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Estimation of Genetic variability and Correlation Coefficient for yield and its components and Root Length in Faba Bean Genotypes under Water Stress

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Abstract: Determine and improving drought tolerance genotype is a major goal of plant breeding to face climate change .The productivity of faba bean in Egypt is affected by abiotic stress especially drought stress .The present study aimed assessing sixty faba bean genotypes, consists of fifty four finish families selected from 180 lines based on it seed yield and six check Egyptian cultivars to estimates of genetic variability, heritability , genetic advance and phenotypic correlations coefficient of seed yield and components in faba bean genotypes under water stress .This assessment was carried out in field experiment under water regimes consisting of three systems (100%, 75% and 50% of field capacity), through two locations (Ismailia , North Sinai governorates) during tow successive growing seasons (2019\2020 and 2020\2021). The field experiments were laid out in split-plot with randomized complete block design with four replications, where the main plots were allocated to three watering levels (100%75%and 50% of field capacity), while the subplots were a located the genetic material (60 genotype of faba bean). The results cleared that the phenotypic coefficient of variation and Genotypic coefficient variation (GCV) were higher for number of branches/plants, number of pods/plants, number of seed/pods, seed yield/plot dry mater production, harvest index and water use efficiency. The obtained results are indicating greats for improvement of these character by simple selection .The high broad since heritability estimate, which recorded in tow season (2019-2020 and 2020-2021) for dray matter production (89.91 and 76.33 , respectively) , harvest index (86.08 and 81.81 , respectively) , seed index (79.69 and 84,o6), number of seed/pod (65,0 and 65.1 , respectively), water use efficiency (86.61 and 78.19 respectively) and root length (86.78 and 81.27, respectively) traits indicated less influence of environment on respective character. Hence, direct selection can be followed to improve faba bean genotypes for this trait is early maturing genotypes. In addition, the high heritability coupled with high genetic advance absolved indicated the most of studied trait were mainly governed by additive gene action and are greatly influence for direct selection for genetic improvement by pedigree selection methods of heritable trait. Positive and highly significant correlation was observed of study characters. The strong as so giving on of these characters can be give importance during selection to improve the yield potential of faba bean.

Keywords: Faba bean; correlation confection; genetic advance; genetic variability, heritability

INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the most cultivated legume crops in the world that enhances soil productivity and offers a valid source of protein (20–30%) for humans and animals (Qahtan *et al.,* 2021). In addition, a good source of mineral nutrients, vitamins and numerous bioactive compounds. Moreover, its ability to fix atmospheric nitrogen makes this legume useful in crop rotation and an important tool in reducing the concentration of the N_2-greenhouse gas in the atmosphere. Most faba bean genotypes are susceptible to abiotic stress. A lack of appropriate genetic background and reasonable tolerance to environmental stresses are the main causes of the yield's instability. The primary objectives of faba bean breeding programs are high yield and tolerance to stresses (Maalouf *et al.,* 2019). Generating genotypes of beans that are adapted to the environmental conditions in which faba bean is cultivated is the most effective strategy to overcome the abiotic stresses of faba bean production (Alharbi and Adhikari, 2020). It is undeniable that genetic variations created through mutations or hybridizations enable the selection of the genotypes adapted to environmental factors such as drought, temperature, and salt soil, as a biotic stress (Banerjee *et al.,* 2022). Drought stress affects plant organ growth by altering the morphological and physiological features of plants crop (Cordea and Borsai, 2021). The mechanism involved in adapting plants to drought is variation in the ratio of root/shoot dry mass (Turner, 1996 and El-Enany *et al.,* 2013). Drought stress results in growth reduction and decreases the growth of the shoot and root of faba bean plants. This reduction may be due to decreased photosynthesis, the growth of the plant, expansion, and the division of plant cells (Sundaravalli, 2005 and Rodriguez *et al.,* 2008). Despite its importance, the faba bean subjects to drought stress throughout its lifetime due to water scarcity. Increasing the drought tolerance and crop water use continue to be growing issues of concern, because of the increasing demand for water and improved environmental quality by the human population (Hatfield *et al.,* 2001). Grain legumes are commonly used for food and feed all over the world and are the main source of protein for over a billion people worldwide, but their production is at risk from climate change. Water deficit significantly reduce the yield of grain legumes, and the faba bean is considered particularly susceptible. The genetic improvement of faba bean for drought adaptation (water deficit tolerance) by conventional methods breeding is time-consuming and laborious, since it depends mainly on selection and adaptation in multiple sites. The lack of high-throughput screening methodology and low heritability of advantageous traits under environmental stress challenge breeding progress (Muktadir *et al.,* 2020). Therefore, this study was carried out with the following objectives to evaluate sixty populations of faba bean for seed yield and seed yield components and some seed quality under three levels of irrigation. These objectives are to estimate each of the water use efficiency for investigated populations. Also, to

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estimate the genetic variability, heritability and genetic advance as percent of means among the traits conferring drought tolerance in faba bean. In addition to examine the relationships among studied traits for effective selection of drought tolerant faba bean.

MATERIALS AND METHODS

Sixty populations of faba bean consists of fifty-four Finnish families and six check Egyptian cultivars used as materials in this study. The fifty-four Finnish families of faba bean (No. 7 to 60) were received from Helsinki University; Finland (Khazaei *et al.,* 2014a and Khazaei *et al.,* 2014b). These Finnish populations are individuals were produced from crossing between (Mélodie/2 x ILB 938/2). The Mélodie/2-parent was selected from a French low vicine-convincing cultivar with high water use efficiency of (WUE). While the ILB 938/2-parent was selected from an Ecuadorian landrace with relatively high water use efficiency (WUE). While the six check cultivars (No. 1 to 6, via. Misr-1, Nubari-1, Nubari-2, Nubari-3, Sakha-3 and Sakha-4) were obtained by Legumes Research Department, Field Crops Research Institute (FCRI), Agricultural Research Center (ARC), Giza, Egypt. The number and populations code of faba bean, which used in this study are listed in Table (1).

Table (1): List of the faba bean populations used in this study

No.	Populations Code	No.	Populations Code	No.	Populations Code
1	Misr-1	21	M x I F6	41	M x I F6
2	Nubari-1	22	M x I F6	42	M x I F6
3	Nubari-2	23	M x I F6	43	M x I F6
4	Nubari-3	24	M x I F6	44	M x I F6
5	Sakha-3	25	M x I F6	45	M x I F6
6	Sakha-4	26	M x I F6	46	M x I F6
7	M x I F6	27	M x I F6	47	M x I F6
8	M x I F6	28	M x I F6	48	M x I F6
9	M x I F6	29	M x I F6	49	M x I F6
10	M x I F6	30	M x I F6	50	M x I F6
11	M x I F6	31	M x I F6	51	M x I F6
12	M x I F6	32	M x I F6	52	M x I F6
13	M x I F6	33	M x I F6	53	M x I F6
14	M x I F6	34	M x I F6	54	M x I F6
15	M x I F6	35	M x I F6	55	M x I F6
16	M x I F6	36	M x I F6	56	M x I F6
17	M x I F6	37	M x I F6	57	M x I F6
18	M x I F6	38	M x I F6	58	M x I F6
19	M x I F6	39	M x I F6	59	M x I F6
20	M x I F6	40	M x I F6	60	M x I F6

Experimental sites and growing seasons:

Two Field Experimental sites were used in this work, the first one was done in Ismailia-Agriculture Research Station; under fresh water (The Nile River), while the second was done in North Sinai Governorate (underground water; ranged from: 3800-4200 ppm over the cultivated season). In two winter, seasons, 2017/2018 and 2018/2019, it cultivated 180 fabe bean genotypes from Finland, were selected the best 54 according to its seed yield and yield components. Through, the two-winter season; 2019/2020 & 2020/2021, the fifty-four Finnish families selected and six check Egyptian cultivars under evaluated under three watering levels; 100%, 75% and 50% of field capacity.

Experimental design and its management:

The experiments were laid out in split-plot with randomized complete block design arrangement and four replications. The main plots were allocated to the three watering levels (100%, 75% and 50% of field capacity) as presented in Table (2) while, the sub plots were allocated to the genetic materials (60 genotypes of fabe bean). The plot area was 5.25 m^2 (20-plants; 25 cm between plants and 1.00 m between drip lines) and four replications. All agricultural practices were carried out according to standard commercial recommendation for faba bean production in each location at the proper time. Total amount of irrigation water/fad. /Season; during the two winter seasons 2019-2020 and 2020-2021 for three watering levels: 100% (T1); 75% (T2) and 50% (T3) of field capacity under drip irrigation was presented in Table (2). The water requirement was estimated using the FAO Penman-Monteith equation (Cai *et al.,* 2007)

Properties of experimental Soil:

Regarding the properties of the experimental soil according to its analysis physio-chemical components are described in Table (3).

Table (2): Total amount of irrigation water/fad. /Season; during the two winter seasons

Items	Three Watering Levels based on Field Capacity					
	100%		75%		50%	
	1st season	2nd season	1st season	2nd season	1st season	2nd season
Total amount of irrigation water / fad. / season (m^3)	1250.00	1375.00	937.50	1031.25	625.00	687.50

Table (3): Physio-chemical properties of soil for Ismailia-Agriculture Research Station

Parameters	Years	
	2019-2020	2020-2021
Sand (%)	90.10	91.70
Silt (%)	5.40	6.30
Clay (%)	2.90	3.20
Soil pH	6.60	6.80
Textural class	Sandy loam	Sandy loam
Organic carbon (%)	0.91	0.94
Organic matter (g/kg)	2.64	2.87
Total N (%)	0.06	0.08
Available P (mg/kg)	30.00	32.20
Ca^{2+} (cmol/kg)	325.50	331.31
Mg^{2+} (cmol/kg)	0.14	0.16
Na^{+} (cmol/kg)	0.25	0.22
K^{+} (cmol/kg)	0.17	0.15
Al^{3+} (cmol/kg)	0.08	0.05

-Data Collection:

Data was collected on the following growth parameters :

1 .Seed Yield and its components:

- Plant height (average of 5-plants; cm).
- Number of branches /plant (average of 5-plants) .
- Number of pods /plant (average of 5-plants).
- Number of seeds / pod (average of 10-pods).
- -100seeds weight (seed index).
- Seed yield / plant (average of 5-plants).
- Seed yield /plot (kg).
- Dry matter production / plot (aboveground phytomass).
- Harvest index = seed yield / total aboveground phytomass.(%)
- Expected Seed Yield / fad. =

$$\frac{\text{Seed yield} / Plot\ x\ \ 4200\ m^2}{5.25\ m^2}$$

2. Drought Tolerance Parameters Water Use Efficiency (WUED):

The water use efficiency based on dry weight was calculated according to Ehdaie and Waines (1993) formula as a ratio of aboveground phytomass dry yield (kg/m3) to total water consumed (TWC) by the crop plants as a follow: WUE (kg•m-3) = Y / TWC

2-Root System:

-Sampling, washing and extraction of roots:

Soil cores were taken from each experimental unit (one row) at one location, between plants within row. A 56 mm diameter tube auger with serrated edge (Böhm, 1979) was manually driven into the soil. Cores of soil root were obtained from depth 45 cm. prior to wash roots; the soil samples were soaked in water for about 4 hours to facilitate root extraction. The soil-root mixture was stirred by hand until it was homogenous suspension. The stirring was stopped for a few minutes to allow the heavy soil particles to settle down. Root tended to float in this suspension. Then, the suspension without the settled soil particles was poured on to sieve with mesh size of mm^2. The process of suspension and decantation was repeated until all roots were transferred to the sieve. Faba bean roots were, then, collected from the sieve by tweezers and put into flat plastic dish contacting water. A little organic debris was picked up and removed by tweezers. The root samples were kept on small plastic bags and frozen until root length could be measured.

Measuring root length:

Root length was measured using the intersection method of Tennant (1975). For counting the number of intersections, a convenient shallow tray with size of 30 x 40 cm made of glass was used. A paper with a grid of 2 cm^2 was placed under the tray; the grid must be visible; the wet root segments were then poured on the tray with some water and positioned randomly over the grid with forceps. Sometimes the long-branched roots were cut into smaller pieces. Finally, counts were made of the intersections of roots segments with the vertical and horizontal grid lies using a hand counted to facilitate the counting procedure. Root length, then, calculated using the following formula:

$R = 1.57$ x N. Tennant (1975)

Where:

R: Total root length in centimeters.

1.57: Length conversion factor depends on the grid unit using in the counting (grid unit is likely related to crop which its root is to be measuring).

N: Number of intersections counted

Data Analysis

1-Analysis of variance:

Data for two seasons was subjected to analysis of variance (ANOVA) using the Generalized Linear Model (GLM) procedure of the Statistical Package for Social Science (SPSS) version 20 (SPSS Inc., Chicago IL). Means were separated using Duncan Multiple Range Test (DMRT) at $P \leq 0.01$ and ≤ 0.05 levels of significance.

Table (4): ANOVA table for expected mean squares in mixed modal when (w) was fixed and (p) random.

S.O. V	D. F.	Expected mean squares
Replications	(r-1)	
Water levels (w)	(w-1)	δ^2ea + rp δ^2w
Main Plot Error (a)	(r-1) (w-1)	δ^2ea
Populations (p)	(p-1)	δ^2eb + rδ^2wg + rw ($\sum p^2 j$ / p-1)
Water Levels x Populations (wxg)	(w-1) (p-1)	δ^2eb + rδ^2wg
Subplot error (b)	(r-1) (wp -w)	δ^2ep
Total Variation	rwp-1	

2. Genotypic (δ^2g) and Phenotypic (δ^2p) Variances:

Genotypic (δ^2g) and phenotypic (δ^2p) variances were estimated according to Burton and De Vane (1953) as a follow:

- $\delta^2 g = \dfrac{MSg - MSe}{r}$
- $\delta^2 p = \delta^2 g + \delta^2 e$
- $\delta^2 e = MSe$

Where:

δ^2g: genotypic variance

δ^2p: phenotypic variance

δ^2e: environmental variance

MS_g: Mean square due to populations.

MS_e: Error mean square.

r: number of replications

3. Phenotypic (PCV %), Genotypic (GCV %) and Environmental (ECV %) coefficients of variation:

The phenotypic coefficient of variation (PCV %), Genotypic coefficient of variation (GCV %) and Environmental coefficient of variation (ECV %) were estimated by method of Burton (1952) and Johnson *et al.* (1955)

$$[\text{PCV} = \frac{\delta\, p}{\bar{x}} \text{ x } 100] \qquad [\text{GCV} = \frac{\delta\, g}{\bar{x}} \text{ x } 100]$$

$$[\text{ECV} = \frac{\delta\, e}{\bar{x}} \text{ x } 100]$$

Where:

δp: Phenotypic standard deviation.

δg: Genotypic standard deviation.

δe: Environmental standard deviation.

$\bar{X}$: Grand mean for the characteristic.

In addition to, the phenotypic coefficient of variation (PCV%), Genotypic coefficient of variation (GCV%) and environmental coefficient of variation (ECV%) were classified according to Sivasubramanian and Menon (1973) as:

Low:	0-10%.
Moderate:	10- 20%.
High:	> 20%.

4. Broad Sense Heritability (h^2_B):

Broad sense heritability (h^2_B) was expressed as the percentage of the ratio of δ^2g to δ^2p as described by Allard *et al.* (1960)

$$h^2_B = \frac{\delta g}{\delta p} \text{ x } 100$$

Where:

h^2_B: Heritability in broad sense

δg: Genotypic variance

δp: Phenotypic variance

Then, broad sense heritability was categorized according to Robinson *et al.*, (1949) as:

Low:	0-30%.
Moderate:	30- 60%.
High:	> 60%.

5. Genetic Advance (GA):

Genetic Advance (GA) and percentage of the mean (GAM) assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al.* (1955) as:

Where:

GA: Expected genetic advance

K: Standardized selection differential at 5% selection intensity (K = 2.063)

σ^2p: Phenotypic variance

σ^2g: Genotypic variance

The genetic advance as percentage of mean (GAM) was computed as: GAM (%) =x 100

Where:

GAM: Genetic advance as percentage of mean

GA: Expected genetic advance

X: Grand mean of a character

Then, the genetic advance as percentage of mean was categorized as:

Low:	0-10%.
Moderate:	10- 20%.
High:	> 20%.

6.a. Phenotypic correlation coefficients:

In many natural systems, changes in one attribute are accompanied by changes in another attribute and that a definite relation exists between the two. In other words, there are correlations between the two variables. A correlation, whatever its nature, is the ratio of the appropriate covariance to the product of the two standard deviations **(**Falconer and Mackay, 1996**)**. Accordingly, the following symbols will be used throughout the estimation of phenotypic correlation coefficients are**:**

$$rph_{xy} = \frac{\mathrm{cov}\ ph_{xy}}{\delta\ ph_x \cdot \delta\ ph_y}$$

Where:

x and y: the two characters under consideration
$r\ ph_{xy}$: the phenotypic correlation between the two characters x and y
Cov_{ph}: the covariance of the two characters x and y
δ^2 and δ: the variance and standard deviation

The phenotypic correlation coefficient was estimated **(MSTAT-C program; 1986)** using data derived from the previous treatments and genotypes under investigation. The objective was to determine the association between forage yield traits, seed yield and/or seed yield components. Besides, the question of whether the magnitude of such correlation can be altered due to change of genetic materials was also under consideration.

6.b. Testing of the significance of correlation coefficients:

Singh and Chaudhary (1979**)** collated between two methods for testing the significance of correlation coefficients and they maintenance that, the observed value of correlation coefficients is compared with the tabulated value for (n - 2) degrees of freedom. The tabulated values are given in Table (7) page 63 of Fisher and Yates (1938). If the observed value is more than the tabulated one, the correlation coefficients is said to be significant. The other way to test the null hypothesis (r = 0) is through the application of [t] test as fallow:

$$t = r\sqrt{\frac{n-2}{1-r^2}}$$

Where:

r: correlation coefficient.
n: total number of observations.

This [*t*] value is tested against the table value of [t] for (n - 2) degrees of freedom. In fact, these are the same values as given in Table (7) of Fisher and Yates (1938). Nonetheless, in our study, we used two forecited methods for testing the significance of correlation coefficients.

RESULTS AND DISCCUSSION

For various reasons to use of faba bean, the varietal requirement in term of plant type, seed type, maturity, pattern of use and growth are diverse from region to region. Therefore, faba bean breeding program has become more complex and no single variety and / or population can be suitable for all the objectives. Thus, there is need to develop varieties suitable for a specific region and / or use. Therefore, genetic diversity is of great importance and plays a crucial role in focusing faba bean improvement.

Genetic Variability, Heritability and Genetic Advance of Seed yield and its Components and Root Length. Genetic variability, heritability and genetic advance of twelve seed yield and its components and root length of sixty faba bean populations exposed to three irrigation levels were estimated and summarized in Tables (5-8). The phenotypic variance (δ2p) and phenotypic coefficient of variation (PCV %) were slightly higher than corresponding genotypic variance (δ2g) and genotypic coefficient of variation (GCV %) for all the studied characters indicated the presence of less environmental effect (δ2e and ECV %) upon the concerned characters .The values of phenotypic (PCV %) genotypic (GCV %) and environmental (ECV %) coefficients of variation were categorized as low (<10%), moderate (10 to 20%) and high (>20%) based on the divided by Sivasubramanian and Menon (1973) and exposed in Tables (5-8). According to the present study; the phenotypic coefficient of variations (PCV) and genotypic coefficient of variation (GCV) were higher for number of branches/ plant, number of pods/plant, number of seeds/pod, seed yield/plot, dry matter production, harvest index and water use efficiency as shown in Tables (5-8). The obtained results are indicating greater scope for improvement of these characters by simple selection. On the contrary of these conclusions, low estimates of the genotypic coefficient of variation (GCV) were recorded for plant height character indicated that, the environmental factors had more influence on the expression of this character than the genetic factors, suggesting the limited scope for improvement of this character by direct selection of high performing genotypes. In this regard, Abd Azizi and Osman (2015) found that the phenotypic variance was always greater than the genotypic variance for the entire seed yield and traits under study. The highest phenotypic variance among yield component were observed on number of pods and number of seeds per plant and seed weight were 88.86, 89.01 and 66.86, in respectively .

Sharma *et al.* (2017) found that, the genotypes recorded highly significant variation for studied characters indicated the presence of sufficient variability for these characters, thus, there is a lot of scope for selection. One of the ways of assessing the variability is through examining the range of variation. They added that, the genotypic coefficient of variations (GCV) and phenotypic coefficient of variations (PCV) were higher for plant height (54.87 and 54.98; respectively), biological yield/ plant (27.50 and 27.59; respectively), seed yield/plant (26.36 and 27.09; respectively) and primary branches/plant (23.54 and 23.92; respectively) indicating greater scope for improvement of these characters by simple selection. In addition, high heritability estimate indicates less influence of environment on studied characters. Hence, direct selection can be followed to improve early maturing genotypes. High estimates of genetic advance (GA) coupled with substantial amount of heritability indicated selection for such characters would result in the improvement of characters in the desired direction as the character was governed by additive gene action. High heritability coupled with low GA indicates non-additive gene action .

Hiywotu *et al.* (2022) mentioned that the selection based on phenotypic expression of individual accessions for these traits might be easy due to relatively small contribution of the environment to the phenotype, meaning that most of the variation is genetic rather than environmental. The heritability exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. If, low heritability coupled with low genetic advance indicates such character was highly influenced by environment and selection would be ineffective for those traits. The high range of values indicated the good scope for selection of suitable basic material for breeders for further improvement. Besides that, broad sense heritability indicates the percentage of transfers of traits from this generation to next. Depending upon the heritability of the traits characters were categorized into high heritable, medium heritable and low heritable traits. Based on this simple definition, the high broad sense heritability estimate (> 60, according to Robinson *et al.* (1949), which recorded in the two seasons; 2019-2020 and 2020-2021 for dry matter production (89.91 and 76.33; respectively), harvest index (86.08.40 and 81.18; respectively), water use efficiency (86.61 and 78.19; respectively) and root length (86.78 and 81.27; respectively) and seed index (79.69and 84.06 respectively) traits. These indicates less influence of environment on respective characters, which cleared in Tables (5 and 8). Hence, direct selection can be followed to improve faba bean genotypes for these traits in early maturing genotypes. Moreover, high heritability coupled with low genetic advance and genetic advance as percentage of mean for seed index and root length traits indicates non-additive gene action. Where the genetic advance values for these two traits were 17.50, 13.84, 10.50, 13.78, 13.92, 11.05, 17.32, 15.36 and 14.04, 12.39 in respectively. In addition, low broad sense heritability indicates predominance of non-additive gene action indicating the scope for breeding. Whereas, high estimates of GA coupled with substantial amount of heritability, indicate that selection for such characters would result in the improvement of characters in the desired direction as additive genes govern the character. High heritability coupled with low genetic advance indicates non-additive gene action. The heritability exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. In addition, high broad sense heritability was coupled with high genetic advance as percent of mean indicated that most likely the heritability of these characters was due to additive gene effects and selection might be effective for these characters. On the other hand, the variations of the heritability values and genetic advances were found to be independent for some cases under study, thereby reflecting that high heritability was not always associated with high genetic advance. The low broad sense heritability, which recorded in the two seasons; 2019-2020 and 2020-2021 for number of pods/plant (Table 6), indicates predominance of non-additive gene action and scope for breeding. In addition, high broad sense heritability was coupled with high genetic advance as percent of mean indicated that most likely the heritability of those characters was due to additive gene effect and selection might be effective for these characters. Moreover, high heritability coupled with low genetic advanced indicates non-additive gene action. The heritability exhibited due to favorable influence for such traits may not be rewarding. If low heritability coupled with low genetic advanced indicates such character was highly influenced by environment and selection would be in effective for that trait. Therefore, the use of genetic material offers positive opportunities for improving the productivity of faba bean as a primary and main objective of this study. In this respect, Hanelt and Mettin (1989) also, recorded high heritability estimates for 100-seed weight (94.33 %) and number of seeds per pod (89.04%). The result of genetic advance as percent of means an increase of 9.60% to 107.33% magnitude made by selection. Positive and highly significant correlations were observed for seed yield and each of number of pods per plant and plant height. Therefore, it is concluded that these two traits may be considered as the selection criteria for the improvement of seed faba bean. Toker (2004) was grown eight faba bean genotype in order to estimate the broad sense heritability. He mentioned the heritability for plant height, number of stems and pods per plant, seed yield biological yield, 100-seed weight, dry to flowering and maturity estimated as 83, 63, 43, 62,52,99,97 and 97% respectively. In addition, in this regard, Hamza (2017) added that the estimates of broad sense heritability (h2) generally were high to moderate for all studied traits. The height estimates of broad sense heritability was scribed as 94.32% for 100-seed weight ,89.04% for number of seed /pod and 89.03% for dry to 90% maturity. High estimates of her its ability indicated that selection based on mean would be successful in proving these traits. Addition to the number of pods/plant was record the highest genetic advance of mean 107.33% followed by number of seed / pods 57.85% and100-seed weight 57.51%.

Phenotypic Correlation Coefficients for Seed yield and seed Yield Components :

In the present study, phenotypic correlation coefficients for twelve seed yield, seed yield components and root length of sixty faba bean populations affected by three irrigation levels during 2019-2020 and 2020-2021-seasons were estimated and summarized in Table (8). Positive and highly significant correlation was observed among all studied characters. The strong association of these characters can be giving importance during selection to improve the yield potential of faba bean. Bora *et al.* (1998) motional that the seed yield correlated significant positive with number of pods per plant (0.950) and plant height (0.496). Musallam *et al.* (2004) there is strong correlation between biomass at maturity and seed yield in faba bean genotypes that maintain high biomass under drought show drought tolerance response and this can be targeted in breeding programs .The correlation coefficient among all agronomic traits (Plant height, number of branches, first fruit node, number of pods / plants, number of seeds / plant and seed yield / plant). They mentioned that; the improvement of seed yield in faba bean is linked with these traits (number of pods per plant and plant height) and selection of these traits might have good impact on yield. They added that; the correlation helps breeders to identify the characters that could be used as selection criteria in breeding programmed. These results suggested that improvement of grain yield in faba bean is linked with these traits (number of pods per plant and plant height) and selection of these traits might have good impact on yield. In this connect, Elshafei *et al.* (2019) reached to the same findings and mentioned that the selection of the most traits of faba bean crop might be good impact on seed yield and its yield attributes. In addition, Tadele *et al.* (2021) mentioned that; any improvement of traits with significant positive correlation would result in a substantial increment on seed yield of faba bean crop. The result indicated any improvement of traits with significant positive correlation would result in a substantial increment. They added that; the phenotypic expression of the correlation gets modified under the influence of environment and genotypic correlation provides measures of genetic association between traits and is more reliable than phenotypic correlation and this helps to identify the traits to be utilized in breeding.

Table (4): Analysis of variance for plant height, number of branches / plant and number of pods /plants sixty faba bean populations affected by three irrigation levels during two seasons; 2019-2020 and 2020-2021.

Analysis of Variance:	Three Seed yield Traits					
	Plant Height (cm)		Number of Branches/Plant		Number of Pods / Plant	
	2019-20	2020-20	2019-20	2020-20	2019-20	2020-20
Phenotypic Variance (δ^2p)	66.64	104.37	10.40	9.16	44.27	26.59
Genotypic Variance (δ^2g)	38.62	48.94	4.74	6.38	8.01	4.30
Environmental Variance (δ^2e)	55.43	95.34	6.66	2.78	36.26	22.29
Phenotypic Coefficients of Variation (PCV %)	10.08	13.47	71.82	61.77	31.99	30.92
Genotypic Coefficients of Variation (GCV %)	6.90	8.25	46.30	51.55	13.61	8.04
Environmental Coefficients of Variation (ECV %)	7.34	10.65	54.91	34.03	28.95	19.11
Broad Sense Heritability (h^2_B)	46.89	37.53	41.55	69.65	18.09	16.18
Genetic Advance (GA)	9.77	9.88	2.89	4.35	2.48	1.78
Genetic Advance as Percentage of Mean (GAM)	10.51	9.75	61.47	88.75	11.94	6.97

Note: Classify of PCV %, GCV % and ECV % according to Sivasubramanian and Menon (1973) as: Low: 0-10%; Moderate: 10- 20% and High: > 20%. Categorize of broad sense heritability according to Robinson *et al.* (1949) as: Low: 0-30%; Moderate: 30- 60% and High: > 60%. Categorize of genetic advance as percentage of mean according to Johnson *et al.* (1955) as: Low: 0-10%; Moderate: 10-20% and High: > 20%.

Table (5): Analysis of variance for number of seeds / pods, seed index and seed yield / plant of sixty faba bean populations affected by three irrigation levels during two seasons; 2019-2020 and 2020-2021.

Analysis of Variance:	Three Seed yield Traits					
	Number of Seeds / Pod		Seed Index		Seed Yield / Plant	
	2019-20	**2020-21**	**2019-20**	**2020-21**	**2019-20**	**2020-21**
Phenotypic Variance (δ^2p)	35.79	19.17	62.29	45.29	63.57	56.96
Genotypic Variance (δ^2g)	23.37	13.25	49.64	38.07	45.05	32.78
Environmental Variance (δ^2e)	12.52	5.92	12.65	7.22	18.53	24.18
Phenotypic Coefficients of Variation (PCV %)	139.13	101.81	10.54	8.85	8.93	8.33
Genotypic Coefficients of Variation (GCV %)	112.18	84.64	9.41	8.12	7.52	6.32
Environmental Coefficients of Variation (ECV %)	82.29	56.58	42.81	3.54	4.82	5.43
Broad Sense Heritability (h^2_B)	65.02	69.11	79.69	84.06	70.85	57.55
Genetic Advance (GA)	8.02	6.24	12.98	11.67	11.65	8.96
Genetic Advance as Percentage of Mean (GAM)	186.61	145.15	17.32	15.36	13.05	9.89

Note: Classify of PCV %, GCV % and ECV % according to Sivasubramanian and Menon (1973) as: Low: 0-10%; Moderate: 10- 20% and High: > 20%. Categorize of broad sense heritability according to Robinson *et al.* (1949) as: Low: 0-30%; Moderate: 30- 60% and High: > 60%. Categorize of genetic advance as percentage of mean according to Johnson *et al.* (1955) as: Low: 0-10%; Moderate: 10-20% and High: > 20%.

Table (6): Analysis of variance for seed yield / plot, dry matter production and harvest index of sixty faba bean populations affected by three irrigation levels during two seasons; 2019-2020 and 2020-2021

Analysis of Variance:	Three Seed yield Traits					
	Seeds Yield / Plot		Dry matter Production		Harvest index (%)	
	2019-20	**2020-21**	**2019-20**	**2020-21**	**2019-20**	**2020-21**
Phenotypic Variance (δ^2p)	27.52	45.80	89.04	77.29	35.06	67.84
Genotypic Variance (δ^2g)	20.39	23.27	80.06	59.00	30.18	55.02
Environmental Variance (δ^2e)	7.13	22.53	8.98	18.29	4.88	12.82
Phenotypic Coefficients of Variation (PCV %)	293.08	375.97	115.64	130.82	25.86	30.39
Genotypic Coefficients of Variation (GCV %)	252.28	267.98	109.65	114.30	23.99	27.37
Environmental Coefficients of Variation (ECV %)	149.17	26370	36.72	63.64	9.65	13.21
Broad Sense Heritability (h^2_B)	74.09	50.81	89.91	76.33	86.08	81.10
Genetic Advance (GA)	8.02	7.09	17.50	13.84	10.52	13.78
Genetic Advance as Percentage of Mean (GAM)	477.99	394.05	214.51	206.06	45.92	50.85

Note: Classify of PCV %, GCV % and ECV % according to Sivasubramanian and Menon (1973) as: Low: 0-10%; Moderate: 10- 20% and High: > 20%. Categorize of broad sense heritability according to Robinson *et al.* (1949) as: Low: 0-30%; Moderate: 30- 60% and High: > 60%. Categorize of genetic advance as percentage of mean according to Johnson *et al.* (1955) as: Low: 0-10%; Moderate: 10-20% and High: > 20%.

Table (7): Analysis of variance for expected seed yield / fad, water use efficiency and root length of sixty faba bean populations affected by three irrigation levels during two seasons; 2019-2020 and 2020-2021

Analysis of Variance:	Water Use Efficiency		Root Length	
	2019-20	2020-21	2019-20	2020-21
Phenotypic Variance (δ^2p)	60.72	46.90	61.50	54.62
Genotypic Variance (δ^2g)	52.59	36.67	53.37	44.39
Environmental Variance (δ^2e)	8.13	10.23	8.13	10.23
Phenotypic Coefficients of Variation (PCV %)	98.93	119.51	5.53	4.21
Genotypic Coefficients of Variation (GCV %)	91.57	105.68	5.16	3.79
Environmental Coefficients of Variation (ECV %)	36.00	55.82	2.01	1.82
Broad Sense Heritability (h^2_B)	86.61	78.19	86.78	81.27
Genetic Advance (GA)	13.92	11.05	14.04	12.39
Genetic Advance as Percentage of Mean (GAM)	175.80	192.78	9.91	7.06

Note: Classify of PCV %, GCV % and ECV % according to Sivasubramanian and Menon (1973) as: Low: 0-10%; Moderate: 10- 20% and High: > 20%. Categorize of broad sense heritability according to Robinson *et al.* (1949) as: Low: 0-30%; Moderate: 30- 60% and High: > 60%. Categorize of genetic advance as percentage of mean according to Johnson *et al.* (1955) as: Low: 0-10%; Moderate: 10- 20% and High: > 20%.

Table (8): Phenotypic Correlation Coefficients for Twelve Seed yield, seed yield Components and Root Length of Sixty Faba Bean Populations Affected by Three Irrigation Levels during two Seasons; 2019-2020 (Above Diagonal) and 2020-2021 (Below Diagonal)

Characters	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
1. Plant Height (cm)	----	0.57	0.41	0.58	0.65	0.69	0.30	0.57	0.18	0.33	0.60	0.64
2. Number of Branches / Plt.	0.68	----	0.33	0.42	0.51	0.40	0.47	0.50	0.45	0.40	0.44	0.39
3. Number of Pods / Plant	0.59	0.42	----	0.38	0.43	0.49	0.39	0.60	0.58	0.46	0.46	0.64
4. Number of Seeds / Pod	0.51	0.37	0.39	----	0.56	0.33	0.52	0.29	0.56	0.44	0.60	0.39
5. 100-Seeds Weight	0.66	0.39	0.45	0.49	---	0.50	0.49	0.43	0.52	0.49	0.44	0.69
6. Seed Yield / Plant	0.61	0.58	0.64	0.47	0.35	----	0.58	0.69	0.58	0.51	0.46	0.65
7. Seed Yield / Plot	0.43	0.49	0.39	0.60	0.58	0.46	----	0.65	0.52	0.61	0.58	0.39
8. Expected Seed Yield / fad.	0.48	0.50	0.61	0.44	0.62	0.54	0.55	----	0.41	0.45	0.36	0.58
9. Aboveground Phytomass	0.77	0.55	0.35	0.46	0.77	0.68	0.55	0.49	----	0.38	0.49	0.49
10. Harvest Index	0.18	0.48	0.61	0.58	0.65	0.49	0.43	0.13	0.58	----	0.58	0.50
11. Water Use Efficiency	0.37	0.52	0.49	0.36	0.57	0.66	0.49	0.46	0.29	0.54	----	0.65
12. Root Length	0.48	0.38	0.43	0.49	0.39	0.60	0.58	0.46	0.49	0.68	0.66	----

For testing the significant of correlation coefficients, "*t*" value for n-2 at 0.05 and 0.01 levels are 0.159 and 0.208, respectively

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تقدير التباين الوراثي ومعامل الارتباط المظهري لمحصول البذور ومكوناته وطول الجذر في الطرز الوراثية للفول البلدي تحت الإجهاد المائي

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المستخلص : يعد تحسين التراكيب الوراثية للفول البلدي لتحمل الجفاف هدفاً رئيسياً لتربية النباتات لمواجهة تغير المناخ التي تؤثر بدورها على إنتاجيته في مصر، خاصة الإجهاد اللاحيوى وبشكل خاص إجهاد الجفاف. من هذا المنطلق أجريت الدراسة الحالية بهدف تقييم 60 تركيب وراثي من الفول المصري تكونت من 54 عائلة، سبق وأن اختيرت من بين 180 سلالة بناءاً على محصول البذور، بالإضافة إلى ستة أصناف مصرية لتقديرات التباين الوراثي، والتوريث، والتقدم الوراثي، ومعامل الارتباط المظهرية في محصول البذور ومكوناته وطول الجذر في تلك التراكيب الوراثية للفول تحت ظروف الضغط المائي. تم إجراء تجربة حقلية تحت ثلاثة أنظمة مائية تكونت من (100٪ 75٪ و50٪ من السعة الحقلية) وذلك في موقعين (الإسماعيلية، شمال سيناء) خلال موسمي الزراعة المتتاليين (2019 / 2020 و2020/ 2021). تم استخدام تصميم القطع المنشقة مرة واحدة، بقطاعات الكاملة العشوائية، حيث تم تخصيص قطع الأرض الرئيسية لمستويات الري الثلاثة (100٪ 75٪ و 50٪ من السعة الحقلية)، بينما خصص للقطع الفرعية ال60 تركيب وراثي من الفول البلدي. أوضحت النتائج أن معامل التباين المظهري كان أعلى بالنسبة لعدد الفروع/ النبات، عدد القرون/ النبات، عدد البذور/ القرون، محصول البذور/ نبات، انتاج المادة الجافة، مؤشر الحصاد وكفاءة استخدام المياه، وهذا يعزز امكانية تحسين هذه الصفات عن طريق الانتخاب البسيط. أشارت تقديرات كفاءة التوريث بمعناها العام خلال الموسمين (2019/ 2020 و2020/ 2021) إلى أنها بلغت (91 . 89 و 33 . 76) لانتاج المادة الجافة، (08 . 86 و 81 . 81) لدليل الحصاد، (69 . 79 و 84) لوزن 100 بذرة، (01، 65 و 10 . 65) لعدد البذور/ قرن، ، (61 . 86 و 19 . 78) لكفاءة استخدام المياه، (78 . 86 و 27 . 81) لطول الجذر. أشارت النتائج إلى ان ارتفاع قيمة كفاءة التوريث خلال الموسمين لصفة إنتاج المادة الجافة وغيرها إلى نقص تأثير البيئة على الصفات مما يسمح بإمكانية الانتخاب المباشر لتحسين صفات التراكيب الوراثية للفول البلدى في وقت مبكر. كذلك لوحظ أن درجة التوريث المرتفعة اقترنت بالتقدم الوراثي العالي مما يشير إلى أن معظم الصفات المدروسة يحكمها بشكل أساسي الفعل الجيني الإضافي ولها تأثير كبير على الانتخاب المباشر من أجل التحسين الوراثي عن طريق طرق اختيار النسب للصفات الوراثية، ولوحظ ارتباط إيجابي ودلالة عالية في صفات الدراسة. يمكن إعطاء الحذر الشديد لهذه الصفات أهمية أثناء الاختيار لتحسين إمكانات العائد من الفول الفول البلدى خاصة تحت ظروف الجفاف.

الكلمات المفتاحية : الفول البلدى، معامل الارتباط، مقدار التحسن الوراثى المتوقع، التباين الوراثى، كفاءة التوريث