AN INVESTIGATION ON GENETIC VARIABILITY FOR DIFFERENT QUANTITATIVE AND QUALITATIVE TRAITS OF WHEAT (*Triticum Aestivum L*) GENOTYPES

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KEYWORDS	ABSTRACT
Wheat, Quantitative Traits, Genetic Diversity, Qualitative traits, Principle Component Analysis	Wheat is the most important fasten diet of country's population and major cereal crop of the country. The proposed research study was conducted in experimental field of plant breeding & molecular genetics department, Faculty of Agriculture, University of Poonch, Rawalakot during 2016. Twenty-five genotypes of wheat were used as source population. Data on diverse quantitative & qualitative traits like Plant height, peduncle length, seed length, 1000 seed weight etc. was recorded from randomly selected guarded plants from each line of experimental unit. Performance and diversity of wheat lines was assessed for certain morphological traits, grain yield and its components using principle component analysis and cluster analysis. On basis of overall performance, it was concluded that three quantitative traits showed remarkable variation, which were plant height, peduncle length and stem diameter. Maximum linkage distance was showed between cluster A and cluster B, so members of these clusters showed variability among themselves. Thus, these genotypes could further be used in breeding programs for maximizing yield.

INTRODUCTION

Wheat is the major fasten food for the majority of the population and main cereal crop of country. In formulating agricultural policies, it occupies central position (Mohammadi, Mirasi, Saeidi & Amiri, 2015). Value of wheat added in agriculture is 10.1 and in GDP 2.2. Production of cultivated wheat during the year 2013 was 24.2 while the estimated target was 25.5 which represented the loss of 5.1%. Wheat provides human nutrition and food security so its role in human life is more valuable. In Pakistan production of wheat crop is now became an important occupation of native farmers. In wheat breeding program one of the primary goal is to develop varieties with high genetic potential and combination of alleles for increasing yield. The knowledge about presence of genetic diversity among species and individuals of the species is very important because the crossing two different genotypes allows transgressive segregation which resulted in higher yield of offspring than their parents (Khodadadi, Fotokian & Miransari, 2011).

The most important strategy to improve crop is crossing dissimilar genotypes. Selection of parents is very important in hybridization. Genetic distance between the parents is very vital to get benefit from transgressive segregation (Bharadwaj, 2012). Another scientist (Aharizad, Sabzi, Mohammadi & Khodadadi, 2012) studied genetic diversity of different wheat collected from different parts of world. The genetic diversity could be the result of geographical effect through evolution and therefore traits could be reasoned as a role of variety (Aharizad et al., 2012). For parental selection during hybridization, presence of genetic diversity is prerequisite for successful breeding programs. In crossing nurseries most diverse parents' selection is highly valuable for potential recombination to increase yield (Shahryari, Mahfoozi, Mollasadeghi & Khayatnezhad, 2011). Statistical approaches or techniques are today available for estimating the genetic diversity, tracing among the diverse situations as studied (Pordel & Maragheh, 2013; Baranwal, Mishra, Vishwakarma, Yadav & Arun, 2012; Jlibene & Nsarellah, 2011).

Therefore, objective of current study is to study genetic diversity in wheat genotypes for different monogenic and polygenic traits, and to classify genotypes into various groups. Results obtained from PCA and cluster analysis are may be different from each other. The Principle components analysis is therefore avoided while using cluster analysis. In case large variation is shown by first two components then grouping of genotypes using these two traits is useful method (Mardi, Naghavi, Kazemi, Rashidi, Ahkami, Salehi & Katsiotis, 2011). UPGMA and Ward's methods are popular algorithms used for the cluster analysis. UPGMA, Ward's, SLINK, and CLINK studying genetic variance between the genotypes and to classifying them in PAST, the UPGMA is most reliable technique in agreement with the relation of the family founded as on their hereditary material (Kumar, Singh & Jaiswal, 2013). The present research study focused on investigating the genetic divergence among various wheat genotypes for qualitative and quantitative traits and to select the genotypes on the basis of their position in various group.

MATERIALS AND METHODS

Current research trail was conducted at University of Poonch, Rawalakot Pakistan. Total 25 genotypes of wheat were evaluated in the experiment. BARS-2009 was used as check variety. Sowing was done in November 2016. Wheat lines were sown in rows, keeping row to row distance as one foot. The recommended NPK fertilizer was used in the field in two sections, one during time and second during the germination, at vegetative stage and at the booting stage.

Experimental Design: Experiment was laid out in augmented design using check variety.
Inter Culture practices: the weeding and hoeing were regularly done during experiment.

Qualitative and Quantitative Parameters

Following parameters were studied during experiment like Plant height, stem diameter, the peduncle length, 100 seed weight, 1000 seed weight, color at maturity, awning habit, glume attachment, glume pubescence, shoulder width, shoulder shape, beak shape, seed color, Seed surface, seed shape, seed size, Seed brush, seed germ size, seed groove, seed hardness, sheath wax, auricle anthocyanin and ear size.

Table 1 List of Genotypes Used in Current Study

Genotypes	Genotypes	Genotypes	Genotypes
3169	3176	3185	3193
3170	3177	3186	
3171	3179	3187	
3172	3180	3188	
BARS-2009	3181	3189	
3173	3182	3190	
3174	3183	3191	
3175	3184	3192	

STATISTICAL ANALYSIS

The obtained data was analyzed for significance using the method of (Sneath-1 & Sokal-2, 1973) with the help of computer software 'Statistica' www.statsoft.com. PCA or principle component analysis and cluster analysis were done on the basis of Euclidian distance and K-mean clustering following the method of (Kumar, Lal, Ruchi & Upadhyay, 2009) using PAST software.

RESULTS OF STUDY

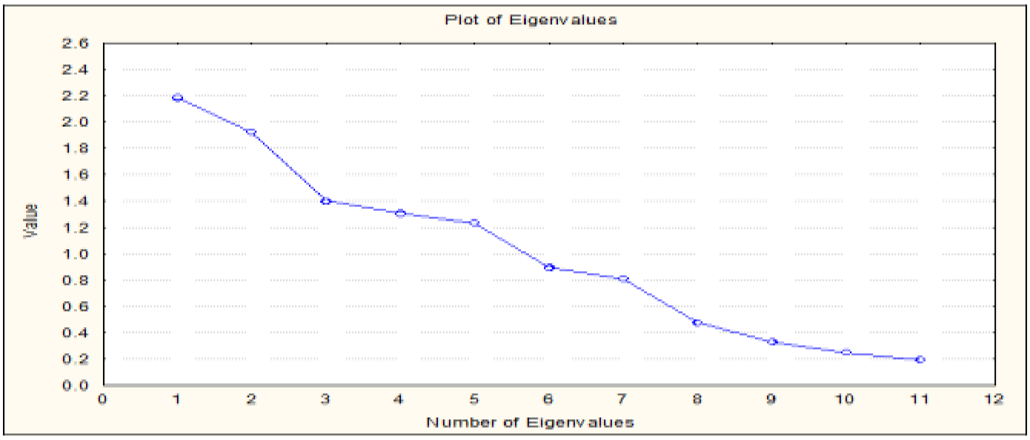
Principle Component Analysis of Quantitative Traits

PCA was performed for several morphological characters of wheat genotypes shown on table 01 (Table. 2). To classify genotypes in groups different methods were used (Bauer et al., 2007). The five variables with greater than Eigen value were studied. Results stated that first factor showed the highest Eigen value (2.184 %) and minimum Eigen value of (1.234%). Overall 73% variability was contributed by these traits among 25 genotypes. The factor 2 recorded maximum value of (17.47) % followed by factor 3 (12.70%), of the total variance explained as studied by (Youssefian, Kirby & Gale, 1992).

Table 2: Principal Component Analysis for Morpho-Physiological Traits

	Eigen Values	Total Variance (%)	Cumul. Eigen Value	Cumul. Variance (%)
Factor1	2.18	1.23	1.23	19.86
Factor2	1.92	17.47	4.11	37.33
Factor3	1.40	12.70	5.50	50.03
Factor4	1.30	12.70	6.81	61.87
Factor5	1.23	11.23	8.04	73.10

Figure 1 Plot of Eigen Values for Morphological Traits



Factor Loading for Quantitative and Qualitative Traits

Factors loading for several traits was shown in (Table 03). Maximum positive load was recorded by (0.76) along with glume length (0.15), whereas plant height (-0.76) along with peduncle length (-0.69) expressed highest negative load. Seed width had highest positive load value in the factor 01 so it could be called as valuable factor for the enhance biomass character. Results showed that factor 2 enclosed highest positive load values of variables like plant height (0.39) followed by peduncle length (0.49). Minimum negative load value of character such as seed length along with beak length (-0.57). As factor 02 recorded the highest positive load of factors like, peduncle length (0.49). Therefore, this is considered as primary factor to “yield improvement”.

Factor 03 enclosed the highest positive load of the traits like stem diameter (0.57) along by beak length (0.53) whereas minimum negative load value of the factors like the glume length (-0.57) along with awn length (-0.48) and seed length (-0.31). As factor 3 held the maximum positive load of factor like stem diameter so this factor can be called as effective factor for yield characters. According to the results of (Bauer, Drici, Drinic & Micid, 2007; Fotokian, Shahnejat & Taleie, 2002) studied analysis based on the PCA is more reliable in finding the difference between genotypes.

Table 3 Factor Loadings for Morphological Traits

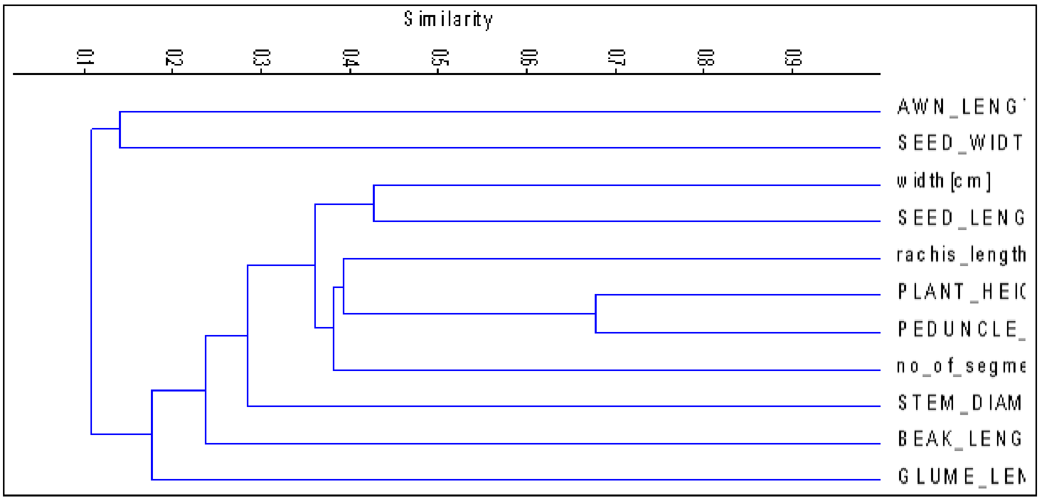
	Factor1	Factor 2	Factor 3	Factor 4	Factor 5
Glume length	0.15	-0.03	-0.57	-0.18	-0.64
Glume Width	-0.31	-0.71	-0.14	0.07	0.31
Beak length	-0.07	-0.57	0.53	0.01	0.03
Rachis length	-0.73	-0.33	-0.23	0.1	0.01
No of segments	-0.35	0.06	-0.04	0.71	0.01
Awn length	0.10	0.10	-0.48	-0.32	0.43
Plant height	-0.76	0.39	-0.20	-0.19	-0.03
Peduncle length	-0.69	0.49	0.08	-0.24	0.15
Stem diameter	-0.31	-0.02	0.57	-0.61	-0.16
Seed length	0.03	-0.57	-0.31	-0.40	0.32
Seed width	0.32	0.49	0.06	0.07	0.62

Glume length, Glume Width, Beak length, Rachis length, No of segments, Awn length, Plant height, Peduncle length, Stem diameter, Seed length, Seed width

Cluster Analysis for Quantitative Traits (Hierarchical Cluster)

Cluster analysis showed the relationship among the studied traits. Dendogram was constructed by using PAST, using eleven quantitative traits (plant height, peduncle length, seed width, seed length, glume length, glume width, beak length, rachis length, no of segments, awn length and stem diameter) showed two main clusters, clusters named A and cluster B. Cluster A includes only two parameters which are awn length and seed width. Whereas main cluster B contained two sub-clusters named b1 and b2. Sub cluster b1 includes eight variables i.e.; peduncle length, seed length, plant height etc. While sub cluster B2 includes one variable i.e. glume length. (Ali et al., 2008) who studied that cluster analysis can be useful for finding high yielding genotype of wheat.

Figure 2 Dendogram for Qualitative & Quantitative Traits based on Euclidean Distance



K-Mean Clustering

Analysis of Variance

Analysis of variance was done between and within the 8 traits of 25 five wheat genotypes and shown in (Table 04). The plant height along with peduncle length, seed weight, seed diameter and number of segments revealed non-significant results which stated that the results might because of various environmental stresses (Miralles & Slafer, 1995).

Table 4 Analysis of Variance Between and Within 05 Morphological Traits

	Between		Within			Significant
	SS	DF	SS	DF	F	p
Glume width	0.05	3.00	1.10	21.00	0.32	0.81
Beak length	0.01	3.00	0.05	21.00	0.97	0.43
Rachis length	0.27	3.00	2.78	21.00	0.68	0.58
No. of segments	2.51	3.00	21.79	21.00	0.81	0.50
Awn length	5.71	3.00	63.65	21.00	0.63	0.61
Plant height	11.3	3.0	11.7	20.0	6.4	0.00**
Peduncle length	13.1	3.0	9.9	20.0	8.8	0.00**
Stem diameter	1621.76	3.00	707.60	21.00	16.04	0.00**
Seed length	1.11	3.00	6.60	21.00	1.18	0.34
Seed width	0.01	3.00	0.02	21.00	1.59	0.22
Glume length	0.00	3.00	0.01	21.00	0.84	0.49

Glume length, Glume Width, Beak length, Rachis length, No of segments, Awn length, Plant height, Peduncle length, Stem diameter, Seed length, Seed width

Members in Four Clusters

Members from four clusters were arranged in (Table. 5) Cluster 1 includes seven members BARS-2009, 3173, 3174, 3177, 3188, 3191, 3192. Cluster 2 consisted of nine members includes 3169, 3172, 3176, 3179, 3182, 3185, 3186, 3187, 3193. Cluster 3 consisted of three members includes 3181, 3183, 3184 and cluster 4 includes six members (3170, 3171, 3175, 3180, 3189, 3190). Pattern of distribution indicated that cluster 2 had maximum number of genotypes along with cluster 1 whereas minimum number of genotypes were on cluster 3 and 4 (Raic, Mocak, Rohacik & Sokilvicova, 2009).

Table No.5 Members of Clusters

Clusters	No. of Members	Members name
Cluster1	07	BARS-2009, 3173, 3174, 3177, 3188, 3191, 3192.
Cluster2	09	3169, 3172, 3176, 3179, 3182, 3185, 3186, 3187, 3193
Cluster3	03	.3181, 3183, 3184
Cluster4	06	3170, 3171, 3175, 3180, 3189, 3190

Euclidean Distances Between Clusters

Euclidean distances between clusters were shown in (Table 6). Cluster 2 correlated with cluster 1at the linkage distance of 2.644. Cluster 3 correlate with cluster 1 at the linkage distance of 8.6909. Cluster 4 correlate with cluster 1 at the linkage distance of 4.785. Cluster 3 correlate with cluster 2 at the linkage distance of 6.097. Custer 4 correlate with cluster 2 at the linkage distance of 7.3911. Cluster 4 correlate with cluster 3 at the linkage distance of13.451.

Table 6 Euclidean Distances between Clusters

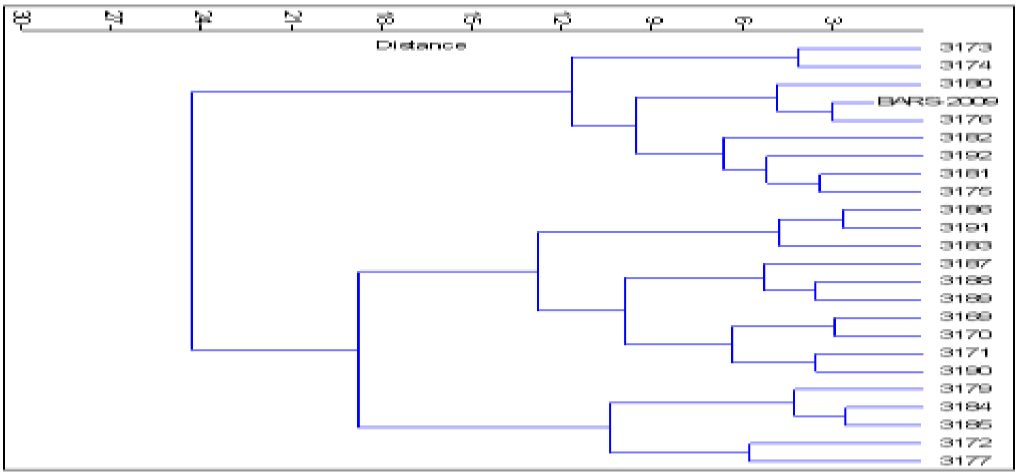
	Cluster No. 1	Cluster No. 2	Cluster No. 3	Cluster No. 4
Cluster No. 1	0			
Cluster No. 2	2.64	0		
Cluster No. 3	8.69	6.09	0	
Cluster No. 4	4.78	7.39	13.45	0

Cluster Analysis for Assessment of Wheat Genotypes

The cluster analysis was shown as Dendrogram indicating the estimated relations between the wheat genotypes. Reif, Zhang, Dreisigacker, Warburton, Ginke, Hoisington, Bohn &

Melchinger, 2005) studied the genetic distance among wheat genotypes using cluster analysis. A Dendrogram was constructed by PAST, using the twenty-five wheat genotypes which showed two clusters named as A and B. Main cluster A includes two sub clusters a1 and a2. Sub cluster A1 includes two genotypes (3173and 3174) while the sub-cluster A2 includes seven genotypes includes (3180, BARS-2009, 3176, 3182, 3192, 3181, 3175). Main cluster B was divided into two sub-clusters cluster b1 and b2. Sub cluster b1 include ten lines (3186,3191,3181,3187,3188,3189,3169,3170,3171,3190) while sub cluster B2 consist of five genotypes including (3179,3184,3185,3172,3177). In cluster A 3180, 3181 and 3192 are outliers and cluster B contains 3 outliers (3183, 3187 and3179). In dendogram, line (3176) showed strong correlation with BARS-2009. Also lines3181 and 3175 at linkage distance near about 6 are showing homology in qualitative characters with BARS-2009. As these lines are showing relatedness with BARS-2009, so we can use them further in breeding programs for improvement of qualitative characters. (Fu et al., 2006) studied wheat genotypes with same range of results.

Figure 3 Dendogram Constructed for Wheat Genotypes



DISCUSSION

Wheat is the main cereal crop of the world; therefore, it is very important to create genetic variability by artificial crossing techniques to make high yielding varieties for increasing yield. On the basis of PCA analysis it is clear that five factors had highest Eigen values 2.18, 1.92. 1.40, 1.30 and 1.23 which indicated the contribution of large genetic variability by these traits. These traits could be of primary importance for selecting genotypes. Zaman, Paul, Kabir, Mahbub & Bhuiya, 2005) also studied the pattern of genetic divergence through principle component analysis. In factor 1 seed weight (0.32) and glume length (0.15) exhibited maximum positive load so these traits need to improve for enhancing biomass production. To improve yield factor two need to pay attention because factor 02 had maximum positive load for peduncle length (0.49) which is important yield related traits. Yield could also be improved by selecting variable from factor 02 as it enclosed highest positive load for stem diameter (0.57). Current findings were supported by earlier researchers (Langade, Ram, Vishwakarma & Sharma, 2013). Factor 3 had maximum load of (0.71) for number of segments so this factor is valuable for improving yield also.

Two main clusters located at greater genetic discussion are typically focused to select the genotypes for enhancing yield. Seed width from cluster A and stem diameter from cluster B could be improved as they are located at two different positions in two main clusters. Plant height, peduncle length and stem diameter show the significant difference so these traits could be used as selection criteria for genotypes. Cluster analysis for assessment of wheat genotypes suggested that two main clusters were located at genetic distance of 30.

Maximum genetic variation was shown by genotypes located in the cluster A and B named 3173 and 3177 because these two genotypes could be used to improvement the qualitative and quantitative traits. The genetic variability is need to focus while doing any experiment. Important traits such as plant height, stem diameter, peduncle length should be improved through selection based on variability among the genotypes. Some previous scientists also studied same parameters to enhance genetic variability (Verma, Singh, Vishwakarma & Tripathi, 2006; Kumar et al., 2013; Singh, Vishwakarma & Singh, 2014).

CONCLUSION

This study concluded that among the eleven quantitative traits three traits showed remarkable variation, which were plant height, peduncle length and stem diameter. Thus, these traits can be focused in further breeding programs. Whereas, variation in rest of the two traits could be created by bringing more gene pool into breeding programs. Maximum linkage distance was showed between cluster A and cluster B, so the members of these clusters showed variability among themselves. Thus, these genotypes can further be used in breeding programs to exploit the existing variability in them. Genetic variability could be enhanced by crossing genetic divergent parents. Quantitative traits could be improved through field trail by combining favorable alleles from both parents. Effect of various biotic and abiotic stresses could be reduced in order to obtain desired results.

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