Title Modification: A Study of Improving the Performance and Genetic Traits of Yellow Maize (*Zea mays* L.) Using Foliar Humic Acid to Achieve Sustainable Productivity

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Abstract

This study was conducted at the Research and Experimental Farm, College of Agriculture, University of Kirkuk, during the spring season of 2025, with the aim of evaluating the growth and yield performance of five maize (*Zea mays* L.) genotypes — Drakma, TORRO, Fito, Julie, and Holland — under the effect of three concentrations of humic acid (0, 20, and 40 g L^{-1}). The experiment was arranged in a split-plot design within a randomized complete block design (RCBD) with three replications. Each experimental unit consisted of four rows, each three meters long, with 20 cm spacing between plants. The soil was prepared by double plowing and fertilized with phosphorus and nitrogen according to recommended standards. The qualitative traits studied included protein percentage, oil percentage, specific weight, bulk density, carbohydrate percentage, and ash content. Data were statistically analyzed using the SAS program, and genetic, environmental, and phenotypic variances were estimated, in addition to heritability and expected genetic advance. The results demonstrated a clear superiority of the maize genotypes when treated with humic acid compared to the untreated control, with the genotype TORRO exhibiting the most pronounced enhancement across all evaluated traits. Protein content increased markedly under the TORRO × 40 $g \cdot L^{-1}$ interaction, reaching 10.36%, in contrast to the lowest value recorded in the control treatment of Drakma (6.18%). Oil percentage showed a similar trend, as the Holland × 40 $g \cdot L^{-1}$ interaction achieved the highest value of 5.15%, whereas the control treatment of Julie registered the lowest oil content (3.57%). Specific weight reached its maximum under the TORRO × 40 $g \cdot L^{-1}$ interaction (78.64 $g \cdot hL^{-1}$), compared with the lowest value (70.84 $g \cdot hL^{-1}$) observed in Drakma without humic acid. Bulk density also improved significantly, with the TORRO × 20 $g \cdot L^{-1}$ interaction recording the highest value (0.791 $g \cdot cm^3$), while the Fito control treatment exhibited the lowest density (0.708 $g \cdot cm^3$). Carbohydrate percentage reached its highest level under TORRO × 20 g L^{-1} (75.33%), compared with the lowest value of 70.59% observed in the Fito × 40 g L^{-1} interaction. Ash percentage followed a similar pattern, attaining its maximum under TORRO × 20 g L^{-1} (2.00%), whereas the minimum value (1.52%) occurred in the Fito × 40 g L^{-1} treatment.

Keywords: TORRO - Humic acid - Genetic standards - Genetic structures

Introduction

This study was conducted at the Research and Experimental Farm, College of Agriculture, University of Kirkuk, during the spring season of 2025, with the aim of evaluating the growth and yield performance of five maize (*Zea mays* L.) genotypes — Drakma, TORRO, Fito, Julie, and Holland — under the effect of three concentrations of humic acid (0, 20, and 40 kg/L). The experiment was arranged in a split-plot design within a randomized complete block design (RCBD) with three replications. Maize (*Zea mays* L.) is one of the world's most strategic agricultural crops due to its diverse applications in food and industry. It serves as an essential food source for humans, a major feed component for livestock, and a raw material in starch and oil production, in addition to its growing role in biofuel manufacturing (1). Maize is characterized by its wide adaptability to various environmental and climatic conditions, which has contributed to its extensive cultivation worldwide. Its economic importance lies in its contribution to food security and in providing alternative energy resources, making it a focal point for agricultural research and scientific attention (2). Developing new maize cultivars has become crucial to addressing climate change challenges and meeting the increasing demands of global markets (3). Recent statistics indicate that the United States ranked first globally in maize production in 2024, with a total yield of approximately 377.6 million tons. Similarly, Egypt recorded a 21% increase in maize imports during the first nine months of 2024, reaching about 5.7 million tons compared to 4.7 million tons during the same period of the previous year (4). In Iraq, maize cultivation has expanded significantly; in Kirkuk Governorate alone, the cultivated area reached about 300,000 dunams in the same year. In the Al-Qala’a Saleh region, about 650 dunams were planted with yellow maize and 250 dunams with white maize, with an average yield of 650 kg per dunam, according to data from the Ministry of Water Resources. Additionally, Iraq’s agricultural exports exceeded 1.5 million tons of various crops (5). Genetic variation is a fundamental component of crop improvement programs, as it forms the basis for developing both quantitative and qualitative traits (6) . Analyzing these variations enables the estimation of genetic and phenotypic coefficients of variation and the determination of heritability (7), which facilitates the prediction of genetic gain from selection processes. Such analyses are crucial for identifying the most influential genetic traits that can serve as reliable indicators in plant breeding programs (3). Humic acid is a naturally occurring organic compound that has demonstrated significant efficacy in promoting plant growth and productivity, particularly in maize (8) . It enhances the physical and chemical properties of soil by improving moisture retention and aeration (9), thereby providing a better root growth environment. It also facilitates the absorption of essential nutrients such as phosphorus and potassium, improves water-use efficiency, and consequently enhances plant growth and yield (10). Furthermore, humic acid helps reduce the accumulation of toxic heavy metals such as cadmium and zinc in roots while increasing their concentration in leaves (3), thereby improving plant tolerance to environmental stress (11). It also stimulates soil microbial activity, contributing to the decomposition of organic matter and the continuous release of nutrients (12). This, in turn, increases biomass and improves plant qualitative traits such as chlorophyll concentration and photosynthetic rate. In maize (13), several studies have shown that humic acid application enhances grain quality traits, which directly reflects on total yield (14).

The objectives of this study were centered on assessing the field performance and productivity of five maize genotypes while simultaneously determining the most effective concentration of humic acid through the evaluation of three application levels and their influence on key plant traits. In addition, the study aimed to estimate the components of phenotypic variance and related parameters, quantify heritability, and predict the extent of potential genetic improvement, thereby providing a comprehensive understanding of the genotypic responses under varying humic acid treatments.

Materials and Methods

The field experiment was carried out at the Research and Experimental Station of the College of Agriculture, University of Kirkuk, during the spring season of 2025. A split-plot design within a randomized complete block design (RCBD) was adopted, with three replications. The main plots were assigned to foliar application treatments of humic acid at three concentrations (0, 20, and 40 g L^{-1}), while the subplots included five maize genotypes: Drakma, TORRO, Fito, Julie, and Holland. The experimental field was prepared by performing two perpendicular plowing passes using a moldboard plow, followed by leveling and smoothing operations. Triple superphosphate (P_2O_5) was applied as a source of phosphorus at a rate of 200 kg/ha, and urea fertilizer (46% N) was used as a nitrogen source at a rate of 200 kg/ha, divided into two equal doses: the first at planting and the second one month later, following the recommendations of *(15)*. Each replication consisted of three main plots corresponding to the humic acid concentrations, and each main plot contained five subplots to which the maize genotypes were randomly distributed (*7*). Each experimental unit comprised four rows, each 3 meters long, with a 0.75-meter spacing between rows and 20 cm between plants. A buffer distance of 1 meter was maintained between experimental units, main plots, and blocks to ensure adequate isolation (*12*). Two to three seeds were sown per hill, and thinning was performed one week after germination to maintain one healthy plant per hill. The study included the evaluation of several qualitative traits representing grain quality and physiological efficiency including protein percentage oil percentage specific weight bulk density carbohydrate percentage and ash percentage to provide a comprehensive assessment of the performance of the maize genotypes under different humic acid treatments

Statistical and Genetic Analysis

The data collected from the experiment were subjected to statistical analysis using a randomized complete block design (RCBD) arranged in a split-plot layout. Mean comparisons were performed using Duncan's Multiple Range Test (DMRT), and all statistical analyses were carried out using the SAS software package for general analysis of variance (ANOVA). In addition, the GENES software was employed to estimate genetic parameters, variance components, heritability, and expected genetic advance (*16*).

1. Variance Components and Coefficients of Phenotypic, Genotypic, and Environmental Variation

The three types of variances were estimated according to the method described by (17) at each level of potassium concentration, as follows:

σP2=σG2+σE2\sigma_P^2 = \sigma_G^2 + \sigma_E^2σP2=σG2+σE2 σE2=MSer\sigma_E^2 = \frac{MSe}{r}σE2=rMSe σG2=(MSg−MSe)r\sigma_G^2 = \frac{(MSg - MSe)}{r}σG2=r(MSg−MSe)

The phenotypic and genotypic coefficients of variation were calculated according to (18), and the classification ranges suggested by (19), (20),. (21) were used, as follows:

- Less than 10% → Low variation
- Between 10% and 30% → Moderate variation
- Greater than 30% → High variation

Where:

PCV=σPX¯×100PCV = \frac{\sigma_P}{\bar{X}} \times 100PCV=X¯σP×100
GCV=σGX¯×100GCV = \frac{\sigma_G}{\bar{X}} \times 100GCV=X¯σG×100

and:

- PCVPCVPCV: Phenotypic Coefficient of Variation
- GCVGCVGCV: Genotypic Coefficient of Variation
- σP\sigma_PσP: Phenotypic standard deviation
- σG\sigma_GσG: Genotypic standard deviation
- X¯\bar{X}X¯: General mean of the trait

2. Heritability and Expected Genetic Advance as a Percentage of the Mean

Broad-sense heritability (HB.S.2H^2_{B.S.}HB.S.2) was estimated following the method proposed by. (22). The heritability values were categorized according to the ranges reported by (23), (24), and (25) as follows:

- Less than 40% → Low heritability
- Between 40–60% → Moderate heritability
- Greater than 60% → High heritability

HB.S.2=σG2σP2H^2_{B.S.} = \frac{\sigma_G^2}{\sigma_P^2}HB.S.2=σP2σG2

The Expected Genetic Advance (G.A.) was estimated according to the classification of (19):

- Less than 10 → Low improvement potential
- Between 10–30 → Moderate improvement potential
- Greater than 30 → High improvement potential

The expected genetic advance was calculated using the following formula:

G.A.=K×HB.S.2×σPG.A. = K \times H^2_{B.S.} \times \sigma_PG.A.=K×HB.S.2×σP

where:

- G.A.G.A.G.A.: Expected genetic advance
- KKK: Selection differential constant (1.40 at 20% selection intensity)
- HB.S.2H^2_{B.S.}HB.S.2: Broad-sense heritability
- σP\sigma_PσP: Phenotypic standard deviation of the trait

The Expected Genetic Advance as a Percentage of the Mean (E.G.A%) was estimated according to the method of (26), using the equation:

E.G.A%=G.A.X¯×100E.G.A\% =\frac{G.A.}{\bar{X}} \times 100E.G.A%=X¯G.A.×100

where:

- E.G.A%E.G.A\%E.G.A%: Expected genetic advance as a percentage of the mean
- G.A.G.A.G.A.: Expected genetic advance

- X¯\bar{X}X¯: General mean of the trait

Results and Discussion

4.1 Evaluation of Genotypes, Humic Acid Spraying, and Their Interaction on the Studied Traits

The results of the analysis of variance presented in Table (1) revealed significant differences at the 1% probability level for both maize genotypes and humic acid foliar application, as well as their interaction, in most of the studied traits. However, the differences were not significant for specific weight, ash content, and carbohydrate percentage, whereas oil percentage showed significance at the 5% level. Developing high-yielding genotypes with desirable agronomic and qualitative characteristics remains essential for improving maize productivity, particularly under varying environmental conditions where both genetic potential and environmental factors play a crucial role (*27*). The study of genetic diversity serves as a valuable tool to identify genotypes with high adaptability and resilience to environmental stresses, ensuring enhanced productivity and grain quality (*28*). Humic acid, as a bioactive organic compound, has demonstrated its efficacy in stimulating vegetative growth, improving nutrient uptake, and enhancing photosynthetic efficiency (*29*). These physiological improvements contribute directly to grain quality in terms of starch and protein accumulation and grain weight (*30*). Furthermore, the interaction between genetic background and humic acid treatments is a promising approach to optimizing plant responses, identifying genotypes that maximize the benefits of such biostimulants, thereby supporting sustainable agriculture and food security under climate change conditions (*31*).

Protein Percentage (%)

Table (2) shows significant differences among the maize genotypes for protein percentage. The TORRO genotype recorded the highest value (9.32%), while Drakma had the lowest (6.48%). This variation may be attributed to genetic differences influencing nitrogen uptake and storage efficiency. Previous studies have indicated that genes such as *ZmNRT2.5* regulate nitrate transport, enhancing protein accumulation (*32; 14*). Regarding the effect of humic acid, foliar application at 40 g·L^{-1} resulted in the highest protein percentage (8.35%) compared with 7.79% at 20 g·L^{-1}, likely due to the improved nutrient uptake—especially nitrogen—and enhanced photosynthetic activity (*33*). The interaction between TORRO and 40 g·L^{-1} humic acid yielded the highest protein content (10.36%), while Drakma without application showed the lowest (6.18%), emphasizing the significance of genotype × management interaction in improving grain quality (*34; 35*).

Oil Percentage (%)

Table (3) indicates significant variation among genotypes in oil content, where Holland recorded the highest value (4.72%) and Julie the lowest (3.62%). This can be attributed to genetic factors influencing oil biosynthesis and accumulation pathways (*11*). The application of 40 g L^{-1} humic acid led to the highest oil percentage (4.21%) compared with 4.05% at 20 g L^{-1} due to humic acid's role in enhancing nutrient absorption and physiological activity (*32*). The genotype × humic acid interaction was significant; Holland × 40 g·L^{-1} produced the highest oil percentage (5.15%), while Julie × 0 g L^{-1} was the lowest (3.57%), confirming the importance of genetic–environmental interactions (*36*).

Specific Weight (g·hL^{-1})

According to Table (4), genotypes differed significantly in specific weight. TORRO recorded the highest (76.40 g·hL^{-1}), while Drakma had the lowest (71.27 g·hL^{-1}).

This variation results from genetic effects on seed physical properties, including cell density, solid matter content, and biochemical composition (*37*). Although humic acid concentrations did not show significant direct effects, the interaction was significant—TORRO × 40 g L^{-1} achieved the highest value (78.64 g·hL^{-1}), and Drakma × 0 g·L^{-1} the lowest (70.84 g·hL^{-1}). These findings emphasize genotype-specific responses to humic acid and its role in improving physical seed traits through enhanced nutrient assimilation and plant metabolism (*38*).

Bulk Density (g·cm^{3})

The results in Table (5) reveal significant genotypic differences in bulk density. TORRO had the highest mean (0.781 g·cm^{3}) and Drakma the lowest (0.720 g·cm^{3}). This variation arises from differences in seed chemical composition (oil, moisture, and organic matter), which affect density and structural integrity (*39*). Among humic acid treatments, 40 g L^{-1} produced the highest bulk density (0.757 g·cm^{3}) compared with 0.746 g·cm^{3} at 20 g·L^{-1}, reflecting humic acid's role in improving soil structure, nutrient uptake, and plant metabolism (*40*). The genotype × humic acid interaction was also significant—TORRO × 20 g L^{-1} recorded the highest density (0.791 g·cm^{3}), whereas Fito × 0 g L^{-1} was the lowest (0.708 g·cm^{3}). Such variations highlight the importance of genotype × environment interactions in physiological trait expression (*41*).

Carbohydrate Percentage (%)

Table (6) shows significant genotypic differences in carbohydrate content. TORRO recorded the highest (73.44%) and Fito the lowest (71.36%). These differences reflect genetic variation in photosynthetic efficiency, sugar metabolism, and starch biosynthesis. No significant differences were observed among humic acid treatments alone. However, the interaction between genotype and humic acid was significant; TORRO × 20 g·L^{-1} recorded the highest carbohydrate percentage (75.33%), while Fito × 40 g L^{-1} had the lowest (70.59%). This emphasizes the importance of integrating genetic selection with optimal humic acid management to maximize carbohydrate accumulation (*42*).

Ash Percentage (%)

Table (7) revealed significant genotypic differences in ash percentage. TORRO recorded the highest (1.87%) and Fito the lowest (1.67%). These differences arise from genotypic variation in the uptake and translocation of mineral nutrients, with ash serving as an indicator of total mineral content. Humic acid alone had no significant effect, but the interaction was significant; TORRO × 20 g·L^{-1} showed the highest (2.00%), while Fito × 40 g L^{-1} had the lowest (1.52%). This demonstrates that optimal genotype × humic acid combinations enhance mineral absorption and physiological activity, including photosynthesis and carbohydrate storage (*43; 44*).

Estimation of Genetic Parameters

Variance and Coefficient Analysis under Humic Acid Treatments: Analysis of variance revealed considerable differences in maize traits across the three humic acid concentrations (0, 20, and 40 kg·L^{-1}). Genetic, environmental, and phenotypic variances varied among traits, indicating that several traits possess moderate-to-high genetic variability and can be effectively improved through selection (*45*).

Broad-Sense Heritability:

Most studied traits showed high broad-sense heritability across all humic acid concentrations, except for ash and carbohydrate content under the 0 kg·L^{-1}

treatment, which exhibited low heritability values. This pattern suggests a strong genotype × environment interaction influencing selection efficiency (*46*). Expected Genetic Advance (%): Expected genetic advance varied from low to high depending on the trait and humic acid concentration. At 0 kg·L^{-1}, values were generally low, while higher concentrations improved selection efficiency. Traits with high genetic advance are suitable for direct selection, whereas those with low values may require hybridization or environmental manipulation to enhance genetic gain (*47*).

Conclusions

The results of this study clearly indicated that the TORRO genotype was the most superior among the tested maize genotypes in all evaluated traits demonstrating the highest genetic potential for improving grain quality and physiological performance. Foliar application of humic acid at 40 kg·L^{-1} markedly enhanced growth traits nutrient uptake and overall physiological activity contributing directly to increased grain yield and total biomass. The interaction between the high-performing TORRO genotype and humic acid treatment resulted in optimal carbohydrate distribution and maximized expression of superior traits. These findings underscore the critical importance of selecting genetically superior genotypes and integrating them with biostimulant management strategies such as humic acid application to achieve enhanced maize productivity and efficient utilization of environmental and nutritional resources.

Table 1. Analysis of Variance (ANOVA) for the Studied Traits

SOURCE OF VARIATION	**D.F**	**PROTEIN (%)**	**OIL (%)**	**SPECIFIC WEIGHT (G·HL^{-1})**
Replications	2	0.133	0.313	25.00
Genotypes	2	1.529**	0.102*	1.72 n.s
Error A	4	0.048	0.016	2.22
Humic Acid	5	9.935**	1.396**	31.78**
Genotype × Humic	10	1.937**	0.202**	5.35**
Error B	30	0.034	0.029	0.99
Source of Variation	**d.f**	**Ash (%)**	**Carbohydrate (%)**	**Bulk Density (g·cm^3)**
Replications	2	0.0904	5.66	0.00196
Genotypes	2	0.0212 n.s	0.65 n.s	0.00052**
Error A	4	0.0081	0.42	0.00015
Humic Acid	5	0.0639*	5.23**	0.00514**
Genotype × Humic	10	0.0485*	3.95**	0.00071**
Error B	30	0.0221	0.36	0.00011

- Notes: *Significant at P ≤ 0.05* - Significant at P ≤ 0.01 - n.s = non-significant

Table 2. Mean Effect of Genotypes, Humic Acid Concentrations, and Their Interaction on Protein Content (%)

GENOTYPE	0 KG·HA⁻ ¹	20 KG·HA⁻ ¹	40 KG·HA⁻ ¹	MEAN OF GENOTYPES
Drakma	6.18 j	6.77 i	6.48 ij	6.48 d
TORRO	9.30 b	8.31 d	10.36 a	9.32 a
Fito	7.87 ef	7.64 f	7.17 h	7.56 c
Julie	7.57 fg	8.96 c	8.19 de	8.24 b
Holland	8.09 de	7.28 gh	9.56 b	8.31 b
Mean of Humic Acid	7.80 b	7.79 b	8.35 a	—

- **Note:** Means followed by different letters within a column or row are significantly different at $P \leq 0.05$; means with the same letter are not significantly different.

Table 3. Mean Effect of Genotypes, Humic Acid Concentrations, and Their Interaction on Oil Content (%)

GENOTYPE	0 KG·HA⁻ ¹	20 KG·HA⁻ ¹	40 KG·HA⁻ ¹	MEAN OF GENOTYPES
Drakma	3.94 ef	4.15 cde	4.06 def	4.05 b
TORRO	4.07 def	3.80 fg	4.29 bcd	4.05 b
Fito	4.47 b	4.08 def	4.00 def	4.18 b
Julie	3.48 h	3.80 fg	3.57 gh	3.62 c
Holland	4.56 b	4.44 bc	5.15 a	4.72 a
Mean of Humic Acid	4.10 ab	4.05 b	4.21 a	—

- **Note:** Means followed by different letters within a column or row are significantly different at $P \leq 0.05$; means with the same letter are not significantly different.

Table 4. Mean Effect of Genotypes, Humic Acid Concentrations, and Their Interaction on Specific Weight ($g\cdot hL^{-1}$)

GENOTYPE	0 KG·HA⁻¹	20 KG·HA⁻¹	40 KG·HA⁻¹	MEAN OF GENOTYPES
Drakma	71.34 gh	70.84 h	71.62 fgh	71.27 d
TORRO	73.86 cde	78.64 a	76.69 b	76.40 a
Fito	74.21 cde	73.95 cde	72.92 efg	73.70 bc
Julie	72.67 efg	73.10 d-g	73.57 cde	73.11 c
Holland	74.95 bcd	73.31 def	75.26 bc	74.51 b
Mean of Humic Acid	73.41 a	73.97 a	74.02 a	—

- **Note:** Means followed by different letters within a column or row are significantly different at P ≤ 0.05; means with the same letter are not significantly different.

Table 5. Mean Effect of Genotypes, Humic Acid Concentrations, and Their Interaction on Bulk Density ($g\cdot cm^3$)

GENOTYPE	0 KG·HA⁻¹	20 KG·HA⁻¹	40 KG·HA⁻¹	MEAN OF GENOTYPES
Drakma	0.711 f	0.727 ef	0.722 ef	0.720 d
TORRO	0.772 abc	0.791 a	0.782 ab	0.781 a
Fito	0.740 de	0.708 f	0.765 bc	0.738 c
Julie	0.772 abc	0.766 bc	0.758 cd	0.765 b
Holland	0.740 de	0.740 de	0.759 cd	0.746 c
Mean of Humic Acid	0.747 b	0.746 b	0.757 a	—

- **Note:** Means followed by different letters within a column or row are significantly different at P ≤ 0.05; means with the same letter are not significantly different.

Table 6. Mean Effect of Genotypes, Humic Acid Concentrations, and Their Interaction on Carbohydrate Content (%)

GENOTYPE	0 KG·HA⁻ ¹	20 KG·HA⁻ ¹	40 KG·HA⁻ ¹	MEAN OF GENOTYPES
Drakma	71.60 efg	72.45 cde	72.00 def	72.02 b
TORRO	71.64 efg	75.33 a	73.36 bc	73.44 a
Fito	72.32 c-f	71.18 fg	70.59 g	71.36 c
Julie	72.86 bcd	71.68 efg	72.17 def	72.24 b
Holland	72.11 def	71.98 def	73.56 b	72.55 b
Mean of Humic Acid	72.11 a	72.52 a	72.33 a	—

- **Note:** Means followed by different letters within a column or row are significantly different at P ≤ 0.05; means with the same letter are not significantly different.

Table 7. Mean Effect of Genotypes, Humic Acid Concentrations, and Their Interaction on Ash Content (%)

GENOTYPE	0 KG·HA⁻ ¹	20 KG·HA⁻ ¹	40 KG·HA⁻ ¹	MEAN OF GENOTYPES
Drakma	1.65 bc	1.70 bc	1.77 abc	1.71 b
TORRO	1.70 bc	2.00 a	1.91 ab	1.87 a
Fito	1.57 c	1.75 abc	1.69 bc	1.67 b
Julie	1.86 ab	1.69 bc	1.52 c	1.69 b
Holland	1.76 abc	1.75 abc	1.88 ab	1.79 ab
Mean of Humic Acid	1.70 a	1.78 a	1.75 a	—

- **Note:** Means followed by different letters within a column or row are significantly different at P ≤ 0.05; means with the same letter are not significantly different.

Table 8. Genetic Parameters of Studied Traits under First Environment (0 kg·ha⁻ ¹ Humic Acid)

STUDIED TRAITS	PROTEIN (%)	OIL (%)	SPECIFIC WEIGHT (G·HL⁻ ¹)	BULK DENSITY (G·CM³)	CARBOHYDRATE (%)	ASH (%)
Genetic Variance (σ²G)	1.20	0.80	0.0002	0.12	0.0037	0.03
Error Variance (σ²E)	0.67	1.08	0.0003	0.10	0.0067	0.17
Environmental Variance (σ²Env)	0.01	0.20	0.0001	0.02	0.0003	0.20
Standard Error	0.01	0.25	0.0001	0.02	0.0004	0.25
Phenotypic Variance (σ²P)	1.21	1.00	0.0002	0.14	0.0041	0.23
Standard Error of Phenotype	0.44	0.37	0.0001	0.05	0.0015	0.09
Genotypic Coefficient of Variation (GCV, %)	14.03	1.22	1.66	8.47	3.56	0.24
Environmental Coefficient of Variation (ECV, %)	1.28	0.61	1.22	3.07	1.09	0.62
Phenotypic Coefficient of Variation (PCV, %)	14.09	1.37	2.06	9.01	3.72	0.67
Broad-Sense Heritability (H², %)	99.18	79.88	64.78	88.41	91.39	13.23
Expected Genetic Advance (GA)	1.53	1.12	0.01	0.46	0.08	0.09
Expected Genetic Advance (%)	19.56	1.53	1.87	11.15	4.76	0.12

Supplementary Table 8. Genetic Parameters of Studied Traits under Second Environment (20 kg·ha^{-1} Humic Acid)

STUDIED TRAITS	PROTEIN (%)	OIL (%)	SPECIFIC WEIGHT (G·HL^{-1})	BULK DENSITY (G·CM^3)	CARBOHYDRATE (%)	ASH (%)
Genetic Variance (σ^2G)	0.73	2.17	0.0009	0.0387	0.0124	1.53
Error Variance (σ^2E)	0.40	4.39	0.0005	0.0390	0.0087	1.43
Environmental Variance (σ^2Env)	0.02	0.61	0.00001	0.0126	0.0003	0.06
Standard Error	0.03	0.75	0.00001	0.0155	0.0003	0.08
Phenotypic Variance (σ^2P)	0.75	2.79	0.0009	0.0513	0.0127	1.59
Standard Error of Phenotype	0.27	1.02	0.0003	0.0187	0.0046	0.58
Genotypic Coefficient of Variation (GCV, %)	10.95	1.99	4.16	4.85	6.25	1.71
Environmental Coefficient of Variation (ECV, %)	1.90	1.06	0.41	2.77	0.90	0.34
Phenotypic Coefficient of Variation (PCV, %)	11.11	2.26	4.18	5.59	6.31	1.74
Broad-Sense Heritability (H^2, %)	97.09	77.95	99.03	75.42	97.97	96.12
Expected Genetic Advance (GA)	1.18	1.82	0.04	0.24	0.15	1.70
Expected Genetic	15.11	2.46	5.80	5.90	8.66	2.34

Advance (%)						

Supplementary Table 21. Genetic Parameters of Studied Traits under Third Environment (40 kg·ha^{-1} Humic Acid)

STUDIED TRAITS	**PROTEIN (%)**	**OIL (%)**	**SPECIFIC WEIGHT (G·HL^{-1})**	**BULK DENSITY (G·CM^3)**	**CARBOHYDRATE (%)**	**ASH (%)**
Genetic Variance (σ^2G)	2.599	1.364	0.0003	0.326	0.002	0.649
Error Variance (σ^2E)	1.394	2.116	0.0002	0.181	0.016	0.765
Environmental Variance (σ^2Env)	0.003	0.174	0.00002	0.001	0.022	0.101
Standard Error	0.004	0.213	0.00003	0.001	0.026	0.124
Phenotypic Variance (σ^2P)	2.602	1.538	0.0003	0.327	0.024	0.750
Standard Error of Phenotype	0.950	0.562	0.0001	0.119	0.009	0.274
Genotypic Coefficient of Variation (GCV, %)	19.30	1.58	2.36	13.54	2.53	1.11
Environmental Coefficient of Variation (ECV, %)	0.67	0.56	0.62	0.56	8.34	0.44
Phenotypic Coefficient of Variation (PCV, %)	19.31	1.68	2.44	13.55	8.72	1.20
Broad-Sense Heritability (H^2, %)	99.88	88.68	93.59	99.83	8.40	86.56
Expected Genetic	2.26	1.54	0.02	0.80	0.02	1.05

Advance (GA)						
Expected Genetic Advance (%)	27.00	2.08	3.20	18.93	1.02	1.45

References

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