

Performance evaluation of faba bean genotypes under irrigation supplementary conditions

Zainab Hameed Abdullah Alkhalidy¹, Abdullah M.S. Al-Dabbagh², Mohammed S. AlTaweel¹, Maan Mohammed Salih¹, Huthaifa M. Ibrahim¹ Dalal N. Mahmood¹,

1-Center for Arid Farming and Conservation Agricultural Research, University of Mosul. Iraq.

2-Department of Horticulture and Landscape Engineering, College of Agriculture and Forestry, University of Mosul, Mosul, Iraq.

Zainab.1991@uomosul.edu.iq
abdullah.aldabbagh@uomosul.edu.iq
draltweel@uomosul.edu.iq
maan.m.salih@uomosul.edu.iq
dalal.nabeel@uomosul.edu.iq
Huthaifa.mahdi@uomosul.edu.iq

Corresponding author. maan.m.salih@uomosul.edu.iq Orcid ID: 0009-0002-7083-3596

Abstract

A field experiment was conducted during the 2023–2024 growing season at the University of Mosul Research Station to evaluate the performance of thirteen genetic combinations of (*vicia faba* L.) Under supplementary irrigation conditions, it was designed (RCBD) with three replicates.

Analysis of variance showed highly statistically significant differences ($P \leq 0.01$) between genotypes for all quantitative traits studied. Genotype (4: FLIP17-065FB) recorded the highest significant values for plant height (149.70 cm), pod length (12.40 cm), green biological yield (4064.00 g plant⁻¹), and green pod yield (1268.00 g plant⁻¹).

The number of seeds / pods and weight of 100 seeds showed the highest Broad-sense heritability (0.966 and 0.963, respectively), along with high expected genetic advance (41.91 percent and 48.57 percent, respectively), This demonstrates the predominance of additive gene action and the potential efficiency of direct selection to improve these traits. Correlation analysis revealed positive genetic

correlations between plant height, seeds per pod, and green pod yield. Genotypes (4: FLIP17-065FB), (11: FLIP17-078FB) and (5: FLIP17-066FB) showed potential as parental lines for improving bean productivity under supplementary irrigation.

Keywords: Faba bean, Supplementary irrigation, Heritability, genetic Parameters.

Introduction

Leguminous crops, especially beans (*Vicia faba* L.), play a pivotal role in sustainable agricultural systems due to their high nutritional value and biological ability to fix atmospheric nitrogen. This property contributes significantly to improving soil fertility and thus reducing dependence on chemical fertilizers [1,2]. Faba bean cultivation is widespread in the Mediterranean basin, West Asia and North Africa, regions that are increasingly vulnerable to climate instability and fluctuations in rainfall patterns, especially under semi-arid conditions [3].

Recent climate projections indicate an increased frequency of late-season drought events, intensified episodes of water stress, and increased evaporation rates within these regions [4]. Although beans show a moderate degree of tolerance to abiotic stresses, exposure to water shortages during sensitive growth stages, especially flowering and pod filling, can significantly reduce crop productivity [5,6]. These decreases are typically associated with poor photosynthesis efficiency, disruption of assimilation transmission from source tissue to

pelvic tissue, and accelerated leaf aging [7].

In this context, supplementary irrigation has emerged as an effective agricultural practice to mitigate the harmful effects of water stress without relying on expensive complete irrigation systems [8]. Providing carefully regulated amounts of water in critical growth stages helps stabilize yield, and improve water use efficiency, and promote sustainable production in water-limited environments [9]. However, the response of bean genotypes to supplemental irrigation varies according to their adaptive physiological and anatomical characteristics, including root system efficiency, osmotic adaptability, evaporative cooling efficiency, and phenological flexibility [10,11].

Genotype $\times$ environment (G $\times$ E) interactions remain a major challenge in predicting field performance, as genotypes that exhibit superior productivity under favorable conditions may lose their advantage when exposed to drought stress [12]. Previous field investigations have shown significant genetic variation between bean genotypes in terms of

morphological and yield-related traits, accompanied by relatively high inheritance estimates and significant genetic progression of many productivity-related characteristics. These results support the effectiveness of direct selection in bean breeding programs [13].

Accordingly, the current study was conducted to achieve the following objectives: (1) Evaluation of agronomic performance of thirteen faba bean genotypes under complementary irrigation conditions; (2) identify genotypes characterized by superior crop stability and water use efficiency; (3) analyze the genetic relationships between traits associated with adaptation to water shortage stress; (4) Develop practical recommendations that may support breeding strategies and crop management practices in environments with limited water resources.

2. Materials and methods

2.1 Experimental site and environmental conditions

The field experiment was conducted during the 2023–2024 winter growing season at the Research Station of the College of Agriculture and Forestry, University of Mosul in Mosul, Iraq (36.33° north, 43.15° east; 223 meters above sea level).

Soil samples were collected and analyzed for their physical and chemical properties following standard laboratory methods [14,15].

Chemical properties

pH Soil Reaction	7.6
Available nitrogen	2.3 mg/kg
Available phosphorus	109 mg/kg
Available potassium	11.8 mg/kg

Physical properties

Clay	15.2
Silt	61.75
Sand	23.05
Soil texture	Silty Loam

2.2 Plant Material

Thirteen faba bean genotypes were used in this study. Genotypes were selected to provide variation in their genetic background and morphological characteristics according to internationally accepted germplasm evaluation criteria [16,17]. Genotype codes and their origins are shown in the following table.

Genotypes	Name	Pedigree
1	Flip19-221FB	Selection from BPL 2236
2	Flip19-222FB	Selection from ILB504
3	Flip19-223FB	ILB445-32122-1/TR2010
4	FLIP17-065FB	ILB360
5	FLIP17-066FB	selection for heat from Shambat
6	FLIP15-160FB	S 88094-8-1-32025-3/TR2010
7	FLIP17-071FB	S 88135-3-2-1
8	FLIP17-072FB	ILB1270
9	FLIP17-076FB	NA112 XWRB7/63/1/2
10	FLIP15-149FB	S 88094-6-4-32107-1/TR2010
11	FLIP17-078FB	selection for heat from Shambat
12	FLIP17-079FB	selection for heat from Shambat
13	Basabeer	Bulk1/3-1993

2.3 Experimental design and field preparation

The experiment was arranged using a randomized complete block design (RCBD) with three replicates. Processors were randomly distributed within each block using the randomization procedure available in the R statistical software environment [18]. Each experimental plot of land has an area of 1.8 square metres² and consists of three rows, each 2 meters long. The distance between rows was maintained at 45 cm, while the distance between plants within rows was 20 cm. Rows were oriented north – south to improve light interception efficiency [19].

2.4 Agricultural practices and data collection

The field was plowed to a depth of approximately 25 cm and then leveled before sowing. Seeds were planted manually to a depth of 3–5 cm, with seeds distributed in two rows per experimental unit [20].

Phosphorus and potassium fertilizers were added before planting according to soil testing recommendations. Nitrogen fertilizer in the form of urea (46% N) was applied in two equal doses: the first during the branching stage (4–6 leaves) and the second at the beginning of flowering [21].

Supplementary irrigation was provided during the main growth stages, especially branching, flowering and pod formation, according to soil moisture status and crop water requirements estimated from reference evaporation [22,23].

Data were collected from ten randomly selected plants within the net plot area of each experimental unit following standard evaluation protocols [16,17]. The following traits were recorded: plant height (cm), branches/ plant, length of pod (cm), seeds/ pod, green biological yield (g plant⁻¹), green pod yield (g plant⁻¹), harvest index (%), weight of 100 dry seeds (g).

2.5 Statistical analysis

ANOVA was performed using SAS software according to the linear model of RCBD:

$$Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$

where Y_{ij} represents the observed value, μ the overall mean, τ_i the genotype effect, β_j the block effect, and ε_{ij} the random error term. Means were separated using Tukey's test at $\alpha = 0.05$.

Genetic variance components and quantitative inheritance parameters were estimated according to the procedures of Falconer & Mackay [24] and Johnson et al. [25]:

- "Phenotypic variance"
 $\sigma_p^2 = (MS_g - MSE)/r$

- "Genotypic variance"
 $\sigma_g^2 = (MS_g - MSE)/r$
- "Environmental variance"
 $\sigma_e^2 = MSE$
- "Broad-sense heritability"
 $H^2 = (\sigma_g^2 / \sigma_p^2) \times 100$
- "Genotypic variation coefficient" $GCV = (\sqrt{\sigma_g^2 / \bar{X}}) \times 100$
- "Phenotypic variation coefficient" $PCV = (\sqrt{\sigma_p^2 / \bar{X}}) \times 100$
- "Genetic advance" $GA = K \times \sigma_p \times H^2$ where $K = 2.063$ at 5% selection intensity
- "Percentage of genetic advance"
 $GA\% = (GA / \bar{X}) \times 100$

3. Results

3.1 Phenotypic performance of genotypes

Table (1) shows the analysis of variance for the studied characteristics. Highly statistically significant differences ($P \leq 0.01$) were detected between the thirteen bean genotypes for all quantitative traits evaluated.

Table (1). Mean squares from analysis of variance for 13 faba bean genotypes.

S.O.V.	PH cm	NB P	PL cm	NSP	GBY g/pl	GPY g/pl	HI %	100- SW g
Reps	0.788	4	0.015	0.561	27	12	82.564	0.398
Genotyp es	309.56 1**	3.123 **	9.270 **	27.274 **	1805712. 481**	131380.0 77**	129.32 2**	1913.1 04**
Error	11.28 8	0.23 1	0.364	0.314	45394.66 0	43280.67 0	58.776	24.425

Table notes: PH = Plant Height (cm); NBP = Number of Branches per Plant; PL = Pod Length (cm); NSP = Number of Seeds per Pod; GBY = Green Biological Yield (g plant^{-1}); GPY = Green Pod Yield (g plant^{-1}); HI = Harvest Index (%); 100-SW = Hundred Seed Weight (dry, g). ** and *** indicate significance at $P \leq 0.01$ and $P \leq 0.05$, respectively.

Table (2) showed that genotype (4) exhibited superior performance in six out of the eight evaluated traits, recording the highest mean values for plant height (149.70 cm), pod length (12.40 cm), green biological yield (4064.00 g plant^{-1}), green pod yield

(1268.00 g plant^{-1}), harvest index (33.27%), and 100-seed dry weight (153.53 g). In contrast, genotype (3) produced the lowest green pod yield (603.00 g plant^{-1}), whereas genotype (11) recorded the highest number of seeds per pod (4.40 seeds).

Table (2). Mean performance of morphological and yield-related traits for the studied genotypes.

Genotypes	PH cm	NBP	PL cm	NSP	GBY g/pl	GPY g/pl	HI %	100- SW g
1	122.90 f	3.80 g	9.15 cd	2.60 d	1823.00 d	863.50 bc	47.50 a	90.14 fg
2	129.40 cde	4.60 efg	5.55 e	2.90 d	2850.00 c	1042.00 ab	36.32 a-d	98.23 ef
3	123.30 ef	4.30 fg	9.05 cd	3.10 bcd	1838.00 d	603.00 c	32.93 a-d	68.49 h
4	149.70 a	5.30 de	12.40 a	3.00 cd	4064.00 a	1268.00 a	33.27 a-c	153.53 a
5	132.10 c	4.50 efg	9.15 cd	3.10 bcd	2773.50 c	1098.00 ab	39.60 abc	131.98 b
6	120.50 f	6.60	8.55 d	2.90 d	2115.00	710.00	33.36	83.53 g

		ab			d	ab	a-d	
	125.30			3.60	2522.50	1039.50	41.30	120.83
7	def	4.20 g	9.25 cd	bc	c	ab	ab	cd
	144.70		9.55		3810.00			95.35
8	ab	6.80 a	bcd	2.80 d	ab	800.50	21.89 d	ef
		6.60			2730.50		34.75	102.70
9	130.40	ab	11.90 a	3.70 b	c	963.50	a-d	e
		5.60	9.20	3.10	3813.50	1356.00	35.49	
10	148.60 a	cd	cd	bcd	ab	a	a-d	66.50 h
		6.20	10.16		3626.50	1035.00	32.21	100.80
11	139.40 b	abc	bc	4.40 a	b	ab	bcd	e
	125.30	5.10	10.40		2806.00	723.50	29.14	117.90
12	def	def	b	3.70 b	c	bc	bcd	d
	125.40	5.90			3687.00	735.00	25.83	127.33
13	def	bcd	11.75 a	2.90 d	ab	bc	cd	bc

Note: Means followed by the same letter within a column are not significantly different at the 0.05 probability level according to Tukey's test.

3.2 Variance Components and Quantitative Genetic Parameters

Estimates of variance components revealed that the genotypic variance component (σ_g^2) exceeded the environmental variance component (σ_e^2) for most studied traits (Table 3). The traits number of seeds per pod and 100-seed weight exhibited the highest proportions of genotypic to phenotypic variance (96.6% and 96.3%, respectively), followed by plant height (89.8%). This pattern was reflected in the broad-sense heritability estimates (H^2), which ranged from 0.966 for number of seeds per pod to 0.286 for harvest index.

The phenotypic coefficient of variation (PCV) values slightly exceeded the genotypic coefficient of variation (GCV) values for all traits. However, the differences between PCV and GCV were very small for number of seeds per pod (0.36%) and 100-seed weight (0.46%), indicating minimal environmental influence on the phenotypic expression of these traits. Conversely, wider differences between PCV and GCV were observed for green pod yield (10.77%) and harvest index (12.37%), reflecting their greater sensitivity to environmental fluctuations.

The expected genetic advance under 5% selection intensity (GA%) ranged from 14.74% for plant height to 51.39% for green biological yield.

High genetic advance values were also recorded for number of seeds per pod (41.91%) and 100-seed weight

(48.57%), suggesting substantial potential for improvement through direct selection [25].

Table (3). Estimates of variance components and quantitative genetic parameters for the studied traits.

Genetic paramete rs	PH cm	NBP	PL cm	NSP	GBY g/pl	GPY g/pl	HI %	100- SW g
σ^2_p	110.71 2	1.195	3.333	9.301	632167. 267	72647. 139	82.291	653.98 5
$\pm$ S.E.p	$\pm$ 8.357	$\pm$ 0.090	$\pm$ 0.252	$\pm$ 0.702	$\pm$ 47719. 232	$\pm$ 5483.7 79	$\pm$ 6.212	$\pm$ 49.366
σ^2_g	99.424	0.964	2.969	8.987	586772 .607	29366. 469	23.515	629.56 0
$\pm$ S.E.g	$\pm$ 13.028	$\pm$ 0.132	$\pm$ 0.390	$\pm$ 1.146	$\pm$ 75908 .242	$\pm$ 6391. 319	$\pm$ 6.978	$\pm$ 80.363
σ^2_e	11.288	0.231	0.364	0.314	45394. 660	43280. 670	58.776	24.425
$\pm$ S.E.e	$\pm$ 1.044	$\pm$ 0.021	$\pm$ 0.034	$\pm$ 0.029	$\pm$ 4196.7 38	$\pm$ 4001.2 99	$\pm$ 5.434	$\pm$ 2.258
h^2 (bs)	0.898	0.807	0.891	0.966	0.928	0.404	0.286	0.963
PCV (%)	7.967	20.445	18.826	21.055	26.875	29.563	26.586	24.494
GCV (%)	7.550	18.367	17.769	20.696	25.893	18.796	14.212	24.032
GA	19.465	1.817	3.350	6.070	1520.2 71	224.44 5	5.340	50.713
GA (%)	14.738	33.991	34.548	41.908	51.388	24.617	15.650	48.573
Mean	132.07 7	5.346	9.697	14.485	2958.4 23	911.73 1	34.122	104.40 6

Table notes: σ_p^2 = phenotypic variance; σ_g^2 = genotypic variance; σ_e^2 = environmental variance; H^2 = broad-sense heritability; PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; GA = expected genetic advance; GA% = percentage of genetic advance.

3.3 Phenotypic (rp) and genetic (rg) correlation coefficients

Positive genetic associations

Plant height showed a strong positive genetic association with green pod yield, ($r_g = 0.846$) and green biological yield ($r_g = 0.852$). This result suggests that taller plants tend to produce greater biomass and higher productivity than pods, possibly due to better vegetative growth and higher assimilation production.

The number of seeds per pod was positively associated with green pod yield, ($r_g = 0.627$), suggesting that increasing the number of seeds within the pod directly contributed to improving overall yield. A weaker positive relationship was observed between the number of seeds per pod and pod length ($r_g = 0.230$).

Pod length had a moderate positive genetic association with the weight of 100 seeds ($r_g = 0.500$), showing that longer pods were generally associated with larger, heavier seeds. This relationship is important because seed size and weight are key components of crop quality and market preferences.

Negative genetic associations

A strong negative genetic relationship was found between the number of branches per plant and the harvest

index ($r_g = -0.852$). Similarly, biological yield showed a strong negative correlation with harvest index ($r_g = -0.825$). These relationships suggest that excessive vegetative growth may reduce the efficiency of assimilation division toward the reproductive organs, resulting in a decrease in the conversion of total biomass into economic return.

In addition, the number of branches per plant showed a very weak negative correlation with green pod yield, ($r_g \approx -0.015$), indicating that increased branching did not contribute positively to productivity under supplementary irrigation conditions and may instead promote unnecessary vegetative growth.

Phenotypic versus Genotypic Correlations

Comparison of phenotypic and genetic correlations showed that genetic correlations were generally higher for most important agronomic traits, especially those related to plant height and pod yield. This suggests that the observed phenotypic relationships were largely influenced by genetic yield and could therefore be useful in selection programs.

On the other hand, some phenotypic correlations were weaker or different from the corresponding genetic

correlations, especially with regard to the number of branches per plant and pod yield. This difference reflects the influence of environmental variation on trait expression and demonstrates that phenotypic performance alone may not always provide an accurate estimate of the true genetic relationship between traits.

Overall, the results suggest that genetic correlations analysis can provide valuable information for indirect selection and for identifying effective traits to improve crop performance in bean breeding programs under complementary irrigation conditions.

Table (4). phenotypic (above the diameter) and genetic (below the diameter) correlation coefficients between the studied traits.

Traits	PH	NBP	PL	NSP	GBY	GPY	HI	100-SW
PH	1.000	0.329	0.278	0.435	0.807	0.510	-0.286	0.145
NBP	0.349	1.000	0.364	0.238	0.423	-0.047	-0.607	-0.068
PL	0.258	0.362	1.000	-0.027	0.369	0.068	-0.352	0.478
NSP	0.465	0.253	-0.032	1.000	0.223	0.406	0.120	0.002
GBY	0.852	0.543	0.431	0.230	1.000	0.433	-0.346	0.364
GPY	0.846	0.015	0.208	0.627	0.552	1.000	0.299	0.128
HI	-0.314	-0.852	-0.283	0.227	-0.825	0.409	1.000	-0.062
100-SW	0.147	-0.088	0.500	0.004	0.388	0.186	-0.056	1.000

Practical implications of correlation analysis

Indirect selection: Strong positive genetic correlations between plant height, number of seeds per pod, and green pod yield, suggest that these traits can be used as indirect selection criteria to predict final productivity. Their early expression and ease of measurement increase their practical value in educational programs.

Vegetative – reproductive balance: The strong negative relationship between branching and harvest index suggests that excessive vegetative growth may reduce reproductive

efficiency. Therefore, balanced selection methods, such as the Smith–Hazel selection index, can help improve crop performance while maintaining acceptable vegetative growth.

Breeding priorities: Breeding programs should focus on improving the number of seeds per pod and the weight of 100 seeds because both traits have shown positive genetic associations with pod productivity and relatively high genetic susceptibility, indicating a good potential response to selection.

4. Discussion

4.1 The importance of phenotypic variation in early selection programs

The superior genotype performance (4) of many crop components may be related to the accumulation of favorable alleles associated with vegetative growth, crop composition and composition, contributing to stable productivity under complementary irrigation conditions [26]. Traits such as plant height and pod length are generally relatively stable across environments, which may explain the consistent performance of some genotypes [27].

4.2 Effects of components of variation and genetics on breeding programs

High-scale heritability values ($H^2 > 0.80$) combined with significant genetic progression ($GA\% > 40\%$) for traits such as number of seeds per pod and weight of 100 seeds indicate that added genetic advance play a major role in controlling these traits. This suggests that direct phenotypic selection in early separate generations can be effective for improving these traits [28].

In contrast, the relatively low heritability ($H^2 = 0.286$) and genetic advance ($GA\% = 15.65\%$) estimated for the harvest index may reflect a stronger environmental impact or

involve non-additive genetic influences such as dominance and genetic interaction. Therefore, improving this trait may require more advanced parenting methods, including family selection or multi-environment evaluation [29].

4.3 Interpretation of correlation patterns and their applications in indirect selection

Strong positive genetic correlations between plant height and number of seeds per pod with green pod yield provide useful criteria for indirect selection. Because these traits are expressed early and have relatively high heritability, they may serve as practical indicators of productivity potential while reducing the time and cost required for field evaluation [24].

On the other hand, the strong negative correlation between the number of branches and the harvest index ($r_g = -0.852$) reflects the physiological competition between vegetative growth and reproductive development. Over-allocation of assimilation to vegetative organs may reduce the availability of assimilation for pod filling and seed development [30]. Therefore, the use of multi-attribute selection indicators, especially the Smith–Hazel indicator, may contribute to a better balance between vegetative strength and economic return [31].

5. Conclusions and recommendations

5.1 conclusions

Significant genetic variation was detected among the studied genotypes for all quantitative traits, providing a strong basis for effective selection and crop improvement.

Genotype (4: FLIP17-065FB) showed outstanding performance in a number of productivity and quality characteristics, while genotypes , (11: FLIP17-078FB) and (5: FLIP17-066FB) also showed positive results. These findings highlight its suitability as a potential source of parenthood in future parenting programs.

The predominance of additive gene action work was evident for traits such as number of seeds per pod and 100-seed weight. High estimates of heredity and genetic progress suggest that direct selection can effectively improve these traits.

- Significant positive genetic correlations were observed between plant height, number of seeds per Pod, and green Pod yield. Therefore, these qualities can be indirect indicators of choice for maximum productivity.

5.2 Practical recommendations

- Genotypes (4), (11) and (5) can be considered valuable parental material for hybridization programs aimed at enhancing productivity potential and quality traits

These structures can be entered into outcome comparison experiments in order to determine the superior ones

- It is recommended to apply path coefficient analysis to distinguish direct and indirect effects between productivity-related traits and determine the most effective selection criteria.

- Further evaluation of superior genotypes under diverse environmental conditions and growing seasons is necessary to verify their stability and adaptability to climate change.

- Breeding efforts should focus on reducing the negative relationship between branching traits and harvest index through appropriate hybridization schemes, thus improving the balance between vegetative growth and economic yield.

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