**GENETIC VARIATION OF MORPHO-PHYSIOLOGICAL CHARACTERS IN WHEAT**

**Abstract**

Wheat (*Triticum aestivum L*.) is a globally important staple crop, yet its production is challenged by climate variability, soil constraints, and genetic limitations. Despite extensive breeding efforts, limited studies have comprehensively analyzed morpho-physiological traits across diverse wheat genotypes under agroecological zone (AEZ-9) conditions in Bangladesh. Therefore, this study was conducted with 17 wheat genotypes following a Randomized Complete Block Design (RCBD) with three replications at the Field Laboratory of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh, from December 2023 to April 2024 to assess genetic variability, heritability, expected genetic advance, and interrelationships among key morpho-physiological traits. The results revealed significant genetic variation among the genotypes for all studied traits. High heritability coupled with high genetic advance was observed for grain-filling rate, 1000-grain weight, and yield per plant, indicating strong additive gene effects and potential for selection. Correlation analysis showed that grain-filling rate, spike number, and days to maturity were positively associated with yield, suggesting their importance in wheat improvement programs. Path coefficient analysis further confirmed the direct contribution of grain-filling rate to yield. These findings highlight the potential of grain-filling rate and spike number as selection criteria for enhancing wheat yield under AEZ-9 conditions. These traits should be prioritized in wheat breeding programs to enhance yield stability under AEZ-9 conditions.

**Keywords:** Breeding, Genotypes,Agroecological zone, Heritability, Genetic Advance, Additive gene, Path coefficient

**1. Introduction**

Wheat is the most widely cultivated cereal crop in the world and serves as a staple food for approximately 40% of the global population, contributing 20% of total dietary calories and proteins worldwide [1]. It accounts for nearly 30% of total cereal production and remains a crucial source of calories for human consumption [2]. The historical development of wheat, from its early domestication to modern plant breeding and the Green Revolution, has significantly enhanced global food security. As a result, wheat has become one of the most productive and essential crops in the 21st century [3].

However, wheat production faces several challenges, particularly due to climate variability. Extreme weather events such as droughts and heat waves, along with unpredictable rainfall patterns, adversely affect yield stability. Additionally, soil constraints, including poor nutrient content and salinity, further limit productivity. Moreover, genetic limitations within current wheat varieties restrict their adaptability to changing environmental conditions, necessitating the development of improved genotypes [4].

Genetic variation, a fundamental component of breeding programs, refers to the natural differences in DNA sequences among individuals within a species. This variability allows breeders to select and combine desirable traits to enhance future generations of crops, thereby increasing resilience, productivity, and adaptability [5]. Among the key morpho-physiological traits influencing wheat yield, plant height, grain filling rate, spike number, and 1000-grain weight are of particular importance [6]. The extent of genetic variation in these traits enables breeders to select high-yielding genotypes, making an understanding of their heritability and genetic advance essential for developing improved wheat varieties.

Both phenotypic and genotypic variability play a crucial role in identifying superior wheat genotypes. The presence of a wide range of phenotypic expressions—observable characteristics influenced by underlying genetic variations—allows plant breeders to implement targeted selection for desirable traits such as high yield, disease resistance, and stress tolerance [7]. Essentially, greater variability increases the likelihood of identifying exceptional genotypes within a population.

Despite extensive research on wheat breeding, limited studies have comprehensively analyzed morpho-physiological traits across diverse wheat genotypes under AEZ-9 conditions, a specific agroecological zone of Bangladesh. To address this gap, the present study evaluates genetic variation, heritability, and the correlation among morpho-physiological traits in 17 wheat genotypes. By examining these factors, the study aims to provide insights into genetic improvement strategies for enhancing wheat productivity in this region.

**2. Materials and Methods**

**2.1 Experimental site and soil**

The field study was conducted at the Field Laboratory of Genetics and Plant Breeding of Bangladesh Agricultural University, Mymensingh during the period from December 2023 to April 2024. Geographically, the site is located at 24°43'21"N latitude and 90°25'24"E longitude, with an elevation of 23 meters above sea level. The soil at the experimental site belongs to the Sonatala series within the Old Brahmaputra Floodplain (AEZ-9) [8]. To comprehensively understand the study conditions, weather data and the detailed physicochemical characteristics of the soil at the experimental field are outlined in Tables 1, 2, and 3, respectively.

**Table 1** Weather data regarding monthly average air temperature, rainfall, relative humidity, and sunshine hours at the experimental site during the study period December 2023 to April 2024

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Months | Monthly Average temperature (0C) | Rainfall(mm) | Relative humidity (%) | Sunshine (hrs/day) |
| Maximum | Minimum | Average |
| December 2023 | 26.85 | 14.70 | 19.47 | 0.00 | 86.30 | 09.12 |
| January 2024 | 25.11 | 13.52 | 18.24 | 03.21 | 76.13 | 07.42 |
| February 2024 | 27.28 | 16.31 | 22.29 | 08.40 | 69.33 | 09.46 |
| March 2024 | 32.04 | 19.62 | 27.35 | 73.22 | 53.49 | 10.41 |
| April 2024 | 34.72 | 23.88 | 29.64 | 87.23 | 47.57 | 10.17 |

 **Table 2** Physical properties of initial soil

|  |  |  |
| --- | --- | --- |
| 1. Physical Characteristics of Soil
 | Results | Methods |
| Sand (%) (0.0-0.02 mm) | 20 | Hydrometer  |
| Silt (%) (0.02-0.002 mm) | 67 |
| Clay (%) (<0.002 mm) | 13 |
| Soil textural class | Silt loam |
| Particle density (g/cc) | 2.60 | [9] |
| Bulk density (g/cc) | 1.35 | [10] |
| Porosity (%) | 46.67 |  |

**Table 3** Chemical properties of initial soil

|  |  |  |
| --- | --- | --- |
| 1. Chemical Characteristics of Soil
 | Results  | Methods  |
| pH | 6.50 | Glass Electrode pH meter [11] |
| Organic carbon (%) | 1.29 | Wet oxidation [12] |
| Total Nitrogen (%) | 0.101 | Semi-micro Kjeldahl [13] |
| Available Phosphorus (P) (ppm) | 6.57 | Olsen [14] |
| Exchangeable Potassium (K) (me%) %) | 0.077 | Ammonium acetate Extraction [15] |
| Available Sulfur (S) (ppm) | 12.5 | CaCl2 Extraction [16] |
| Available Zinc (Zn) (ppm) | 0.92 | [17] |

**2.2 Experimental Design and Treatments**

The experiment was conducted using seventeen wheat genotypes, namely Bijoy, Sourab, Prodip, Balaka, Gourab, AYTC P-48, E-4, Pavan, Protiva, Kolyansona, Durag, Sufi, Ananda, BAW 1054, Akbar, Shatabdi, AYT P-59 A-7, and Peacock. A **randomized complete block design (RCBD)** with three replications was employed to ensure statistical reliability. Each experimental plot measured **2.5 m × 1 m**, with wheat seeds sown at a density of **120 kg ha⁻¹**.The plots contained **10 rows per plot**, maintaining a **row-to-row spacing of 20 cm**, as recommended by Hossain et al. [18]. Furthermore, the distance between adjacent blocks was set at **75 cm**, as also noted by Rana et al. [19].

**2.3 Crop management**

To ensure an adequate supply of essential nutrients, the experimental plots were fertilized with 174 kg Urea, 76 kg TSP, 120 kg MoP, 56 kg gypsum, 4 kg ZnSO4, and 7 kg Na2B4O7·10H2O per hectare, following the recommendations of Ahmmed et al. [20]. Two-thirds of the N, along with the entire amounts of P, K, S, zinc (Zn), and boron (B), were applied as a basal dose during the final land preparation. The remaining one-third of nitrogen was applied 17 days after sowing, following the first irrigation, in accordance with the Fertilizer Recommendation Guide-2018 [20].

The seeds of 17 wheat genotypes were sown on December 21, 2023, and all intercultural operations were carried out uniformly across genotypes. Thinning was performed 25 days after sowing to maintain optimal plant density, while weeding was conducted whenever necessary to minimize competition. The field was irrigated twice, with the first irrigation applied at the crown root initiation stage and the second at the peak tillering stage. Since the genotypes exhibited variations in maturity duration, harvesting was carried out between March 25 and April 20, 2024, depending on the specific maturity period of each genotype.

**2.4 Data Collection**

Pre- and post-harvest data were collected by selecting five random plants from the center of each plot to ensure unbiased sampling. During the growth stages, data were recorded on days to anthesis, days to maturity, and grain-filling duration. In addition to these parameters, various growth and yield-related traits were assessed, including the number of spikes per plant, the number of spikelets per spike, and 1000-seed weight. These measurements provided a comprehensive evaluation of the genotypic variations in wheat performance.

**2.4.1 Estimation of Genotypic and Phenotypic Variances**

The genotypic and phenotypic variances were estimated according to Johnson *et al*. [21].



Where,

δ2g = genotypic variance

MSV = mean square for genotype

MSE = mean square for error

r = number of replications

δ2ph = δ2g + δ2e

Where,

δ2ph = phenotypic variance

δ2g = genotypic variance

 δ2e = environmental variance (MSE)

**2.4.2 Estimation of Genotypic and Phenotypic Coefficients of Variation**

The genotypic and phenotypic coefficients of variation were calculated according to the formula suggested by Burton [22]. Both genotypic and phenotypic coefficients of variation are expressed in percentage.

Genotypic coefficient of variation (G.C.V.) = 

Where,

δg = Genotypic standard deviation.

= Population mean

Similarly, the phenotypic coefficient of variation was calculated from the following formula:

Phenotypic coefficient of variation (P.C.V.) = 

Where,

δph = phenotypic standard deviation

= Population mean.

**2.4.3 Estimation of Heritability**

Heritability in the broad sense (h2b) was estimated by the formula suggested by Johnson *et al*. [21] and Hanson *et al*. [23] as the proportion of genotypic variance to phenotypic variance.

 Heritability in broad sense, h2b (%) = 

Where,

h2b (%) = heritability in broad-sense

 δ2g = genotypic variance

δ2ph = phenotypic variance

**2.4.4 Estimation of Genetic Advance (GA)**

The expected genetic advance (GA) for different characters under selection was estimated by the formula as suggested.

Genetic Advance (GA) = h2b.k. δph

Where,

h2b (%) = heritability in broad-sense

k= selection intensity, the value of which is 2.06 at 5% selection intensity, and

δph= phenotypic standard deviation.

The genetic advance was then expressed in percentage of mean according to Comstock and Robinson [24] as follows,

GA (%) =

Where,

GA= genetic advance

= population mean

**2.4.5 Estimation of Correlation Coefficients**

The correlation coefficients were calculated from the mean data of different characters for each pair of characters in all possible combinations following the formula used by Singh and Choudhary [25].

r = 

Where,







∑xy = sum of the products of the x and y variable traits.

∑x = sum of the variable x,

∑y = sum of the variable y,

∑x2, ∑y2 = The sum of squares of x and y variable respectively, and

N = The number of observations.

Vx = Variance of variable x,

Vy = variance of variable y.

**2.4.6 Estimation of Path Coefficients**

The path analysis coefficients, as described by Dewey and Lu [26], were obtained by solving the simultaneous equations using the Gaussian Elimination method. In this study, grain yield per plant was considered the resultant variable (effect), while eight yield-related traits were treated as causal factors influencing yield. The following sets of simultaneous equations were formulated based on the cause-and-effect relationships among these traits.

rly = Ply + r12P2y + r13P3y + r14P4y + r15P5y + r16P6y + r17P7y + r18P8y

r2y = r21Ply + P2y + r23P3y + r24P4y + r25P5y + r26P6y + r27P7y + r28P8y

r3y = r31Ply + r32P2y + P3y + r34P4y + r35P5y + r36P6y + r37P7y + r38P8y

r4y = r41Ply + r42P2y + r43P3y + P4y + r45P5y + r46P6y + r47P7y + r48P8y

r5y = r51Ply + r52P2y + r53P3y + r54P4y + P5y + r56P6y + r57P7y + r58P8y

r6y = r61Ply + r62P2y + r63P3y + r64P4y + r65P5y + P6y + r67P7y + r68P8y

r7y = r71Ply + r72P2y + r73P3y + r74P4y + r75P5y + r76P6y + P7y + r78P8y

r8y = r81Ply + r82P2y + r83P3y + r84P4y + r85P5y + r86P6y + r87P7y + P8y

riy = Correlation co-efficient between Y and ith character (I = 1, 2, 3, ……8)

y = Grain yield/plant

Piy = Path coefficient due to ith charcter (i = 1, 2, 3, ……………8)

1 = Days to anthesis

2 = Days to maturity

3 = Days to grain filling

4 = Grain filling rate

5 = Spikes/plant

6 = Spikelet/spike

7 = Grain/plant

8 = 1000-grain weight

Total correlation between I and y, i.e. rly was partitioned as follows-

Ply = The direct effect of 1 on y

r12P2y = The indirect effect of 1 via 2 on y

r13P3y = The indirect effect of 1 via 3 on y

r14P4y = The indirect effect of 1 via 4 on y

r15P5y = The indirect effect of 1 via 5 on y

r16P6y = The indirect effect of 1 via 6 on y

r17P7y = The indirect effect of 1 via 7 on y

r18P8y = The indirect effect of 1 via 8 on y

After calculating the direct and indirect effects of the characters, residual effect (R) was calculated using the following formula suggested by Singh and Choudhury, [27].



Where,

= R2

Piy = Direct effect of the characters on yield

riy = Correlation coefficient of the characters with yield

Therefore,

Residual effect = 

**2.5 Statistical analysis**

The experimental data were analyzed using R programming software (version 4.2.2) based on a three-factor Completely Randomized Design (CRD). Analysis of variance (ANOVA) was performed to determine the significance of treatment effects, and Tukey’s Honest Significant Difference (HSD) test was used for pairwise comparisons at the 5% significance level, following the methodology outlined by Gomez and Gomez [28].

**3. Results and Discussion**

**3.1 Growth Periods and Grain Filling Rate of Different Wheat Genotypes**

Significant variations were observed among the wheat genotypes in terms of anthesis, maturity, and grain filling duration. The genotype *Durag* reached anthesis approximately 15 days later than *Pavon* and required the maximum time to attain spike maturity. In contrast, *Kolyansona*exhibited the shortest maturity period. *Durag* also had the longest grain-filling duration but exhibited the lowest grain-filling rate. Conversely, AYTC P-48 E-4 recorded the highest grain-filling rate, followed by Peacock. This variation can be attributed to the fact that the duration and rate of grain growth in wheat are significantly influenced by both genotypic differences and environmental conditions [29].

**Table 4. Mean performance of growth periods and grain filling rate of selected wheat genotypes**

|  |  |  |  |
| --- | --- | --- | --- |
| **Sl. No.** | **Genotypes** | **Growth periods**  | **Grain filling rate****(mg/day)** |
|  **Days to anthesis**  | **Days to maturity**  | **Days to grain filling**  |
| 1. | Bijoy  | 71.67 b | 93.33 b-d | 21.67 d-f | 0.69 g |
| 2. | Sourav  | 70.00 bc | 95.67 bc | 25.67 b-d | 0.80 ef |
| 3. | Prodip  | 69.00 bc | 94.67 b-d | 26.67 bc | 0.77 ef |
| 4. | Balaka  | 68.33 bc | 93.33 b-d | 25.00 b-d | 0.96 bc |
| 5. | Gourav  | 69.33 bc | 93.00 b-d | 23.33 b-f | 0.86 de |
| 6. | AYTC P-48 E-4 | 69.00 bc | 89.00 cd | 20.00 ef | 1.16 a |
| 7.  | Pavon  | 65.67 c | 95.67 bc | 27.00 b | 0.59 h |
| 8. | Protiva  | 67.67 bc | 84.67 b-d | 22.00 c-f | 0.91 cd |
| 9. | Kolyansona  | 69.33 bc | 87.33 d | 19.67 f | 0.74 fg |
| 10. | Durag  | 80.33 a | 117.3 a | 37.00 a | 0.40 j |
| 11.  | Sufi  | 68.67 bc | 93.33 b-d | 24.67 b-e | 0.78 ef |
| 12. | Ananda  | 78.00 a | 114.0 a | 36.00 a | 0.52 i |
| 13. | BAW 1054 | 68.67 bc | 91.67 b-d | 23.00 b-f | 0.85 de |
| 14. | Akbar  | 68.00 bc | 93.00 b-d | 25.00 b-d | 0.75 fg |
| 15. | Shatabdi  | 70.67 b | 91.67 b-d | 21.00 d-f | 0.84 de |
| 16. | AYT P-59 A-7 | 67.67 bc | 90.67 b-d | 23.00 b-f | 0.84 de |
| 17. | Peacock  | 70.00 bc | 97.00 b | 27.00 b | 1.0 b |

In a column, figures with the same letter (s) or without a letter do not differ significantly whereas figures with dissimilar letters differ significantly

**3.2 Yield Components of Various Genotypes of Wheat**

Significant variations were observed among the wheat genotypes in yield-contributing traits, as presented in Table 5. Ananda produced 41.8% more spikes than Prodip, while Sourav exhibited a 33.36% increase in effective spikelets compared to AYTC P-48 E-4. Similarly, the Peacock genotype recorded 36.11% more grains than AYTC P-48 E-4, which had the lowest grain count. However, despite having fewer grains, AYTC P-48 E-4 produced the heaviest seeds among all genotypes. Furthermore, Peacock achieved a 47.36% higher grain yield than AYTC P-48 E-4, which recorded the lowest yield.

This higher grain yield might have been associated with the genetic makeup of the parental material of these varieties, as they were grown under similar soil, climatic, input, and crop management conditions, as noted by Das and Biswas [30]. Moreover, previous research has identified numerous quantitative trait loci (QTLs) associated with grain yield, further supporting the genetic basis of yield differences. For instance, Ndlovu et al. [31] reported the detection of 93 QTLs under well-watered conditions in maize, emphasizing the role of genetic factors in yield variation.

**Table 5. Mean performance of yield and yield contributing characters of selected wheat genotypes**

|  |  |  |
| --- | --- | --- |
| **SL. NO.** | **Genotypes** | **Characters**  |
| **Spike per plant (no.)** | **Spikelets per spike (no.)** | **Grains per spike (no.)** | **1000-grain weight (g)** | **Yield/****plant (g)** |
| 1. | Bijoy  | 5.6 a-c | 11.89 b-d | 22.83 b | 25.22 h | 3.44 d-f |
| 2. | Sourav | 4.66 c-e | 13.25 a | 20.08de | 43.96 b | 4.12 cd |
| 3. | Prodip  | 3.8 e | 12.28ab | 23.37 b | 41.67 c | 3.94 d |
| 4. | Balaka  | 4.46 a | 11.66b-e | 18.69 ef | 43.99 b | 5.10 ab |
| 5. | Gourav  | 4.13 e | 10.13 fg | 19.96 de | 41.91c | 3.79 de |
| 6. | AYTC P-48 E-4 | 4.86 b-e | 8.83 h | 16.03 h | 49.78 a | 4.64 bc |
| 7. | Pavon  | 3.86 e | 9.23 gh | 17.59 fg | 30.62 g | 3.15 ef |
| 8. | Protiva  | 4.00 e | 10.52 ef | 21.34 cd | 36.79 d | 4.04 cd |
| 9. | Kolyansona  | 4.13 e | 11.09 b-f | 24.06 ab | 28.95 g | 2.89 f |
| 10. | Durag  | 3.80 e | 10.80 d-f | 20.96 d | 35.94 de | 3.03 f |
| 11. | Sufi  | 4.40 e | 10.92 c-f | 18.01 fg | 37.89 d | 4.00 cd |
| 12. | Ananda  | 6.53 a | 10.69 d-f | 17.14 gh | 33.07 f | 3.85 d |
| 13. | BAW 1054 | 4.40 de | 11.00 c-f | 22.66 bc | 41.53 c | 3.93 d |
| 14. | Akbar  | 5.46 a-d | 9.98 f-h | 19.96 de | 36.02 de | 3.76 de |
| 15. | Shatabdi  | 5.8 ab | 9.92 f-h | 17.66 fg | 32.57 f | 3.55 d-f |
| 16. | AYT P-59 A-7 | 4.13 e | 11.16 b-f | 20.59 d | 40.31 c | 3.88 d |
| 17. | Peacock  | 5.66 a-c | 12.12 bc | 25.09 a | 34.41 ef | 5.49 a |

In a column, figures with the same letter (s) or without a letter do not differ significantly whereas figures with dissimilar letters differ significantly

**3.3 Coefficient of Variation, Heritability, and Genetic Advance for Different Morpho-Physiological Characters**

**3.3.1 Growth Characters**

The phenotypic and genotypic coefficients of variation exhibited minimal differences for growth-related traits in wheat, indicating strong genetic control over these characteristics (Table 6). Additionally, the high heritability coupled with a high genetic advance suggests that these traits are primarily governed by additive gene action, highlighting their potential for effective selection in breeding programs [32].

**3.3.2 Yield Components**

Moderate differences between genotypic and phenotypic variation were observed for the number of spikes and spikelets (Table 6). However, this difference was more pronounced for grain number and least for 1000-seed weight. The high heritability and genetic advance recorded for various yield traits suggest that these characteristics are predominantly controlled by additive gene action, making them highly heritable as exhibited by Shankar et al. [33] and Bharali et al. [34].

**3.3.3 Yield of Wheat**

The phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation, indicating a relatively low environmental influence on yield per plant (Table 6). Moreover, the moderately high heritability, coupled with a high genetic advance, suggests that yield was primarily governed by additive gene action. Consequently, further selection for yield per plant is expected to enhance overall productivity. These findings further indicate that the association among these traits was predominantly under genetic control, highlighting the preponderance of genetic variance in the expression of yield-related characters [35].

**Table 6. Coefficient of variation, heritability and genetic advance of growth periods, grain fillings rate, yield components, and yield of selected wheat genotypes**

|  |  |  |  |
| --- | --- | --- | --- |
| **Character** | **Coefficient of variation (%)** | **Heritability****(%)** | **Genetic advance (%)** |
| **Genotypic** | **Phenotypic**  |
| Growth periods  |
| Days to anthesis  | 12.71 | 13.39 | 69.01 | 21.94 |
| Days to maturity  | 10.16 | 11.06 | 81.19 | 25.15 |
| Days to grain filling  | 18.40 | 20.92 | 77.30 | 33.31 |
| Grain filling rate (mg/day) | 22.09 | 22.79 | 93.93 | 44.09 |
| Yield components  |
| Spike number  | 18.01 | 21.69 | 68.93 | 30.80 |
| Spikelets number  | 9.72 | 11.36 | 73.30 | 17.15 |
| Grains number  | 12.69 | 13.35 | 90.39 | 24.86 |
| 1000-grain weight(g)  | 16.65 | 16.92 | 96.78 | 33.73 |
| Yield/plant (g) | 16.33 | 18.79 | 75.51 | 29.23 |

**3.4 Correlation Coefficient Among Different Morpho-Physiological Characters**

Days to anthesis exhibited a strong positive correlation with days to maturity (r = 0.858) and grain-filling period (r = 0.694), indicating that a delay in anthesis extended both maturity duration and grain-filling time (Table 7). Similarly, the maturity period was highly correlated with the grain-filling period (r = 0.945), suggesting a direct relationship between these traits. Furthermore, the grain-filling rate showed a strong positive correlation with yield per plant (r = 0.670) and 1000-grain weight (r = 0.550), highlighting its significant contribution to final yield.

Additionally, the spike number displayed a significant correlation with yield per plant (r = 0.390) and exhibited the highest correlation with 1000-grain weight (r = 0.969), underscoring the importance of spike density in yield formation. Overall, these findings suggested that selection for traits such as grain-filling rate, spike number, and days to maturity could enhance yield potential in wheat genotypes, as suggested by Surin et al. [36].

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Character | Maturity period | Grain filling period | Grain filling rate | Spike Number | Spikelet number | Grain number | 1000-grain weight | Yield/plant  |
| Days to anthesis | 0.858\*\* | 0.694\*\* | -0.034 | 0.144 | 0.141 | 0.148 | 0.054 | 0.357\*\* |
| Maturity period |  | 0.945\*\* | 0.012 | 0.083 | 0.101 | 0.125 | 0.107 | 0.435\*\* |
| Grain filling period  |  |  | 0.348\* | 0.132 | 0.052 | 0.078 | 0.132 | 0.428\*\* |
| Grain filling rate  |  |  |  | 0.816\*\* | -0.006 | -0.226 | 0.550\*\* | 0.670\*\* |
| Spike Number |  |  |  |  | 0.056 | -0.131 | 0.969\*\* | 0.390\*\* |
| Spikelet number |  |  |  |  |  | 0.543\*\* | -0.291\* | 0.221 |
| Grain number |  |  |  |  |  |  | 0.214 | 0.440\*\* |
| 1000-grain weight  |  |  |  |  |  |  |  | 0.507\*\* |

**Table 7. Correlation coefficient among different morpho-physiological characters of selected wheat genotypes**

\*\* =Significant at 1% level of probability, \* =Significant at 5% level of probability

**3.5 Path coefficient analysis**

Path analysis revealed the direct (underlined) and indirect effects of key morpho-physiological traits on grain yield per plant in 17 wheat genotypes (Table 8). Grain filling rate exhibited the strongest positive direct effect on yield, while 1000-grain weight showed a notable negative direct effect. This aligns with the findings of Han et al. [37]. Moreover, Knezevic et al. [38] reported that grain weight as a grain yield component is determined by genetic and environmental factors (temperature, light, nutrients, water). Indirect contributions from the grain filling period and spike number were also significant, emphasizing their role in yield determination.

**Table 8. Path analysis showing the direct (underlined) and indirect effect of some morpho-physiological characters on grain yield per plant of selected wheat genotypes**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Character | Days to anthesis | Maturity period | Grain filling period | Grain filling rate | Spike number  | Spikelet number | Grain number | 1000-grain weight | Yield/plant |
| Days to anthesis | **-0.3632** | -0.2979 | 0.7473 | 0.0186 | 0.2455 | 0.0418 | 0.0165 | -0.0518 | 0.357\*\* |
| Maturity period | -0.3117 | **-0.347** | 1.0177 | -0.0065 | 0.1415 | 0.0300 | 0.0139 | -0.102 | 0.435\*\* |
| Grain filling period  | -0.2521 | -0.2181 | **1.0769** | -0.1912 | 0.2250 | 0.0154 | 0.0087 | -0.1266 | 0.428\*\* |
| Grain filling rate  | 0.0123 | -0.0041 | 0.3747 | **-0.5495** | 1.3913 | -0.0017 | -0.0252 | -0.5276 | 0.670\*\* |
| Spike Number | -0.0523 | -0.0288 | 0.1421 | -0.4484 | **1.7050** | 0.0166 | -0.0146 | -0.9295 | 0.390\*\* |
| Spikelet number | -0.0512 | -0.0350 | 0.0560 | 0.0032 | 0.0954 | **0.2970** | 0.0607 | 0.2052 | 0.221 |
| Grain number | -0.0537 | -0.0434 | 0.0840 | 0.1242 | -0.2233 | 0.1613 | **0.1118** | 0.2791 | 0.440\*\* |
| 1000-grain weight  | -0.2496 | -0.3971 | 0.1421 | -0.3022 | 1.5621 | -0.2017 | -0.2325 | **0.1851** | 0.507\*\* |

\*\* =Significant at 1% level of probability, \* =Significant at 5% level of probability;

**4. Conclusion**

This study revealed significant genetic variation among 17 wheat genotypes for key morpho-physiological traits under AEZ-9 conditions in Bangladesh. High heritability and genetic advance for grain-filling rate, 1000-grain weight, and yield per plant suggest that these traits are primarily controlled by additive gene action, making them ideal for selection in breeding programs. Correlation and path analysis confirmed that grain-filling rate, spike number, and days to maturity positively influenced yield, with grain-filling rate showing the strongest direct effect. These findings emphasize the importance of grain-filling rate and spike number as selection criteria for wheat improvement. Future breeding efforts should focus on these traits to develop high-yielding, stress-tolerant wheat varieties, ensuring greater productivity and adaptability under variable environmental conditions.

**References**

[1] Acevedo, M., Zurn, J., Molero, G., Kumar Singh, P., He, X., Aoun, M., Juliana, P., Bockleman, H., Bonman, M., El-Sohl, M., Amri, A., Coffman, R., & McCandles, L. (2018). The role of wheat in global food security (pp. 81–110). <https://doi.org/10.4324/9780203733301-4>

[2] Plourde, A. (2023). Wheat (pp. 121–130). Elsevier eBooks. <https://doi.org/10.1016/b978-0-323-95295-8.00027-7>

[3] Curtis, T., & Halford, N. G. (2014). Food security: The challenge of increasing wheat yield and the importance of not compromising food safety. The Annals of Applied Biology, 164(3), 354–372. <https://doi.org/10.1111/aab.12108>

[4] Hossain, A., & Teixeira da Silva, J. A. (2013). Wheat production in Bangladesh: Its future in the light of global warming. AoB PLANTS, 5, pls042. <https://doi.org/10.1093/aobpla/pls042>

[5] Koyun, H., Koncagül, S., & Karakuş, K. (2016). Significance of Genetic Diversity in Farm Animal Production.

[6] Liu, J., Wang, D., Li, M., Jin, M., Sun, X., Pang, Y., Yan, Q., Liu, C. M., & Liu, S. (2024). QTL Mapping for Agronomic Important Traits in Well-Adapted Wheat Cultivars. Agronomy, 14(5), 940. <https://doi.org/10.3390/agronomy14050940>

[7] Ali, Y., Atta, B. M., Akhter, J., Monneveux, P., & Lateef, Z. (2008). Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm.

[8] UNDP, F. (1988). Land resources appraisal of Bangladesh for agricultural development. *Report*, *2*, 212-221.

[9] Kretz, R. (1974). Physical Constants of Minerals in West, RC, ed. Handbook of chemistry and physics. Chemical Rubber Co, 55, B193-B197.

[10] Cresswell, H. P., & Hamilton, G. (2002). Particle size analysis. In N. J. McKenzie, H. P. Cresswell, & K. J. Coughlan (Eds.), Soil physical measurement and interpretation for land evaluation (pp. 224–239). CSIRO Publishing.

[11] Michael, A. M. (1965). Determination of soil pH by glass electrode pH meter. Journal of Agricultural Science, 65(2), 143-145.

[12] Walkley, A., & Black, I. A. (1934). An examination of the Degtjareff method for determining soil organic matter, and a proposed modification of the chromic acid titration method. Soil Science, 37(1), 29-38.

[13] Bremner, J. M., & Mulvaney, C. S. (1982). Nitrogen-total. In A. L. Page, R. H. Miller, & D. R. Keeney (Eds.), Methods of Soil Analysis. Part 2. Chemical and Microbiological Properties (pp. 595-624). American Society of Agronomy, Soil Science Society of America.

[14] Olsen, S. R., Cole, C. V., Watanabe, F. S., & Dean, L. A. (1954). Estimation of available phosphorus in soils by extraction with sodium bicarbonate. U.S. Department of Agriculture Circular, (939).

[15] Knudsen, D., Peterson, G. A., & Pratt, P. F. (1982). Lithium, sodium, and potassium. In A. L. Page, R. H. Miller, & D. R. Keeney (Eds.), Methods of Soil Analysis. Part 2. Chemical and Microbiological Properties (pp. 225-246). American Society of Agronomy, Soil Science Society of America.

[16] Williams, C. H., & Steinbergs, A. (1959). Soil sulphur fractions as chemical indices of available sulphur in some Australian soils. Australian Journal of Agricultural Research, 10(3), 340-352.

[17] Kalambe, N. (2021). Estimation of zinc from soil sample.

[18] Hossain, M. M., Rana, M. S., Nasim, M. R., Rahaman, S., Jote, J. F., Shahrin, K. R., Begum, M., & Hasan, A. K. (2024). Optimizing Wheat Growth and Yield: The Synergistic Effects of Nitrogen and Silicon Levels. Asian Journal of Research in Crop Science, 9(4), 185–195. <https://doi.org/10.9734/ajrcs/2024/v9i4310>

[19] Rana, M. S., Ahmed, M., Nasim, M. R., Hossain, M. M., Jolly, N. Y., Shahrin, K. R., Hoque, M. A., Kader, M. A., & Hasan, A. K. (2024). Effect of Sowing Date and Plant Growth Regulators on Growth and Yield Attributes of Wheat (Triticum aestivum L.) Grown at AEZ-9 of Bangladesh. Asian Journal of Research in Crop Science, 9(4), 215–227. https://doi.org/10.9734/ajrcs/2024/v9i4312

[20] Ahmmed, S., Jahiruddin, M., Razia, M. S., Begum, R. A., Biswas, J. C., Rahman, M., Ali, M. M., Islam, S. K., Hossain, M. M., Gani, N., Hossain, G. A., & Satter, M. A. (2018). Fertilizer recommendation guide–2018. Bangladesh Agricultural Research Council (BARC), Farmgate, Dhaka.

[21] Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans.

[22] Burton, G. W., & De Vane, D. E. (1953). Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material.

[23] Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza 1. Agronomy journal, 48(6), 268-272.

[24] Comstock, R. E., & Robinson, H. F. (1952). Estimation of average dominance of genes. Heterosis, 2, 494-516.

[25] Singh, S. K., Singh, V. P., Srivastava, S., Singh, A. K., Chaubey, B. K., & Srivastava, R. K. (2018). Estimation of correlation coefficient among yield and attributing traits of field pea (*Pisum sativum* L.). Legume Research-An International Journal, 41(1), 20-26.

[26] Dewey, D. R., & Lu, K. (1959). A correlation and path‐coefficient analysis of components of crested wheatgrass seed production 1. Agronomy Journal, 51(9), 515-518.

[27] Singh, R. K., & Chaudhary, B. D. (1981). Biometrical methods in quantitative genetic analysis.

[28] Gomez, K. A., & Gomez, A. A. (1984). Statistical procedures for agricultural research. John Wiley & sons.

[29] Giménez, V. D., Serrago, R. A., Abeledo, L. G., Ciampitti, I. A., & Miralles, D. J. (2024). Comparative analysis of wheat and barley yield performance across temperate environments. <https://doi.org/10.1016/j.fcr.2024.109339>

[30] Das, N., & Biswas, P. S. (2017). Molecular Characterization of Parental Lines of Rice Aiming to Address High Yield and Nutritional Quality Under Drought and Cold Stress Condition. 4(2), 51–60. <https://doi.org/10.18488/JOURNAL.68.2017.42.51.60>

[31] Ndlovu, N., Gowda, M., Beyene, Y., Chaikam, V., Nzuve, F. M., Makumbi, D., McKeown, P. C., Spillane, C., & Prasanna, B. M. (2024). Genomic loci associated with grain yield under well-watered and water-stressed conditions in multiple bi-parental maize populations. Frontiers in Sustainable Food Systems. <https://doi.org/10.3389/fsufs.2024.1391989>

[32] Patial, M., Kumar, M., Bishnoi, S. K., Pal, D., Pramanick, K. K., Shukla, A. K., & Gandhi, S. (2023). Genetic variability and trait association for grain yield in barley (*Hordeum vulgare* L.). Journal of Cereal Research, 15(2). <https://doi.org/10.25174/2582-2675/2023/133530>

[33] Shankar, K., Suresh, G., Tiwari, N., & Ajmera, S. (2024). Analysis of Genetic Variability, Heritability and Genetic Advance for Yield and Yield-related Traits of Linseed (*Linum usitatissimum* L.). Journal of Advances in Biology & Biotechnology, 27(10), 1596–1604. <https://doi.org/10.9734/jabb/2024/v27i101584>

[34] Bharali, V., Yadla, S., Fiyaz, R. A., Rao, V. S., & Jukanti, A. K. (2024). Genetic inheritance studies in rice (*Oryza sativa* L.) for grain protein, quality and yield. *Electronic Journal of Plant Breeding*, *15*(3), 604–611. <https://doi.org/10.37992/2024.1503.079>

[35] Abd El-Mohsen, Ashraf A., S. R. Abo Hegazy, and Moemen H. Taha. "Genotypic and phenotypic interrelationships among yield and yield components in Egyptian bread wheat genotypes. J." Plant Breed. Crop Sci 4.1 (2012): 9-16.

[36] Surin, S., Verma, N., Bhargaw, P. K., Kumari, M., & Mishra, D. K. (2024). Studies on Genetic Variability, Correlation and Path Coefficient Analysis for Yield and Yield Contributing Traits in Bread Wheat (*Triticum aestivum* L.). *Journal of Experimental Agriculture International*. <https://doi.org/10.9734/jeai/2024/v46i62490>

[37] Han, Y., Zhao, P., Zhao, Y., Liu, M., Guo, E., Wang, G., & Zhang, A. (2024). Transcriptome Sequencing and Metabolome Analysis Reveals the Regulatory and Molecular Mechanism of Grain Filling Rate in Foxtail Millet (*Setaria italica* L.). <https://doi.org/10.20944/preprints202404.1190.v1>

[38] Knezevic, Desimir, Adriana Radosavac, and Milica Zelenika. "Variability of grain weight per spike in wheat grown in different ecological conditions." Acta Agriculturae Serbica 20.39 (2015): 85-95.