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Evaluation of Wheat Genotypes for Genetic Variability, Genetic Potential and Yield Related Attributes in Agro-Climatic Conditions of Dera Ismail Khan

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Assessing wheat genotypes for genetic variability, yield potential, and heritability of yield-related traits is essential for developing high-yielding, climate-resilient wheat cultivars. Eighteen wheat genotypes were evaluated using a Randomized Complete Block Design (RCBD) with three replications at the Faculty of Agriculture Research Field, Gomal University, Dera Ismail Khan. Genotypes were subjected to investigation for analysis of variance (ANOVA), broad-sense heritability, and cluster analysis. Traits scored involve days to 50% headings, days to maturity, plant height, number of grains spike^{-1}, flag leaf area, number of spikelet’s spike^{-1}, grain yield plant$^{-1,}$ and 1000-grains weight. Data collected was subjected to Statistic v.8.1 and SPSS. All traits depicted excellent variation among genotypes and were classified as highly significant ($p < 0.01$). Variation analysis involving GCV and PCV resulted in medium to high values for days to maturity & number of spikelet’s spike^{-1}, while low ranged for flag leaf area, plant height, grain yield plant^{-1}, number of grains spike$^{-1,}$ and 1000-grains weight. Heritability of broad sense was recorded as in high ranges for traits like plant height, flag leaf area, grain yield plant^{-1}, number of grains spike^{-1}, number of spikelets spike$^{-1,}$ and 1000-grain weight. Genetic advances in percent of mean showed an elevated magnitude in plant height, grain yield plant^{-1}, number of grains spike^{-1}, flag leaf area, and 1000-grains weight. Cluster analysis clustered eighteen genotypes into six clusters, based on the best performance for different yield-related attributes, and hence recommended the genotypes under study to be utilized in breeding programs for developing high-yielding wheat cultivars.

Keywords: Genotypic Variance, Phenotypic Variance, Heritability, GCV, PCV

Introduction:

Wheat (*Triticum aestivum* L.) is globally recognized as the most important cereal crop. It is a self-pollinated species with a hexaploid genetic makeup ($2n = 6x = 42$), possessing the AABBDD genome. This crop holds significant economic value among the Triticum genus and belongs to the Poaceae family. Its origin is traced back to the arid and semi-arid regions of the Middle East and Asia [1]. It is considered the most used staple grass being an important food source for Europeans, Africans, and Asians [2].

Almost 40% of the daily dietary needs are fulfilled by wheat due to its composition of useful elements such as iron, magnesium, and Vitamins like B & E [3]. Wheat comprises vitamins, lipids, and minerals accompanied by starch protein and legume protein, giving it a nutritional advantage over meat-based diets, which typically lack significant fiber content [4].

Wheat is among the three most consumed cereal crops and contributes hugely to global food security in the fast-changing climate [5]. It has the status of the most used staple crop in Pakistan. It is cultivated in Pakistan on a very large scale from north to south leading Pakistan to the position of the world's tenth-largest grower of wheat in terms of hectare yield ratio and hectare production ratio. Its widespread cultivation has also significantly boosted the fertilizer industry, with usage nearly tripling compared to thirty years ago. Additionally, wheat in Pakistan exhibits diverse characteristics and responds effectively to various crop management practices. The development of new seed varieties is the main driver of sustainable crop production. Leading varieties currently offer yield potentials of 60 to 75 months per acre, though actual yields can fluctuate due to climate conditions and various stress factors, indicating that further improvements are possible [6]. Wheat production in Pakistan is severely affected by various stresses leading to the loss of several spikelets and grain weight & size [5] in which Khyber Pakhtunkhwa is substantially affected by diverse climatic conditions from north KP to South KP. Ongoing global climate change is expected to worsen the issue of stagnant wheat productivity in many wheat-growing regions around the world [7].

Wheat yields in Pakistan remain significantly below their potential, but further improvements can be achieved by adopting high-yielding varieties and implementing advanced farming systems to maximize the productivity of local wheat cultivars. To reach this goal, breeders must thoroughly understand and effectively manipulate yield and related traits in wheat. Traits Any wheat breeding program can address these challenges by identifying genetic diversity, sorting out the top yield-performing lines, evaluating their genetic advancement and heritability, and screening the available wheat germplasm for various yield-related traits [8]. Variability studies can potentially assist in the development process of varieties in the selection segment while Genetic variation and phenotypic variation can help project an analogy of various yield-associated attributes [9]. Grain yield is related to many attributes and it has been shown that a complex trait elevation in its production can only be reached by developing and executing a proper and managed screening process of yield and related traits in wheat and focus being diverted on manipulation of wheat attributes to procure diverse and varied germplasm pool that can contribute to breeding processes all over the world [10]. For breeding purposes, the breeder must correctly select the target crop's improvement by identifying variations in desired qualities [11]. Genetic diversity and its ratio are the basis of plant breeding. Production of high-yielding, diverse, and efficient species of wheat plant in a breeding process will result in an enhanced yield average overall which is entirely dependent on genetic diversity. To obtain a genuine and enhanced production from a breeding initiative the role of variability in specific yield-related attributes is essential and hence must be studied to exploit the genetic basis of a wheat crop [12]. High production statistics can be achieved as much as possible because in a process of breeding, diversity, and variation studies are immensely important and such studies can improve the selection process of a crop. According to [13]; the germplasm identification, classification, and stratifying of the germplasm is the ultimate tool of significance in plant breeding. This study aimed to evaluate wheat genotypes for yield-related attributes based on total variability, heritability, and cluster analysis, and to screen out potential candidate genotypes performing best in the agro-climatic condition of Dera Ismail Khan. These candidate lines will act as base materials for developing climate-resilient wheat varieties for the semi-arid conditions of Dera Ismail Khan.

Materials & Methods:

To evaluate genetic diversity through genotypic and phenotypic variations, including their respective coefficients of variation, as well as to examine heritability in the broad sense and potential genetic advance, a total of eighteen (18) wheat genotypes and two (2) local check varieties were sourced from the Arid Zone Research Center, Dera Ismail Khan (Table 1). The experimental plot was organized in randomized block design with three replications in the research area of the Faculty of Agriculture, Gomal University, Dera Ismail Khan. Sowing was carried out in the Rabi season, November 2023.

Table 1. List of genotypes used in this study.

S.No	**Genotype Source**	Annotation
1	IEYT2018-19E#8	M1
2	IEYT 2018-19 E#12	M2
3	IEYT2018-19E#13	M3
4	IEYT2018-19E#18	M4
5	IEYT2018-19E#24	M5
6	IEYT2018-19E#30	M6
7	IEYT2018-19E#32	M7
8	IEYT2018-19E#35	M8
9	IEYT2018-19E#36	M9
10	IEYT2018-19E#38	M10
11	IEYT2018-19E#53	M11
12	IEYT2018-19E#58	M12
13	IEYT2018-19E#63	M13
14	IEYT2018-19E#65	M14
15	IEYT2018-19E#66	M15
16	IEYT2018-19E#68	M16
17	IEYT2018-19E#70	M17
18	IEYT2018-19E#74	M18
19	BORLAUG	CHECK
20	PIRSABAK-15	CHECK

Preparation of Land:

The research area was subjected to mechanical deep plowing thrice after which was subjected to the operation of a rotavator one time, recommended dosages of fertilizers (80-160 kg/ha of nitrogen, 50-90 kg/ha, and potassium at 60 kg/ha) were applied.

Data Recording Procedure:

All the data for research was recorded with a selection intensity of 5%, hence five best-performing plants were randomly marked and data was recorded for days to 50% headings, days to maturity, plant height (cm), flag leaf area (m^2), numbers of spikelet spike^{-1}, number of grains spike^{-1}, grain yield plant^{-1} (gm), 1000-grain weight (gm). Days to 50% heading were measured from the date of sowing to the day when 50% of plants in a row produced spikes. Plant height was measured in cm from the base of the plant to the tip of the spike. Flag leaf area (m^2) was calculated from the flag leaf length and width. Spikelets produced by a single spike were counted manually. A single spike was thrashed and the number of grains produced was counted manually and expressed as grains spike^{-1}. Yield plant plant^{-1} (gm) and 1000-grain weight (gm) were calculated by measuring weighing balance.

Analysis of Variance (ANOVA):

To estimate the variance of recorded data to obtain a null hypothesis related to zero variance amid genotypes data was processed through the procedure by [14]. Statistical software "Statistics v.8.1" was used for the analysis of data.

Heritability Estimation:

To analyze broad sense heritability (H^2_{BS}), obtained data was subjected to the calculation by the formula proposed in the study of [15];

$$H^2_{B.S} = V_g / V_p$$

Where

H^2_{BS} = Heritable nature of broad sense

V_g = Variance of genotypic nature

V_p = Variance of phenotypic nature

Genotypic Coefficient of Variance and Phenotypic Coefficient of Variance:

To estimate the genotypic coefficient of variance (GCV) and Phenotypic Coefficient of variance (PCV), the means of the data obtained were subjected to calculation via the formula of [14].

Phenotypic Coefficient of Variance:

$PCV_{(\%)} = (V_p)^2 / X\ (100)$

V_p= Variance of Phenotype

X = mean of a sample

Genotypic Coefficient of Variance:

$GCV_{(\%)} = (V_g)^2 / X\ (100)$

V_g = Variance of Genotype

X = mean of a sample

Genetic Advance:

Genetic advance estimation recording was carried out using the procedure by [16] & [14] process;

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

GA: genetic advance

K = 2.06 (selection intensity constant at 5%)

h^2 = Heritability.

GA as % of mean (GAM) = (GA / X) (100)

Cluster Analysis:

Cluster analysis was conducted following the protocol outlined by, using a Euclidean distance threshold of 10 as the standard for linkage distance.

Results:

Analysis of Variance:

Variation studies via analysis of variance (ANOVA) illustrated highly significant variance for all parameters amid the studied genotypes which concludes the presence of desirable attributes for improvement via crop selection and screening processes in under-research breeding material.

Days to 50% Heading:

The analysis of mean squares revealed highly significant variation among the genotypes under study (Table 2). Range estimates for variation revealed the lowest value of 97.33 and maximum value of 100.48 days. It took 107.67 days for genotype M13 to reach days to 50% headings while minimal days to 50% headings were taken by genotype M10 and M12 at 97.33 days respectively. The value of Genetic variance for days to 50% headings was 4.24 and the value of phenotypic variance was 12.14.

Table 2. Mean squares of twelve agro-morphological characters of eighteen wheat accessions.

	DF	DH	DM	PH	FLA	NSS	NGS	GYP	1000GW
Replication	2	8.0185	5.5556	4.778	2.004	9.3889	4.667	73.1852	6.3996
Genotypes	17	**20.6362****	**21.8039****	**858.517****	**129.057****	**12.8627****	**409.225****	**48.4924****	**240.728****
Error	34	7.9009	6.0458	4.774	3.535	2.8987	6.686	2.4205	4.326
SE of Mean		1.62	1.41	1.26	1.08	0.98	1.49	0.89	1.2

Table 1. Stratification of eighteen genotypes in clusters.

S. No	Cluster One	Cluster Two	Cluster Three	Cluster Four	Cluster Five	Cluster Six
1	M1	M3	M6	M10	M11	M13
2	M2	M8	M7	M14	M12	M15
3	M4	M9	M16			
4	M5		M17			
5	M18					

Table 5. Stratification of traits based on means into clusters.

Parameters	Cluster one	Cluster two	Cluster three	Cluster four	Cluster five	Cluster six
Days to 50% headings	99.4±0.76	101.22±0.96	100.77±2.58	98.83±2.12	97.66±0.47	104±5.18
Days to maturity	139.73±1.62	137.88±3.83	141.55±0.87	139.5±4.00	136.16±1.64	140.66±2.35
Plant height	136.36±4.79	95.51±4.87	124.52±5.58	112.55±9.92	106.35±4.12	108.6±15.50
Flag leaf area	31.58±3.45	35.30±6.56	38.39±5.50	43.98±12.69	37.24±5.33	43.89±12.8
No spikelets spike^{-1}	20.4±1.51	22.33±1.85	20.22±2.78	21.66±2.35	21.5±2.12	20.66±3.77
No of grains spike^{-1}	47.8±4.72	68.66±7.05	44.7±6.06	71.16±5.89	53.83±1.17	68.16±10.13
Grain yield plant^{-1}	27.73±3.66	24.33±5.77	27±3.61	26.83±6.83	28.16±1.64	26.5±7.30
1000-grain weight	41.33±5.70	23.55±1.38	33.66±5.67	45.83±5.89	26.5±7.77	41.16±12.49

The coefficient of variation analysis registered a value of 9.98 for the genotypic coefficient of variance and 16.88 for the phenotypic coefficient of variance. Broad sense heritability revealed a value of 34.95% for days to 50% headings while the estimate of probable genetic advance stood at 2.50 along with the value of genetic gain listed at 2.49 (Table 3).

Days to Maturity:

The estimation of the mean square for this trait presented highly significant variation in genotypes (Table 2). The minimum value of the range was recorded as 134 days to maturity while on the other hand highest value of the range was recorded as 143.66 days to maturity. Genotype M15 took the highest 143.67 days to maturity while the days to maturity taken by genotype M3 was minimum amid all genotypes being 134 days. Variation estimates of (GV) stood at 5.25 and (PV) stood at 11.29 and in the same regard, the coefficient of variation estimates was recorded for (GCV) as 10.52 while (PCV) as 15.41. Broad sense heritability stood at 46.49 % and Genetic advance studies revealed a value of 3.21 for days to maturity while genetic advance as a percent of mean value was recorded as 2.3 (Table 3).

Plant Height (cm):

Mean square estimates for this trait also revealed highly considerable differences amid genotypes (Table 2). The minimum plant height range was recorded as 90.03 cm while the maximum plant height range was recorded as 140.13. M1 depicted a maximum plant height of 140 cm and genotype M8 illustrated the smallest plant height of 90 cm in all the genotypes. Variation at (GV) level was 248.38 and in (PV) it was 289.35. In the same genetic potential analysis, the coefficient of variation value for (the GCV) level was 1.96, and (the PCV) was 1.98. Broad sense heritability was recorded at 98.35%, with a genetic advance of 34.46 and a genetic advance as a percentage of the mean calculated at 29.75% for the parameter (Table 3).

Flag Leaf Area (m^2):

Mean square analysis results depicted a strong variation in the genotypes for this trait (Table 2). minimum range for the said parameter was estimated at 26.34 cm^2 while on the contrary highest range was depicted as 52.96 cm^2. Genotype M14 had the highest flag leaf area of 52.96 cm^2 while the minimum mean value was depicted by genotype M18 as 26.34 cm^2. Variation at the genotypic level (GV) was 41.84 while variation at the phenotypic level was recorded as 45.37. In the same analysis, it was noticed that the coefficient of variation values of the (GCV) level and (PCV) level were 5.01 and 5.21 respectively. Broad sense heritability revealed a value of 92.20 % and genetic advance showed a value of 12.79 while the genetic advance as a percent of mean or genetic gain value was recorded as 35.14 (Table 3).

Numbers of Spikelet Spike^{-1}:

Mean square analysis suggested this important trait indicated the presence of strong and significant values in variation (Table 2). The minimum value of the range was 17.33 and the highest magnitude of range was recorded as 24. Genotype M3 presented the highest number of spikelet spike^{-1} at 24.00 while the lowest for genotype M16 was 17.33. Variation was recorded at the genetic level (GV) as being 3.32 and phenotypic level as 6.22 while it was registered that the coefficient of variation at the genotypic level (GCV) was 14.16 and at the phenotypic level (PCV) it was 19.38. The broad sense heritability value was 53. 39 % and Probable genetic advance was 2.74 while genetic gain or genetic advance in terms of percent mean was recorded being 13.27 (Table 3).

Number of Grains Spike^{-1}:

The mean square depicted that all the genotypes presented high diversity and a highly significant amount of variation (Table 2). The minimum value of the range was recorded as 37.33 while the range was recorded as maximum at 76.66. Genotype M9 depicted 76.66 numbers of grains spike^{-1} as the highest value followed by genotype M7 as 37.33 as the lowest. The value of variation in terms of (GV) stood at 134.17 and (PV) value as140.86. The coefficient of such variations was also investigated which presented values of 2.83 and 2.90

for both (GCV) and (PCV), respectively. Broad sense heritability was recorded as 95.25%. Similarly, the probable genetic advance value was 23.28, and genetic advance as a percent of the mean value stood at 42.47 (Table 3).

Table 3. Range, mean, coefficients of variation, and broad sense heritability estimates of various quantitative characters of eighteen wheat accessions and one check.

Parameters	Range	Mean	GV	PV	GCV	PCV	h^2BS%	GA	GG
Days to 50% headings	97.33-107.66	**100.48****	4.24	12.14	9.98	16.88	34.95	2.50	2.49
Days to maturity	134-143.66	**139.56****	5.25	11.29	10.51	15.41	46.49	3.21	2.30
Plant height	90.03-140.13	**115.82****	284.58	289.35	1.96	1.98	98.35	34.46	29.75
Flag leaf area	26.34-52.96	**36.406****	41.84	45.37	5.01	5.21	92.20	12.79	35.14
Number of spikelets spike^{-1}	17.33-24	**20.667****	3.32	6.22	14.16	19.38	53.39	2.74	13.27
Number of grains spike^{-1}	37.33-76.66	**54.833****	134.17	140.86	2.83	2.90	95.25	23.28	42.47
Grain yield plant^{-1}	21-31.66	**26.593****	15.35	17.77	8.08	8.69	86.38	7.50	28.21
1000-grain weight	21-51	**34.407****	78.80	83.12	3.68	3.78	94.795	17.80	51.74

Grain Yield Plant^{-1} (gm):

Mean square analysis resulted in demonstrating a highly diverse nature of all genotypes for said parameter (Table 2). The minimum value of range for this parameter was 21 g while the highest range value for said parameter was 31.66 g. M14 had the best performance of 31.66 g followed by lowest by genotypes M3 and M9 as 21.00, respectively. Variation analysis indicated that (GV) stood at 15.35 and (PV) stood at 17.77. While finding out variation coefficients for said parameter it was observed that (GCV) value was recorded as being 8.08 and (PCV) value was recorded as being 8.69. Broad sense heritability value stood at 86.38 % and genetic advance value was registered as being 7.50 while genetic advance as a percent of mean value stood at 28.21 (Table 3).

1000-Grain Weight (gm):

Mean square analysis results indicated that all the genotypes under study were highly diverse from each other (Table 2). The minimum range of said parameter was recorded as 21 g while the maximum value of range stood at 51 g. The highest mean value was given by genotype M18 as 51 g and the lowest by genotype M12 as being 21 g. Variation calculation of (GV) and (PV) values stood at 78.80 and 83.12, respectively and coefficient of variation presented values of 3.68 and 3.78 for (GCV) and (PCV) respectively. The broad sense heritability value recorded was 94.79% and the genetic advance value was estimated as being 17.80 while the Genetic advance presented a magnitude of 51.74 (Table 3).

Cluster Analysis:

All the genotypes were analyzed for classification intro clusters keeping in view the entire traits to find out the best performing genotypes for every trait. In this regard, cluster analysis was executed which presented six clusters of varied genotypes (Table 4).

Eighteen genotypes were arranged into clusters which maximum number of genotypes was arranged in Cluster One where five genotypes were lined up whereas the minimum number of genotypes was present in Cluster Four, Cluster Five, and Cluster Six where only two genotypes were present in each cluster respectively while remaining cluster two and cluster three possessed three and four genotypes respectively (Table 4) (Figure 1).

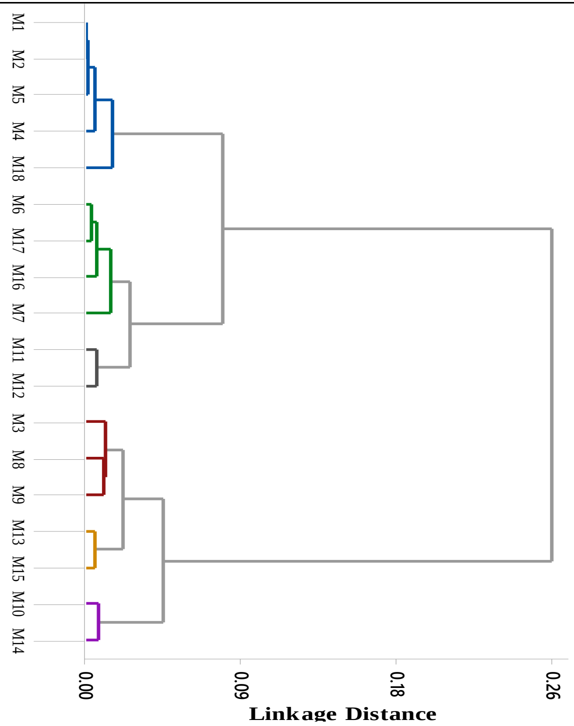

Figure 1. Graphical representation of eighteen genotypes into clusters via Ward's method (1963).

Genotypes under study were classified according to their mean values for each trait after being subjected to the calculation of grand means (Table 5). For the first trait of days to 50% headings, it was registered that the highest performance was presented by genotypes in cluster six where the mean value for said trait was found to be highest. For the trait of days to maturity, the highest mean performance was given by genotypes in cluster three. Plant height had its highest mean value from the genotypes of cluster one. Flag leaf area mean was registered highest in cluster four and several spikelet's spike-1 mean depicted its highest value in cluster two. Some grains spike-1 had its highest mean performance by genotypes in cluster two. The trait of grain yield plant had the highest mean value from cluster five. 1000-grain weight depicted good performance in cluster four (Table 5).

Discussion:

Investigated parameters depicted highly significant variation amid genotypes which indicates their potential for exploitation for beneficial attributes in a breeding process. Research suggests that genotypes in this study can be manipulated and a potentially considerable breeding process can be carried out for desired traits.

Analysis of variance indicated that there is a significant and considerable magnitude of variation present in genotypes which can be exploited for breeding. Researchers in [17][18] along with research by [19] and [20] found similar results for GCV and PCV by our findings suggesting environment had affected the expression of this character. Heritability estimates were in the medium range which indicated the amount of genetic control was medium, while genetic advance possessed a low magnitude of genetic advance and this magnitude of genetic advance when coupled with medium heritability suggests that there is very little impact of additive gene effect, these findings were in contrast to findings by [21].

ANOVA suggested that there was very high diversity amid all genotypes for said parameter and such estimates favor breeders to enhance or manipulate this trait. GCV was slightly lower than PCV hence concluding that the environmental effect on this trait was present while findings of [20][22][21] & [23] indicated the existence of low amounts of GCV and PCV for said trait. Broad sense heritability was up to medium range which was favored by the results of [24] and this was coupled by low genetic advance suggesting additive gene action was inconsiderable and selection might not be that effective for this trait.

Variance studies suggested a considerable and notable amount of variation in genotypes favoring the selection process for further breeding. GCV and PCV values were slightly varying from each other, up to a very minimal extent, and hence can be ignored indication, that plant height had a very low impact on environmental surroundings corroborating with [25] and [21] while findings by [26] contradicted our findings. High heritability coupled with high genetic advance suggested the presence of additive gene effect while also suggesting that heritability is straight-driven and not complex corroborating with findings of [27][25] and [28].

ANOVA estimates suggested this trait was potentially good for the selection process as it had highly considerable variation. GCV and PCV dissimilarities were also found to be very minimal which indicated the inconsiderable effect of the environment's mask on expression patterns as evident in studies of [29] [30] and [22]. Similar to our findings, high heritability coupled with medium-ranged genetic advance suggesting some effect of additive gene action was also found in the studies of [24]

Variance estimates indicated that this parameter was also a potential candidate for selection amid the breeding process as the variance was intense. GCV and PCV magnitude was slightly considerable which leads to the conclusion of the presence of minor environmental effects similar to the findings of [31] and [32]. High heritability coupled with a low genetic advance in this study suggested that it's influenced by additive gene effect and such statistics had been also found by [25] [33] [34] [32] and [26].

ANOVA had a P value of highly significant status for this trait suggesting its favorable position amid future breeding processes. The difference in numbers between GCV and PCV was also obtained as negligible and indicated the absence of environmental influence on illustration of this parameter similar to findings by [35] while [23] and [36] High heritability percentage coupled with high genetic advance suggested such trait had straightforward inheritance pattern similar to findings by [28][23] and [37]

For this trait, ANOVA was also evident of highly significant variation in genotypes. GCV and PCV magnitude difference was minimal which suggested genetic control was more than environmental control and hence breeding will be effective for this trait in such genotypes likewise to [24] [23] while high heritability with low genetic advance suggested by studied investigations of [25] was also evident in our studies suggesting that additive gene expression was imprinted on trait inheritance pattern.

ANOVA presented statistics indicating a highly significant aspect of variation for this attribute. GCV and PCV had very minor differences in their quantity and hence suggested that 1000-grain weight was influenced by the genetic aspect rather than the environmental aspect likewise to [23] [38] & [21]. High heritability coupled with medium genetic advance indicated somewhat the effect of additive gene action on inheritance same as findings by [25].

Conclusions:

All the traits depicted highly significant variation among genotypes indicating their potential to be utilized during future breeding programs while cluster analysis suggests cluster one had second best performance for trait of 1000-grains weight and genotypes in this cluster like M1, M2, M4, M5, and M18 can be exploited for development of 1000-grains weight. Genotypes in cluster two involved M3, M8, and M9 which performed best for a number of grains spike^{-1} with second best to cluster four for the same parameter involving genotypes like M10 and M14 which also performed excellently in flag leaf area trait as well as 1000-grains weight. Cluster three performed considerably in days to 50% headings and days to maturity with genotypes like M6, M7, M16, and M17. Cluster five involved genotypes like M11 and M12 and performed best for a number of spikelets spike^{-1}. Cluster six performed best for traits like days to maturity, flag leaf area, number of grains spike^{-1}, and 1000-grains weight. All eighteen genotypes clustered in six clusters can be exploited for the improvement of different yield-related traits, hence developing climate-smart and high-yielding wheat cultivars for the agro-climatic conditions of Dera Ismail Khan.

Conflict of Interest:

All the authors declare no conflict of interest.

Authors Contributions:

Muhammad Mohibullah and Nasr Ullah Khan conceived the idea and drafted the manuscript. Muhammad Israr Qureshi, Rida Nasir, Muhammad Zubair, Adnan Shehzad, and Nimra Qayyum experimented and collected the data. Ali Asghar and Jamal Abdul Nasir analyzed the data. Habib Ur Rehman provided technical assistance during the experiment. All authors proofread the final manuscript.

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