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## Research Article

### ACCESSIONS DISSECTION OF WHEAT (*TRITICUM AESTIVUM*) USING CLUSTER AND PRINCIPAL COMPONENT ANALYSIS

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## Abstract

A research trial for sixty-two (62) wheat accessions was conducted at Arid Zone Research Centre, D. I. Khan, Khyber Pakhtunkhwa, Pakistan to check variations in germplasm, heritability and genetic advance. The experiment was triplicated with randomized complete block design (RCBD) with plot size 18x5m<sup>2</sup>. Data were recorded for days to headings, days to maturity, flag leaf area, plant height, No. of tillers plant<sup>-1</sup>, peduncle length, spike length, spikelet spike<sup>-1</sup>, No. of grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, 1000-grains weight and further subjected to Analysis of Variation (ANOVA) and Least Significant Differences amongst the means to check the significant at 5% probability level. For phenotypic and genotypic correlation high magnitude of (71.19%) was recorded in spike density and lowest in plant height (1.89%). Whereas for GCV maximum was noted for spike length (14.64%). Maximum Hbs and GA was estimated in plant height with values (98.06%) and (35.95%) respectively. Whereas the trait spikelets spike<sup>-1</sup> exhibited minimum values for Hbs (26.29%) and GA (1.46%). High heritability means the trait Plant height is additively controlled. The grain yield plant<sup>-1</sup> was higher in peduncle length, tillers plant<sup>-1</sup>, thousand grain weight, grain number spike<sup>-1</sup> and spike density. Grain yield plant<sup>-1</sup> was recorded as highest by genotypes in Cluster-I and Cluster-IV. Principal component analysis presented an eigen value of greater than 1 for first four components and contributed to 73% of total variation while important yield related attributes were highest in PC1 and PC2.

**Keywords:** *Wheat, heritability, genetic advance, cluster analysis.*

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## 1. Introduction

Pakistan is amongst top ten Wheat (*Triticum aestivum* L.) growers of the world and 75% of the farmers in Pakistan tend to grow wheat due to its high demand in the country as well as good export values. Wheat was cultivated over an area of 9043 thousand hectares and production was recorded as 27.643 million tonnes which depicts an increase of 5.4%

over previous year (Pakistan Economic Survey, 2022-2023).

It is a vital source of carbohydrates and has the capability to produce upto 20% of the food reserves of the world (Farzi and Bigloo, 2010). New varieties of wheat are being developed by the breeders with the aim of improving the yield potential of wheat. It is an important cereal crop following rice, it enjoys an indispensable and significant rank



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in agriculture and the economic domain of the country.

Crop improvement plays essential role in providing wider scope for selection in genetic variability. Heritability studies of characters indicate to which extent such characters can be achieved. Heritability is helpful in selection process whereas the genetic advance is known to be predictor of genetic gain in upcoming generations (Najeeb *et al.*, 2009). Heritability study is an excellent indicator of transmission of characters and selection of elite genotypes from existing pool of germplasm (Devesh *et al.*, 2018).

In Wheat crop phenotypic and genotypic variance, heritability estimates, genetic advance provide assessment about genetic behaviour and degree of variation have been studied by Cheema *et al.*, 2006. Principal component analysis assists in accumulation of small number of informative variable data from already prevalent large scale of information (Devesh *et al.*, 2019). Correlation studies have been reported by (Farooq *et al.*, 2018) showed beneficial understanding of inheritance patterns of traits which have influence on the yield of the crop. Genotypic and phenotypic association studies have been reported that correlation facilitates the selection process for a particular trait like yield and yield related attributes. (Verma *et al.*, 2019).

For dissection of genetic material / accession it is very meaningful if the available lot is dissected or divided into groups on the basis of morphological traits, correlation, genetic components like heritability, genetic gains and genetic advance and other breeding tools. Amongst them it is best to study principal component analysis and cluster analysis. Where there is a diverse germplasm then cluster analysis is very helpful. Because in cluster analysis it becomes easy to select the plant with required traits amongst the favorable clusters. Principal component analysis is known to provide few and concise

amount of principal components from a large amount of variation. Focusing the importance of clustering and finding out the principal component of variation following cogent objectives were designed;

1. Evaluation and comparison of wheat germplasm on the basis of morphology.
2. Screening the germplasm into components and cluster for better selection cluster analysis.

## 2. MATERIALS AND METHODS

A research trail for sixty-two (62) wheat accessions was conducted at Arid Zone Research Centre, D. I. Khan, Khyber Pakhtunkhwa, Pakistan to check variations in germplasm, heritability and genetic advance. The experiment was triplicated with randomized complete block design (RCBD) with plot size 18x5m<sup>2</sup>. Data were recorded for days to headings, days to maturity, flag leaf area, plant height, no. of tillers plant-1, peduncle length, spike length, spikelet spike-1, no of grains spike-1, grain yield plant-1, 1000-grains weight and further subjected to Analysis of Variation (ANOVA) and Least Significant Differences amongst the means to check the significant at 5% probability level. Fertilizers containing nitrogen and phosphorous doses were provided as per recommendation during sowing to harvesting process. Focus was given to twelve parameters by collecting five random plants from each replication and plot. Collected data was evaluated via analysis of variation (Steel *et al.*, 1997). In this study the genotypic and phenotypic coefficients of variations were (Singh and Chaudhary, 1985) to obtain idea regarding variability by formula

$$V_p (\%) = \frac{\sqrt{PV}}{\bar{X}} \times 100 \quad V_g (\%) = \frac{\sqrt{GV}}{\bar{X}} \times 100$$

$V_p$  = phenotypic variance,  $V_g$  = genotypic variance,  $\bar{X}$  = sample mean

$$h^2_{BS} = V_g/V_p * 100$$

Where,  $h^2_{BS}$ : Broad Sense Heritability (Falconer, 1989),  $V_g$ : genotypic variance,  $V_p$ :

phenotypic variance. Genetic advance studies were performed using formula of (Allard, 1960).

$$\text{Genetic advance (as percent of mean)} = k \times h \times \frac{\sqrt{\text{Phenotypic variance}}}{\text{Mean value of treat}} \times 100$$

GA: genetic advance, K: constant = 2.06 at 5% selection intensity,  $h^2$ : Heritability. Genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation was studied with the help of procedure by Kwon and Torrie (1964). Where,  $V_p$  = phenotypic variance,  $V_g$  = genotypic variance,  $\bar{X}$  = sample mean

$$\text{Genetic advance (as percent of mean)} = k \times h \times \frac{-b \pm \sqrt{\text{phenotypic variation}}}{\text{Mean value of treat}} \times 100$$

GA: genetic advance, K: constant = 2.06 at 5% selection intensity,  $h^2$ : Heritability. Genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation Kwon and Torrie (1964).

$$\text{Phenotypic correlation: } (r_p) = \frac{\text{PCov}_{xy}}{\sqrt{\text{PV}_x \cdot \text{PV}_y}}$$

$r_p$  = phenotypic correlation,  $\text{PCov}_{xy}$  = phenotypic covariance of x and y character,  $\text{PV}_x$  = phenotypic variance of x character,  $\text{PV}_y$  = phenotypic variance of y character

We studied broad sense of Where,  $h^2_{BS}$ : Broad Sense Heritability (Falconer, 1989),  $V_g$ : genotypic variance,  $V_p$ : phenotypic variance. Genetic advance studies were performed using formula of (Allard, 1960). heritability in terms of ratio via formula of (Falconer, 1989).

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$$\text{Genotypic correlation: } (r_g) = \frac{\text{GCov}_{xy}}{\sqrt{\text{GV}_x \cdot \text{GV}_y}}$$

$r_g$  = genetic correlations,  $\text{GCov}_{xy}$  = genetic covariance between x and y character,  $\text{GV}_x$  = genotypic variance of x character,  $\text{GV}_y$  = genotypic variance of y character.

Cluster analysis Ward's protocol (1963) with Euclidian diversity distance being 10 as standard for linkage distance. software Minitab 18 was applied for Principal Component Analysis.

**Table 1. Source and origin of the wheat accession used in the experiment**

Annotation	Origin	Annotation	Origin	Annotation	Origin
A1	MXI18-19	A21	MXI18-19	A41	MXI18-19
	MTESTIGOSBW-4		M40ES27SA1811-70		M40ES27SA1811-207
A2	MXI18-19	A22	MXI18-19	A42	MXI18-19
	MTESTIGOSBW 9		M40ES27SA1811-74		M40ES27SA1811-210
A3	MXI18-19	A23	MXI18-19	A43	MXI18-19
	MTESTIGOSBW-17		M40ES27SA1811-81		M40ES27SA1811-216
A4	MXI18-19	A24		A44	MXI18-19
	M40ES27SA1811-4				M40ES27SA1811-217
A5	MXI18-19	A25	MXI18-19	A45	MXI18-19
	M40ES27SA1811-6		M40ES27SA1811-94		M40ES27SA1811-222
A6	MXI18-19	A26	MXI18-19	A46	MXI18-19
	M40ES27SA1811-12		M40ES27SA1811-97		M40ES27SA1811-224
A7	MXI18-19	A27	MXI18-19	A47	MXI18-19
	M40ES27SA181-16		M40ES27SA1811-102		M40ES27SA1811-229
A8	MXI18-19	A28	MXI18-19	A48	MXI18-19
	M40ES27SA1811-18		M40ES27SA1811-103		M40ES27SA1811-239
A9	MXI18-19	A29	MXI18-19	A49	MXI18-19
	MA0ES27SA1811-26		M40ES27SA1811-107		M40ES27SA1811-247

A10	MXI18-19	A30	MXI18-19	A50	MX116-17
	M40ES27SA1811-28		M40ES27SA1811-110		MULTMISCBW-6
A11	MXI18-19	A31	MXI18-19	A51	MX116-17
	M40ES27SA1811-34		M40ES27SA1811-119		
A12	MXI18-19	A32	MXI18-19	A52	MX116-17
	M40ES27SA181-38		M40ES27SA1811-142		MSIBWM368A-48
A13	MXI18-19	A33	MXI18-19	A53	MX116-17
	M40ES27SA1811-41		M40ES27SA1811-145		MSIBWM368A-54
A14	MXI18-19	A34	MXI18-19	A54	MX116-17
	M40ES27SA1811-46		M40ES27SA1811-146		MSIBWM368A-56
A15	MXI18-19	A35	MXI18-19	A55	MX116-17
	M40ES27SA1811-57		M40ES27SA1811-147		MSIBWM368A-98
A16	MXI18-19	A36	MXI18-19	A56	MX116-17
	M40ES27SA1811-59		M40ES27SA1811-147		MSIBWM368A-131
A17	MXI18-19	A37	MXI18-19	A57	MX116-17
	M40ES27SA1811-62		M40ES27SA1811-148		MSIBWM368A-133
A18	MXI18-19	A38	MXI18-19	A58	MX116-17
	M40ES27SA1811-64		M40ES27SA1811-169		MSIBWM368A-134
A19	MXI18-19	A39	MXI18-19	A59	MX116-17
	M40ES27SA1811-67		M40ES27SA1811-170		MSIBWM368A-183
A20	MXI18-19	A40	MXI18-19	A60	MX116-17
	M40ES27SA1811-68		M40ES27SA1811-180		MSIBWM368A-184
		A41	MXI18-19	A61	MX116-17
			M40ES27SA1811-207		M511BWM368A-351
				A62	MX116-17
					M511BWM368A-353

### 3. Result and Discussion

**Genetic Variance:** Analysis of variance for twelve agro-morphological attributes resulted in highly significant dissimilarities among studied genotypes (Table 2). Variations and coefficients of variations in terms of genotypic and phenotypic variations, broad sense heritability and probable genetic advance in terms of percentage mean for said attributes are listed in (Table 3). Genotypic coefficient of variation was ranged as high in spike density followed by mid ranged in spike length, no. of tillers plant<sup>-1</sup>, no of spikelets spike<sup>-1</sup> and low ranged in days to maturity, time to 50% heading in days, peduncle length, grain yield plant<sup>-1</sup>, flag leaf area, 1000-grains weight and grains number spike<sup>-1</sup> and plant height.

However, phenotypic coefficient of variation was higher in all attributes which reflects environmental dominancy in these characters. (Table 3).

Broad sense heritability was recorded as highest in plant height, no. of grains spike<sup>-1</sup>, 1000-grains weight, flag leaf area, spike density, grain yield plant<sup>-1</sup>, peduncle length, days to 50% headings and days to maturity and moderate for no. of tillers plant<sup>-1</sup>, spike length, no of spikelets spike<sup>-1</sup>. While genetic advance was highest for plant height, no of grains spike<sup>-1</sup> while it was recorded as moderate for 1000-grains weight, flag leaf area, grain yield plant<sup>-1</sup>, peduncle length and low for days to 50% headings, days to maturity, no. of tillers plant<sup>-1</sup>, spike length, no of spikelets spike<sup>-1</sup> and spike density (Table

3). Results reveal that the trait yield can be improved via manipulation of said attributes. Alemu *et al.*, 2020 also found similar heritability and genetic advance values for days to 50% headings and spike length, Elbashier *et al.*, 2019 for days to maturity, Kalimullah *et al.*, 2012 for flag leaf area and spike density, Bhushan *et al.*, 2013 and Jamil *et al.*, 2017 recorded similar magnitude for no. of tillers plant<sup>-1</sup> and no of spikelets spike<sup>-1</sup>, Bayisa *et al.*, 2020 and Gerema 2021 for plant height, no of grains spike<sup>-1</sup> and 1000-grains weight, Devesh *et al.*, 2018 for peduncle length, Khan *et al.*, 2019 and Saleem *et al.*, 2008 for grain yield plant<sup>-1</sup>. Heritability accompanied by genetic advance studies is more helpful in understanding genetic gain during selection process rather than studying heritability alone (Johanson *et*

*al.*, 1955). Genetic advance was recorded as highest with high heritability for plant height and no of grains spike<sup>-1</sup> which is indicative of additive gene action on this trait and selection could prove healthy in the initial generations. Kalimullah *et al.*, 2012 and Munir *et al.*, 2007 suggested similar findings in their studies. High amount of heritability recorded with little genetic development for time in days to 50% headings, time required for maturity and spike density indicate non-additive gene action on their expression hence limitations might be faced by breeders for exploitation of these traits. Heritability along with genetic advance was lowest in no. of spikelets spike<sup>-1</sup> which is an indication of potent inheritance path of this attribute by studied genotypes with non-additive gene action on the trait.

**Table 2. Mean, mean squares and standard error of means for seven quantitative characters of sixty two wheat genotypes**

Trait	Mean	Mean squares	SE (Mean)
Days to 50% headings	104.8	96.091**	1.59
Days to maturity	141.44	55.69**	1.56
Flag leaf area	38.27	251.31**	1.35
No of tillers plant <sup>-1</sup>	10.83	12.79**	1.1
Plant height	113.52	938.19**	1.43
Spike length	11.42	9.241**	1.11
Peduncle length	19.09	116.20**	1.33
No. of spikelets spike <sup>-1</sup>	21.65	11.20**	1.34
No. of grains spike <sup>-1</sup>	53.06	458.54**	1.45
Grain yield plant <sup>-1</sup>	21.64	207.34**	1.46
1000-grains weight	36.13	292.07**	1.37
Spike density	1.02	0.69**	0.08

\*\*= Highly Significant (p < 0.05)

**Correlation analysis:** Correlation was estimated at phenotypic and genotypic level and results are given in (Table 4). Yield-related attributes such as grain yield per plant showed highly significant associations with peduncle length, grains number per spike, number of tillers per plant, thousand grain weight, and density of spikes for both phenotypic and genotypic levels. There was also a highly significant negative relationship with days to 50% heading. The number of spikelets per spike had a considerably higher association at the genotypic level and a significant correlation at the phenotypic

level. Other attributes exhibited non-significant associations with grain yield per plant in both positive and negative directions at phenotypic and genotypic levels (Table 4). Other attributes varied in their associations with each other. For example, time to 50% heading was observed positively related with days to maturity and flag leaf area at both levels, a significantly positive association with plant height at both levels, a significantly negative association with thousand grain weight at the genotypic level, and a highly significant negative association with grain number per spike and spike

density. Time taken for maturity had a highly significant relationship with flag leaf area at both levels and significant associations with plant height and thousand grain weight. The number of tillers per plant had a significant correlation with thousand grain weight at both levels and a strong significant correlation with spike density at both levels. Flag leaf area showed a significant positive correlation with the number of spikelets per spike and the number of grains per spike at both phenotypic and genotypic levels. The

number of spikelets per spike had a highly significant association with the number of grains per spike.

Finally, 1000-grain weight had a significant association with the number of tillers per plant at both levels of correlation (Table 4). Likewise estimates of correlation were recorded in studies by Habib *et al.*, 2020, Elbasher *et al.*, 2019, Iqbal *et al.*, 2017, Din *et al.*, 2018, Kalimullah *et al.*, 2012, and Gerema 2021.

Table 3. Various Genetic parameters for yield components of wheat.

Traits	GV	PV	GCV	PCV	H(%)	GA(%)
Days to 50% headings	29.5	37.08	5.65	6.33	79.53	9.97
Days to maturity	16.12	23.44	7.21	8.69	68.78	6.86
Flag leaf area	81.93	87.44	3.6	3.72	93.7	18.05
No of tillers plant <sup>-1</sup>	3.05	6.68	13.7	20.2	45.65	2.43
Plant height	310.7	316.8	1.87	1.89	98.06	35.95
Spike length	1.83	5.57	14.6	25.6	32.82	1.59
Peduncle length	36.95	42.28	5.23	5.59	87.39	11.7
No. of spikelets spike <sup>-1</sup>	1.93	7.33	12.4	24.2	26.29	1.46
No. of grains spike <sup>-1</sup>	150.7	157.1	2.67	2.73	95.96	24.77
Grain yield plant <sup>-1</sup>	66.98	73.38	3.94	4.13	91.27	16.1
Thousand grains weight	95.45	101.2	3.34	3.44	94.36	19.55
Spike density	0.22	0.24	68.1	71.2	91.37	0.93

\*\*= Highly Significant (p < 0.05)

Table 4. Genotypic and phenotypic correlation for various traits in wheat genotypes

Paramete	DH	DM	FLA	NTP	PH	SL	PL	NSS	NGS	GYP	1000-	SD
DH		<b>0.50*</b>	<b>0.41*</b>	-	<b>0.28*</b>	0.16 <sup>N</sup>	-	0.11 <sup>N</sup>	-	-	-	-
DM	<b>0.50*</b>		<b>0.44*</b>	0.05 <sup>N</sup>	<b>0.29*</b>	-	0.07 <sup>N</sup>	0.11 <sup>N</sup>	-	0.21 <sup>N</sup>	<b>0.3*</b>	0.12 <sup>N</sup>
FLA	<b>0.40*</b>	<b>0.44*</b>		0.02 <sup>N</sup>	-	0.08 <sup>N</sup>	-	<b>0.41*</b>	<b>0.27*</b>	0.14 <sup>N</sup>	0.01 <sup>N</sup>	0.09 <sup>N</sup>
NTP	-	-	-		0.03 <sup>N</sup>	0.08 <sup>N</sup>	0.23 <sup>N</sup>	0.19 <sup>N</sup>	0.13 <sup>N</sup>	<b>0.51*</b>	<b>0.32*</b>	<b>0.34*</b>
PH	<b>0.26*</b>	<b>0.30*</b>	-	-		0.01 <sup>N</sup>	<b>0.49*</b>	-	-	0.01 <sup>N</sup>	0.17 <sup>N</sup>	-
SL	0.06 <sup>N</sup>	-	0.03 <sup>N</sup>	-	-		-	<b>0.35*</b>	0.09 <sup>N</sup>	-	-	<b>0.26*</b>
PL	-	0.04 <sup>N</sup>	-	0.17 <sup>N</sup>	<b>0.50*</b>	-	-	-	-	<b>0.33*</b>	<b>0.41*</b>	0.21 <sup>N</sup>
NSS	-	-	<b>0.47*</b>	-	-	0.02 <sup>N</sup>	-		<b>0.43*</b>	<b>0.32*</b>	0.01 <sup>N</sup>	<b>0.41*</b>
NGS	-	-	<b>0.26*</b>	0.11 <sup>N</sup>	-	0.07 <sup>N</sup>	-0.11	<b>0.52*</b>		<b>0.49*</b>	0.13 <sup>N</sup>	<b>0.57*</b>
GYP	-	0.21 <sup>N</sup>	0.13 <sup>N</sup>	<b>0.53*</b>	0.04 <sup>N</sup>	-	<b>0.34*</b>	<b>0.36*</b>	<b>0.48*</b>		<b>0.50*</b>	<b>0.66*</b>
1000-	-	<b>0.30*</b>	-	<b>0.32*</b>	0.17 <sup>N</sup>	-	<b>0.41*</b>	-	0.12 <sup>N</sup>	<b>0.50*</b>		0.12 <sup>N</sup>
SD	-	0.13 <sup>N</sup>	0.09 <sup>N</sup>	<b>0.41*</b>	-	<b>0.35*</b>	0.21 <sup>N</sup>	<b>0.56*</b>	<b>0.59*</b>	<b>0.66*</b>	0.12 <sup>N</sup>	

\* and \*\* significant at 5% and 1% level of significance respectively.

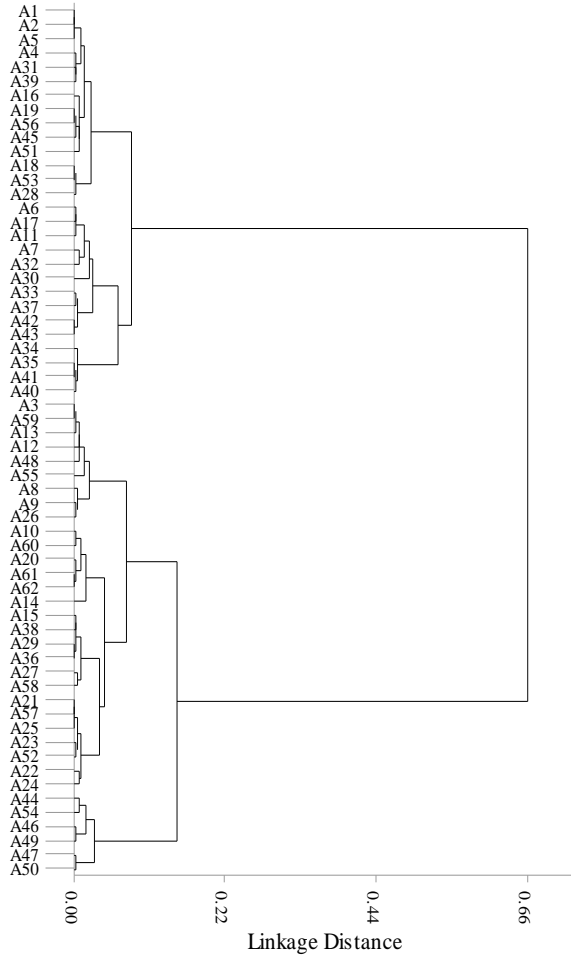
**Cluster analysis:** Investigations for cluster analysis were followed by Euclidean variation distance following Ward's method. This investigation led to accumulation of genotypes into six clusters (Table 5) (Figure 1). Cluster analysis resulted in minimum of four genotypes in Cluster-V to maximum of nineteen spikelets genotypes in Cluster-IV. Cluster-I had fourteen genotypes, Cluster-II had nine genotypes, Cluster-III had ten genotypes and Cluster-VI had six genotypes (Table 5). Mean analysis for clusters was performed and all the characters were studied on the basis of mean performance in each cluster. Days to 50% headings had high performance in terms of mean value in Cluster-V, days to maturity in Cluster-IV, flag leaf area in Cluster-VI, no of tillers plant<sup>-1</sup> in Cluster-IV, plant height in Cluster-I,

spike length in Cluster-III, peduncle length in Cluster-I, no of spikelets spike<sup>-1</sup> in Cluster-II, no of grains spike<sup>-1</sup> had highest mean performance in Cluster-II, grain yield plant<sup>-1</sup> in Cluster-I, 1000-grains weight in Cluster-IV and spike density in Cluster-II (Table 6). Future selection processes can be efficient if selection is made from Cluster-IV regarding yield related attributes as it had good performance for many traits such as days to maturity, flag leaf area, grain yield plant<sup>-1</sup> and 1000-grains weight. Cluster-II also depicted good results for grain yield plant<sup>-1</sup>, no of grains spike and spike density. Cluster-I also showed promising results for grain yield plant<sup>-1</sup>. Genotypes in Cluster-V can be selected for the trait days to 50% headings and in Cluster-VI for flag leaf area trait (Table 6).

**Table 5. Detail of sixty-two genotypes in six clusters**

S.	Cluster I	Cluster	Cluster III	Cluster IV	Cluster V	Cluster VI
1	A1	A3	A6	A10	A34	A44
2	A2	A59	A17	A60	A35	A54
3	A5	A13	A11	A20	A41	A46
4	A4	A12	A7	A61	A40	A49
5	A31	A48	A32	A62		A47
6	A39	A55	A30	A14		A50
7	A16	A8	A33	A15		
8	A19	A9	A37	A38		
9	A56	A26	A42	A29		
10	A45		A43	A36		
11	A51			A27		
12	A18			A58		
13	A53			A21		
14	A28			A57		
15				A25		
16				A23		
17				A52		
18				A22		
19				A24		

**Figure 1.** Analysis of cluster for 12 morpho- yield traits in wheat genotypes via ward’s method (1963).



**Principal Component Analysis:**

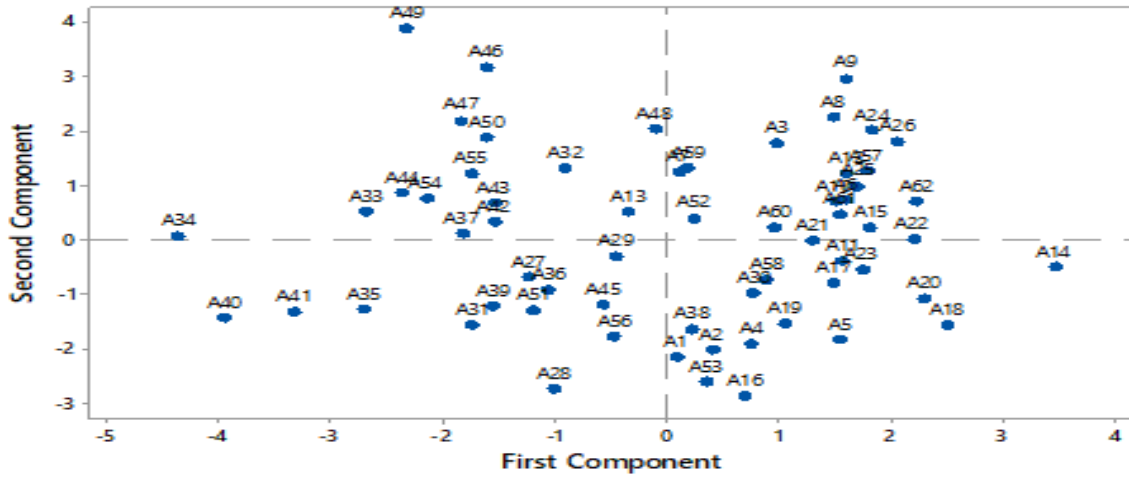
Principal component analysis was performed so that significant variance in genotypes under investigation could be studied. Mean data was used to analyze traits. It was observed that first four components had eigen value greater than 1 and were accomplice to 73% of total variation in twelve traits of sixty two genotypes (Table 7) also shown by scree plot (Figure 2). PC1 had an eigen value of 3.10 and accounted for 25.9% of total variation. PC1 had positive association with attributes such as time to maturity (0.093), flag leaf area (0.131), tillers number plant<sup>-1</sup> (0.310), spike length (0.061), peduncle length (0.157), spikelets number per spike (0.299), grains per spike (0.414), grain yield plant (0.491), weight of thousand grains (0.267) and spike density (0.461). PC2 had eigen value of 2.35 and accounted for 19.6% of total variation and showed positive association with days to 50% heading (0.191), flag leaf area (0.334), spike length (0.325), number of spikelets spike (0.312), number of grains spike (0.255) and spike density (0.068). PC3 depicted an eigen value of 2.08 and accounted for 17.4% of total variation with positive association to attributes such as number of grains spike (0.188) and spike density (0.048). PC4 had

**Table 6.** Grouping based on mean of different clusters of sixty two wheat genotypes

Parameters	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI
Days to 50%	102.28±3.	104.29±4.86	108.53±7.19	102.17±2.93	110.33±4.90	109.78±7.47
Days to maturity	141.14±3.	140.04±3.62	144.60±3.66	141.36±3.62	140.66±2.26	139.72±8.50
Flag leaf area	32.65±5.5	36.71±7.23	43.14±8.82	39.12±7.78	28.11±4.50	49.72±10.28
No. of tillers	10.74±1.8	10.09±1.82	11.06±1.73	11.90±1.99	9.90±2.74	9.09±1.91
Plant height	132.52±7.	97.37±7.91	127.98±11.10	100.22±9.17	130.61±5.35	100.08±4.47
Spike length	10.85±1.5	12.04±1.82	12.51±1.50	10.97±2.02	10.19±0.54	12.24±0.75
Peduncle length	26.13±3.7	14.12±1.89	16.58±6.59	19.11±5.11	20.26±4.70	13.55±3.19
No of spiklets	21.06±1.5	23.11±1.97	22.03±1.98	21.63±1.87	19.15±0.86	21.98±1.78
No of grains	47.44±5.5	64.63±7.82	45.95±5.32	62.54±8.34	28.29±3.04	47.22±8.73
Grain yield plant <sup>-1</sup>	24.64±6.4	24.53±6.71	22.41±9.20	24.64±4.57	6.97±2.98	9.40±1.99
1000-grain weight	42.48±6.1	26.47±3.58	35.53±7.75	42.86±4.69	21.87±4.62	24.99±10.18
Spike density	0.97±0.48	1.29±0.43	0.6±0.49	1.22±0.46	0.54±0.07	0.55±0.03



**Figure 2.** Score plot showing the eigenvalue of different principle components on the basis of studied parameters.



**Table 7. Principal components (PCs) of yield related traits among wheat genotypes**

Statistical Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Eigen value	3.108	2.352	2.09	1.21	0.807	0.606	0.557	0.399	0.332	0.228
Proportion	0.259	0.196	0.174	0.101	0.067	0.051	0.046	0.033	0.028	0.019
Cumulative	0.259	0.455	0.629	0.73	0.797	0.848	0.894	0.927	0.955	0.974
DH	-0.226	0.191	-0.536	0.064	0.171	0.017	0.134	0.044	0.315	-0.301
DM	0.093	-0.034	-0.57	-0.22	-0.132	-0.474	0.081	0.212	0.21	0.102
FLA	0.131	0.334	-0.394	-0.32	-0.03	0.23	0.105	-0.563	-0.416	0.188
NTP	0.31	-0.116	-0.09	0.251	0.802	0.116	0.238	-0.049	0.09	-0.02
PH	-0.109	-0.393	-0.358	0.351	-0.281	0.166	-0.032	0.126	-0.321	-0.332
SL	0.061	0.325	-0.057	0.645	-0.007	-0.386	-0.388	-0.329	-0.124	-0.069
PL	0.157	-0.507	-0.053	0.153	-0.276	0.195	0.159	-0.548	0.395	0.045
NSS	0.299	0.312	-0.172	0.192	-0.177	0.618	-0.296	0.339	0.251	0.212
NGS	0.414	0.255	0.188	-0.23	-0.162	-0.053	-0.022	-0.138	0.277	-0.69
GYP	0.491	-0.162	-0.056	-0.04	0.002	0.011	0.104	0.244	-0.503	-0.251
GW	0.267	-0.358	-0.137	-0.27	0.192	-0.138	-0.709	-0.061	0.066	0.128
SD	0.461	0.068	0.048	0.229	-0.243	-0.301	0.36	0.111	0.061	0.382

eigen value of 1.21 and accounted for 10.1% of total variance with positive association to days to 50% heading (0.064), number of tiller plant (0.251), plant height (0.351), spike length (0.645), peduncle length (0.153), number of spikelets spike (0.192) and spike density (0.229). According to above results it was revealed that parameters such as number of grains spike<sup>-1</sup>, number of spikelets spike<sup>-1</sup>, number of tillers plant<sup>-1</sup>, 1000-grain weight,

grain yield plant<sup>-1</sup> and spike density contributed significantly to variation in PC1, spike length, flag leaf area, number of grains spike<sup>-1</sup> and number of spikelets spike<sup>-1</sup> in PC2, number of grains spike<sup>-1</sup> and spike density in PC3 and plant height, number of tillers plant<sup>-1</sup>, spike density and spike length in PC4. Polygon obtained via principal component analysis depicted that genetic behaviour of sixty two genotypes diverse

from broad genetic background to narrow genetic background in which highly diverse broad genetic background genotypes included A49, A9, A14, A18, A16, A28, A40 and A34 being at the pinnacle of polygon whereas less diverse with narrow genetic background were genotypes A37, A42, A29, A60, A21, A15 and A22 (Figure 2).

### Conclusion

In this research it has been found that selection is made from Cluster-IV for yield related attributes best lot of genotypes can be obtained which can further be expedited in breeding and research programme. Moreover, in Component analysis studies, it has been elucidated that PC1, PC2, PC3 and PC4 for the parameters like number of grains spike<sup>-1</sup>, number of spikelets spike<sup>-1</sup>, number of tillers plant<sup>-1</sup>, 1000-grain weight, grain yield plant<sup>-1</sup> and spike density contributed significant variation. Yield-related attributes such as grain yield per plant showed highly significant associations with peduncle length, grains number per spike, number of tillers per plant, thousand grain weight, and density of spikes for both phenotypic and genotypic levels. There was also a highly significant negative relationship with days to 50% heading. The number of spikelets per spike had a considerably higher association at the genotypic level and a significant correlation at the phenotypic level. High amount of heritability recorded with little genetic development for time in days to 50% headings, time required for maturity and spike density indicate non-additive gene action on their expression hence limitations might be faced by breeders for exploitation of these traits. Heritability along with genetic advance was lowest in no of spikelets spike<sup>-1</sup> which is an indication of potent inheritance path of this attribute by studied genotypes with non-additive gene action on the trait.

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