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Research Article

The richness of diversity in a core collection of bread wheat (*Triticum aestivum* L.)

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Abstract
Diversity evaluation provides opportunity to assess genetically important distinct traits that will effectively contribute to improvement of genotypes. Assessing genetic diversity in a core collection is key to find out the ways to efficient utilization of genetic resource. Wheat cultivars spinning over a century were collected from the Indian Institute of Wheat & Barely Research (IIWBR), Karnal, made up of a core collection. The core set of data was analysed by multivariate methods. The experimental material consisted of ~100 genotypes which were evaluated in an Augmented Randomized Block Design. Quantitative characters like no. of grain per spike, no. of spikelet per spike, test weight and spike length were found to be the key yield contributing traits. Principal component analysis (PCA) and cluster analysis of eight quantitative characters and genotypes fall into three principal component and three cluster respectively. Based on these experiment first and third cluster genotypes have high associated with PCI and PCIII. These principal components were made by grouping them high yield contributing traits. Genotypes in these clusters have higher values for yield contributing traits then the total average of traits. Genotypes belonging to superior clusters could be considered to very useful to developing high yielding varieties and other breeding activities.

Keyword
Principal Component Analysis (PCA), Cluster Analysis, Wheat

Introduction

The total cultivated area of wheat in the world is around 220.11 million ha (2016-17) with production of 758.2 million tonnes and a forecast of 749.5 million tonnes (2017-18) while the average global productivity of wheat is 3405 kg per ha FAO(2017). The major wheat producing countries are China followed by India, USA, and France. India's share in the world area is about 12.5 percent, whereas it occupies 13.1 % in total wheat production. In India, wheat is the second most important crop after rice occupying 30.42 million hectares with a production of 98.38 million tonnes and the average productivity of 3.1 tonne per hectare in 2016-17. Uttar Pradesh, Punjab and Haryana are the important states from the point of both area and production (Anonymous, 2017). Development of high-yielding varieties requires a thorough knowledge of the existing genetic variation in a crop. One of the main objectives of any breeding program is to produce high yielding varieties for release as cultivars to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines are to be selected for further manipulation to achieve the target. Introduction of new cultivars can be made from one region to the other easily and may be used for further manipulation to develop breeding lines Jamal *et al.*(2009). The present study aims to evaluate wheat germplasm released in India spanning a period of 100 years (1906-2006) procured from IIBWR. This core collection was then analysed for eight quantitative agro-morphological characters. Diversity analysis is a efficient approach to utilized genetic variation present in a core collection Hodgkin *et al.*(1995) Zhang *et al.*(2011). The core collection is a effective tool to capture maximum genetic diversity by minimizing the number of genotypes Frankel (1984).

Materials and Methods

The set of 98 genotypes (94 core set genotypes and four check varieties) Indian bread wheat genotypes (Table 1) collected from the Indian Institute of Wheat & Barely Research (IIWBR), Karnal, Haryana; based on the multivariate analysis for eight agro-morphological traits was evaluated at Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, using Augmented Randomized Block Design (Federer, 1956) to estimate genetic variation for the traits in *Rabi* 2013-14. Cluster analysis was carried out of mean all eight traits namely plant height (cm), days to 50% flowering, days to maturity, number of spikelets per spike, spike length (cm), number of seeds per spike, test weight (gm) and yield per plant (gm) was performed, based on genetic distance matrix of the

94 germplasm accessions along with four checks, applying the UPGMA (Unweighted Pair-Group Method using Arithmetic average) clustering method (Michener *et al.,* 1957). Principal component analysis reduced the data by minimizing number of variables that were correlated to each other called principal components. Scatter dendrogram biplot to show the variation patterns. Quantitative traits were analyzed by cluster and principal component analysis with the help of software program 'SPSS' v 16.0. Cluster analysis identified variables which are further clustered into main group and subgroups using Ward's method. The genotypes as well as traits in each cluster were also analyzed for basic statistics. The genotypes were sown with a row to row distance of 20 cm and 0.5 m distance in between blocks and each genotype was sown in 3 lines of 2 m length in *Rabi* 2013-14. Check varieties were repeated in each block. Recommended cultural practices were followed to grow a healthy crop and for proper expression of genotypes. Three random but robust plants from inner rows were tagged from each plot for data collection. A total of eight quantitative traits were taken at appropriate crop growth stage, in to the consideration.

Results and Discussion

Multivariate data analysis techniques that are reduced complexity of data sets and simplified results. These include principal component analysis and hierarchic clustering analysis (HCA). Principal component analysis is suitable to identify and determination of independent principal components that are effective on plant traits separately. It reflects the most dominant and largest contributor to the total variation. It helps breeders to genetic improvement traits such as yield that have low heritability, specifically in early generations via indirect selection for traits effective on this Golparvar *et al.(*2003) , Leilah *et al*.(2005), Golparvar *et al.,(* 2006). The eigenvalues are often used to determine how many factors to retain. The sum of the eigenvalues is usually equal to the number of variables. The bi-plot helps to visualize the first three principal components are often the most important in reflecting the variation patterns among genotypes and the traits associated with these are more useful in differentiating genotypes (Fig.1 & Fig.2).

Principal component analysis (PCA) identified important largest contributor by reduced them. It is also grouping them of total variation into few components (Sharma, 1998). In the present study, first three components account for about 63.708 % of total variation giving a clear idea of the structure underlying the variables analyzed. However, the criterion of cut-off limit for the coefficients of the proper vectors greater than 0.3 having a large enough effect to be considered important (Fig 2). Therefore, in this analysis the first factor retains the information contained in 2.52 of the original variables. PCA for the first three principal components of these data are given in table 2. Five principal components PC 1 to PC 5 , which are extracted from the original data and having latent roots greater than one, accounting nearly 75% of the total variation. Suggesting first these principal component scores might be used to summarize the original eight variables in any further analysis of the data. Out of the total principal components retained, PC1, PC2 and PC3 with values of 31.50 %, 17.17 % and 15.03 % respectively contributed more to the total variation and in addition to PC1, PC2 and PC3 with values of 31.50 %, 48.67 % and 63.70 % cumulative variance (%) respectively contributed to the total variation. This values was useful for deciding priories of PC i.e. PC1 is more important than PC3 (Table 2). Characters with highest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero (Chahal and Gosal, 2002). It was suggested varieties were grouping them into few different cluster with relatively high contribution of few characters rather than small contribution from each character (Fig 1). The first principal component accounted for 31.50% of total variance indicating that plant height (cm), no. of grains per spike and no. of spikelets per spike were the variables that contributed most positively and also registered those with high yield component values. The second component accounted for 17.177 % of total variance which identified component variables (days to 50% flowering and test weight (gm) presenting positive contributions and the main characters responsible for classification. The third principal component accounted for 15.032% was positively associated with spike length (cm) and days to maturity. This component was negatively associated with yield (gm/plant) differentiating those genotypes with their characteristics (Table 2, Table 3). The overall comparison or association of levels of similarity among genotypes and among traits under study are depicted as Fig. 1 & Fig 4 respectively. In conclusion, indirect selection *via* traits like no. of grains per spike, no. of spikelets per spike which have higher heritability relative to seed yield and strongly associated with this trait is emphasized in this study for genetic improvement of yield. Similar results were found in bread wheat genotypes Golparvar *et al.* (2006) & Arain *et al.(*2011).

On the basis of their greater intercluster distance of genotypes (Table 1, Fig 1), high value of cluster mean according to the character to be improved (Table 4). These genotypes could be used in hybridization programme for improvement of

different plant characters (Table 1). From principal component analysis (PCA) the first three principal components explained 63.708% of the total variation, suggesting that traits such as plant height, days to flowering, days to maturity and grain yield contributing traits are the principal discriminatory traits in the germplasm (Table 2 & 3). The diverse parents from various clusters are helpful in planning and broadening the breeding programme by planning the crosses and increased use of heterosis and genetic diversity especially for grain yield in our country (Fig 1).

The generated information can be helpful in reducing the overall time required to screen large populations for potential breeding stock. Genotypes were showing high plant height and days to 50% flowering may be useful as potential donors for increasing total plant biomass. The genotypes with late maturity, longer spikes and high no. of grain per spike, high no. spikelets per spike with high test weight might serve as potential donors for increasing grain yield of predominant wheat varieties. It is concluded that the genetic variation existing in the germplasm set can efficiently be utilized in genetic improvement of bread wheat.

Analyses performed by the UPGMA grouped 98 genotypes into total three clusters based on two step cluster analysis (Table 1, Fig. 1). Genotypes which are falling under different clusters had diverse parent and it could be used for hybrid programme to get the higher heterotic effect. Sanni *et al.,* 2012 also reported similar findings from cluster analysis of the rice germplasm for agro-morphological traits diversity. First and third cluster were associated with PC1 (0.253 & 0.297), Second cluster with PC2 (1.11823) and third cluster 3 with PC1 (0.99402) (Table 2). It is suggested that cluster first and third more important in terms of plant yield contributing genotypes and traits. Number of genotypes fall into cluster 28, 42 and 28 in first, second and third cluster respectively and average performance of traits in each cluster is shown (Table 3).

In first cluster 28 genotypes were classified and the average values of genotypes in this cluster for plant height (cm) (110.2), days to 50% flowering (67.54) and no. of spikelet per spike (43.01) were higher than the total mean of all genotypes (91.35, 65.41 and 42.28) respectively. Third cluster comprises 28 genotypes and this group were highest values with respect to days to maturity (155.43), no. of grains per spike (59.50), test weight (40.33 g), average grain yield (31.80 g) than the total mean of all genotypes (153.74, 57.27, 30.03 and 21.39) respectively. Members of this group are suitable for breeding programs aimed at improving the yield (Table 4). Crossing among existing genotypes in first and third group provided more possibility to having more genetic variance and optimal genotypes with respect to yield performance. In the second cluster 42 genotypes were classified. These genotypes were lower rate of almost all traits (Table 4). These genotypes can be removed for core collection to avoid efforts, labour and cost. Apart from genotypes, variable traits were also grouping them into few number based on comparative levels of similarity (Fig 3). In this figure yield per plant is closely associated with test weight and spike length, means these traits were highest contributed to yield per plant. Day to maturity and plant height were highest cluster distance means these traits were lowest contributed to yield per plant.

Cluster analysis based on the three principal components grouped the lines into the three clusters (Fig. 1, Table 1). Average value of component for each cluster is shown in table 4. In the first cluster were highest value with respect to first component (**0.25309**) and third component (0.99402). Third cluster had highest values for second component (1.11823) (Table 2). Therefore, these genotypes of this cluster can be used for increase in grain yield in breeding programs. First and third cluster genotypes have associated with high yield component. Second cluster had not associated with any component. Genotypes of this cluster cannot use for increase yield associated characters in breeding programs.

Studied were shown the existence of considerable genetic variation among the genotypes in cluster first and third. These genotypes may be considered for further selection and breeding. However, these genotypes should also be tested in multi-location trials to confirm their superiority and may then be used as parents in hybridization programme to develop high yielding varieties along with desirable character. Parents may be selected from those clusters which had significant genetic distance for crossing in order to obtain genetic recombination and transgressive segregation in the subsequent generations. These clusters positively associated with PCI and PCIII. Among these high yielding principal component characters like no. of grain per spike, no. of spikelet per spike and test weight have majorly contributing to yield. Since above mention promising genotypes and distinct majorly yield contributing traits identified in this experiment, However further research across location and years needs to be done in order to corroborate the results obtained in the present investigation. These genotypes and traits could be very useful in developing high yielding varieties with desirable traits.

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Table 1. List of genotypes used in experiment were grouping them into three cluster

Sr. No.	Genotype	Cluster	Distance	Sr. No.	Genotype	Cluster	Distance
1	PBC TYPE 11	1	25.997	50	WL 410	3	17.832
2	A 115	2	12.915	51	WL 711	2	17.422
3	A 90	2	9.457	52	DL 153-2(KUNDAN)	3	13.917
4	8A	2	16.854	53	HD 2285(GOBIND)	2	15.989
5	NP 111	2	13.532	54	HD 2385	1	9.560
6	NP 165	3	18.873	55	HI 784 (SWATI)	1	24.741
7	C 518	3	18.854	56	HUW 206	1	7.301
8	NP 710	2	16.861	57	J 405	2	19.571
9	NP 721	1	20.447	58	K 8020 (TRIVENI)	1	22.960
10	C 591	2	15.953	59	K 8027 (MAGHAR)	3	19.938
11	HYB 11	1	18.320	60	PBN 142(KAILASH)	3	11.834
12	NP 809	2	11.143	61	PBW 226	1	13.596
13	NP 832	3	14.895	62	RAJ 1482	2	12.480
14	NI 179	2	19.631	63	RW 3016	3	19.921
15	NP 890	2	20.142	64	GW 120	2	15.280
16	NP 770	2	19.030	65	DWR 39 (PRAGATI	1	8.663
17	HY 5	2	21.058	66	HS 86	2	20.307
18	C 286	1	12.804	67	PBN 51	3	19.628
19	HYB 633	1	18.414	68	SAGARIKA	3	15.576
20	NP 825	1	17.549	69	NARMADA 112	1	17.850
21	NP 852	1	12.748	70	UTKALIKA	3	31.633
22	SAFED LERMA	2	11.211	71	HP 1493	2	24.015
23	KHARCHIA 65	2	23.164	72	HUW 37	2	14.596
24	C 306	1	27.218	73	HUW 213	3	12.569
25	NP 824	1	25.907	74	UP 1109	3	10.840
26	SONORA 64	3	12.856	75	AKW1071(PUNA)	2	17.431
27	NP 884	2	12.646	76	DL 788-2(VIDISHA)	3	19.145
28	HD 1949(MOTI)	2	9.910	77	HP 1633 (SONALI)	2	26.141
29	HD 1982	2	20.979	78	HP 1761(JAGDISH)	3	14.098
30	HD 2177	2	15.113	79	HPW 147	2	21.457
31	HD 2189	2	16.019	80	HS 295	3	16.479
32	HS 1138-6-4	2	16.913	81	HS 365	1	19.530
33	HW 657	2	12.651	82	K 9644 (ATAL)	1	15.666
34	HYB 65	1	20.001	83	NIAW 34	3	15.733
35	IWP 72	3	14.787	84	PBW 396	1	18.909
36	J 1-7	1	12.067	85	HPW 89 (SURABHI)	3	21.724
37	K 78	1	22.117	86	HD 2864 (URJA)	1	13.781
38	LAL BAHADUR	1	13.009	87	HS 375 (HIMGIRI)	2	17.548
39	NARMADA 4	2	13.745	88	HS 420 (SHIVALIK)	3	15.198
40	NARMADA 195	2	10.406	89	K 7903 (HALNA)	1	18.782
41	UP 215	2	5.085	90	K 8434 (PRASAD)	1	11.011
42	UP 262	1	24.644	91	K 9162	1	20.860
43	UP 368	2	10.616	92	K 9533 (NAINA)	2	14.573
44	WG 357	2	20.450	93	RAJ 3777	3	13.463
45	GW 40	2	25.574	94	RAJ 4037	3	8.715
46	J 24	2	13.138	95	HD2967 (Check)	3	24.640
47	HD 2329	2	12.296	96	PBW 644 (Check)	3	33.025
48	HD 2135	3	21.506	97	WH1021 (Check)	3	24.652
49	HUW12	2	22.575	98	RSP 561 (Check)	3	27.494

Table 2. Principal Component analysis of wheat genotypes with their eigenvalue, variance explained (%) and Cumulative variance (%).

Clusters Analysis	PC_1	PC_2	PC_3
Cluster I	**0.25309**	-0.28045	**0.99402**
Cluster II	-0.36733	-0.55852	-0.46795
Cluster III	**0.29791**	**1.11823**	-0.29209
Eigenvalue	2.520	1.374	1.203
Variance Explained (%)	31.500	17.177	15.032
Cumulative variance (%)	31.500	48.677	63.708

Table 3. Coefficients and vectors associated with the first three principal components

Traits	Eigen Vector			Communalities
Spike length (cm)	-0.007	-0.049	**0.580**	**0.607**
Days to maturity	-0.040	0.064	**0.601**	**0.643**
Yield (gm/plant)	**0.372**	-0.018	-0.214	0.663
No. of grains per spike	**0.324**	-0.083	0.081	0.488
No. of spikelets per spike	**0.336**	-0.015	0.081	0.600
Plant height (cm)	**0.354**	-0.099	-0.024	0.514
Days to 50 % flowering	-0.151	**0.628**	0.022	0.826
Test weight (gm)	-0.004	**0.524**	-0.005	0.755

Table 4. Mean values for three clusters based on eight yield contributing traits

Cluster	Freq.	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of spikelets per spike	Spike length (cm)	No. of grains per spike	Test weight (gm)	Avg. yield per plant (gm)
I	28	110.2	67.54	153.68	43.01	11.23	57.93	28.08	20.28
II	42	83.74	64.69	152.38	40.79	10.47	52.79	26.37	13.43
III	28	85.49	65.93	155.43	42.58	11.39	59.50	40.33	31.80
Mean	98	91.35	65.41	153.74	42.28	11.09	57.27	30.03	21.39
S.E.	-	7.21	1.94	2.92	8.22	1.10	3.91	7.09	4.15

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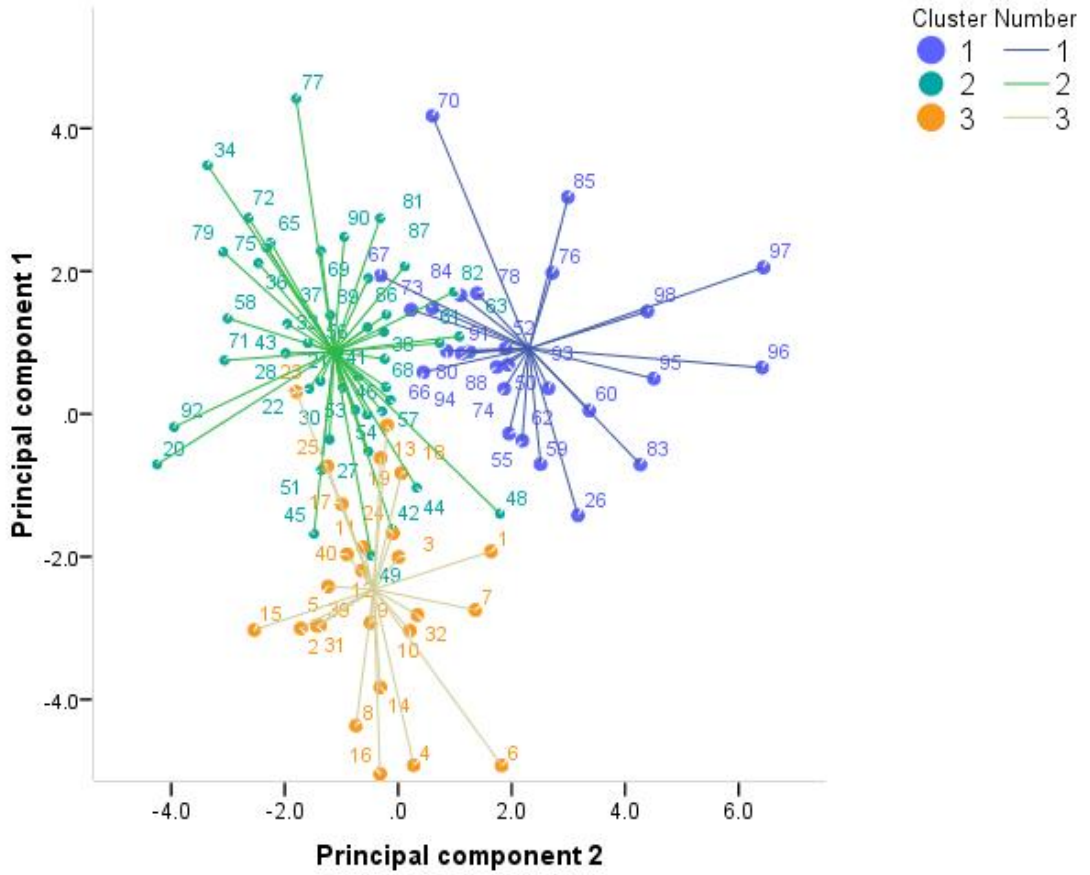

Fig. 1. Genotypes by traits score biplot of 98 Indian wheat varieties on the basis of 8 agro- morphological characters, comparison between two principal components

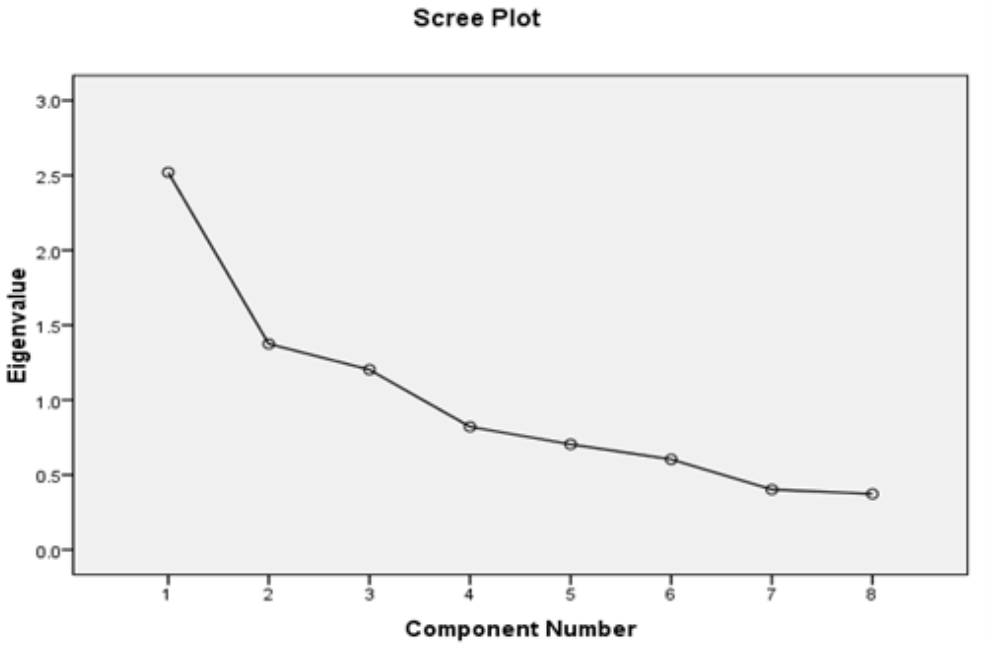

Fig. 2. Comparison between components and their Eigen values

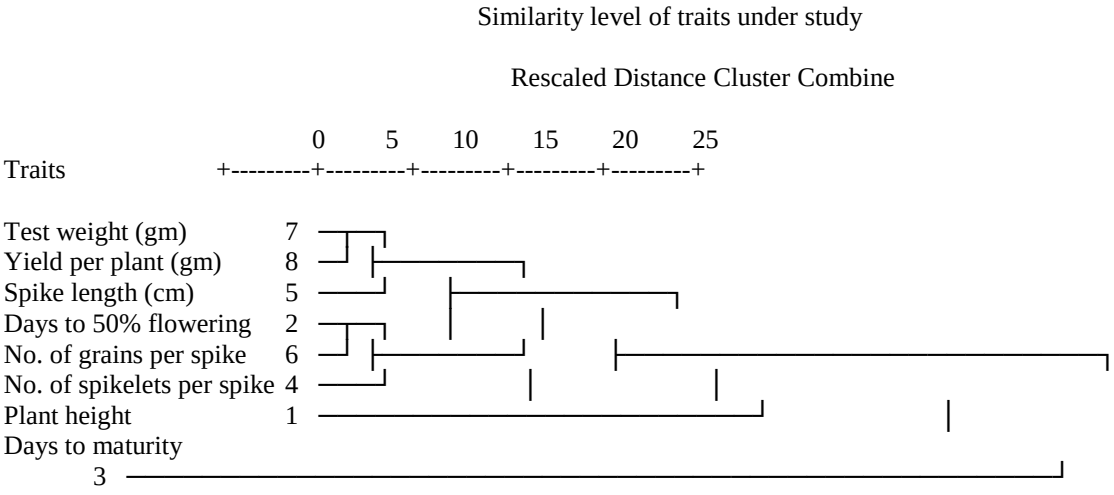

Fig. 3. Comparative levels of similarity among traits under study