Short Communications

Indian Journal of Agricultural Sciences **82** (11): 978–84, November 2012

Genetic diversity analysis for moisture stress adaptive and quality traits in bread wheat (*Triticum aestivum*)*

D T KALLESH [1], G P SINGH[2], ANJU M SINGH[3], ARVIND AHLAWAT[4] and R K SHARMA[5]

Indian Agricultural Research Institute, New Delhi 110 012

Received: 14 February 2011; Revised accepted: 17 September 2012

Key words: Bread wheat, Genetic diversity, Morpho-physiological traits, Moisture stress

India achieved remarkable progress in wheat production during the last four decades and is the second largest wheat producer in the world with the production touching a record level of 93.90 mt during 2011–12 (Anonymous 2012). Food security in the world is challenged by increasing food demand and threatened by declining water availability (Zwart and Bastiaanssen 2004). Water deficit is one of the most severe stresses faced by the sustainable crop productivity all over the world. World wide, yield losses each due to drought are estimated to be around 500 million USD (Sharma and Lavanya 2002).

Water deficit is considered to be among the most severe environmental stresses and the major constraint on plant productivity; losses in crop yield due to water stress probably exceeds the loss from all other causes combined (Rampino *et al.* 2006). The deficit has an evident effect on plant growth that depends on both severity and duration of the stress (Araus *et al*. 2002, Bartel and Souer 2004).

Drought tolerance is the function of various morpho-physiological and biochemical characters (Mitra 2001). A severe drought stress during post-flowering stages like anthesis or post anthesis causes loss of chlorophyll, cell electrolyte leakage, flag leaf yellowing and grain pre-maturation (Beltrano and Ronco 2008). In past, different morpho-physiological traits have been potentially utilized for screening genotypes of different crops under water stress conditions. However, success of breeding under stress conditions is limited (Hollington and Steele 2007), but an understanding of the genetic basis of drought tolerance in crops based on various morpho-physiological traits is also a pre-requisite for a geneticist to evolve superior genotype through either conventional or genetic engineering method (Chen *et al.* 2004). Therefore, identification and analysis of plant traits with sound and positive association with drought tolerance and high productivity under drought is necessary (Condon *et al*. 2004, Rauf and Sadaqat 2008).

Similarly the local landraces are well adapted in stress environments and farmers prefer landraces due to their ability to produce some yield even in difficult conditions where modern cultivars are less reliable (Brush 1999).

Obtaining accurate estimates of the genetic diversity among the germplasm sources may increase the efficiency of plant breeding (Barrett and Kidwell 1998). Evaluation of genetic diversity levels among the adapted germplasm can provide predictive estimates of genetic variation among the segregating progeny for cultivar development (Manjarrez-Sandoral *et al.* 1997). Studying variation among the germplasm lines of known potentialities can generate information helpful to the breeders to choose suitable parents for purposeful hybridization (Sharma 2008). Improving the productivity of wheat under moisture stress is one of the primary goals of the wheat breeding programmes in India. A wide array of material including wheat land races, local varieties, advance lines, and crosses with ancestral species are being used by different wheat breeding programmes in the country to generate the necessary genetic diversity. Better understanding of the genetic basis of this variability will improve the efficiency of wheat improvement for drought tolerance. This present study was undertaken to assess the genetic diversity of moisture stress adapted traits and so that suitable genotypes can be recommended for incorporation in the breeding programmes for the development of stress tolerant genotypes.

Field experiments were conducted at Experimental Farm, Division of Genetics, Indian Agricultural Research Institute, New Delhi, India (28° 41' North latitude and 77°13' East

* Short note

Based on complete M Sc thesis of the first author submitted to IARI, New Delhi

[1] Ph D Student (e mail:kalleshdt@gmail.com), [2,3] Senior Scientist (e mail: gyanendrapsingh@hotmail.com, anju_mahendru@yahoo.co.in, [4] Technical Officer (e mail: ahlawatarvind@yahoo.com), [5] Principal Scientist (e mail: sharma.rk.rk@gmail.com), Division of Genetics, [5]Principal Scientist (e mail: romiarora@yahoo.com), Division of Plant Physiology

latitude, 228 m above mean sea level). The area is semi-arid, subtropical climate with alluvial soil which is slightly alkaline with clay loam texture and low organic matter. The experiment was sown in two agronomic conditions (rainfed and restricted irrigation conditions) during crop season 2008–09. Material for the present study comprised 150 genotypes of bread wheat meant for all the agronomic conditions like timely sown irrigated conditions, late sown irrigated conditions and also timely sown rainfed conditions.

The experiment was laid out in alpha lattice design with two replications and two conditions of sowing (rainfed and restricted irrigated conditions). Each genotype was planted with the help of self propelled Norwegian seed drill. The gross plot size of the experiment was 1.38 m × 4.0 m, with rows at 23 cm apart. The standard cultivation practices prescribed for wheat under irrigated conditions were followed precisely. The field observations were recorded in crop growing season. The data were recorded on 10 plants from each plot for most of the traits. The observation on days to germination, tillers/m, days to heading, flag leaf area, relative water content, canopy temperature depression, days to maturity, number of grains/spike, 1 000- grain weight, and harvest index, protein content, sedimentation value and grain yield/plot. The canopy temperature depression (CTD) was measured at anthesis of the unirrigated crop using a portable infrared thermometer (Model AG-42) with a view of 2.5^0. The measurements were taken at the time of anthesis and 10 days after anthesis. Relative water content and membrane thermal stability was estimated using standard procedures. The flag leaf area was measured as per Muller (1991) and also utilizing a Licor leaf area meter at flowering (stage 61, Zadok's scale, Zadoks *et al.* 1974). Kernel hardness was measured using Single Kernel Characterization System 4100. The protein content of grain was measured by Kjeltech method using Autokjeltech 3 100 system. The SDS-sedimentation value for gluten strength was measured manually. The hectoliter weight for estimating the plumpness of the grains was measured using instrument designed by Directorate of Wheat Research, Karnal. The flour recovery percentage was worked out using Brabender senior mill. The statistical analysis was carried out using software MSTAT C (1989). The D^2 analysis was done as per Mahalanobis (1936) and Rao (1952).

Divergence analysis of 150 wheat genotypes was carried out and results with respect to both the conditions (restricted irrigation and rainfed) and the pooled analysis over both the agronomic conditions are presented in the Tables 1–3. In any crop improvement programme, genetic diversity has been considered as an important factor which is also an essential prerequisite for hybridization programme for obtaining high-yielding progenies

Direct group constellation was formed using the D^2 values for each of the characters. All the 150 wheat genotypes

Table 1 Group constellation of the 150 wheat genotypes based on Mahalanobis D^2 values

Cluster	Agronomic condition	No. of genotypes	Genotypes included
Cluster I	Res. irrigation	30	CBW 9, CBW 12, CBW 14, CBW 23, CBW 24, CHIRIYA 1, DBW 15, DBW 17, DBW 39, DBW 44, CBW 52, DBW 59, DBW 77, FLW 7, FLW 12, FLW 18, HW 2032, HW 2023, HW 4022, HW 4018, HW 5209, HD 2733, HD 2819, HD 2864, HD 2932, HD 2967, HD 2987, HS 420, HALNA, HUW 468
	Rainfed	35	CHIRIYA 1, HD 2864, HD 2932, HD 2967, HD 2987, HS 420, HALNA, HUW 468, HD 2781, WH 542, UAS 316, TEPOCA/RABE, SW-85-5422, SHANGHAI 1, SEMONG 2, RNB 1001, NL 838, NIAW 8319, DBW 66, DBW 58, CHIRIYA 3, WH 760, MORROCCO, C 306+*LR* 24, C 306+*LR* 28, HW 4026, HW 4024, HW 3018, HW 2071, HW 2039, HW 2025, PASTOR, OPATA, VOROBY, PBW 65
	Pooled	18	WH 760, MORROCCO, WH 1021, BPW 892, C 306+*LR* 24, C 306+*LR* 28, CBW 25, CBW 38, CBW 39, CNO79/PRULLA, DBW 14, CHIRIYA 7, CHIRIYA 3, HW 5207, SR 36 (LMPG), COOK, COOK 2, TR 380-14,
Cluster II	Res. irrigation	21	DBW 28, DBW 43, FLW 6, FLW 11, FLW 13, GW 273, GW 322, GW 326, HW 2005, HW 2006, HW 2045, HW 2066, HW 5206, HD 2189, HD 2329+*LR*28, HD 2643, HD 2781, HD 2824, HD 3016, HP 1913, HUW 510
	Rainfed	18	CBW 12, DBW 15, HW 5206, HD 2329+*LR* 28, HUW 510, WH 730, PC-OE-BW-02, PBW 590, NL 838, K 0607, HUW 541, DBW 50, BPW 892, CBW 38, CBW 39, COOK 2, UGN 7, MACS 2496
	Pooled	15	HUW 234, HS 365, HD 2985, HD 2944, HD 2923, HD 2329+*LR* 24, HD 2329+*LR* 37, HW 5210, HW 4026, HW 4024, HW 3018, HW 2071, UGN7, BAVIACORA, MACS 2496,
Cluster III	Res. Irrigation	18	WH 730, UP 2698, UP 2511, SUZ-2-81-13-1, RAJ3765, PC-OE-BW-02, PBW 142, PBW 590, PBW 550, PBW 502, PBW 373, PBW 343, NL 838, NIAW 1415, MACS 6222, LOK 45, K 0607, HUW 541

Continued

Table 1 *Concluded*

Cluster	Agronomic condition	No. of genotypes	Genotypes included
	Rainfed	28	CBW 9, CBW 14, CBW 23, HD 2733, FLW 11, GW 326, HD 2643, PBW 550, PBW 502, PBW 373, PBW 343, MACS 6222, LOK 63, FLW 3, CBW 42, DBW 14, CHIRIYA 7, WH 1021, CNO79/PRULLA, HUW 234, HD 2985, HD 2944, HD 2923, HW 5210, MP 4010, LOK 62, KAUZ/AA//KAUZ, HW 5207
	Pooled	29	WH 542, UAS 316, TEPOCA/RABE, SW-85-5422, SHANGHAI 1, SEMONG 2, RNB 1001, NL 838, NIAW 8319, NIAW 845, NIAW 34, NW 2036, NW 1014, MP 3224, LOK 63, LOK 1, LOK BOLD, J 24+*LR* 24, FLW 15, FLW 9, FLW 5, FLW 4, FLW 3, FLW 1, DBW 66, DBW 58, DBW 50, DBW 42, DBW 16,
Cluster IV	Res. irrigation	33	WH 542, UAS 316, TEPOCA/RABE, SW-85-5422, SHANGHAI 1, SEMONG 2, RNB 1001, NL 838, NIAW 8319, NIAW 845, NIAW 34, NW 2036, NW 1014, MP 3224, LOK 63, LOK 1, LOK BOLD, J 24+*LR* 24, FLW 15, FLW 9, FLW 5, FLW 4, FLW 3, FLW 1, DBW 66, DBW 58, DBW 50, DBW 42, DBW 16, DBW 14, CHIRIYA 7, CHIRIYA 3
	Rainfed	22	DBW 17, DBW 39, DBW 44, CBW 52,DBW 28, DBW 43, FLW 6, FLW 13, GW 273, GW 322, HW 2005, HW 2006, HW 2045, NIAW 845, NIAW 34, NW 2036, NW 1014, MP 3224, LOK 1, LOK BOLD, J 24+LR 24, FLW 15, NL 838, NIAW 1415, MACS 6222, LOK 45, K 0607, HUW 541
	Pooled	33	WH 730, UP 2698, UP 2511, SUZ-2-81-13-1, RAJ3765, PC-OE-BW-02, PBW 142, PBW 590, PBW 550, PBW 502, PBW 373, PBW 343, CS2A/2M-LR 28, LMPG, DBW 11, NEPAL 5, NIAW 8201, NW 1012, MACS 6273, MP 4010, LOK 62, KAUZ/AA//KAUZ, HI 1500, PASTOR, OPATA, VOROBY, PBW 65
Cluster V	Res. irrigation	25	WH 760, MORROCCO, WH 1021, BPW 892, C 306+*LR* 24, C 306+*LR* 28, CBW 25, CBW 38, CBW 39, CNO79/PRULLA, HUW 234, HS 365, HD 2985, HD 2944, HD 2923, HD 2329+*LR* 24, HD 2329+*LR* 37, HW 5210, HW 4026, HW 4024, HW 3018, HW 2071, HW 2039, HW 2025
	Rainfed	25	DBW 59, DBW 77, FLW 7, FLW 12, FLW 18, HW 2032, HW 2023, HW 4022, HW 4018, HW 5209, HD 2819, HW 2066, HD 2189, HD 2824, HD 3016, HP 1931, SR 36(LMPG), COOK, TR 380-14, BAVIACORA, CS2A/2M-LR 28, LMPG, DBW 11, NEPAL 5, NIAW 8201,
	Pooled	33	CBW 9, CBW 12, CBW 14, CBW 23, CBW 24, CHIRIYA 1, DBW 15, DBW 17, DBW 39, DBW 44, CBW 52, DBW 59, FLW 11, FLW 13, GW 273, GW 322, GW 326, HW 2005, HW 2006, HW 2045, HW 2066, HW 5206,M HW 2039, HW 2025, DBW 43, FLW 6, , HD 2189, HD 2329+*LR*28, HD 2643, HD 2781, HD 2824, HD 3016, HP 1913,
Cluster VI	Res. irrigation	23	HW 5207, SR 36 (LMPG), COOK, COOK 2, TR 380-14, UGN7, BAVIACORA, MACS 2496, CS2A/2M-LR 28, LMPG, DBW 11, NEPAL 5, NIAW 8201, NW 1012, MACS 6273, MP 4010, LOK 62, KAUZ/AA//KAUZ, HI 1500, PASTOR, OPATA, VOROBY, PBW 65
	Rainfed	22	UP 2698, UP 2511, SUZ-2-81-13, RAJ 3765, PBN 142, NIAW 1415, LOK 45, FLW 9, FLW 5, FLW 4, FLW 1, DBW 16, CBW 25, HD 2329+*LR* 24, HD 2329+*LR* 28,NW 1012, MACS 6273, HI 1500, HUW 510, HUW 541, NIAW 34, HW 5210
	Pooled	23	DBW 77, FLW 7, FLW 12, FLW 18, HW 2032, HW 2023, HW 4022, HW 4018, HW 5209, HD 2733, HD 2819, HD 2864, HD 2932, HD 2967, HD 2987, HS 420, HALNA, HUW 468, MP 3224, LOK 1, LOK BOLD, J 24+LR 24, FLW 15,

were grouped into six clusters in both the conditions as well as in the pooled analysis. The details of the each of the cluster are presented in the Table 1. Under the restricted irrigated conditions, among the six clusters, cluster IV contained 33 genotypes and cluster I had 33 genotypes while 25 genotypes were included in cluster V. Twenty genotypes were grouped in cluster VI and 21 genotypes were included in cluster II, while cluster III was represent by minimum number (18) of the genotypes.

In the rainfed conditions group constellation, maximum number of genotypes (35) was contained by cluster I. Cluster II had 28 genotypes, whereas, cluster V was represented by 25 genotypes. Twenty two genotypes each were included in cluster IV and VI. Minimum numbers (18) of genotypes were included in cluster II.

In the pooled analysis over the restricted irrigated

Table 2 Cluster means of 150 wheat genotypes grouped in six cluster based on 13 characters

Cluster	Sowing condition	Early vigour	No. of tillers	Days to heading	Flag leaf area	RWC	CTD	Days to maturity	Grains/ spike	TKW	Harvest index	Protein (%)	SDS value	Grain yield/plot
Cluster I	Rainfed.	2.80	89.20	77.82	19.92	57.89	4.73	131.22	43.85	36.91	0.40	11.98	36.23	1 060.5
	Res. irri.	2.84	74.35	78.37	19.36	57.20	3.87	131.41	36.50	46.21	0.41	12.36	41.33	1 347.2
	Pooled	3.10	85.55	76.25	23.42	64.36	3.89	128.60	41.40	40.78	0.39	12.45	45.36	1 189.9
Cluster II	Rainfed.	3.68	105.57	75.46	20.35	53.38	4.61	125.36	41.77	36.99	0.40	11.36	58.00	1 456.8
	Res. irri.	3.19	71.033	74.96	22.62	67.01	3.26	126..66	33.97	45.66	0.38	11.99	56.00	1 265.8
	Pooled	3.24	88.09	75.63	21.92	48.00	2.33	128.32	33.78	46.33	0.40	12.58	46.00	1 457.9
Cluster III	Rainfed.	3.22	83.02	81.87	21.32	68.70	5.64	134.63	56.68	37.82	0.38	13.36	47.00	1 302.5
	Res. irri.	3.15	75.27	79.33	26.00	60.00	4.18	132.06	46.52	47.64	0.41	13.01	45.00	1 633.2
	Pooled	2.84	87.35	83.94	22.09	53.00	4.69	135.80	43.41	36.99	0.37	13.02	46.00	1 298.4
Cluster IV	Rainfed.	2.58	99.34	86.67	29.32	68.92	5.15	135.47	45.71	34.25	0.39	12.52	42.00	1 008.3
	Res. irri.	3.35	83.62	82.26	27.36	61.98	4.20	133.88	37.83	39.64	0.40	12.64	46.00	1 658.9
	Pooled	3.40	101.98	80.97	24.98	63.82	4.56	132.64	41.22	38.15	0.38	12.55	43.00	1 455.1
Cluster V	Rainfed.	3.60	103.84	79.84	30.33	60.00	4.31	130.41	47.66	33.47	0.36	11.64	46.00	1 237.6
	Res. irri.	2.67	76.71	84.25	24.69	63.23	4.79	136.41	35.98	42.56	0.36	12.01	46.00	1 309.1
	Pooled	2.80	86.95	79.78	26.33	65.90	4.69	132.64	39.21	41.33	0.40	12.00	45.00	1 265.9
Cluster VI	Rainfed.	3.23	102.20	79.99	20.35	51.69	5.64	134.25	37.89	39.99	0.39	12.33	41.00	1 454.2
	Res. irri.	3.23	114.20	81.20	22.62	53.82	4.40	133.21	38.99	44.51	0.40	12.45	40.00	1 698.6
	Pooled	3.22	82.40	79.87	00.09	54.69	4.88	132.17	47.31	41.56	0.41	12.36	39.68	1 422.3

Table 3 Intra and inter-cluster distance for 13 characters under rainfed, restricted irrigation and pooled over the two conditions

Cluster I	Sowing conditions	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	Res. irri.	2.784	3.432	3.846	2.936	2.985	3.369
	Rainfed	2.663	2.416	2.922	2.789	3.698	3.756
	Pooled	2.856	2.964	4.564	4.245	2.489	4.236
Cluster II	Res. irri.		2.778	4.558	5.018	2.716	2.889
	Rainfed		2.847	4.193	4.658	5.698	5.169
	Pooled		2.134	5.213	3.266	3.186	4.123
Cluster III	Res. irri.			3.205	3.458	3.158	3.325
	Rainfed			2.725	3.258	4.001	3.158
	Pooled			3.128	3.149	3.069	4.020
Cluster IV	Res. irri.				2.921	3.256	3.445
	Rainfed				2.658	2.698	2.425
	Pooled				2.689	3.025	2.964
Cluster V	Res. irri.					2.695	2.654
	Rainfed					3.014	3.741
	Pooled					2.569	3.269
Cluster VI	Res. irri.						2.653
	Rainfed						2.781
	Pooled						2.896

conditions and the rainfed conditions, cluster IV and V had 33 genotypes each and cluster III contained twenty nine genotypes, while cluster VI had twenty two genotypes. Eighteen and fifteen genotypes were included in cluster I and II, respectively. Some of the genotypes were included in the same clusters under both conditions of evaluation, as well as in pooled analysis representing the genetic relatedness with each other and consistency of performance over the agronomic conditions.

The cluster means of each of the thirteen characters was calculated and are presented in Table 2. A perusal of Table 2 shows that under rainfed conditions, maximum cluster mean for the character grain yield/plot was observed for the cluster II (1 456.8) followed by cluster VI (14.52.2). The minimum cluster mean under the rainfed conditions was observed for the cluster IV (1 008.3). Under restricted irrigation conditions, maximum cluster mean was observed for cluster VI (1 698.6), followed by cluster IV (1 658.9) and cluster III (1 633.2). The minimum cluster mean was observed for the cluster I for the character grain yield/plot under restricted irrigated conditions. In the pooled analysis over the rainfed and restricted irrigation conditions, the maximum cluster mean was observed for cluster II (1 457.9), followed by cluster IV (1 455.1) and cluster VI (1 422.3). The minimum cluster mean was observed for cluster I (1 189.0).

The cluster mean analysis of 12 yield-contributing traits are presented in the Table 2 for rainfed conditions, restricted irrigation conditions and the pooled analysis over the two agronomic conditions. It is evident from the Table that cluster analysis for the characters namely early vigour, days to maturity, grain yield, number of grains/spike, grain weight/spike and canopy temperature depression might be considered to have contributed the most of the total genetic diversity of the genotypes. The relative contribution of yield *per se* towards genetic divergence was very high. Similar observations have been made by Singh and Chatrath (1993) and Jagdev (1993). A perusal of the cluster means of pooled analysis indicated that the cluster II containing minimum genotypes (15), also has lower means for the characters days to heading, days to maturity, number of grains/spike and grain weight/spike, while, highest cluster means were observed for the traits plant height and 1 000-grain weight. The genotypes which were having longer plant stature, bold grains, earliness and less grain number, could be used for breeding for short duration for stress environments. This is because the yielding potential of the genotypes was found to be coupled with many component traits. The contribution of the traits such as 1 000-grain weight, days to heading to the total genetic divergence may be due to the great influence of selection towards uniformity for early maturity, size and texture of the grains. Thus, these traits offered scope for the selection of the trait for identifying genetically diverse parents for hybridization programmes for breeding drought-tolerant high-yielding varieties suited to differential moisture availability situations based on multiple cropping systems.

The intra- and inter-cluster values are presented in the Table 3. From the perusal of the Table 3, it could be seen that intra-cluster distance was maximum for cluster III (3.205), followed by cluster IV (2.921) and cluster I (2.784), while cluster II (2.778) and cluster VI (2.653) had little lower values of intra-cluster distance in restricted irrigated conditions. Under rainfed sowings, cluster V exhibited highest

intra-cluster distance (3.014), followed by cluster II (2.847), cluster VI (2.781), III (2.725), I (2.663) and IV (2.658). Pooled analysis revealed maximum intra-cluster distance for the cluster III (3.128), followed by VI (2.896), I (2.856), IV (2.689), V (2.569) and II (2.134). Thus genotypes included within the cluster III, IV and I revealed maximum diversity.

The highest inter cluster distance was noted between cluster II and cluster IV (5.018) which is followed by cluster II and III (4.558), I and III (3.846), cluster III and IV (3.458) and minimum inter cluster distance was recorded for (2.654) in the restricted irrigation conditions. Under rainfed sowings, maximum inter-cluster distance was recorded for clusters II and V (5.698) and minimum inter-cluster distance was observed for clusters I and II (2.416).

In the pooled analysis over restricted irrigation and rainfed conditions, highest inter-cluster distance was observed between clusters II and III (5.213), followed by cluster I and III (4.564), cluster I and VI (4.236), cluster II and VI (4.123). Minimum cluster distance was observed between clusters I and V (2.489).

One of the important aspects of the present investigation was to classify 150 genotypes into different clusters based on the genetic distances. This aspect is important in sense that in long run, it will help to avoid repetition of genetically similar genotypes in hybridization. This has been achieved by resorting to assignment of these genotypes into groups and studying their inter- and intra-group diversity. As evident from Table 3, the D^2 analysis led to the formation of six groups in both the conditions of evaluation, i e restricted irrigation and the rainfed conditions.

The perusal of 150 genotypes revealed that the genotypes were belonging to different eco-geographical areas were included in the same cluster. This indicated that there is no association between clustering pattern and eco-geographical distribution of the genotypes. Also, the clustering of genotypes from different eco-geographical locations into one cluster could be attributed to make possible free exchange of breeding material from one place to other (Sharma and Hore 1997). This may also be due to the fact that the unidirectional selection practised for a particular trait at several place produced similar phenotypes which were aggregated in one cluster irrespective of their distant geographical origin. On the other hand many genotypes originating from one place were scattered over different clusters. Such genetic diversity among the genotypes of common geographic origin could be due to factors like heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability. This fact is also supported by wide inter-cluster differences among them.

SUMMARY

A study was conducted to work out the genetic divergence for yield, morpho-physiological and quality traits in timely sown restricted irrigated and rainfed conditions. In the pooled analysis, cluster IV and V had 33 genotypes each and cluster III contained 29 genotypes, while cluster VI had 22 genotypes. Eighteen and 15 genotypes were included in cluster I and II, respectively. Maximum intra-cluster distance was reported in cluster III followed by VI, II, I and IV and minimum intra-cluster distance was found for cluster V. Genotypes included in III, VI and II revealed maximum diversity among themselves. Highest inter-cluster distance was observed between cluster II and III followed by I and III, I and VI. Moderate inter-cluster distance was noticed between II and IV in the pooled analysis. Parentage of 150 genotypes revealed that genotypes were belonging to different eco-geographical areas were included in the same cluster. This indicated that there is no association between clustering pattern and eco-geographical distribution of genotypes.

REFERENCES

Anonymous. 2012. *Progress Report of All India Coordinated Wheat and Barley Improvement Project*, 74 pp. Sharma Indu (Ed.). Directorate of Wheat Research, Karnal.

Araus J L, Slafer G A, Reynolds M P and Royo C. 2002. Plant breeding and water relation in C_3 cereals: What to breed for? *Annals of Botany* **89**: 925–40

Barrett B A and Kidwell K K. 1998. AFLP–based genetic diversity assessment among wheat cultivars from Pacific Northwest. *Crop Science* **38:** 1261–71.

Bartel D and Souer E. 2004. Molecular responses of higher plants to dehydration. *(in) Plant Responses to Abiotic Stress*, pp 9–38. Hirt H and Shinozaki K (Eds). Springer-Verlag, Berlin and Heidelberg, Germany.

Beltrano J and Ronco M G. 2008. Improved tolerance of wheat plants (*Triticum aestivum* L.) to drought stress and re-watering by the arbuscular mycorrhizal fungus *Glomus claroideum*: effect on growth and cell membrane stability. *Brazilian Journal of Plant Physiology* **20**(1): 29–37.

Brush S. 1999. Genetic erosion of crop populations in centres of diversity: a revision. *(in) Proceedings of the Technical Meeting on the Methodology of the FAO World Information and Early Warning Systems on Plant Genetic Resources,* pp 34–44. Prague, 21–23 June 1999, Rome, Italy.

Chen F, Zhoghu He, Xia X, Lillemo M and Morris C. 2004. A new puroindoline b mutation present in Chinese winter wheat cultivar Jingdong 11. *Journal of Cereal Science* **42:** 267–9.

Hollington P A and Steele K A. 2007. Participatory breeding for drought and salt tolerant crops. *(in) Advances in Molecular Breeding Toward Drought and Salt Tolerant Crops*, pp 455–78. Jenks M A, Hasegawa P M and Jain S M (Eds). Springer Verlag.

Mahalanobis P C. 1936. On the generalized distance in statistics. *Proceedings of the National Academy of Science* India **2:** 49–55.

Mitra J. 2001. Genetics and genetic improvement of water stress traits for durum wheat improvement under Mediterranean conditions. *Journal of Agricultural Science* **137**: 139–45.

MSTAT C. 1989. MSTAT-C Software, Version 1.4. Crop and Soil Science Department, Michigan State University, East Lancing, MI.

Muller J. 1991. Determining leaf surface area by mean of linear measurements in wheat and triticale. *Archiv fuchtungs frschung*

21(2): 121–3.

Rampino P, Pataleo S, Gerardi C, Mita G and Perrotta C. 2006. Drought stress response in wheat: physiological and molecular analysis of resistant and sensitive genotypes. *Plant Cell and Environment* **29:** 2 143–52.

Rauf S and Sadaqat H A. 2007. Effects of varied water regimes on root length, dry matter partitioning and endogenous plant growth regulators in sunflower (*Helianthus annus* L.). *Journal of Plant Interactions* **2**(1): 41–51.

Sharma B D and Hore D K. 1997. Yield attributes of rice (*Oryza sativa*) under acid, low phosphorus and high iron soil of north-east region of India. *Indian Journal of Agricultural Sciences* **67** (12): 580–2.

Sharma K K and Lavanya M. 2002. Recent development in transgenic for abiotic stresses in leagumes of semi-arid tropics. *JIRCAS Working Report*, pp 61–73.

Sharma Rajeev K. 2008. Genetic divergence among some differentially heat tolerant genotypes of wheat. *Agricultural Science Digest* **28(1):** 69–70.

Singh K N and Chatrath R. 1983. Genetic divergence in bread wheat under sodic conditions. *Wheat Information Service* **76:** 35–38.

Yadav Rajbir, Singh S S, Jain Neelu, Singh G P and Prabhu K V. 2010. Wheat production in India: Technologies to face future challenges. *Journal of Agricultural Sciences* **2 (2):** 164–73.

Zadoks J C, Chang T T and Konzak C F. 1974. A decimal code for the growth stages of cereals. *Weed Research* **14**: 415–21.

Zwart S J and Bastiaanssen W G M. 2004. Review of measured crop water productivity values for irrigated wheat, rice, cotton and maize. *Agricultural Water Management* **69:** 115–33.