



Research Note

Genetic diversity analysis in Exotic germplasm accessions of Wheat (*Triticum aestivum* L.) by cluster analysis.

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(Received: 9th May 2015; Accepted: 10th Oct 2015)

Abstract

The present investigation was planned to assess genetic diversity for yield, yield contributing traits and resistance to spot blotch disease of wheat in two hundred exotic germplasm accessions of bread wheat. The germplasm along with 4 checks were evaluated in augmented block design at G.B. Pant University of Agriculture & Technology, Pantnagar during 2013-14. The genotypes were evaluated for eight quantitative traits and spot blotch incidence. The germplasm accessions showed wide variability for the studied traits and these were grouped into different clusters using Non-hierarchical Euclidean cluster analysis. On this basis, 200 wheat accessions were categorized into 8 clusters. The intra cluster distance was maximum for the cluster VII (2.431) and minimum for the cluster VIII (1.813). Inter cluster distance was maximum between cluster I and VIII (7.263) and minimum between cluster III and IV (2.292). So, larger the distance between the clusters better the chances of getting transgressive segregants.

Keywords

Bread wheat, germplasm, genetic diversity, yield, spot blotch

Wheat (*Triticum aestivum* L.) is the most widely grown crop and an essential component of the global food security mosaic, providing one-fifth of the total calories for the world's population (Reynolds *et al.*, 2011). In India the crop ranks second in terms of total production next to rice. It is largely grown in Indian states like Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra, Gujarat, West Bengal, Uttarakhand and Himanchal Pradesh. These states contribute about 98% of total wheat production in the country and play an appreciable role of supplying carbohydrates, proteins and minerals.

Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development. One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to obtain transgressive segregants, genetic distance between parents is necessary (Joshi *et al.*, 2004). The higher genetic distance between parents, the higher heterosis in progeny can be observed (Joshi and Dhawan, 1966; Anand and Murrty, 1968). Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to <http://ejplantbreeding.com>

be used in crossing nurseries to enhance the genetic recombination for potential yield increase. Some appropriate methods, cluster analysis, PCA and factor analysis, for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity, and study interaction between the environment are currently available (Bhatt, 1970; Carves *et al.*, 1987; Mohammadi and Prasanna, 2003).

It is widely accepted that evaluation and cataloguing of genetic resources (GR) is an essential prerequisite for a successful breeding programme, which facilitates utilization of diverse germplasm. By using the diversity analysis tools we can quantify the degree of genetic divergence amongst different populations (Jaiswal *et al.*, 2010). The aim of this study was to identify genetically divergent germplasm accessions possessing desirable yield traits and resistance to spot blotch. Spot blotch caused by [*Bipolaris sorokiniana* (Sacc. In Borok) Shoem] earlier to be a major disease of north eastern plains zone (NEZP) of the country now due to changing climatic conditions its incidence has significantly increased in north western plains zone (NWZP), therefore, analyzing diversity for spot blotch resistance along with yield traits would help identification of better donors to be used in breeding programme.

Field experiment was conducted in N. E. Borluag Crop Research Centre (NEBCRC), G.B. Pant University of Agriculture and Technology, Pantnagar, Distt. U.S. Nagar, Uttarakhand during

rabi, 2013-14. The Crop Research Centre is situated at 29°N latitude, 79°29' E longitude and at an altitude of 243.84 m above the mean sea level.

The experimental material consisted of two hundred exotic germplasm accessions including four checks, two each resistant (Chirya 3 and Francolin) and susceptible (Sonalika and Ciano T79) was evaluated in Augmented Block Design (ABD). Each genotype was grown in 2 rows of 1 m long plot with 23 cm distance between rows. The recommended cultural practices were adopted to raise good crop. The data were recorded for 9 characters viz., days to 75% heading, days to maturity, plant height, spike length, number of spikelets per spike, number of grains per spike, thousand grain weight, grain yield and Area under Disease Progress Curve (AUDPC) based on disease severity. Disease severity was recorded on each plant using the double digit scale (00-99) developed as a modification of Sarri and Prescott's severity scale to assess foliar blight diseases in wheat (Sarri and Prescott, 1975) by visually scoring the percent diseased area on the flag (F) and penultimate (F-1) leaves. Data recorded on the above characters were subjected to Non-hierarchical Euclidean cluster analysis (Spark, 1973).

The analysis of variance revealed highly significant differences among the genotypes for days to 75% heading, number of grains per spike, grain yield and also for AUDPC. The data is presented in table 1. Maximum number of days to 75% heading were recorded in case of accession No. 120 (106.62) and minimum in accession No.95 (73.37). Maximum number of days to maturity was recorded in case of accession No. 123(155.25) and minimum in accession No.93 (98.0). The accession No. 85 attained maximum height of 123.31cm and accession No.143 attained minimum (73.91 cm). The range of spike length was observed from 7.46 - 14.71 cm with a general mean of 11.11. Coefficient of variation was 12.79%. The range of spikelets/spike was observed from 13.12- 27.12. (Fig. 1). The accession No. 94 attained maximum number of grain per spike of 63.75 and accession No. 109 attained minimum (29.5) (Fig. 2) with a general mean of 41.72 Coefficient of variation was 8.34%. The accession No. 188 attained maximum thousand grain weight of 53.79g and accession No. 38 attained minimum (23.03g.) (Fig. 3) with a general mean of 35.88. Coefficient of variation was 12.58 %. The accession No. 166 attained maximum grain yield of 344.06g and accession No. 74 attained minimum (61.56 g.) (Fig. 4) with a general mean of 174.29. Coefficient of variation was 40.39 %. The range of AUDPC value was from 36.43 to 2411.68 with general mean of 1097.70.

The germplasm accessions were highly variable for disease severity as revealed by the AUDPC value. Out of 200 accessions, 17 accessions were observed highly resistant, 7 resistant, 87 moderately resistant, 3 highly susceptible and 86 accessions were observed moderately susceptible (Table 2).

The Non-hierarchical Euclidean cluster analysis grouped 200 exotic germplasm accessions into eight distinct clusters (Table 3). Distribution pattern of all genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits. Earlier studied have also reported substantial genetic divergence in wheat materials (Deshmukh *et al.*, 1999; Roy *et al.*, 2004; Verma *et al.*, 2006; Singh *et al.*, 2006; Iqbal *et al.*, 2007; Jaiswal *et al.*, 2010; Verma *et al.*, 2013). The average intra and inter cluster distances have been presented in (Table 4). The intra cluster distance of cluster VII was 2.431, which revealed maximum genetic diversity among its constituents followed by cluster III (1.949), cluster II (1.946), cluster IV (1.940), cluster V (1.878), cluster I (1.859), cluster VI (1.825) and cluster VIII (1.813).

Inter cluster distance being maximum between cluster I and VIII (7.263) followed by cluster I and II (5.251), cluster V and VIII (5.223) and cluster VII and VIII (5.221) indicate that the genotypes of cluster I and VIII and cluster II and V are distantly related to each other. It showed that genotypes with maximum distance resulted in higher yield and there are more chances of getting transgressive segregants which can be used in breeding programme.

On the other hand minimum inter cluster distance was recorded between cluster III and IV (2.292) followed by cluster III and V (2.367) and cluster V and VII (2.435), indicating that genotypes of cluster III and IV and V and VII possess gene which have similar expression. Hence these can be used for backcross breeding programme. This is in accordance with the findings of Bashyal *et al.* (2011).

There were variable mean values for different characters in different clusters (Table 5). Cluster I bears lowest mean value for days to maturity (107.4). Similarly for plant height cluster VII bears lowest value (93.01) and cluster III consists of tall type plants with mean value 106.16. Cluster II consists of genotypes with longest spikes having mean value 12.72. Maximum numbers of spikelets were found to be in cluster VIII (25.32) and minimum (17.18) in cluster I. Cluster VIII consists of genotypes bearing maximum grains per spike



with mean value of 56.33, whereas grain weight was highest in genotypes of cluster XVII (2.57) indicating that the genotypes bears bold grains. Thousand grain weights were found to be maximum for cluster VIII mean value of 44.01.

The analysis of variance revealed highly significant differences among the genotypes for days to 75% heading, number of grains per spike, grain yield and AUDPC value. The characters which have sufficient variability suggested that a crossing programme involving diverse genotypes may lead to an overall improvement in crop. Inter and intra cluster distance provide index of genetic diversity between and within clusters. It would be desirable to choose the donor from different clusters. Larger the distance between the clusters better the chances of getting transgressive segregants. These findings suggested that the experimental material had sufficient diversity for yield traits as well as severity to spot blotch. Diversity in these characters may be exploited by restoring to hybridization which would be subsequently released into the development of superior lines for yield and spot blotch resistance.

Acknowledgement

The authors pose sincere thanks to CIMMYT, Mexico for financial support from Seeds of Discovery (SeeD 2012-021) project and Director, Experiment Station, GBPUAT, Pantnagar for providing necessary facilities for carrying out the investigation.

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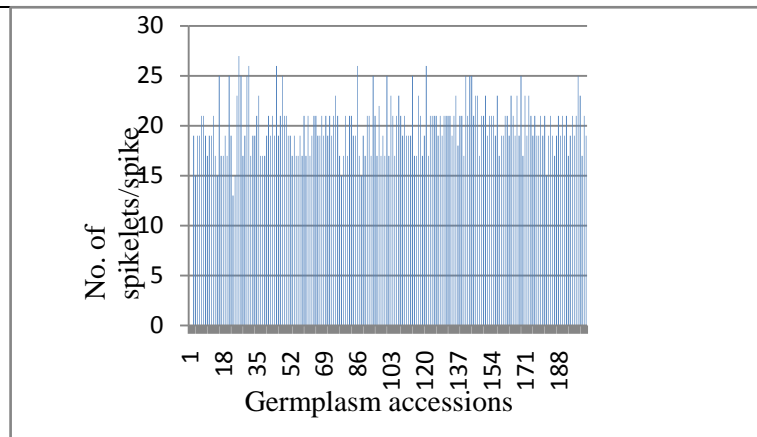


Fig.1. Variation of No. of spikelets/spike in germplasm

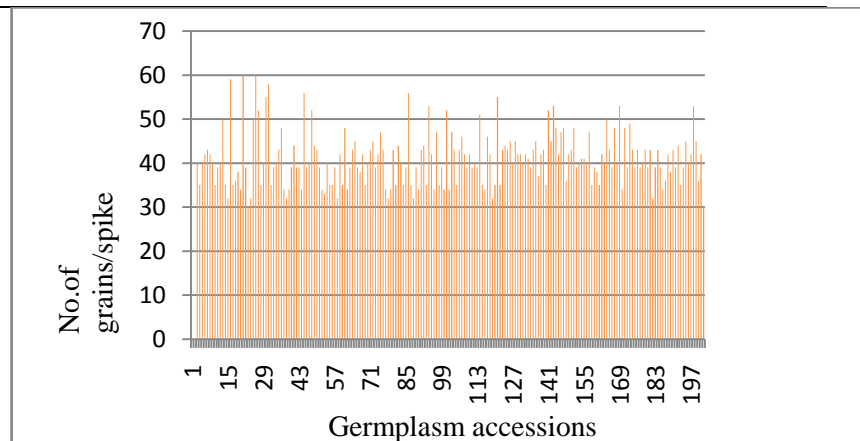


Fig.2. Variation of No. of grains/ spikelet in germplasm

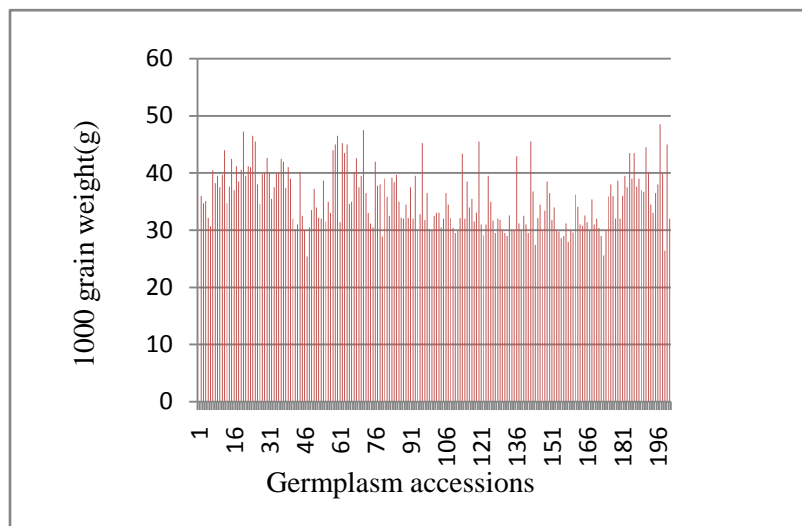


Fig.3. Variation of No. of 1000 grain weight in germplasm

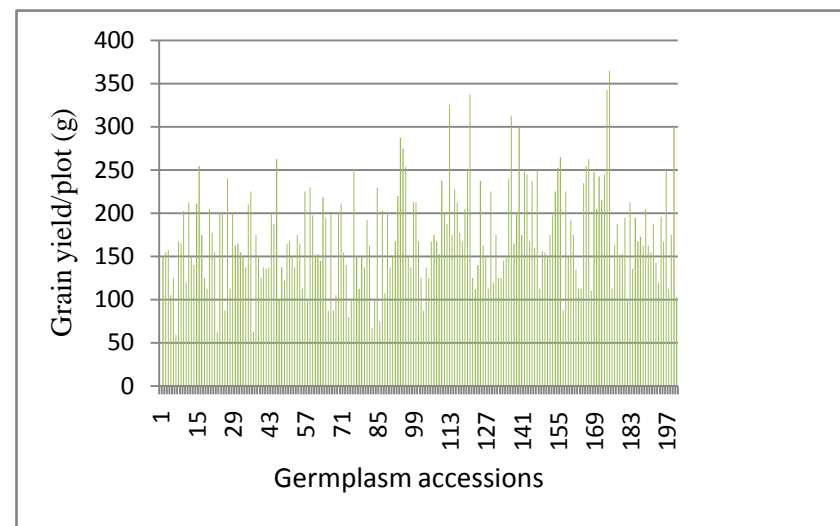


Fig.4. Variation of yield/plot(g) in germplasm accessions



Table 1. Mean, range and least significant differences in the germplasm accessions

Sl. No	Character	Genotype		Checks			CV%	CM	AVSB	AVDB	AVAC	
		General Mean	Range	Ciano-T79	Chirya3	Sonalik a						Francolin
1	Days to 75% heading	94.2	73.37-106.62	100.0	94.25	99.5	95.75	4.319	6.72	13.45	15.03	11.88
2	Days to maturity	125.87	98.0-155.25	140.25	128.0	139.75	127.0	6.66	14.25	28.50	31.86	25.19
3	Plant height	100.54	73.91-123.31	97.83	97.5	100.91	100.33	4.75	7.53	15.06	16.84	13.32
4	Spike length	11.11	7.46 - 14.71	12.0	10.50	10.50	11.37	12.79	2.27	4.54	5.075	4.012
5	No. of spikelets per spike	20.08	13.12-27.12	21.5	19.5	19.50	18.5	9.02	2.83	5.66	6.33	5.00
6	Number of grains per spike	41.72	29.5-63.75	43.75	37.75	40.2	37.5	8.34	5.30	10.60	11.8	9.37
7	1000 grain weight	35.88	23.03-53.79	32.78	34.78	35.58	36.22	12.58	7.009	14.01	15.67	12.39
8	Grain yield	174.29	61.56-344.06	167.5	136.8	165.0	174.3	40.39	103.93	207.8	232.41	183.73
9	AUDPC	1097.70	36.43-2411.68	1476.25	1012	903.62	1159.8	38.21	695.28	1390.5	1554.7	1229.1

CM= Least significance differences between the mean of two check varieties.

AVSB = Least significance differences between the adjusted value of two selections in the same block

AVDB= Least significance differences between the adjusted value of two selections in the different blocks

AVAC= Least significance differences between the adjusted selection value and a check mean

Table 2: AUDPC values of 200 germplasm accessions

Spot blotch resistant/ susceptible	Total No. of accessions	AUDPC range
Highly resistant	17	0
Moderately resistant	87	568.5-1248
Resistant	7	157.5-496
Moderately susceptible	86	1256.5-1912.5
Susceptible	3	2029.5-2346



Table 3. Grouping of various accessions according to their position in eight clusters

Cluster No.	Accessions	No. of accessions
Cluster 1	Accession no. 13, 33, 129, 169, 170, 177, 178, 179, 180, 189, 198	11
Cluster 2	Accession no. 2, 9, 18, 21, 30, 36, 41, 46, 57, 64, 65, 77, 101, 134, 137, 146, 152, 164, 173, 181, 182, 184	22
Cluster 3	Accession no. 22, 26, 38, 50, 54, 55, 56, 58, 62, 71, 78, 86, 87, 90, 94, 98, 103, 106, 114, 115, 122, 125, 130, 133, 138, 149, 150, 153, 158, 162, 185, 190, 197,	33
Cluster 4	Accession no. 4, 8, 14, 16, 24, 27, 28, 42, 44, 52, 60, 66, 76, 84, 96, 97, 111, 121, 123, 126, 135, 143, 147, 157, 163, 187, 192, 196	28
Cluster 5	Accession no. 1, 3, 17, 23, 25, 29, 32, 37, 39, 40, 45, 47, 48, 49, 63, 69, 79, 82, 85, 88, 89, 93, 105, 107, 110, 113, 118, 119, 141, 142, 145, 151, 160, 161, 165, 166, 167, 194, 200	39
Cluster 6	Accession no. 5, 10, 12, 20, 34, 68, 72, 92, 100, 104, 108, 109, 112, 116, 117, 120, 124, 128, 132, 136, 140, 148, 156, 159, 168, 172, 183, 188	28
Cluster 7	Accession no. 6, 7, 11, 19, 31, 35, 51, 53, 59, 67, 70, 73, 74, 75, 80, 83, 91, 95, 99, 127, 139, 144, 154, 155, 171, 186, 191, 193, 195, 199	30
Cluster 8	Accession no. 15, 43, 61, 81, 102, 131, 174, 175, 176	9

Table 4. Estimate of average intra and inter cluster distances for eight clusters

	1	2	3	4	5	6	7	8
1	1.859	5.257	3.387	4.906	3.380	3.688	4.674	7.263
2		1.946	3.962	2.934	3.996	2.896	4.93	2.565
3			1.949	2.292	2.367	2.903	2.600	4.991
4				1.940	2.587	2.468	2.438	3.181
5					1.878	2.532	2.435	5.223
6						1.825	3.188	4.352
7							2.431	5.221
8								1.813



Table 5. Cluster mean value for different characters

Clusters	Characters							
	DH	DM	PH	SL	SLS	GRS	TGW	GY
Cluster I	81.38	107.64	103.51	10.67	17.18	38.57	32.12	138.26
Cluster II	90.82	120.72	102.20	12.72	23.68	51.22	41.42	220.90
Cluster III	93.77	126.42	106.16	11.20	20.75	42.45	29.30	145.67
Cluster IV	98.53	132.60	97.24	11.87	21.42	43.69	36.18	190.97
Cluster V	93.14	124.00	104.14	10.26	17.64	35.98	34.46	212.33
Cluster VI	92.44	119.15	98.49	11.80	19.81	39.92	42.00	133.35
Cluster VII	99.25	134.95	93.01	9.36	18.36	38.03	33.79	140.91
Cluster VIII	99.46	136.53	98.31	12.45	25.35	56.33	44.10	231.12

DH: Days to heading, DM: Days to maturity, PH: Plant height, SL: Spike length, SLS: No. of spikelets per spike, GRS: Grains per spike, TGW: Thousand grain weight, GY: Grain yield