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Environmental Variation on Genetic Divergence of Wheat (Triticum aestivum L.)

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Abstract
Variations among 45 wheat genotypes were studied on multivariate scale through Mahalanobis' D^2 statistics at saline and non-saline environments. In the both environment, the genotypes were grouped themselves into five different clusters. Number of genotypes in each cluster varied with the environments. In non-saline environment, cluster II was the largest having 13 genotypes. While, under saline condition, the cluster II also had the highest number of genotypes (16). The distance within cluster were always less than the distances between clusters. The cluster III and IV, I and V and II and V exhibited wide distance between them in non saline, Again cluster III and IV, I and V, I and II and IV and V were distinctly different from others. Cluster mean for yield and its components indicated that twelve genotypes in the cluster V had good performance under non-saline and five genotypes under saline in the cluster IV had good performance. Number of spikes per plant and days to maturity in non-saline environment and number of grains per spike and days to heading in saline environment contributed maximum towards divergence among 45 genotypes.

Key words: Environmental variation, Salinity, Non-salinity, Genetic diversity, Wheat

Introduction

Genetic diversity between the genotypes is crucial for effective breeding programme as the genetically diverge genotypes produce high heterotic effects and consequently result desirable segregate for developing high yielding varieties. Creation of genetic variability and selection of materials from the variant are the major tools of any plant breeding program. Lack of genetic variability is one of the main constraints for developing wheat variety. Selection of diverse parents from distant my lead to have a wide gene combination for quantitative improvements of a crop variety (Jin, 1981). Multivariate analysis with D^2 technique measures the amount genetic diversity in a given population in respect of several characters (Naidu and Satanarayana, 1991). Genetic investigation of quantitative characters become complicated when more than one environments is considered. Because the gene expression may vary with change of environment (Naidu and Satanarayana, 1991). Hence the present investigation was carried out in two different environments to identify genetically diverse parents and also to study influence of environments on character expression and clustering pattern in wheat.

Materials and Methods

The experiment was conducted at the Experimental Farm of the Regional Agricultural Research Station, Rahmatpur, Barisal which lies at the 22^0 42″ North latitude and 90^0 23″ East longitude at an elevation of 4 meter above the sea level. It belongs to the Non-calcareous Grey Floodplain Soils (Non saline, Ganges Tidal Alluvium) under AEZ 13 (BARI, 1997). The genotypes (Table 1) were grown in pot culture under semi-controlled environment (inside plastic green house) and natural light during the season of 2008-2009. The materials were evaluated under control (non-saline) and 16 dS/m salinity level following a randomized complete block design. Salt solution was prepared artificially by dissolving calculated amount of commercially available NaCl with tap water to make 160 m M NaCl solution. The salt solution was applied with an increment of 40 m M at every alternate day till the respective concentrations were attained. Plants in control were irrigated with tap water. Treatment solution was applied in excess so that extra solution dripped out from the bottoms of the pots. Treatments began 12 days after sowing and were continued for 10 days, after which the pots were flushed with tap water to leach out the accumulated salt and the plants were irrigated with tap water until maturity (Ashraf and McNeilly, 1988; Aziz *et al.*, 2005, 2006). Data on yield and yield contributing parameters were recorded from two environments. All data were subjected to genetic analysis following Mahalanobis' (1936) generalized distance (D^2) as extended by Rao (1952).

Table 1. List of wheat entries with pedigree used in salinity screening

Sl. No.	Genotype code	Variety/Line/Pedigree	Source
1	G1	Akber	Wheat Research Centre, BARI, Joydebpur, Gazipur
2	G2	Ananda	
3	G3	Barkat	
4	G4	Kanchan	
5	G5	Aghrani	
6	G6	Kalyansona	
7	G7	Sonalika	
8	G8	Protiva	
9	G9	Sourav	
10	G10	Gourab	
11	G11	Shatabdi	
12	G12	NL-644	
13	G13	BL-1022PVN/BUC	
14	G14	SW89-5124*2/FASAN CMBW91Y03050F-030TOPM-2Y-010M-010M-010Y-010M	
15	G15	JUN/PRL	
16	G16	BL-1040 JUNCO//YD/PCI	
17	G17	AKR/4/1AS58/3/KAL/BB//ALD	
18	G18	Barkat/Bulbul	
19	G19	K-44 PEL73280/ART71/4/TZPP//TRM46/CN067//PROTOR/5/PRE DG/NAC//PF7748	
20	G20	ICTAL123/3/RAWAL87/VEE/HD2285 BD(JO)86-0JO-3JE-010JE-010JE-HRDI-RC5DI	
21	G21	Sourav*2/CATBIRD BD(D1)1040B-0DI-HRDI-RC3DI	
22	G22	Chirya-3	
23	G23	Chirya-7	
24	G24	PVN/BL1022	
25	G25	POVON-76 VCM//CNO/743*/KAL/BD	
26	G26	RAWAL-87	
27	G27	ND/VG9144//KAL/BB/3/YACO/4/CHTL/5/BAW-824 BD(DI)8875-ODI-010DI-010DI-5DI-1DI-RCIDI	
28	G28	PVN/3/BOW//CROW//BUC/PVC	
29	G29	AGR/KAN	
30	G30	K9107	
31	G31	HP1724	
32	G32	YIE86-60774	
33	G33	AKR/BALAKA//FAN/PVN	
34	G34	NL-297*2/LR25	
35	G35	G162/BL1316//NL-297	
36	G36	BL1910=ZSH23/HLB15//NL297	
37	G37	G162/BL1316//NL-297	
38	G38	Akbar/Balaka	
39	G39	KAN/6/COQ/F61.70//CNDR/3/OLN/4/PAO/5/MRNG/ALDA N//CNO	
40	G40	KRL 1-4	
41	G41	GAA/KEA/GAA	
42	G42	NL297*3/NANZING7840	
43	G43	BL2124=SW89-5193/RR21	
44	G44	FANG60//RL6043/4*NAC	
45	G45	RAWAL87//BUC/BJY	

Results and Discussion

Significant variations among the genotypes for all the seven characters of the two environments were observed. In the both environment, the genotypes were grouped themselves into five different clusters (Table 2 and 3). Number of genotypes in each cluster varied with the environments. In non-saline environment, cluster II was the largest having 13 genotypes followed by cluster V with 12 genotypes, cluster III had 9 genotypes, cluster IV containing 6 genotypes and cluster I had 4 genotypes. While, under saline condition, the cluster II also had the highest number of genotypes (16) followed by cluster III having 10 genotypes. Cluster V had 8 while, cluster 1 and cluster IV containing 6 and 5 genotypes, respectively. Clustering pattern of the genotypes in wheat was influenced by the environment.

Table 2. Distribution of 45 wheat genotypes to different clusters under non-saline condition

Cluster	Number of genotypes	Genotypes falling in cluster
I	4	G6, G17, G25, G26, G34
II	13	G1, G2, G5, G16, G19, G22, G28, G30, G31, G39, G40, G41, G44
III	9	G3, G9, G15, G18, G20, G29, G32, G42, G43
IV	6	G4, G8, G14, G21, G23, G38
V	12	C7, G10, G11, G12, G13, G24, G27, G33, G35, G36, G37, G45

Table 3. Distribution of 45 wheat genotypes to different clusters under saline condition

Cluster	Number of genotypes	Genotypes falling in cluster
I	6	G1, G15, G18, G27, G32, G34
II	16	G2, G3, G6, G7, G9, G14, G17, G19, G20, G23, G25, G26, G28, G29, G39, G45
III	10	G4, G5, G16, G21, G22, G35, G37, G38, G41, G44
IV	5	G8, G12, G33, G40, G24
V	8	C10, G11, G13, G30, G31, G36, G42, G43

Average intra and inter cluster distances (D^2) of five clusters at non-saline and saline environment are presented in Table 4 and 5, respectively. It appears that the distance within cluster were always less than the distances between clusters suggesting more wide variation between the genotypes of different clusters. The highest inter cluster distance (≈ 6) was observed between cluster III and IV in the both environments. Again, the highest intra cluster distance (≈ 3) was found in the both environments in cluster V. While, it was lowest (0.3) for the cluster I. It suggests that the genotype in the cluster V estimated higher distinctly different from the others in both environments. The distance between cluster II and IV and cluster I and III had minimum values suggesting that genotypes belonging to theses cluster less diversified in both environments.

Table 4. Average intra (bold) and inter cluster D values among five clusters of wheat genotypes under non-saline condition

Cluster	I	II	III	IV	V
I	**0.28**	3.98	2.73	3.80	4.86
II		**1.85**	3.65	2.50	4.34
III			**2.08**	6.18	3.72
IV				**1.00**	3.93
V					**3.13**

Table 5. Average intra (bold) and inter cluster D values among five cluster of wheat genotypes under saline condition

Cluster	I	II	III	IV	V
I	**0.35**	4.56	2.91	3.89	5.68
II		**1.61**	4.30	2.68	3.78
III			**2.53**	6.05	3.18
IV				**0.79**	4.14
V					**3.05**

The mean value for seven characters of the various clusters is presented in Table 6 and 7 for non-saline and saline environment, respectively. It appears that cluster I had early matured, dwarf plants with lower spikes per plant, lower grains per spike, lower grain weight and lower grain yield in both environments. The genotypes included in the cluster V were late in maturity and produced tallest plant, highest number of spikes per plant and grains per spike, 1000-grain weight and grain yield per plant under non- saline

environment. While, under saline environment, cluster IV had late maturing plant and produced bold sized grain with highest grain yield. This indicates the presence of high yielding genotypes in these clusters. Under saline environment, cluster V produced tallest plant with maximum spikes per plant and grains per spike.

Table 6. Cluster mean for the characters studied in wheat genotypes under non-saline environment

Character	Cluster				
	I	II	III	IV	V
Days to heading	55	56	59	63	60
Days to maturity	98	102	103	104	105
Plant height (cm)	65	71	74	71	79
Spikes/plant (No.)	4.0	4.8	5.1	5.6	6.0
Grains/spike (No.)	38.3	40.18	43.8	52.2	50.0
1000- grain weight	35.5	41.5	45.0	47.5	50.2
Grain yield (g/plant)	4.96	6.67	6.31	7.15	7.56

Table 7. Cluster mean for the characters studied in wheat genotypes under saline environment

Character	Cluster				
	I	II	III	IV	V
Days to heading	53	55	54	59	57
Days to maturity	97	101	98	103	102
Plant height (cm)	62	69	65	67	74
Spikes/plant (No.)	2.8	3.2	3.9	4.1	5.3
Grains/spike (No.)	23.3	25.9	31.1	36.1	39.8
1000- grain weight	30.3	33.1	37.3	44.8	39.2
Grain yield (g/plant)	2.01	3.24	4.37	6.34	3.88

Contributions of the characters towards divergence are presented in Table 8. The positive absolute values of vector 1 and negative values for vector II for the traits indicated the responsibility of primary differentiation and the negative absolute values for vector I and positive values for vector II for the characters indicated the responsibility of secondary differentiation. The canonical variate analysis revealed that the vectors (vector I and II) for number of spikes per plant and days to maturity were positive in non saline environment. While, under saline environment, number of grains per spike and days to heading were positive. Such results indicated that these characters contributed maximum towards divergence among 45 genotypes. On the other hand, negative vectors (Vector I and II) indicating lowest contribution towards the divergence among the 45 genotypes.

Table 8. Relative contributions of seven characters to total divergence

Characters	Non-saline		Saline	
	Vector I	Vector II	Vector I	Vector II
Days to heading	-0.0138	0.2157	0.0318	-0.1675
Days to maturity	0.0529	-0.0361	-0.0298	-0.0211
Plant height (cm)	-0.2973	-0.4669	-0.1437	-0.2796
Spikes/plant No.)	0.1373	0.0189	-0.0198	-0.0133
Grains/spike (No)	-0.6358	-0.3320	0.4538	0.2188
1000- grain weight	-0.1987	-0.0898	-0.0667	-0.1025
Grain yield (g/plant)	0.3011	-0.1805	-0.2503	-0.2011

Nimbalkar *et al*. (2002) studied genetic divergence of 24 wheat cultivars and grouped in 12 clusters and observed the highest and lowest intra cluster distance were observed in cluster II and I, respectively. Among the characters examined the number of grains per spike, 1000-grain weight and number of productive tillers contributed considerably to the genetic divergence in the wheat cultivars. Suri and Sharma (1999) grouped 200 wheat genotypes into 16 clusters and reported that grain yield and tiller number were major contributors towards genetic divergence. Miah and Shamsuddin (2000) grouped 16 wheat genotypes into six distinct clusters and described that grain yield, grain weight, number of grains per spike and grain filling period contributed maximum to the total divergence.

The number of genotypes in each cluster varied with the environments. Distribution of genotypes into different clusters was at random and distribution changed with the environments (Islam *et al.,* 1997 and Naidu and Satyanarayana, 1991).

The falling of same genotyped in different clusters could be explain as wide genetic divergence in the features created through selection and genetic drift (Murty *et al*., 1965 ; Murly and Anand 1966). The variation in the clustering pattern of genotypes might be due to differences in the environments studied which emphasis on the importance of multi environmental studies for quantitative assessments of genetic diversity (Naidu and Satyanarayana 1991). Variation in clustering pattern was also observed by Rao and Auryawanshi (1988) and Islam *et al.* (1997). Some authors observed in bread and durum wheat clustering that revealed instability due to relatively lesser divergence, whereas the widely divergent clusters remained distinct in different environment (Raut *et al.,* 1985; Singh *et al*., 1980). So cluster stability was dependent on divergences.

Conclusions

Considering the all characters it appears that twelve genotypes in the cluster V had good performance under non-saline environment. While, under saline environment, five genotypes in the cluster IV had good performance. The results also indicates that the cluster III and IV, I and V and II and V exhibited wide distances between them in non-saline. Again, under saline, the cluster III and IV, I and V, I and II and IV and V were distinctly different from the others. Parental materials selected from these cluster would be give broad spectrum of variation when they are hybridized for salinity breeding.

References

Ashraf, M. and McNeilly, T. 1988. Variability in salt tolerance of nine spring wheat cultivars. *J. Agron. Crop Sci*., 160: 14-21.

Aziz, M.A.; Karim, M.A.; Hamid, M.A.; Khaliq, Q.A. and Hossain, M. 2005. Salt tolerance in mungbean: growth and yield response of some selected mungbean genotypes to NaCl salinity. *Bangladesh J. Agri. Res*., 30 (4):529 - 535.

Aziz, M.A.; Karim, M.A.; Hamid, M.A.; Khaliq, Q.A. and Karim, A.J.M.S. 2006. Salt tolerance of mungbean at different growth stage: effect of NaCl salinity on yield and yield components. *Bangladesh J. Agri. Res*., 31(2): 313-322.

BARI (Bangladesh Agricultural Research Institute). 1997. Annual Report. 1996-97. BARI. Joydebpur. Gazipur.

Islam, M.S.; Rasual, M.G.; Mia, F.U.; Khatun, F. and Rouf, F.M.A. 1997. Environment variation on genetic divergence in mustard. *Bangladesh J. Pl. Breed. Genet*. 10(162): 25-28.

Jain, H.J. 1981. Evolving a new production technology of pulse crops News. 1: 1-2.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proc. Natl. Inst. Sci. India.* 2: 69-55

Miah, M.A.E. and Shamsuddin, A.K.M. 2000. Genetic divergence in bread wheat (*Triticum aestivum* L.) for source-sink characters. *Bangladesh J. Pl. Breed. Genet.* 13 (2): 19-24.

Murty, B.B. and Anad, I.J. 1966. Combining ability and genetic diversity in varieties of *Linium usitatisimum. Indian J. Genet*. 26: 21-36.

Murty, B.R.; Mathur, J.B.L. and Arunachalam, V. 1965. Self incompatibility and genetic divergence in *Brassica compestis* var. Samson. Sankhya (B). 27: 271-278.

Nimbalkar, C.A.; Navale, P.A. and Biradar, A.B. 2002. Generalized D^2 and genetic diversity in wheat. *J. Maharastra Agril. Univ*. 27 (1): 43-45.

Naidu, N.V. and Satayanarayna, A. 1991. Studies on the genetic divergence over environments in Mungbean Vigna radiata (L) Wilczck. *Indian J. Genet*., 51(4); 271-278.

Rao, C.R. 1952. Advance statistical method in biometrical research. Ed. John Willey and Sons. New York.

Rao, S.K. and Auryawanshi. 1988. Genotype x environments interaction in the genetic diversity of urd germplasm collections. *Legumes Res.*, 11: 15-20.

Raut, S.K.; Manjaya, J.G. and Khorgade P.W. 1995. Selection criteria in wheat. *PKV Res. J*. 19 (1): 17-20.

Singh, D.; Kumar, P. and Chauhan, B.P.S. 1980. Genetic diversity for some qualitative characters in barley. *Indian J. Genet.* 40: 391-395.

Suri, V. and Sharma, S.C. 1999. Genetic diversity in relation to number of cluster in wheat (*Triticum aestivum* L.). *Crop Improvement*., 26 (2): 208-215.