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## ORIGINAL RESEARCH PAPER

# Grain yield performance, correlation, and cluster analysis in elite bread wheat (*Triticum aestivum* L.) lines

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70060, Pakistan\* Corresponding author. Email: [saimamir\\_nia@yahoo.com](mailto:saimamir_nia@yahoo.com)**Abstract**

Wheat is a leading cereal, playing a crucial role in feeding the hungry world and improving global food security. The present study was undertaken to comparatively analyze the extent of genetic diversity for various quantitative traits among the wheat material exotic to Pakistan, received from CIMMYT (The International Maize and Wheat Improvement Center), Mexico. Nineteen advanced lines from the Semi-Arid Wheat Yield Trial (SAWYT) were studied along with a local cultivar, considered a control (NIA-Amber). Data were recorded on nine important agro-morphic traits. The compared genotypes differed significantly ( $p \leq 0.05$ ) in the studied traits, where line V6 produced the highest mean grain yield ( $6,049 \text{ kg ha}^{-1}$ ) and maximum 1,000-grain weight (45.0 g). Other lines, V19, V17, and V2, also showed superiority in yield (5,723, 5,150, and 5,067  $\text{kg ha}^{-1}$ , respectively). Days to heading established a significant positive association with days to maturity ( $r = 0.7995$ ), plant height ( $r = 0.3168$ ), spike length ( $r = 0.2696$ ), and spikelets per spike ( $r = 0.4391$ ). The important yield associated trait, 1,000-grain weight, had a highly significant positive correlation ( $r = 0.6833$ ) with grain yield. Cluster analysis for various quantitative traits showed important information about genetic diversity for the studied traits among wheat genotypes. Hence, selection of genotypes for higher grain yield based on these traits could be useful for future breeding.

**Keywords**

exotic wheat; crop improvement; analysis of variance (ANOVA); inter-relationship; Euclidean distance

**Introduction**

Wheat (*Triticum aestivum* L.) is the principal food source of people globally and occupies a central position in the agriculture sector. It ranks second after rice as a source of calories for consumers in emerging countries [1]. Wheat is planted on more than 240 million ha with production of 757.92 million metric tons [2]. Crop yields can be enhanced by increasing either area under cultivation or yield per unit area. However, principally it is difficult to increase the wheat planting area due to the cultivation of some other crops in the field. The renowned Green Revolution, along with innovative management practices, has enhanced wheat productivity [3,4]. Therefore, the development of improved genotypes which produce high grain yield is a durable option for breeders to increase yield per unit area along with better management practices. The knowledge of traits contributing to high yield has been considered complex as yield is a polygenic character and is influenced by environmental changes [5–8]. It

is paramount to determine traits contributing to grain yield to enhance the breeding efficiency through meaningful selection criteria [9]. Traits like optimum plant height, grain number per spike, and a 1,000-grain weight contribute to wheat yield [10–12]. Estimation of correlation to find out the degree of interrelationship among various yield associated traits is an important issue which shows complex chain of associations [13,14]. Therefore, it is important to work out the interrelationship of yield and other related traits for efficient selection of improved genotypes. Moreover, similarity among the wheat genotypes was evaluated using cluster analysis based on the agro-morphic traits by exploiting Euclidean distance. Other researchers have also used cluster analysis to study the morphological similarity among the genotypes [15,16]. A dendrogram based on the Euclidean distance obviously separated different elite wheat genotypes, indicating better response towards the agro-morphic characteristics.

In Pakistan, wheat breeding programs are primarily designed for higher yields and development of cultivars resistant to biotic and abiotic stresses. Wheat is the leading crop among cereals, particularly due to the proteins with remarkably good physicochemical properties [17]. Evaluation and identification of superior lines from introduced plant materials is the fundamental step in a crop improvement program. Promising genotypes with high yield, good adaptation, and agronomically desirable characteristics could reliably be exploited for commercial cultivation. Moreover, the use of elite wheat material for development of superior high yielding genotypes endowed with resistance to biotic and abiotic stresses is the need of the hour to cope up with the desired crop production in order to feed the fast growing human population.

The present work was aimed at evaluating exotic wheat genotypes in order to generate additional information for efficient selection, better utilization, and adaptation. It is expected that genotypes showing some improvement in grain yield and other associated traits will be selected and utilized in future breeding programs. Moreover, grouping on the basis of clusters could be helpful in making a concrete conclusion and future use of the genotypes for crossing purposes or varietal development.

## Material and methods

The present experiment was carried out to evaluate the elite wheat genotypes (Semi-arid Wheat Yield Trial) for yield and yield associated traits in bread wheat. The list of parents/pedigree of the genotypes is presented in [Tab. 1](#). Twenty genotypes, including NIA-Amber as a local control genotype, were planted at the experimental farm of the Nuclear Institute of Agriculture (NIA), Tando Jam (25.4281° N, 68.5307° E). The experiment was laid out in randomized complete block design with three replications during the Rabi (spring) season (mid-November) 2013–2014. Experimental plots had six rows of 5 m length, spaced 30 cm apart for each genotype per replicate. The recommended dose of fertilizers N:P<sub>2</sub>O<sub>5</sub>:K<sub>2</sub>O at 120:60:50 kg ha<sup>-1</sup> was applied and all recommended agronomic practices were adopted for raising a normal healthy crop. Observations from the central four rows were recorded on 10 randomly selected and tagged plants per genotype or line for nine quantitative traits, viz., days to heading and maturity, plant height (cm), spike length (cm), dry weight per spike (g), spikelets per spike, grains per spike, 1,000-grain weight (g), and grain yield (kg ha<sup>-1</sup>). All cultural practices were performed during the cropping season according to wheat production technology. Analysis of variance was applied to the data according to the method suggested by [18], Tukey's HSD (honestly significant difference) test was used to compare means, and correlation coefficient (*r*) for association analysis was calculated according to [19]. Cluster analysis was performed using Multivariate Statistical Package for grouping of genotypes on the basis nine quantitative traits [20].

## Results

The analysis of variance (ANOVA) was carried out and results are presented in [Tab. 2](#). The results revealed significant differences ( $p \leq 0.01$ ) among the genotypes for all the

**Tab. 1** Parentage of genotypes/varieties evaluated in the study.

Genotype	Pedigree/parentage
V1	LOCAL CHECK (NIA-Amber)
V2	MILAN/KAUZ/DHARWAR DRY/3/BAV92//4/PAURAQ
V3	METSO/ER2000/5/2*SERI*3/RL6010/4*YR/3/PASTOR/4/BAV92
V4	WORRAKATTA/2*PASTOR//DANPHE#1
V5	BERKUT/MUU//DANPHE#1
V6	METSO/ER2000//MONARCA F2007/3/WBLL1*2/KKTS
V7	C80.1/3*BATAVIA//2*WBLL1/3/EMB16/CBRD//CBRD/4/...
V8	SLVS/3/CROC_1/AE.SQUARROSA (224)//OPATA/5/VEE/LIRA//...
V9	SNLG/3/EMB16/CBRD//CBRD/4/KA/NAC//TRCH
V10	SNLG/3/EMB16/CBRD//CBRD/4/KA/NAC//TRCH
V11	METSO/ER2000//MUU
V12	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/FRET2/7/MINO
V13	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/FRET2/7/...
V14	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/FRET2/7/...
V15	KA/NAC//TRCH/4/MILAN/KAUZ//DHARWAR DRY/3/BAV92
V16	KA/NAC//TRCH/3/DANPHE#1
V17	KA/NAC//TRCH/3/DANPHE#1
V18	EMB16/CBRD//CBRD/4/BETTY/3/CHEN/AE.SQ//2*OPATA
V19	FRANCOLIN#1/WBLL1
V20	FRANCOLIN#1//WBLL1*2/KURUKU

**Tab. 2** Mean squares from analysis of variance (ANOVA) of various quantitative traits in elite bread wheat genotypes.

Source of variance	df	Days to heading	Day to maturity	Plant height (cm)	Spike length (cm)	Spike dry weight (g)	Spikelets per spike	Grains per spike	1,000-grain weight (g)	Grain yield (kg ha <sup>-1</sup> )
Replications	2	0.800	6.613	2.963	0.537	4.349	2.225	3.785	0.380	32,120
Genotypes	19	40.220**	48.827**	46.838**	2.90**	0.650**	4.510**	120.300**	20.426**	1,174,844**
Error	38	1.379	2.586	7.384	0.242	0.088	0.529	2.280	0.345	15,317
Total	59									

\*\* Significant at 1% level of probability.

characters studied, indicating the presence of sufficient genetic variability among the genotypes. Mean values of the characters measured in 20 genotypes are given in [Tab. 3](#). Statistically significant differences were found among the genotypes for all the analyzed traits. Maximum yield was recorded for V6 (6,049 kg ha<sup>-1</sup>), followed by the genotypes V19, V17, and V2.

The present study showed a significant ( $p \leq 0.05$ ) and positive correlation among the various attributes ([Tab. 4](#)). The highest positive correlation ( $r = 0.7995$ ) was found between days to heading and days to maturity. Plant height was positively and significantly correlated ( $r = 0.3693$ ) with days to maturity, and it was positively but nonsignificantly correlated with days to heading. Spike dry weight showed a highly significant positive correlation with grains per spike ( $r = 0.5175$ ) and spike length ( $r = 0.5548$ ). Spike length established a positive and significant correlation with grains per spike ( $r = 0.5057$ ). Spike length had a negative and nonsignificant association with days to heading, maturity, and grain yield ( $r = 0.1086$ ). Number of spikelets per spike depicted a positive and highly significant correlation with days to heading ( $r = 0.5626$ ), maturity ( $r = 0.5065$ ), and plant height ( $r = 0.4470$ ), but showed a nonsignificant positive correlation with grain yield. Number of grains per spike showed a positive and significant association with spike length ( $r = 0.5123$ ) and spike dry weight ( $r = 0.6233$ ). The important trait,

**Tab. 3** Mean performance of elite wheat genotypes for various quantitative traits.

Genotypes	Days to heading	Days to maturity	Plant height (cm)	Spike length (cm)	Dry weight per spike (g)	Spikelets per spike	Grains per spike	1,000-grain weight (g)	Grain yield kg ha <sup>-1</sup>
V1	75.5 <sup>e</sup>	130.0 <sup>a-e</sup>	103 <sup>bcd</sup>	11.67 <sup>cde</sup>	3.8 <sup>cde</sup>	21.6 <sup>bcd</sup>	57.6 <sup>jk</sup>	37.0 <sup>k</sup>	3,070 <sup>k</sup>
V2	81.0 <sup>a</sup>	129.0 <sup>b-f</sup>	101 <sup>cde</sup>	13.60 <sup>a</sup>	4.2 <sup>abc</sup>	23.4 <sup>a</sup>	64.1 <sup>fgh</sup>	43.0 <sup>c</sup>	5,062 <sup>c</sup>
V3	79.0 <sup>bc</sup>	130.5 <sup>a-d</sup>	99 <sup>def</sup>	10.60 <sup>fg</sup>	3.3 <sup>ef</sup>	22.2 <sup>ab</sup>	55.2 <sup>k</sup>	37.0 <sup>k</sup>	4,407 <sup>gh</sup>
V4	80.5 <sup>ab</sup>	132.0 <sup>a</sup>	104 <sup>abc</sup>	11.33 <sup>c-g</sup>	3.2 <sup>f</sup>	20.6 <sup>cdef</sup>	44.9 <sup>m</sup>	43.7 <sup>bc</sup>	4,755 <sup>d</sup>
V5	75.5 <sup>e</sup>	130.5 <sup>a-d</sup>	106 <sup>ab</sup>	12.20 <sup>bc</sup>	3.2 <sup>f</sup>	21.8 <sup>bc</sup>	57.7 <sup>j</sup>	38.7 <sup>hi</sup>	4,733 <sup>d</sup>
V6	79.0 <sup>bc</sup>	129.5 <sup>a-f</sup>	101 <sup>cde</sup>	11.40 <sup>c-f</sup>	3.9 <sup>bcd</sup>	21.5 <sup>b-e</sup>	58.3 <sup>j</sup>	45 <sup>a</sup>	6,049 <sup>a</sup>
V7	70.5 <sup>g</sup>	118.5 <sup>f</sup>	102 <sup>b-e</sup>	12.80 <sup>ab</sup>	4.5 <sup>a</sup>	20.5 <sup>def</sup>	66.7 <sup>bcd</sup>	38.1 <sup>ij</sup>	4,616 <sup>def</sup>
V8	76.5 <sup>de</sup>	131.5 <sup>ab</sup>	100 <sup>c-f</sup>	10.43 <sup>g</sup>	3.6 <sup>def</sup>	21.6 <sup>bcd</sup>	61.5 <sup>i</sup>	39.0 <sup>ghi</sup>	4,048 <sup>j</sup>
V9	75.5 <sup>e</sup>	128.5 <sup>c-g</sup>	94 <sup>gh</sup>	10.63 <sup>fg</sup>	3.6 <sup>def</sup>	19.7 <sup>fg</sup>	64.2 <sup>e-h</sup>	40.1 <sup>ef</sup>	4,179 <sup>ij</sup>
V10	76.5 <sup>de</sup>	128.0 <sup>d-g</sup>	94 <sup>gh</sup>	10.57 <sup>fg</sup>	3.2 <sup>f</sup>	18.5 <sup>gh</sup>	62.9 <sup>ghi</sup>	37.2 <sup>jk</sup>	4,483 <sup>e-h</sup>
V11	77.0 <sup>de</sup>	128.5 <sup>c-g</sup>	102 <sup>b-e</sup>	11.87 <sup>b-e</sup>	4.0 <sup>a-d</sup>	22.0 <sup>b</sup>	72.2 <sup>a</sup>	39.5 <sup>fgh</sup>	4,152 <sup>ij</sup>
V12	73.5 <sup>f</sup>	124.0 <sup>i</sup>	97 <sup>fg</sup>	11.50 <sup>c-f</sup>	3.6 <sup>def</sup>	20.3 <sup>ef</sup>	68.9 <sup>b</sup>	38.9 <sup>ghi</sup>	4,641 <sup>de</sup>
V13	76.0 <sup>de</sup>	126.0 <sup>ghi</sup>	102 <sup>b-e</sup>	13.27 <sup>a</sup>	4.0 <sup>bcd</sup>	20.4 <sup>def</sup>	62.1 <sup>hi</sup>	41.05 <sup>d</sup>	4,349 <sup>hi</sup>
V14	77.5 <sup>cd</sup>	127.5 <sup>efg</sup>	98 <sup>efg</sup>	13.40 <sup>a</sup>	4.4 <sup>ab</sup>	21.4 <sup>b-e</sup>	67.5 <sup>bc</sup>	40.1 <sup>def</sup>	4,425 <sup>fgh</sup>
V15	80.0 <sup>ab</sup>	131.0 <sup>abc</sup>	99 <sup>def</sup>	11.87 <sup>b-e</sup>	3.6 <sup>def</sup>	21.2 <sup>b-e</sup>	66.0 <sup>c-f</sup>	40.9 <sup>de</sup>	4,068 <sup>j</sup>
V16	76.5 <sup>de</sup>	127.0 <sup>fgh</sup>	107 <sup>a</sup>	10.97 <sup>efg</sup>	4.4 <sup>ab</sup>	21.5 <sup>b-e</sup>	64.8 <sup>d-g</sup>	40.1 <sup>def</sup>	4,592 <sup>d-g</sup>
V17	77.5 <sup>cd</sup>	129.0 <sup>b-f</sup>	102 <sup>b-e</sup>	11.97 <sup>bcd</sup>	4.3 <sup>abc</sup>	22.0 <sup>b</sup>	66.6 <sup>b-e</sup>	43.96 <sup>b</sup>	5,150 <sup>c</sup>
V18	64.5 <sup>h</sup>	116.5 <sup>j</sup>	91 <sup>h</sup>	11.40 <sup>c-f</sup>	3.2 <sup>f</sup>	18.4 <sup>h</sup>	57.2 <sup>jk</sup>	39.76 <sup>fg</sup>	4,312 <sup>hi</sup>
V19	77.0 <sup>de</sup>	127.5 <sup>efg</sup>	102 <sup>b-e</sup>	12.20 <sup>bc</sup>	3.2 <sup>f</sup>	22.2 <sup>ab</sup>	61.5 <sup>i</sup>	44.0 <sup>ab</sup>	5,723 <sup>b</sup>
V20	76.0 <sup>de</sup>	124.5 <sup>hi</sup>	100 <sup>c-f</sup>	11.07 <sup>d-g</sup>	3.3 <sup>f</sup>	20.7 <sup>c-f</sup>	52.4 <sup>l</sup>	44.4 <sup>ab</sup>	4,628 <sup>def</sup>
Mean	76.250	127.48	100.43	11.737	3.7619	21.078	61.615	40.545	4,572.0
HSD (5%)	1.9410	2.6581	4.4914	0.9568	0.4913	1.2026	2.4960	0.9713	122.68

Means of the same column followed by the same letter do not differ significantly at 5% level of probability.

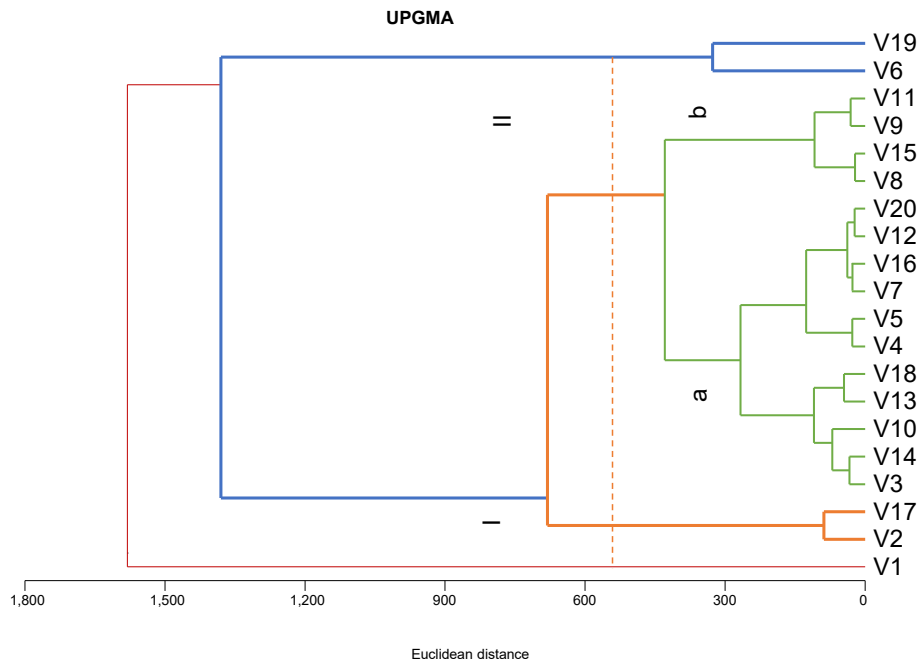
**Tab. 4** Correlation coefficient (*r*) among yield and yield related traits, VIZ. Days to heading (DH), days to maturity (DM), Grains per spike (GPS), plant height (PH), dry spike weight (DSW), spike length (SL), spikelets per spike (SPS), 1,000-grain weight (TGW), and grain yield (GY kg ha<sup>-1</sup>) in bread wheat genotypes.

Traits	DH	DM	PH	SPL	DSW	GSP	SPS	TGW
DM	0.7995**	1						
PH	0.3693*	0.3168*	1					
SL	0.0362	-0.1285	0.2696*	1				
DSW	0.0504	0.0303	0.1092	0.4088**	1			
SPS	0.5839**	0.5574**	0.4391**	0.2571*	0.3683*	1		
GSP	-0.0813	-0.1302	-0.0760	0.3163*	0.5192**	0.1306	1	
TGW	0.3145*	0.0930	0.2073	0.1992	-0.0313	0.1989	-0.2290	1
GY	0.2154	0.0028	0.1374	0.1782	0.0517	0.2039	-0.0543	0.683**

\* Significant at 5%; \*\* significant at 1%.

1,000-grain weight, developed a highly significant and positive correlation with grain yield ( $r = 0.6789$ ), whereas a positive but nonsignificant association was observed with all other studied traits, except number of grains per spike. Moreover, a negative nonsignificant correlation was also established between 1,000-grain weight and number of grains per spike ( $r = -0.219$ ). Thousand-grain weight developed a strong positive correlation with grain yield [20].

The mean data regarding yield and yield components, along with other associated phenological traits, were used to construct the dendrogram to get insight about the grouping of the genotypes. The cluster analysis grouped the 17 genotypes into two main



**Fig. 1** UPGMA dendrogram of Euclidean distance revealing the genetic relationships among the 20 studied wheat lines based on quantitative traits.

clusters, i.e., Cluster I and Cluster II, while the genotype V1 remained separate from the main clusters (Fig. 1). The genotypes V6 and V19 clustered into a separate clade, which represented the highest yielding genotypes as compared to the others. Cluster I consisted of two genotypes (V2 and V17), which took maximum number of days to heading and had a higher spike dry weight and the maximum of number of spikelets per spike. Moreover, these two genotypes made the second high yielding group among the studied genotypes. Cluster II consisted of A and B subgroups. The sub-Cluster A was further divided into two groups, i.e., A-I (V3, V14, V10, V13, and V18) and A-II (V4, V5, V7, V16, V12, and V20). These genotypes were characterized as tall lines with grain yield near to the overall mean population yield. The sub-Cluster B consisted of four genotypes, i.e., V8, V15, V9, and V11, and they were the lowest yielding genotypes as compared to the other groups/lines.

## Discussion

The analysis of variance indicated that the evaluated material has significant genetic variations which could be utilized in breeding programmes for improvement of bread wheat genotypes to enhance the crop productivity. These results are in agreement with the previous work [7] concerning agronomically important traits in bread wheat genotypes. Jan et al. [21] also reported highly significant differentiation among the genotypes for grain yield.

The grain yield remains the prime objective of all wheat breeding programs. Correlation results indicated that early maturity, the tall-dwarf plant height (101 cm), and the highest 1,000-grain weight (45 g) contributed to higher yield in the V6 genotype. The early maturing genotypes are important for late sowing time conditions to escape the effects of high temperature, especially during the reproductive stage [22–25]. Significant differences were also recorded for 1,000-grain weight among the genotypes [26]. Tall-dwarf wheat varieties are of significant interest for breeders to achieve maximum grain yield, hence these genotypes may be selected for breeding genotypes with the desired stature and enhanced produce. Higher yield in V19 and V17 could have resulted from the higher number of spikelets per spike and 1,000-grain weight. The number of spikelets per spike contributes significantly to final grain yield [27,28]. The reasons for

higher yield in V2 could be due to the longest spike length (13.61 cm) and maximum number of spikelets per spike (23.4). The trait spikelets per spike was earlier found to be highly and significantly correlated with spike length [11].

The correlation coefficient between yield components depicts a complex chain of interacting association [13]. It is an important statistical technique which can assist wheat breeders in selecting crop plants for increased grain yield. The association among different characters is the consequence of linked genes and their pleiotropic effects, while the phenotypic correlation is the result of environment [29] and is an observable association between two traits. Ali et al. [30] reported a positive and highly significant correlation between spike length and grain yield. However, these results do not coincide with Fellahi et al. [31] who rather reported a significant and positive association between number of spikelets per spike and grain yield. A significant positive correlation between plant height and spikelets per spike was also reported [32]. Moreover, a positive association between yield and 1,000-grain weight was also noted [33].

The trait number of grains per spike was negatively but nonsignificantly associated with days to heading and maturity. Gelalcha et al. [34] also confirmed the negative and significant correlation between days to heading and grains per spike. Grain yield was negatively and nonsignificantly correlated with days to heading and days to maturity. Plant height developed a negative but nonsignificant association with grains per spike. Similarly, spike length was negatively but nonsignificantly correlated with days to maturity. A negative nonsignificant association was also noted between spikelets per spike and grains per spike. Spike dry weight established a negative but nonsignificant association with days to maturity. This indicates that careful selection for these traits will result in improved wheat yield as some of the yield-contributing traits are correlated with one another. Therefore, selection in one of the traits will indirectly result in improved associated components. Overall, an intensive selection for spike length, spikelets per spike, grains per spike, and seed index will ultimately improve seed yield in wheat [35]. Cluster analysis based on quantitative traits, which provides insight about similarity among genotypes by estimating Euclidean distance [15], can be exploited to improve the wheat germplasm with diverse characteristics by selecting diverse lines for hybridization from various clusters [36].

## Conclusion

The genotypes investigated were significantly different for all the traits analyzed. Grain yield was highly and significantly correlated with 1,000-grain weight, whereas all the other traits were positively but nonsignificantly correlated with grain yield. Cluster analysis further strengthened our findings in selecting the better performing lines by grouping them on the basis of the characteristics. Hence, V6 and V19 clustered together were the highest yielding genotypes (6,049 and 5,723 kg ha<sup>-1</sup>, respectively), followed by the genotypes V2 and V17 in Cluster I, and they could be recommended for a future wheat improvement program.

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### Wydajność plonu ziarna, korelacja i analiza skupień w elitarnych liniach pszenicy (*Triticum aestivum* L.)

#### Streszczenie

Pszenica (*Triticum aestivum* L.) jest jednym z najważniejszych zbóż, odgrywającym kluczową rolę w zaspokajaniu potrzeb żywnościowych ludności i poprawie globalnego bezpieczeństwa żywnościowego. Niniejsze badania podjęto w celu przeprowadzenia analizy porównawczej stopnia różnorodności genetycznej wybranych cech ilościowych u linii pszenicy egzotycznych dla Pakistanu, otrzymanymi z Meksyku (CIMMYT; The International Corn and Wheat Improvement Center). Dziewiętnaście linii pochodzących z Semi-Arid Wheat Yield Trial (SAWYT) badano razem z lokalną odmianą NIA-Amber, przyjętą jako kontrola. Dane rejestrowano dla dziewięciu ważnych cech agro-morfologicznych. Porównywane genotypy różniły się istotnie ( $p \leq 0,05$ ) pod względem badanych cech. Linia V6 dała najwyższy średni plon ziarna ( $6049 \text{ kg ha}^{-1}$ ) i największą masę 1000 ziarniaków ( $45,0 \text{ g}$ ). Linie V19, V17 i V2 również wykazały wysoki plon (odpowiednio  $5723$ ,  $5150$  i  $5067 \text{ kg ha}^{-1}$ ). Liczba dni do kłoszenia była istotnie dodatnio skorelowana z wysokością roślin ( $r = 0,7995$ ), dniami do dojrzałości ( $r = 0,3168$ ), długością kłosa ( $r = 2696$ ) i liczbą kłosków w kłosie ( $r = 0,4391$ ). Ważna cecha wpływająca na plon – masa 1000 ziarniaków – była wysoce dodatnio skorelowana z plonem ziarna ( $r = 0,6833$ ). Analiza skupień dla różnych cech ilościowych dostarczyła ważnych informacji o różnorodności genetycznej badanych cech między genotypami pszenicy, dlatego też wybór genotypów dla uzyskania wyższego ziarna w oparciu o te cechy może być przydatny do przyszłej hodowli.