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Genetic Variability and Path Coefficient Analysis in Advanced Bread Wheat Lines Using Alpha Lattice Design

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ABSTRACT

The current study was carried out to genetic variability and coefficient analysis. Out of the morpho physiologic features, the highest grain yield was recorded in MPG09 at 5784 kg ha⁻¹, followed by MPG39 at 5777 kg ha⁻¹ and MPG24 at 5496 kg ha⁻¹. All these features of spring wheat show high positive correlations with each other, as demonstrated by the results of this study. Moreover, days to maturity were closely related to plant height, with $rg = 0.30$, $P = 0.05$, and flag leaf area, with $rg = 0.31$, $P = 0.05$. Plant height showed very strong correlations with flag leaf area, spikelets spike-1, and thousand-grain weight with values of $rp = 0.33$, $P = 0.01$; $rp = 0.35$, $P = 0.01$; and $rp = 0.31$, $P = 0.05$, respectively. Similar positive genetic correlations were recorded for peduncle length with $rg = 0.40$, $P = 0.01$, for spikelets spike-1 with $rg = 0.75$, $P = 0.01$, and for thousand-grain weight with $rg = 0.69$, $P = 0.01$. As a statistical method, the path coefficient analysis is used. However, plant height, biological yield, and flag leaf area showed decent indirect effect on grain production. Besides, days to maturity and 1000-grain weight variables had positive indirect effects on the time taken till heading. Similarly, indirect pathways through days to maturity were positive for grain yield: 1000-grain weight added 0.30, tillers per square meter added 0.10, and days to heading added 0.08. Thus, wheat genotypes MPG09 and MPG39 with higher production can be considered for use in future breeding programs to increase wheat productivity.

INTRODUCTION

Wheat is a cereal grain and is known as *Triticum aestivum* L. Also, it belongs to the family Poaceae and the genus *Triticum*. It occupies the second position in the hierarchy of the necessity for edible staple grains in the global market after rice [1]. *Triticum aestivum*, originating from Southwest Asia, is a self-pollinated crop and is often referred to as the "king of cereals" [1]. It covers the largest surface area among food crops globally and accounts for approximately 20% of human calorie consumption. Durum wheat, a variety of *Triticum aestivum*, is cultivated in about 218 million ha of

fertile land globally, with an average yield increasing from 2.3 to 4.6 tonnes [2].

Wheat stands in a vital position not only as a valuable cash crop on a global scale but also as a key crop for food security [3]. The significance of wheat is revealed the importance as a global trade volume. Wheat is typically sown, in October, November, and December, and collected in May and June. In Pakistan, during the last growing season, 24.946 million tonnes of wheat were produced on a cultivated area of 8,825 thousand



hectares. However, there was a 2.1% decrease in the sown area compared to the previous year, leading to a drop in production from 27.464 to 26.394 million tonnes due to various factors like reduced sowing land, dry conditions, lack of irrigation water, heat waves, and lower nutrient output [4].

Grain yield is one of the complex quantitative traits and it is influenced by environmental conditions as well as different yield-contributing traits. The use of genotypic selection is not efficient; selection should be done based on yield components and morphological and physiological traits. Exploiting current genomic variability in wheat is essential for developing high-yielding varieties adaptable to changing climates. Better heredity of wheat genotypes is necessary for higher yields under different agro ecological conditions [5]. Genetic diversity is crucial for breeding varieties with increased yield, wider adaptation, documented traits on high quality and the ability for pest and illness resistance. Further, correlation and path coefficient analysis have fully informed the relationship of selection of desired yield and various yield features to the researchers. This information is important in developing selection criteria for crop production enhancement, as [6]. Multi-trait path analysis shows the indirect, direct, positive, and negative impacts of certain yield attributes on the total yield helping plant breeders to find potential traits for enhancing the yield of crops [7].

MATERIALS AND METHODS

Experimental Materials and Design

The present studies were conducted at the Cereal Crop Research Institute (CCRI), Pirsabak

Nowshera from 2022 to 2024. The climate of CCRI is humid and sub-tropical type with hot summers and cold winters and total rainfall is 322 mm. The highest average temperature in Pirsabak Nowshera is 42° centigrade in June and the lowest is 10 ° centigrade in January. The material and design comprised 64 wheat genotypes, arranged in an alpha lattice design with two replications in this experiment. Each replication involved sowing 64 advanced wheat lines in four rows, keeping a consistent row-to-row distance of 0.25 cm. Data collection occurred at both the plot level and on a per-sample plant basis, encompassing twelve phenological and morphological parameters, following parameters were studied; days to heading, days to maturity, plant height in centimeters, flag leaf area in square centimeters, tillers per square meter, spikelets per spike, spike length, chlorophyll content, 1000-grain weight, biological yield, and grain yield.

Statistical Analysis

Statistical analysis involved variance analysis as per the method proposed by Steel and Torri (1980). Mean separation was conducted using the least significant difference (LSD) test, and ANOVA for all studied traits was determined by using the MSTATC. Genotypic and phenotypic correlations for various morphological, physiological, and biochemical traits were computed for both genotypic and phenotypic correlations using TNAUSTAT software, following the procedure outlined by Singh and Chaudhry (1997). TNAUSTAT software was used for genotypic and phenotypic correlations. The procedure described by Singh and Chaudry (1997) was used for measuring different morphological, physiological and biochemical traits.

RESULT AND DISCUSSION

Table 1

Mean square of 64 advanced bread wheat lines regarding days to heading, days to maturity, plant height, flag leaf area, peduncle length, tiller meter-2.

Source of Variance	Df	Days to Heading	Days to Maturity	Plant Height	Flag Leaf Area	Peduncle Length	Tillers meter ⁻²
REPS	1	2.67	3.78	105.13*	10.52	2.25	1.13
GENO.(unadjusted)	63	15.18**	3.15**	52.28**	19.03**	9.53**	2390.97**
Blocks within Reps/ Block	14	3.12	2.78	39.73	6.77	1.76	1037.41
GENO. (adjusted)	63	15.13**	3.10*	51.56**	19.15*	9.57**	2355.02**
RCB	63	3.12	1.97	25.32	9.53	2.47	705.53
Intra block error	49	2.73	1.74	21.20	9.02	2.34	534.37
CV		1.40	0.80	4.60	11.60	3.60	8.39

**= 1% significant and *=5% significant.

Table 2

Mean square of 64 advanced bread wheat lines regarding chlorophyll content, spike length, spikelets per spike, 1000-grains weight, grain yield, biological yield.

Source of Variance	Df	Chlorophyll Content	Spike Length	Spikelets Spike ⁻¹	1000-grain Weight	Grain yield	Biological yield
REPS	1	48.16**	6.36**	12.76*	72.08**	506521.125	96141.125
GENO.(unadjusted)	63	13.88**	1.25**	3.21**	21.75**	772070.5536**	3488545.649**
Blocks within Reps/Block	14	6.28	0.47	1.86	6.35	266429.2679	1900483.625
GENO. (adjusted)	63	13.25**	1.23**	3.15**	21.61**	746287.6336**	3374600.526**
RCB	63	4.53	0.39	1.50	4.79	183139.3115	1054938.629
Intra block error	49	3.53	0.32	1.22	3.81	159342.1811	711685.0513
CV		4.04	4.94	5.95	4.25	8.98	6.88

**, * significant at 1% and 5% respectively.

Table 3

Correlation of phenotypic characteristics (Above Diagonal) and correlation of genotypic characteristics (Below diagonal) for different traits of wheats

	DH	DM	PH	PDL	FLA	TM	SPK	SL	CC	TGW	GY	BY
DH		00.26*	-00.05	-00.12	00.08	-00.14	00.02	-00.21	-00.05	00.12	-00.17	-00.27*
DM	00.35**		00.10	-00.04	00.16	-00.06	-00.02	-00.03	-00.16	00.13	00.00	00.01
PH	-00.02	00.30*		00.24	00.33**	-00.14	00.20	00.35**	00.08	00.31*	00.10	00.14
PDL	-00.28*	-00.11	00.40**		00.07	00.03	00.13	00.34**	00.09	00.01	00.07	00.15
FLA	00.08	00.31*	00.29*	00.18		-00.07	00.20	00.15	-00.11	00.17	00.11	00.01
TM	-00.13	00.09	-00.15	00.05	-00.06		-00.02	-00.12	-00.19	-00.34**	00.07	00.20
SPK	00.13	-00.02	00.10	00.10	00.07	-00.03		00.45	00.11	-00.05	-00.07	-00.06
SL	-00.26*	-00.08	00.75**	00.72**	00.13	-00.22	00.42**		00.10	00.21	00.12	00.11
CC	-00.06	-00.23	-00.07	00.17	-00.17	-00.25*	00.18	00.25*		-00.01	00.06	00.22
TGW	00.09	00.14	00.69**	-00.03	00.44**	-00.52**	00.15	00.48**	00.05		00.16	00.01
GY	-00.16	-00.04	00.01	00.17	00.00	00.12	-00.14	00.13	00.04	00.19		00.62**
BY	-00.25*	-00.03	-00.02	00.25*	-00.17	00.31	-00.22	00.10	00.25*	00.03	00.67**	

DH = days-to-heading, DM = days-to-maturity, PH = plant-height, FLA = flag-leaf-area, TM = tiller-per-meter, SL = spike-length, SPKS = spikelets-per-spike, CC = chlorophyll-content, TGW = 1000-grains-weight, GY = grain-yield and BY = biological-yield.
 **, * significance at 1% and 5%, respectively.

Table 4

Path coefficient analysis for various traits

	DH	DM	PH	PDL	FLA	TM	SL	SPKS	CC	TGW	BY	Total Indirect Effect	Total direct Effect
DH	0.21	0.19	0.04	-0.28	-0.07	-0.15	-0.08	-0.10	-0.01	0.19	0.02	-0.25	-0.04
DM	0.08	0.54	-0.56	-0.10	-0.26	0.10	0.01	-0.03	-0.03	0.30	0.01	-0.49	0.05
PH	0.00	0.16	-1.89	0.39	-0.24	-0.17	-0.06	0.30	-0.01	1.49	0.00	1.87	-0.02
PDL	-0.06	-0.06	-0.75	0.99	-0.15	0.06	-0.06	0.29	0.02	-0.06	-0.03	-0.80	0.19
FLA	0.02	0.17	-0.56	0.17	-0.82	-0.06	-0.04	0.05	-0.02	0.94	0.00	0.67	-0.15
TM	-0.03	0.05	0.28	0.05	0.05	1.14	0.02	-0.09	-0.03	-1.13	-0.02	-0.86	0.28
SL	0.03	-0.01	-0.18	0.10	-0.06	-0.03	-0.58	0.17	0.02	0.33	0.02	0.39	-0.19
SPK	-0.06	-0.04	-1.41	0.71	-0.10	-0.25	-0.24	0.40	0.03	1.03	-0.02	-0.36	0.04
CC	-0.01	-0.13	0.14	0.17	0.14	-0.28	-0.10	0.10	0.12	0.10	-0.01	0.12	0.24
TGW	0.02	0.07	-1.30	-0.03	-0.36	-0.60	-0.09	0.19	0.01	2.16	-0.03	-2.11	0.05
BY	-0.04	-0.02	-0.01	0.17	0.00	0.13	0.08	0.05	0.00	0.41	-0.15	0.78	0.63

DH =days-to-heading, DM = days-to-maturity, PH = plant-height, FLA = flag-leaf-area, TM = tiller-per-meter, SL = spike-length, SPS= spikelets-per-spike, CC = chlorophyll-content, TGW = 1000-grains-weight, GY = grain-yield and BY = biological-yield

This investigation was performed to study the genotypic variation, correlation, and path coefficient analysis for some important traits of 64 bread wheat genotypes. Days to heading, days to

maturity, plant height in centimeters, flag leaf area in square centimeters, tillers per square meter, spikelets per spike, spike length, chlorophyll

content, 1000-grain weight, biological yield, and grain yield were the variables recorded.

The collection heading date of the 64 genotypes was between 111-121 days with an average of 117 days. The shortest lifetime of 111 days characterized the MPG11 line, while the longest lifetime was 121 days that of the MPG27 genotype. The least significant difference (LSD 5%) for heading was 3.30 days. Previously, [8] studied 180 genotypes with days to heading ranging from 60 to 96 days in Alpha lattice design during 2017-18. Days to heading was observed with significantly negative phenotypic association for biological yield ($r_p = -0.27$, $P = 0.05$). Same association of heading with maturity ($r_G = 0.42^{**}$) and ($r_G = 0.39^{**}$) were reported by [8].

Maturity period for a set of 64 diverse genotypes spanned 160-167 days, with an average of 163 days. MPG31 was shortest at a minimum of 160 days while the longest at a maximum period was MPG26 at 167 days LSD 5% for the minimum detectable difference in maturity was 2.70 days. [9] evaluated 49 wheat genotypes with maturity ranging from 126 to 143 days in simple lattice design during 2016-17. The days taken for a plant to reach maturity had a strong positive correlation with both the plant height, ($r_G = 0.30$; $P = 0.05$), and the FLA (flag leaf area), ($r_G = 0.31$; $P = 0.05$). Plant height presented a strong association with peduncle length (at $r_G 0.40$ and $P 0.01$), flag leaf area (at $r_G 0.29$ and $P 0.05$), number of spikelets per spike (at $r_G 0.75$ and $P 0.01$), and 1000-grain.

The height of the plant of all genotypes of wheat varied from 80.9 cm to 109.9 cm, with an average of 99.3 cm. The lowest height of plant (80.9 cm) was recorded for MPG62, while the highest plant height of 109.9 cm belonged to both cases of MPG27 and MPG41. [10] observed plant height ranged from 88.70 to 110 cm for a set of 54 genotypes evaluated in randomized block design during 2014-15. The least significant difference (LSD 5%) for plant height was 9.3 cm. Plant height presented a strong association with peduncle length (at $r_G 0.40$ and $P 0.01$), flag leaf area (at $r_G 0.29$ and $P 0.05$), number of spikelets per spike (at $r_G 0.75$ and $P 0.01$), and 1000-grain weigh. similar association i.e., positive significant genotypic correlation of plant height with peduncle length ($r_G = 0.88^{**}$) was reported by [5].

Leaf flag area ranged from 19.4 to 33.8 cm in terms of flag leaf area, with a mean of 26.0 cm and a coefficient of variation of 1.60%. Moreover, the smallest flag leaf area was noted in the variety MPG31-19.4 cm, and the largest one was that of the variety MPG42, with 33.8 cm. The LSD 5% for flag leaf area was 6.0 cm². [11] noted flag leaf area for 10 wheat genotypes varied from 21.29 to 36.41 cm² in randomized block design during 2018-19. Leaf -area showed significant positive correlation with 1000-grains weight ($r_G = 0.44$, $P = 0.01$). only, same association of flag leaf area with 1000-grain weight ($r_G = 0.37^{**}$) was recorded by [12].

The range observed for peduncle length of wheat genotypes was between 36.85 and 49.05 cm, with an average of 42.11 cm. The shortest peduncle length recorded was 36.85 cm for MPG22, while the longest peduncle length was 49.05 cm reported for MPG41 [13] noted peduncle length for 28 wheat genotypes varied from 21.37 to 49.33 cm in randomized complete block design during 2020-2022. The least significant difference (LSD 5%) for peduncle length was 3.10 cm. peduncle-length showed significant positive genotypic inter-relation with biological yield ($r_G = 0.25$, $P = 0.05$). Same result of peduncle length with spikelets spike⁻¹ ($r_G = 0.78^{**}$) was reported by [5] in their research work.

The tillers m⁻² ranged from 205.36 to 353.36 with an average of 276.11. However, the highest number of tiller m⁻² (353.36) was recorded for MPG43, and the minimum number of tiller m⁻² (205.36) was noted for MPG29 (Table-4). Similarly, the least significant difference (LSD 5%) for tillers m⁻² was 46.31. tiller meter⁻² had significant positive association (based on genotypes) with biological-yield ($r_G = 0.31$, $P = 0.05$). Contradictory link of tiller meter⁻² with chlorophyll content ($r_G = 0.36^{**}$) was reported by [14] for set of 16 wheat genotypes.

The average chlorophyll content ranged between 38.67 to 53.38 μ mol meter⁻² (Table 4) with an average of 46.44 μ mol meter⁻². The maximum value for chlorophyll content (53.38 μ mol meter⁻²) was recorded for MPG05, while the minimum value for chlorophyll content (38.67 μ mol meter⁻²) was recorded for MPG29. The least significant difference (LSD 5%) for chlorophyll content was 3.76 μ mol meter. Patil et al. (2023) observed a chlorophyll content range of 41.52 to

48.23 μmol^{-1} for a set of 21 genotypes evaluated in randomized block design during 2021-22. chlorophyll concentration had a strong positive relationship with bio-yield ($r_G=0.25$, $P=0.05$).

Length of spike ranged between 9.93 cm to 13.52 cm with a mean length of 11.51 cm. shortest spike length recorded was 9.93 cm was in MPG31, while longest spike length of 13.52 cm was observed in MPG07. The LSD 5% (least significant difference) regarding spike length was 1.14 cm. [13] noted spike length for 28 wheat genotypes ranged from 7.97 to 14.00 in randomized complete block design during two consecutive years (2020-2022). spike length had significant positive phenotypic relationship with spikelets spike⁻¹ ($r_P=0.45$, $P=0.01$). Similar association of spike length with spikelet spike⁻¹ ($r_G=0.44^{**}$) was reported [1] in their experiment.

The values for spikelet length of spike-1 varied from 16.13 to 21.17, with an average of 18.50 for the different genotypes. The highest number of spikelets per spike was 21.17 in MPG06, and the lowest spikelets per spike with a value of 16.13 was in MPG32. The LSD 5% value was 2.21. [15] noted spikelets spike⁻¹ ranged from 12.86 to 25.43 for 114 pre-breeding lines in randomized block design during 2010-11. For spikelets spike⁻¹, which represented the smallest difference considered statistically significant. Likewise, Varsha et al (2019) showed significant positive genotypic relationship of spikelets spike⁻¹ with 1000-grain weight ($r_G=0.56^{**}$).

with a mean 1000 grain-weight of wheat advance lines ranged between 39.18 to 52.93 g with a mean of 45.97 g. The maximum weight was 1000 grains corresponding to 52.93g for MPG29, and a minimum weight of 1000 grains corresponding to 39.18g for MPG26, The LSD 5% (least significant difference) for 1000 grain-weight was 3.91g. [15] noted 1000 grain weight ranged from 26.94 to 69.11g for 114 pre-breeding lines in randomized block design during 2010-11.

Average values for wheat grain-yield were recorded between 2916 to 5784 kg ha⁻¹, with a mean of 4457 kg ha⁻¹. Similarly, the maximum grain yield was recorded for wheat advance line MPG09, which amounted to 784 kg ha⁻¹. The

minimum amount of grain-yield of 2916 kg ha⁻¹ was observed in MPG27. The least significant difference (LSD 5%) for grain yield was 802.18 Kg ha⁻¹. A statistically significant positive association was also noted between grain-yield and biological-yield. [16] recorded grain yield for 55 wheat lines with a check cultivar which varied from 2835 to 7125 under a Randomized Complete Block Design. [6] revealed significant positive genotypic correlation of grain yield with biological yield ($r_G = 0.62^{**}$).

The range from the mean values of biological yield was from 9131 to 1503 kg ha⁻¹ as indicated in Table 5. The overall mean for the biological production was 12319 kg ha⁻¹. The wheat advance line MPG45 showed the minimum value of biological yield that was 9131 kg ha⁻¹ with the highest value of biological yield recorded for MPG 40 was 15031 kg ha⁻¹. recorded value for LSD 5% (least significant difference) of biological-yield (Kg ha⁻¹) was 1690 Kg ha⁻¹. [17] recorded biological yields ranging from 13750 to 18945 for 64 wheat lines tested in a simple lattice design.

CONCLUSIONS

This study examined 64 genotypes of wheat, showing statistically significant variations in different phenotypic and morphologic features. Genotypes of interest were assigned specific traits, MPG31 for early-maturity, MPG05 for high chlorophyll content, MPG43 for highest-tillers-per-square meter, MPG29 for highest amount of 1000-grains-weight, MPG09 (5784 kg/ha), MPG39 (5777 kg/ha) and MPG24 (5496 kg/ha) noted for highest-grain-yield, and MPG40 for highest biological-yield. Statistically positive genetic correlations were examined in various key traits included in this study, including plant height as well as peduncle length with spikelets spike⁻¹ and biological yield, highlighting the coordinated genetics control and potential for simultaneous improvement through breeding efforts. Path coefficient analysis highlighted the cause-and-effect relationships between traits, with features like 1000-grains-weight, tillers and peduncle-length showing direct effects on grain yield.

REFERENCES

1. Chauhan, S., Gupta, A., Tyagi, S. D., & Singh, S. (2023). Genetic Variability, Heritability and Genetic Advance Analysis in Bread Wheat (*Triticum aestivum* L.) Genotypes. *International Journal of Plant & Soil Science*, 35(19), 164–172. <https://doi.org/10.9734/ijpss/2023/v35i193538>
2. Haile, T. (2022). Genetic variability, divergence, and path coefficient analysis of yield and yield related traits of Durum wheat (*Triticum turgidum* L. var. Durum) genotypes at Jamma district, south wollo zone, amhara region, Ethiopia. *Journal of Plant Science and Phytopathology*, 6(2), 075–083. <https://doi.org/10.29328/journal.jpss.1001078>
3. Crespo-Herrera, L. A., Crossa, J., Huerta-Espino, J., Vargas, M., Mondal, S., Velu, G., Payne, T. S., Braun, H., & Singh, R. P. (2018). Genetic Gains for Grain Yield in CIMMYT's Semi-Arid Wheat Yield Trials Grown in Suboptimal Environments. *Crop Science*, 58(5), 1890–1898. <https://doi.org/10.2135/cropsci2018.01.0017>
4. Government of Pakistan., (2019). Economic survey of Pakistan.
5. Ullah, N., Ullah, H., Afridi, K., Alam, M., Jadoon, S. A., Khan, W. U., Ahmad, M., & Uddin, H. (2018). Genetic variability, heritability and correlation analysis among morphological and yield traits in wheat advanced lines. *Biyolojik Çeşitlilik ve Koruma*, 11(1), 166–180. <https://dergipark.org.tr/en/pub/biodicon/isue/55718/761852>
6. Baye, A., Berihun, B., Bantayehu, M., & Derebe, B. (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. *Cogent Food & Agriculture*, 6(1), 1752603. <https://doi.org/10.1080/23311932.2020.1752603>
7. Kumar, R., Singh, S. K., Bagare, V., Singh, A., Pathak, V. N., Yadav, V., & Kumar, R. (2023). Path Coefficient Analysis for Yield and Its Attributing Traits in Wheat (*Triticum aestivum* L.). *International Journal of Plant & Soil Science*, 35(20), 651–658. <https://doi.org/10.9734/ijpss/2023/v35i203849>
8. Gerema, G., Lule, D., Lemessa, F., & Mekonnen, T. (2020). Morphological characterization and genetic analysis in bread wheat germplasm: A combined study of heritability, genetic variance, genetic divergence and association of characters. *Agricultural Science and Technology*, 12(4), 301–311. <https://doi.org/10.15547/ast.2020.04.048>
9. Seyoum, E. G., & Sisay, A. (2021). Genetic variability, heritability and genetic advance study in bread wheat genotypes (*Triticum aestivum* L.). *Advances in Bioscience and Bioengineering*, 9(3), 81–86.
10. Rajput, R. S., & Kandalkar, V. (2018). Combining ability and heterosis for grain yield and its attributing traits in bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(2), 113–119.
11. Ahmad, A., Iqbal, M. N., Anjum, M. M., Khan, B., Khan, S., Ullah, S., Ullah, R., & Afridi, M. Y. (2023). Genetic Attributes and Correlation Studies for Important Traits in Wheat Under Irrigated and Rainfed Conditions. *Gesunde Pflanzen*, 75(6), 2387–2400. <https://doi.org/10.1007/s10343-023-00884-7>

12. Ayer, D., Sharma, A., Ojha, B., Paudel, A., & Dhakal, K. (2017). Correlation and path coefficient analysis in advanced wheat genotypes. *SAARC Journal of Agriculture*, 15(1), 1–12. <https://doi.org/10.3329/sja.v15i1.33155>
13. Bhatt, B., Swati, N., Jaiswal, J. P., Khan, R., Joshi, S., & Chaudhary, D. (2023). Assessment of Genetic Variability for Morpho-physiological and Yield Traits in Bread Wheat (*Triticum aestivum* L.). *International Journal of Environment and Climate Change*, 13(11), 2283–2291. <https://doi.org/10.9734/ijecc/2023/v13i113390>
14. Prasad, J., Dasora, A., Chauhan, D., Rizzardi, D. A., Bangarwa, S. K., & Nesara, K. (2021). Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.) genotypes. *Genetics and Molecular Research*, 20(2), 1-6. <http://dx.doi.org/10.4238/gmr19419>
15. Nukasani, V., Potdukhe, N. R., Bharad, S., Deshmukh, S., & Shinde, S. M. (2013). Genetic variability, correlation and path analysis in wheat. *Journal of Cereal Research*, 5(2).
16. Sabaghnia, N., Janmohammadi, M., Bashiri, A., & Asghari-Shirghan, R. (2014). Genetic variation of several bread wheat (*Triticum aestivum* L.) genotypes based on some morphological traits. *Agronomy Science*, 69(1), 44–54. <https://doi.org/10.24326/as.2014.1.5>
17. Fikre, G., Alamerew, S., & Tadesse, Z. (2015). Genetic Variability Studies in Bread Wheat (*Triticum Aestivum* L.) Genotypes at Kulumsa Agricultural Research Center, South East Ethiopia. *Journal of Biology Agriculture and Healthcare*, 5(7), 89–98.