Original Research Article

Development of faba bean genotypes for broomrape tolerant and foliar diseases resistancein F_2factorial crosses.

ABSTRACT

Two fieldexperiments were conductedatSakhaAgriculturalResearch Station, Kafr El-Sheikh, Egypt .The first experiment was in a naturally *Orobanche*free field and the second one was in a naturally *Orobanche*-infested field.In each experiment sixteen F_2 crosses and their parents were sown. The sixteen F_2 crosseswere produced by a4x4 factorial mating design in F_1 and selfed to give F_2-crosses.The data were then analyzedusing a line x tester design. The main objective of this study was to induce new promisingfaba bean genotypes that are able to produce high yield, resistance to foliar diseases and broomrape tolerance.Significant differences among all genotypesmean square were observed for all studied traits under bothgrowth conditions. The parents, crosses and their interaction mean squares were detected for all traits in the two environments. Mean squares of lines were significant for flowering date at both environments, number of seeds per plant and 100-seed weight in infested soil conditions. Mean squares of testers were significant for chocolate spot at the two conditions; rust disease,plant height, No. of pods and seeds,seed yield per plant and 100-seed weight under normal condition. Lines x testers mean squares were significant for all traits in both conditions, except for number of branches and 100-seed weight L1 and L4 and the parental testers T4 were considered more resistance parents tofoliardiseases under both environments. The crosses; L2 x T3, L2 xT4, L3 x T2, L3 x T4 and L4 x T4 were considered resistantto foliar disease and had an earlier flowering date. The testers, T3 and T4showed significantly the highest values of number of seeds per plant, seed yield per plant and 100-seed weightunder both conditions, while the crosses; L3 x T4 and L4 x T4 hadthe highest values for seed yield per plant and 100-seed weight under both conditions.The parental L2 and T4 were considered good combiners for chocolate spot and rust diseases under both environmental conditions, while L1 and T4 performed as good combiner parents fornumber of seeds and seed yield per plant. The cross; L2x T3 performed as good specific combiner cross for foliar diseases under both conditions. The crosses;L1x T3, L2 xT3, L3 x T4 and L4 x T4 had highly significant (sij) values for theNo. of seeds and seed yield per plant under infested soil condition. The phenotypic coefficient of variation (PCV) values ranged from 5.52% to 84.01% and genotypic coefficient of variation (GCV)values ranged from 3.18% to 79.21%.Broad-sense heritability (H) ranged from 72.98% to 99.29%,and narrow sense heritability $^{(}h^{2)}$ranged from 2.3% to 21.38%. Expected genetic advance (Ga) ranged from 0.03 to 0.71, and predicted genetic advance (Ga%) ranged from 8.21% to 10.86%.

Key words: Broomrape, chocolate spot, combining ability, genetic advance,heritability, rust.

INTRODUCTION

Faba bean (*Viciafaba* L.) is one of the oldest cropgrown by human and is used as a source of protein in the human diet, as well as a fodder and forage crop for animals. Additionally, it is used as a source of nitrogen in the biosphere and plays an important role in crop rotation, reducing energy costs, improving soil physical conditions and decreasing the incidence of diseases and weed populations.

The total faba bean cultivation area in Egypt annually is about 198.000 feddan with production of about 281.000 tons with in average yield of 9.2 ardab per feddan,(ardab=155kg) approximately 67% of the from essential human consumption needs**[1]**.

There are several reasons for the decline in area, such as the improved productivity per unit due to reduced susceptibilityto biotic **[2]**and abiotic stresses**[3]**. Broomrape is one of the serious constraints of faba bean in North Africa, the Nile Valley and sub-Saharan African countries where more than 30% of faba bean is produced. Chocolate spot and rust have

Mediterranean region and Middle East, *Orobanche spp*. infest about 16 million hectares**[4]**.It obtains its carbohydrates from the host's phloem, and water and minerals from the host's xylem. It poses a constant threat to legume production **[5]**.*O. crenata* is the most widely spread parasite in the Mediterranean region and West Asia**[6]**.Estimated yield losses range from 7% to 80% depending on the levels of infestation **[7]**. Chemical, physical and biological control methods are used against this weed, but they are not usually effective enough. The production of tolerant cultivars combined with other methods could be the best way to minimize yield losses and reduce soil infestation.

Chocolate spot (*Botrytis fabae*) and rust (*Uromycesvicia-fabae*) disease have been recorded as a serious disease in the North Delta region. Fungus attacks leaves, stems and pods. Chocolate spot disease management is based mainly on the expensive fungicides. Application and modification of the cultural practices have shown partial protection **[8]**.It can cause yield losses of 27 to 80%.

To address these challenges, this study was aimed to develop faba bean varieties with high yield, broomrape tolerant and resistance to foliar diseases like chocolate spot and rust.

MATERIALS AND METHODS

As a complement to previous F_1 studies**[9]**we conducted an F_2 study of the sixteen crosses and their parents, which were grown in a naturally *Orobanche* free fieldas the first experiment. The second experiment involved growing the materials in a naturally *Orobanche*-infested field to evaluate tolerance to *Orobanche*. The main objective of this study was to induce new promising faba bean genotypes capable of producing high yield, resistance to rust and chocolate spot as foliar diseases and broomrape tolerance.The study was carried out at the Experimental Farm at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, Egypt, during the three growing seasons of 2019-2020, 2020-2021 and 2021-2022. Eight faba bean (*Viciafaba* L.) genotypes were used as parents,selected based on genetic diversity, differences in growth habit, disease reactions, broomrape tolerance and differences in yielding ability. Thebotanical group and agronomic characters are presented in Table 1. Almany, Giza 843 Misr 3 and Najeh were used as testers, while the four genotypes namely; Line 1, Line 2, Line 3 and Line 4 were used as lines in a factorial mating design that produced sixteen crosses.

Table (1): Names, pedigree, flowering date and agronomical characters of faba bean genotypes used in this investigation.

Genotype	Pedigree	Agronomical characters	
		Flowering date	Characteristics
Line 1	(Giza 843 x Misr 1)	Early	Tolerant to *Orobanche* and resistant to foliar diseases.
Line 2	(Giza 2 x Misr 1)	Early	Tolerant to *Orobanche* and resistant to foliar diseases.
Line 3	(Giza 843 x Giza 2)	Medium	Tolerant to *Orobanche* and resistant to foliar

			diseases.
Line 4	(Sakha 3 x Giza 2)	Late	Tolerant to *Orobanche* and resistant to foliar diseases.
Almany	Introduction from Germany	Medium	Resistant to foliar diseases
Misr 3	L667 x (Cairo 241 x Giza 461)	Medium	Tolerant to *Orobanche*
Giza 843	561/2076/85 x 461/845/83	Early	Tolerant to *Orobanche*
Najhe	INRAT, Tunisia	Early	Tolerant to *Orobanche*

In the 2019-2020 season, the parental genotypes were sown under insect wire-cages at the Sakha Agricultural Research Station, Egypt, on two successive sowing dates, namely the 1st and 15th of November to ensure synchronization of flowering periods for the parental genotypes. Once the plants began to flower, hand crosses were made. Female flowers were emasculated at the late bud stage, before the anthers dehisced by slitting the dorsal surface of the flower with fine forceps, and pollen grains were transferred from the male parent to the emasculated flowers of the female parent.

In the 2020-2021 season, seeds of the parents and their sixteen F_1 hybrids were sown to produce F_2 seeds for evaluation in the next season. In the 2021-2022 season, seeds of the parents and their sixteen F_2 generations were evaluated in two adjacent experiments. The first experiment was conducted under normal conditions (*Orobanche*seeds-free), while the second experiment was sown in heavily naturally infested soil with *O.crenata* seeds. Each experiment was designed in a randomized complete block design (RCBD) with three replicates. The experimental plot consisted of one ridge for each parent and six ridges for each F_2 generation. Each ridge was 3 m long, 60 cm apart, with 20 cm between hills on one side of the ridge and a single seed was planted per hill. Cultural practices were applied as recommended for ordinary faba bean production in the area.

The data were recorded based on guarded individual plants that were labeled for different genotypes on the following characters:flowering date, chocolate spot and rust diseases reaction, broomrape reaction, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and seed yield per plantand dry weight spike broomrape per plot.

Reaction to chocolate spot and rust diseases was assessed according to the disease scales suggested by **Bernier et al [10]**: (1) highly resistant, (3) resistant, (5) moderately resistant, (7) susceptible and (9) highly susceptible.

The line x tester analysis according to **Kempthorne[11]** was done in the case of genotypes that were significant to estimate the variance due to general and specific combining abilities of the tested lines, testers and line x testers interaction. According to **Kempthorne[11]**, the variance of general and specific combining abilities can be computed from the covariance of full sib (F.S) and half sib (H.S) families.

Where:

$$\sigma^2 gca = Cov\ H.S = 1+F \text{ per } 4 \times \sigma^2_A, \text{ with } F=1,\ \sigma^2_A = 2\sigma^2 gca$$

$$\sigma^2 sca = \{1+F \text{ per } 2\}^2 \sigma^2_{D,} \text{ with } F=1,\ \sigma^2_D = \sigma^2 sca$$

Where F is the coefficient of inbreeding that ranged from 0 to 1 with open pollenated varieties to completely pure lines, respectively.

Table (2): Line X tester analysis of variance including parents according to Kempthorne's Method[11].

S.O.V	**d f**	**MS**	**EMS**
Replication	r-1		
Genotype (G)	(g-1)		
Parents	(P-1)		
Parent's vs. crosses	1		
Crosses	(C-1)		
Lines	(l-1)	Ml	$\sigma^2 e + r \sigma^2 2lt + r\sigma^2 l$
Testers	(t-1)	Mt	$\sigma^2 e + r \sigma^2 lt + r\sigma^2 t$
Lines x testers	(l-1) (t-1)	Mlt	$\sigma^2 e + r \sigma^2 lt$
Error	(r-1) (g-1)	Me	$\sigma^2 e$

Where: the MS due to lines(M_l) and testers (Mt) were tested against MS due to lines x testers (M_{lxt}) and the latter is , in turn, tested against MS due to error (Me)**[12].**

The genetical parameters,including genotypic variance (V_g) and phenotypic variance (V_{ph}) were computed according to the fermula suggested per**Burton** [**13**]. For each trait, PCV% and GCV% were calculated based on the methods provided by **Burton** [**13**]**.**Broad-sense heritability (H) was calculated according to **Lush Jay** [**14**]. The range of heritability was categorized as suggested by **Johnson etal**[**15**]: low (< 30%), moderate (30-60%) and high (> 60%).

Narrow sense heritability (h^2) estimates were calculated as **Acquaah** [**16**]. According to **Stansfield** [**17**], the classification of narrow-sense heritability is as follows: low (< 20%), moderate (20-50%), and high (> 50%). For each character , expected genetic advance (Ga) and predicted genetic advance as percent(Ga%) were estimated following the methods outlined by **Fehr** [**18**] assuming selection of the top 5% of genotype plants and using narrow- sense heritability (h^2%) to calculate the expected genetic advance (Ga) . The range and frequency are as follows: low (less than 10), moderate (10-20) and high (more than 20).

The phenotypic (PCV) and genotypic coefficients of variation (GCV) were computed as per**Burton** [**13**]**.**

$$\mathrm{PCV} = \frac{Vph}{\bar{\mathrm{X}}}\,\mathrm{x}100 \text{ and } \mathrm{GCV} = \frac{Vg}{\bar{\mathrm{X}}}\,\mathrm{x}100\,.$$

The mathematical model for the GGE biplot analysis has been explained by**Ruswandi et al [19].**

RESULTS AND DISCUSSION

Legume production in the Mediterranean countries suffers considerable damage from infestation with the root-parasitic weed (*O.crenata*) and foliar diseases such as rust and chocolate spot, which can cause devastating yield losses in faba bean, lentil, pea and other crops in its native distribution area around the Mediterranean. Many attempts have been made to devise control methods against *Orobanche*spp.,various methods have been suggested for broomrape control to minimize its damage to crop productivity. These methods include cultural practices such as sowing dates, hand pulling and crop rotation, biological control by releasing phytomyza and chemical control using glyphosate and other herbicides. However, the best approach is the induction of resistance in cultivars. Therefore, the main objective of this study is to induce new promising faba bean genotypes that are able to produce high yield, broomrape tolerant, and resistant to both of rust and chocolate spot foliar diseases.

Analysis of variance

The analysis of variance estimation shown in Table 3revealedhighly significant differences among genotypes for all studied traits. These results indicate the presence of genotypic differences among the genotypes.

Table 3: Mean squares from analysis of variance of the studied traits, evaluated under normal and infestation with broom rape environmental conditions.

SOV	d.f	Chocolate spot reaction		Rust reaction		Flowering date	
		Normal	Infested	Normal	Infested	Normal	Infested
Rep	2	0.31ns	0.24ns	0.30ns	0.37ns	7.43ns	1.28ns
Genotypes	23	1.57**	1.11**	3.60**	2.94**	39.55**	29.51**
Parents (P)	7	1.58**	1.66**	4.90**	3.91**	60.86**	52.29**
P vs. C	1	0.45ns	0.01ns	4.10**	2.67**	38.44*	8.15*
Crosses (C)	15	1.64**	0.93**	2.96**	2.51**	29.68**	20.31**
Lines (L)	3	1.57ns	0.86ns	2.87ns	2.54ns	73.30**	33.54**
Testers (T)	3	3.43*	2.22*	6.14*	4.54ns	28.72ns	35.46ns
L x T	9	1.07*	0.53**	1.93**	1.82**	15.46*	10.85*
Error	46	0.29	0.15	0.35	0.37	6.73	5.98
σ^2gca		0.02	0.014	0.036	0.024	0.494	0.328
σ^2sca		0.228	0.110	0.484	0.458	2.628	0.1.169
σ^2gca/σ^2sca		0.087	0.127	0.074	0.052	0.188	0.280

Table 3 .cont.

SOV	df	Plant height (cm)		Number of branches per plant		Number of pods per plant	
		Normal	Infested	Normal	Infested	Normal	Infested
Rep	2	3.85ns	13.14ns	0.09ns	0.25ns	5.83ns	5.45ns
Genotypes	23	347.66**	293.891**	1.31**	0.60*	186.02**	129.06**
Parents (P)	7	524.48**	451.97**	0.77*	0.57ns	100.42**	58.44**
P vs C	1	669.99**	167.22**	19.29**	2.61**	1866.53**	519.57**
Crosses (C)	15	243.65**	205.23**	0.36ns	0.49ns	113.94**	135.98**
Lines (L)	3	37.54ns	135.33ns	0.27ns	0.15ns	144.49*	219.33ns
Testers (T)	3	641.44*	389.16ns	0.66ns	1.32*	286.87**	143.90ns
L x T	9	179.76**	167.22**	0.29ns	0.32ns	46.11**	105.55**
Error	46	19.88	17.20	0.21	0.26	4.41	5.25
σ^2gca		2.219	1.320	0.003	0.006	2.360	1.060
σ^2sca		54.190	49.066	0.041	0.059	14.010	32.900
σ^2gca/σ^2sca		0.041	0.027	0.073	0.102	0.168	0.032

Table 3 .cont.

SOV	df	Number of seeds per plant		Seed yield per plant		100-seed weight		Broomrape dry weight
		Normal	Infested	Normal	Infested	Normal	Infested	Infested
Rep	2	8.41ns	2.90ns	20.05ns	7.35ns	16.41ns	27.06ns	13.34ns
Genotypes	23	1328.06**	1195.87**	1149.04**	789.19**	161.19**	148.76**	117.45**
Parents (P)	7	739.69**	439.01*	818.09**	317.28**	226.88**	141.62**	40.01*
P vs C	1	19609.33**	2067.97**	14504.18**	2666.94**	609.24*	1021.55**	145.80**
Crosses (C)	15	383.87**	1490.94**	413.15**	884.23**	128.62**	93.90*	234.52**
Lines (L)	3	458.56ns	295728*	135.31ns	1254.25ns	289.08**	201.29*	68.23**
Testers (T)	3	1234.03*	1627.95ns	1371.27**	951.84ns	202.00*	113.96ns	17.38ns
L x T	9	222.79**	956.49**	186.38**	738.36**	50.68ns	51.41ns	62.70**

Error	46	25.15	34.19	23.93	4.91	28.99	37.39	9.92
σ^2gca		5.593	18.559	7.874	5.065	2.706	0.470	2.885
σ^2sca		70.078	302.99	55.625	244.383	12.644	1.475	16.984
σ^2gca/σ^2sca		0.080	0.061	0.142	0.021	0.214	0.318	0.170

Significant differences were observed among all genotypes mean squares for all studied characters.The parental genotypes are not related and are derived from different genetic backgrounds.Therefore, the expected selection programs in these materials in the segregating generation would not be limited only to superior specific hybrids and improvement would be expected. The genotypes are partitioned into parents, crosses and their interaction.Highly significant mean squareswere found for parents for in studied traits under both conditions, except for number of branches per plant under infested broomrape condition. Meanwhile, highly significant mean squares of crosses were detected for all studied traits at the two environmental conditions,except for number of branches per plant under both condition, reflecting the diversity of the parents for these studied traits and indicating that this diversity could be transmitted to the progenies.

However, mean squares of parents vs. crosses as an indication of average heterosis overall crosses showed a highly significant mean square for all studied traits under both conditions, except for chocolate spot reaction under both conditions, indicating the presence of hybrid vigor for an expected traits.

The mean squares of lines were significant and/or highly significant for flowering date and 100-seed weight under both conditions, while number of pods per plant was significant under normal condition, in addition to the number of seeds per plantand broomrapedry weight per plant under infested broomrape conditionwere significant and highlysignificant, respectively.

The mean squares of the testers were significant and/or highly significant for chocolate spot reaction at the two conditions, rust reaction, plant height, number of pods per plant, number of seeds per plant, seed yield per plant, and 100-seed weight under normal condition and number of branches per plant under infested broomrape condition.

Line x testers mean squares were significant and/or highly significant for all studied traits at the two conditions, except for number of branches per plant and 100-seed weight under both conditions, revealing the overall differences between these crosses.

Faba bean cultivars genetically varied from each other in one or more characteristics. The analysis of variance revealed highly significant differences between the tested genotypes for all characters under investigation, indicating wide genetic variability for all studied characters and hence, the feasibility for genetic improvements using such genetic pools of faba beans (Tables 2 to 4).

From the data shown in Table 3, it could be concluded that the σ^2gca/σ^2sca ratio was less than one for all studied traits.This would indicate that, non-additive genes seem to be responsible to inheritance of these traits. In other words, non-additive genetic types, especially dominance appear to control most of the genetic variance associated with all studied traits. In such cases, a bulk method would be fruitful to eliminate the effect of dominance in the advanced segregating generations, and then full-sib family selection could be realized.

Mean performance

The mean performance of the four lines, four testers and their F_2generation crosses for chocolate spot and rust reactions, and flowering date under normal free soil and broomrape infested conditions are presented in Table 4.

Table 4: Mean performance of the eight faba bean parental genotypes and their F_2 generations for broomrape tolerance, rust and chocolate spot resistance.

Genotypes	Chocolate spot reaction		Rust reaction		Flowering date (day)	
	Normal	Infested	Normal	Infested	Normal	Infested

Lines								
L1			3.31	3.40	2.07	2.83	57.00	55.67
L2			4.59	5.00	4.00	4.33	43.33	42.67
L3			4.05	4.33	4.00	4.30	50.00	49.33
L4			3.00	3.07	2.00	2.37	44.67	44.33
Testers								
T1- (Almany)			4.00	4.00	4.07	4.13	53.33	52.00
T2- (Misr 3)			4.53	4.33	5.33	5.67	52.33	51.00
T3- (Giza 843)			5.00	5.00	4.33	4.67	51.67	50.67
T4- (Najeh)			3.23	3.33	2.00	2.67	51.67	50.33
Crosses								
C1	**Line-1**	**T-1**	4.16	4.50	4.33	4.67	59.66	55.78
C2		**T-2**	4.21	4.27	3.56	3.67	56.07	50.29
C3		**T-3**	4.47	4.47	5.27	5.47	55.50	53.98
C4		**T-4**	3.95	3.97	4.36	4.53	51.23	50.50
C5	**Line-2**	**T-1**	4.46	4.47	4.68	4.80	54.10	52.50
C6		**T-2**	3.53	4.00	3.67	4.07	47.25	46.63
C7		**T-3**	2.33	3.10	2.33	2.67	49.11	49.10
C8		**T-4**	3.00	3.67	2.67	3.00	49.17	47.92
C9	**Line-3**	**T-1**	4.80	4.47	5.23	5.33	52.49	51.25
C10		**T-2**	3.22	3.60	3.33	3.67	50.29	49.17
C11		**T-3**	3.89	4.03	3.89	4.23	52.22	51.83
C12		**T-4**	3.07	3.23	3.00	3.83	49.98	47.79
C13	**Line-4**	**T-1**	4.63	4.80	5.20	5.33	50.33	49.56
C14		**T-2**	3.37	4.30	4.03	4.67	49.74	46.68
C15		**T-3**	4.66	4.80	5.33	5.50	52.33	48.07
C16		**T-4**	3.00	3.17	2.80	3.03	53.33	52.27
LSD 0.05			0.88	0.64	0.98	1.00	4.26	4.01
LSD 0.01			1.77	0.84	1.30	1.33	5.67	5.35

Regarding the reaction to foliar diseases (chocolate spot and rust), L1, L4 and T4 (Najeh) were considered highly resistant, with chocolate spot estimated mean values of 3.31, 3.00, and 3.23 under normal condition, and 3.4, 3.07 and 2.33 under infested condition, respectively. Meanwhile the rust estimated mean values were 3.07, 2.00 and 2.00 under normal condition, and 2.82, 2.23 and 2.67 under infested condition, respectively.

The crosses; L2 x T2, L2 xT4, L3 x T2, L3 x T4 and L4 x T4 were also identified as resistance crosses for the traits in view.Additionally, the cross; L2 x T3 exhibited the lowest values for foliar disease reactions under both environments. The parental lines; L1 and L4 showed the significantly lower values for flowering date (earlier parents) under both environments, while, the crosses; L2 x T2, L2 xT3, L2 x T4, L3 x T4 and L4 x T2 showed the earlierflowering crosses under normal as well as infested soil condition.

Among the tested parents, L1 had the tallest parent values (143.33 and 138.33) under normal as well as infested soil conditions, while the shortest parent was L3 under both environments. On the other hand, the tallest cross plants were observed in the crosses; L4 xT4 and L3 xT4 under normal condition with no significant differences between them. Meanwhile, the shortest plants were observed in the cross; L3 x T1 under normal soil condition. It is generally observed that all parents and their crosses showed shorter plants in infested soil condition compared to plants under normal soil conditions. This might be the negative effect of broomrape on the plants at infested soil plants.

For number of branches per plant, L1 and L2 line parents and T3 (Giza 843) tester parent had the highest values of the trait in question under both environments, while for crosses; L1 x T4, L2 x T4, L3 x T1, L3 x T4 and L4 xT4 had the significantly highest values for the trait under test at both environments, however, L3 x T2 cross showed the highest value (5.14) of number of branches under normal soil condition.

For numberof pods per plant, L1 line parent gave the significantly highest values (42.75, 27.37 pods)under both normal and infested soil conditions, respectively. While, the crosses L1 x T4, L2 x T4 registered the significantly highest number of pods under normal soil condition with no significant different of both and the crosses; L1 x T3 and L3 xT1 produced the highest number of pods under infested soil condition. The line parent; L1 and the tester parent; T4 produced the highest values of number of seeds per plant under both conditions, while The line parent; L2 and the tester parent; T1,T2 and T4 had the highest significant values for the trait in view at infested soil condition. The crosses; L1 x T1, L1 x T3 and L1 xT4 had the significantly highest values under normal as well as infested soil conditions for the trait in consideration. While, the crosses; L2 x T4 and L4 xT4 showed the highest number of seeds under normal soil condition without a significant difference of both.

For seed yield per plant, the line parent; L1 and the tester parents;T3 and T4 revealed the highest values of seed yield per plant under normal condition, while the tester parents;T1, T2 and T4 had the highest values of the trait in view under infested soil condition. The crosses; L1 x T4, L3 x T2, L3 x T4 and L4 xT4 had the significantly highest values of the trait under test under normal condition and the crosses; L1 x T3, L2 x T3 and L3 xT4 showed the highest values under infested soil condition.

For 100-seed weight, the line parents; L1 and L2and the tester parents;T1, T2, T3 and T4 gave the significantly highest values for the trait in question under both tested environments. Meanwhile, the crosses; L2 x T2, L2 x T3, L2 x T4, L3 xT4 and L4 xT4 showed the significantly highest values under normal as well as infested soil conditions.

Generally, the lower mean values of seed yield and its studied components were observed under broomrape infested condition compared with normal free soil. This could be attributed to broomrape reducing the yield of host plants (faba bean) by affecting the partitioning of assimilates and nutrients and not bydirect toxic effect.

Joel[20] and Abbes et al[21]reported that broomrape acts as a strong sink, depriving the host of water, minerals and organic nutrients with a consequent negative impact on the growth of the host plant. **Press etal[22]**reported that parasitic plants such as broomrape can affect host productivity by extracting water, nutrients and organic components from the host` vascular system and also by impacting on host physiology, and then impairing the hosts ability to acquire resources. These results were in agreement with those reported by **Attia[23], El-Denary et al[24],and Soliman et al[25].**

Table 5: Mean performance of the four faba bean genotypes and their F$_2$ generations for plant height, number of branches per plant and number of pods per plant traits under normal and infested soil.

Genotypes			Plant height (cm)		Number of branches per plant		Number of pods per plant	
			Normal	Infested	Normal	Infested	Normal	Infested
Lines								
L1			143.33	138.33	4.23	4.03	42.75	27.37
L2			134.67	130.48	3.86	3.51	33.87	25.53
L3			120.00	118.67	3.11	3.08	27.55	21.89
L4			133.33	130.00	3.67	3.64	25.86	22.67
Testers								
T1 (Almany)			125.50	103.33	3.10	2.67	28.97	15.33
T2 (Misr 3)			113.82	110.49	3.09	3.02	25.30	22.63
T3 (Giza 843)			148.33	108.33	4.33	3.33	34.33	28.70
T4 (Najhe)			150.00	121.67	3.83	3.67	32.85	28.16
Crosses								
C1	**Line-1**	**T-1**	134.75	123.92	4.84	3.21	43.57	34.80
C2		**T-2**	134.40	127.99	4.66	3.56	43.32	30.57
C3		**T-3**	147.50	127.08	4.83	4.13	43.83	38.33
C4		**T-4**	150.03	142.67	4.90	4.43	53.56	34.96
C5	**Line-2**	**T-1**	140.21	132.59	4.41	3.69	42.41	23.22

C6		**T-2**	138.79	124.23	4.34	3.13	34.36	21.35
C7		**T-3**	134.44	105.81	4.81	3.60	38.45	36.54
C8		**T-4**	146.11	132.94	5.61	4.07	56.11	27.11
C9	**Line-3**	**T-1**	126.84	121.44	4.45	4.18	40.86	36.55
C10		**T-2**	126.51	116.53	5.14	3.63	42.25	25.38
C11		**T-3**	147.92	124.17	4.88	3.35	39.28	24.24
C12		**T-4**	149.49	129.25	5.02	4.33	47.18	41.16
C13	**Line-4**	**T-1**	135.75	132.30	4.17	3.48	35.52	26.03
C14		**T-2**	143.37	129.45	4.77	3.73	41.00	24.19
C15		**T-3**	128.89	118.29	4.56	3.62	33.08	19.24
C16		**T-4**	156.50	124.91	4.63	4.20	41.00	32.08
LSD 0.05			7.31	6.81	0.75	0.82	3.44	3.76
LSD 0.01			9.75	9.08	1.01	1.11	4.59	5.01

Table 6: Mean performance of the four faba bean genotypes and their F_2 generations for number of seeds per plant, seed yield per plant, 100-seed weight and broomrapedry weight traits under normal and infested soil.

Genotypes			**Number of seeds per plant**		**Seed yield per plant (g)**		**100-seed weight (g)**		**Broomrape dry weightper plant (g)**
			Normal	**Infested**	**Normal**	**Infested**	**Normal**	**Infested**	**Infested**
Lines									
L1			93.71	67.53	73.17	48.88	78.27	72.41	14.25
L2			81.24	73.21	61.12	51.93	75.24	71.03	14.15
L3			69.40	67.40	51.12	46.78	73.75	69.39	21.41
L4			66.70	61.86	37.41	32.41	56.30	52.40	23.30
Testers									
T1 (Almany)			55.76	40.45	44.20	28.11	79.27	62.59	18.55
T2 (Misr 3)			76.96	74.86	59.63	53.63	77.49	71.67	13.30
T3 (Giza 843)			102.33	67.09	85.57	47.08	84.89	70.33	15.46
T4 (Najhe)			92.33	80.90	75.80	57.51	82.20	71.09	17.93
Crosses									
C1	**Line-1**	**T-1**	127.21	92.81	89.26	62.84	70.14	67.91	8.76
C2		**T-2**	103.73	87.86	77.48	65.33	74.68	74.41	12.31
C3		**T-3**	125.93	121.63	86.92	83.67	69.10	68.81	4.48
C4		**T-4**	138.50	96.50	106.07	71.78	76.57	74.41	12.92
C5	**Line-2**	**T-1**	113.24	62.30	83.36	44.37	73.67	71.40	12.25
C6		**T-2**	106.92	58.38	85.61	45.99	80.08	78.91	19.21
C7		**T-3**	103.33	91.69	91.06	80.32	88.21	87.82	10.86
C8		**T-4**	125.68	69.81	111.60	54.43	88.68	82.19	9.36
C9	**Line-3**	**T-1**	105.74	100.95	85.30	77.09	80.68	76.38	8.27
C10		**T-2**	114.67	55.42	100.56	42.91	87.70	78.13	26.07
C11		**T-3**	114.58	57.31	92.26	43.33	80.51	75.76	14.33
C12		**T-4**	118.82	100.19	100.33	81.74	84.41	81.63	4.96
C13	**Line-4**	**T-1**	101.68	72.22	75.28	51.07	74.06	70.79	15.17
C14		**T-2**	114.30	43.83	90.61	33.90	79.27	77.27	30.67
C15		**T-3**	98.14	50.38	72.80	33.78	74.25	67.25	14.91
C16		**T-4**	124.53	87.23	109.27	66.70	87.88	76.60	10.95
LSD 0.05			8.23	9.59	8.03	3.64	8.84	0.04	5.16
LSD 0.01			10.97	12.79	10.70	4.85	11.78	13.38	13.38

The highest seed yield per plant, belonged to T3 under normal condition, while T4 had the highest yield under broomrape infection and the heaviestbroomrape dry weight. In terms of the F_2 crosses, C4, C8, C10, C12 and C16 performed better under normal condition, and C3, C7 and C12 showed higher performance under broomrape infection conditions compared to the other crosses, while the lowest performing cross was C15 under both growth conditions. Among the parents, the heaviest 100 seed weight was obtained from L1, T1 and T4 under normal condition, while L1 and T2had the highest weight under broomrape infection. However, the heaviest 100 seed weight for crosses was observed in C7 and C8 under both conditions. With respect to the reaction to broomrape infection tolerance, the parental genotypes L1, L2, L3, T2 (Misr3) and T3 (Giza843) were highly tolerant (Table 5).The hybrid crosses ranged from high tolerant in C3(L1 x T3Giza 843), C7 (L2 x T3Giza 843) and C12 (L3 x T4Najeh),to moderate resistant in C10 (L3 x T2 Misr3) and C11 (L3 x T3 Giza 843), withmeanvalues for broomrape dry weight of4.48,10.86,4.96, 26.07 and 14.33 in F_2 generations, respectively.

The lowest mean values for seed yield and its components were obtained under broomrape infested condition compared with normal free soil. These results were in agreement with **Attia[23], El-Denary et al [24]and Soliman et al [25]**, who reported that the number of branches per plant was significantly reduced with *Orobanche* infestation.

Combining ability effects:

General combining ability effects in this study were found to be significantly different for most traits (Table 7, 8 and 9). High positive values of GCA (desirable) would be highly appreciated for yield and its components traits. Conversely, for broomrape tolerance, resistance to rust and chocolate spot foliar diseases and flowering date, high negative effects would be useful (desirable) from a breeding perspective.

Theoretically, as estimate of general combining ability effect (ĝi)of parent is not absolute value. It actually depends upon the group of parent to which this particular parent was crossed in the crossing system. If the parent has exactly average in its combination ($x_j..$) as the general average performance of the parents in their combinations (x…), the expected estimate of (ĝi)would be zero. Significant departure from zero, wherever the direction would indicate that the parent is much better or much poorer than the overall average of the parents involved in the test.

The parent line L1 showed significant and highly significant positiveeffect(ĝi)forplant height under infested soil condition,numberof pods and number of seeds per plant under both tested environmental conditions and for seed yield per plantunder infested soil condition.

The parent line L2 exhibited a significantnegativeeffect (ĝi) for flowering date and 100-seed weight under normal soil condition and for rust disease reaction under both environmental conditions.

The parent line L3 showed highly significant positive effects (ĝi)for numberof pods per plant and seed yield per plant under infested soil condition and for 100-seed weight under normal condition.

The tester parent T4 had highly significant negative effects (ĝi)for chocolate spot and rust disease reactions under environmentalconditions, plant height, number of pods and seeds per plant and seed yield per plant under both soil conditions, andfor the number ofbranches per plant under soil infested condition and 100-seed weight under normal condition.

However, based on the obtained results, it can be concluded that, the line parent L2 is considered as good combiner parent for foliar diseases reaction and flowering date especially undernormal soil condition. Additionally, the tester parent T4 is considered as good combiner parent for chocolate spot and rust disease reactions as well as yield components i.e., number of pods and seeds and seed yield per plant under normal as well as infested soil conditions.On the other hand, the parentsL4 and T3 performed poorer as combiner parents in this present genetic material.The good combiner parents i. e., L2 and T4 have the ability in possessadditive genes to the crosses in which this involved in.Similar results were reported by **El-Refaey[26], Stoddard et al[27], El-Rodeny[28], Abou- Moustafa[29], Shalaby[30]and Abd El-Maksoud et al [31].**

Significant (Ŝij)innegative effects were observed for chocolate spot and rust diseases reactions in the cross; L2 x T3 under both tested environments (Table 10). Highly significant positive effect were of (Ŝij)was found for plant height under both environments in the cross;

L3 x T3. There were no significant effects of (Ŝij)for numberof branches per plant in all crosses under normal soil and infested soil conditions.

For the number of pods per plant, highly significant (Ŝij) inpositive effects were detected in the crosses; L2 x T4 and L4 xT2 at normal soil condition (Table 11).At infested soil condition, the crossesL2 x T3 and L3 xT4 exhibited significant (Ŝij). Significant and/or highly significant(Ŝij)wereobserved for number of seeds per plant in the crosses; L1 x T3 under both conditions, L1 x T1, L3 xT2, L3 xT3 and L4 x T2 under normal soil condition and L2 x T3, L3 x T1, L3 xT4 and L4 xT4 under infested soil condition. For seed yield per plant, highly significant (Ŝij)was found in the cross; L3 x T2 under normal soil condition, while highly significant inter and intra allelic interactionswere detected in the crosses; L1 x T2, L1 x T3, L2 xT3, L3 x T1, L3 x T4, L4 xT1 and L4 x T4 for seed yield per plant under infested soil condition(Table 12). One cross i.e., L2 x T3 exhibited a highly significant (Ŝij) for 100–seed weight under normal soil condition.The crosses; L2 x T3 and L3 x T4exhibited significant(Ŝij) forbroomrape dry weight.Similar resultswere obtained by **El-Metwallyet al [32], Ahmad [33], Haridy et al [34], Gehanet al [35] and Ibrahime et al [36].**

Table 7: Estimates of general combining ability (GCA) effects for chocolate spot reaction, rust reaction and flowering date traits.

Genotypes	Chocolate spot reaction		Rust reaction		Flowering date	
	Normal	Infested	Normal	Infested	Normal	Infested
Lines						
L1	0.40ns	0.25ns	0.40ns	0.30ns	3.56**	2.42*
L2	-0.47ns	-0.24ns	-0.64*	-0.65*	-2.14*	-1.15ns
L3	-0.05ns	-0.22ns	-0.12ns	-0.01ns	-0.81ns	-0.20ns
L4	0.12ns	0.21ns	0.36ns	0.35ns	-0.61ns	-1.07ns
LSD 0.05	0.52	0.37	0.57	0.56	2.29	2.26
LSD 0.01	0.69	0.50	0.77	0.75	2.29	3.04
Testers						
T1	0.72**	0.51**	0.88**	0.75**	2.09*	2.06ns
T2	-0.21ns	-0.01ns	-0.33ns	-0.26ns	-1.21ns	-2.00ns
T3	0.04ns	0.05ns	0.22ns	0.19ns	0.24ns	0.53ns
T4	-0.54*	-0.54**	-0.77**	-0.68*	-1.12ns	-0.59ns
LSD 0.05	0.52	0.37	0.57	0.55	1.68	2.26
LSD 0.01	0.69	0.50	0.77	0.75	2.29	3.04

Table 8: Estimates of general combining ability (GCA) effects for plant height, number of branches per plant and number of pods per plant traits.

Genotypes	Plant height		Number of branches per plant		Number of pods per plant	
	Normal	Infested	Normal	Infested	Normal	Infested
Lines						
L1	1.58ns	4.57*	0.06ns	0.06ns	3.84**	4.93**
L2	-0.20ns	-1.95ns	0.04ns	-0.15ns	0.59ns	-2.68*
L3	-2.41ns	-3.00 ns	0.12ns	0.10ns	0.16ns	2.10 ns
L4	1.03ns	0.39ns	-0.22ns	-0.01ns	-4.59**	-4.35**
LSD 0.05	3.45	3.73	0.34	0.32	1.68	2.18
LSD 0.01	4.65	5.02	0.45	0.42	2.26	2.94
Testers						
T1	-5.71**	1.72ns	-0.28ns	-0.14ns	-1.65 ns	0.42ns
T2	-4.33*	-1.30ns	-0.03ns	-0.26ns	-2.00*	-4.36**
T3	-0.41ns	-7.01**	0.02ns	-0.10ns	-3.58**	-0.15ns
T4	10.44**	6.60**	0.29ns	0.49**	7.23**	4.09**
LSD 0.05	3.45	3.73	0.34	0.32	1.68	2.18
LSD 0.01	4.65	5.02	0.45	0.42	2.26	2.94

Table 9: Estimates of general combining ability (GCA) effects for number of seeds per plant, seed yield per plant, 100 seed weigh and broomrape dry weight traits.

Genotypes	Number of seeds per plant		Seed yield per plant		100 seed weight		Broomrape dry weight per plot
	Normal	Infested	Normal	Infested	Normal	Infested	
Lines							
L1	9.03**	21.67**	-1.18ns	12.20**	-6.75 **	-4.22ns	-3.85**
L2	-2.52ns	-7.49*	1.80ns	-2.42*	3.29*	4.47ns	-0.55ns
L3	-1.36ns	0.44ns	3.50ns	2.56 **	3.96 *	2.37ns	-0.06ns
L4	-5.15**	-14.61 **	-4.12*	-12.34**	-0.50ns	-2.63ns	4.46**
LSD 0.05	2.95	5.74	3.68	1.90	2.97	6.05	2.85
LSD 0.01	3.98	7.74	4.46	2.56	4.01	8.15	3.84
Testers							
T1	-2.85ns	4.04ns	-7.81**	0.14ns	-4.73**	-3.99ns	-2.35ns
T2	-4.91**	-16.66**	-2.55ns	-11.67**	1.07ns	1.57ns	8.60**
T3	-4.32**	2.22ns	-5.35**	1.57ns	-1.35ns	-0.69ns	-2.32ns
T4	12.07**	10.40**	15.71**	9.96**	5.02**	3.11ns	-3.93**
LSD 0.05	2.95	5.74	3.68	1.90	2.97	6.05	2.85
LSD 0.01	3.98	7.74	4.46	2.56	4.01	8.15	3.84

Table 10: Estimates of specific combining ability (SCA) effects for chocolate spot, rust resistance, and flowering date traits for the sixteen F_2 crosses.

Genotypes			Chocolate spot reaction		Rust reaction		Flowering date	
			Normal	Infested	Normal	Infested	Normal	Infested
C1	Line-1	T-1	-0.75ns	-0.31ns	-0.93ns	-0.67ns	1.95ns	1.09ns
C2		T-2	0.23ns	-0.02ns	-0.49ns	-0.65ns	1.67ns	-0.35ns
C3		T-3	0.23ns	0.12ns	0.66ns	0.70ns	-0.35ns	0.81ns
C4		T-4	0.30ns	0.21ns	0.76ns	0.63ns	-3.26ns	-1.54ns
C5	Line-2	T-1	0.41ns	0.15ns	0.46ns	0.41ns	2.10ns	1.38ns
C6		T-2	0.41ns	0.20ns	0.66ns	0.70ns	-1.44ns	-0.33ns
C7		T-3	-1.04*	-0.76*	-1.23*	-1.15*	-1.04ns	-0.49ns
C8		T-4	0.21ns	0.40ns	0.10ns	0.05ns	0.38ns	-0.55ns
C9	Line-3	T-1	0.34ns	0.13ns	0.49ns	0.31ns	-0.85ns	-0.82ns
C10		T-2	-0.31ns	-0.22ns	-0.20ns	-0.34ns	0.26ns	1.15ns
C11		T-3	0.10ns	0.15ns	-0.20ns	-0.22ns	0.74ns	1.29ns
C12		T-4	-0.14ns	-0.06ns	-0.09ns	0.25ns	-0.14ns	-1.63ns
C13	Line-4	T-1	0.00ns	0.03ns	-0.02ns	-0.05ns	-3.20ns	-1.64ns
C14		T-2	-0.33ns	0.04ns	0.02ns	0.30ns	-0.48ns	-0.47ns
C15		T-3	0.70ns	0.49ns	0.77ns	0.68ns	0.66ns	-1.61ns
C16		T-4	-0.37ns	-0.56ns	-0.77ns	-0.92ns	3.02ns	3.72ns
LSD 0.05			1.03	0.74	1.15	1.12	4.59	4.52
LSD 0.01			1.39	1.00	1.30	1.51	6.18	6.08

Table 11: Estimates of specific combining ability (SCA) effects for plant height, number of branches per plant and number of pods per plant traits for the sixteen F_2 crosses.

Genotypes			Plant height		Number of branches per plant		Number of pods per plant	
			Normal	Infested	Normal	Infested	Normal	Infested
C1	Line-1	T-1	-1.21ns	-8.21*	0.32ns	-0.49ns	-0.85ns	-0.28ns
C2		T-2	-2.94ns	-1.12ns	-0.12ns	-0.01ns	-0.75ns	0.27ns
C3		T-3	6.24ns	3.68ns	0.00ns	0.39ns	1.34ns	3.81ns
C4		T-4	-2.08ns	5.66ns	-0.20ns	0.11ns	0.26ns	-3.80ns
C5	Line-2	T-1	6.03ns	6.98ns	-0.10ns	0.20ns	1.22ns	-4.25ns
C6		T-2	3.23ns	1.64ns	-0.43ns	-0.23ns	-6.47**	-1.34ns
C7		T-3	-5.04ns	-11.07**	-0.00ns	0.07ns	-0.81ns	9.63**
C8		T-4	-4.22ns	2.46ns	0.53ns	-0.04ns	6.05**	-4.04ns
C9	Line-3	T-1	-5.14ns	-3.12ns	-0.14ns	0.44ns	0.12ns	4.30ns
C10		T-2	-6.85ns	-5.02ns	0.29ns	0.02ns	1.86ns	-2.09ns
C11		T-3	10.64**	8.33*	-0.01ns	-0.43ns	0.46ns	-7.45**
C12		T-4	1.36ns	-0.19ns	-0.14ns	-0.03ns	-2.44ns	5.23*
C13	Line-4	T-1	0.33ns	4.35ns	-0.08ns	-0.15ns	-0.49ns	0.23ns

C14 **C15** **C16**		**T-2**	6.57ns	4.51ns	0.26ns	0.23ns	5.35**	3.16ns
		T-3	-11.83**	-0.94ns	0.01ns	-0.04ns	-0.99ns	-6.00**
		T-4	4.94ns	-7.92*	-0.19ns	-0.05ns	-3.88*	2.60ns
LSD 0.05			6.91	7.45	0.67	0.63	3.36	4.36
LSD 0.01			9.30	10.04	0.90	0.85	4.52	5.88

Table 12: Estimates of specific combining ability (SCA) effects for number of seeds per plant, seed yield per plant, 100 seed weigh and broomrape dry weight traits for the sixteen F_2 crosses.

Genotypes			**Number of seeds per plant**		**Seed yield per plant**		**100 seed weight**		**Broomrape dry weight**
			Normal	**Infested**	**Normal**	**Infested**	**Normal**	**Infested**	**Infested**
C1 **C2** **C3** **C4**	**Line-1**	**T-1**	6.21*	-10.93ns	7.13ns	-8.21**	2.24ns	0.51ns	1.50ns
		T-2	-15.20**	4.82ns	-9.91**	6.10**	0.99ns	1.45ns	-5.91*
		T-3	6.40*	19.71**	2.34ns	11.20**	-2.17ns	-1.88ns	-2.82ns
		T-4	2.59ns	-13.60*	0.43ns	-9.08**	-1.06ns	-0.08ns	7.22*
C5 **C6** **C7** **C8**	**Line-2**	**T-1**	3.79ns	-12.28*	-1.74ns	-12.04**	-4.26ns	-4.70ns	1.69ns
		T-2	-0.46ns	4.49ns	-4.75ns	1.38ns	-3.64ns	-2.75ns	-2.31ns
		T-3	-4.64ns	18.93**	3.50ns	22.47**	6.90*	8.44ns	0.26ns
		T-4	1.32ns	-11.14*	2.98ns	-11.81**	1.00ns	-0.99ns	0.36ns
C9 **C10** **C11** **C12**	**Line-3**	**T-1**	-4.86ns	18.44**	-1.50ns	15.68**	2.09ns	2.39ns	-2.78ns
		T-2	6.12*	-6.39ns	8.50*	-6.68**	3.31ns	-1.42ns	4.07ns
		T-3	5.45 ns	-23.38**	3.00ns	-19.51**	-1.47ns	-1.52ns	3.24ns
		T-4	-6.70*	11.33ns	-9.99**	10.51**	-3.93ns	0.55ns	-4.53ns
C13 **C14** **C15** **C16**	**Line-4**	**T-1**	-5.13ns	4.77ns	-3.90ns	4.57*	-0.07ns	1.80ns	-0.40ns
		T-2	9.55**	-2.92ns	6.16ns	-0.79ns	-0.66ns	2.72ns	4.15ns
		T-3	-7.21*	-15.26*	-8.84*	-14.15**	-3.27ns	-5.04ns	-0.69ns
		T-4	2.79ns	13.41*	6.57ns	10.38**	4.00ns	0.52ns	-3.05ns
LSD 0.05			5.90	11.48	7.36	3.80	5.95	12.11	5.71
LSD 0.01			7.95	15.48	9.91	5.12	8.01	16.31	7.96

Coefficients of variability:

Phenotypic (PCV) and genotypic (GCV) coefficients of variability were estimated for all studied traits (Table 13). It could be observed that PCV was relatively higher than the corresponding GCV and the difference was represented by environmental variance. However, it could be observed that, PCV% values ranged from 5.52% for number of branches per plantto 84.01% forplant height under infested soil condition, while GCV%values ranged from 3.18% for number of branches per plant under infested soil condition to 79.21% for plant height under normal soil condition. The estimates of PCV and GCV were relatively high for all studied traits in all crosses. The values of PCV for all traits were close to GCV values, indicating little environmental effects on the expression of these traits. Generally, a high GCV value of traits might suggest the possibility of improving these traits through selection. In this concern, **Kalia and Pathania[37] and Solieman and Ragheb[38]**recorded similar trend results on faba bean.

Heritability and genetic advances:

Broad sense heritability estimates, as shown in Table13, ranged from 72.48% for 100-seed weight under infested soil condition to 99.29% for seed yield per plant under infested soil condition. However, the values of broad-sense heritability are generally considered high according to the categories suggested by **Johanson[39]** either under normal or infested soil conditions.

Narrow-sense heritability estimates were listed in Table, 13. The values ranged from 2.3% for number of branches per plant under normal soil condition to 21.38% for number of seeds per plant at normal soil condition. According to the classification of narrow- sense heritability by **Stansfield[40]**, all estimates are considered as low(<20%).

The low estimates of narrow-sense heritability could be logical results, because, as mentioned before, the non-additive genes are mainly responsible to inheritance all studied traits in the present investigation either under normal or infested soil conditions.In turn, the additive genes are considered a low source of genetic variance, subsequently lowering the estimates of narrow-sense heritability.

The expected genetic advance (Ga) or predicted (Ga%) genetic gain upon selecting the top 5% of the population are presented in Table 13. The predicted genetic advance (Ga%) ranged from 0.71for number of branches per plant at normal soil condition to 13.95for Broomrape dry weight per plant under infested soil condition, respectively.

However, it could be observed that the lowest value of narrow-sense heritability (2.30%) was coupled with the lowest values of Ga (0.03) and Ga% (0.71). On the other side, the highest value of narrow-sense heritability (29.48%) was coupled with the highest values of Ga (21.38) and Ga%(10.86).

Table 13: Mean average($\bar{x}$), Phenotypic(PCV) and genotypic (GCV) coefficients of variation, broad-senseheritability (H), narrow sense (h^2), expected genetic advance (Ga) and predicted genetic advance (Ga%) for studied under normal and infested soil conditions.

Studied traits	Environment condition	$\bar{X}$	PCV	GCV	H	h^2	Ga	Ga%
Chocolate spot disease reaction	Normal	3.85	13.60	11.09	81.57	15.19	0.23	5.88
	Broomrape	4.05	9.17	7.93	86.52	15.09	0.19	4.68
Rust disease reaction	Normal	3.81	31.48	28.37	90.14	11.92	0.27	7.06
	Broomrape	4.14	23.68	20.67	87.28	9.72	0.20	4.79
Flowering date	Normal	51.53	25.58	21.23	82.98	14.98	1.12	2.17
	Broomrape	49.98	19.68	15.70	79.74	13.35	0.86	1.73
Plant height per plant	Normal	137.94	84.01	79.21	94.28	7.66	1.70	1.23
	Broomrape	124.79	63.12	58.10	92.04	6.70	1.23	0.98
No. of branches per plant	Normal	4.39	9.92	8.31	83.75	2.30	0.03	0.71
	Broomrape	3.64	5.52	3.18	75.66	11.39	0.11	2.89
No. of pods per plant	Normal	38.64	64.48	56.67	97.63	15.19	2.64	6.38
	Broomrape	28.27	28.17	21.80	95.03	11.66	1.45	5.12
No. of seeds per plant	Normal	104.01	69.74	61.11	97.12	7.18	2.86	2.75
	Broomrape	75.59	58.28	51.11	96.70	21.38	8.21	10.86
Seed yield per plant	Normal	81.81	37.22	31.47	96.00	12.02	4.56	5.58
	Broomrape	55.57	47.01	40.05	99.29	8.74	2.74	4.93
100 seed weight	Normal	78.31	69.07	55.96	81.02	20.01	3.03	3.87
	Broomrape	73.55	61.66	44.69	72.48	13.01	1.80	2.45
Broomrape dry weight	Broomrape	14.74	39.17	32.76	69.95	17.29	2.05	13.95

This GGE biplot provides a visual representation of how different genotypes perform under different environments, helping to identify which genotypes are best suited for specific conditions. In the GGE biplot shown in Fig. 1, the genotypes are represented by points on the plot, with their positions indicating their performance under different environments. The genotypes C3, C7, C9 and C12 are located in the sector representing the broomrape infested environment,indicating that theymay not have performed as well under those conditions. The genotypes C4, C16, C8 and C10 are situated in the sector representing the normal environment, indicating that they performed well under those conditions.

Fig. 2 shows that C12, which falls into the center of concentric circles, is an ideal cross in terms of higher yield ability and stability, compared to the rest of the crosses. Additionally, C4, C16, C3 and C9 located on the next two concentric circles, may be considered desirable or favorable genotypes. **Yan et al [41]** reported that, the selection of superior genotypes in target environments is an important objective of plant breeding programs.

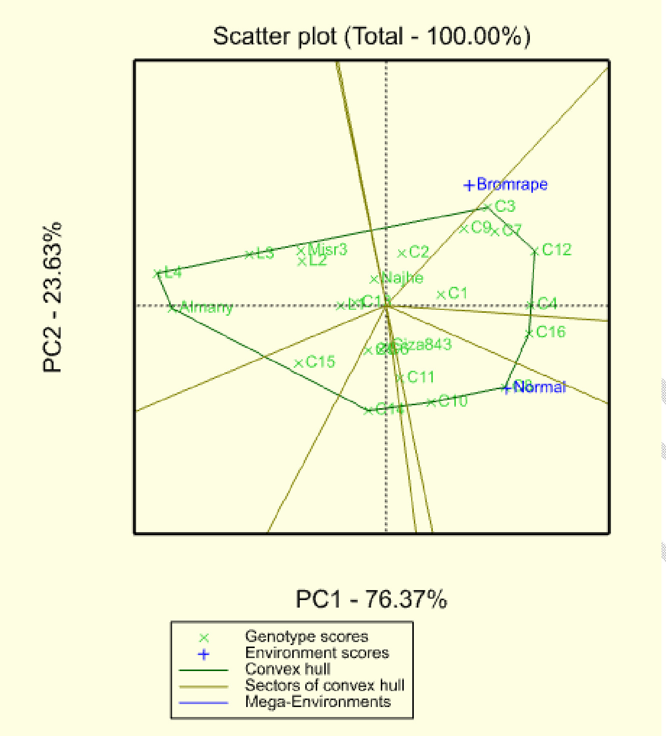

Fig. 1: Mega-environment for seed yield of twenty four faba bean genotypes across normal and broomrape infest environments.

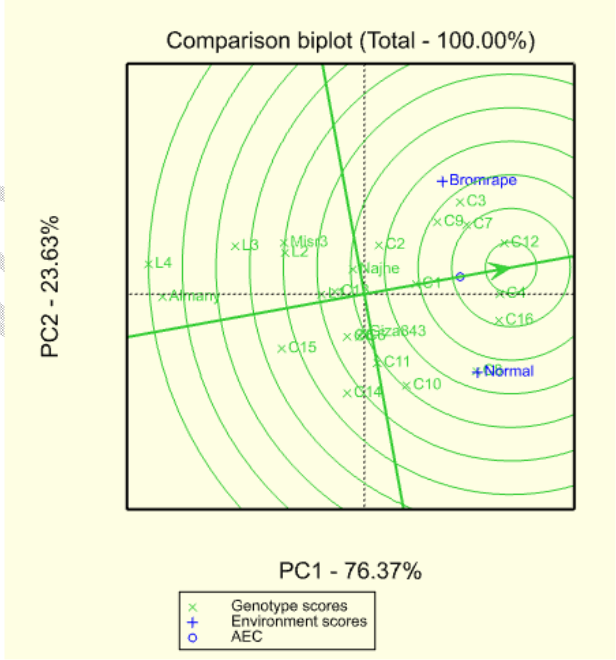

Fig. 2: Ideal genotypes for seed yield of twenty four faba bean genotypes across normal and broomrape infest environments.

In Fig. 3, a line with a single arrow passes through the biplot origin and the average environment (small circle) and is referred to as the average environment axis (AEA). The arrow points to higher mean performance for the genotypes. The line perpendicular to AEA and passes through the biplot origin points to higher performance variability or less stability in both direction (grand mean) **[41]**. The top-ranked crosses were C12 and C4, followed by C16, C7, C3 and C8; the lowest-ranked genotype were T1 (Almany) and L4.Similarly, prior publications by**AbdEl-Aty et al [42],Doraetet al [43]and Soliman et al [44]**have demonstrated significant variations among faba bean genotypes in agronomic traits under broomrape -free and infested soil conditions.

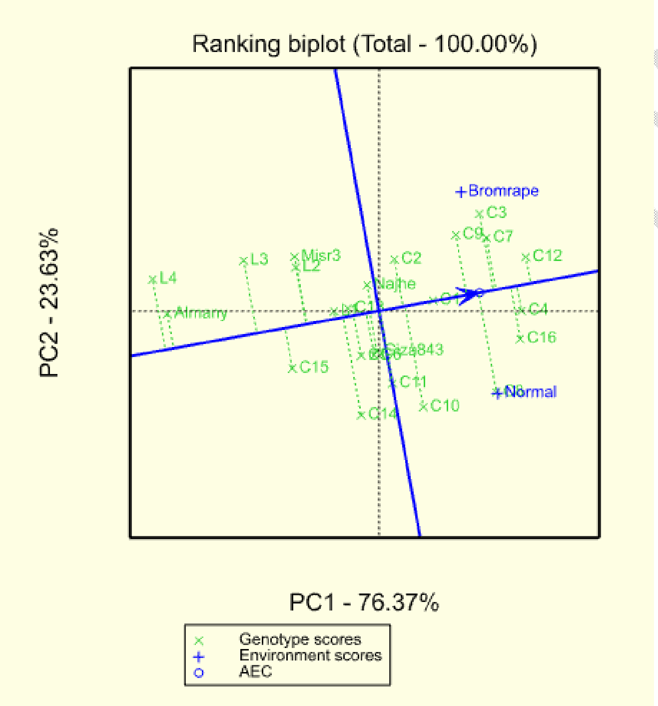

Fig. 3: Means vs. stability biplot for seed yield of twenty four faba bean genotypes across normal and broomrape infest environments.

CONCLUSION

This study highlights the importance of breeding for tolerant to broomrape and resistance foliar diseases in faba bean production in Egypt. By identifying genetic variations and selecting promising crosses, researchers can work towards developing resilient and high-yielding faba bean varieties that can thrive in challenging conditions. This research contributes to the overall goal of ensuring food security and sustainable agriculture in Egypt. In this study, eight parents and their 16 F_2 crosses were evaluated under normal and broomrape infested soil conditions revealing significant genetic variations. Developing genotypes tolerant to broomrape and resistant to foliar diseases is essential for sustainable faba bean productivity. Selection in the different crosses especially in C3, C7, C9 and C12 could lead to the release of resilient and productive faba bean varieties.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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