Research Article

Performance Evaluation, Estimation of Genetic and Phenotypic Correlation Coefficients, and Path Coefficient Analysis of Quantitative Traits in Triticale Genotypes Grown under Different Seeding Rates

Hussein Ali Hindi[1], Liwaa Nahedh Faisal[2], Yaseen Obaid Noori Ahmed Sharif*[3] and Tariq Raad Thaer Al-Mafarji[4]

[1]Department of Field Crops, College of Agriculture, Tikrit University, Tikrit, Iraq; [2]Department Education. Samarra Industrial Secondary School. Salah al-Din Education Directorate . Vocationa. Ministry of Education. Iraq; [3]Department of Field Crops, College of Agriculture, Kirkuk University, Kirkuk, Iraq; [4]Department of Medicinal and Industrial Plants, College of Medicinal and Industrial Plants, University Kirkuk, Kirkuk, Iraq.

Abstract | This study was conducted on a sandy loam soil, to evaluate the performance, estimate certain genetic parameters, and perform path coefficient analysis of vegetative growth and yield traits for six Triticale genotypes (Triticosecale x Wittmack), namely Farah, Amal 7, Al-Muhand, LIRON 3, LIRON 4, and LIRON 6. The genotypes were sown at three seeding rates of 140, 160, and 180 Kg ha^{-1}. The experiment followed a randomized complete block design (R.C.B.D.) with three replications and split-plot arrangement, where seeding rates were assigned to main plots and genotypes to subplots. The results indicated that the seeding rate of 140 Kg ha^{-1} outperformed other rates for most studied traits, except total biological yield, which was higher at 160 and 180 Kg ha^{-1}. Among genotypes, Farah exhibited the highest means for grains per spike, biological yield, and grain yield. Grain yield showed significant positive phenotypic correlations with tiller number per m^2, spike length, and total biological yield. Path coefficient analysis revealed that grains per spike and 500-kernel weight had the greatest direct effects on grain yield.

Received | July 17, 2025; **Accepted** | October 17, 2025; **Published** | February 23, 2026
***Correspondence** | Yaseen Obaid Noori Ahmed Sharif, Department of Field Crops, College of Agriculture, Kirkuk University, Kirkuk, Iraq; **Email:** yaseenobaidnoori@uokirkuk.edu.iq
Citation | Hindi, H.A., L.N. Faisal. Y.O.N.A. Sharif and T.R.T. Al-Mafarji. 2026. Performance evaluation, estimation of genetic and phenotypic correlation coefficients, and path coefficient analysis of quantitative traits in triticale genotypes grown under different seeding rates. *Pakistan Journal of Agricultural Research,* 39(1): 77-88.
DOI | https://dx.doi.org/10.17582/j.pjar/2026/39.1.77.88
Keywords | Triticale, Genotypes, Seeding rates, Path coefficient analysis

Introduction

Triticale, also known as hexaploid wheat, represents a successful attempt by scientists to develop a man-made crop combining the traits of wheat (*Triticum*) and rye (*Secale*). This is achieved by chromosome doubling of the sterile hybrid to produce a polyploid plant. Triticale is characterized by a higher protein content and lysine level compared to wheat, with an increase of about 4% (Mohammed *et al.*, 2025).

This crop has numerous favorable features. It can be grown in areas that experience spotty rainfall, alongside barley or as a substitute for it, as it is better adapted to drought conditions. This is significant in areas plagued by limited rainfall during the winter growing months of the year, or with scarce water supplies stemming from the construction of dams and subsequent water releases stemming from international agreements. Triticale also performs well on soil that is not suitable for other crops such as sandy, highly acidic, and nutritionally deficient soil varieties (Ismail and Al-Fahady, 2012; Fayhaa *et al.*,2025; Mohammed *et al.*, 2025). Despite the fact that triticale contributes to economic returns and plays a dual role in crop production, Iraqi farmers have not given enough attention to its cultivation, which is rather being given to soft wheat, durum wheat, and barley. Even though the purchase of triticale is approved by the Iraqi Ministry of Trade at all silos in the country, the number of areas of cultivation has remained very limited, if not nonexistent. This reflects the need to encourage its cultivation and adopt scientific practices that ensure high productivity. Seeding rates are one of the most important of these practices; it establishes plant density and provides, under conditions of vegetative growth, an appropriate environment for the growth of the crop. The optimal rate reduces intraspecific competition, while during the grain-filling stage, it increases (Alnori and Ahmad, 2012; Younis and Al-Hasans, 2019).

The use of promising genotypes is a very important factor for increasing triticale grain yield. Introduction of new genotypes by insertion, along with exploiting genetic variation, is required to identify the most productive varieties in specified environmental conditions. A genotype that gives good performance in a specific environment might not yield under a similar intensity in another environment. Grain yield is a complex character in all breeding and improvement programs for triticale because it is governed by a large number of genes and highly influenced by environmental conditions (Al-Mafarji and Al-Jubouri, 2023a). The genetic and phenotypic correlation studies between grain yield and its components aim to determine the most influential characters and establish them as indicators for selection for improving the yield. There are two types of yield indicators used in this regard: direct indicators, represented by the estimates of heritability, and indirect indicators, such as correlation coefficients and path coefficient analysis (Mahmood *et al.*, 2025).

The objectives of the study are the evaluation of the productivity of tested genotypes, determination of the most promising ones, and specifying the best seeding rate that provides the highest grain yield. Determination of genetic and phenotypic correlations of certain growth traits and yield components with grain yield was also estimated in this paper, in addition to carrying out path coefficient analyses to identify the direct and indirect effects of the most influential traits on grain yield, thus enabling their adoption as effective selection indicators for improving triticale productivity.

Materials and Methods

A field experiment was conducted during the 2024–2025 winter cropping season at the Samarra Directorate of Agriculture Research Station, Salah Al-Din Governorate, located at 34.09° N latitude and 43.51° E longitude. The study aimed to evaluate the response of growth and yield traits of six Triticale (*Triticosecale × Wittmack*) genotypes to three seeding rates, estimate genetic parameters, and perform path coefficient analysis. The experiment included two factors: the first factor was three seeding rates (140, 160, and 180 Kg ha^{-1}), and the second factor was six Triticale genotypes, as detailed in Table 1.

Table 1: *Names, pedigree, and sources of Triticale genotypes.*

No.	Genotype	Pedigree	Source
1	Farah	LOCAL CHECK*	Ministry of Science
2	Amal 7	LOCAL CHECK*	Ministry of Science
3	Al-Muhand	LOCAL CHECK*	Ministry of Science
4	LIRON-3	LIRON_2/5/DIS B5/...	MXI07-08
5	LIRON-4	LIRON_2/5/DIS B5/...	MXI07-08
6	LIRON-6	LIRON_2/5/DIS B5/...	MXI07-08

Soil samples were randomly collected from different field locations at 30 cm depth before sowing to estimate physical and chemical properties, as shown in Table 2.

The experimental field was plowed using a moldboard plow, followed by disc harrowing. Each replication was divided into three main plots randomly assigned to the three seeding rates. Each main plot included

Table 2: *physical and chemical properties of field soil at 30 cm depth.*

Trait	pH	E.C	Available N	Available P	Available K	Organic matter	Sand	Clay	Silt	Texture
Unit	–	dS m^{-1}	mg kg^{-1} soil	mg kg^{-1} soil	mg kg^{-1} soil	%	%	%	%	–
Value	7.7	3.2	22	7	45	0.9	79.7	17.0	3.3	Sandy loam

six subplots randomly assigned to the six genotypes. Nitrogen fertilizer in the form of urea (N 46%) was applied at 200 Kg ha^{-1} in two splits: the first at sowing and the second 25 days after sowing. Phosphorus was applied as triple superphosphate (P2O5 46%) at 200 Kg ha^{-1} at soil preparation. Potassium was applied as potassium sulfate at 200 Kg ha^{-1} at soil preparation (Sebahi, 2011).

The weeds were controlled using a pesticide 2.4, D before planting (Sharif et al; 2024a).

Each main plot area was 12 m^2. Five rows were planted per experimental unit with 20 cm spacing between rows. Seeds were sown manually in each row. Each replication included 18 experimental units, totaling 54 units. Sowing was conducted on 25 November 2024. Irrigation was applied as needed, and weeds were removed manually. At full maturity (25 May 2025), experimental units were harvested, and the following traits were recorded:

Vegetative growth traits:

- Number of tillers per m^2 (X1)
- Flag leaf area (cm2) (X2)
- Days from sowing to maturity (X3)
- Spike length (cm) (X4)

Yield and yield components:

- Number of grains per spike (grain $spike^{-1}$) (X5)
- 500-kernel weight (g) (X6)
- Total biological yield (Kg ha^{-1}) (X7)
- Grain yield (Kg ha^{-1}) (X8)

Data were statistically analyzed using a randomized complete block design with split-plot arrangement. Means were compared using Duncan's multiple range test (Al-Rawi and Khalaf Allah, 2000).

Genetic analysis

Phenotypic and genetic correlation coefficients between traits and grain yield were estimated following (Walter, 1975) and tested for significance against tabulated r-values at the appropriate degrees of freedom. Path coefficient analysis was performed to determine direct and indirect effects of studied traits on grain yield according to (Al-Zubaidi and Al-Jubouri, 2016). The scale used for path effects is shown in Table 3.

Table 3: *Scale of path coefficient effects.*

Effect	Negligible	Low	Moderate	High	Very high
Value range	0–0.09	0.10–0.19	0.20–0.29	0.30–0.99	>1.00

Results and Discussion

Analysis of variance

The results of the analysis of variance (Table 4) showed that the effect of seeding rates was highly significant for all studied traits, except for days from sowing to maturity, which was significant at the 5% probability level. This is because seeding rate is a major factor influencing the optimal environment for crop growth by balancing plant competition, which affects vegetative growth and yield components (Al-Dahi, 2021; Sharif *et al*., 2024b).

The effect of genotypes was significant at 1% probability for most traits, except grain yield per unit area, which was significant at a lower level. This variation was ascribed to differences in the genetic makeup of the genotypes, which manifested in growth and yield attributes. This is in view of (Al-Dulaimi 2020; Alshamary *et al*., 2025). The interaction between the two factors was highly significant for most traits and statistically significant for days to maturity and spike length, while the number of grains per spike was not statistically significant. It follows, therefore, that the tested genotypes reacted to the three seeding rates differently, which consequently brought about variation in growth traits and grain yield components.

Total number of tillers (m^2)

It can be seen in Table 5 that as determined by Duncan's multiscale test, seeding rates, genotypes, and their interaction had a significant impact on the total number of tillers m^2. The highest average yield of 302.55 tillers m^2 was observed when the seeding rate was 140 kg ha^{-1}, whereas with a seeding rate of

Table 4: *Mean squares of the studied traits from ANOVA.*

M.S.								d.f	S.O.V
X8	X7	X6	X5	X4	X3	X2	X1		
7434.47	2022.22	0.143	0.629	1.46	5.01	1.02	10.720	2	R
*17706674.11	2099605.11**	34.79**	252.29**	74.12**	45.90*	276.99**	3148.38**	2	A
8263.30	97686.11	0.17	0.48	0.268	4.57	0.93	11.520	4	R(A)
683363.86*	5097373.33**	30.81**	164.11**	21.940**	11.84**	248.38**	6993.760**	5	B
218945.79**	398212.22**	0.25**	3.051	0.99*	1.32*	3.83**	352.58**	10	AB
33832.79	63184.81	0.08	1.642	0.400	0.566	0.539	27.548	30	Error

180 kg ha^{-1}, it followed with the least average yield of 276.11 tillers m^2. It is likely that because of the lower seeding rate, there was decreased competition for nutrients and environmental resources, which allowed for better vegetative growth, whereas a higher seeding rate reduced the number of lateral branches (Batool *et al*., 2022).

Table 5: *Effect of seeding rates, genotypes, and their interaction on total tiller number (m^2).*

Genotype	140 Kg ha^{-1}	160 Kg ha^{-1}	180 Kg ha^{-1}	Mean
Farah	345.00 a	311.33 ef	294.33 hi	350.22 a
Amal 7	331.00 b	330.33 b	300.00 ef	326.33 b
Al-muhand	310.67 cd	317.67 c	291.67 f	300.78 b
Liron-3	259.00 hij	253.00 jk	245.33 k	252.44 e
Liron-4	267.67 h	258.00 j	254.67 j	260.11 d
Liron-6	302.67 de	296.67 ef	281.67 g	293.67 c
Mean	302.55 a	288.83 b	276.11 c	$\bar{x}$=289.17

Observed significant differences between the means, with the highest average for Farah (350.22 tillers m^2). The most inferior, Liron-3, came up with the lowest average of 252.44 tillers m^2. In addition, this variation shows the genetic reason, whether the genotypes are responding to environmental and climatic conditions, referring to previous studies of Nwry *et al*., 2021.

In the case of interaction between seeding rates and genotypes, the mean for Farah × 140 kg ha^{-1} was highest (345.00 tillers m^2), while Liron-3 × 180 kg ha^{-1} recorded the minimum average under these conditions (245.33 tillers m^2).

Flag leaf area (cm^2)

Significant differences between the means of seeding rates, genotypes, and their interactions are indicated in Table 6 for flag leaf area. The highest mean (31.326 cm^2) was recorded for the 140 kg ha^{-1} rate, while the lowest mean (23.55 cm^2) was given by the 180 kg ha$^-$ rate. This has been attributed to increased leaf area at low seeding rates due to less intra-plant competition that enabled the plants to utilize the growth resources optimally. The above explanation is consistent with the findings by Shah *et al*. (2016).

The genetic differences between the genotypes were also highly significant, and the highest mean flag leaf area was seen in Farah with 34.828 cm^2, while the lowest, 21.293 cm^2, was seen in Liron-3. Indeed, these differences reflected genetic responses under favorable environmental conditions, as stated by Al-Mafarji and Al-Jubouri (2024).

The interaction of seeding rates and genotypes was also significant, and the highest flag leaf area was 39.350 cm^2 from Farah × 140 kg ha^{-1} while the lowest was 18.093 cm^2 belonging to Liron-3 × 180 kg ha^{-1}.

Table 6: *Effect of seeding rates, genotypes, and their interaction on flag leaf area (cm^2).*

Genotype	140 Kg ha^{-1}	160 Kg ha^{-1}	180 Kg ha^{-1}	Mean
Farah	39.350 a	35.236 b	32.943 c	34.828 a
Amal 7	26.033 b	30.780 d	25.373 g	30.464 b
Al-Muhand	29.103 e	31.326 d	27.390 f	30.553 b
Liron-3	24.133 g	21.653 h	18.093 f	21.293 e
Liron-4	30.993 d	28.300 ef	22.233 h	27.175 c
Liron-6	25.300 g	22.200 h	19.143 i	22.214 d
Mean	31.326 a	28.382 b	23.55 c	$\bar{x}$=27.754

Days from sowing to full maturity (days)

There are substantial differences in the number of days from planting to full maturity due to seeding rates, genotypes, and their interactions, according to the results shown on Table 7. The 140 kg ha^{-1} seeding rate had the shortest period of 164.055 days, while the longest was at the 180 kg ha^{-1} seeding rate, at 167 days. It has been explained that the shorter duration in cases of low seeding rates is because competition for growth resources is minimal at an early stage, hence accelerating the plant's transition from vegetative to productive growth (Al-Zaidi and Al-Abody, 2024).

Among genotypes, Al-Muhandis was the earliest at an average of 164.111 days, followed by Amal 7 and Liron-6, while Liron-3 was the slowest and reached up to 167.111 days. This variation is because of genetic cause and the response of different genotype to temperature and photoperiod, as Ahmad (2017) .

There was a significant interaction between seeding rates and genotype. The shortest maturation period was noted for the cross of Amal 7 × 140 kg ha^{-1} with 162.666 days, while the longest was observed for the cross of Liron-3 × 180 kg ha^{-1} with 169.333 days.

Table 7: *Effect of seeding rates, genotypes, and their interaction on days from sowing to full maturity (days).*

Genotype	140 Kg ha^{-1}	160 Kg ha^{-1}	180 Kg ha^{-1}	Mean
Farah	164.333 gh	166.00 c-f	164.000 i-j	166.11 b
Amal 7	162.666 k	164.666 f-i	163.00 j-k	164.777 cd
Al-Muhand	168.00 b	163.00 b-k	165.333 e-h	164.111 d
Liron-3	165.666 d-g	166.333 c-e	169.333 a	167.111 a
Liron-4	164.000 j-i	165.000 e-i	167.333 b-c	165.444 b-c
Liron-6	163.666 k-i	163.666 j-k	165.666 d-g	164.333 d
Mean	167.00 a	164.777 b	164.055 b	$\bar{x}$=163.314

Spike length (cm)

Significantly, as shown by the results in Table 8, there is a difference between seeding rates, genotypes, and their interactions with respect to spike length. The rate of 140 kg ha^{-1} scored the highest average (12.111 cm), while 180 kg ha^{-1} had the lowest average (8.055 cm). A high rate of seeding causes heightened competition for light and nutrients during ear formation that negatively affects vegetative growth, hence reducing the length of ears, as evidenced in the work by Basietva, (2023).

The average length of spikes in the genotypes was highest in Amal 7, which was 12.111 cm, while Liron-3 and Liron-6 showed the minimum, 8.666 and 8.111 cm, respectively. This variation reflects differences in the duration of the period from spike formation to flowering completion, which affected spike growth, consistent with Kaleri *et al.* (2016).

The interaction between seeding rates and genotypes was significant. The combination Amal 7 × 140 Kg ha^{-1} gave the highest spike length (15.00 cm), whereas Liron-6 × 180 Kg ha^{-1} recorded the lowest (6.666 cm). This result was supported by the significant positive phenotypic correlation between spike length and days from sowing to physiological maturity (Table 13).

Table 8: *Effect of seeding rates, genotypes, and their interaction on spike length (cm).*

Genotype	140 Kg ha^{-1}	160 Kg ha^{-1}	180 Kg ha^{-1}	Mean
Farah	13.333 b	11.333 cd	9.333 g-h	11.333 b
Amal 7	15.00 a	12.333 bc	9.000 g-h	12.111 a
Al-Muhand	12.666 b	10.666 de	8.333 hi	10.555 c
Liron-3	10.333 d-f	8.333 hi	7.333 i-j	8.666 e
Liron-4	11.333 cd	9.333 g-h	7.666 i-j	9.444 d
Liron-6	10.000 e-f	7.666 i-j	6.666 j	8.111 e
Mean	12.111 a	9.944 b	8.055 c	$\bar{x}$=10.037

Number of grains per spike (grain.spike^{-1})

Results in Table 9 showed significant differences among seeding rates, genotypes, and their interaction for grain number per spike. The lowest seeding rate (140 Kg ha^{-1}) achieved the highest mean (43.751 grain.spike^{-1}), significantly higher than the medium rate (39.661 grain.spike^{-1}), while the highest rate (180 Kg ha^{-1}) gave the lowest mean (36.274 grain.spike^{-1}). The decrease at higher seeding rates is due to higher plant density, which limits dry matter accumulation and spike development, especially during early grain formation, consistent with (Zangana and Aljburi, 2023; Dumlu, 2025).

Genotypic differences were evident. Farah recorded the highest mean (45.983 grain.spike^{-1}), whereas Amal 7 gave the lowest (32.973 grain.spike^{-1}). The superior performance of Farah is associated with its later maturity, allowing prolonged leaf activity and greater flag leaf area, enhancing photosynthesis and dry matter accumulation. This result was supported by the genetic correlation between flag leaf area and the number of grains per spike (Table 13), and similar findings were reported by Abd El-Aty *et al.* (2025).

The interaction between seeding rates and genotypes was significant. Farah × 140 Kg ha^{-1} gave the highest grain number per spike (49.480), whereas Amal 7 × 180 Kg ha^{-1} recorded the lowest (29.523 grain. spike^{-1}). This can be explained by the significant positive phenotypic correlation between flag leaf area and the number of grains per spike (Table 13).

Table 9: *Effect of seeding rates, genotypes, and their interaction on number of grains per spike (grain.spike^{-1}).*

Genotype	140 Kg ha^{-1}	160 Kg ha^{-1}	180 Kg ha^{-1}	Mean
Farah	49.480 a	45.960 b	42.190 cd	45.983 a
Amal 7	36.403 g-i	32.993 j	29.523 k	32.973 e
Al-Muhand	42.510 cd	38.493 fg	34.247 i-j	38.310 d
Liron-3	43.913 bc	41.550 cd	38.870 ef	41.444 b
Liron-4	45.527 b	38.213 fg	35.233 i-j	39.657 c
Liron-6	44.993 b	40.757 de	37.263 f-g	41.004 b
Mean	43.751 a	39.661 b	36.274 c	x̄=39.895

Weight of 500 grains (g)

Results in Table 10 indicated significant differences among seeding rates, genotypes, and their interactions for 500-grain weight. The 140 Kg ha^{-1} seeding rate recorded the highest mean (21.694 g), significantly higher than the 180 Kg ha^{-1} rate, which gave the lowest mean (18.916 g). The reduction at higher seeding rates is due to increased plant density, which reduces dry matter accumulation in source organs (leaves) and its translocation to sinks (grains), thus lowering grain weight, consistent with (Al-Hasan and Anwar, 2016).

Genotypic variation was evident. Amal 7 and Liron-4 recorded the highest means (22.277 and 22.444 g, respectively), while Farah showed the lowest mean (18.111 g). This result can be attributed to the negative correlation between grain number per spike and 500-grain weight, as Farah had the highest grain number per spike (Table 9), it is worth noting that there is an inverse relationship between the number of grains per spike and the 500-grain weight, and this result is consistent with (Al-Mafarji and Al-Jubouri, 2024).

The interaction between seeding rates and genotypes was significant. Amal 7 × 140 Kg ha^{-1} and Liron-4 × 140 Kg ha^{-1} recorded the highest 500-grain weights (24.00 and 24.333 g, respectively), whereas Farah × 180 Kg ha^{-1} gave the lowest (16.833 g). This was supported by a significant positive phenotypic correlation between spike length and 500-grain weight (Table 13).

Table 10: *Effect of seeding rates, genotypes, and their interaction on weight of 500 grains (g).*

Genotype	140 Kg ha^{-1}	160 Kg ha^{-1}	180 Kg ha^{-1}	Mean
Farah	19.333 g-h	18.166 h	16.833 i	18.111 d
Amal 7	24.000 a	22.166 b	18.833 g	22.277 a
Al-muhand	20.000 de	20.666 c	17.833 h	18.888 c
Liron-3	22.166 b	20.666 c	19.666 e-f	20.833 b
Liron-4	24.333 a	22.166 b	20.833 c	22.444 a
Liron-6	20.333 cd	19.166 g-h	17.666 h	19.055 c
Mean	21.694 a	20.194 b	18.916 c	x̄=20.268

Table 11: *Effect of seeding rates, genotypes, and their interaction on total biomass yield (kg ha^{-1}).*

Genotype	140 Kg ha^{-1}	160 Kg ha^{-1}	180 Kg ha^{-1}	Mean
Farah	12,210 e-g	12,440 c-f	12,766.7 a	12,472.233 a
Amal 7	11,853 c	11,936.7 g	12,410 b	12,066.8 c
Al-Muhand	11,850 gh	11,943.3 g	12,206.7 e-g	12,000 c
Liron-3	11,946.7 g	12,066.7 fg	12,326.7 d-g	12,113.366 c
Liron-4	11,233.3 i	11,266.7 i	11,450 i	11,316.666 d
Liron-6	12,110 d	12,490 b	12,623.3 b	12,407.766 b
Mean	11,867.216 b	12,023.9 a	12,297.233 a	x̄=12,062.797

Total biomass yield (kg.ha^{-1})

Data in Table 11 revealed that seeding rates 160 and 180 Kg ha^{-1} achieved the highest total biomass yields, recording means of 12,297.233 and 12,023.916 Kg ha^{-1}, respectively, compared to 140 Kg ha^{-1}, which had the lowest mean (11,867.216 Kg ha^{-1}). The increase in total biomass at higher seeding rates is attributed to higher plant density, leading to greater overall vegetative production, in agreement with (Zawar *et al*., 2025).

Genotype Farah recorded the highest mean for this trait (12,472.233 kg ha^{-1}), whereas genotype Liron-4 had the lowest mean (11,316.666 kg ha^{-1}). This increase in the Farah genotype can be attributed to its higher mean biological yield per plant, which consequently enhanced the total biological yield. Moreover, the genetic correlation was positive and significant between 500-grain weight and total biological yield (Table 13), and similar results were reported by (Ahmed and Alhabbar, 2025).

The interaction between genotype Farah and the seeding rate of 180 kg ha^{-1} achieved the highest mean value for this trait (12,766.7 kg ha^{-1}), whereas the interaction between genotype Liron-4 and the seeding rate of 140 kg ha^{-1} recorded the lowest mean (11,233.3 kg ha^{-1}). This can be explained by the significant positive phenotypic correlation between 500-grain weight and biological yield, as well as the significant negative phenotypic correlation of the same trait with the number of tillers per m^2.

Total grain yield (kg.ha^{-1})

Results in Table 12 showed significant differences among seeding rates, genotypes, and their interactions for total grain yield. The 140 Kg ha^{-1} seeding rate recorded the highest mean (5,312.61 kg.ha^{-1}), while 180 Kg ha^{-1} gave the lowest mean (3,336.47 kg.ha^{-1}). The superior performance of the 140 Kg ha^{-1} rate is attributed to its favorable impact on the main yield components, namely total spike number per m^2, grains per spike, and 500-grain weight, which collectively enhanced total grain yield per unit area, in agreement with (Abdalkarim *et al*., 2022; Al-Samarrai and Hindi., 2024).

The genotype Farah recorded the highest mean grain yield of 4690.94 kg ha^{-1}, whereas the genotypes Liron-3 and Al-Muhandis exhibited the lowest means of 3905.19 and 4020.59 kg ha^{-1}, respectively. This superiority of genotype Farah can be attributed to its advantage in one of the main yield components, namely the number of grains per spike, which resulted from the increased flag leaf area and consequently enhanced the total grain yield per unit area. This finding was supported by the significant positive genetic correlations between the number of tillers per m^2 and spike length with grain yield (Table 13) and is consistent with the results reported by (Ahmed and Alhabbar., 2025; Al-Mafarji and Al-Jubouri 2023b).

The interaction between genotype Farah and the seeding rate of 140 kg ha^{-1} produced the highest mean grain yield (6199.2 kg ha^{-1}), whereas the interaction between genotype Al-Muhandis and the seeding rate of 180 kg ha^{-1} gave the lowest mean (3199.1 kg ha^{-1}). This can be explained by the phenotypic correlations between the number of tillers per m^2, spike length, and grain yield of Triticale (Table 13). Moreover, this result was further confirmed by the high direct effects revealed by the path coefficient analysis between the number of grains per spike and 500-grain weight with grain yield of Triticale (Figure 1). These findings suggest that the two mentioned traits can be effectively used as selection criteria for improving grain yield.

Table 12: *Effect of seeding rates, genotypes, and their interaction on total grain yield (kg ha^{-1}).*

Genotype	140 Kg ha^{-1}	160 Kg ha^{-1}	180 Kg ha^{-1}	Mean
Farah	6,199.2 a	4,496.1 de	3,377.5 g	4,690.94 a
Amal 7	5,401.7 b	4,474.2 de	3,518.1 g	4,464.68 b
Al-Muhand	4,888.9 cd	3,973.7 f	3,199.1 g	4,020.59 d
Liron-3	4,634.9 cd	3,916.1 f	3,302.4 g	3,951.90 d
Liron-4	5,461.2 b	3,946.6 f	3,302.4 g	4,236.77 c
Liron-6	5,289.8 b	4,245.3 ef	3,316.9 g	4,283.99 c
Mean	5,312.61 a	4,175.36 b	3,336.47 c	$\bar{x}$=4,274.811

Genetic and phenotypic correlation with total grain yield

Table 13 presents genetic and phenotypic correlation coefficients between the studied traits and total grain yield. The genetic correlation of total grain yield was significantly positive with total spike number per m^2 (0.964**), spike length (0.598**), and positively significant with total biomass yield (0.546*). Total spike number per m^2 was highly positively correlated with spike length (0.641**) and total biomass yield (0.708**). Leaf area was highly positively correlated with grains per spike (0.654**). Days from sowing to physiological maturity showed a significant positive genetic correlation with spike length (0.538**). Spike length was positively correlated with total biomass yield (0.538*), and 500-grain weight had a highly significant positive genetic correlation with total biomass yield (0.596**).

Phenotypic correlation analysis showed that total grain yield was highly positively correlated with total spike number per m^2 (0.744**) and total biomass yield (0.619**), and significantly positive with spike length (0.554*). Spike length had a significant negative phenotypic correlation with total spike number per m^2 (-0.576*) but positively correlated with days to maturity (0.572*). Grains per spike had

Table 13: *Genetic and phenotypic correlations of studied traits with total grain yield.*

Traits	X8	X1	X2	X3	X4	X5	X6	X7
X8	1.000	-0.964**	0.256	-0.059	0.598**	-0.181	0.345	0.546*
X1	-0.744**	1.000	-0.252	-0.133	-0.641**	-0.032	-0.079	-0.708**
X2	0.269	-0.215	1.000	-0.383	0.397	0.654**	0.358	-0.068
X3	-0.001	-0.015	-0.363	1.000	-0.638**	0.134	-0.342	0.233
X4	0.554*	-0.576*	0.392	-0.572*	1.000	-0.222	0.538*	-0.008
X5	-0.161	-0.033	0.642**	0.115	-0.227	1.000	-0.412	0.241
X6	0.297	-0.064	0.342	-0.306	0.522*	-0.402	1.000	-0.596**
X7	0.619**	-0.571*	-0.007	0.219	0.031	0.211	-0.558*	1.000

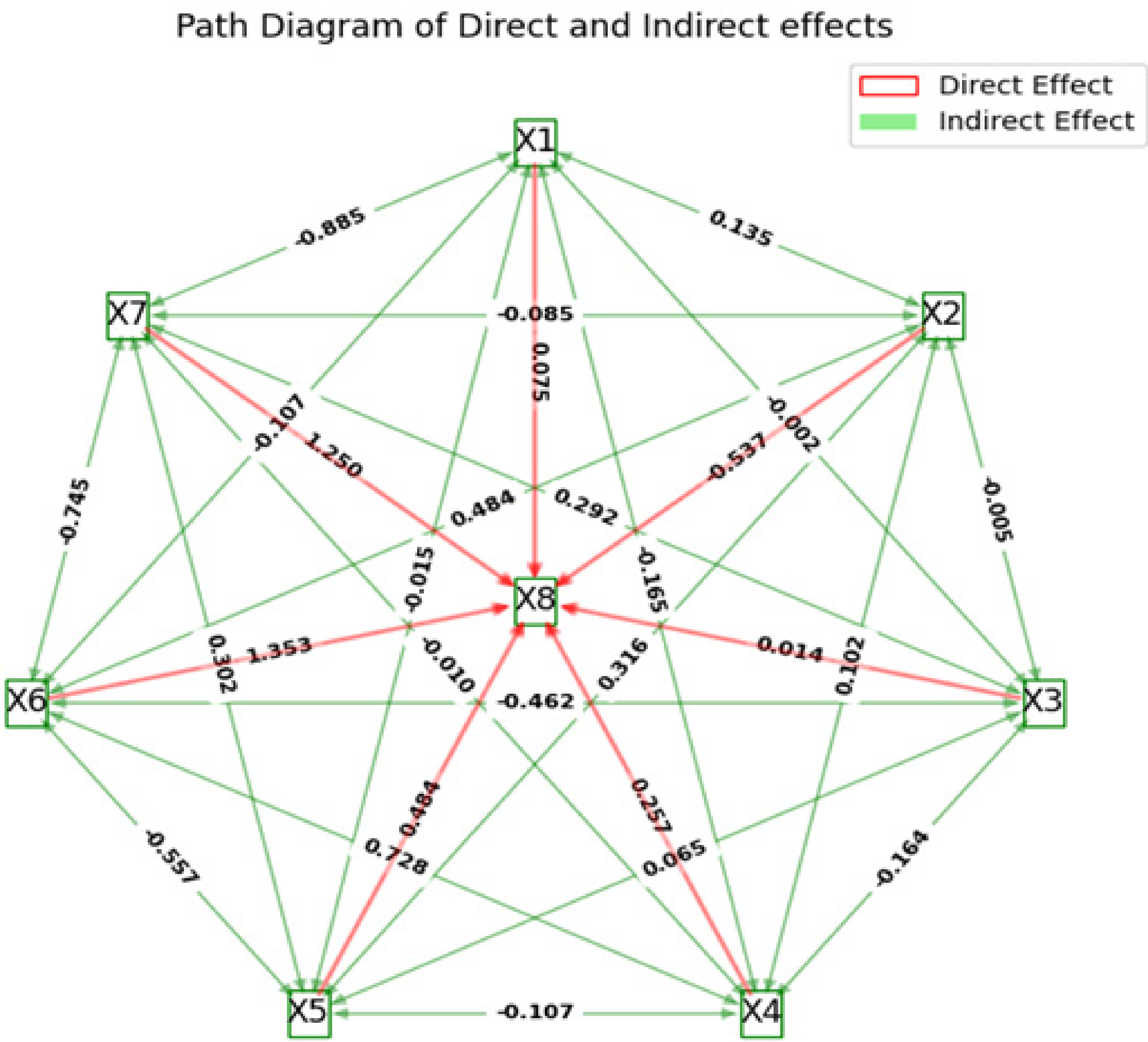

Figure 1: *Phenotypic path coefficient analysis of the studied traits with grain yield*

a highly significant positive phenotypic correlation with leaf area (0.642**). Five-hundred-grain weight was positively correlated phenotypically with spike length (0.522*) and total biomass yield (0.558*) and negatively correlated with total spike number per m^2 (-0.571*). These results are consistent with (Aziz and Al-Zubaidy, 2024; Mishra *et al*., 2025; Madab., 2025; Assad and Hindi., 2025). who reported both positive and negative significant genetic and phenotypic correlations among yield-related traits.

Path coefficient analysis

Path coefficient analysis (Figure 1) revealed that the direct effects of traits on total grain yield varied considerably. The direct effect was high for total spike number per m^2 (0.537), grains per spike (0.728), and 500-grain weight (1.353), while it was low for the remaining traits. Indirect effects were also notable: total spike number per m^2 exhibited a strong negative indirect effect via total biomass yield (-0.885). Leaf area showed a moderate positive indirect effect through spike length, and a high positive indirect effect via grains per spike (0.316) and 500-grain weight (0.484). Days from sowing to physiological maturity had a high negative indirect effect on 500-grain weight (-0.462) but a high positive indirect effect on total biomass yield (0.702). Spike length exerted a high positive indirect effect on 500-grain weight, while grains per spike had a high positive indirect effect on both 500-grain weight and total biomass yield. Total biomass yield exhibited a strong positive indirect effect on total grain yield (0.745).

These results align with (Sabri and Ahmed, 2018; Neykov, 2024; Omer and Al-Layla, 2024; Sharif *et al*., 2024) who reported that specific yield components exerted significant direct effects on the total grain yield of Triticale. The analysis highlights the critical role of grains per spike, 500-grain weight, and total spike number in determining yield, and emphasizes the importance of considering both direct and indirect pathways in selection and breeding programs.

Conclusions

Based on the obtained results of this study, it can be concluded that all six tested triticale genotypes could be successfully grown under conditions of Samarra city using a seeding rate of 140 kg/ha^{-1}. This rate gave the highest averages for vegetative growth traits, as well as for total grain yield and its components, thus making it economically feasible for triticale growers. Among the genotypes, Farah showed the highest total grain yield per unit area, performing best under these conditions. The number of grains per spike and 500-grain weight traits may prove effective selective indicators in a triticale yield improvement program, since path coefficient analysis showed a strong direct effect of these two traits on total grain yield.

Acknowledgments

There are no individuals or organizations to acknowledge for this work.

Novelty Statement

This presents a new avenue in the realm of the genetic performance evaluation of triticale plant species through the assessment of performance, estimation of genetic and phenotypic correlation coefficients, and path coefficient analysis for quantitative traits under different cultivation rates. The results, thus obtained, provide precise scientific data that could enable the researcher and farmer to identify the best genotypes and to come up with improved agricultural management for better yields.

Authors' Contributions

Hussein Ali Hindi and Liwa Nahed Faisal: Contributed to the practical part of the research.
Yassin Obaid Nouri Ahmed Sharif and Tariq Raad Thaer Al-Mufarji: Contributed to the theoretical part by writing the article and conducting a statistical data analysis.
All authors have read and approved the final manuscript.

Conflict of interest

Conflict of Interest The authors declare no financial, personal, or professional conflicts of interest that might influence the outcome or interpretation of the content of the study.

Generative AI and AI-assisted technology statement

The artificial intelligence analysis of all sections of this manuscript showed that none of the text plagiarized and was with a score of zero.

References

Abdalkarim, P., J. Aziz, and K. mstafa. 2022. Response of Bread Wheat Varieties (*Triticum aestivum* L.) to Seeding rates under the environmental conditions of sulaymaniyah governorate. Kirkuk University J. Agric. Sci., 13(4): 346-354. https://doi.org/10.58928/ku22.13427

AbdEl-Aty, M.S., M.K. Mohammed, E.I. Shimaa, A.M.E. Mohammed, S.S. Mohammed, and H.A.Ahmad. 2025. Evaluation of some bread wheat genotypes for low nitrogen fertilization using different stress tolerance indices. Egypt. J. Agron., 47(3): 381–392. https://doi.org/10.21608/agro.2025.369974.1651

Abdullah, A. and J. Rafaat. 2020. The Impact of Seeding Rate and Locations on Some Grass Pea (*Lathyrus sativus*) Lines for Growth, Forage and Seed Yield in Sulaimani Region. Tikrit J. Agric. Sci., 20(1): 20-37. https://doi.org/10.25130/tjas.20.1.3

Ahmad, U. 2017. Evaluating seed rate, cutting, and nitrogen level: Study of yield and yield components of Triticale. Pak. J. Biotechnol., 14(2): 193–204. https://nja.pastic.gov.pk/PJBT/index.php/PJBT/article/view/1205

Ahmed, R.A. and Z. Alhabbar. 2025. Foliar application of potassium to enhance growth and yield of bread wheat cultivars under rainfed and supplementary irrigation. Passer J. Basic Appl. Sci., 7(2): 616–622. https://doi.org/10.24271/psr.2025.512358.2022

Al-Dahi, W.T.A. 2021. Effect of planting dates and seed quantities on some productive and genetic traits of Triticale (*Triticum durum* desf.) inputs (PhD thesis). Department of Field Crops, College of Agriculture and Forestry, University of Mosul, Iraq.

Al-Dulaimi, O.Z.A.M.S. 2020. Effect of variety, salicylic acid stimulation, and humic acid addition on growth, yield, and quality of Triticale wheat (Triticosecale × Wittmack) (PhD thesis). Department of Field Crops, College of Agriculture, University of Tikrit, Iraq.

Al-Hasan, A. and A. Anwar. 2016. The interaction effect of locations and seeding rates on yield and its components of some oat (*Avena sativa* L.) varieties under Rain fed conditions. Kirkuk University J. Agric. Sci., 7(1): 33-44. https://doi.org/10.58928/ku16.07104

Al-Mafarji, T.R.T. and J.M.A. Al-Jubouri, 2023. Combining Ability and Gene Action of Half Diallel Crosses in Bread Wheat (*Triticum aestivum* L.). IOP Conf Ser Earth Environ Sci., 1262(5). https://doi.org/10.1088/1755-1315/1262/5/052027

Al-Mafarji, T.R.T. and K.A. Al-Jubouri. 2024. Diagnosis of growth traits of genotypes (*Triticosecale x Wittmack*) tolerant to nitrogen stress and estimation of some genetic parameters. Euphrates J. Agric. Sci., 16(2): 388–399. http://dx.doi.org/10.13140/RG.2.2.36089.48486

Al-Mafarji, T. and J. AL-Jubouri. 2023a. Heterosis, Correlations and Path Analysis of Grain Yield Components in Bread Wheat (*Triticum aestivum* L.). Kirkuk University J. Agric. Sci., 14(3): 34-46. https://doi.org/10.58928/ku23.14304

Alnori, M. and R. Ahmad. 2012. Effect of seeds size and plants spacing on yield and its components of two synthetic varieties of corn (Zea mays L.). Mesopotamia J. Agric., 40(0): 83-93. https://doi.org/10.33899/magrj.2012.62170

Al-Rawi, K.M. and A.A. Khalaf Allah. 2000. Design and analysis of agricultural experiments. University of Mosul, Printing and Publishing House Foundation, Ministry of Higher Education and Scientific Research.

Al-Samarrai, R.S.K. and H.A. Hindi. 2024. Effect of Different Spray Concentrations of Zinc on the Growth Traits and Yield of Six Row Barley Varieties. In IOP Conference Series: Earth Environ. Sci., (Vol. 1371, No. 5, p. 052076). IOP Publishing. https://doi.org/10.1088/1755-1315/1371/5/052076

Alshamary, W.F.A., Y.O.N.A. Sharif, N.E. Noori, and A.-M.S. Kahlel. 2025. Effect of Moisture Depletion Rate and Irrigation Water Depth on the Productivity and Water Use Efficiency of Soybean Crop (*Glycine max* L.) Merr. under Drip Irrigation and Fixed Sprinkler Irrigation Systems. Agric. Sci. Digest., 45(2): 222–227. https://doi.org/10.18805/ag.DF-651

Al-Zaidi, A.J.H. and A.K.M. Al-Abody. 2024. Response of bread wheat (*Triticum aestivum L.*) and Triticale (*Triticosecale × Wittmack*) varieties at different levels of phosphate fertilization under Basra governorate conditions. Euphrates J. Agric. Sci., 16(3): 172–185. https://iasj.rdd.edu.iq/journals/journal/issue/15236

Al-Zubaidi K.M.D. and K.K.A. Al-Jubouri. 2016. Design and analysis of genetic experiments. Amman (Jordan): Al-Wadah Publishing House.

Assad, N.I. and H.A. Hindi. 2025. Effect of Spraying with Nano Potassium on of Quality Traits of Genotypes of Bread Wheat (*Triticum aestivum* L.) Under the Conditions of Kirkuk. In IOP Conference Series: Earth Environ.

Sci., (Vol. 1487, No. 1, p. 012078). DOI: https://doi.org/10.1088/1755-1315/1487/1/012078

Aziz, F. and K. Al-Zubaidy. 2024. Correlation, Genetic and Phenotypic Path Coefficient Analysis in Maize (*Zea mays* L.). J. Med. Indust. Plant Sci., 2(1): 52-61. https://doi.org/10.32894/MEDIP.24.1.6

Basieva, M. 2023. Influence of seeding rates on productive qualities of winter triticale in the foothill zone conditions. In E3S Web of Conferences (Vol. 431, p. 01018). EDP Sci. https://doi.org/10.1051/e3sconf/202343101018

Batool, A., S. Aleeym, A. Newaz, M.I. Khan, W. Arshad, M. Aslam, S. Ali, and M. Zeehan. 2022. Evaluation of the impact of variable seed rates on growth, productivity, and yield attributes of different wheat (*Triticum aestivum L.*) genotypes of Baran area. J. Pak. Res., 35(2): 285–302. https://dx.doi.org/10.17582/journal.pjar/2022/35.2.285.302

Dumlu, B., H. Metvin, K. Uymran, B. Jan, A. Hali, and T. Aras. 2025. Assessment of genetic diversity in wheat (*Triticum aestivum* L.) genotype for cold tolerance, agronomic and quality traits. Crop Pasture Sci. J., 76(1): 1–17. https://doi.org/10.1071/cp25047

Fayhaa Muhammad Najm, Hind Tahseen Ibrahim, Raed Amer Ali Alsahoo, Ibrahim Ayad Jihad, Qais R.M.A.Z. 2025. oRGINAL article. J. Anim. Healt. Product., 13(s1): 39–48. https://doi.org/https://dx.doi.org/10.17582/journal.jahp/2024/13.s1.39.48

Ismail, N. and M.Y. Al-Fahady. 2012. Phenotypic stability for yield, its components and quality characters of introduced lines of triticale (x. triticosecale wittmack) under limited rainfall condition in northern of iraq. Mesopotamia J. Agric., 40(0): 238-251. https://doi.org/10.33899/magrj.2012.62241

Kaleri, S.K., A. Arshad, B. Abdul Wahid, F.V. Nasreen, N. Hailong, F.A. Tanweer, H.K. Sajid, and K. Mohsin. 2016. Performance of some wheat varieties basis on yield and yield-contributing characters. Int. J. Biol. Biotechnol., 13(4): 571–574.

Madab, D.S., H.A. Hindi, Y.O.N.A. Sharif, and T.R.T. Al-Mafarji. 2025. Nature in inheritance of yield and its components in different mating designs of cotton genotypes (*Gossypium hirsutum* L.). Natur. Engineer. Sci., 10(2): 495–509. https://doi.org/10.28978/nesciences.1740074

Mahmood, E.T., T.R.T. Al-Mafarji, M.B. Al-Ethawi, K.K. Ahmed, S.H.I. Al-Ani, and K.P. Korolev. 2025. Correlation analysis of growth, yield, and quality traits in maize (Zea mays L.) hybrids under different plant densities. In IOP Conference Series: Earth Environ. Sci., (Vol. 1538, No. 1, p. 012041). IOP Publishing. https://doi.org/10.1088/1755-1315/1538/1/012041

Mishra, U., C. Shailja, V.S. Kandalkar, and A.K. Sharma. 2025. Genotypic and phenotypic correlation coefficients, path coefficients, and the implication of discriminant selection index for genetic improvement in advanced wheat (*Triticum aestivum L.*) cultivars. Int. J. Advan. Biochem. Res., 9(8): 232–240. https://www.doi.org/10.33545/26174693.2025.v9.i8Se.5136

Mohammed, M.D., T.K. Karyagdi, A.M. Qneed, I.A. Jihad, Q.R. Lahhob, M. Mudhafar, H.A. Alsailawi, and A.A. Ayada. 2025. Molecular characterization and zoonotic potential of giardia species in livestock with respect to their transmission dynamics and host adaptation. J. Anim. Health Prod., 13(s1): 411–421. https://doi.org/https://dx.doi.org/10.17582/journal.jahp/2025/13.s1.411.421

Mohammed, M.H., L.S. Mohammed, and A.H. Anees. 2025. The use of spraying brassinolide to improve the genotypes yield of Triticale X Trititcosecal wittmack. Tikrit J. Agric. Sci., 25(2): 1-14. https://doi.org/10.25130/tjas.25.2.1

Neykov, N. 2024. Correlation, path-coefficient, and principal component analysis of yield and some characters related to the productivity of Triticale genotypes. Bulgarian J. Agric. Sci., 30(5): 807–812. https://journal.agrojournal.org/page/en/details.php?article_id=4781

Nwry, R.G., S.H. Abdulqader, and S.A. Hussain. 2021. Effect of plant population and cultivars on growth, yield and its component of bread wheat (*Triticum aestivum* L.) under the rain-fed condition in Kurdistan- Iraq. Tikrit J. Agric. Sci., 21(3): 41-51. https://doi.org/10.25130/tjas.21.3.5

Omer, A.A. and M.J. Al-Layla. 2024. Estimation genetic parameter, genotypic and phonotypic correlation, path and cluster analysis of quantitative traits for Bread Wheat genotypes in Erbil under rain- fed condition. J. Med.

Industr. Plant Sci., 2(3): 23-23. https://doi.org/10.32894/MEDIP.24.3.4

Sabri, Z. and A. Ahmed. 2018. Performance Evaluation and path coefficient analysis for six genotypes of barley (Hordeum vulgare L.) under different plant densities. Mesopotamia J. Agric., 46(3): 179-190. https://doi.org/10.33899/magrj.2018.161499

Sebahi, J. 2011. Guide to the use of chemical and organic fertilizers in Iraq. Guidance Bulletin.

Shah, W.A., H. Zafar, A. Roohul, A. Shazymar, I.A. Muhammad, and Ikramullah. 2016. Effect of irrigation levels and seed rates on wheat production. Pure Appl. Biol., 5(4): 895–905. http://dx.doi.org/10.19045/bspab.2016.50113

Sharif, Y.O.N.A., A.S.H. Al-Mafrajy, and Z.M.M. Albarzenje. 2024. Evaluation of the Effectiveness of 2.4-D 72% Herbicide in Combating Weedy Leaves Associated with Different Varieties of Forage Sorghum (*Sorghum bicolor* L.) and Its Effect on Growth Characteristics. In IOP Conference Series: Earth Environ. Sci., (Vol. 1371, No. 5, p. 052020). IOP Publishing. https://doi.org/10.1088/1755-1315/1371/5/052020

Sharif, Y.O.N.A., D.S. Madab, and H.A. Hindi. 2024. Estimation of Path Analysis and Genetic Parameters for Sorghum (*Sorghum bicolor* (L.) Moench) Varieties in Different Environments. IOP Conference Series: Earth Environ. Sci., 1371(5). https://doi.org/10.1088/1755-1315/1371/5/052035

Walter, A.B. 1975. Manual of quantitative genetics (3rd ed.). Washington State University Press.

Younis, S. and A.M. Al-Hasans. 2019. Effect of plant densities on growth characters, silage and grain yield on corn (Zea mays L.). Mesopotamia J. Agric., 45(2): 305-312. https://doi.org/10.33899/magrj.2019.161318

Zangana, D.D. and J.M. Aljburi. 2023. Impact of hydrogel and its relationship to yield, some of its components and grain quality of bread wheat genotypes (Triticum aestivum L.). In IOP Conference Series: Earth Environ. Sci., (Vol. 1214, No. 1, p. 012042). IOP Publishing. https://doi.org/10.1088/1755-1315/1214/1/012042

Zawar, S., W. Muhammad, and M.A. Muhammad. 2025. Optimizing wheat yield through seed rate and planting method interactions: A study for enhanced crop productivity and food security. Pure Appl. Biol. J., 14(2): 94–105. http://dx.doi.org/10.19045/bspab.2025.140011