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Genetic Variability, Heritability and Genetic Advance of Seed Yield and Its Components for Some Promising Genotypes of Faba Bean

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ABSTRACT



A field experiment designed in randomized complete block design with three replicates was used to evaluate nine promising faba bean lines in F₆ with three cultivars: Giza 716, Giza 843 and Sakha 1 under natural infection of chocolate spot disease at the Agricultural Research Station farm in Etay Al-Baroud during 2018/2019 and 2019/2020. Mean squares due genotypes were highly significant for all studied traits in both seasons as a clear evidence for the wide diversity between these genotypes in their pedigree and these genotypes will differ in their performances for all traits. Line 8, 9 and 3 had highly significant values for most of the traits. All genotypes showed a moderate resistance for chocolate spot except Giza843, Line2 and 4 in both seasons. The genetic variance was the large part in phenotypic variation compared to the environmental variation in all traits and this may be clear that the diversity in all genotypes performances were due the wide genetic diversity of all genotypes. Generally, plant height, 100-seed weight and seed yield/plant had high PCV, GCV and h² values which indicated that this trait is controlled by genetic factor and higher chance to improve this trait through selection. Seed yield/plant, seed yield/plot and seed yield/fad significant negative associated with chocolate spot infection in both seasons. The phenotypic similarity matrix between all genotypes ranged from 12.20 to 118.66. the highest similarity values were showed between Line 8 and Line 6 followed by Giza 843 and Giza 716 and Line 7 and Line 2.

Keywords: Genetic Variability, Heritability, Faba bean.

INTRODUCTION

Faba bean (Vicia faba, L.) is the first legume crop in Egypt, as it is considered a daily food for the majority of the Egyptian people because of its great nutritional value, as it is a major source of protein and is one of the most important alternatives to animal protein in Egypt, where the protein ratio in dry seeds ranges from 35:40% (Sharaan et al., 2004 and Mahdi et al., 2021). Therefore, there is great interest from the government to increase the harvested area of faba bean by encouraging farmers, providing improved seeds and production requirements, and improving the price policy of the crop. Despite these strenuous efforts of the government, there is a significant decline in the harvested area with faba beans in Egypt, as that area reached about 70682 feddans in 2019 (FAOSTAT, 2019). The great decline in the harvested area of faba bean due to many factors, the most important factor is due to the large spread of broom rape and chocolate spot (Botrytis fabae) disease, which caused great losses in the yield. As well as the inability of the crop to compete with wheat and some contract crops such as sugar beet crop, which occupied a large area of the faba beans. In addition to the absence of resistant varieties to both broom rape (Fernández-Aparicio et al., 2016) and chocolate spot (Abou-Elhagag and Salman 2001), that can be cultivated in places infested with both broom rape and chocolate spot. From this standpoint, the role of the faba bean breeder is increasing in Egypt in finding new high-yield genotypes

tolerant to both broom rape and chocolate spot, through which the area of the faba bean grown can be, increased again (Maalouf et al., 2011 and El-Hosary 2020). Therefore, the faba bean breeder will initially search for new variances in the faba bean population, but the breeder in most cases faces great difficulty in exhausting most of the genetic variances in the Egyptian faba bean population. In addition to the lack of modern methods and tools in plant breeding, so, the breeder depends most of the time on traditional breeding methods that depend mainly on estimating the components of the phenotypic variance to link the phenotypic differences between those genotypes with the genetic variation, a method (Aziz and Osman, 2015) that has proven to be very successful in most cases and through it the faba bean breeder was able, to breed many developed varieties.

Cross Mark

Heritability and genetic advance are great selection parameters. The estimation of heritability together with the genetic advance is the most useful to predict the gain according to selection compared with the selection based on heritability alone. Heritability determines to which degree difference among phenotypes as a result of genetic causes. Heritability is used to show to which degree a trait is inherited to the offspring generation. This magnitude suggests the extent to which improvement can be achieved through selection. The genetic advance achieved in each breeding cycle depends on how the additive gene effect is beneficial (Hassan, 1991). Kalia and Sood (2004) found on

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faba bean high heritability and high genetic advance for pod yield/plant which indicated high additive gene action and the possibility of trait improvement through selection. The high heritability with low genetic advance in any traits, almost referred to the dominant effect of the gene, and hence these traits can be improved by hybridization. Johnson *et al.* (1955) showed that the estimation of heritability together with the coefficient of variation is usually useful to the resulting effect of selection than heritability alone. This was mainly because heritability is a ratio of genotypic and phenotypic variances and varies greatly in accordance with the sample size, the environment, and the character of the population.

In the end, the current study is considered a new try to find new faba bean genotypes with high-yielding and tolerance to chocolate spot, depending on the associated of phenotypic differences of those genotypes with the genetic variation and determining the amount of genetic advance of those genotypes.

MATERIALS AND METHODS

A field experiment was conducted at the Agricultural Research Station farm in Etay Al-Baroud to evaluate nine promising lines of municipal beans in the sixth generation with three commercial varieties: Giza 716, Giza 843 and Sakha 1 under natural infection in the field conditions for chocolate spot disease during the two growing seasons 2018 / 2019 and 2019/2020. The name pedigree and of the faba bean genotypes are shown in Table 1.

 Table 1. Name and pedigree of the twelve faba bean genotypes used in the study.

8	
Genotypes names	Pedigree
Giza 716	461/842/83 x 503/453/83
Giza 843	561/2076/85Skh x 461/845/83
Sakha 1	Giza716 x 620/283/85
Line 1	Sakha1 x Giza 40
Line 2	Giza 843 x Sakha 1
Line 3	Sakh1 x Nubaria 1
Line 4	Nubaria 1 x TW
Line 5	Giza 716 x TW
Line 6	Sakha 1 x TW
Line 7	Giza 716 x Giza 40
Line 8	Giza 716 x Nubaria 1
Line 9	Nubaria 1 x Giza 40

During the two seasons all genotypes were sowing on 20^{th} of November in an experiment designed in randomized complete block design with three replicates. Each plot consisted of 4 rows, each row was four meters long and 60 cm apart (plot size was 12 m²). Seeds were sown on both sides of the ridge with two seeds /hill with 25 cm hill spaces.

The all other agricultural practices were done as recommended. No pesticide treatments were applied, the crop was provided with normal irrigation.

Data recorded:

in the two seasons 10 guarded plants were randomly taken at harvest to measure the following records plant height (cm), no. of branches/plant, no. of pods/plant, no. of seeds/pod, 100-seed weight (g), seed yield/plant (g), seed yield/plot (kg) and seed yield/fad (erdab). While, disease severity and reaction chocolate spot (*Botrytis fabae*) were recorded at the first of April according to ICDARDA (Bernier *et al.*, 1984) scale from 1-9 (1 highly resistant, 3 resistant, 5 moderate resistant, 7 susceptible 9 highly susceptible).

Statistical Analysis:

Data were subjected to the analyses of variance (ANOVA) for randomized complete block design (RCBD) with three replicates for each season individually followed by compared means with LSD at levels probability of 5% and 1%, according to Gomez and Gomez (1984). Broad sense heritability (H) was estimated by using variance components method (Fehr, 1987). The genotypic and phenotypic variances (δ^2 g and δ^2 ph) were calculated from the partitioning the expected mean squares (Table 2) as follows:

 Table 2. Expectation mean squares (M.S) for the ordinary analysis of variance for individually

scason.			
SOV	DF	MS	EMS
Replications	(r-1)	M r	
Genotypes	(g-1)	Мg	$\delta^2 e + r \delta^2 g$
Error	(r-1)(g-1)	Me	δ²e

Where: r is replicates number and g is genotypes number.

 $\delta^2 g$ and $\delta^2 e$ refers to genotypic and error variance, respectively. The pertinent mean squares expectation (Table 2) as follows: $\delta^2 g = (Ma - Me)/r$, and $\delta^2 ph = (\delta^2 g + \delta^2 e/r$, where $\delta^2 e = Me$.

The genotypic and phenotypic coefficients of variation (GCV and PCV%) for each character were calculated by using the following formulas:

$$PCV = \frac{\sqrt{\delta^2 P}}{\overline{X}} x \ 100$$
$$GCV = \frac{\sqrt{\delta^2 P}}{\overline{X}} x \ 100$$

Where: $\delta^2 p$ and $\delta^2 g$ are the phenotypic and genotypic variances. \overline{X} is the grand mean of trait.

Broad sense heritability (H) was calculated as follows: $H = (\delta^2 g / \delta^2 ph) x 100$ (Allard, 1960).

RESULTS AND DISCUSSIONS

1.Analysis of variance.

Analysis of variance of all genotypes in both seasons of this study is presented in Table 3. Mean squares due genotypes were highly significant for all studied traits in both seasons. The significant mean square of all tested genotypes (nine lines and three cheeks) consider a clear evidence for the wide diversity between these genotypes in their pedigree and these genotypes will differ in their performances for all traits. In the previous studies of Eman *et al.*, (2017), Abbas *et al.*, (2012) and Talaat and Abdallah (2008) found a wide diversity among the Egyptian faba bean genotypes in all growth, yield and yield components traits. The significant genotypic differences in faba bean for plant height, pod number /plant and 100-seed weight were shown before by Kumar *et al.*, (2017).

Troite	DE	2018/201	9	2019/202	0
TTaits	D. r —	Genotypes	Error	Genotypes	Error
Plant height (cm)	11	429.92**	22.32	450.43**	22.88
Branches number/plant	11	3.42**	0.49	6.15**	0.26
Pod number/plant	11	67.62**	5.68	95.35**	7.68
Seeds number/pod	11	1.80**	0.12	2.72**	0.17
100-seed weight (g)	11	198.03**	14.50	300.14**	19.78
Seed yield/plant (g)	11	130.06**	6.90	117.71**	12.03
Seed yield/plot (kg)	11	6.69**	0.34	6.52**	0.64
Seed yield/fad (erdab)	11	34.11**	1.73	33.26**	3.24

Table 3.Genotypes mean squar	es for all the studied	traits in 2018/2019 a	nd 2019/2020	growing seasons

2. Mean performances.

Growth, seed yield and yield component traits.

The results in Table 4 indicated that all tested genotypes significantly differ in their performances for all studied traits during the two seasons of the study. For plant height the results showed that Line 8 had highly significant desirable values for plant height (117.48 and 118.66 cm), branches number/plant (4.55 and 4.12), pods number /plant (18.20 and 20.20), seed number/pod (3.92 and 4.32), 100seed weight (79.92 and 85.40 g), seed yield/plant (32.19 and 31.51 g), seed yield/plot (7.27 and 7.23 kg) and seed yield/fad with averages of 16.41 and 16.33 erdab in the first and second seasons, respectively. In the same way, Line 9 ranked the second class after Line 8 where it gave also highly significant desirable values for plant height (114.68 and 116.08 cm), branches number/plant (4.03 and 3.80), number of pods/plant (18.89 and 20.78), seeds number/pod (3.74 and 4.11), 100-seed weight (76.13 and 83.36 g), seed yield/plant (30.89 and 29.61 g), seed yield/plot (6.96 and 6.79 g) and seed yield/fad (15.73 and 15.34 erdab) in both seasons respectively. Also, Line 3 gave excellent means for all the previous traits without any significant differences with Line 8 and line 9 in all studied traits except number of pods/plant in the two seasons.

All tested genotypes differ in their performances in both seasons. Similar results were obtained before by Eman *et al.* (2017) who found that the Egyptian faba bean genotypes differ significantly in growth and yield and Sakha I were the lowest in growth traits in the two seasons. On the other side Abbas *et al.* (2012) found that Sakha I cultivar had the highest values for growth traits (plant height and number of branches/plant) compared with Giza716 and Giza 40 cultivars. Also, Talaat and Abdallah (2008) found that Giza 716 was higher than Sakha 1 and Giza 40 in all yield and its components traits and this really associated with the difference in genetic contributions of the genotypes.

Table 4. Mean performance of twelve faba bean genotypes for all the studied traits in 2018/2019 and 2019/2020 seasons.

Trait	Plant hei	ght (cm)	Branches (n	umber/plant)	Pods (nun	ber/plant)	Seeds (number/pod)		
genotype	2018/19	2019/20	2018/19	2019/20	2018/19	2019/20	2018/19	2019/20	
Giza 716	103.77 ^{cd}	105.06 ^{cd}	3.44 ^{bc}	3.00 de	13.05 bc	13.85 ^{bc}	3.10 de	3.34 ^{de}	
Giza 843	99.31 de	99.95 ^{de}	2.98 ^{cd}	3.17 de	11.33 cd	12.09 cd	2.75 ^{ef}	2.89 ef	
Sakha 1	109.78 ^{bc}	105.02 ^{cd}	2.98 ^{cd}	3.17 de	7.92 ^e	7.88 ^e	3.77 ^{ab}	4.14 ^a	
Line 1	109.78 ^{bc}	111.14 ^{bc}	3.50 bc	3.33 ^{cd}	12.54 ^{bc}	13.42 bc	3.52 bc	3.87 abc	
Line 2	102.47 ^d	104.27 ^d	3.68 bc	3.80 abc	10.36 cde	10.91 cde	3.13 cde	3.44 ^{cd}	
Line 3	111.33 ^{ab}	112.70 ^{ab}	4.29 ^{ab}	3.96 ^{ab}	14.82 ^b	16.30 ^b	3.61 ^{ab}	3.97 ^{ab}	
Line 4	102.50 ^d	104.16 ^d	3.76 abc	3.48 bcd	9.44 ^{de}	9.58 ^{de}	3.17 ^{cd}	3.49 bcd	
Line 5	89.36 ^f	89.54 ^f	2.28 ^d	2.61 ^e	12.86 bc	13.88 ^{bc}	2.20 g	2.19 ^g	
Line 6	95.13 ef	96.50 ^e	2.28 ^d	2.61 ^e	12.53 bc	13.15 ^{bc}	2.54 ^{fg}	2.66 fg	
Line 7	111.55 ^{ab}	112.92 ^{ab}	4.11 ab	3.96 ^{ab}	9.61 de	9.56 ^{de}	3.73 ^{ab}	4.10 ^a	
Line 8	117.48 ^a	118.66 ^a	4.55 ^a	4.12 ^a	18.20 a	20.02 a	3.92 ^a	4.32 ^a	
Line 9	114.68 ^{ab}	116.08 ab	4.03 ^{ab}	3.80 abc	18.89 ^a	20.78 ^a	3.74 ^{ab}	4.11 ^a	

Means followed by the same letter for each genotype are not significantly different by Duncan test (p<0.05)

Table 4. Cont.

Constant	100-seed	100-seed weight (g)		Seed yield/plant (g)		l/plot (kg)	Seed yield/fad (Erdab)	
Genotypes	2018/19	2019/20	2018/19	2019/20	2018/19	2019/20	2018/19	2019/20
Giza 716	70.59 ^{cd}	74.79 ^{cd}	24.80 °	24.50 cde	5.58 °	5.57 ^{cde}	12.61 °	12.58 cde
Giza 843	67.56 ^{de}	70.66 de	28.50 ^b	27.09 bcd	6.46 ^b	6.08 bcd	14.58 ^b	13.73 bcd
Sakha 1	78.01 ab	62.41 f	20.68 de	19.53 ^g	4.66 de	4.48 ^g	10.51 de	10.12 g
Line 1	74.68 bc	79.80 ^{bc}	29.38 ^{ab}	27.99 abc	6.62 ab	6.42 abc	14.94 ^{ab}	14.50 abc
Line 2	69.71 ^d	74.03 ^d	20.41 de	19.91 ^{fg}	4.57 de	4.54 ^{fg}	10.33 de	10.26 fg
Line 3	75.74 ^{ab}	80.93 ^{ab}	30.73 ^{ab}	29.99 ^{ab}	6.92 ^{ab}	6.88 ^{ab}	15.62 ab	15.54 ^{ab}
Line 4	69.73 ^d	73.81 ^d	19.00 e	18.90 ^g	4.26 ^e	4.30 ^g	9.63 ^e	9.71 ^g
Line 5	60.79 ^f	62.41 f	22.90 cd	21.74 efg	5.21 ^{cd}	4.79 efg	11.76 ^{cd}	10.82 efg
Line 6	64.72 ef	66.44 ef	21.76 de	21.95 efg	4.89 de	4.84 ^g	11.04 de	10.93 efg
Line 7	75.88 ^{ab}	81.09 ab	24.80 °	23.62 def	5.59 °	5.42 def	12.61 °	12.24 def
Line 8	79.92 ^a	85.40 ^a	32.19 a	31.51 a	7.27 ^a	7.23 ^a	16.41 a	16.33 a
Line 9	76.13 ^{ab}	83.36 ^{ab}	30.89 ^{ab}	29.61 ab	6.96 ab	6.79 ^{ab}	15.73 ^{ab}	15.34 ^{ab}

Chocolate spot severity and reactions.

For the infection with chocolate spot (Botrytis fabae) diseases, recorded under natural field conditions in all tested genotypes during the two seasons are presented in Table 5. All genotypes showed a moderate resistance except Sakha 1, Line 2 and Line 4 in both seasons as well as Line 6 in the first season, among most genotypes for measured traits. Line 8 showed the lowest severity to chocolate spot infections (4.0 and 4.3%) followed by Line 3 (4.1 and 4.5%) then Giza 843 (4.7 and 5.5%) in the first

and second seasons, respectively. On the other side, Line 2 was the most susceptible genotype where it showed the highest chocolate spot severity percentages with averages of 8.1 and 7.4% in the first and second seasons, respectively. Many researchers described the variation of the resistance on the Egyptian faba bean genotypes such as Abbas *et al.*, (2012) who found that Giza 716 and Sakha 1 were more resistance than Giza 40 to chocolate spot infections. In the same way, Waly *et al.*, (2019) indicted that Nubaria 1 followed by Misr 1 were more resistance to chocolate spot than Sakha 3 and Giza 40. Moreover, El-Sayed *et al.*, (2011) confirmed that Giza 716 and Sakha 2 scored the lowest infections with chocolate spot while, Giza 40 was high susceptible genotype.

Table 5. Chocolate spot severity percentage of all tested genotypes under the field infection during 2018/2019 and 2019/2020 growing seasons.

Genotypes	Disease severity %	Reaction	Disease severity %	Reaction
	2018/	19	2019/	20
Giza 716	5.6	MR	6.2	MR
Giza 843	4.7	MR	5.5	MR
Sakha 1	7.8	S	7.2	S
Line 1	5.0	MR	5.2	MR
Line 2	8.1	S	7.4	S
Line 3	4.1	MR	4.5	MR
Line 4	8.0	S	7.6	S
Line 5	6.2	MR	6.5	MR
Line 6	6.9	S	6.5	MR
Line 7	6.2	MR	6.5	MR
Line 8	4.0	MR	4.3	MR
Line 9	4.7	MR	5	MR

3. Genetic variability and heritability.

Genetic variability and heritability for all traits of twelve faba bean genotypes are showed in Table 6. The obtained data revealed that genetic variance components were highly significant for all studied traits, it could be detect that the genetic variance was the large part in phenotypic variation compared to the environmental variation in all traits and this may be clear that the diversity in all genotypes performances were due the wide genetic diversity of all genotypes (Table 1). In all studied traits except number of branches/plant and number of pods/plant a less differ between phenotypic coefficients of variation and genotypic coefficients of variation were observed. The low difference between GCV% and PCV% for all studied traits indicating the negligible of environmental effect on all traits. However, PCV% was higher than GCV% for number of branches and pods/plant in both seasons, confirmed the presence of a significant environmental effect, which is expected for these traits. the narrow gap between PCV and GCV variation in faba bean have been observed in studies before this narrow gap between PCV and GCV indicated that the variability between genotypes due to the genetic constitution of the genotypes was larger than variability due to the environmental factors (Hamza et al., 2017). The high PCV and GCV values consider a clear indication of the low effect of environmental factors in the expression of traits and the higher chance to improve the traits through selection breeding (Ejara et al., 2016). In the first season the broad sense Heritability ranged from 49.92 for number of branches/plant to 75.73% for seed yield/fad while the broad sense heritability ranged in the second season form 46.17% for number of pods/plant to 70.87% for number of seeds /pod. The results also showed that h² of seed yield/plant, seed yield/plot and seed yield/fad were 74.83, 75.72 and 75.73% in the first season and reduced to 59.43, 60.68 and 60.68% for the three traits, respectively in the second season. The large variability in h^2 of these traits during the two seasons consider a clear evidence for the large environmental effect on these traits (threshold traits).

Table 6. Genotypic and phenotypic coefficients of variability and heritability for all the studied traits of all the studied faba bean genotypes in 2018/19 and 2019/20 seasons.

	P	V	GV		E	V	PCV		GCV		h ²	
Traits	2018/19	2019/20	2018/19	2019/20	2018/19	2019/20	2018/19	2019/20	2018/19	2019/20	2018/19	2019/20
Plant height (cm)	97.41	101.68	66.06	69.81	31.35	31.87	9.33	9.42	7.68	7.81	67.81	68.66
Branches number/plant	0.98	0.49	0.49	0.23	0.49	0.26	28.68	20.47	20.26	13.91	49.92	46.17
Pod number /plant	16.00	22.29	10.32	14.61	5.68	7.68	31.80	35.10	25.54	28.41	64.51	65.54
Seeds number /pod	0.40	0.60	0.28	0.42	0.12	0.18	19.35	21.83	16.19	18.38	70.00	70.87
100-seed weight (g)	45.09	66.50	30.59	46.72	14.50	19.78	9.33	10.71	7.69	8.97	67.84	70.25
Seed yield/ plant (g)	27.42	29.64	20.52	17.61	6.90	12.03	20.53	22.05	17.76	16.99	74.83	59.43
Seed yield /plot (kg)	1.40	1.62	1.06	0.98	0.34	0.64	20.57	22.65	17.90	17.64	75.72	60.68
Seed yield /fad (erdab)	7.13	8.24	5.40	5.00	1.73	3.24	20.57	22.65	17.90	17.64	75.73	60.68

It was reported that use of both the genetic advance and heritability of traits consider more effective parameter in determining how much progress can be made through selection than used each of them individually (Johnson *et al.*, 1955). Our findings, showed high heritability accompanied with high to moderate genetic advance was presented for plant height, 100-seed weight and seed yield/fad. High heritability with the high genetic advance of these traits confirmed the possibility to select of high performing genotypes to improvement of the traits and the effectiveness of phenotypic performance selection to improve these traits. While, traits with high to moderate heritability, indicates that these traits will respond moderate to high for phenotypic selection. Also, high h² and GAM value of traits indicates the possibility of transferring these traits from parents to their offspring (Singh, and Ceccarelli 1996). Generally, plant height, 100seed weight and seed yield/plant had high PCV, GCV, H2 and GA values which indicated that this trait is controlled by genetic factor and higher chance to improve this trait through selection. The moderate heritability with the low genetic advance of branches number/plant, seeds number/pod and seed yield/plot due the epistatic gene action, (Kalia and Sood 2004) so the mass selection may be ineffective in improving the seed yield per plant in these four genotypes.

4. Phenotypic correlation coefficient (r_{ph}).

The phenotypic correlation coefficients (r_{ph}) among all faba bean traits in both seasons of the study are presented in Table 7. Seed yield/fad significant positive associated with seed yield/plant (0.97** and 0.96**) and seed yield/plot (1.00** and 1.00**) in the contrast of this seed yield/fad significant negative correlated with chocolate spot infection (-0.92** and -0.96**) in both seasons, respectively. In the same way a significantly positive associated between seed yield/plant and seed yield/plot were shown with correlation coefficients of 0.96** and 0.95** in both seasons, respectively. Also, seed yield/plant and seed yield/plot negatively significant correlated with chocolate spot infection in both seasons. The obtained data revealed that number of seeds/pod and 100-seed weight positively significant associated with plant height and number of branches/plant and negatively significant associated with pods number/plant in both seasons. Finally, 100-seed weight positively correlated with number of seeds/pod (0.99** and 0.99**) in the first and second seasons, respectively. In all other cases all growth and yield traits insignificant negative associated with chocolate spot infection.

The negative correlation between faba bean yield and chocolate spot infection were observed by Kim *et al.*, (2015) who found a negative and significant associated between seed yield and each of diseases chocolate spot and rust indicate the negative impact of chocolate spot and rust on seed yield faba bean.

Table 7.Phenotypic correlation coefficients among all the studied traits of the examined faba bean genotypes in 2018/19 and 2019/20.

	Plant height (cm)	Branches number/ plant	Pod number/ plant	Seeds number/ pod	100-seed weight (g)	Seed yield /plant (g)	Seed yield/ plot (kg)	Seed yield/ fad (erdab)	Disease severity %
Plant height (cm)	-	0.74**	-0.72**	0.99**	0.97**	0.45	0.44	0.44	-0.28
Branches number/plant	0.57	-	-0.54	0.77**	0.74**	0.47	0.45	0.45	-0.36
Pod number/plant	-0.74**	-0.60*	-	-0.78	-0.72**	0.26	0.27	0.27	-0.40
Seeds number/pod	0.99**	0.64*	-0.80**	-	0.99**	0.38	0.37	0.37	-0.21
100-seed weight (g)	0.98**	0.59*	-0.73**	0.99**	-	0.45	0.44	0.44	-0.28
Seed vield/plant (g)	0.42	0.16	0.26	0.35	0.43	-	0.96**	0.97**	-0.95**
Seed vield/plot (kg)	0.48	0.22	0.19	0.42	0.49	0.95**	-	1.00**	-0.94**
Seed vield/fad (erdab)	0.48	0.22	0.19	0.42	0.49	0.96**	1.00**	-	-0.92**
Disease severity %	-0.36	-0.05	-0.30	-0.28	-0.36	-0.96**	-0.93**	-0.96**	-

Values upper the diagonal refers to correlation coefficient between traits in 2018/19 and the lower one refers to correlation coefficient between traits in 2019/20.

* and ** referred significant at both 5% and 1% levels of probability, respectively.

5. The phenotypic similarity matrix.

Based on the quantitative data of studied traits cluster analysis according to Lance and Williams (1967) method divided the twelve genotypes to 11 main groups (Table 8).with regard to similarity matrix are shown in dendrogram the results showed that the phenotypic similarity among all tested faba bean genotypes ranged from 12.20 to 118.66. The highest similarity values were showed between the two Line 8 and Line 6 (118.66) followed by the similarity between Giza 843 and Giza 716 (114.68) and the similarity between Line 7 and Line 2 (75.88). on the other side, Sakha 1 and Line 1 showed the lowest similarity with all tested genotypes (12.20 and 14.79) for both genotypes, respectively. The low similarity between most of tested genotypes may be clear evidence for the wide genetic diversity between these genotypes.

 Table 8.cluster groups and similarity between all tested genotypes.

Cluster	1st Item	2nd Item	Similarity
1	Line 8	Line 6	118.658
2	Giza 843	Giza 716	114.677
3	Line 7	Line 2	75.884
4	Cluster 2	Line 3	62.096
5	Cluster 4	Cluster 3	55.755
6	Cluster 5	Cluster 1	44.344
7	Cluster 6	Line 5	33.143
8	Cluster 7	Line 9	29.898
9	Cluster 8	Line 4	25.485
10	Cluster 9	Line 1	14.788
11	Cluster 10	Sakha 1	12.198



Figure 1. Dendrogram of cluster analysis of the examined twelve faba bean genotypes based on growth and yield traits across the two seasons of the study.

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التباين الوراثي و التوريث في محصول البذور ومكوناته لبعض التراكيب الوراثية الواعدة من الفول البلدي فايز السيد والى 1, رضا على إبراهيم 1 و جهاد محمد عبد الوهاب ² 1 قسم بحوث المحاصيل البقولية- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية- الجيزة-مصر ² قسم بحوث أمراض الخضر- معهد بحوث أمراض النبات- مركز البحوث الزراعية- الجيزة- مصر

تم عمل تجربة حقلية مصممة فى نظلم القطاعات الكاملة العشوائية من مكررات لتقييم تسعة سلالات واعدة من الفول فى F6 مقارنة مع ثلاثة أصناف تجارية هى جيزة716 ، وجيزة848 ، وسخا1 تحت الإصابة الطبيعية بمرض التبقع الشوكولاتى فى مزرعة محطة البحوث الزراعية بايتاى. البارود خلال عامى 2019/2018 و 2020/2019. كان التباين الراجع للتراكيب الوراثية معنوياً لجميع الصفات المدروسة فى كلا الموسمين ، أعطت السلالات8 و 9 و3 متوسطات معنوية عالية لمعظم الصفات. أظهرت جميع التراكيب الوراثية معنوياً لجميع الصفات المدروسة فى كلا الموسمين ، أعطت السلالات8 و 9 و3 متوسطات معنوية عالية لمعظم الصفات. أظهرت جميع التراكيب الوراثية معنوسطة للتبقع الشوكولاتى ما عدا جيزة 843 وسلالة 2 و4 فى كلا الموسمين. كان التباين الوراثى يمثل الجزء الأكبر من التباين المظهرى مقارنة بالتباين البينى فى كل الصفات وهذا يوضح أن الإختلاف فى متوسطات أداء هذه التراكيب يرجع إلى التباين الوراثى الكبير بين تلك التراكيب. بشكل عام ، كان لارتفاع النبات ووزن 100 بذرة ومحصول البنور / نبات قيم عالية من PCV و GCV و ² مما يشير إلى أن هذه الصفات يتحكم فيها عامل وراثي وهذاك فرصة عالية لتحسين هذه الصفة من ووزن 100 بذرة ومحصول البنور / نبات قيم عالية من PCV و GCV و ² مما يشير إلى أن هذه الصفات يتحكم فيها عامل وراثي وهذاك فرصة عالية الموسمين. تراوحت قيم خلال الانتخاب. كان إرتبط محصول البنور / نبات ، محصول البذور /قطعة ، محصول البذور /فنان سلبي معنوى بالإصابة البتبع الشوكولاتى فى كل الموسمين. تراوحت قيم مصفوفة التشابه بين كل التراكيب الوراثية ما بين 12.00 إلى 13.60 للهرت أعلى قيم التشابه بين التركيب بين السلالة 6 متبوعة بالصف جيزة 716 و و كذلك السلالة 7 مع السلالة 2.