Hill Wheat from Indian Himalayas: A Rich Source of Diversity

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Two hundred and sixty four hill wheat germplasm collections were grown at VPKAS Experimental Farm, Hawalbagh, Almora, for two consecutive years 2002-03 and 2003-04 in an augmented design. These were evaluated for 15 quantitative traits. All the genotypes were grouped into 15 clusters using non-hierarchical Euclidean analysis showing existence of high genetic diversity in the material. High coefficient of variability was observed for grain yield/plant, grain weight/spike and biomass/plant. First eight vectors explained more than 80% of the total variation. The highest intercluster distance was obtained between cluster X and XV (17.27). The intracluster distance was the maximum in cluster IV (4.73) and minimum in cluster V (2.30). Crossing between superior genotypes of diverse cluster is expected to generate transgressive segregants for grain yield, spike length, 1000-grain weight, effective tillers/plant, biomass/plant, early flowering and maturity.

Key Words: *Triticum aestivum,* Germplasm evaluation, Divergence, Hill wheat

Introduction

Wheat (*Triticum aestivum* L. em Thell.) is the most important crop of *rabi* (winter) season in North-Western Himalayas. The bread wheat (*Triticum aestivum*) is the most important species, occupying about 90% of the total wheat area. The genus *Triticum* is extremely variable and grows in habitats ranging from sea level to elevation of 3,500 m. Diverse agroclimatic conditions, different cultural practices and geographical conditions have generated substantial genetic diversity in this crop. Genetic diversity is the basic building block of any crop improvement programme (Kumar and Singh, 1997) as genetic variation among parents is highly essential to derive superior progeny (Chen *et al.*, 1994; Smell, 1995) and success of any hybridization programme depends upon selection of suitable parents of diverse origin (Selvarani and Chendirasekaran, 2000). Genetic divergence is one criterion for selecting parents to generate crosses that give transgressive segregant in subsequent generations. Multivariate analysis is a powerful tool in quantifying the degree of divergence present in the biological population at genotypic level. The use of multivariate analysis has been emphasized by many workers (Singh, 1994; Redhu *et al.*, 1995). Although several breeders in different crops have used D^2 statistics, but non-hierarchical Euclidean cluster analysis suggested by Beale (1969) and Spark (1973) is capable of overcoming the limitations of Mahalanobis D^2 statistics. These procedures characterize genetic divergence using the criterion of similarity and dissimilarity based on aggregates effect of a number of agronomically important characters.

The pace and magnitude of genetic improvement generally depend on the extent of genetic variability in segregating generation which largely depends on the genetic diversity of the parents. It is, therefore, logical to assess the genetic divergence in the available germplasm for identification of diverse genotypes. The present investigation was, therefore, undertaken to study the nature and extent of genetic variability and genetic divergence in 264 germplasm lines using non-hierarchical Euclidean cluster analysis to identify the donor for yield and yield contributing characters.

Materials and Methods

Two hundred and sixty four hill wheat germplasm accessions were collected from the Uttarakhand hills of Indian Himalayas during different explorations. These accessions along with three checks, *viz.*, Sonalika, VL *Gehun* 804 and HS 240 were evaluated under medium fertility (N: P_2O_5: K_2O: 120: 60: 40 kg/ha), irrigated conditions at VPKAS Experimental farm, Hawalbagh (29º36'N, 79º40' E and 1250 msl) during *rabi* 2002-03 and 2003-04 in an augmented block design consisting of 6 blocks with each block having 47 plots and checks repeated in each block. Each plot comprised of two rows of 3 m length with inter and intra-row spacing 0.3 m and 0.1 m, respectively. The crop received 60 kg/ha N, 60 kg/ha P_2O_5 and 40 kg/ha K_2O as basal dose and 30 kg/ha N as a top dressing after first irrigation and at joining stage. Three irrigations (50 mm each) were provided to the crop in addition to 263.8 mm and 63.0 mm rainfall during *rabi* 2002-03 and 2003-04, respectively.

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Observations were recorded on fifteen quantitative characters, namely, days to 75% spike emergence, days to 80% maturity, flag leaf length, flag leaf width, peduncle length, plant height, effective tillers per plant, spike length, number of spikelets per spike, biomass per plant, number of grains per spike, grain weight per spike, grain yield per plant, 1000-grain weight and harvest index. Five competitive plants were randomly selected for recording observations. Genetic divergence was studied using non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark ,1973). The SPAR 1 package developed by Indian Agricultural Statistical Research Institute (IASRI), New Delhi, was used for statistical analysis.

Results and Discussion

Genetic variability and divergence is of great interest to the plant breeder as it plays a vital role in framing a successful breeding programme (Mehetre *et al*., 1994; Goel *et al*., 2005). The greater the genetic heterogeneity, the more is the probability of getting diverse recombinants exhibiting high heterosis for the quantitative traits of economic importance.

A wide range of variation was observed for almost all the characters (Table 1). On the basis of pooled data promising genotypes were identified with respect to days to 75% spike emergence, days to maturity, plant height, effective tillers per plant, spike length, biomass per plant, number of grains per spike and grain yield per plant. Maximum range was observed for plant height (74.5 - 123.17 cm), while flag leaf width had the least range (0.86 – 2.09 cm). Genotype VHC (BD) 38B was the tallest (123.17 cm) and VHC (LK)-1 was the shortest (74.5 cm). These may be crossed with each other in order to develop semi, tall genotypes which is the requirement of hill farmers as fodder is an important component of hill farming. Accessions VHC (BD) 8, VHC (BD) 19 and VHC (BD) 20A had the highest spike length, grain yield and number of tillers, respectively (Table 2). Among the six best accessions, VHC 6314 had high spike length and high number of grains/spike and VHC (BD) 39 was the tallest with high biomass/plant These accessions may be used as donors/parents for their respective characters in developing high yielding genotypes with desired traits. Wide range of variation for plant height, spike length, 100-seed weight and total tillers was also reported by Ajlouni and Jaradat (1997).

The coefficient of variability was the highest for grain yield/plant and lowest for days to maturity. Plant height, days to 75% spike emergence, days to maturity spike

length and number of spikelets/spike were the traits having CV value of less than 10%. On the contrary, rest of the traits had CV values above 10% ranging from 11.85% for 1000-grain weight to 36.58% for grain yield. It can be inferred that, in the present study, all characters except plant height, spike emergence, days to maturity, spike, length and number of spikelets per spike showed wide variations suggesting sufficient scope for further improvement for majority of characters. However, for improvement in plant height, spike emergence, days to maturity, spike length and number of spikelets per spike, there is need for introgressing the variability from outside sources.

Non-hierarchical Euclidean cluster analysis proved useful for estimating the genetic divergence in 264 wheat genotypes which were grouped into 15 different non-overlapping clusters. The grouping indicated a large amount of genetic divergence among the genotypes. The appropriate cluster arrangement as determined by F test revealed that the 15 clusters were the most suited in pooled analysis. Cluster V consisted of highest number of accessions (48) which showed the highest value for peduncle length (21.10 cm), plant height (118 cm), harvest index (44%) and days to 75% spike emergence (128) whereas, cluster X had the lowest number of accessions (1) and had maximum value for peduncle length (21.10 cm) and plant height (118 cm). Cluster XII had the highest value for days to 75% spike emergence (128), spike length (10.7 cm), number of spikelets/spike (25), therefore, may be important for developing early flowering genotypes with higher number of grains/spike. Cluster IV consisted of 5 accessions and had maximum value for flag leaf width (1.7 cm), number of grains/spike (62) and grain weight/ spike (2.01 gm). This is an important cluster which can provide donors for number of grains/spike and grain weight, the two major yield attributes. Cluster VI showed the highest value for flag leaf length (20.78 cm), effective the tillers/plant (14), biomass/plant (44.26 g) and grain yield/plant (20.71 g). This is most important cluster from yield point of view as the donors for effective tillers/plant, biomass/plant and grain yield/plant can be selected from this cluster. Cluster VII had 15 accessions and had highest value for days to maturity (166). Cluster XIII consisted of 24 accessions while cluster XIV contained 11 accessions which had the highest value for 1000-grain weight (37.53 g). This cluster can be useful in developing genotypes with higher grain weight. Interestingly, the grouped genotypes collected/originated from different

Table 1. Range, coefficient of variability and associated variance for various characters

S.No.	Characters	Season	Range	CV %	Eigen roots	% Variation
1	Days to 75%	I	114.28-133.28	2.55	3.07	20.47
	spike emergence	II	114.83-134.17	2.77	3.53	23.53
		Pooled	118.78-131.78	2.03	3.199	21.32
2	Days to maturity	I	153.17-170.83	2.46	2.604	17.36
		II	154.39-170.72	1.85	2.508	16.72
		Pooled	157.44-169.11	1.51	2.438	16.25
3	Flag leaf length	I	10.76-27.52	13.32	1.963	13.09
	(cm)	II	9.54-24.74	15.52	2.013	13.42
		Pooled	11.9-23.5	12.18	1.702	11.35
4	Flag leaf width	I	0.89-2.09	14.65	1.278	8.52
	(cm)	II	0.62-2.09	20.17	1.295	8.64
		Pooled	0.86-2.09	15.25	1.395	9.3
5	Peduncle length	I	0.71-28.11	25.34	1.08	7.2
	(cm)	II	3.4-22.9	25.19	1.092	7.28
		Pooled	2.24-25.18	23.15	1.048	6.99
6	Plant height (cm)	I	72.61-126.61	8.08	0.982	6.54
		II	60.67-130	9.35	0.907	6.05
		Pooled	74.5-123.17	6.75	0.928	6.19
7	Effective tillers/	I	4.72-17.39	24.72	0.843	5.62
	plant	II	4.39-17.39	28.16	0.857	5.72
		Pooled	4.78-17.78	20.58	0.89	5.93
8	Spike length	I	5.68-12.52	10.86	0.686	4.57
	(cm)	II	6.5-12.27	11.84	0.691	4.61
		Pooled	6.51-11.64	9.26	0.654	4.36
9	Number of	I	10.94-38.94	11.05	0.608	4.06
	spikelets/spike	II	15.67-42	9.96	0.534	3.56
		Pooled	16.89-33.22	7.82	0.528	3.52
10	Biomass/plant	I	7.62-44.97	28.67	0.487	3.25
	(g)	II	8.99-68.99	36.91	0.51	3.4
		Pooled	16.22-49.55	19.88	0.505	3.37
11	Number of	I	34-68	13.82	0.411	2.74
	grains/spike	II	30.06-72.39	18.42	0.35	2.33
		Pooled	32.72-68.72	12.98	0.455	3.03
12	Grains weight/	I	0.73-2.29	30.26	0.362	2.41
	spike (g)	II	0.56-3.62	21.55	0.319	2.13
		Pooled	0.97-2.48	20	0.391	2.6
13	Grain yield/	I	2.98-17.32	34.15	0.332	2.22
	plant (g)	II	3.86-33.64	36.58	0.222	1.48
		Pooled	6.48-21.25	30.67	0.377	2.52
14	1000-grain	I	20.11-43.65	14.96	0.273	1.82
	weight (g)	II	17.52-48.93	11.36	0.152	1.01
		Pooled	22.84-42.53	11.85	0.282	1.88
15	Harvest index%	I	16.08-74.4	21.61	0.02	0.13
		II	21.03-68.96	14.76	0.021	0.14
		Pooled	21.22-62.02	15.05	0.208	1.39

places falls into same cluster thus indicated their close affinity. Further, distribution of genotypes from same place into different clusters suggested that the geographical diversity may not necessarily be related with genetic diversity (Table 2). Redhu *et al.* (1995), Desmukh *et al.* (1999), Suri and Sharma (1999) and Bergale *et al.* (2001) also found no relationship between geographical and genetic distance. Further, the genotypes of the same cluster had little divergence from each other with respect of the aggregate effect of the fifteen characters examined. Therefore, the hybridization among the genotypes of the same cluster is not desirable for developing good segregates.

The estimates of inter and intra-cluster distances provide index of genetic diversity among and within the clusters. In pooled data, intra-cluster values ranged from 2.29 (cluster V) to 4.73 (cluster IV) indicating that cluster V and IV consisted individuals of minimum and maximum diversity, respectively (Table 3). Broadly, it can be concluded that relatively less divergence exists in cluster V, whereas individuals in cluster IV are more divergent. However, cluster XV showed zero intra-cluster distance since it had only one genotype. The inter-cluster distance of cluster X and XV was found the maximum (17.265), while cluster V and XIII had the least (2.29) suggesting wide diversity between the cluster X and XV

Table 2. Minimum and maximum values for morphological characters in hill wheat germplasm

Characters	Minimum				Maximum			
	Genotypes	Origin	Value	Group	Genotype	Origin	Value	Group
Days to 75% spike emergence	Noo1, Noo2, Noo34 VHC(BD)83, VHC6244	Nepal Uttarkashi Pithoragarh	119	I, IX	VHC6206	Champawat	132	VII
Days to 80% maturity	Noo75C VHC6102 VHC6248	Nepal Dwarahat Berinag	157	X,V,IX	Noo3	Nepal	169	VII
Plant height (cm)	VHC(LK)-1	Namhole, Shimla	74.5	IV	VHC(BD)38B	Rudraprayag	123.17	XIV
Effective tillers per plant	VHC6149 VHC6168	Gairsain Karnprayag	5	III	VHC(BD)20A VHC(BD)48	Tharali Tehri	18	VI, XIII
Spike length (cm)	VHC6241	Berinag	6.51	V	VHC(BD)8 VHC(BD)27	Almora Rudraprayag	11.64	VI, XII
Biomass per plant (g)	VHC6185 VHC6187	Lohaghat Barakot	6.22	I,III	VHC(BD)19	Tharali	49.55	VI
Number of grains per spike	VHC6409	Garur	25	V	VHC(BD)56	Tehri	68.72	IV
Grain yield per plant (g)	Noo31A	Nepal	6.48	XII	VHC(BD)19	Tharali	21.25	VI
1000-grain weight (g)	VHC(BD)56	Tehri	22.84	VIII	VHC(BD)75	Uttarkashi	42.53	XIV

Table 3. Average intra and inter-cluster distance D values in hill wheat germplasm

Season	Clusters	I	II	II	IV	V	VI	VII	VIII	IX	X	XI	XII	XII	XIV	XV
I	I	**2.58**														
II		**2.69**														
Pooled		**2.97**														
I	II	3.53	**2.72**													
II		5.04	**2.57**													
Pooled		5.28	**2.90**													
I	III	3.25	3.82	**2.92**												
II		3.92	4.81	**3.25**												
Pooled		3.54	3.21	**2.50**												
I	IV	6.18	3.26	4.75	**2.97**											
II		6.90	3.51	7.25	**2.66**											
Pooled		7.36	4.96	6.05	**4.73**											
I	V	2.98	2.40	4.46	5.24	**2.72**										
II		3.58	3.08	4.28	5.11	**2.21**										
Pooled		2.51	4.24	2.86	7.47	**2.30**										
I	VI	5.45	3.24	5.66	4.15	3.76	**3.34**									
II		5.51	4.33	6.37	4.46	3.83	**2.41**									
Pooled		7.73	4.26	6.45	5.82	6.49	**3.49**									
I	VII	2.33	2.86	3.70	5.13	3.10	4.19	**2.38**								
II		4.19	3.51	4.59	4.06	2.63	4.27	**2.26**								
Pooled		4.09	4.84	2.78	6.15	3.96	7.17	**2.73**								
I	VIII	4.17	3.34	3.94	4.00	4.85	4.39	2.50	**2.63**							
II		5.93	3.51	5.48	4.51	3.31	3.44	3.49	**3.06**							
Pooled		3.35	3.17	2.73	5.61	2.60	4.98	3.03	**2.56**							
I	IX	4.11	3.24	4.18	4.81	4.40	5.63	3.61	4.13	**3.19**						
II		4.01	4.36	4.17	5.99	3.02	4.72	3.91	5.17	**2.66**						
Pooled		3.74	2.77	2.60	6.64	2.73	5.98	4.49	3.03	**2.35**						
I	X	5.42	3.84	5.03	4.58	4.76	5.88	5.34	5.48	4.70	**3.70**					
II		4.61	3.12	6.04	4.06	2.47	4.43	3.17	4.36	4.20	**2.30**					
Pooled		11.87	9.38	10.69	11.47	11.53	10.97	12.15	11.03	9.73	**0.00**					
I	XI	14.08	13.56	12.86	13.36	14.38	15.04	14.32	14.04	13.15	13.64	**0.00**				
II		3.94	4.17	2.80	5.86	2.74	5.07	2.47	3.84	3.24	4.56	**2.60**				
Pooled		3.50	4.46	3.58	7.36	3.19	6.93	3.96	3.06	2.76	10.75	**2.54**				
II	XII	6.70	3.01	6.23	3.23	3.75	4.69	3.57	3.11	5.13	3.35	4.57	**2.44**			
Pooled		6.02	4.08	3.83	5.66	5.13	5.62	3.35	3.32	4.48	11.45	4.35	**3.12**			
II	XIII	5.42	3.91	5.02	6.17	2.54	4.11	4.54	2.93	4.05	4.35	3.89	4.24	**2.70**		
Pooled		4.04	3.25	3.33	7.09	2.29	4.90	4.88	2.63	2.52	10.64	3.72	4.86	**2.45**		
II	XIV	4.45	3.15	5.79	4.87	2.14	3.41	3.99	3.72	3.86	2.23	4.60	3.98	2.95	**2.25**	
Pooled		5.51	2.88	4.41	6.50	4.26	4.93	5.51	3.61	3.77	9.83	4.13	5.07	3.70	**2.73**	
II	XV	11.71	11.30	10.53	12.60	10.99	11.98	11.19	10.85	11.41	11.77	10.45	10.96	10.90	11.73	**0**
Pooled		11.13	12.36	11.61	13.48	11.10	13.11	10.90	10.74	11.30	17.27	10.03	10.25	12.02	11.98	**0**

Bold values denote intra-cluster distance

and a close relationship between cluster V and XIII. It may be inferred that intercrossing between the individuals of X and XV may give desirable segregants.

Cluster means for various characters exhibited significant differences. Maximum mean value for flag leaf length (20.78 cm), effective tillers/plant (14), biomass/plant (44.26 g) and grain yield/plant (20.71 g) were obtained in cluster VI which included nine genotypes. Cluster X which contained only one accession (NOO75C) showed maximum mean value for peduncle length (21.10 cm), plant height (118 cm), grain weight/spike (2.01 g) and harvest index (44%). Minimum mean value for spike length (8.56 cm) and number of spikelets/spike (19) was obtained in cluster I which included 13 genotypes. Cluster IV consisted of 5 genotypes which had minimum mean value for peduncle length (9.32 cm) and plant height (85 cm). Cluster VII showed minimum value for biomass/plant (22.88 g), while cluster XI showed minimum mean value for grain yield/plant (7.57 g). Cluster XV showed minimum value for flag leaf length (14.40 cm) and number of grains/spike (43). It is indicated that these genotypes are genetically divergent from other genotypes and exhibit superiority in aggregate performance of the above traits. These genotypes consisted of different combinations of traits individually.

On the basis of genetic divergence cluster III, IV and VI are important for yield and yield attributes. Therefore, the individuals of these clusters should be given utmost importance while framing a strategy for high grain yield. Similarly, for improving 1000-grain weight cluster XIV should get due importance. Hence, intercrossing the individuals of diverse clusters followed by pedigree or modified bulk pedigree may resort to developing superior recombinants in the segregating population.

Acknowledgements

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