INNSPUB

International Journal of Biosciences | IJB |
ISSN: 2220-6655 (Print), 2222-5234 (Online)
http://www.innspub.net
Vol. 9, No. 1, p. 34-44, 2016

RESEARCH PAPER OPEN ACCESS

Multivariate analysis for yield contributing traits in wheat- *Thinopyrum bessarabicum* addition and translocation lines

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Key words: PCA, Cluster analysis, Correlation, Wheat, Phenotypic traits, Addition and translocation lines.

http://dx.doi.org/10.12692/ijb/9.1.34-44 Article published on July 18, 2016

Abstract

For world food security development of high yielding cultivars through identification of genetic diversity is also an important tool. The objective of the present experiment was to get complementary information about different yield contributing characters and to identify the diversity among addition and translocation lines which would assist the plant breeders in making their selection for developing high yielding cultivars. Twenty one wheat genotype including seven wheat- *T bessarabicum* addition and nine translocation lines along with amphiploid, CS, Genaro and two BC1 self fertile lines were grown to study thirteen phenotypic characteristics in two year field experiment, using a randomized complete block design (RCBD) with three replications. Multivariate statistical analysis was used to understand the data structure and trait relations. Simple correlation coefficients depicted highly significant correlation of grain yield per plant with the number of seeds, seed weight per spike, and significant association with spike weight and days to heading. Principal component analysis revealed that five components explained 87% of the total variation among traits. The first PCA contributes maximum portion of total variability (29%) and was more related to spike weight, number of seeds per spike, seed weight per spike, days to heading and grain yield per plant. Cluster analysis assigned 21 genotypes into four clusters. Multivariate statistical analysis revealed that this genetic stock has potential to enhance yield of wheat cultivars and traits like spike length, spike weight, number of spike per plant, number of grain per spike, grain weight per spike, and 1000 grain- weight should be used as selection criteria.

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Introduction

Wheat is one of the first domesticated food crops and for 8000 years has been the basic staple food of the major civilizations of Europe, West Asia and North Africa, and is grown as principle crop. Wheat is grown in an area of 9.17 million hectare in Pakistan and produced 25.03 million tons in 2014-2015, which is below the target of 26.3 million tones fixed by government for rabi season (MNFS&R, 2015). According to a forecast, the demand for wheat will be more than doubled by 2030 and output will reach 28 million tons, so the demand will greater than supply with increasing population and decreasing cultivated area in our country. The country is likely to face a deficit in wheat. This information indicated that if production technology remains the same with escalating population and diminishing cultivable area, the deficit of wheat will be much larger. Therefore appropriate policy measures are needed to address the likely deficit in wheat (Nazli *et al*., 2012). One of the strategies to get an increase in wheat production and developing high yielding varieties particularly under climate change depends to investigate the extent of genetic diversity of our plant genetic resources. As world's wealth of plant genetic resources has much value for world food security. Grain yield in wheat is a multifaceted character and is determined by the interaction of a number of attributes. Adequate knowledge of genetic association of these attributes with yield is of great importance to breeders for developing suitable selection strategy for genotypes to be crossed and making an improvement in complex characters like grain yield which showed little response to direct selection (Fellahi *et al*., 2013). For this purpose morphological traits have been successfully used for assessment of genetic diversity and cultivar development as they provide a simple approach of quantifying genetic variation (Fufa *et al*., 2005). Genetic diversity analysis in germplasm collection assists in classification of germplasm and identification of core collection with possible efficacy for specific breeding goal (Mohammadi and Prasanna, 2003). Recently, several studies have been conducted in order to give an idea about the factors responsible for grain yield in wheat aiming to develop high yielding cultivars through indirect selection (Fellahi *et al*., 2013). In this regard the use of multivariate statistical algorithms is an important tactic for classification of germplasm and analysis of genetic relationships and diversity among breeding material (Mohammadi and Prasanna, 2003).

A large number of suitable statistical methods are available which include principal component analysis, factor analysis and cluster analysis for the selection of parent genotypes, detection of genetic variability, centre of origin, study of interaction among the environments and tracking the course to crop evolution (Mostafa *et al*., 2011).

Correlation coefficient (Brame *et al*., 1984) is also an important statistical method which can help wheat breeders in this regard. Seven statistical procedures have been used by Leilah and Al-Khateeb (2005) to study the relationship between wheat grain yield and its components. Studies have been demonstrated that the pattern of correlation among grain yield with other traits varies in different sets of genotypes and growth environments. A negative correlation between plant height and grain yield of wheat has been found by Moghaddam *et al*. (1998). The experimental study of Khokhar *et al*. (2010) revealed positively and significant correlation among yield per plant, peduncle length and number of grain per spike.

The principal component analysis is another multivariate statistical technique use for complex data sets to explore and simplify them. Each PC is a linear combination of the original variables, and so it is often possible to assign the meaning to what the components represent (Lewis and Lisle, 1998). In some bread wheat genotypes Mohamed, (1999) found that two factors (grain yield and spike density) accounted for 80.8% of variation among traits. Genotypes can be classified into main groups and subgroups on similarity and dissimilarity basis by cluster analysis. This technique is useful for parental selection in breeding programs (El-Deeb and Mohamed, 1999) and crop modeling (Jaynes *et al*., 2003).

By using cluster and principal component analysis, 113 accessions of barley have been evaluated by Ahmad *et al*., (2008). Ali *et al*., (2008) evaluated seventy wheat genotypes for variability parameter including cluster analysis for eight traits. Aharizad *et al*., (2012) applied cluster analysis using Wards algorithm and squared Euclidean distances and assigned 94 bread wheat inbred lines into three groups. Collaku (1989) and Leilah and Al-Khateeb (2005) illustrated that number of tillers and 1,000-seed weight positively improved yield potential. The 1,000-seed weight was reported by many researchers as the variable most closely related to grain yield and was often used in selecting high yielding wheat cultivars (Deyong, 2011; Rymuza *et al*., 2012). The objective of present research work is to establish the amount of genetic variability and interrelationships among the gene pool, to find out the morphological traits most responsible for high yield, screening the gene pool for these morphological traits and to identify best parents to initiate a hybridization program.

Materials and methods

Field experiments

Present study consisted of twenty one wheat genotypes involving nine wheat- *Th.bessarabicum* translocation lines, seven addition lines with amphiploid, CS, Genaro and two BC1 self fertile lines (Table 6) obtained from Dr. Abdul-mujeeb Kazi, Wheat Wide Crosses and Cytogenetics, NARC Islambabad. The material was raised in year of 2012-13 and 2013-14 at the National Agricultural Research Center Islamabad Pakistan, in randomize complete block design (RCBD) with three replications. Each plot consisted of one row of 2.5 m length spaced at 30 cm between rows and 15 cm between plants. Other recommended cultural practices for wheat production were followed during the growing seasons. Five competitive plants were randomly selected (excluding border plants) recording biometrical measurements on days to heading, days to maturity, plant height, flag leaf area, spike length, spike weight, number of spike per plant, number of grain per spike, grain weight per spike and 1000 grain weight, grain yield per plant, plant biomass and harvest index.

Statistical analysis

Simple linear correlation

A simple linear correlation was used when there is only one predictor variable, matrix of simple correlation between grain yield and its components was computed according to (Snedecor, 1956). The significance of correlation was tested against the value of t-tabulated at (n-2) degree of freedom. Where, n is number of genotypes (Snedecor, 1956).

Principal components analysis

Principal components analysis is a mathematical procedure used to classify a large number of variables (items) into major components and determine their contribution to the total variation. The first principal component is accounted for the highest variability in the data, and each succeeding component accounts for the highest remaining variability as possible (Everitt and Dunn, 1992).The main advantage of principal component analysis is reducing the number of dimensions without much loss of information.

Cluster analysis

Cluster analysis was used for arranging variables into different clusters to find the clusters that their cases within are more similar and correlated to one another comparing to other clusters. This procedure was performed using a measure of similarity levels and Euclidean distance (Everitt, 1993; Eisen *et al*., 1998). All statistical analyses were performed using soft ware's SPSS14 and Minitab-16.

Results and discussion

Phenotypic Variability

Table 1 indicates the minimum and maximum values, arithmetic mean and standard deviation of all seven *Thinopyrum beassarabicum* disomic addition lines, CS, amphiploid, nine Thinopyrum bessarabicum translocation lines and two BC1 self fertile lines for all estimated variables. For most of the measured traits a large level of phenotypic variation was observed. Therefore plant height varied from 57.67 (Tr-2) to 101.67 cm (CS), number of spikes per plant from 8 (Tr-6) to 14 (7JJ,Tr-2,Tr-4 and CS/Bess//Genaro), spike length from 7.33cm (CS) to 16 cm (3JJ), single spike weight from 1.08g (2JJ) to 3.25g (Tr-3JJ 2n = 2X = 44), number of grains per spike from 18.67 (6JJ) to 73.67 (4JJ), seed weight per spike ranged from 0.60g (Tr-1) to 2.34g (Tr-7), thousand–grain weight varied from 21.24 (1JJ) to 48.10g (Tr-5), leaf area from 13.99cm^2 (2JJ) to 30.03cm^2 (3JJ), number of days to heading from 133.33 days (Tr-4) to 169.33 days (Amphiploid), number of days to maturity from 176.67 (Tr-3) to 208 days (Amphiploid), grain weight per plant from 4.96g (Tr-1) to 14.66g (Tr-7), biological yield from 16.66g (7JJ) to 59.73g (Tr-3) and harvest index from 8.44 (Tr-3) to 50.59 (7JJ). Data represented that all the addition and translocation lines owing to the presences of various genes scattered on different *Th. bessarabicum chromosomes* have potential to improve yield as these lines have performed superior in almost all the traits studied from its parent CS.

Table 1. Basic statistics (minimum and maximum values, means and standard deviation) for the estimated variables of Wheat-*Thinopyrum bessarabicum* addition and translocation material).

Parameter	Minimum	Maximum	Mean	Std. Deviation
Plant height	57.67	101.67	80.9686	10.43898
No of spikes /plant	8.00	14.00	11.2860	1.95005
Spike length	7.33	16.00	11.1919	2.27475
Single Spike weight	1.08	3.25	2.3519	0.62803
No of seeds /spike	18.67	73.67	49.9362	15.39217
Seed weight spike	0.60	2.34	1.4819	0.54349
1000 grain weight	21.24	48.10	32.3233	7.85251
Leaf area	13.99	30.03	21.0290	4.57252
Days to heading	133.33	169.33	149.2305	8.27151
Days to maturity	176.67	208.00	187.8410	7.06674
Grain yield per plant	4.96	14.66	10.0329	2.83551
Biological yield	16.66	59.73	37.6329	11.66455
Harvest index	8.44	50.59	29.1452	10.85378

Table 2. A matrix of simple correlation coefficient (r) for the estimated variables of wheat-*Th. bessarabicum* addition and translocation lines.

	PH	SPP	SPL	SPW	SSP	SSPW	TGW	LA	DH	DM	Y/PL	BY
SPP	-.276											
	.225											
SPL	-.095	-.115										
	.681	.621										
SPW	-.317	-.464*	.379									
	.161	.034	.090									
SSP	-.181	-.047	.168	.533*								
	.433	.841	.466	.013								
SSPW	-.140	-.234	.481*	.676**	.674**							
	.546	.307	.027	.001	.001							
TGW	-.384	.164	.298	.415	-.038	.090						
	.085	.479	.190	.061	.869	.697						
LA	.332	-.606**	.333	.498*	.022	.177	.262					
	.142	.004	.140	.022	.924	.444	.251					
DH	.266	-.038	-.029	-.349	-.371	-.148	-.418	.041				
	.244	.870	.899	.121	.098	.522	.059	.858				
DM	.003	-.306	.257	.064	.009	.141	-.411	.045	.687**			
	.989	.178	.261	.783	.971	.542	.064	.846	.001			
Y/PL	-.286	.135	.272	.529*	.663**	.675**	.147	.029	-.489*	-.128		
	.209	.559	.233	.014	.001	.001	.526	.900	.025	.581		
BY	-.071	-.450*	-.081	.499*	.063	.079	.479*	.344	-.524*	-.326	-.017	
	.758	.041	.728	.021	.786	.735	.028	.127	.015	.149	.942	
HI	-.156	.447*	.227	-.093	.311	.254	-.208	-.234	.078	.154	.563**	- 776**
	.500	.042	.323	.688	.170	.266	.365	.306	.736	.505	.008	.000

* Correlation is significant at the 0.05 level (2-tailed), ** Correlation is significant at the 0.01 level (2-tailed). PH= Plant height, SPP= Spike/Plant, SPL= Spike length, SPW= Spike weigh, SSP= Seed/spike, SSPW=Single spike seed weight, TGW= 1000 Grain weight, DH=Days to heading, DM= Days to maturity, Y/Pl= Grain yield/Plant, BY= Biological yield, HI= harvest Index

Simple correlation analysis

The linear relationship between two variables is measured by the simple linear correlation. A correlation Coefficient (r) value of -1 or +1 indicates perfect correlation; the values which are close to -1 indicate high negative correlation. In contrary, values close to +1 indicates high positive correlation and if there is no linear association between variables, the correlation is zero.

Results of correlation analysis among characters are listed in Table 2. These results reveals that plant biomass is significantly and positively correlated with spike weight and thousand grains weight, while it is significantly and negatively correlated with number of spike per plant and days to heading. So to get higher kernel weight the traits like increased plant biomass and maximum spike weight might be selected.

Table 3. Loadings of PCA for the estimated traits of wheat.

Parameter	PC 1	PC 2	PC 3	PC 4	PC 5
Plant height	-.342	-.264	.405	-.431	.608
No of spikes /plant	-.272	.553	-.647	.232	.129
Spike length	.466	.192	.367	.555	.288
Single Spike weight	.896	-.143	.227	.064	-.177
No of seeds /spike	.672	.401	.066	-.421	-.124
Seed weight / spike	.757	.327	.331	-.106	-.045
1000 Grain weight	.499	-.308	-.435	.590	.147
Leaf area	.386	-.485	.502	.115	.436
Days to heading	-.603	.138	.629	.252	-.113
Days to maturity	-.170	.243	.779	.214	-.416
Grain yield per plant	.729	.533	-.109	-.189	.120
Biological yield	.485	-.785	-.195	-.104	-.195
Harvest index	.043	.915	.034	.038	.251
Eigenvalue	3.794	2.846	2.375	1.259	1.031
Proportion	29.181	21.89	18.271	9.686	7.932
Cumulative (%)	29.181	51.072	69.343	79.029	86.961

Table 4. Genotypes included in four clusters.

Groups	Genotypes
Cluster I	1JJ, 3JJ44, Tr-7, 3JJ, 2JJ, CS, Amphloid, CS/Bess//Gen, CS/Bess//Pavon
Cluster II	5JJ, Genaro, 3JJ42, Tr-2, 7JJ
Cluster III	4JJ, Tr-6, Tr-1, Tr-4, Tr-5
Cluster IV	6JJ, Tr-3

Grain yield per plant showed highly significant and positive correlation with number of grain per spike, single spike seed weight, significant and positive correlation with spike weight, negative and significant association with days to heading. Days to maturity showed highly significant and positive correlation with days to heading.

Leaf area represented significant and positive correlation with spike weight while highly significant negative correlation with number of spikes per plant. 1000 grain weight showed positive correlation with number of spike per plant, spike length, spike weight, single spike seeds weight. Single spike seed weight showed highly significant and positive correlation with spike weight and number of grains per spike while significant and positive correlation with spike length. Number of grains per spike indicated significant and positive correlation with spike weight and spike weight showed negative and significant correlation with number of spikes per plant. Harvest index has depicted highly significant and positive correlation with grain yield per plant, significant and positive correlation with number of spikes per plants while highly significant and negative correlation with plant biomass. Moghaddam *et al.*, (1998) showed a negative correlation between plant height and grain yield. They attributed that to the lower number of grains/spike with the tallest wheat plants. Kumbhar *et al.* (1983) and Mohamed, (1999) had shown that grain weight/ spike, biological yield and number of spikes/m^2 were closely related to grain yield/m^2. The differential relations of yield components to grain yield may be attributed to environmental effects on plant growth (Asseng *et al.*, 2002). So to get maximum yield per plant the traits like spike weight, single spike seed weight, spike length, number of grains per spike, number of spikes per plant must be selected.

Table 5. Mean and standard deviation for four clusters.

Genotype	Cluster I	Cluster II	Cluster III	Cluster IV
P height	87.81 ±7.80	68.47 ±6.44	79.93 ±8.65	84 ±0
spike/pl	11.52 ±1.85	11.93 ±1.98	10.73 ±2.52	10 ±0.47
spike l	11.80 ±2.83	11.07 ±1.29	10.97 ±1.87	9.33 ±2.83
Ssp weight	2.14 ±0.78	2.49 ±0.56	2.74 ±0.23	2.00 ±0.08
seed/spi	47.48 ±14.10	58.47 ±5.56	57.47 ±12.46	20.83 ±3.06
SW/Spike	1.47 ±0.51	1.74 ±0.54	1.53 ±0.56	0.75 ±0.02
1000GW	29.09 ±7.26	30.99 ±5.21	37.69 ±8.29	36.79 ±11.89
leaf area	21.63 ±5.55	17.60 ±3.39	22.68 ±3.30	22.77 ±0.45
Days to H	153.26 ±8.25	147.13 ± 6.88	146.89 ±9.10	142.22 ±2.99
Days to M	189.67 ±7.78	188.20 ±4.74	187.53 ±7.72	179.50 ±4.01
GY/Pl	9.92 ±2.55	11.65 ±2.05	9.35 ±2.93	7.21 ±3.06
BY	31.12 ±11.25	32.32 ±9.98	49.65 ±4.27	54.01 ±8.09
HI	33.42 ±7.10	31.05 ±6.87	18.87 ±5.88	13.92 ±7.76

P height= Plant height, Spike/Pl= Spike/Plant, Spike l= Spike length, Ssp weight= Single spike weigh, Seed/Spi= Seed/spike, SW/Spike= Seed weight/Spike, 1000GW= 1000- Grain weight, Days to H=Days to heading, Days to M= Days to maturity, GY/Pl= Grain yield/Plant, BY= Biological yield, HI= harvest Index,

Table 6. Germplasm Pedigree.

Genetic Stock	Pedigree
Tr-1	6BS.6BL-6J (CS/Th.bess//CSph/3/4*Prinia
Tr-2	1DS.1JS
Tr-3	3JS.3BL, (CS/Th.bess//CSph/3/3*Prinia
Tr-4	1AS.1AL-1JL
Tr-5	7DS.7DL-4J, (CS/Th.bess//CSph/3/4*Prinia
Tr-6	6JS.7DL, (CS/Th.bess//CSph/3/4*Prinia
Tr-7	5JS.5DS.5DL
Amphiploid	CS/*Thinopyrum bessarabicum*
1JJ	CS+1JJ (2n = 6x= 42+2= AABBDD+1JJ)
2JJ	CS+2 JJ (2n = 6x= 42+2= AABBDD+2JJ)
3JJ	CS+3 JJ (2n = 6x= 42+2= AABBDD+3JJ)
4JJ	CS+4 JJ (2n = 6x= 42+2= AABBDD+4JJ)
5JJ	CS+5JJ (2n = 6x= 42+2= AABBDD+5JJ)
6JJ	CS+6JJ (2n = 6x= 42+2= AABBDD+6JJ)
7JJ	CS+7JJ (2n = 6x= 42+2= AABBDD+7JJ)
3JJ42	CS+Tr 3J (2n = 6x= 42 = AABBDD+Tr3J)
3JJ44	CS+Tr 3JJ (2n = 6x= 42+2= AABBDD+Tr3JJ)
CS/bess//Pav	CS/Th. bess//Pavon (7x = 49 =42+7 = AABBDDJ)
CS/bess//Gen	CS/Th. bess//Genaro (7x = 49 =42+7 = AABBDDJ)

Principal components analysis

PCA (Principal component analysis) divulge the importance of the largest contributor to the total variation at each axis of differentiation (Sharma, 1998). The values obtained by PCA called Eigen values are often used to settle on how many factors to retain. The results in table 3 and graphically represented in fig 1 estimated wheat variable into five principal components factors with Eigen values more than one which all together explained 86.961 of total variability (Table 3). The first component (PC1) was highly correlated with, spike weight (r = 0.896), number of seeds per spike (r = 0.672), seed weight per spike (r = 0.757), days to heading (r = -0.603) and grain yield per plant (r = 0.729). Meanwhile, the PC2 was highly correlated with number of spikes per plant (r = 0.553), grain yield per plant (r = 0.533), biological yield (r = - 0.785) and harvest index (r = 0.915).

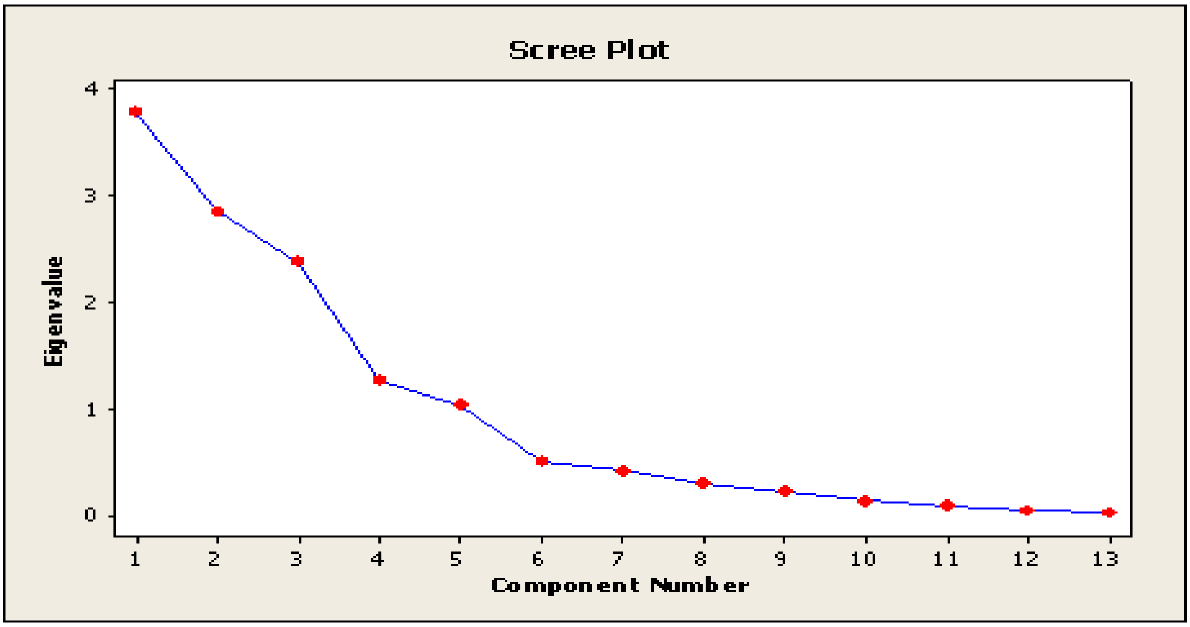

Fig. 1. Scree plot showing Eigen values in response to number of components for the estimated variables of bread wheat genotypes.

Third component (PC3) was also highly correlated with number of spikes/plant (r = -0.647), leaf area (r = 0.502), days to heading (r= 0.629) and days to maturity (r = 0.779) while PC4 and PC5 were related with spike length (r = 0.555), TKW (r = 0.590) and plant height (r = 0.608) respectively. Data in Table 3 shows that PC1 accounted for about 29.181% of total variation, PC2 contribute 21.890% PC3 contribute 18.271%, while PC4 and PC5 explained 9.686% and 7.932% respectively. Hence, PCA indicated that days to heading, days to maturity, flag leaf area, spike length, spike weight, grains number per spike, grain yield per plant, thousand-kernel weight and plant biomass exposed to be the important variables affecting yield. It was reported by Yin *et al.* (2002), that the grain yield was divided into three components, namely, number of spikes/m2 , number of kernels/spike, and 1000 grain weight. Furthermore, Leilah and Al-Khateeb (2005) stated that harvest index, biological yield, spike diameter, number of spikes/m^2, spike length, grain weights/spike, and 100-grain weight were the most important factors in contributing to grain yield.

Cluster analysis

Cluster analysis sequestrates genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters (Jaynes *et al.*, 2003). The cluster analysis performed on the basis of means for thirteen traits indicated that, genotypes formed four clusters (Fig.2).

The cluster I include nine genotypes, cluster II include five genotypes while cluster III and VI have five and two genotypes respectively. Members of each cluster are presented in Table 4. Although cluster analysis grouped genotypes together with greater morphological similarity, the clusters did not necessarily include all genotypes from same origin. Zubair *et al*., (2007), Ahmad *et al*., (2008) and Ali *et al*., (2008) also reported lack of association between morpho-agronomic traits and origin. Mean values along with standard deviation for each cluster (Table 5) revealed that genotypes in the cluster I are 1JJ, 3JJ44, Tr-7, 3JJ, 2JJ, CS, Amphloid, CS/Bess//Gen, CS/Bess//Pavon showed maximum mean value for plant height, spike length, days to heading, days to maturity and harvest index, The harvest index as a quantitative trait indicating plant efficiency to distribute dry matter for grain and it is one of the main purposes at the breeding programs of cereals to introduced genotypes with high harvest index (Zarei *et al*., 2010) while genotypes in cluster II are 5JJ, Genaro, 3JJ42, Tr-2, 7JJ showed maximum mean value for no of pikes per plant, number of seeds per spike, seed weight per spike and grain yield per plant, members of this group are suitable for breeding programs aimed at improving the yield. Saeed Aharizad *et al* 2012 also found the similar results and concluded the traits likes number of spikelets per plant, 1000-grain weight, grain yield per plant, spike length are main traits contributing towards yield. Cluster III genotypes are 4JJ, Tr-6, Tr-1, Tr-4, Tr-5 represented maximum mean values for single spike weight, 1000-grain weight and IV showed maximum leaf area and plant biomass. So the representative addition and translocation lines along with amphiploid of cluster I can be used for induction of maximum plant height, spike length, days to heading, days to maturity and harvest index.

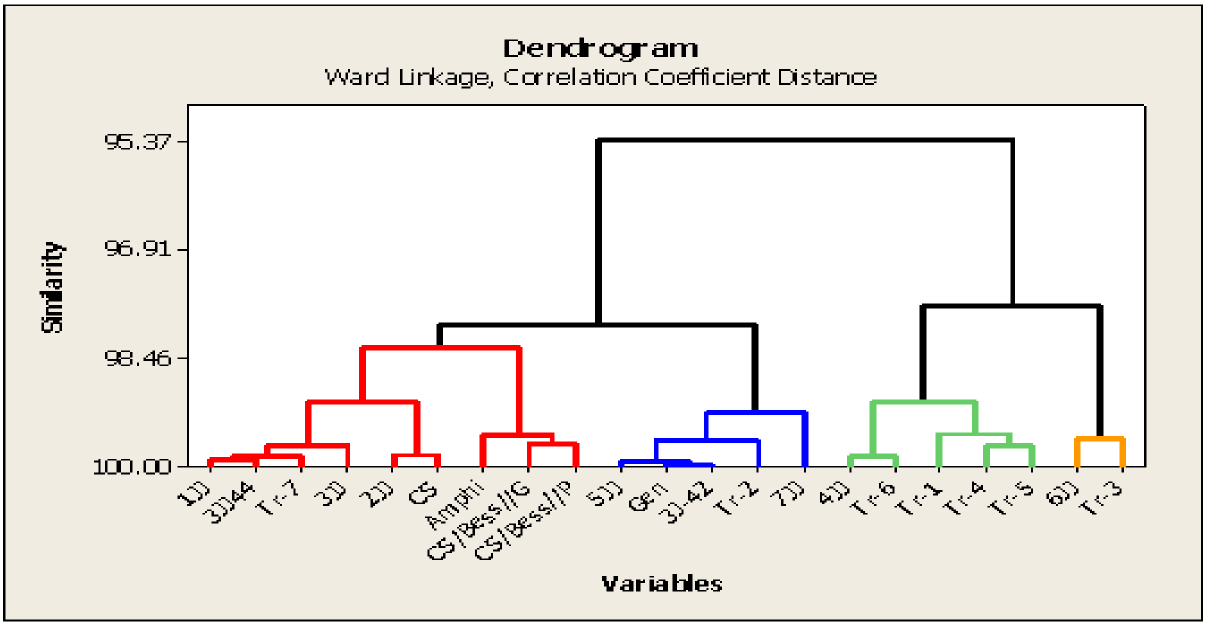

Fig. 2. Tree diagram based on 21 wheat genotypes using Ward's method.

The genotypes in the cluster II can be used for improving maximum no of pikes per plant, number of seeds per spike, seed weight per spike and grain yield per plant, while genotypes in III and IV can be used for the improvement in plant height, days to heading, days to maturity and maximum leaf area, plant biomass respectively. Therefore these addition lines and translocation lines could be exploited to transfer desired traits in hybridization programs to develop high yielding wheat varieties. Similarly, Khodadadi *et al.* (2011) categorized wheat cultivars into seven groups. Yousuf *et al.* (2008) formed four distinct clusters to arrange seventy wheat genotypes.

The cluster diagram showed three main clusters (Figure 3). Cluster 1 included plant height, Spike length, leaf area, 1000-grain weight and plant biomass showing close relationship. Due to lowest linkage distance 1000-grain weight and plant biomass were closest in this cluster, while plant height was outlier in this cluster. Second cluster included single spike weight, seed weight per spike, number of seeds per spike and grain yield per plant. This cluster emphasized the importance of traits in indirect selection of a complex trait like grain yield. These traits are relatively easy to analyze and select. Other statistical techniques like correlation analysis and factor analysis could not explain the relationship among grain yield per plant and other traits with such clarity as cluster analysis. Third cluster exhibited relation between number of spikes per plant and harvest index. While in the last cluster strong correlation was observed between days to heading and days to maturity.

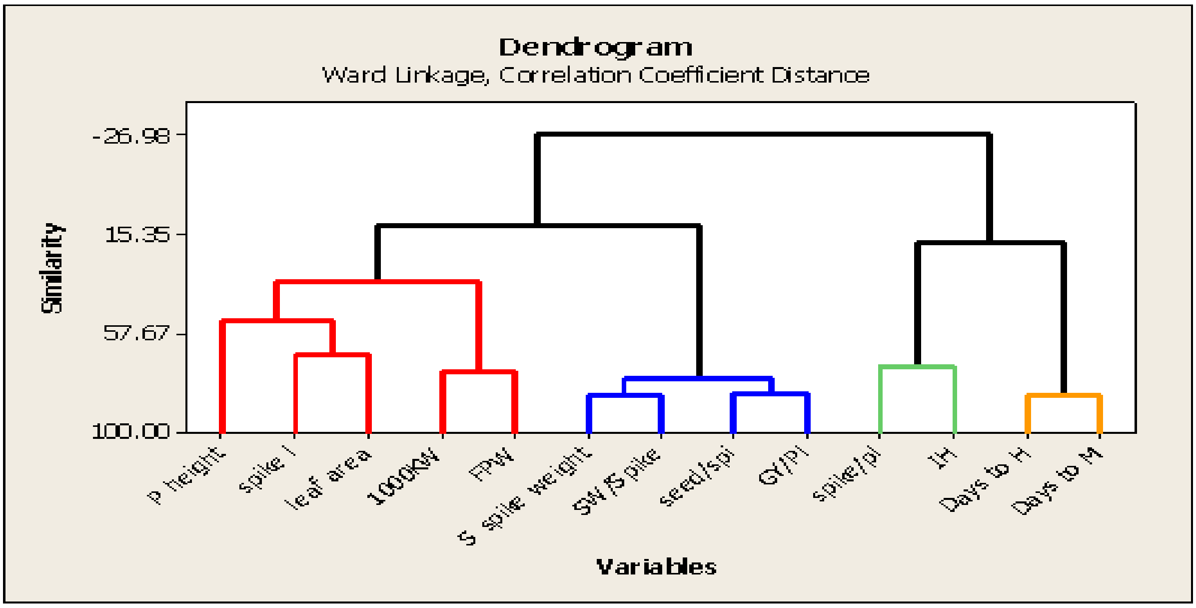

Fig. 3. Tree diagram based on 13 morphological traits in wheat genotypes using Ward's method.

Conclusion

Results indicated adequate variability in the wheat-*Th. bessarabicum* addition and translocation lines along with amphiploids and two BC1 self fertile lines to initiate a breeding program. Multiple statistical procedures were used to study variation and relationships between thirteen measured traits in these genetic stocks of bread wheat. Results showed that all the lines performed superior than their parental line CS in traits like spike length, spikes number per plant, seed number per spike, thousand kernel weight, single spike weight and yield per plant, harvest index and plant biomass. As these lines might possess various genes distributed on different pairs of chromosomes or chromosomal segments from *Th. bessarabicum,* having potential to contribute in mounting wheat grain yield. Therefore it can be concluded to select these lines and traits as selection criteria in the breeding programs aiming to higher yield. It is also recommended that, final selection of traits cannot be done on the basis of single statistical method, it is necessary to use multivariate statistical analysis for screening important traits and parental lines in wheat breeding programs.

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