

## MULTIVARIATE STATISTICAL ANALYSIS FOR YIELD AND YIELD COMPONENTS IN BREAD WHEAT PLANTED UNDER RAINFED CONDITIONS

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### Abstract

Crop yields of major cereals including wheat are not increasing at the targeted growth rates to feed the rising demands stemming from increase in the human population. Variability in germplasm is always the key to improvement and to assess the extent of variation is never ending process in a plant breeding program. Out of several methods available for assessing the variability, multivariate analysis is one of the most important and widely used methods. Present study was designed to find diversity patterns among 30 wheat lines of hexaploid wheat from CIMMYT nursery planted for two years (i.e. 2013-14 and 2014-15) in two replicates to seek genetic variability amongst genotype in rainfed conditions. Thirteen quantitative traits were determined phenotypically. Three genotypes viz., 27, 28 and 29 performed well with higher values of yield and yield components that may be considered as tolerant to rainfed conditions. The Principal Component Analysis (PCA) grouped all germplasm into four major components explaining over 75% of genetic variation. Cluster analysis classified studied traits into seven groups. Days to heading (DH) and days to maturity (DM) had highest positive loading in first component, while most of yield components had positive loading in second component. It can be concluded that wheat yield can be improved in Pakistan by employing breeding programme in terms of crosses and heterosis in determined different parent clusters.

**Key words:** Principal component analysis, Multivariate analysis, Cluster analysis, Crop yield, Wheat germplasm, Rainfed condition.

### Introduction

Wheat a widely cultivated cereal is main source of human nutrition supports about 35% of world population and provide 20% daily protein and food calories to 4.6 billion world's population (Flister & Galushko, 2016). Wheat is second major crop of the world with global production of 735.3 million tonnes and total area under cultivation is about (Anon., 2015). Pakistan is 9<sup>th</sup> largest wheat producer with 9180 thousand hectares of area is under wheat cultivation. With 2.5% annual increase in population of Pakistan the wheat demand will increase by 30 million tons in 2030 (Nazli *et al.*, 2012). It is urgency of time to increase wheat production for eradication of food insecurity from country, for that different methods and factors that could lead to increase yield must be sorted out (Sokoto *et al.*, 2013). Wheat breeding focuses on development of wheat lines with desirable characters that are capable of producing high yield under range of environments (Tahmasebi *et al.*, 2013). Success of breeding program depends upon understanding and examining the variation among the traits and interaction between different traits that ultimately contribute to yield of a crop (Mary & Gopalan, 2006). The selection of better cultivars is primarily based upon the ability of cultivar to produce high yield under range of environments. Genetic variability and heritability of a variety are important factors determining the effectiveness of yield and other yield components (Aycicek & Yildirim, 2006a; Baenziger *et al.*, 2011).

Three main components contribute to wheat grain yield namely number of productive spike, number of grains per spike and grain weight. And on individual plant level spike number, spikelet number per spike, grain number per spikelet, and grain weight are main components of wheat

yield. Various studies report negative correlation among these yield traits but this correlation might be genotype dependent (Cuthbert *et al.*, 2008; Wang *et al.*, 2009; Deng *et al.*, 2011). Grain yield is product of many agro-physiological traits and biotic and abiotic stresses also affect the final yield so identification of key traits increasing tolerance to these stresses might be helpful in increasing yield. In addition, incorporation of these traits by conventional breeding or by understanding molecular and physiological basis of these traits into breeding program might also increase wheat yield.

Improvement in genetic diversity of wheat begins right after its domestication but with changing environment desired improvement in productivity could not be achieved. Early source of attaining genetic diversity was through hybridization, phenotypic selection or through introduction from specific areas. The final aim of selection or screening is to develop varieties which are high yielding, biotic and abiotic stress tolerant, early maturing, lodging and shattering resistant varieties which had led to the emergence of new cropping systems (Arya *et al.*, 2013). Being a complex trait, yield is controlled by multiple genes and pleiotropic genes and at the same time is influence by environmental conditions. So selection of genotypes only on yield will be misleading, it is necessary to get information about various other factor like information on nature and magnitude of variation in population, association of character with yield and among themselves and the extent of environmental influence on the expression of these characters (Yagdi, 2009; Tsegaye *et al.*, 2012). Greater the variability among the genotypes greater will be the opportunity for development of variety with desirable characteristics (Khan *et al.*, 2003; Aycicek & Yildirim, 2006b).

Multivariate analysis is commonly used for the determination of genetic variability among larger set of wheat lines. Among these methods cluster analysis, multidimensional scaling (MDS), principal component analysis (PCA) and principal coordinate analysis (PCoA) are most commonly exploited methods (Brown-Guedira, Thompson, Nelson, & Warburton, 2000). Of all the above mentioned multidimensional analyses principal component analysis is important for finding regularities among data. Basically PCA transforms the closely correlated data sets into new system of traits and separate them from non correlated components (Janmohammadi, Movahedi, & Sabaghnia, 2014). Current investigation aims at exploring important traits related to yield and to explore effective selection criteria that can be used for improving wheat yield. Keeping in view all scenario experiment was conducted to evaluate genotypes for yield and yield component under rainfed conditions.

### Material and Methods

Advance lines from CIMMYT Elite Bread Wheat Yield Trail (EBWYT) nursery were planted under rain fed conditions at National Agricultural Research Centre, Islamabad, Pakistan during 2013-14 and 2014-2015 in two replications, following alpha lattice design comprising four meter in four rows for each genotype. The detail of the germplasm used is provided in Table 1. The soil type of experimental site was moderately fine textured, non-saline, with pH 7.9, slightly calcareous, and electrical conductivity (EC) of 0.21dS/m. The agronomic practices were kept uniformly to run the whole experiment. For measuring 13 traits separately, 10 plants were randomly selected/ tagged from two central rows for each replicate. The traits recorded include: biomass (B), days to heading (DH), days

to maturity (DM), flag leaf length (FL/L), flag leaf width (FL/W), grain yield (GY), harvest index (HI), leaf area (LA), plant height (PH), spike length (S/L), spikelets per spike (Sp/S), tillers per plant (TL), thousand grain weight (TW). The collected data of all selected traits was statistically analyzed using R software for Principal Component Analysis (PCA) and Cluster analysis (CA) to seek genetic diversity amongst the morphological and quality traits. The correlation matrix is drawn based on PCA. The statistically significant principal components were sorted out by employing Eigen significant criteria after Hussain *et al.* (2014) and Kaiser *et al.* (1960).

### Results and Discussion

Basic statistics for all the studied traits is presented in Table 2 that showed high heritability for grain yield (19%), followed by leaf area (12%) and tillers per plant (10%); while the least value for genetic variability was recorded for days to heading (1%) and days to maturity (2%). Improvement of these traits through simple selection is difficult as they account for least variability. Results from summary statistics show that there was vast diversity among genotypes based on estimated traits (Table 2). Such a high variability plays a vital role in breeding program to meet desired objectives of breeding such as breeding for high yield, resistance to disease, stress tolerance and high quality. High value of coefficient of variation for grain yield shows that its values differs greatly across the genotypes, while the least value exhibits for phenological traits such as days to heading and maturity of genotypes varied within a small range as those of Aharizad *et al.* (2012). The results from the analysis of variance (ANOVA) showed that genotypes differ significantly across the year and replicates (Table 3a&b).

**Table 1. The list of germplasm used in the experiment.**

S. No.	Entry No.	Germplasm/line
1	501	LOCAL CHECK "NARC-2011"
2	502	MUNAL #1
3	503	BECARD #1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ
4	504	PRL/2*PASTOR/3PFAU/WEAVER*2//CHAPIO
5	505	TACUPETO F2001*2/BRAMBLING//KIRITATI/2*TRCH
6	506	KACHU//KIRITATI/2*TRCH
7	507	KIRITATI//HAW234+LR34/PRINIA/3/BAJ #1
8	508	KIRITATI//HAW234+LR34/PRINIA/3/BAJ #1
9	509	MUTUS//ND643/2*WBLL1
10	510	ND643/2*WBLL1/4/WHEAR/KAKUNA/3/C80.1/3*BATAVIA//2*WBLL1
11	511	BAJ #1/KISKADEE #1
12	512	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/PRL/2*PASTOR/..
13	513	WHEAR/VIVITSI//WHEAR/3/FRNCLN
14	514	QUAIU*2/KINDE
15	515	MUU/FRNCLN//FRANCOLIN #1
16	516	WAXWING*2/TUKURU/3/2*WHEAR/VIVITSI//WHEAR
17	517	DANPHE #1*2/CHYAK
18	518	MUTUS*2/HARIL #1
19	519	MUTUS*2//ND643/2*WBLL1
20	520	FRNCLN/NIINI #1//FRANCOLIN #1
21	521	FRNCLN/3/ND643//2*PRL/PASTOR/4/FARCOLIN #1
22	522	FRNCLN/3/KIRITATI//HUW234+LR34/PRINIA/4/FRANCOLIN #1
23	523	WBLL1*2BRAMBLING*2//BAVIS
24	524	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
25	525	CROC_1/AE.SAQUARROSA (205)//BORL95/3/PRL/SARA//TSI/.....
26	526	FRET2*2/4/SNI/TRAP#1/3/KAZ*2/TRAP//KAUZ/5/KIRITATI/.....
27	527	PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI/5/...
28	528	MUNAL*2/CHONTE
29	529	WAXWING*2/TUKURU/2*FRNCLN
30	530	FRANCOLIN #1/CHONTE//FRNCLN

**Table 2. Summary statistics for agro-morphological traits.**

	Min	Max	Mean	S.E. Mean	LSD	CV
Area	26.57	43.36	34.43	0.74	1.52	0.12
Biomass	1.40	2.05	1.74	0.03	0.06	0.08
DTH	105.67	110.00	108.16	0.21	0.44	0.01
DTM	139.34	148.17	143.07	0.46	0.94	0.02
FLL	19.12	26.80	22.54	0.34	0.69	0.08
FLW	1.76	2.23	2.02	0.02	0.04	0.06
GY	0.47	0.92	0.65	0.02	0.05	0.19
HI	39.77	54.68	46.95	0.57	1.17	0.07
PH	78.17	94.96	86.73	0.62	1.26	0.04
SPL	9.38	11.46	10.37	0.09	0.18	0.05
Spls	18.42	21.83	20.26	0.15	0.30	0.04
TILL	5.42	7.83	6.46	0.12	0.25	0.10
TKW	35.21	41.66	38.24	0.31	0.63	0.04

Min: Minimum value, Max: Maximum value, Mean: Average value, S.E. Mean: Standard error mean, LSD: Least significant difference, CV: Coefficient of variation

Area: Leaf area, Biomass: Above ground biomass, DTH: Days to heading, DTM: Days to maturity, FLL: Flag leaf length, FLW: Flag leaf width, GY: Grain yield, HI: Harvest index, PH: Plant height, SPL: Spike length, Spls: Spikelets per spike, TILL: Tillers per plant, TKW: 1000 grain weight

**Table 3a. Analysis of variance (ANOVA) table agro-morphological traits evaluated for two years under rainfed conditions.**

	DF	TKW	HI	GY	FLW	FLL	Area	TILL	PH	SPLS	SPL
Genotype	29	28.68***	923***	0.31***	0.1317***	33***	206***	5.26***	129.9***	6.56***	4.021***
Rep	1	63.15***	17987***	14.312***	0.1729*	83**	219.	8.71*	8.7	58.4***	18.998***
Year	1	59.32***	23573***	7.511***	0.4951***	3337***	6173***	92.01***	62.5	0.8	0.008
Genotype: Rep	29	33.92***	675***	0.268***	0.1099***	24**	134***	4.17**	115.9***	3.31	2.725**
Genotype: Year	29	34.78***	1185***	0.554***	0.1298***	41***	202***	2.73	182.5***	5.98***	4.395***
Rep: Year	1	148.15***	24121***	13.118***	0.1827*	0	173.	20.54**	1416.1***	18.23**	2.45
Genotype: Rep:Year	29	41.76***	838***	0.421**	0.0522	11	78	2.08	74.1**	3.96*	2.299*
Residuals	2	1000.3	58	0	0.0442	12	60	2.06	40	2.54	1.308

Area: Leaf area, Biomass: Above ground biomass, DTH: Days to heading, DTM: Days to maturity, FLL: Flag leaf length, FLW: Flag leaf width, GY: Grain yield, HI: Harvest index, PH: Plant height, SPL: Spike length, Spls: Spikelets per spike, TILL: Tillers per plant, TKW: 1000 grain weight. For grain yield (19%), followed by leaf area (12%) and tillers per plant (10%); while the least value for genetic variability was recorded for days to heading (1%) and days to maturity (2%)

**Table 3b. Analysis of variance (ANOVA) for biomass and phenological traits evaluated for two years under rainfed conditions.**

	DF	DW	DTH	DTM
Genotype	29	0.219***	57***	83.2*
Rep	1	14.36***	5649***	179.2.
Year	1	0.576***	4811***	372.1**
Genotype: Rep	29	0.138***	69***	73
Genotype: Year	29	0.305***	70***	104.3**
Rep:Year	1	3.162***	5336***	74.7
Genotype: Rep: Year	29	0.171***	66***	77.9.
Residuals	2	0.039	3	54.8

DF: Degree of freedom, DW: above ground plant dry weight, DTH: Days to heading , DTM: Days to maturity

**Correlation analysis:** Diversification of wheat accession based on their yield was already assessed by planting them under rainfed conditions (Rymuza *et al.*, 2012). The literature reported that different environmental conditions do not only affect on wheat performance but also on correlation between different yield and morpho-physiological characters (Sabo *et al.*, 2002; Weber, 2008; Głowacka, 2010). Pearson correlation coefficient between grain yield and all studied traits are given in Table 4. There was strong and significant positive correlation ( $p < 0.05$ ,  $r > 0.5$ ) for grain yield associated with spikelets per spike ( $r = 0.85^{**}$ ) and thousand grain weight ( $r = 0.76^{**}$ ), while it had moderately high significant correlations with rest of traits except days to heading and days to maturity. Grain yield had a significant and negative correlation with days to heading, while it had non-significant and negative correlation with days to maturity. Positive association between grain yield and 100 grain weight was shown by

Leilah & Khateeb (2005) and Bibi *et al.* (2017). Positive correlation of grain yield and plant height was reported by Leilah & Khateeb (2005), Gracia del Moral *et al.* (2003) and Slafer *et al.* (2005). The positive correlation between grain yield and spikelets per spike imply that wheat yield is sink limited, more the number of kernals more will be the yield and increasing spikelets per spike will lead to increase in grain yield. Positive association between days to heading and days to maturity reported in present study was in agreement with Ajmal *et al.* (2013). All other correlations among studied traits are listed in Table 4. It has been observed from the results that grain yield had positive associations with yield components, leaf area, biomass and plant height suggesting the need to emphasis on these traits for improving grain yield under rainfed conditions. The negative association with days to maturity suggest that genotypes which complete their life cycle prior to environmental extremities had higher yield.

**Table 4. Correlation analysis for agro-morphological traits evaluated for two cropping years.**

	Area	Biomass	DTH	DTM	FLL	FLW	GY	HI	PH	SPL	Spls	TILL
Biomass	0.23											
DTH	-0.50**	-0.38*										
DTM	-0.51**	-0.15	0.57**									
FLL	0.12	0.1	-0.19	-0.06								
FLW	-0.01	0.26	-0.39*	-0.01	0.69**							
GY	0.28	0.65**	-0.54**	-0.37*	0.31	0.49**						
HI	-0.19	0.17	0.04	-0.02	0.28	0.48**	0.34					
PH	0.58**	0.3	-0.27	-0.32	0.08	0.11	0.37*	0.12				
SPL	0.27	0.46**	-0.38*	-0.27	0.12	0.41*	0.44*	0.09	0.60**			
Spls	0.3	0.55**	-0.58**	-0.41*	0.11	0.25	0.85**	0.19	0.40*	0.35		
TILL	0.1	0.2	-0.08	-0.08	0.54**	0.59**	0.57**	0.61**	0.34	0.27	0.37*	
TKW	0.11	0.46*	-0.46**	-0.27	0.01	0.22	0.76**	0.1	0.22	0.31	0.77**	0.25

Area: Leaf area, Biomass: Above ground biomass, DTH: Days to heading, DTM: Days to maturity, FLL: Flag leaf length, FLW: Flag leaf width, GY: Grain yield, HI: Harvest index, PH: Plant height, SPL: Spike length, Spls: Spikelets per spike, TILL: Tillers per plant, TKW: 1000 grain weight

**Table 5. Principal component analysis table for agro traits evaluated under rainfed conditions.**

Traits	PCA 1	PCA 2	PCA 3	PCA 4
Leaf area	-0.4576523	0.51909687	-0.54482125	-0.05391835
Biomass	-0.6549836	0.0985511	0.28987416	0.21878227
Days to heading	0.6904522	-0.34218495	0.08132759	0.45619967
Days to maturity	0.498782	-0.45163373	0.25089434	0.29813829
Flag leaf length	-0.3957605	-0.58494683	-0.39434951	-0.38394354
Flag leaf width	-0.5815153	-0.62712802	-0.16601664	-0.21638955
Grain yield	-0.9140054	-0.05800956	0.28098048	-0.03387616
Harvest index	-0.3492855	-0.663123	0.06022278	0.20221578
Plant height	-0.5782341	0.25325016	-0.42565696	0.53932757
Spike length	-0.631348	0.10166495	-0.21474118	0.4177937
Spikelets per spike	-0.8226689	0.18640195	0.36366517	-0.04706342
Tillers per plant	-0.5942071	-0.60034361	-0.14785103	0.15166346
1000 grain weight	-0.6869026	0.16004711	0.56181286	-0.06383748
Eigenvalue	5.050806	2.274032	1.413113	1.078771
Variance percent	38.852352	17.492551	10.870099	8.29824
Cumulative variance percent	38.85235	56.3449	67.215	75.51324

**Principal component analysis (PCA):** The PCA is usually used to simplify the complex data into simple components called principal components. First principal component accounts for maximum variability in data than all other components (Leilah & Al-Khateeb, 2005). In the present study, the principal component analysis divided data into four main components accounting for 75.51% of variations. First principal component had eigen value 5.05 and accounted for 38.85% of variation. The PC2, PC3 and PC4 accounted for 17.49% 10.87 and 8.29% of variation and had eigen values 2.27, 1.41 and 1.07 respectively (Table 5). Days to heading and days to maturity had highest positive loading in the 1<sup>st</sup> component (Table 5). Leaf area, plant height, spikelets per spike, 1000 grain weight, spike length and biomass had positive loading in 2<sup>nd</sup> component, while 1000 grain weight, spikelets per spike, biomass, grain yield, days to maturity, days to heading and harvest index had positive loading in 3<sup>rd</sup> component. In the 4<sup>th</sup> principal component, plant height, days to heading, spike length, days to maturity, biomass, harvest index and tillers per plant had highest positive loading. First two components accounted for 56.34% of total variation (Table 5).

The connections between the different factors and genotypes with respective principal components are further explained by the principal component biplots is given in Fig. 1. In PCA, a higher correlation is exhibited by the smaller angles among vectors of the same direction. Genotypes having higher value of particular trait were plotted closer to the vector line and further in the direction of that particular vector, often on the vertices of the convex hull. Most of the genotypes were scattered in the positive side of the 1<sup>st</sup> principal component, with genotypes such as 8, 7, 5 and 2 excelling in yield which was contributed mostly by high 1000 grain weight and spike lets per spike as well as optimum values for other yield components (Fig. 1). Genotypes such as genotype 8, 7, 5 and 2 were dispersed in the positive side of the excelling principle components such as optimum values for yield and other yield components.

Most of breeding program utilizes the diverse parents which are genetically far apart from one another, and population from them will have high performance, cluster analysis usually finds the extent of genetic diversity and groups the organisms with similar parents into one cluster. Cluster analysis based on genotypes

group the whole set of genotypes into seven major clusters based on their morphological performance. Cluster analysis usually finds the extent of genetic diversity and groups the organisms with similar parents into one cluster (Shinwari *et al.*, 2013; Mohammadi *et al.*, 2015). The cluster analysis divided the genotypes into 7 major clusters with maximum number of genotypes in cluster 1 while cluster 4 having only 2 genotypes. Genotypes 527, 528 and 529 had higher mean value for grain yield, 1000 grain weight and spikelets per spike so were grouped in one cluster (Fig.

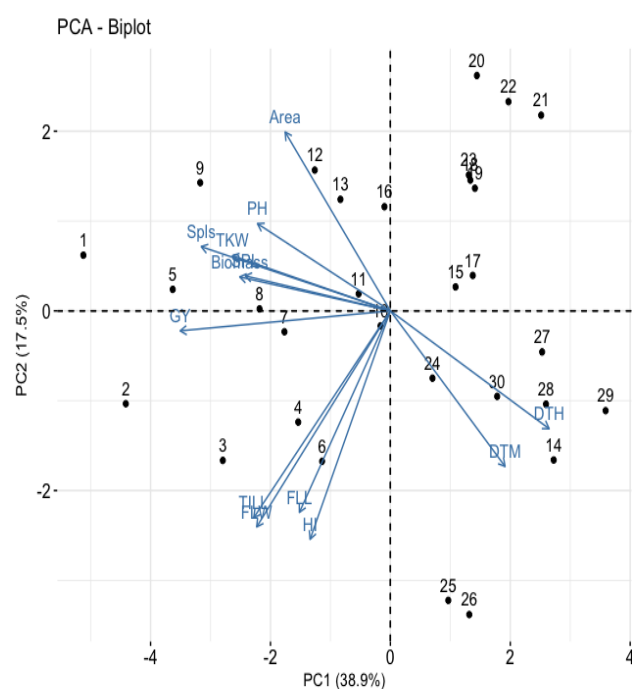


Fig. 1. PCA Biplot for Agro morphological traits with number showing genotypes.

## Conclusion

Present study was aimed at finding diversity patterns in selected 30 wheat lines of hexaploid wheat from CIMMYT nursery grown in rainfed condition. Three genotypes namely 27, 28 and 29 performed well with higher values of yield and yield components and may be considered as tolerant to rainfed conditions. The present study can be used as benchmark for selection of genotypes for further screening, genotyping and testing for improving yield and yield components.

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2). Two lines viz., 7 and 8 grouped in one cluster take maximum days to maturity, while 2, 4, 6, 30 in one cluster and 7, 8 in closely related cluster were short statured plants. Genotypes 27, 28 and 29 had higher value of yield components so can be released as varieties after further testing (Fig. 2). These lines can also be used as parents in hybridization program to produce high yielding varieties. The present study is helpful in designing crosses between different parents thus will be helpful in improving wheat yield by maximizing the genetic diversity.

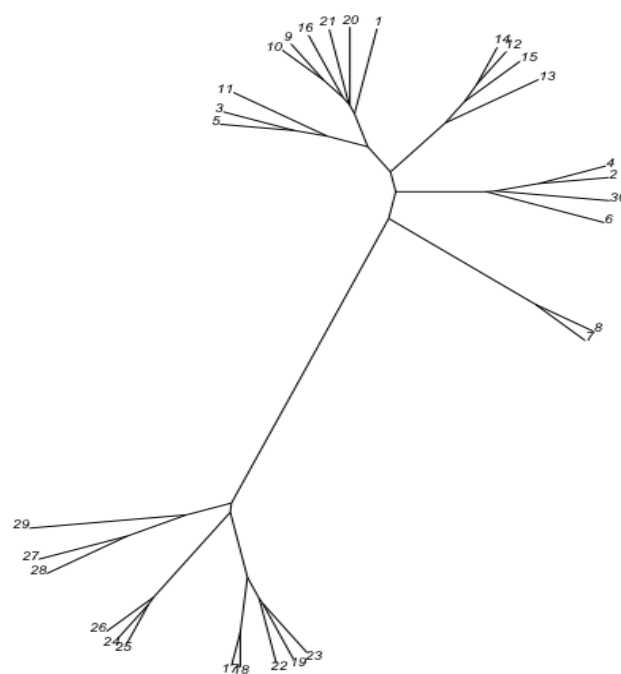


Fig. 2. Cluster analysis dividing genotypes in 7 major clusters based on morphological data.

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