

Comparison of Yield and Identification of Effective Traits on Yield of Some Wheat Genotypes in Baghlan Province

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ABSTRACT

Wheat is Afghanistan's primary staple food crop, and improving its productivity is essential. Selecting high-yield varieties is a key approach to enhancing wheat production. This study aims to compare the average yields of 17 wheat genotypes cultivated in Baghlan province and identify traits that significantly impact yield. The experiment was conducted during the winter season of 2022-2023 at the research farm of the Agriculture Faculty of Baghlan University. The soil was sandy loam, and a randomized complete block design (RCBD) with three replications and 17 treatments was used. Fifteen traits of these genotypes were evaluated. Analysis of variance showed highly significant differences in all characteristics (at the <1% significance level). Kabali, Lalmi 17, Chonta, and Wahdat demonstrated the highest yields among the varieties. Correlation coefficient analysis revealed that grain yield per m² had a significant positive correlation with traits such as the number of grains per spike, grain weight per spike, spike weight, grain yield per plant, biological yield per plant, stem height, biological yield per m², and harvest index. In the regression analysis (stepwise method), the number of grains per spike, spikes per m², and 1000-grain weight remained in the final model ($R^2 \approx 0.86$). Path analysis indicated that the number of grains per spike, spikes per m², 1000-grain weight, and days to flowering had the most substantial direct effects on grain yield. Cluster analysis classified the genotypes into three groups. Based on the results, the high-yielding varieties identified in this study are recommended for cultivation in Baghlan province and can be utilized in breeding programs. For future breeding efforts to develop high-yielding wheat varieties, the number of grains per spike, number of spikes per m², thousand-grain weight, and days to flowering should be prioritized as selection traits.

ARTICLE INFO

Article history:

Received: Mar 19, 2024

Revised: Jul 13, 2024

Accepted: Nov 6, 2024

Keywords:

Afghanistan; Cluster analysis; Correlation coefficient; Grain yield; Path analysis; Regression; Wheat

To cite this article: Lateif, M. (2024). Comparison of Yield and Identification of Effective Traits on Yield of Some Wheat Genotypes in Baghlan Province. *Journal of Natural Science Review*, 2(Special Issue), 407–418. <https://doi.org/10.62810/jnsr.v2iSpecial.Issue.139>

Link to this article: <https://kujnsr.com/JNSR/article/view/139>



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Introduction

Afghanistan is an agricultural country, with approximately 80% of its population directly or indirectly involved in agriculture (Muradi & Boz, 2018). Despite this, about 54.5% of people

live below the poverty line (World Bank Group, 2021). Cereal grains are considered the primary food crop globally, providing 70% of the population's diet, 75% of total carbohydrates, and 6-15% of the protein required for human nutrition (WHO, 2003). Among cereals, wheat (*Triticum aestivum* L.) is a major crop and the most critical source of nutrition in Afghanistan (Ahmadzai et al., 2019), supplying significant amounts of energy, starch, protein, vitamins, and dietary fiber (Shewry & Hey, 2015). Wheat is grown on 2.2 million hectares in Afghanistan, yielding 4.5 million tons (2.2 tons per hectare) (United States Department of Agriculture, 2023). However, productivity per unit area is low in Baghlan province, which does not meet the current population's needs. Therefore, increasing productivity is essential, either by expanding the cultivated area (Singh et al., 2021) or enhancing yield per unit area (Michel & Makowski, 2013).

Selecting high-yielding varieties is one way to increase productivity per unit area (Ullah et al., 2021). Grain yield, a complex trait influenced by environmental factors and multiple genes, is crucial for identifying the best genotypes (Grafius, 1960). Numerous traits and their interactions affect wheat yield, and understanding these relationships provides valuable selection tools for developing high-yield varieties (Egesel & Kahrman, 2013). Varieties with high yields can be selected based on molecular, physiological, and morphological markers (Soltabayeva et al., 2021). Morphological traits, which are easy to measure and highly heritable, provide a reliable and rapid approach for screening plant communities and improving yield (Yap & Harvey, 1972). Statistical analyses, including correlation, regression, path, and multivariate methods, are used in wheat breeding programs to enhance selection efficiency (Egesel & Kahrman, 2013).

The correlation coefficient of yield with various traits is essential for breeding programs (Mollasadeghi & Shahryari, 2011), as it reveals which traits are most strongly associated with grain yield (Vaghela et al., 2021). However, correlation analysis alone cannot determine indirect effects between traits, so multivariate analysis is needed (Moghaddam et al., 1998). Path analysis can identify independent variables' direct and indirect effects on the dependent variable (Ojha et al., 2018; Dewey & Lu, 1959; Sunil et al., 2018). Stepwise regression analysis helps exclude ineffective traits and retain only those significantly contributing to yield variation in the final model (Farih et al., 2021). Singh et al. (2021) evaluated advanced bread wheat varieties and found that grain yield was significantly correlated with harvest index, biological yield per plant, plant height, days to maturity, days to flowering, and tiller count per plant, suggesting that selection based on these traits could maximize yield.

Similarly, Mecha et al. (2017) reported that grain yield had positive correlations with grain filling period, productive tiller count per plant, spikelet number per spike, spike length, 1000-kernel weight, kernel count per spike, biological yield per plot, and harvest index. Path analysis revealed that biological yield, 1000-kernel weight, harvest index, and kernel count per spike directly affected yield. Siahbidi et al. (2013) found that 1000-kernel weight, peduncle length, spike density per m², and fertile tiller count were retained in the final regression model, accounting for 50% of yield variation. Tahmasebi et al. (2013) studied 15

wheat lines and observed that most traits showed significant differences; 1000-grain weight, spike count, and plant height positively correlated with yield and remained in the final regression model. Ojha et al. (2018) reported significant positive correlations between grain yield and spike density per m², plant height, spike weight, spike length, grain count per spike, flag leaf length, and 1000-grain weight. Path coefficient analysis revealed that spike density per m², spike weight, grain count per spike, flowering time, and 1000-grain weight had the most direct positive effects on grain yield.

Given the importance of selecting high-yielding varieties and identifying effective yield traits, this research aims to evaluate the yield of 17 wheat genotypes from Baghlan province and identify the traits influencing yield.

Material and methods

In this study, 17 winter wheat genotypes sourced from Baghlan province and an agriculture research station were evaluated during the 2022-2023 season at the research farm of the Agriculture Faculty, Baghlan University (566 m altitude, 36.5° N latitude, 68.38° E longitude). A randomized complete block design (RCBD) with three replications was used. Each 3 m² plot (2 m × 1.5 m) included six rows with 25 cm row spacing and 5 cm between plants within each row. Urea fertilizer was applied three times at 8.3 g/m²—during field preparation, stem elongation, and flowering. Each plot also received 25 g/m² of DAP. Observations were recorded for 15 traits, including days to flowering, days to physiological maturity, grain weight per spike, grain count per spike, spike weight, spike length, grain yield per plant, biological yield per plant, 1000-grain weight, effective tiller count, plant height, spike density per m², biological yield per m², grain yield per m², and harvest index. The Harvest index was calculated as the ratio of grain yield to biological yield.

For data analysis, the normal distribution of residuals was checked using Kolmogorov-Smirnov and Shapiro-Wilk tests in SPSS 26. Analysis of variance (ANOVA) for each trait was conducted, with mean separation using Duncan's multiple range test in SAS 9.4. Pearson's correlation analysis was used to measure relationships between traits, stepwise regression analysis identified the most impactful traits on grain yield, path analysis determined direct and indirect trait effects, and cluster analysis classified genotypes. All multivariate analyses were performed in SPSS 26.

Results and Discussion

The analysis of variance revealed highly significant variation ($p < 0.01$) across all measured traits in the 17 wheat genotypes, as shown in Table 2. This variation reflects substantial genetic diversity among the genotypes, which can be advantageous for future selection in wheat breeding programs. Rasool et al. (2021) also observed significant variation among genotypes in their study based on most morphological characteristics.

The comparison of mean values for studied traits (Table 3) indicates that the Lalmi 15 and Kabul 013 genotypes matured earliest at 116 ± 0.47 days, while the Surkha genotype matured latest at 166.7 ± 0.27 days. Similarly, Rasool et al. (2021) reported a range of 161 to 170 days

for maturity, with an average of 166.92 days. As illustrated in Table 2, the number of grains per spike varied between 55 and 25.4, with the Jozjan variety having the highest grain count per spike and Surkha the lowest. Thousand-kernel weight averaged 42.27 g, ranging from 56.3 g to 37.3 g; Surkha presented the heaviest kernel weight, while Kabali had the lowest. Finally, grain yield per m², an essential trait for selecting cultivars, ranged from 404.4 g to 600 g, averaging 514.02 g. Kabali yielded 596 ± 7 g, Lalmi 17 yielded 586.6 ± 47.1 g, Chonta yielded 571.7 ± 53.4 g, and Wahdat yielded 557.2 ± 33.8 g per m². The lowest yield belonged to Zarddana, with 404.4 g per m². Based on these findings, the Kabali, Lalmi 17, Chonta, and Wahdat varieties are recommended for cultivation in Baghlan province.

Table 1. Descriptive statistic of 15 traits in 17 bread wheat

Traits	Minimum	Maximum	Mean	Std. Deviation	Skewness	Kurtosis
DTF	115.0	144.0	120.29	5.93	3.16	10.07
DTPM	153.0	167.0	156.90	3.33	1.37	2.39
GW/S (gr)	1.2	2.8	1.77	0.33	0.56	0.32
NG/S	19.9	60.8	42.33	7.64	-0.50	0.82
WS(gr)	0.4	9.9	6.38	1.99	-1.33	2.49
LS (cm)	8.4	12.4	10.08	0.92	0.32	-0.32
GY/P (gr)	6.5	13.7	9.78	1.88	0.18	-0.76
BY/P (gr)	13.3	29.1	20.46	3.70	0.13	-0.56
1000GW (gr)	34.0	58.9	42.27	5.49	1.52	2.42
NET	3.0	9.0	5.60	1.32	0.26	-0.16
PH (cm)	76.2	133.2	88.16	10.36	2.88	9.56
NS/m ²	195.7	451.3	305.23	66.97	0.18	-1.04
BY/m ² (gr)	886.7	1913.3	1218.17	218.95	1.57	3.44
HI (%)	25.8	52.5	42.61	5.05	-0.79	2.01
GY/m ² (gr)	353.3	666.7	514.02	79.71	0.18	-0.78

Table 2. Analysis of variance in RCBD design for 15 traits in bread wheat

SOV	df	MS							
		DTF	DTPM	GW/S (gr)	NG/S	WS(gr)	LS (cm)	GY/P (gr)	BY/P (gr)
rep	2	0.41 ns	8.37*	0.02 ns	5.51 ns	1.97 ns	0.26 ns	1.8ns	25.5 ns
treat	16	105.9**	30.45**	0.25**	137.1**	9.96**	1.53**	8.44**	24.88**
error	32	1.25	1.58	0.05	22.27	1.07	0.54	1.22	7.41
CV		0.93	0.8	12.44	11.15	16.2	7.28	11.27	13.3
R ²		0.98	0.91	0.72	0.76	0.83	0.59	0.78	0.65

Table 3. Continuation

SOV	df	MS						
		1000GW (gr)	NET	PH (cm)	NS/m ²	BY/m ² (gr)	HI (%)	GY/m ² (gr)
rep	2	32.68*	5.28*	19.6 ns	13751.7**	57862.3**	1.59 ns	10228.1 ns

treat	16	72.62**	2.37*	292.2**	7160.5**	123829**	56.4**	10610.2**
error	32	8.78	1.22	20.47	2567.4	9371.3	11.96	4039.4
CV		7.01	19.7	5.13	16.6	7.95	8.13	12.38
R2		0.81	0.55	0.88	0.63	0.87	0.7	0.6

Table 4. Average of studied traits with their standard error in 17 breadwheat

genotype	DTF	DTPM	GW/S (gr)	NG/S	WS(gr)	LS (cm)	GY/P (gr)	BY/P (gr)
Hazarana	121.7bc±	157.7bcd	1.54def±	35.7de±0	5.03ef±0.5	10.5abc±	7.2e±0.1	15.4e±1.3
Lalmi	0.27	e±0.72	0.04	.53	7	0.24	8	8
Zardana	120.7bcd	160b±0.4	1.59def±	37.6cde±	6.62abcde	10.9ab±0	9.5bcd±	20.3bcde
	±0.54	7	0.16	2.96	f±0.45	.81	0.59	±1.01
Lalmi4	118efg±0	154g±0.4	1.51ef±0.	39.6bcde		9.2cd±0.		16.1e±1.
	.47	7	14	±2.62	4.68f±0.12	16	7e±0.2	2
Hazarana	121.7bc±	158.3bcd	1.43f±0.0	34.6e±3.	6.08bcdef	10.9ab±0	8.3de±0	18.6cde±
Abi	0.72	±0.27	8	58	±0.44	.22	.75	1.6
Jozjan	116g±0.4	158bcde±			7.87ab±0.	11.3a±0.	11.6ab±	23.1abc±
	7	0.47	2.5a±0.12	55a±2.84	28	29	0.31	0.6
Kabali	117.7fg±	154g±0.4	1.62cdef±	43.4bcde	7.03abcd±	9.2cd±0.	9.6bcd±	20.4bcde
	0.27	7	0.05	±0.43	0.78	34	0.26	±1.14
Lalmi17	119def±0	154g±0.4	1.9bcde±	45.5bc±1	7.12abcd±	10.1abcd	9.7bcd±	20.3bcde
	.47	7	0.1	.71	0.61	±0.15	0.48	±2.04
Daralamn	117.7fg±	154.7fg±0	2.03bc±0.	40.3bcde	6.9abcde±	10.1abcd	11.1abc	22.3abcd
07	0.54	.72	03	±2.93	0.33	±0.2	±0.54	±1.62
Sorkha	142.3a±0	166.7a±0.	1.44f±0.1	25.8f±2.4	6.6abcdef	10.9ab±0	9.6bcd±	25.7a±0.
	.72	27	1	9	±0.25	.14	0.3	31
Safidac	119def±0	157.3cde	1.47f±0.0	39cde±1.	5.48def±0.	10.3abcd	7.9de±0	17.2de±0
	.47	±0.98	3	31	44	±0.58	.06	.72
Solh2002	119def±0	156.7cdef	1.71bcdef	44.9bc±0	8.24a±0.6	9.1cd±0.	12.6a±0	24.2ab±2
	.47	±0.72	±0.02	.8	8	24	.37	.03
Wahdat	122.3b±0	157.7bcd	2.04bc±0	48.6ab±0	7.52abc±0.	9.8bcd±	11.1abc	21.4abcd
	.72	e±0.72	.02	.75	57	0.33	±0.78	±1.17
Chonta	118efg±0	155.7efg±	1.82bcde	46.2bc±2	7.62abc±0	8.9d±0.2	11.6ab±	21.5abcd
	.47	0.98	f±0.14	.9	.49	9	0.84	±1.73
Mazar99	120cde±	158.7bc±	1.75bcdef	44.1bcd±	7.7abc±0.5	10.7ab±0	11.1abc	23.2abc±
	0.47	1.09	±0.13	2.04	5	.44	±0.86	1.91
Roshan	117fg±0.	156defg±	1.78bcdef	42.7bcde	7.63abc±0.	10abcd±	10.9abc	21.6abcd
	47	0.47	±0.17	±2.49	49	0.25	±0.71	±1.16
Lalmi15	119def±0	154.3g±0.	2.08b±0.	48.3ab±1	5.77cdef±0	9.8bcd±	8de±0.1	17.6de±0
	.47	72	1	.53	.7	0.19	8	.79

	116g±0.4	153.7g±0.	1.95bcd±	48.3ab±1	0.55g±0.0	9.6bcd±	9.4cd±0	19bcde±
Kabul 013	7	54	0.06	.3	7	0.19	.51	1.38

Table 5. Continuation

genotype	1000GW (gr)	NET	PH (cm)	NS/m ²	BY/m ² (gr)	HI (%)	GY/m ² (gr)
Hazarana	43.1cd±0	4.7bc±0.	86.6bcd±	334.4abc±3	1262.2bcd±5	44abc±0.	553.9abc±13
Lalmi	.65	54	1.6	1.2	4.3	96	.2
Zardana	42.3cd±1	5.9abc±0	86.1bcd±	272.8cd±27.		40.8bc±1.	
	.85	.24	1.9	6	992.2g±32.1	71	404.4e±20.9
Lalmi4	38d±1.08	4.7bc±0.	80.6cd±2.	335.8abc±2	1188.9bcdef	39.2c±0.4	466.1bcde±
		45	54	7.1	±74	2	27.2
Hazarana	42cd±2.2	5.7abc±0	89.4bc±1.	314.7abcd±	1071.1efg±34	41.8bc±1.	447.2cde±11
Abi	8	.55	98	34.8	.9	16	.1
Jozjan	45.5c±1.5	4.7bc±0.	84.3bcd±	223.8d±12.	1176.7bcdef±	44.7abc±1	523.9abcde±
	7	14	1.56	6	61.3	.12	14.5
Kabali	37.3d±1.4	5.9abc±1	80.1d±1.6	409.2a±24.	1268.9bcd±8	46.8ab±0.	
	4	.2	5	4	4	96	596.7a±50.5
Lalmi17	41.7cd±0.	5.5abc±0	86.6bcd±	312.9abcd±	1334.4bc±53.	43.7abc±1	586.6ab±47.
	75	.61	2.2	30.2	9	.91	1
Daralamno		5.5abc±0	87.3bcd±2	252.9cd±17.	1195.6bcdef	44.9abc±	536.1abcd±2
7	51b±3.33	.71	.01	9	±66.5	0.68	7.5
Sorkha	56.3a±1.	6.7ab±0.	124.9a±3.	375.9ab±21.		29.3d±1.4	554.4abc±2
	9	45	6	2	1893.3a±8.7	3	9.1
Safidac	37.8d±1.3	5.4abc±0	85.9bcd±	287.8bcd±3	1008.9fg±50.	41.2bc±0.	416.1de±22.
	2	.47	1.96	4.7	3	26	7
Solh2002	38.2d±1.	7.3a±0.6	83.6bcd±	322.2abcd±	1113.3defg±4	48.6a±2.2	543.9abc±43
	06	8	1.84	36.9	2.8	6	.9
Wahdat	41.9cd±0	5.5abc±0	90.3b±1.5	273.3cd±30.	1264.4bcd±3	44abc±1.	557.2abc±33
	.72	.58	2	9	6.4	46	.8
Chonta	39.3d±0.	6.4ab±0.	83.3bcd±1	325.7abc±2	1216.7bcde±	46.9ab±3.	571.7abc±53.
	69	84	.77	6.3	17.5	89	4
Mazar99	39.4d±1.	6.4ab±0.	89.5bc±2.	343abc±13.		39.5c±0.1	531.1abcd±5
	14	41	87	1	1344.4b±18.7	5	.6
Roshan	41.3cd±1.	6.2ab±0.	87.3bcd±2	308.6bcd±3	1188.9bcdef	43.6abc±	516.7abcde±
	39	19	.74	7.5	±82	2.37	37.6
Lalmi15	43.1cd±0	3.8c±0.3	87bcd±2.1	246.6cd±4.	1151.1cdefg±	40.1bc±0.	461.7cde±8.
	.75	4	3	9	25.4	87	5
Kabul 013	40.5cd±0	4.8bc±0.	86.1bcd±	249.4cd±15	1037.8efg±59	44.1abc±	457.2cde±24
	.89	25	0.85	.6	.8	0.57	.9

Correlation Analysis

The correlation coefficients among the studied traits are presented in Table 4; days to physiological maturity positively correlated with days to flowering, spike length, and stem height. Kernel weight per spike showed a significant positive correlation with grains per spike, grain yield per plant, biological yield per plant, plant height, and grain yield per m² while correlating negatively with spikes per m². Grain yield per plant positively correlated with grain weight per spike, grains per spike, spike weight, biological yield per plant, harvest index, and overall grain yield per plant. Thousand-kernel weight was negatively correlated with the number of spikes per m². Biological yield per m² showed a significant positive correlation with grain weight per spike, grains per spike, spike weight, biological yield per plant, plant height, and grain yield per m². Grain yield per m² was significantly positively correlated with grain weight per spike, grains per spike, spike weight, grain yield per plant, biological yield per plant, stem height, biological yield per m², and harvest index. Singh et al. (2021) found that grain yield had strong positive correlations with days to maturity, 50% flowering, biological yield per plant, harvest index (%), plant height, and tillers per plant. Maurya et al. (2020) reported a positive correlation of grain yield per plant with days to flowering, maturity, spike length, and tiller count. Tahmasebi et al. (2013) observed that thousand-grain weight, spike count, and plant height were significantly positively correlated with grain yield.

Table 5. Correlation coefficient between 15 studied traits in 17 bread wheat

Traits	DTF	DT PM	GW/ S	NG/S	WS	LS	GY/P	BY/P	TGW	NET	PH	NS /m ²	BY/m ²	HI
DTPM	0.7**	1												
GW/S	0.02	0.23	1											
NG/S	-0.04	0.21	0.94**	1										
WS	0.25	0.43	0.30	0.29	1									
LS	0.57*	0.72**	0.26	0.09	0.16	1								
GY/P	-0.08	0.28	0.60*	0.60*	0.63**	-0.01	1							
BY/P	-0.03	0.40	0.7**	0.72**	0.65**	0.15	0.94**	1						
TGW	0.14	0.10	0.45	0.12	0.12	0.46	0.19	0.19	1					
NET	-0.11	0.08	-0.46	-0.37	0.39	-0.28	0.43	0.27	-0.35	1				
PH	0.33	0.58*	0.7**	0.68**	0.26	0.45	0.37	0.58*	0.27	-0.34	1			
NS/m ²	-0.11	-0.22	-0.64**	-0.46	0.12	-0.43	-0.22	-0.23	0.63**	0.52*	-0.42	1		
BY/m ²	0.11	0.13	0.57*	0.60*	0.48*	0.05	0.38	0.51*	0.10	-0.18	0.58*	0.15	1	
HI	-0.18	-0.09	0.35	0.39	0.33	-0.33	0.63**	0.54*	0.05	0.31	0.11	0.08	0.30	1
GY/m ²	0.01	0.07	0.61*	0.65**	0.52*	-0.11	0.56*	0.63**	0.09	-0.02	0.52*	0.15	0.91**	0.68**

Regression Model

The stepwise regression analysis results for all studied traits were significant at the 1% level (Table 5). Grain yield per m² was used as the dependent variable, with other traits (excluding harvest index, biological yield, and grain yield per plant) as independent variables. Grains per spike explained 39% of the variation in grain yield per m². When spikes per m² were added to the model, these traits explained 64.1% of the yield variation. The thousand-kernel weight added last accounted for an 86.5% explanation of the yield variation in the final model. Fouad (2018), using a stepwise method, identified grains per spike, spikes per plant, and 100-grain weight as significant contributors to yield. Tahmasebi et al. (2013) identified spike count, plant height, and thousand-grain weight as yield-influencing components that explained 73.2% of yield variation. Nazem & Arzani (2013) found that grains per spike, spike count per plant, and thousand-grain weight explained 47% of the yield variation per plant.

Table 6. Regression analysis of studied traits in 17 bread wheat

Step	a	b ₁	b ₂	b ₃	Adjusted R Square	VIF	P-value model
NG/S	251.94	6.021			0.390	1.35	<0.001
NS/m ²	-130.89	8.452	0.919		0.641	2.20	<0.002
TGW	-959.65	9.644	1.624	13.63	0.865	1.76	<0.003

Path Analysis

Path analysis is crucial for understanding the causal relationships between yield and traits with significant effects. As shown in Table 5, grains per spike had the strongest positive direct effect on grain yield (1.14), followed by spikes per m² (1.06), thousand-kernel weight (0.67), and days to flowering (0.20). Grains per spike also had a positive indirect effect through thousand-kernel weight but negatively impacted spikes per m² (-0.48) and days to flowering (-0.06). The analysis also indicated that spikes per m² positively influenced days to flowering (0.01) but had negative indirect effects on grains per spike (-0.52) and thousand-kernel weight (-0.46). Thousand-kernel weight positively affected grains per spike but had a negative indirect effect through spikes per m² (-0.71) and days to flowering (-0.03). Days to flowering indirectly affected grain yield positively via spikes per m² (0.06) but had negative effects through grains per spike (-0.31) and thousand-kernel weight (-0.11). Rameez et al. (2012) reported that thousand-grain weight, spike length, and days to heading positively affected wheat, while tiller count per plant, plant height, grain per spike, and peduncle length negatively impacted yield. Kiran et al. (2020) showed that biological yield per plot, harvest index, grain growth rate 14 days after anthesis, and productive tillers positively impacted grain yield, with biological yield exerting the strongest indirect positive effect on yield.

Table 7. Direct and indirect effect of traits on grain yield

Traits	correlation coefficient	direct effect	N of G/s	N of S/m ²	of 1000 GW	D to FL
N of G/s	0.70	1.14	-	-0.48	0.09	-0.06
N of S/m ²	0.09	1.06	-0.52	-	-0.46	0.01
1000 GW	0.08	0.67	0.15	-0.71	-	-0.03
D to FL	-0.15	0.20	-0.31	0.06	-0.11	-

Cluster Analysis

The 17 wheat genotypes were grouped into three clusters based on the studied traits, using squared Euclidean distance and Ward's method (Fig. 1). Cluster 1 included seven genotypes, Cluster 2 had nine, and Cluster 3 contained one cultivar. Cluster 1 had the highest spike length but lower values for most other traits. Cluster 2 showed the highest values for grain weight per spike, grains per spike, spike weight, grain yield per plant, harvest index, and grain yield

per plant, with lower days to maturity, indicating early-maturing genotypes. The genotype in Cluster 3 showed the highest values for thousand-kernel weight, productive tiller count, plant height, spike density per m², and biological yield. These genotypes could be used as parents in hybridization programs to develop high-yielding wheat varieties.

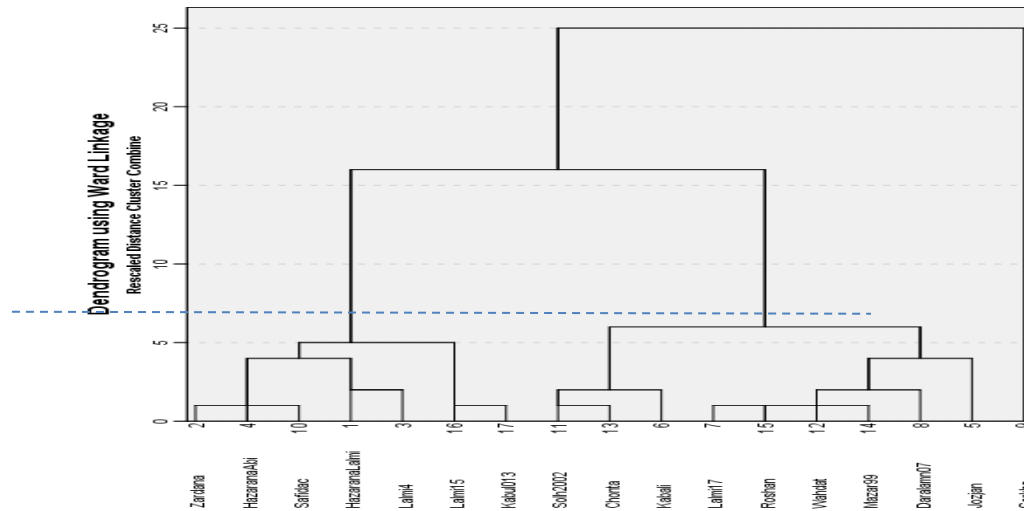


Fig 1. Cluster diagram of 17 bread wheat genotypes based on studied traits

Table 8. Mean and standard error of three clusters for 17 bread wheat

cluster	DTF	DTF	GW/S	NG/S	WS	LS	GY/P	BY/P
1	119.6±0.6	156.5±0.9	1.7±0.1	40.4±2	5.7±0.3	10.2±0.2	8.2±0.3	17.7±0.6
2	119±0.5	156.1±0.5	1.9±0.1	45.6±1.3	7.5±0.1	9.9±0.2	11±0.3	22±0.4
3	142.3±0	166.7±0	1.4±0	25.8±0	6.6±0	10.9±0	9.6±0	25.7±0

Table 9. Continuation

cluster	1000GW	NET	PH	NS/m ²	BY/m ²	HI	GY/m
1	41±0.8	5±0.3	85.9±0.9	291.6±13.2	1101.7±35.4	41.6±0.6	458.1±16.9
2	41.7±1.3	5.9±0.2	85.8±1	308±17	1233.7±23.9	44.7±0.8	551.5±8.9
3	56.3±0	6.7±0	124.9±0	375.9±0	1893.3±0	29.3±0	554.4±0

Conclusion

This research evaluated 17 wheat genotypes cultivated in Afghanistan's Baghlan province. Analysis of variance revealed highly significant differences among the studied traits (at a 1% significance level). Based on the comparison of means, the Kabali, Lalini 17, Chonta, and Wahdat genotypes exhibited the highest yields, respectively. Correlation analysis showed that grain yield per square meter had positive and significant correlations with grain weight per spike, number of grains per spike, spike weight, grain yield per plant, biological yield per plant, stem height, biological yield per square meter, and harvest index. In stepwise regression analysis, the number of grains per spike, number of spikes per square meter, and

thousand kernel weight remained in the final model ($R^2 \approx 0.86$). Path analysis indicated that the number of grains per spike, number of spikes per square meter, thousand kernel weight, and days to flowering had the strongest direct effects on grain yield. Cluster analysis classified the genotypes into three distinct groups. Based on these findings, the varieties with the highest yields are recommended for cultivation in Baghlan province and can be utilized in future breeding programs. Furthermore, the number of grains per spike, number of spikes per square meter, thousand kernel weight, and days to flowering should be considered key selection traits in future breeding programs to enhance wheat genotype yields.

Conflict of Interest: The author(s) declared no conflict of interest.

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