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THE GENETIC EXPLOITATION OF WHEAT FOR DIFFERENT YIELD RELATED TRAITS BY PRINCIPAL COMPONENT ANALYSIS

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The research was conducted to assess the genetic variability, pattern of grouping, and to search out the diverse genotypes for improvement of wheat germplasm for yield. The germplasm was collected from different research institutes like AARI, NIBGE and UAF. The important wheat parameters for which the data were recorded were days to heading, days to maturity, height of the plants, peduncle length, length of the spikes, width of leaves, length of leaves, area of leaves, spikelets number per spike, grains number per spike, weight of grains per spike, tillers number per plant, weight of thousand grains, and the yield per plant. The results showed the analysis of variance had significant values for all traits. Multivariate analysis was used to unlock genetic diversity present within germplasm. The first and second PC being the most diverse components showed 28.4 and 42.2% of variation during 2013-14. Biplot based on the 2013-14 data collected represented that days to heading, peduncle length, spike length, flag leaf area, 1000-grain weight and number of spikelets per spike contributed greatly in diversity. Graph based on the 2013-14 data recorded showed that genotypes Karawan-2, N-50, N-42, BAYA'S, PBW-450, AS-2002, Nacozari, Pastor, Kareiga, N-3, CHAM-4, NING-8319, A-6, Kohistan-97, FSD-08, Chakwal-97, GA-2002, B-119, Sandal, T.D-1, N-63, Pirsabak-2005, Mexipak-65 and Punjab-81 were present at distance from other varieties with respect to PC-1 and PC-2, so these were more diverse genotypes and could be used for improvement of wheat germplasm for further breeding program.

Keywords: Genetic diversity, wheat germplasm, genetic association, principal component analysis

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INTRODUCTION

Human population is depending directly on plants to get their food. Common bread wheat is one of the major crops, which is widely grown in Pakistan as well as whole of the world as a major food cereal. We are far behind to meet the increasing demand of population and we must work efficiently through proficient source management such as the breeders who try to produce new varieties that can also give more production in a wide range of environments (Rauf *et al*., 2017). The yield of the wheat in more affected due to the high temperature (Challinor *et al.*, 2014). It is now being grown in areas, which are too hot and are not good for its cultivation and growth.

The wheat genotypes can be exploited and used for the development of varieties having good qualities like growing in the changing environment and fulfill the needs of the rapid growing population. The diversity in the germplasm plays a key role in the development of a variety through selection and other breeding program. The selection that is carried out for production of better performing combinations had been reported in the self-pollinated plants like in wheat (Franco *et al*., 2001; Jatasara and Paroda, 1983; Kumar *et al*., 2009). Assessing the variability could be very helpful for the analysis of diversity in the genotypes (Cox *et al*., 1986; Smith, 1984) and introduction of the valuable yield parameters from the wild germplasm to the local genetic material (Thompson *et al*., 1998). The genetic variability had been studied in different crops like wheat (Maric *et al*., 2004; Kumar *et al*., 2009; Maqbool *et al*., 2010; Sajjad and Khan, 2009).

Among different algorithmic techniques that were used for the variability analysis, multidimensional scaling, cluster and principal component, and principal coordinate are now being used for assessing the genetic diversity (Thompson *et al*., 1998; Melchinger 1993; Brown and Guedira *et al*., 2000). The plant scientists are using principal coordinate as well as the principal component analysis for analysis of diversity in the germplasm (Schut *et al*., 1997; Kantety *et al*., 1995; Barrett and Kidwall, 1998; Thompson *et al*., 1998). The research was carried out by taking one hundred genotypes and having the importance of diversity for the improvement of the wheat crop and considering the advantages and disadvantages of the different designs and tools being used for the variability analysis with the objectives to assess the genetic variability for the fourteen parameters, to know the pattern of grouping of the wheat genotypes and to search out the diverse wheat genotypes for their exploitation as promising material in further breeding program for improvement of wheat yield.

MATERIALS AND METHODS

One hundred genotypes collected from Ayub Agricultural Research Institute (AARI), National Institute of

Biotechnology & Genetic Engineering (NIBGE) and University of Agriculture, Faisalabad (UAF) were grown during the years 2013-14 at experimental site of Department of Plant Breeding & Genetics. RCBD design was used and two replications (due to lack of resources) of each genotype were sown in rows of about 5 m long and 15 cm apart, and 30 cm was the space between the plants of each genotype. The seeds of each genotype were sown using a dibbler, which made holes in the well prepared soil and 2-3 seeds of each genotype were dropped in well and gently covered the soil for germination. The climatic conditions had been presented in Fig. 1 and Fig. 2. The plants were thinned as plucking the weak and small plants and keeping only one healthy plant in each hole. The genotypes were sown using the randomization procedure. Four irrigations were applied and all the agronomic and plants protection measures were undertaken to have the good crop stand to get healthy crop.

At maturity the data were recorded for the ten random plants of each genotype and their averages were calculated for further analysis.

Figure 1. **Minimum, maximum and average temperature recorded during 2014.**

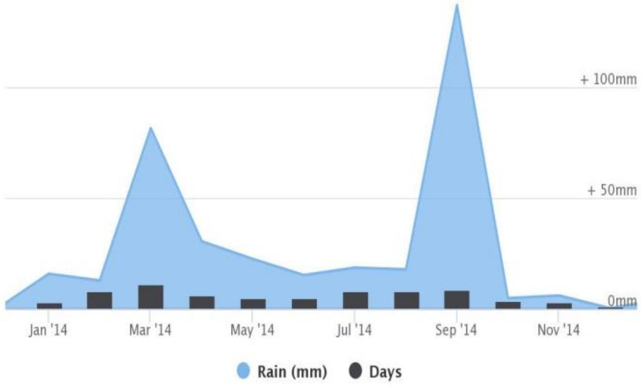

Figure 2. **Average rainfall amount (mm) and rainy days during 2014.**

The characters for which the data were recorded were days to heading, days to maturity, height of the plants, peduncle length, length of the spikes, width of leaves, length of leaves, area of leaves, spikelet's number per spike, grains number per spike, weight of grains per spike, tillers number per plant, weight of thousand grains, and the yield per plant.

The analysis of the variance (ANOVA) from each of the genotype was carried out accordingly to Steel and Torrie (1997). The phenotypic variation was analyzed using PCA according to the Everitt and Dunn (1992) using the software Xlstat.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) carried out for data recorded during 2013-14 showed significant results for all the factors i.e., genotypes, replications and treatments. The genotypes, treatments and genotype into treatment interaction showed highly significant results for most of the traits as compared to replications as shown in Table 1. The replications showed significant results for plant height, 1000 grain weight and yield per plant. The genotypes showed an increase for all the parameters studied in comparison to controls. The genetic variation was found to be more prominent for the traits like

Table 1. Mean sum of squares for 14 traits of wheat during 2013-14

EFFECT	DF	DH	DM	PH	PL	SL	Lw	LL	LA	SP/S	G/S	GWT/S	T/PL	1000G WT	Y/PL
REP	1	1.75	0.09	153.64*	3.08	1.55	0.18	2.02	44.74*	0.36	9.93	0.41**	0.6	10.56*	45.86*
GEN	99	4.15**	3.14**	123.03**	21.37**	8.43**	0.08**	20.77**	162.34**	4.77**	296.61**	0.44**	6.8**	514.87**	28.42**
TRT	1	11568**	10932**	106.87	967.08**	9626**	2.92**	81.91**	3333.2**	1580**	2046**	1.64**	13273**	9757**	2.41*
G x T	99	5.77**	4.75**	111**	25.78**	5.03**	0.08**	20.45**	144.49**	3.59**	265.57**	0.63**	5.5	311.85**	27.12
Res	199	1.32	1.03	43.26	9.36	2.58	0.05	11.08	86.38	2.04	43.24	0.2	3.9	26.3	21.71
Total	399	32.41	30.15	80.3	18.82	29	0.07	15.97	127.76	7.09	166.25	0.37	15261	242.95	24.73

* significant at 0.01, ** significant at 0.05; DH; days to heading, DM; days to maturity, PH; Plant height,PL; Peduncle length, SL; Spike length, LW; Leaf width, LL; Leaf length, LA; Leaf area, SP/S; Spikelets per spike, G/S; Grains per spike, GWT/S; Grain weight per spike, T/PL; Tillers per plant, 1000GWT; Thousands grain weight, Y/p ; Yield per plant

plant height, spikelets per plant, peduncle length, and number of seeds in one panicle, days for both heading and maturity (Shafi *et al.,* 2014). The treatments also showed highly significant results for most of the characters and significant results for yield per plant except for plant height, which showed non-significant results. The genotypes into treatment interaction showed highly significant results for most of the parameters except for number of tillers and yield per plant.

Table 2 shows a range of values of the observed traits and reported that the early genotypes took 99 days to heading while late genotypes took 105 days to heading. The genotypes took a maximum of 135 days to maturity and a minimum 129 days. The range for plant height is 54.13 to 113.66 cm and peduncle length range from 18 to 37 cm. Results for the height of the plant were found to be the same as described by Gulnaz *et al.* (2011) while studying the germplasm of Pakistan and CIMMYT. The spike length gave maximum 14.5 cm and minimum 8.1 cm value. The leaf width ranges from1.6 to 2.7cm while leaf length showed 14 cm minimum value and 33 cm as maximum. The data for leaf area ranges from 23 to 75 cm$^{2.}$ The genotypes gave 17 minimum spikelets per spike and 25 maximum. The number of grains per spike ranged from 29 to 80 while the range for grain weight per spike is 1.49 to 5.7 g. The data for tillers per plant is ranged from 21 to 25 while 1000 grain weight showed 24 g as minimum value and 69 g as maximum value same as Masood *et al*. (2005). The genotypes showed minimum 11.20 g yield per plant and 38.2 g as maximum value for the yield per plant. The minimum value for yield per plant for the germplasm of West Bengal was 6.30 and maximum value for the yield was 13.7 the both the ranges were low than found in the study (Kotal *et al.*, 2010).

The variation and structure of the population were analyzed by using the procedure of principal components for the data recorded during 2013-14. The contribution of the variation, Eigen values, principal components, and the Eigen vectors for the five main components were given in the Table 3. During the year 2013-14, first five principal components (PCs) accounted the major variation (68.3% of the total). The 1st PC accounted 28.45% of the variation containing major source of diversity for spike length, leaf width, leaf length, leaf area and the 1000-grain weight with positive Eigen vectors while yield / plant and days to maturity were having negative values for Eigen vectors. The second component of PCA contributed about 13.73% of the variation for different traits with highest values for days to heading, spikelets per spike, grains per spike and yield per plant while leaf area and leaf length gave negative Eigen vectors. The first and second PCs showed the variation 37.80 and 22.88 percent (Pirdashti *et al.*, 2012). The 3rd and 4th PCs accounted for 9.9 and 9.04% of variation respectively for morphological traits with highest loading values days to heading, days to maturity and grain weight per spike for 3rd and plant height, grains weight per spike and 1000 grain weight for 4th PC. The 5th PC contained 7.18% of variation for yield per plant with positive Eigen vectors as given in Table 4.

A principal component biplot showed that variables are super imposed on the plot as vectors. Biplot represent the association among different traits and the length of the lines also called the vectors showed the share of the different

Table 2. The descriptive statistics for fourteen parameters of wheat

Variable	DH	DM	PH	PL	SL	Lw	LL	LA	SP/S	G/S	GWT/S	T/PL	1000GWT	Y/PL
Minimum	99.67	129.67	54.13	18	8.1	1.6	14	23.8	17	29	1.49	21	24	11.2
Maximum	105.33	135.33	113.66	37	14.5	2.7	33	75.9	25	80	5.7	25	69	38.2
Mean	101.87	131.68	86.57	25.32	10.68	1.92	22.21	43.17	20.22	44.96	2.34	22.8	51.02	19.05
Std. dev	1.77	1.52	8.79	3.76	1.35	0.2	4.22	11.4	1.89	15.68	0.72	0.85	16.67	5.18

DH; days to heading, DM; days to maturity, PH; Plant height,PL; Peduncle length, SL; Spike length, LW; Leaf width, LL; Leaf length, LA; Leaf area, SP/S; Spikelets per spike, G/S; Grains per spike, GWT/S; Grain weight per spike, T/PL; Tillers per plant, 1000GWT; Thousands grain weight, Y/p ; Yield per plant

Table 3. Principal component analysis Eigen values, variability percentage and cumulative values

Variables	PC-1	PC-2	PC-3	PC-4	PC-5
Eigen value	3.98	1.92	1.39	1.27	1.01
Variability (%)	28.45	13.73	9.9	9.04	7.18
Cumulative %	28.45	42.18	52.07	61.12	68.3

Table 4. The principal components for fourteen parameters of wheat

Variables	DH	DM	PH	PL	SL	Lw	LL	LA	SP/S	G/S	GWT/S	T/PL	1000GWT	Y/PL
PC-1	0.08	-0.21	0.03	0.37	0.38	0.32	0.42	0.44	0.30	0.00	0.07	0.02	0.32	-0.02
PC-2	0.46	-0.12	-0.19	0.06	0.13	-0.19	-0.26	-0.26	0.32	0.39	0.22	0.28	0.16	0.37
PC-3	0.19	0.44	-0.33	0.13	-0.07	0.07	-0.03	0.00	0.00	-0.43	0.49	-0.41	0.09	0.18
PC-4	0.02	-0.35	0.54	0.06	0.10	-0.33	-0.10	-0.21	-0.17	-0.35	0.35	-0.04	0.35	-0.10
PC-5	-0.04	-0.39	0.04	-0.10	-0.15	0.13	-0.07	0.02	-0.03	0.01	-0.32	-0.55	0.15	0.60

parameters in the variation. Biplot based on the 2013-14 data represented that days to heading, peduncle length, spike length, flag leaf area, 1000-grain weight and number of spikelets per spike contributed greatly in diversity. Other traits showed less contribution towards diversity. As the vectors for peduncle length and spike length are close to each other it means that they are significantly positively correlated with each other. Similarly, 1000 grain weight and spike length wer significantly positively correlated. Days to maturity and 1000 grain weight are significantly negatively correlated with each other as shown in Fig. 3. The grain yield was negatively linked with that of flowers initiation (Kandic *et al*., 2009; Dadbakhsh *et al*., 2011; Abdolshahi *et al*., 2010).

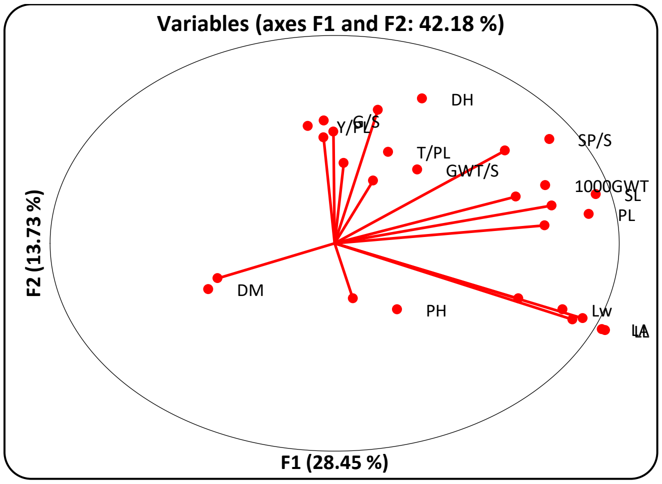

Figure 3. The principal biplot for fourteen parameters of wheat. DH; days to heading, DM; days to maturity, PH; Plant height,PL; Peduncle length, SL; Spike length, LW; Leaf width, LL; Leaf length, LA; Leaf area, SP/S; Spikelets per spike, G/S; Grains per spike, GWT/S; Grain weight per spike, T/PL; Tillers per plant, 1000GWT; Thousands grain weight, Y/p ; Yield per plant

The Scree plot is used to explain percentage variation that is linked with each of the component. Each Eigen value corresponds to a factor and each factor to a one dimension. A factor is a linear combination of the initial variables and all the factors are uncorrelated. The Eigen values and the corresponding factors are sorted by descending order of how much of the initial variability they represent. The Eigen value significance criterion described by Kaiser (1960) was used to select statistically significant principal components. Among 14 components, the five showed value more than 1 (significant) for the year 2013-14. PC-1 showed 28.45% variability with Eigen value 3.98 in germplasm as was presented in Table 3. The first three PCs represented 52% of the total variability (Ahmad *et al.*, 2014). So, selection of genotypes from these PCs will be useful as shown in Fig. 4.

A scatter plot showed that the lines those were close to each other were perceived as the being same when rated on the 14 variables. The PC-1 and PC-2 showed population structure (Fig. 5). Genotypes that are further apart were different from each other with respect to distance between them.

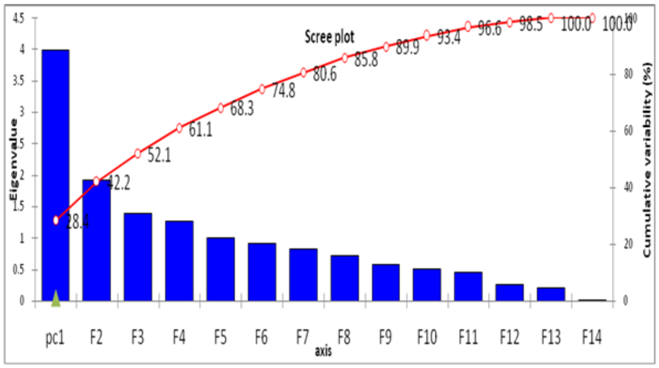

Figure 4. The principal scree plot for fourteen parameters of wheat.

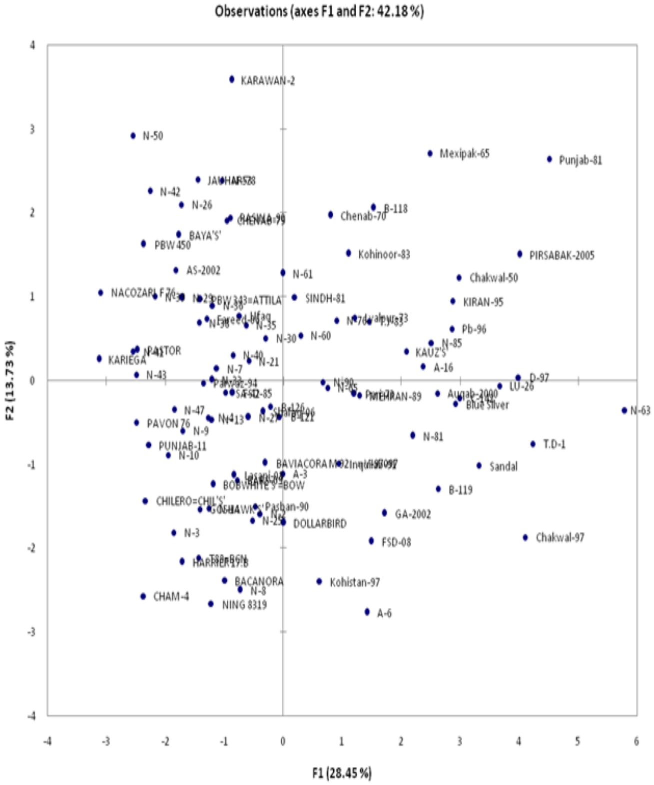

Figure 5. The two dimensional ordination of one hundred genotypes.

Graph based on the 2013-14 data showed that genotypes N-30, N-40, N60, Bobwhite, Baviacora, Lasani-08, Pasban-90, LU-26, Dollarbird, N-25, N-7, Parwaz-94, N-27, N-90, N-65, Mehran-89, Fareed-06, Ufaq and Shafaq-06 were not much different from each other as they are congested in the same area. While genotypes Karawan-2, N-50, N-42, BAYA'S, PBW-450, AS-2002, Nacozari, Pastor, Kareiga, N-3, CHAM-

4, NING-8319, A-6, Kohistan-97, FSD-08, Chakwal-97, GA-2002, B-119, Sandal, T.D-1, N-63, Pirsabak-2005, Mexipak-65 and Punjab-81 were present at distance from other varieties with respect to PC-1 and PC-2 and these genotypes are different. Punjab-81, Mexipak-65, Pirsabak-2005 and chakwal-50 showed maximum diversity from Cham-4, Ning-8319, N-8, Bacanora, Harrier 17.B, and N-3. Chakwal-97 showed maximum diversity from N-50. The genotypes FSD-08, GA-2002, B-119 and Sandal were opposite to N-42, N-26, BAYA's', PBW-450 and AS-(200) (Chahal and Gosal, 2002; Jaynes *et al*., 2003).

***Conclusion*:** It was concluded from the experiment that there was enough variation found in the germplasm for almost all the characters studied as was evident in the analysis of variance. The germplasm was useful for further selection and improvement point of view. The selection from the first three PCs was very useful because they contributed above fifty percent of variation. The more diverse genotypes found in the experiment were Karawan-2, N-50, N-42, BAYA'S, PBW-450, AS-2002, Nacozari, Pastor, Kareiga, N-3, CHAM-4, NING-8319, A-6, Kohistan-97, FSD-08, Chakwal-97, GA-2002, B-119, Sandal, T.D-1, N-63, Pirsabak-2005, Mexipak-65 and Punjab-81 were present at distance from other varieties with respect to PC-1 and PC-2 so these are more diverse genotypes and could be used for improvement of wheat germplasm for further breeding program.

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