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Estimating some genetic parameters for quality traits in oat (*Avena Sativa* L.) under the effect of different potassium foliar spray concentrations

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Abstract

This study was conducted during the winter growing time (2024-2025) at the Agricultural Research and Experimental Station of the College of Agriculture, University of Kirkuk. The experiment was arranged according to a split-plot system within a randomized complete block design (RCBD), with triple replications. The experiment fell into three main plots, which comprised foliar application levels of potassium supplied as potassium sulfate (52% K_2O) at three concentrations (0, 10, and 20 g L^{-1}). Each subplot included thirteen oat genotypes, namely: Alguda, Anatolia, Pimula, Genzania, Hamel, Icarda Short, Kangaroo, Icarda Tall, Mitika, Possum, UC-132, Monte Zuma, and Cayuse. Each block contained 39 experimental units, to which treatments representing all possible combinations of the studied factors were randomly assigned. The quality traits of yield that were evaluated included crude protein (%), crude fiber (%), soluble carbohydrates (%), moisture percentage (%), and ash percentage (%). The results of the study can be summarized as follows: phenotypic variances were greater than both genetic and environmental variances for all traits, and genetic variance exceeded environmental variance at all potassium concentrations. The phenotypic and genotypic coefficients of variation ranged from low to high across the studied traits. For crude protein (%), the phenotypic, genotypic, and environmental coefficients of variation at the three potassium spraying levels (0K, K1, and K2) were generally moderate, while the phenotypic coefficient of variation was high at all concentrations except 0K. For crude fiber (%), the coefficients of variation were low at all three spraying levels. In the case of soluble carbohydrates (%), the coefficients were low at all spraying levels, except at concentration K2, where the phenotypic coefficient of variation was moderate. Regarding moisture percentage (%), the phenotypic and genotypic coefficients of variation were moderate at all three spraying levels, whereas the environmental coefficients were low. For ash percentage (%), the coefficients of variation were moderate at all three spraying levels, except at concentration 0K, where the phenotypic and genotypic coefficients were high.

Broad-sense heritability estimates were moderate to high for all studied traits under the three potassium concentrations (0K, K1, and K2). High heritability values were recorded for crude protein (%), crude fiber (%), and moisture percentage (%), reaching (0.835, 0.682, 0.751), (0.724, 0.724, 0.739), and (0.741, 0.906, 0.713), respectively. High heritability was also observed for soluble carbohydrates (%) and ash percentage (%) at concentrations 0K and K2, amounting to (0.630 and 0.791) and (0.884 and 0.694), respectively, while moderate heritability was recorded at concentration K1, with values of (0.560) and (0.504), respectively. As for the EGA expressed as a rate of the overall mean for the studied traits under the three potassium spraying levels (0K, K1, and K2), high values were obtained for crude protein (%) at all concentrations, reaching (46.42, 31.67, and 31.52), respectively. Similarly, ash percentage (%) showed high expected genetic advance at concentrations 0K and K2, amounting to (57.50 and 32.79), respectively.

Keywords: Genetic parameters, quality traits, potassium, oat

Introduction

Oat (*Avena sativa* L.) belongs to Poaceae and is an important annual herbaceous crop. Numerous studies and research indicate that oats were cultivated in ancient times in different parts of the world. Statistics and estimates for 2013 showed that Russia was among the largest producers of oats, followed by the United States of America, then Canada and Australia (Scapim *et al.*, 2006) [38]. In 2018, the global cultivated area reached approximately 9.50 million hectares, with a total production nearly 23.50 million tons. Germany ranked first in terms of yield per hectare, followed by Denmark and France (USDA, 2018) [40]. In Iraq, the cultivated area in 2018 amounted to about 266.7 kg per dunum, with a total production of approximately 1 ton (Central Statistical Organization, 2018) [15]. Oat is a crop used in both human and animal nutrition; its grains are rich in essential nutrients (Abdullah & Hasan, 2020) [2]. It is considered beneficial for heart, reducing harmful cholesterol levels and high blood pressure, while its fiber contributes to weight-loss diets, facilitates digestion, and helps alleviate constipation (Ahmad, 2014) [15].

Genetic variability constitutes the basic material upon which plant breeders rely to improve both yield and quality traits (Jaber *et al.*, 2024) [27]. Specialists have focused on studying the components of phenotypic variation in quantitative and qualitative traits, such as grain protein content, because of their importance in estimating phenotypic and genotypic coefficients of variation, heritability, and EGA (Hasan & Abdullah, 2021) [22]. Selection programs primarily depend on the presence of genetic variation and on understanding the genetic behavior of such traits (Al-Jubouri *et al.*, 2011) [9]. Breeding crops for high yield and good quality requires knowing both the magnitude and nature of variation within the genetic resources under study (Alatawi *et al.*, 2024) [6]. The availability of genetic diversity represents a continuous source of variation, which forms the basis for selecting plants superior in their productive traits (Hasan *et al.*, 2023) [23]. The phenotype of any individual within a population results from the interaction between genetic makeup and environment, whereas environmental variance refers to differences among plants with identical genetic constitutions (Al-Jubouri *et al.*, 2024) [10]. Genetic variance, on the other hand, reflects differences in the phenotypic expression of plant traits arising from differences in genetic composition despite equal environmental effects (Elyas & Mahfouz, 1985) [17]. In light of these genetic aspects, and in order to determine the most appropriate approach for their improvement, this paper aimed at estimating the components of phenotypic variance, variance coefficients, broad-sense heritability, and EGA expressed as a ratio.

Materials and Methods

The experimentation was made in the Agricultural Research and Experimental Station (Al-Sayyadah area) related to the Faculty of Agriculture, University of Kirkuk, during the 2024-2025 growing season. The soil prepared for the field experiment was plowed by using a moldboard plow in two perpendicular passes, followed by leveling and smoothing operations. Diammonium phosphate fertilizer (DAP) containing 46% P_2O_5 and 18% N was used at a 320 kg ha^{-1} (equivalent to 96 g per experimental unit). Urea fertilizer (46% N) was also applied at the launch of the tillering stage at 200 kg ha^{-1} (Subahi *et al.*, 1992) [39].

Seeds of the oat genotypes listed in Table (1), along with their origin and source, were sown manually.

Table 1: Oat genotypes, their codes, breeding institutions, and sources.

Code	Genotype	Breeding institution	Source
1	Alguda	-	Obtained from the Dept. of Field Crops, Faculty of Agriculture, University of Baghdad
2	Anatolia	-	
3	Pimula	Italy	
4	Genzania	-	
5	Hamel	Italy	
6	Icarda short	ICARDA	Obtained from the Conservation Agriculture Program jointly implemented by the Ministry of Agriculture, University of Mosul, and the International Center for Agricultural Research in the Dry Areas (ICARDA)
7	Kangaroo	Australia	
8	Icarda tall	ICARDA	
9	Mitika	Australia	
10	Possum	Australia	
11	UC-132	USA	Obtained from the Agricultural Research Directorate, Sulaymaniya
12	Monte Zuma	USA	
13	Cayuse	USA	

Narrow- and broad-leaf weeds were removed manually, and the experiment was irrigated according to crop requirements. The experimentation was arranged out using a split-plot method within (RCBD) with triple replications. Each replication included three main plots assigned to the potassium spraying levels.

Each main plot was further divided into thirteen subplots, to which the oat genotypes were randomly allocated. Each experimental unit consisted of four rows, each 3 m long, with a spacing of 0.25 m among rows. The area of each experimental unit was 3 m².

A distance of 0.70 m was left between adjacent experimental units, and 1 m between main plots and between blocks (Hasan *et al.*, 2024) [24]. A fixed number of seeds was sown in each experimental unit based on the thousand-grain weight of each genotype; 105 seeds were planted in each row. The study involved two factors. The first factor was foliar application of potassium at the stem elongation stage, applied as potassium sulfate (52% K_2O) at three concentrations: 0, 10, and 20 g L^{-1}, denoted as K0, K1, and K2, respectively. The second factor consisted of the thirteen oat genotypes included in the experiment.

Genetic Analysis

Genetic analysis was performed separately at each potassium level using the GENES software, as described below.

Genotypic, Phenotypic, and Environmental Variances and Variation Coefficients

The three types of variances were estimated according to the method described by Walter (1975) at each potassium level, as follows:

$$\frac{Msg-Mse}{r} = \sigma_G{}^2 \text{ ، } \sigma_E{}^2 = \frac{Mse}{r}\text{،}^2 \qquad \sigma_E + {}^2\, \sigma_G = \sigma_P{}^2$$

The values of the phenotypic and genotypic variation coefficients were calculated according to the method described by Falconer (1981) [18], and interpreted based on the ranges adopted by Agarwal and Ahmed (1982) [4], Rashid (1989) [36], and Younis *et al.* (2024a) [43]. Accordingly, values lower than 10% were deemed low, values in the middle of 10% and 30% were moderate, and values higher than 30% were high, as follows:

$$P.C.V\ \% = \frac{\sigma_P}{\bar{X}} \times 100 \qquad G.C.V\ \% = \frac{\sigma_G}{\bar{X}} \times 100$$

Where;

- P.C.V = phenotypic coefficient of variation
- G.C.V = genotypic coefficient of variation
- σP = phenotypic standard deviation
- σG = genotypic standard deviation
- X = overall mean of the trait

Heritability and EGA as a Percentage

Broad-sense heritability was calculated according to Hanson *et al.* (1956) [20]. The ranges adopted by Ali (1999) [8] and Mohammed (2000) [32] were used for interpretation, whereby values lower than 40% were deemed low, values between 40-60% were moderate, and values higher than 60% were high, as follows:

$$H^2_{B.S} = \frac{\sigma_G^2}{\sigma_P^2}$$

The (G.A.) was estimated based on the adopted limits of genetic advance, where values less than 10% were low, values between 10-30% were moderate, and values greater than 30% were considered high, according to Abdul-Rahmaan *et al.* (2023) [1], Agarwal and Ahmed (1982) [4], and Younis *et al.* (2024b) [44], using the following equation:

$$G.A = K. \times H^2_{B.s.} \times \sigma P$$

Where;

- G.A = expected genetic advance
- K = constant equal to 76.1 at a selection intensity of 10% of the genotypes
- $H^2B.s$ = broad-sense heritability
- σp = phenotypic standard deviation of the trait

The expected genetic advance as a percentage of the mean (G.A.%) was estimated according to the trait mean based on the method of Kempthorne. (1969) [29].

$$E.G.A = \frac{G.A}{\bar{X}} \times 100$$

Where;

- E.G.A = expected genetic advance as a percentage of the overall mean of the trait
- G.A = expected genetic advance
- X = overall mean of the trait

Results and Discussion

Phenotypic, Genotypic, and Environmental Variances

Table (2) presents the values of phenotypic, genotypic, and environmental variances for the traits. It is evident that phenotypic variance values were greater than both genotypic and environmental variances at all potassium concentrations (K0, K1, and K2) and for all traits. In addition, the proportion of genetic variance contributing to the total variance differed according to the potassium spraying levels. For crude protein (%), the genetic variance was notably high when compared with the environmental variance at all potassium concentrations. These results agree with those noted by Al-Hazzāʿ (2001) [7]. Regarding crude fiber (%), concentration K2 exhibited a higher genetic variance compared with concentrations K0 and K1, whereas the environmental variance was low at concentration K1 and nearly similar at concentrations K0 and K2. Related findings were noted by Gandhi *et al.* (1964) [19], Ayoub (2004) [14], and Humada *et al.* (2024) [25].

In the case of soluble carbohydrates (%), the genetic variance at concentration K2 was high compared with the environmental variance at the same concentration, followed by K1 and then K0. These results are consistent with those obtained by Masood *et al.* (1986) [30]. For moisture percentage (%), the highest genetic variance was recorded at concentration K1, accompanied by a low environmental variance at the same level, followed by concentration K2 and then K0. Comparable findings were reported by Qasim *et al.* (1992) [35]. With respect to ash percentage (%), genetic variance was high at concentration K0, while the corresponding environmental variance was low at the same concentration. At concentration K1, genetic variance was equal to environmental variance, whereas at concentration K2, genetic variance was higher than environmental variance. Similar results were reported by Al-Hazzāʿ (2001) [7], Al-Tawil (2003) [12], Salem (2024) [37], and Omar and Al-Layla (2024) [33].

Phenotypic, Genotypic, and Environmental Coefficients of Variation: This measure is used to estimate the degree of dispersion and variability of traits that differ in their units of measurement, and to compare them to specify the extent of uniformity or greater variability among traits or samples. The outcomes in Table (3) show the values of variances and the phenotypic, genotypic, and environmental coefficients of variation for the studied traits under three potassium spraying concentrations (0K, K1, and K2). These values varied according to the different spraying levels and within the same genotype. Agarwal and Ahmed (1982) [4] and Rashid (1989) [36] proposed interpretive ranges that are commonly adopted, where values lower than 10% are deemed low, values between 10-30% are considered moderate, and values greater than 30% are considered maximal. Accordingly, the coefficients of variation ranged from low too high for all traits.

For crude protein (%), the phenotypic, genotypic, and environmental coefficients of variation at the three potassium spraying levels (0K, K1, and K2) were generally moderate, while the phenotypic coefficient of variation was high at all spraying levels except 0K. For crude fiber (%), all coefficients of variation were low at the three spraying levels. In the case of soluble carbohydrates (%), the coefficients of variation were low at all spraying levels, except at concentration K2, where the phenotypic coefficient of variation was moderate. Regarding moisture percentage (%), the phenotypic and genotypic coefficients of variation were moderate at all three spraying levels, whereas the environmental coefficients were low at all three levels. For ash percentage (%), the coefficients of variation were moderate at all spraying levels, except at concentration 0K, where the phenotypic and genotypic coefficients were high. In general, the results of the phenotypic, genotypic, and environmental coefficients of variation showed differences depending on potassium spraying concentrations. This variation can be attributed to differences in the magnitudes of phenotypic, genotypic, and environmental variances, providing evidence for the importance of studying phenotypic × environment and genotype × environment interactions. High genetic variance values offer plant breeders greater opportunities for selection and improvement of grain quality traits. These findings are consistent with those reported by several researchers, including Daniela *et al.* (2019) [16], Mayuri and Ajay (2020) [31], and Abdul-Rahmaan *et al.* (2024) [46].

G.A as a Percentage

Genetic advance in a selection program primarily depends on the presence of genetic variation and the selection method based on traits associated with yield. The (G.A.%) from the overall mean of the studied trait guides the selection process used to improve the targeted traits. The concept of G.A as a percentage has been discussed by Johanson *et al.* (1955) [28] and Kempthorne (1969) [29], with interpretive ranges suggested by Robinson *et al.* (1951) [47] and Agarwal & Ahmed (1982) [4]: values lower than 10% are low, 10-30% moderate, and greater than 30% high.

Table (4) illustrates the values of G.A as a percentage of the general mean for the studied traits under three potassium spray concentrations (K0, K1, and K2). The results indicate that the G.A percentage was high for crude protein (%) at all concentrations, reaching 46.42%, 31.67%, and 31.52%, respectively. A high G.A percentage was also noticed for ash content (%) at concentrations K0 and K2, amounting to 57.50% and 32.79%, respectively. Moderate values of expected genetic advance percentage were recorded for moisture content (%) at the three spray concentrations (K0, K1, and K2), with values of 20.06%, 23.80%, and 17.35%, respectively. Similarly, moderate values were observed for crude fiber (%) at concentration K2 (10.95%), for soluble carbohydrates (%) at concentration K2 (14.20%), and for ash content (%) at concentration K1 (20.54%). In contrast, low values of G.A advance percentage were noted at the three spray concentrations (K0 and K1) for crude fiber (%) and soluble carbohydrates (%), reaching 9.55% and 9.26% for crude fiber, and 8.78% and 9.02% for soluble carbohydrates, respectively. These results indicate that the selection response (expected genetic advance as a percentage) ranged from moderate to high for most traits, including crude protein. This shows the effectiveness of selection in enhancing such traits (Younis *et al.*, 2022a) [42]. These findings go with those by Premkuma *et al.* (2017) [34], Atar *et al.* (2018) [13], Mayuri & Ajay (2020) [31], and Hasan *et al.* (2025) [21].

Broad-Sense Heritability

Estimating heritability for any quantitative trait is essential, as it helps in determining the most suitable breeding method for improving traits. Broad-sense heritability also indicates the relative contribution of genetic and environmental effects to the phenotypic expression of a trait. According to the ranges suggested by Ali (1999) [8] and Mohammed (2000) [32], values lower than 40% are considered low, 40-60% moderate, and greater than 60% high. As shown in Table (5), broad-sense heritability values for the traits under three potassium concentrations (0K, K1, and K2) ranged from moderate to high. High heritability values were recorded for crude protein (%), crude fiber (%), and moisture content (%), reaching 0.835, 0.682, 0.751; 0.724, 0.724, 0.739; and 0.741, 0.906, 0.713, respectively. High heritability was also observed for soluble carbohydrates (%) and ash content (%) at concentrations 0K and K2, reaching 0.630, 0.791 and 0.884, 0.694, respectively, while at K1, these values were moderate, with 0.560 and 0.504, respectively.

The high broad-sense heritability values for the above traits are attributed to the higher genetic variance in comparison to environmental variance (Table 3) (Younis *et al.*, 2022b) [45]. These findings align with previous studies by Premkuma *et al.* (2017) [34], Atar *et al.* (2018) [13], Mayuri & Ajay (2020) [31], Abdullah *et al.* (2025) [3], Humada *et al.* (2025) [26], and Al-Mafarji *et al.* (2024) [11].

Conclusions

The study found moderate values related to variance and coefficients of variation, and high values for broad-sense heritability. This provides plant breeders with an opportunity to select superior genotypes, as the genetic contribution is clearly expressed in the performance of these genotypes. This is reflected in the moderate-to-high expected genetic advance for most yield traits and their quality components.

Recommendations

A great emphasis should be placed on the superior genetic genotype in subsequent experiments in order to provide it with the greatest opportunity for continued improvement of grain quality traits through selection for other traits. In addition, it should be incorporated into future breeding programs to benefit from its genetic potential after achieving genetic stability, and hybridization should be conducted with other genotypes to transfer desirable traits to and from different genetic backgrounds. Furthermore, potassium spray concentrations higher than 20 g L^{-1} are recommended to determine the extent of oat plant responsiveness to increased potassium levels.

Table 2: Phenotypic, genotypic, and environmental variances.

Studied Traits	K	Phenotypic Variance	Genotypic Variance	Environmental Variance
Crude Protein (%)	K0	1.20	1.00	0.19
	K1	1.24	0.85	0.39
	K2	1.17	0.88	0.29
Crude Fiber (%)	K0	10.73	7.44	3.29
	K1	9.61	6.96	2.64
	K2	13.93	10.29	3.63
Soluble Carbohydrates (%)	K0	10.67	6.72	3.94
	K1	15.86	8.89	6.96
	K2	21.35	16.89	4.45
Moisture (%)	K0	3.05	2.26	0.78
	K1	3.42	3.10	0.31
	K2	3.87	2.76	1.11
Ash (%)	K0	0.28	0.25	0.03
	K1	0.14	0.07	0.07
	K2	0.31	0.21	0.09

Table 3: Phenotypic, Genotypic, and Environmental Coefficients of Variation

Studied Traits	K	Phenotypic CV (%)	Genotypic CV (%)	Environmental CV (%)
Crude Protein (%)	K0	31.55	28.85	12.78
	K1	26.38	21.79	15.83
	K2	23.82	20.65	11.86
Crude Fiber (%)	K0	7.83	6.52	4.34
	K1	7.26	6.18	3.80
	K2	8.42	7.24	4.30
Soluble Carbohydrates (%)	K0	7.91	6.28	4.81
	K1	9.14	6.84	6.05
	K2	10.20	9.07	4.66
Moisture (%)	K0	15.37	13.23	7.81
	K1	14.91	14.20	4.55
	K2	13.82	11.67	7.40
Ash (%)	K0	36.94	34.74	12.56
	K1	23.14	16.44	16.29
	K2	26.84	22.36	14.84

Table 4: Expected Genetic Advance as a Percentage (G.A.%)

Studied Traits	K	Expected Genetic Advance	G.A. (%)
Crude Protein (%)	K0	1.61	46.42
	K1	1.26	31.67
	K2	1.43	31.52
Crude Fiber (%)	K0	3.99	9.55
	K1	3.95	9.26
	K2	4.85	10.95
Soluble Carbohydrates (%)	K0	3.62	8.78
	K1	3.93	9.02
	K2	6.43	14.20
Moisture (%)	K0	2.28	20.06
	K1	2.95	23.80
	K2	2.47	17.35
Ash (%)	K0	0.83	57.50
	K1	0.33	20.54
	K2	0.68	32.79

Table 5: Broad-Sense Heritability (H^2 B.s)

Studied Traits	K	Broad-Sense Heritability
Crude Protein (%)	K0	0.835
	K1	0.682
	K2	0.751
Crude Fiber (%)	K0	0.693
	K1	0.724
	K2	0.739
Soluble Carbohydrates (%)	K0	0.630
	K1	0.560
	K2	0.791
Moisture (%)	K0	0.741
	K1	0.906
	K2	0.713
Ash (%)	K0	0.884
	K1	0.504
	K2	0.694

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