Effect of plant density on gene expression of broad bean (*Vicia faba* L.)

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Abstract

This study, conducted in Nineveh province, Iraq, investigated the inheritance of growth and yield traits in six broad bean genotypes (BASIC, MONARCH, AQUADLGE, HISTAL, CLARO DE LUNA, and LUZ DE OTONO) under three plant densities (66,666, 53,333, and 44,444 plants.ha^{-1}) during the 2024-2025 autumn growing season. The experiment was conducted in a field in the Al-Kuwayr area of Mosul as a factorial experiment with eighteen treatments, following a completely traits except for the number of pods and the percentage of protein in the seeds, where the randomized block design with three replications. The results of the analysis of variance (ANOVA) indicate significant differences among the six genotypes for all the studied differences did not reach significance. The MONARCH genotype gave the highest average dry seed yield, significantly higher than the CLARO DE LUNA and LUZ DE OTONO genotypes. Plants at a density of 66,666 plants.ha^{-1} also recorded the highest average dry seed yield, significantly higher than those at a density of 44,444 plants.ha^{-1}. The highest average dry seed yield was observed in plants with the HISTAL genotype grown at a density of 66,666 plants.ha^{-1}, significantly excelled other interaction treatments. Genotypic variance values were significant (≥0) for all studied traits except for the number of pods and the percentage of protein in the seeds. Environmental variance values were also significant (≥0) for all studied traits. The Heritability Broad Sense values were high for plant height and flowering time. This high heritability indicates that an individual's appearance is strongly influenced by its genotype, suggesting the potential for direct improvements to these traits in subsequent seasons. The expected genotype improvement values, expressed as a percentage of the average trait, were low for flowering time, maturity, number of pods, and percentage of protein in the seeds, and moderate for the remaining traits.

Keywords: Broad beans, plant density, genotypic variance, heritability

Introduction

Broad beans (*Vicia faba* L.) are one of the most important crops of Fabaceae family,. Their importance stems from their use as a food source for humans, as their pods and seeds contain essential nutrients such as carbohydrates, amino acids, vitamins, fats, and several other nutrients. Furthermore, the seeds have a high protein content, ranging from 31.8% to 39.7% [5]and contain 217 IU of vitamin A per 100 grams. They are also high in iron and calcium [24] Their plant residues are used as livestock feed. Additionally, broad beans are important for increasing soil fertility and improving its granular structure when planted in rotation with other legume crops to fix nitrogen and maintain soil fertility and productivity [1]. Studies indicate that the Mediterranean basin is their original habitat. Broad beans have spread to various parts of the world [29]. In Iraq, the cultivated area reached approximately 20,811 dunams in 2022, with an average yield of 1950.2 kg/dunam and a total production of about 40,586 [12]. Globally, the area cultivated with this crop, both as a green and dry crop, reached 2.7 million hectares, with a total production of 9.3 million tons [14].Therefore, it has become imperative for those involved in this crop to work on increasing its productivity per unit area, both quantitatively and

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qualitatively. Plant breeders have a significant role in this through their work on introducing new genotype that are suitable for Iraq's environmental conditions. Genetic evaluation of these combinations is particularly important for informing breeding program recommendations to achieve the genetic improvement sought by plant breeders when genetic information about these varieties is lacking. To a sufficient extent [7].Studying the effect of genetic makeup on growth and yield traits is of particular importance in plant breeding programs. It is the first step towards selecting genetically superior genetic makeups, whether for direct use in agriculture or as parents in hybridization and selection programs. Furthermore, evaluating genetic makeups under different environmental conditions helps in understanding the interaction between genetic makeup and the environment, which is a crucial factor in stabilizing productivity and achieving the highest possible yield [13].Many studies have indicated strong competition for nutrients between reproductive and vegetative growth. Therefore, it has become necessary to find agricultural practices that aim to provide nutrients to the reproductive parts in order to increase production and improve quality. One of the most important of these practices is plant density, which directly affects the efficiency of using environmental resources such as light, water, and nutrients. Determining the optimal plant density contributes to reducing competition between plants and achieving the best plant distribution per unit area, which is reflected positively in morphological and physiological traits and yield components [28].The traits of any crop are a result of genetic and environmental interaction. Therefore, plant breeders should aim to understand the nature of the relationship between plant traits and metabolic processes, as well as phenotypic traits, since these are genetically governed. This understanding is only possible by estimating genetic and phenotypic variations to enable the development of a program for selecting multiple traits simultaneously [4].Estimating the heritability of quantitative traits is among the most important estimations that plant breeders have focused on. It has become clear that by estimating heritability broad sense, the contribution of both genetic and environmental influences to the trait's appearance can be determined. Thus, the heritability value can serve as a measure to determine the relationship between parents and offspring. Heritability is a crucial genetic parameter that must be known for any quantitative trait, as determining the best breeding method for improving a given trait depends on its estimation. Furthermore, its estimation is important for determining the expected genetic advance, which is the most significant application of quantitative heritability theory in plant breeding and improvement programs [8]. Therefore, the current study aims to estimate the heritability, genetic and phenotypic variations, their coefficients, and the Expected Genetic Advance for the traits of the yield and its components for six genotypes of broad beans under study, under the influence of three different plant densities under the conditions of Nineveh Governorate, in order to select the best of these traits in subsequent early generations and more effectively to continue with the good ones in future breeding programs for this crop.

Materials and Methods

This study was conducted during the autumn growing season of 2024-2025 in an agricultural field in the Al-Kuwayr area of Mosul, located at latitude 36.35°N and longitude 43.15°E, at an altitude of 223 meters above sea level [16] The aim was to estimate some genetic parameters under the conditions of Nineveh province for six broad bean genotypes (BASIC, MONARCH, AQUADLGE, HISTAL, CLARO DE LUNA, and LUZ DE OTONO) under the influence of three plant densities (66,666, 53,333, and 44,444 plants.ha^{-1}) (1). The seeds of the six genotypes were sown on 11/16/2024 on rows representing the experimental unit, which

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included three rows, each 2 meters long with 0.75 meters between rows. Thus, the area of the experimental unit was (3 rows × 2 m row length × 0.75 m distance between rows = 4.5 m²). For the three planting distances (20, 25, and 30 cm) between plants, the average was (10 plants per row at a planting distance of 20 cm between plants) with a plant density of (66,666 plants.ha $^{-1}$), (8 plants per row at a planting distance of 25 cm between plants) with a plant density of (53,333 plants.ha $^{-1}$), and (6 plants per row at a planting distance of 30 cm between plants) with a plant density of (44,444 plants.ha $^{-1}$). Thus, the number of plants sown in each experimental unit became (30 plants at a planting distance of 20 cm between plants). (24 plants at a spacing of 25 cm between plants) and (18 plants at a spacing of 30 cm between plants). Sowing was done at a rate of 3 seeds per hole, then thinning to one plant after germination. Agricultural practices were carried out equally for all treatments [23].Data were recorded for ten randomly selected plants per experimental unit. Data were statistically analyzed using SAS software [26] and Duncan's multiple range test was used to compare means at a probability level of 0.05.Phenotypic variance, genetic and environmental variance, and phenotypic and genotypic coefficients of variation were estimated according to [30] as follows.

$$\delta^2 P = \delta^2 G + \delta^2 E$$

Whereas:

Phenotypic Variance = (δ^2 P) Phenotypic variance

Genotypic Variance = (δ^2G) Genotypic variance

Environmental Variance = δ^2E) Environmental variance(

$$\delta^2 G = (\delta^2 \text{ Cultivars} - \delta^2 E) / RB$$

$$\delta^2 E = \text{Mse}$$

Whereas:

Average of cultivars squares= δ^2 Cultivars
Mean squared experimental error = δ^2 E
Mse = δ^2 E

Number of replicates = R

Plant density (3) = B

$$\text{PCV \%} = (\sqrt{\delta^2 P} / \tilde{Y}) \times 100.$$

$$\text{GCV \%} = (\sqrt{\delta^2 G} / \tilde{Y}) \times 100.$$

(PCV) Phenotypic Coefficients of Variation

Genotypic Coefficients of Variance(GCV) Genotypic Coefficients of Variation =

)Ỹ (It is the arithmetic mean of traits

The Heritability Broad Sense H^2(b.s) ratio was estimated by [18]using the following equation:

$$H^2(b.s) = (\delta^2 G / \delta^2 P) \times 100 .$$

The significance of Heritability Broad Sense values was expressed according to the scale presented by [6].

)Less than 40% is low, 40-60% is medium, and more than 60% is high.(

The Expected Genetic Advance E.G.A. was estimated based on the equation provided by [21] as follows.

$$\text{E.G.A.} = [(K \; H^2(b.s) \sqrt{\delta^2 P})].$$

Whereas:

Expected Genetic Advance = Expected Genetic Advance (E.G.A)

K = 2.06 This is the intensity of selection for 5% of plants.

The % Expected Genetic Advance was estimated from the arithmetic mean % E.G.A. as follows:

$$\text{E.G.A. \%} = [(K \; H^2(b.s) \sqrt{\delta^2 P}) / \tilde{Y}] \times 100.$$

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The Expected Genetic Advance limits reported by [25] were adopted as follows:

)Less than 10% is low, 10-30% is medium, and more than 30% is high.(

Results and Discussion

Table (1) presents the results of the analysis of variance for the studied broad bean traits. It shows that the mean squares of the six genotypes were significant for all the studied traits at a 1% probability level, except for the number of pods and the percentage of protein in the seeds, which were not significant. while, the mean squares of the plant density coefficients were significant at a 5% probability level for the maturity date trait, and significant at a 1% probability level for both the total dry seed yield and the dry biological yield. The differences did not reach statistical significance for the remaining traits. However, the effect of the interaction between genotypes and plant density did not reach statistical significance for all studied traits except for 100-seed weight and dry biological yield, where it was significant at the 5% probability level. This aligns with the findings of[11,20,27,31] who reported significant differences between genotypes for growth and yield traits in broad beans.

Table (1): Analysis of variance for studied traits, representing mean squares.

Mean Squares					degrees of freedom	Sources of variation
Number of pods (pod.plant^{-1})	**Maturity date (days)**	**Flowering date (days)**	**Number of branches (branch.plant^{-1})**	**Plant height (cm.plant^{-1})**		
1.711	**66.907**	**4.518**	**2.046**	**11.460**	**2**	**Replicates**
7.466	**50.6407 ** **	**18.907 ** **	**2.205 ** **	**982.440 ** **	**5**	**Genotype**
5.836	**24.685 * **	**0.296**	**0.275**	**57.298**	**2**	**Plant Density**
3.230	**10.285**	**1.629**	**0.269**	**33.206**	**10**	**Genotype × Plant Density**
5.069	**7.103**	**1.067**	**0.235**	**37.096**	**34**	**Experimental Error**

***and ** are significant at probability levels of 0.05 and 0.01, respectively.**

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Table (1) shows the analysis of variance for the studied traits, representing mean squares values.

Mean Squares					degrees of freedom	degrees of freedom
Percentage of protein in seeds	Dry biological yield ($ton.ha^{-1}$)	Total dry seed yield ($ton.ha^{-1}$)	Average weight of 100 seeds (g)	Number of seeds per pod ($seed.pod^{-1}$)		
4.254	49.949	0.940	2.113	0.503	2	Repeats
0.962	14.936 **	4.413 **	1721.207 **	1.423 **	5	Genotype
0.556	211.428 **	4.982 **	205.396	0.026	2	Plant density
0.480	2.517 *	0.335	350.361 *	0.055	10	Genotype × Plant density
0.785	1.235	0.850	172.526	0.114	34	Experimental error

*** and ** are significant at the probability levels of 0.05 and 0.01, respectively.**

The results in Table 2 show significant differences between the studied genotypes for plant height at the Al-Kuwair location. The HISTAL genotype exhibited the highest plant height at 72.000 $cm.plant^{-1}$, significantly higher than the LUZ DE OTONO and CLARO DE LUNA genotypes, which showed the lowest plant height at 50.111 $cm.plant^{-1}$. However, the differences between the three plant densities did not reach statistical significance.The results of the interaction between genotypes and plant density at the Al-Kuwair location indicated that the AQUADLGE genotype, planted at a density of 66,666 $plants.ha^{-1}$, exhibited the highest plant height at 75.533 $cm.plant^{-1}$ showed a significant advantage over some intervention treatments, while the lowest significant plant height was recorded in the CLARO DE LUNA genotype under the same plant density, reaching 48.067 cm.Table (3) shows significant differences between the genotypes for the number of branches per plant at the Al-Kuwair location. The AQUADLGE genotype showed the highest number of branches per plant, reaching 5.066. This was significantly higher than the BASIC and CLARO DE LUNA LUZ DE OTONO genotypes, the latter of which resulted in the lowest number of branches per plant, at 3.866. The effect of plant density did not reach statistical significance among the planted densities. The results of the interaction between genotypes and plant densities at the Al-Kuwair location indicate that plants with the AQUADLGE genotype, grown at a density of 66,666 $plants.ha^{-1}$, produced the highest number of branches per plant, averaging 5,333 $branches.plant^{-1}$, with a significant advantage under certain interaction parameters. Conversely, the lowest number of branches per plant was recorded for plants with the LUZ DE OTONO genotype at a density of 53,333 $plants.ha^{-1}$, at 3,333 $branches.plant^{-1}$.

Table (4) shows significant differences between the genotypes. The HISTAL genotype differed significantly from the others, exhibiting the longest period between planting and flowering, averaging 93.277 days, while the CLARO DE LUNA genotype recorded the shortest period between planting and flowering, averaging 89.388 days. However, the effect of plant density did not reach statistical significance. As for the results of the interaction between genotypes and plant densities, plants with the HISTAL genotype at

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a plant density of 66,666 plants.ha^{-1} recorded the longest time interval between planting and flowering, averaging 94.166 days, with a significant difference compared to most interaction treatments. Conversely, plants with the CLARO DE LUNA genotype at a plant density of 66,666 plants/ha and the LUZ DE OTONO genotype at a plant density of 66,666 plants.ha^{-1} recorded the shortest time interval between planting and flowering, averaging 89.166 days.

Table 2: Effect of genotypes, planting distances, and their interaction on plant height (cm.plant^{-1}).

Average genotype	Plant density plants.ha^{-1}			genotype
	44444	53333	66666	
68.644 a	68.600 a	65.667 a	71.667 a	**BASIC**
71.489 a	65.000 a	74.600 a	74.867 a	**MONARCH**
69.711 a	65.467 a	68.133 a	75.533 a	**AQUADLGE**
72.000 a	70.133 a	72.667 a	73.200 a	**HISTAL**
50.111 b	51.933 b	50.333 b	48.067 b	**CLARO DE LUNA**
50.622 b	50.933 b	50.800 b	50.133 b	**LUZ DE OTONO**
63.763	**62.011 a**	**63.700 a**	**65.578 a**	**Average plant density**

*** The averages that share the same alphabetical letters for each factor and the overlap between them do not differ significantly from each other according to Duncan's test at a probability level of 0.05.**

Table (3): The effect of genotype, planting distances and the interaction between them on the trait of number of branches (branch. plant^{-1}).

average genotype	Plant density (plants.ha- 1)			genotype
	44444	53333	66666	
4.333 b c	4.333 b -e	4.266 b -e	4.400 a -e	**BASIC**
4.600 ab	4.333 b -e	4.666 a -e	4.800 a-c	**MONARCH**
5.066 a	5.133 ab	4.733 a -d	5.333 a	**AQUADLGE**
4.844 a	5.066 ab	4.800 a-c	4.666 a -e	**HISTAL**
3.888 c	3.933 c -f	4.000 c -f	3.733 e f	**CLARO DE LUNA**
3.866 c	4.466 a -e	3.333 f	3.800 d -f	**LUZ DE OTONO**
4.433	**4.544 a**	**4.300 a**	**4.455 a**	**Average plant density**

*** The averages that share the same alphabetical letters for each factor and the overlap between them do not differ significantly from each other according to Duncan’s test at a probability level of 0.05.**

Table (4): Effect of genotype, planting distances and the interaction between them on the flowering time trait (day).

average genotype	Plant density (plants.ha- 1)			genotype
	44444	53333	66666	
92.055 b	92.166 b c	92.166 b c	91.833 b c	**BASIC**
91.722 b	91.500 b -d	91.166 b -d	92.500 a -c	**MONARCH**
91.500 b	91.500 b -d	92.500 a -c	90.500 c -e	**AQUADLGE**
93.277 a	93.166 a b	92.500 a -c	94.166 a	**HISTAL**
89.388 c	89.833 d e	89.166 e	89.166 e	**CLARO DE LUNA**
89.833 c	90.500 c -e	89.833 d e	89.166 e	**LUZ DE OTONO**
91.296	**91.444 a**	**91.222 a**	**91.222 a**	**Average plant density**

*** The averages of factors sharing the same alphabetical order and the interaction between them do not differ significantly according to Duncan's test at a probability level of 0.05.**

The results in Table (5) indicate significant differences between the genotypes. The AQUADLGE genotype recorded the longest maturity date, averaging 173.778 days, significantly different from the CLARO DE LUNA and LUZ DE OTONO genotypes. The latter, in turn, recorded the shortest time between planting and maturity, averaging 167.778 days at the Al-Kuwair location.Regarding the effect of plant densities, the plant density of 44,444 plants.ha^{-1} recorded the longest time from planting to maturity, averaging 172.500 days, significantly different from the plant density of 53,333 plants.ha^{-1}, which recorded the shortest time to maturity, averaging 170.222 days. The results of the interaction between genotypes and plant densities showed that plants with the AQUADLGE genotype, grown at a density of 53,333 plants.ha^{-1}, had the longest maturation time, averaging 175,000 days, with a significant difference compared to some of the interaction parameters for Al-Kuwayr location. Conversely, plants with the LUZ DE OTONO genotype, grown at the same density, had the shortest maturation time, averaging 165,000 days.Tables 6 and 7 show no significant differences between genotypes and plant density. Similarly, the interaction between genotypes and plant densities did not reach statistical significance. Plants with the BASIC genotype, grown at a density of 53,333 plants.ha^{-1}, produced the highest number of pods, 12,533. Plants with the LUZ DE OTONO genotype produced the highest number of seeds per pod at a plant density of 44,444 plants.ha^{-1}, with an average of 8,600 seeds per plant.Table 7 shows significant differences between the genotypes. The MONARCH genotype produced the highest number of seeds per pod, averaging 5,181 seeds per pod, significantly higher than most other genotypes. Plants with the CLARO DE LUNA genotype recorded the lowest average number of seeds per pod, 4,256 seeds per pod. However, the differences in plant density did not reach statistical significance.The results of the interaction between genotypes and plant

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density showed that plants with the MONARCH genotype, at a plant density of 53,333 plants.ha^{-1}, produced the highest number of seeds per pod, 5,326 seeds pod $^{-1}$, plants of the CLARO DE LUNA genotype, under the same plant density, recorded the lowest number of seeds per pod, averaging 4,172 seeds.

Table (5): Effect of genotypes, planting distances, and their interaction on the maturity date trait (days).

average genotype	Plant density (plants.ha^{-1})			genotype
	44444	53333	66666	
171.889 a	172.000 a -d	173.333 a -c	170.333 a -e	**BASIC**
172.667 a	174.000 a b	172.000 a -d	172.000 a -d	**MONARCH**
173.778 a	173.667 a b	175.000 a	172.667 a -d	**AQUADLGE**
172.333 a	173.333 a -c	169.667 b -f	174.000 a b	**HISTAL**
168.778 b	172.000 a -d	166.333 e -f	168.000 d -f	**CLARO DE LUNA**
167.778 b	170.000 a -e	165.000 f	168.333 c -f	**LUZ DE OTONO**
171.203	**172.500 a**	**170.222 b**	**170.888 a b**	**Average plant density**

*** The averages that share the same alphabetical letters for each factor and the overlap between them do not differ significantly from each other according to Duncan's test at a probability level of 0.05.**

Table (6): Effect of genotype, planting distances and the interaction between them on the trait of the number of pods (pod. plant^{-1}).

average genotype	Plant density (plants.ha- 1)			genotype
	44444	53333	66666	
10.800 a	10.800 a	12.533 a	9.067 a	**BASIC**
11.378 a	12.267 a	12.200 a	9.667 a	**MONARCH**
11.156 a	11.333 a	11.533 a	10.600 a	**AQUADLGE**
9.533 a	10.733 a	9.133 a	8.733 a	**HISTAL**
10.044 a	9.467 a	9.800 a	10.867 a	**CLARO DE LUNA**
9.133 a	8.600 a	9.533 a	9.267 a	**LUZ DE OTONO**
10.340	**10.533 a**	**10.788 a**	**9.700 a**	**Average plant density**

*** The averages that share the same alphabetical letters for each factor and the overlap between them do not differ significantly from each other according to Duncan's test at a probability level of 0.05.**

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Table (7): Effect of genotype, planting distances and the interaction between them on the trait of number of seeds per pod (seed.pod-1) for the quer location.

average genotype	Plant density (plants.ha- 1)			genotype
	44444	53333	66666	
4.960 a	4.848 a -c	5.151 a b	4.881 a -c	**BASIC**
5.181 a	5.142 a b	5.326 a	5.076 a b	**MONARCH**
4.610 b	4.531 b -d	4.746 a -d	4.554 b -d	**AQUADLGE**
5.153 a	5.245 a	5.114 a b	5.102 a b	**HISTAL**
4.256 c	4.414 c d	4.172 d	4.182 d	**CLARO DE LUNA**
4.383 b c	4.331 c d	4.281 c d	4.538 b -d	**LUZ DE OTONO**
4.757	**4.752 a**	**4.798 a**	**4.722 a**	**Average plant density**

*** The averages of factors sharing the same alphabetical order and their interaction do not differ significantly according to Duncan's test at a probability level of 0.05.**

The results in Table (8) show significant differences between the genotypes. Plants with the HISTAL genotype produced the highest average weight per 100 seeds, reaching 144.173 g, significantly higher than most other genotypes. Conversely, plants with the LUZ DE OTONO genotype recorded the lowest average weight per 100 seeds, at 109.611 g. However, the differences in plant density did not reach statistical significance. The results of the interaction between genotypes and plant densities indicated that plants with the HISTAL genotype, under a plant density of 66,666 plants/ha, exhibited the highest average seed weight per 100 seeds, reaching 157.65 g, significantly different from most interaction treatments. Conversely, plants with the LUZ DE OTONO genotype, under the same plant density, gave the lowest average seed weight per 100 seeds, at 104.91 g.Table 9 shows significant differences between the genotypes. Plants with the MONARCH genotype excelled, producing the highest average dry seed yield at 4.099 tons.ha^{-1}, significantly different from the CLARO DE LUNA and LUZ DE OTONO genotypes, which gave the lowest average dry seed yield at 2.397 tons.ha^{-1}. Regarding the effect of plant density, the density of 66,666 tons.ha^{-1}, which recorded the highest average dry seed yield at 3.902 tons.ha^{-1}, significantly excelled the density of 44,444 tons.ha^{-1}, which recorded the lowest average dry seed yield at 2.852 tons.ha^{-1}.Furthermore, the results of the interaction between genotypes and plant densities showed that plants with the HISTAL genotype at a density of 66,666 plants/ha/1 had the highest average dry seed yield at 4.625 tons.ha^{-1}, significantly excelled some interaction coefficients. Conversely, plants with the LUZ DE OTONO genotype at a density of 44,444 plants/ha/1 gave the lowest average dry seed yield at 1.841 tons.ha^{-1}. Table (10) shows that the HISTAL genotype gave the highest dry biological yield at 17.440 tons ha^{-1}, while the LUZ DE OTONO genotype gave the lowest dry biological yield at 14.149 tons ha^{-1}.Regarding the effect of plant density, plants with a density of 66,666 plants ha^{-1} gave the highest dry biological yield at 19.256 tons ha^{-1}, significantly different from the two plant densities of 53,333 plants ha^{-1} and 44,444 plants ha^{-1}, which gave the lowest dry biological yield at 12.425 tons ha^{-1}. The interaction between genotypes and plant densities resulted in the highest average dry

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biological yield (DBY) of 22.206 tons/ha at a plant density of 66,666 plants.ha^{-1}, significantly different from most interaction treatments. Conversely, the lowest DBY yield (DBY) of 11.055 tons/ha was recorded at a plant density of 44,444 plants.ha^{-1}.

Table (8): Effect of genotypes, planting distances, and their interaction on the average 100-seed weight (g).

average genotype	Plant density (plants.ha- 1)			genotype
	44444	53333	66666	
131.233 a b	135.53 a -d	118.53 c -e	139.65 a -c	**BASIC**
133.682 a b	138.39 a -c	121.30 b -e	141.35 a -c	**MONARCH**
123.031 b	113.09 d e	139.11 a -c	116.89 c -e	**AQUADLGE**
144.173 a	145.13 a b	129.73 b -e	157.65 a	**HISTAL**
109.702 c	109.67 e	109.65 e	109.79 e	**CLARO DE LUNA**
109.611 c	112.29 d e	111.64 d e	104.91 e	**LUZ DE OTONO**
125.238	**125.682 a**	**121.661 a**	**128.373 a**	**Average plant density**

*** The averages that share the same alphabetical letters for each factor and the overlap between them do not differ significantly from each other according to Duncan's test at a probability level of 0.05.**

Table (9): Effect of genotype, planting distances and the interaction between them on the trait of total dry seed yield (ton.ha^{-1}).

average genotype	Plant density (plants.ha^{-1})			genotype
	44444	53333	66666	
3.692 a	3.170 a -d	3.902 a b	4.004 a b	**BASIC**
4.099 a	3.787 a -c	3.953 a b	4.558 a	**MONARCH**
3.494 a	2.586 b -d	3.989 a b	3.907 a b	**AQUADLGE**
3.870 a	3.682 a -c	3.302 a -d	4.625 a	**HISTAL**
2.592 b	2.043 c d	2.425 b -d	3.308 a -d	**CLARO DE LUNA**
2.397 b	1.841 d	2.341 b -d	3.009 a -d	**LUZ DE OTONO**
3.357	**2.852 b**	**3.318 a b**	**3.902 a**	**Average plant density**

*** The averages that share the same alphabetical letters for each factor and the overlap between them do not differ significantly from each other according to Duncan's test at a probability level of 0.05.**

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Table (10): Effect of genotype, planting distances and the interaction between them on the dry biological yield trait (ton.ha^{-1}).

average genotype	Plant density (plants.ha- 1)			genotype
	44444	53333	66666	
16.414 a b	11.932 g -i	17.293 c d	20.018 b	**BASIC**
15.452 b	12.563 g -i	14.910 e f	18.883 b c	**MONARCH**
16.301 b	13.661 f -h	16.470 d e	18.773 b c	**AQUADLGE**
17.440 a	13.754 f g	16.359 d e	22.206a	**HISTAL**
14.309 c	11.055 i	13.495 f -h	18.376 b -d	**CLARO DE LUNA**
14.149 c	11.587 h -i	13.579 f -h	17.282 c d	**LUZ DE OTONO**
15.678	**12.425 c**	**15.351 b**	**19.256 a**	**Average plant density**

The means of factors sharing the same alphabetical order and their interaction did not differ significantly according to Duncan's test at a probability level of 0.05.

Table 11 indicates that the differences between genotypes and plant density did not reach statistical significance. The table shows that the differences in interaction coefficients between genotypes and plant densities were not significant. Plants with the AQUADLGE genotype at a plant density of 66,666 plants.ha^{-1} gave the highest percentage of protein in the seeds, reaching 23.600, while the lowest percentage of protein in the seeds was recorded in the LUZ DE OTONO genotype at a plant density of 53,333 plants.ha^{-1}, reaching 22.033.

Table 11: Effect of genotypes, planting distances, and their interaction on the percentage of protein in the seeds.

average genotypes	Plant density (plants.ha^{-1})			genotypes
	44444	53333	66666	
a 22.822	a 22.800	a 22.466	a 23.200	**BASIC**
a 23.055	a 22.800	a 22.833	a 23.533	**MONARCH**
a 23.166	a 22.600	a 23.300	a 23.600	**AQUADLGE**
a 23.166	a 23.000	a 23.233	a 23.266	**HISTAL**
a 22.655	a 22.800	a 23.100	a 22.066	**CLARO DE LUNA**
a 22.344	a 22.300	a 22.033	a 22.700	**LUZ DE OTONO**
22.868	**a 22.716**	**a 22.827**	**a 23.061**	**Average plant density**

*** Means sharing the same alphabetical letters for each factor and the interaction between them do not differ significantly according to Duncan's test at a probability level of 0.05.**

The values of phenotypic variances, their total genetic and environmental components, and the genetic parameters for the traits under study in broad beans are shown in Table (12). It is evident from this that the genotypic variance values were significant above zero for all the traits under study except for the number of pods and the percentage of protein in the seeds. The environmental variance values were also significant above zero for all the traits under study. These results are consistent with the findings of [2,3,10,20] regarding the significant values of genetic and environmental variance for some traits in broad beans. The results indicate that genotypic variance values were higher than environmental variance values for plant height, flowering time, number of seeds per pod, and dry biological yield, and lower for all other traits.The highest genotypic variance coefficients were recorded for plant height (16.073) and dry biological yield (18.737), while the highest phenotypic variance coefficients were recorded for plant height (18.697), number of pods (22.336), and dry biological yield (33.239). This aligns with the findings of [3,17,22] who reported varying values for genotypic and phenotypic variance coefficients.

Table (12): Overall average, components of Phenotypic Variance (genetic and environmental), and genetic parameters of the studied traits.

studied traits					Genetic markers
Number of pods (pod.plant^{-1})	**Maturity date (days)**	**Flowering date (days)**	**Number of branches (branch.plant^{-1})**	**Plant height (cm.plant^{-1})**	
0.266 0.393±	4.837 2.446±	1.982 0.910±	0.218 0.106±	105.038 47.282±	**Genotypic Variance**
5.069 1.915±	7.103 2.684±	1.067 0.403±	0.235 0.088±	37.096 14.020±	**Environmental Variance**
5.335	11.940	3.049	0.453	142.134	**Phenotypic Variance**
4.990	1.284	1.542	10.553	16.073	**Genotypic Coefficients of Variance**
22.336	2.018	1.912	15.197	18.697	**phenotypic variation coefficient**
0.049	0.405	0.650	0.482	0.739	**Heritability Broad Sense**
0.237	2.883	2.338	0.669	18.149	**Expected Genetic Advance**
2.296	1.684	2.561	15.097	28.464	**Expected Genetic Advance %**
10.341	**171.204**	**91.296**	**4.433**	**63.763**	**General Average**

Continued from Table (12): The overall average and components of Phenotypic Variance (genetic and environmental) and the genetic parameters of the studied traits.

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studied traits					Genetic markers
Percentage of protein in seeds	**Dry biological yield (ton.ha^{-1})**	**Total dry seed yield (ton.ha^{-1})**	**Average weight of 100 seeds (g)**	**Number of seeds per pod (seed.pod^{-1})**	
0.019 0.052±	1.522 0.719±	0.395 0.214±	172.075 82.989±	0.145 0.068±	**Genotypic Variance**
0.785 0.296±	1.235 0.466±	0.850 0.321±	172.526 65.208±	0.114 0.043±	**Environmental Variance**
0.804	2.757	1.245	344.601	0.259	**Phenotypic Variance**
0.613	7.869	18.737	10.474	8.015	**Genotypic Coefficients of Variance**
3.922	10.591	33.239	14.822	10.705	**معaمل aلaختلaف aلمظeري**
0.024	0.552	0.317	0.499	0.560	**Heritability Broad Sense**
0.045	1.888	0.730	19.095	0.588	**Expected Genetic Advance**
0.197	12.045	21.758	15.247	12.362	**Expected Genetic Advance %**
22.869	**15.678**	**3.358**	**125.239**	**4.758**	**General Average**

Heritability Broad Sense values were high for plant height (0.739) and flowering time (0.650), while they were moderate for number of branches (0.482), maturity time (0.405), number of seeds per pod (0.560), average weight of 100 seeds (0.499), and dry biological yield (0.552), and low for the remaining traits. Previous studies have gave heritability values ranging from low to high for various traits, including those of [11,15,19,20,31] . Table (12) also indicates that the % Expected Genetic Advance values of the average trait ranged from low for flowering time (2.561), maturity time (1.684), number of pods (2.296), and percentage of protein in seeds (0.197), while they were moderate for the remaining traits. [10,15,17,19,20] indicated that the values of genetic improvement varied between low, medium, and high for the studied traits. The results from Table (12) of the genetic parameters show that the values of the phenotypic coefficient of variation were significantly higher than the values of the genotypic coefficients of variation for all traits. This indicates the influence of environmental factors, specifically plant density, on the studied traits to varying degrees. This is because most of these traits are quantitative, and therefore, selection is effective for these traits based on phenotypic characteristics [9].

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