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# Study of genetic parameters and correlations in bread wheat (*Triticum aestivum* L.)

**Saif Saadoun Mohammed[1], Zakariya Bader Al Hamdani[1]***
*Field Crops Department, College of Agricultural and Forestry, University of Mosul, Iraq.*
* *Corresponding author: E-mail:* zakria-bader@uomosul.edu.iq

**ABSTRACT**

The experiment was conducted during the 2023/2024 agricultural season in Al-Qubba village, north of Mosul, to evaluate the performance of ten bread wheat genotypes and their response to nitrogen fertilization in terms of growth and yield traits. A randomized complete block design with a split-plot arrangement was used. Three nitrogen levels (0, 120, 240 kg/ha of urea 46%) were assigned to main plots, and ten wheat genotypes (14BAASH-, AZAD-2, BAOBAB-1, ASEEL-1, Ibaa99, Buhuth22, Mawaddah, Adana99, Baghdad1, Jihan99) were allocated to subplots. Measured traits included plant height, flag leaf area, tiller , spike number-m2, spike length, days to 50% physiological maturity, grains spike-1, 1000-grain weight, biological and grain yield, harvest index, and protein content.Analysis of variance showed that nitrogen levels significantly affected all traits at the 1% level. Genotypic differences were also significant at 1% for most traits, except flag leaf area and harvest index, which were significant at 5%. The interaction between genotypes and nitrogen levels was significant for all traits except spike length., environmental, and phenotypic variances were all greater than zero. Heritability values were generally low, except for moderate values in spike number/m-2and grain yield. The highest phenotypic and environmental coefficients of variation were observed for grain yield and harvest index, while phenotypic coefficients were consistently higher than genetic ones, indicating strong environmental influence on trait expression.

**KEYWORDS:** Bread wheat; Genetic parameters; correlations.

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# دراسة بعض المعالم الوراثية وارتباطاتها الوراثية والمظهرية في حنطة الخبز

سيف سعدون محمد[1]، زكريا بدر الحمداني[1]
قسم المحاصيل الحقلية، كلية الزراعة والغابات، جامعة الموصل، الموصل، العراق.

**الملخص**

أُجريت التجربة خلال الموسم الزراعي 2024/2023 في قرية القبة، شمال الموصل، لتقييم أداء عشرة طرز وراثية من قمح الخبز واستجابتها للتسميد النيتروجيني من حيث صفات النمو والإنتاجية. استُخدم تصميم القطاعات الكاملة العشوائية بترتيب الالواح المنشقة. تم تعيين ثلاثة مستويات من النيتروجين (0، 120، 240 كجم / هكتار من اليوريا 46٪) إلى الالواح الرئيسية، وتم تخصيص عشرة تراكيب وراثية من الحنطة (BAASH-14، **AZAD-2**، **BAOBAB-1**، **ASEEL-1**، **Ibaa99**، **Buhuth22**، **Mawaddah**، **Adana99**، **Baghdad1**، **Jihan99**) إلى لالواح الثانوية و تم قياس الصفات الاتية : ارتفاع النبات، ومساحة ورقة العلم، وعدد الاشطاء وعدد السنابل في المتر المربع، وطول السنبلة، وعدد الأيام 50٪ من النضج الفسيولوجي، وعدد الحبوب لكل سنبلة، ووزن 1000 حبة، والمادة الجافة الكلية (الحاصل البايلوجي) وحاصل الحبوب، دليل الحصاد، ومحتوى البروتين. أظهرت نتائج تحليل التباين أن مستويات النيتروجين أثرت بشكل كبير على جميع الصفات عند مستوى 1٪. كانت الاختلافات الوراثية معنوية أيضًا عند 1٪ لمعظم الصفات، باستثناء مساحة ورقة العلم ودليل الحصاد، والتي كانت معنوية ؟ عند 5٪. كان التداخل بين التراكيب الوراثية ومستويات النيتروجين معنويا لجميع الصفات باستثناء طول السنبلة. كانت جميع التباينات الوراثية والبيئية والظاهرية أكبر من الصفر، كان قيم التباين البيئي أكبر من الوراثي. وكانت قيم الوراثة منخفضة عمومًا، باستثناء قيم متوسطة في عدد السنابل/م$^2$ وإنتاجية الحبوب. ولوحظت أعلى معاملات تباين ظاهرية وبيئية في إنتاجية الحبوب ومؤشر الحصاد، بينما كانت المعاملات الظاهرية أعلى باستمرار من المعاملات الوراثية، مما يشير إلى تأثير بيئي قوي على التعبير عن الصفات.

**الكلمات المفتاحية:** حنطة الخبز؛ المعايير الوراثية؛ الارتباطات.

# INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the most important strategic crops worldwide. It is considered one of the major cereal crops in terms of cultivated area and production, and serves as a vital food source for more than one-third of the world's population, playing a significant role in achieving food security. Wheat is the primary source of energy required by humans due to its balanced composition of proteins and carbohydrates in its grains (Al-Dawoodi & Al-Obaidi, 2014).In 2024, Iraq's wheat production reached approximately 6.5 million tons (FAO Iraq).

Nitrogen fertilizer is among the most important factors that contribute to the growth and productivity of wheat. Nitrogen is one of the most essential nutrients required by plants (Ehsan, 2014). Its availability in the soil in adequate quantities is crucial for achieving good yield (Mohammed et al., 2018). It plays a key role in enhancing photosynthesis, dry matter accumulation, and is essential during various plant growth stages, contributing to increased grain yield (Hassanein, 2020). Nitrogen is also vital in plant nutrition as it is involved in the synthesis of amino acids and proteins (Al-Mawsili, 2016), and increases the protein content in grains and flour by enhancing gluten levels (Al-Ani et al., 2017; Sadiq et al., 2017).Therefore, plant breeders focus on developing and improving high-yielding and resistant genotypes and adapting them to local environments, in addition to improving their quantitative and qualitative traits. Genetic parameters and phenotypic and genotypic variances are considered the foundation for improving any plant population through selection, hybridization, or both (Kaya & Akcura, 2014). Genetic improvement depends on the heritability of traits passed on to progeny. Some growth and yield traits can be estimated under different environmental conditions by evaluating their genotypic and phenotypic traits and the strength of their correlations (Crespo et al., 2017). Heritability is among the most important genetic parameters for selected traits in any breeding program. It influences the expected genetic gain from selection. High heritability of good traits associated with yield does not guarantee the desired genetic gain unless there is a strong and significant positive correlation. (Praveenkumar et al, 2025) indicated the importance of identifying traits affecting yield using different statistical methods, including phenotypic and genotypic correlation coefficients, which show the relationship between yield and its components and among the components .This study aims to estimate several genetic parameters, including phenotypic, environmental, and genotypic variances, as well as broad-sense heritability and phenotypic and genotypic coefficients of variation for several yield-related traits under different nitrogen levels or selection indices influenced by them, in order to improve wheat grain yield through the estimation of broad-sense heritability of the studied traits. Wheat protein is used in the diets of patients who need a rich plant-based source of protein.( Mahmood et al., 2025) It helps promote wound healing and supports the immune system due to its content of important amino acids such as glutamine.( Laidig et al., 2017).

## MATERIALS AND METHODS

The experiment was conducted during the 2023/2024 agricultural season, starting on December 1, 2023, in the village of Al-Qubbah, located in Tel Kaif district, approximately 17 km north of Mosul city. The experiment used a Design (RCBD) with a split-plot arrangement and three replications.

The study involved two factors. The first factor included three nitrogen levels using urea (46% N) at rates of 0, 120, and 240 kg/ha, applied in the main plots. The urea was split into two applications: half after seedling emergence and the other half at the tillering stage. The second factor consisted of ten bread wheat genotypes listed in Table (1), which were assigned to the subplots. Each replication included 30 experimental units resulting from the combinations of the two factors. Each subplot consisted of four rows, each three meters long, with 0.20 m spacing between rows, and a seeding rate of 120 kg/ha (adjusted for each genotype based on weigh1000 grain(g)(Briggs and Aytentefisn ,1980).

Agronomic practices such as irrigation and pest control were carried out as needed. Samples from ten randomly selected plants from the middle rows were taken to measure growth and yield traits.

**Table 1.** Names and Origins of the Wheat Genotypes

| **No.** | **Genotype Name** | **Pedigree/ Source** |
|---|---|---|
| 1 | BAOBAB-1 | MLAN/PASTOR |
| 2 | BAASHA-14 | MLAN/PASTOR |
| 3 | ASEEL-1 | MLAN/PASTOR/3/SHAMISS-3 |
| 4 | AZD-2 | PFAU/MILAN |
| 5 | Mawaddah | Seed Certification / Nineveh |
| 6 | Buhuth 22 | Seed Certification / Nineveh |
| 7 | Ibaa 99 | Seed Certification / Nineveh |
| 8 | Baghdad 1 | Seed Certification / Nineveh |
| 9 | Adna 99 | Seed Certification / Nineveh |
| 10 | Jehan | Seed Certification / Nineveh |

**Studied Traits**

Plant Height (cm): Measured at the physiological maturity stage from the soil surface to the top of the spike excluding the awns.‹Flag Leaf Area ($cm^2$): Calculated from the average of ten flag leaves taken from the main stem of each experimental unit using the following formula (Thomas, 1975:(

Flag Leaf Area = Flag Leaf Length × Maximum Width × Correction Factor (0.95)‹Number of Tillers (per $m^2$): Counted in one row and converted to tillers per square meter, then the average of two middle rows in the experimental unit was taken.‹Number of Spikes (per $m^{-2}$): Counted within one square meter area from the center of each experimental unit.‹Spike Length (cm): Measured from the base to the tip of the spike including the awns, at full spike maturity.‹Days from Sowing to 75% anthesis : The number of days from sowing until 75% of the plants reached anthesis .‹Number of Grains per

Spike: Calculated from the mean of ten randomly selected spikes from each experimental unit ‹1000-Grain Weight (g): One thousand grains were counted from each experimental unit and weighed using a precision balance ‹Biological Yield (g/m²): Total weight of the whole plant (straw + grains) taken from the middle rows, converted to per square meter (Al-Haidari & Al-Baldawi, 2010)‹Grain Yield (g/m2): Grain weight taken from the middle rows and converted to per square meter ‹Harvest Index (%): Calculated as a percentage using the formula: Harvest Index = (Grain Yield / Biological Yield) × 100 ‹ Protein Content (%): Protein percentage was estimated at the laboratory department, Directorate of Agriculture, Nineveh, using a German-made Informatics 8600 device. The device was calibrated and measurements taken from 20g of milled grain sample, and the protein content was read from the device's digital screen.

Statistical and Genetic Analysis of Studied Traits

The following statistical and genetic analysis were conducted: Analysis of variance (ANOVA) of genotypes under different nitrogen fertilization levels using the split-plot design method (Al-Falahy & Al-Zubaidi, 2016)‹Estimation of phenotypic variance components (genotypic, environmental, and interaction) for the proposed traits (Al-Zubaidi & Al-Jubouri, 2016) ‹Estimation of broad-sense heritability for the studied traits. ‹ Estimation of expected genetic gain as a percentage. Estimation of phenotypic and genotypic coefficients of variation ‹Estimation of phenotypic and genotypic correlations.

Estimation of Phenotypic Variance and Its Components:

Phenotypic variance ($\sigma^2$ph) and its components‹genetic ($\sigma^2$g), environmental ($\sigma^2$e), and interaction between genotypes and nitrogen levels ($\sigma^2$gf) – were estimated based on the expected mean square components from the ANOVA table using the following formulas:

$$: \sigma^2 g = (MSg - Mse)/rf; \sigma^2\, gf = (MSgf - MSe)/r; \sigma^2\, e = MSe$$

where MSg, MSgf, and MSe are the estimated mean squares for each genotype, the interaction of genotypes with nitrogen fertilizer levels, and the experimental error, respectively. r is the number of‹replications g is the number of genotypes, and f is the number of nitrogen fertilizer levels. The significance of the three phenotypic variance components (sigma $\sigma^2$e, $\sigma^2$ gf, and $\sigma^2$ g) was tested for zero using Kempthorne's (1957) method, which was explained by Al-Zubaidi and Al-Jubouri (2016). This was done by calculating the variance of each of these variances, and from their square root, the genetic (g) SE, interaction (SE(gf), and environmental (SE(E) standard errors were obtained, as shown in the following equations:

$$SE(\sigma^2 G) = \sqrt{\frac{1}{r^{2f\,2^2}}\left[\frac{2(msg)^2}{k+2} + \frac{2(mse)^2}{k+2}\right]}$$

$$SE(\sigma^2 Gf) = \sqrt{\frac{1}{r^2}\left[\frac{2(msgf)^2}{k+2} + \frac{2(mse)^2}{k+2}\right]}$$

$$SE(\sigma^2 E) = \sqrt{\frac{2(mse)^2}{k+2}}$$

K = degrees of freedom for the target source of variation

Genetic parameter estimation

Broad-sense heritability (($H^2_{b.s}$)

Broad-sense heritability ($H^2_{b.s}$) was estimated according to the equation proposed by Falconer and Mackay (1996): $H2b.s = \sigma 2g/\sigma 2p$.

The significance of broad-sense heritability was expressed according to the scale explained by Ali (1999) (less than 40% low, 40 to 60% medium, and greater than 60% high).

Expected Genetic Improvement (EGA)

Expected genetic improvement in the next generation (EGA), which Falconer and Mackay (1996) termed the response to selection and expressing the difference between the mean of the offspring population resulting from selection and the mean of the original population, was estimated for each trait using the equation proposed by Allard (1961):

$EGA = (i)(h^2 bs)(\sigma\, ph)$ i = the intensity of selection, equal to 2.06 at

The expected genetic improvement from selection was estimated as a percentage of the mean for the trait (ȳ) using the equation presented by Kempthorne (1969), as follows:

$EGA\% = (EGA\ /\ \bar{y})\ x\ 100$ = [(i)($h^2$ b.s)(σph) / ȳ] x 100

The limits for expected genetic improvement were adopted as a percentage, as proposed by Agarwal and Ahmad (1982), as follows: less than 10% is low, between 10% and 30% is medium, and more than 30% is high.

Genetic and Phenotypic Coefficients of Variability (GCV)

The coefficient of variability (COV) in its genotypic and phenotypic forms is defined as the standard deviation (σg or σp), respectively, expressed as a percentage of the mean (ȳ) for the target trait. The following equations, proposed by Moll and Dudly (1952) and Burton (1969), can be used to calculate the COV, respectively:

$GCV = (\sigma g \,/\, \bar{y})\, x\, 100; PCV = (\sigma P \,/\, \bar{y})\, x\, 100$

where

σg = the genetic standard deviation.

σp = the phenotypic standard deviation.

ȳ = the mean for the trait

Genotypic and phenotypic correlations (g) and r for grain yield of a plant with some of its components

The Genotypic and phenotypic correlation coefficients for grain yield and each of its components: number of spikes/m, number of grains per spike, 1000-grain weight, biological yield ($gm^2$), and grain yield ($g/m^2$) were estimated by adopting the results of analysis of variance for these traits

and analysis of covariance, then applying the following two equations (Walter, 1975): were

σg x y = Common genetic variation between the two traits

σph xy = The phenotypic variance shared between the two traits

$\sigma^2$g = Genotypic variation is a trait

$\sigma^2$ph = Phenotypic variation of any

$$rG = \frac{\sigma gxy}{\sqrt{\sigma^2 \text{gx}.\sigma^2 \text{gy}}} \; ; \; rp = \frac{\sigma ph \times y}{\sqrt{\sigma^2 phx.\sigma^2 phy}}$$

## RESULTS AND DISCUSSION

Table (2) shows the results of the analysis of variance for grain yield traits and their components in wheat. It is noted that the mean squares of fertilization levels and genotypes showed significant differences at a 1% probability level for all studied traits, with the exception of flag leaf area (cm2), number of days from sowing to physiological maturity, and harvest index (%). For genotypes, the interaction between the two factors was significant at a 1% probability level for all studied traits, with the exception of flag leaf area (cm2) and harvest index (%), which were significant at a 5% probability level. However, spike length (cm) did not reach the statistical significance level. This means that the cultivars behaved differently at the levels of added nitrogen fertilizer. These results are consistent with Baber et al. (2024) and Mohammad et al. (2024).

**Table 2.** Results of the analysis of variance for the studied traits.

| Source of Variation | D.F | Days to Physiological Maturity | Plant Height (cm) | Flag Leaf Area (cm$^2$) | Number of Branches/m$^2$ | Number of Saplings/m$^2$ | Spike Length (cm) |
|---|---|---|---|---|---|---|---|
| Blocks | 2 | 44.877 | 291.647 | 33.845 | 2922.411 | 11235.144 | 2.212 |
| Fertilization Levels | 2 | 17.244** | 378.091 | 319.710** | 27623.411** | 53732.211** | 6.931** |
| Error A | 4 | 13.811 | 39.717 | 9.922 | 1367.977 | 2705.161 | 0.406 |
| Genotypes | 9 | 10.513* | 181.131 | 32.319** | 9736.222* | 7586.080** | 5.889** |
| genotypes × Fertilization levels | 18 | 15.009** | 90.918 | 30.379** | 6068.225* | 2181.902** | 1.420** |
| Error B | 54 | 4.204 | 28.720 | 14.463 | 2122.411 | 902.809 | 0.964 |

Significant at 1% and 5% probability levels, respectively.(*) and (**)

**Follow Table 2.** Results of the analysis of variance for the studied traits.

| Source of Variation | D.F | Number of Grains/Spike | 1000-Grain Weight | Biological Yield (g/m$^2$) | Grain Yield (g/m$^2$) | Harvest Index (%) | Protein (%) |
|---|---|---|---|---|---|---|---|
| Blocks | 2 | 88.707 | 7.644 | 35724.033 | 32467.676 | 112.914 | 0.668 |
| Fertilization Levels | 2 | 102.014$^{**}$ | 73.677$^{**}$ | 103326.633$^{**}$ | 227642.309$^{**}$ | 1092.963$^{**}$ | 1.135$^{**}$ |
| Error A | 4 | 4.590 | 3.477 | 7818.116 | 8963.671 | 66.179 | 0.058 |
| genotypes | 9 | 49.970$^{**}$ | 25.912$^{**}$ | 47398.982$^{**}$ | 28081.181$^{**}$ | 137.040$^{*}$ | 1.100$^{**}$ |
| genotypes × Fertilization Levels | 18 | 48.679$^{**}$ | 19.060$^{**}$ | 44846.275$^{**}$ | 11669.816$^{**}$ | 239.082$^{**}$ | 0.796$^{**}$ |
| Error B | 54 | 15.294 | 7.088 | 6808.015 | 4628.163 | 54.720 | 0.178 |

Significant at 1% and 5% probability levels, respectively.(*) and (**)

### Components of phenotypic variance:

Table (3) shows the phenotypic variances and their genetic, environmental, and shared components. It is noted that the values of genetic variance, shared variance, and environmental variance were significantly greater than zero for all studied traits, and that the values of environmental variance were higher than the values of genetic variance and shared variance. These results are consistent with (Hamza et al. 2020).

**Table 3.** Components of phenotypic Genotypic variances and standard error of the studied traits.

| **Genetic Parameters** | **Number of days from planting to physiological maturity** | **Plant height(cm$^2$)** | **flag leaf area (cm$^2$)** | **Number of branches/m$^2$** | **Number of saplings/m$^2$** | **Spike length/cm** |
|---|---|---|---|---|---|---|
| Genotypic variation | 0.701 | 16.935 | 1.984 | 845.967 | 742.586 | 0.547 |
| | ±0.506 | ±8.603 | ±1.561 | ±463.430 | ±359.912 | ±0.280 |
| Covariance | 3.602 | 20.733 | 5.305 | 1315.236 | 426.364 | 0.152 |
| | ±1.604 | ±9.753 | ±3.329 | ±653.472 | ±236.920 | ±0.162 |
| Environmental variation | 4.204 | 28.720 | 14.463 | 2122.517 | 902.810 | 0.965 |
| | ±0.794 | ±5.428 | ±2.733 | ±401.118 | ±170.615 | ±0.182 |
| Phenotypic variation | 8.507 | 66.387 | 21.753 | 4283.721 | 2071.760 | 1.664 |
| | ±1.608 | ±9.896 | ±4.111 | ±809.547 | ±391.526 | ±0.314 |

| **Genetic Parameters** | **Number of grains/spike** | **weight of 1000 grains** | **biological yield (g/m$^2$)** | **grain yield (g/m2)** | **harvest index (%)** | **Protein%** |
|---|---|---|---|---|---|---|
| Genotypic variation | 3.853 | 2.091 | 4510.108 | 2605.891 | 9.147 | 0.102 |
| | ±2.389 | ±1.237 | ±2250.212 | ±1333.973 | ±6.594 | ±0.052 |
| Covariance | 11.128 | 3.991 | 12679.420 | 2347.214 | 61.454 | 0.206 |
| | ±5.221 | ±2.058 | ±4746.626 | ±1264.184 | ±25.436 | ±0.085 |
| Environmental variation | 15.295 | 7.089 | 6808.015 | 4628.167 | 54.721 | 0.178 |
| | ±2.890 | ±1.340 | ±1286.594 | ±874.641 | ±10.341 | ±0.034 |
| Phenotypic variation | 30.276 | 13.171 | 23997.543 | 9581.272 | 125.322 | 0.487 |
| | ±5.722 | ±2.489 | ±4535.109 | ±1810.690 | ±23.684 | ±0.092 |

### Genetic parameters (broad-sense heritability, expected genetic improvement, and genetic and phenotypic coefficients of variation)

Table (4) shows that the degree of broad-sense heritability ranges from 0.073 for the trait (harvest index%) to 0.35 for the trait (number of spikes/m$^{-2}$). This is low for all traits. This indicates the appropriate breeding method for the genotypes, as the parents inherited the traits at low levels to the offspring. Therefore, we use the hybridization method to breed these genotypes. Meanwhile, the expected genetic improvement, as a percentage of the average, ranged from 0.307% for the trait (number of days from planting to physiological maturity) and 13.006% for the grain yield ($g/m^2$). The values were low for the traits (flag leaf area, number of grains per spike, harvest index%, and protein content).

Average values were recorded for the traits number of tillers/$m^{-2}$, spike length/$cm^{-1}$, 1000-grain weight, and number of spikes/$m^{-2}$, and high for the trait biological yield ($g/m^{-2}$). From the above, it is clear that the expected genetic improvement as a percentage was between low and medium for all traits. Based on these results, it is likely that genetic improvement for these traits will be achieved in the next selection cycle. Researchers who obtained expected genetic improvement ranged between high, medium, and low. The values of the phenotypic coefficient of variation were higher than the values of the genetic coefficient of variation for all the traits studied, and the highest values for the phenotypic and genetic coefficients of variation were for the traits harvest index (%) and grain yield ($g/m^{-2}$). This is consistent with (Hussanin et al. 2020) and (Abbas et al. 2020).

**Table 4.** Components of phenotypic variance and genetic parameters of the studied traits.

| **Genetic parameters** | **Number of days from planting to physiological maturity** | **Plant height(cm2)** | **flag leaf area ($cm^2$)** | **Number of branches/$m^2$** | **Number of saplings/$m^2$** | **Spike length/cm** | **Number of grains/spike** | **weight of 1000 grains** | **biological yield (g/m2)** | **grain yield (g/m2)** | **harvest index (%)** | **Protein%** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| broad sense | 0.082 | 0.255 | 0.091 | 0.197 | 0.358 | 0.329 | 0.127 | 0.159 | 0.188 | 0.272 | 0.073 | 0.210 |
| G.A | 0.495 | 4.282 | 0.876 | 26.626 | 33.608 | 0.874 | 1.442 | 1.187 | 59.975 | 54.842 | 1.683 | 0.302 |
| %G.A | 0.307 | 4.315 | 1.838 | 7.581 | 12.481 | 7.619 | 3.319 | 3.309 | 6.076 | 13.006 | 3.911 | 3.198 |
| PCV | 1.811 | 8.211 | 9.781 | 18.635 | 16.903 | 11.246 | 12.659 | 10.115 | 15.693 | 23.214 | 26.012 | 7.376 |
| GCV | 0.520 | 4.147 | 2.954 | 8.281 | 10.120 | 6.449 | 4.516 | 4.031 | 6.803 | 12.106 | 7.028 | 3.384 |

Table (5) shows the genetic and phenotypic correlation coefficients between the studied pairs of traits. It is generally noted that the values of the two types of correlation were close in direction (direct or inverse) in most cases, and that the genetic correlations were more valuable than the phenotypic ones in most of them. It is noted that the grain yield trait had a positive and significant genetic correlation at a probability level of 1% for the traits of number of spikes/m$^2$, number of grains per spike, and biological yield g/m$^2$, and the trait of 1000-grain weight( g) did not reach the significance level. As for the phenotypic correlation for the trait of grain yield g/m$^2$, it was positive and significant with the traits of number of spikes/m$^2$, number of grains per spike, and 1000-grain weight (g), and did not reach the significance level for the trait of biological yield g/m$^2$, while the trait of biological yield showed. g/m$^2$ showed a positive and significant genetic correlation with the number of spikes/m$^{-2}$ and the number of grains per spike at the probability level of 1%, but did not reach the level of significance for the trait of 1000-grain weight (g). The phenotypic correlation of the trait of biological yield g/m$^2$ was not significant with the rest of the traits (negative or positive). As for the trait of 1000-grain weight (g), it did not show a genetic or phenotypic correlation with the traits of number of spikes/m$^2$ and number of grains per spike (negative or positive). As for the trait of number of grains per spike, it showed a positive genetic correlation at the probability level of 5% with the trait of number of spikes/m$^2$, and this trait did not show a significant phenotypic correlation with the trait of number of spikes/m$^2$., including Al-Mafarji & Al-Jubouri (2023), Shankar and others (2023), Emnadishetty and Gurjar (2022), Proveenkumar and others (2025).

**Table 5.** Genotypic (above diagonal) and phenotypic (below diagonal) correlation between yield and its components.

| **Traits** | **Number of spikes/m$^{-2}$** | **Number of grains per spike** | **1000-grain weight (g)** | **Biological yield (g/m$^{-2}$)** | **Grain yield (g/m$^{-2}$)** |
|---|---|---|---|---|---|
| Grain yield (g/m$^2$) | 0.880 ** | 0.620 ** | 0.168 | 0.914 ** | 1 |
| Biological yield (g/m$^2$) | 0.776 ** | 0.585 ** | 0.129 | 1 | 0.141 |
| 1000-grain weight (g) | -0.207 | 0.084 | 1 | 0.076 | 0.387** |
| Number of grains per spike | 0.306 * | 1 | 0.047 | -0.067 | 0.552** |
| Number of spikes/m$^2$ | 1 | 0.050 | -0.066 | 0.181 | **0.733 |

(*) and (**) are significant at 1% and 5% probability levels, respectively.

## CONCLUSION

The present study revealed significant genetic variability among wheat genotypes and nitrogen fertilization levels for most agronomic traits, including grain yield and its components. Analysis of variance indicated highly significant effects of genotypes, fertilization levels, and their interaction, suggesting differential genotype responses to nitrogen availability. Genetic, phenotypic, and environmental variances were all significantly greater than zero, with environmental variance contributing more prominently, indicating the influence of environmental factors on trait expression.

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