA under normal and late sown conditions. Genotypes WH147M and MLU 2 used higher heat units and photo thermic quantum for attainment of phenological stages under normal as well as late sown conditions. Thus these genotypes appeared to be photo thermo insensitive to some extent. Thus under heat prone rainfed conditions such genotypes can avoid forced maturity and hence large scale yield loss. Therefore, these genotypes could be used to transfer the stay green character to the genotypes having fast growth, high yield (cluster II under normal sown and cluster IV under late sown) so that their early senescence in rainfed or late sown conditions may be avoided and sustained growth could be achieved by combining stay green post anthesis translocations of carbohydrates to grain sink

The presence of significant genetic variability among the evaluated wheat genotypes suggests an opportunity for improvement of grain yield through hybridization of genotypes from different clusters and subsequent selection from the segregating generations.

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