

Genetic Analysis for Some Faba Bean Agronomic Traits

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1. INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the oldest legume crops grown as a valuable rich protein food besides its contribution to sustainable agriculture by fixing atmospheric nitrogen in symbiosis with the soil bacteria *Rhizobium leguminosarum*. It can excel in different climatic conditions (Singh *et al.*, 2013). Over the past 20 years, Egypt's faba bean

ABSTRACT

This study was conducted at Sakha Research Station, Agricultural Research Center (A.R.C), Egypt during (2021/2022 and 2022/2023) seasons. Eight lines and two testers of faba bean and their sixteen F1's resulted from a line × tester procedure were evaluated under nature foliar diseases infection to identify the kind of gene action, combining abilities and the extent of heterosis for ten important traits. The genotypes were compared using cluster analysis after being grouped in a bi-plot figure. Based on the seed yield data, the biplot-PCA results showed that there were substantial genetic variations between genotypes, response to foliar diseases (Chocolate Spot and Rust), and Maturity date. Estimation of the magnitude of variance due to general and specific combining ability effects (σ^2A/σ^2D) The two hybrids, Sakha1 × RV and Giza 429 × Marina, were the best for the majority of the attributes that were investigated and ought to be taken into account in breeding programs. The parental genotypes Sakha1, Nubaria1, Marina, and Sakha3 depicted their good combining ability. Mid-parent heterosis (MP%) was observed for all studied traits, while heterobeltiosis (BP%) was observed in some crosses for most traits. Based on the heterobeltiasis (BP %), the hybrids Sakha1 × RV 322, Giza 843 × RV 322, and Sakha1 × Marina were the most superior in yield and relevant traits.

KEYWORDS: *Vicia faba*, Line × tester analysis, combining abilities, chocolate spot, and rust disease.

cultivation area has gradually and dramatically shrunk. (Anonymous 2017a) due to unreliable yields, which could be traced back to the susceptibility of the crop to pests, diseases, weeds, parasitic plants, nutrition cost of production inputs, etc. Therefore, a lot of seeds are imported to suit the needs of the growing population (El-Metwally *et al.*, 2013). Chocolate spot (*Botrytis fabae sard.*) and rust (*Uromyces fabae*) diseases are the limiting factors for faba

bean production in the northern parts of Egypt, particularly during wet winter seasons and low temperatures. Ibrahim, *et al.* (1979) mentioned that chocolate spot and rust are the most fungal pathogens attacking the leaves and the stem of faba bean and causing severe yield losses. Mohamed (1982) reported that natural infection with chocolate spot and rust caused yield losses of more than 55% for susceptible cultivars. The infection by chocolate spot (*Botrytis fabae sard*) appears as lesions on leaves, stems, flowers, and pods with oval or oblong brown spot. The entire plant turns black when the number of lesions increases, usually on the upper side of the leaf. In addition, the seeds of severely affected plants turn to reddish-brown, decreasing their market value (Crop Pro 2019). Rust (*Uromyces fabae*) appears white to cream-colored spots on leaves to lesser extension stems, with the severity of the infection the pustules cover most of the leaves, which are dried and fall off. The different methods of diallel analyses are good tools to detect appropriate parents and superior crosses in terms of the investigated traits. The line x tester design can be used to estimate general and specific combining abilities in both self and cross-pollinated plants (Kempthorne, 1957). The discrepancy and differences between the results of the researchers could be due to the divergence among parents and the nature of the studied trait in terms of a number of genes and whether the genes act in additive or non-additive. Ibrahim (2010), obiadalla-Ali *et al.* (2013), and Bishnoi *et al.* (2018) reported that the non-additive gene

action plays an important role in the genetic system of yield and its attributes. Sillero *et al.* (2017) found some genotypes might be promising for use in breeding programs under natural disease infection. Ibrahim *et al.* (2018) utilized the line x tester to figure out genetic parameters for some agronomic traits and reported that additive and non-additive gene effects were more important in the inheritance of these traits which could be improved by the varietal breeding program. The objectives of this work were to determine a) the genetic variation of parental lines, testers, and their F₁- hybrids for seed yield, and yield component traits under natural foliage disease. b) the best hybrids and parents tolerant to diseases, based on GCA and SCA estimates which could be used as a source material for further faba bean improvement, c) the additive and dominant components for various traits.

2. MATERIALS AND METHODS

This study was conducted at Sakha Research Station, Agricultural Research Center (A.R.C), Egypt during two growing seasons 2021/2022 and 2022/2023. Eight parental lines: Nubaria 1 (L₁), Sakha 1 (L₂), Sakha 2 (L₃), Sakha 3 (L₄), Sakha 4 (L₅), Giza 843 (L₆), Giza 3 (L₇) and Giza 429 (L₈) were crossed with two testers: RV322 (T₁) and Marina (T₂) under insect free cages in 2021/2022 seasons to obtain 16 F₁'s seed. Table 1 provides a brief description of plant materials.

Table 1. Pedigree, disease reaction, and date of maturity for the studied faba bean genotypes

Parental lines	Pedigree	Disease reaction	Maturity date
Nubaria 1 Line (L ₁)	(Reina Blanca) introduced from Spain	R	Late
Sakha1 Line (L ₂)	Giza 716 x 620/283/85	R	Early
Sakha2 Line (L ₃)	Rena Blanka x 461/845/83	R.	Medium
Sakha3 Line (L ₄)	Giza 716 (Giza461 x 503/453/83)	HR	Medium
Sakha4 Line (L ₅)	Sakha1 x Giza 3	R	Early
Giza 843 Line (L ₆)	561/2076/85 x 461/843/83	MR	Early
Giza 3 Line (L ₇)	Giza 1 x Dutch 29	MR	Medium
Giza 429 Line (L ₈)	An individual plant selection from Giza402	HS	Medium
Testers			
RV 322	Tester (T ₁) HEL 170, inbred line(China)	S	Very early
Marina	Tester (T ₂) Introduced from Hungary	HR	Late

HR =Highly resistant, R = resistant, MR = moderately resistant, S = susceptible, H.S. = Highly susceptible

2.1. In the 2022/2023 season

In a randomized complete blocks design with three replications, the 16 F₁S seed and their parents were seeded under natural disease infection. Standard agricultural procedures were applied as usually recommended to the faba bean fields. Data were recorded on all plants from each experimental plot. The following traits were recorded: days to flowering, days to maturity, plant height (cm), number of branches/plant, number of pods/ plant, number of seeds/plant, 100-seed weight (g), seed yield/ plant (g.), chocolate spot and rust diseases reaction.

2.2. Disease assessment

According to Bernier et al. (1984), reactions to rust and chocolate spot diseases were noted during the first week of March and mid-February (Table 2). The average monthly agrometeorological data has been recorded during the 2020/2021 season (Fig. 1).

2.3. Statistical analysis

The significance tests and analysis of variance were executed as outlined by (Steel et al., 1997). The combining ability analysis was done using the line x tester approach as suggested by Cochran and Cox (1957) and Kempthorne (1957). Cluster analysis was carried out by the hierarchical cluster analysis procedure of the program SPSS-V.13 for Windows. Minitab statistical software V.17 was utilized to do principal component analysis (PCA). The PCA was employed to ascertain the degree of variation. The relative discriminative power of the axes and their associated characteristics was ascertained using the values derived from PCA (Pradhan et al. 2011). The genotypes were categorized using cluster analysis and clustered in a bi-plot figure. To create a dendrogram tree using the unweighted pair group technique with arithmetic averages (UPGMA), which was suggested by Sokal and Michener in 1958, the cluster analysis was also carried out using the NT-SYS-pc program version 2.0 (Rohlf, 2002).

Table 2. Chocolate spot and rust disease scales (Bernier et al., 1984)

Chocolate spot scale

1	No disease symptoms or very small specks (highly resistant)
3	Few small disease lesions (resistant)
5	Some coalesced lesions, with some defoliation (moderately resistant)
7	Large coalesced sporulating lesions, 50% defoliation, and some dead plants (susceptible)
9	Extensive, heavy sporulation, stem girdling, blackening, and death of more than 80% of plants (highly susceptible)

Rust scale

1	No pustules or very small non-sporulating flecks (highly resistant)
3	Few scattered pustules covering less than 1% of the leaf area, and few or no pustules on the stem (resistant)
5	Pustules common on leaves covering 1-4% of leaf area, little defoliation, and some pustules on the stem (moderately resistant).
7	Pustules very common on leaves covering 4-8% of the leaf area, some defoliation, and many pustules on the stem (susceptible).
9	Extensive pustules on leaves, petioles, and stems covering 8-10% of leaf area, many dead leaves, and several defoliations (highly susceptible).

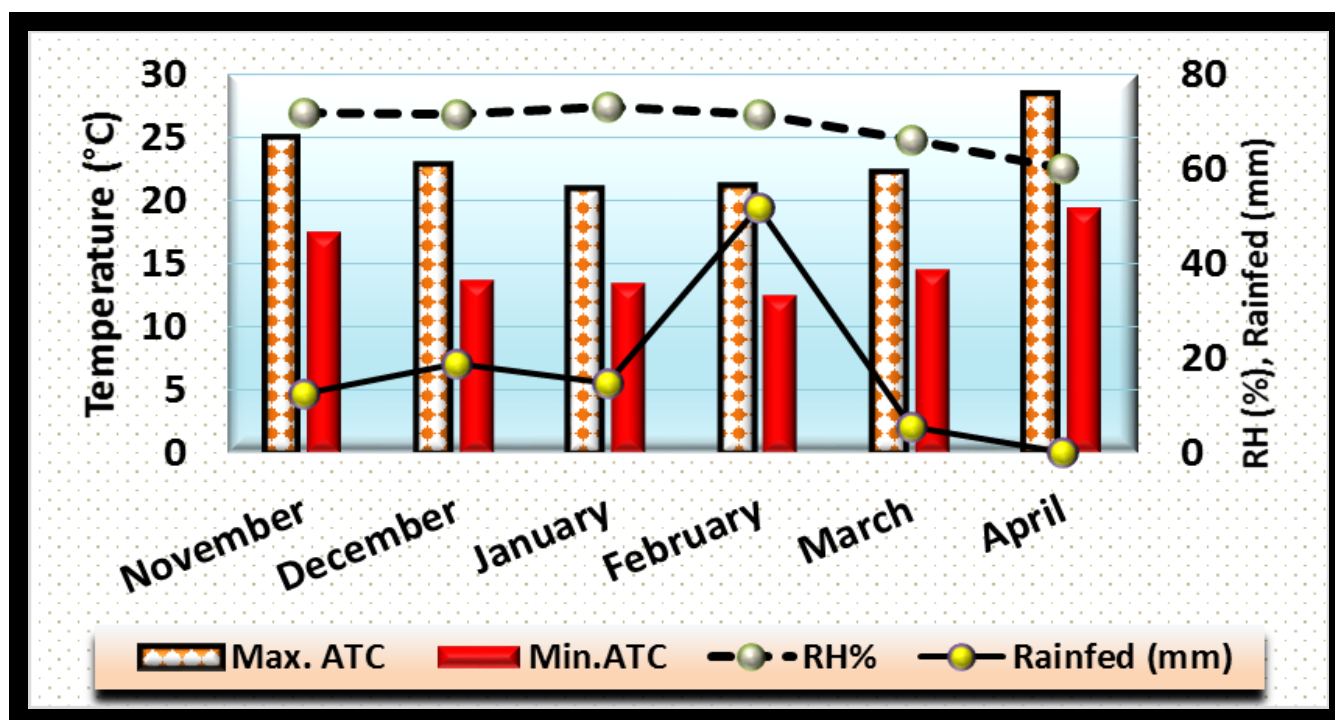


Figure 1. Average of air temperature (ATC), relative humidity (RH%) and rainfed (mm/month) in the 2021/2022 season.

3. RESULTS AND DISCUSSION

3.1. Line x tester analysis

Results of statistical analysis expressed as mean squares for the studied traits Differences among genotypes were highly significant for all traits, indicating wide genetic variability for these traits in hybrids and their parents as shown in Table 3.

The mean squares of the parents and crosses were significant for all the studied traits ($p \leq 0.01$) except a number of branches, illustrating that, a sufficient amount of variation are present for carrying out various analyses in the current study. The significant mean squares of parent vs crosses of most traits refer to the high degree of heterozygosity, i.e., non-additive gene actions in the inheritance of this trait. These results are in line with those noted by Haridy and Amein, 2011, Abou-Zaid et al., 2017, Abd EL-ATY et al., 2018 and Bishnoi et al., 2018.

Means of all traits for the studied parents are shown in Table 4. Marina (T2) gave the highest performance for pods and seeds number

as well as the foliar disease resistance followed by Nubaria 1 (L1) for the number of seeds and disease reactions. However, this cultivar obtained the largest seed yield and 100-seed weight along with the branches number. RV322 (T1) tester was the earliest in flowering and maturity along with the lowest performance in all studied traits.

The mean performance of sixteen crosses are shown in (Table 5). Cross L2 x T1 was the earliest for days to maturity (135 days). As for plant height, Cross L7xT2 produced the tallest plants (140 cm), while cross L1xT1 was the shortest in plant height (76.9 cm). Branches/plant ranged from 1.97 (L5xT1) to 4.29 (L1xT2). L7xT2 recorded the minimal number of both seeds and pods/plant whereas L2xT1 and L4xT2 had the maximum number, respectively. However, L8xT1 was the lowest cross in seed yield/plant and 100-seed weight along with the highest susceptibility for Chocolate and Rust infection.

Table 3. Significance of mean squares due to various sources of variation for line x tester analysis for all studied traits

S.O.V	df.	Flowering date	Maturity date	Plant height/ plant(cm)	Branches No. / plant	Pods No. / plant	Seeds No./plant	Seed yield/ plant(g)	100-seed weight/plant (g)	Disease's reaction	
										Chocolate Spot	Rust
Replications	2	9.96	14.65	20.75	1.03	5.94	35.8	18.32	3.36	0.37	1.07
Genotypes	25	213.95**	337.57**	1901.59**	2.54**	22.28**	312.37**	409.91**	682.08**	3.82**	3.04**
Parents (P)	9	432.97**	507.64**	1646.30**	5.31**	16.58**	265.20**	792.23**	1353.52**	6.61**	4.28*
Crosses ©	15	91.2**	252.97**	1867.0**	1.04	19.53**	350.67**	206.44**	310.33**	2.40**	2.38**
P Vs C	1	84.68**	71.10**	4717.4*	0.06	114.81**	162.48	21.01	228.62**	0.04	1.62**
Lines	7	147.2**	128.76**	59.62**	1.32**	19.92**	435.19**	353.61**	425.37**	1.71**	1.53**
Testers	1	320.3**	2655.2**	27326.8**	4.98**	0.63	456.33*	12	1253.59**	22.01**	22.01**
Line x Tester	7	2.33	34.0**	37.3**	0.24	21.84**	251.05**	87.05**	60.54**	0.29	0.43*
Error	50	5.38	3.40	11.69	0.32	2.26	12.11	6.88	1.25	0.15	0.16

*and ** significant and highly significant at 0.05 and 0.01 respectively.

Table 4. Means of the studied traits for lines and testers parents

Genotype	Flowering date	Maturity date	Plant height/ plant(cm)	Branches No. / plant	Pods No. / plant	Seeds No./plant	Seed yield/ plant(g)	100-seed weight/plant (g)	Disease's reaction	
									Chocolate spot	Rust
Lines										
L₁	77.0	169.3	121.7	6.67	16.67	64.33	73.45	114.17	2.83	2.83
L₂	38.7	141.0	130.0	2.97	18.00	49.33	36.62	74.23	3.00	3.00
L₃	48.0	154.7	126.7	3.00	19.00	58.33	50.64	86.81	3.00	3.00
L₄	51.7	155.7	126.7	3.33	15.67	58.33	46.42	79.59	2.83	2.83
L₅	38.7	139.3	131.7	2.67	20.00	57.33	43.49	75.84	3.00	3.00
L₆	41.0	144.7	130.0	2.67	16.33	42.00	28.25	67.26	5.00	4.67
L₇	45.0	150.0	146.7	3.00	18.67	48.67	30.61	62.89	5.00	4.33
L₈	41.0	151.0	133.3	2.67	18.33	46.33	31.39	67.74	6.67	6.33
Testers										
T₁	34.3	124.3	61.7	1.50	16.33	38.00	12.03	31.67	5.67	4.33
T₂	49.0	164.7	141.7	3.33	23.67	66.00	37.35	56.61	2.50	2.60

Table 5. Mean performance of faba bean crosses for the studied traits

Cross	Flowering date	Maturity date	Plant height/plant(cm)	Branches no. / plant	Pods No./plant	Seeds no./plant	Seed yield/plant(g)	100-seed weight/plant (g)	Disease's reaction	
									Chocolate spot	Rust
L ₁ ×T ₁	53.3	138.3	76.9	4.0	20.8	62.3	43.7	70.1	4.3	4.3
L ₂ ×T ₁	37.7	135.0	86.3	3.0	23.7	84.3	54.3	64.4	4.3	4.3
L ₃ ×T ₁	41.7	151.7	86.7	2.9	17.7	50.7	34.3	67.8	4.3	4.3
L ₄ ×T ₁	43.3	141.7	88.0	2.7	19.7	57.0	39.7	69.6	4.0	4.3
L ₅ ×T ₁	38.3	143.3	83.3	1.9	19.7	61.3	39.3	64.1	4.3	4.3
L ₆ ×T ₁	39.3	136.7	83.3	2.8	24.0	60.7	37.0	61.1	5.0	5.0
L ₇ ×T ₁	40.7	136.7	88.3	2.5	22.3	52.3	29.3	56.1	4.7	4.7
L ₈ ×T ₁	39.3	136.7	88.3	2.8	17.3	42.7	22.0	51.6	5.7	6.0
L ₁ ×T ₂	58.3	161.7	130.0	4.3	21.7	46.7	44.7	95.7	2.8	2.8
L ₂ ×T ₂	44.0	150.7	133.3	3.4	21.0	64.7	46.7	72.2	3.0	3.3
L ₃ ×T ₂	45.0	160.0	130.0	3.5	19.7	47.3	36.0	76.1	2.7	2.7
L ₄ ×T ₂	48.3	160.0	126.3	3.8	25.3	62.3	48.0	77.0	2.3	2.7
L ₅ ×T ₂	43.3	153.3	135.0	3.3	18.0	45.0	33.3	74.2	3.3	3.3
L ₆ ×T ₂	46.7	150.0	133.3	3.1	22.7	52.3	35.0	66.9	4.0	4.0
L ₇ ×T ₂	46.0	150.0	140.0	3.0	16.7	42.0	26.7	63.5	4.0	4.0
L ₈ ×T ₂	43.3	153.3	135.0	3.1	22.0	61.7	37.3	60.5	3.7	3.7

3.2. General and specific combining ability effects in F₁'s

3.2.1. General combining ability:

Table 6 shows estimate of the general combining ability (GCA) effects of the two testers and the parental lines. All traits under study had high positive GCA effects, with the exception of days to flowering and maturity, as well as the chocolate and rust reaction, where a negative GCA is preferable.

For both seed yield/plant and number of seeds, line L₂ displayed the largest GCA impacts ($p \leq 0.01$) (Table 6). For these two traits, this line might be regarded as a good combiner.

The good combiners for days to flowering and maturity were lines L₂, L₈ and T₁ whereas L₅ was for the flowering date only. Also, L₆ and L₇ were for maturity date only. Each of L₁, L₄ and T₂ showed the best GCA performance for seed yield (g), 100-seed weight (g) and resistance to both chocolate spot and rust. There was no line or tester depicted to be a good combiner for all traits. The best-identified combiners can be crossed together to obtain the

potential hybrid populations, which would be useful for enhancing these traits through selection.

3.2.2. Specific combining ability

The SCA effects (Table 7) were positive and significant for hybrids of two parents or at least one parent has a positive GCA effect in most cases. Moreover, some crosses exhibited SCA effects in a reverse trend of their parent's trends. The crosses L₂×T₁, L₅×T₁, L₄×T₂ and L₈×T₂ exhibited positive SCA effects ($p \leq 0.01$) for seed yield(g) in contrast to the significant ($p \leq 0.01$) GCA effects of their parents, also the crosses L₁×T₁, L₃×T₂, and L₅×T₂ for maturity date, while the cross L₇×T₁ showed negative SCA for chocolate spot resistance and the cross L₈ x T₂ was significant for chocolate spot and rust. The SCA effects of each cross were in the opposite directions of their respective parents for each of the traits.

Table 6. Estimates of general combining ability effects of the parental lines & testers on the studied traits.

Genotype	Flowering date	Maturity date	Plant height/plant(cm)	Branches No./ plant	Pods No./plant	Seeds No./plant	Seed yield/plant(g)	100-seed weight/plant (g)	Disease's reaction	
									Chocolate spot	Rust
Lines										
GCA L ₁	11.54**	2.56**	-5.56**	1.03**	0.49	-1.33	6.21**	14.72**	-0.32*	-0.41*
GCA L ₂	-3.46**	-4.60**	0.82	0.01	1.57*	18.67**	12.54**	0.15	-0.24	-0.16
GCA L ₃	-0.96	8.40**	-0.68	0.06	-2.09**	-6.83**	-2.79*	3.75**	-0.41*	-0.49*
GCA L ₄	1.54	3.40**	-1.85	0.13	1.74*	3.83*	5.88**	5.13**	-0.74**	-0.49*
GCA L ₅	-3.46**	0.90	0.15	-0.49*	-1.93**	-2.67	-1.63	1.05*	-0.07	-0.16
GCA L ₆	-1.29	-4.10**	-0.68	-0.22	2.57**	0.67	-1.96	-4.18**	0.59**	0.51**
GCA L ₇	-0.96	-4.10**	5.15**	-0.38	-1.26	-8.67**	-9.96**	-8.40**	0.43*	0.34
GCA L ₈	-2.96**	-2.44**	2.65	-0.17	-1.09	-3.67*	-8.29**	-12.23**	0.76**	0.84**
S.E	1.06	0.84	1.55	0.22	0.65	1.62	1.17	0.41	0.17	0.18
Tester										
GCA T ₁	-2.58**	-7.44**	-23.86**	-0.31**	-0.11	3.08**	-0.50**	-5.11**	0.68**	0.68**
GCA T ₂	2.58**	7.44**	23.86**	0.31**	0.11	-3.08**	0.50**	5.11**	-0.68**	-0.68**
S.E.	0.53	0.42	0.77	0.11	0.32	0.81	0.58	0.24	0.08	0.09

*and ** significant and highly significant at 0.05 and 0.01 respectively

Table 7. Estimates of specific combining ability effects for faba bean hybrids for the studied traits.

Crosses	Flowering date	Maturity date	Plant height/plant(cm)	Branches No. / plant	Pods No. /plant	Seeds No./plant	Seed yield/plant(g)	100-seed weight/plant (g)	Disease's reaction	
									Chocolate spot	Rust
SCA L ₁ ×T ₁	0.08	-4.23**	-2.69	0.18	-0.30	4.75*	0.0003	-7.75**	0.07	0.07
SCA L ₂ ×T ₁	-0.58	-0.40	0.36	0.10	1.45	6.75*	4.33*	1.21	-0.01	-0.18
SCA L ₃ ×T ₁	0.92	3.27**	2.19	0.04	-0.89	-1.42	-0.33	0.94	0.16	0.16
SCA L ₄ ×T ₁	0.08	-1.73	4.69*	-0.25	-2.72**	-5.75*	-3.67*	1.39*	0.16	0.16
SCA L ₅ ×T ₁	0.08	2.44	-1.97	-0.37	0.95	5.08*	3.50*	0.06	-0.18	-0.18
SCA L ₆ ×T ₁	-1.08	0.77	-1.14	0.14	0.78	1.08	1.50	2.18**	-0.18	-0.18
SCA L ₇ ×T ₁	-0.08	0.77	-1.97	0.02	2.95**	2.08	1.83	1.37*	-0.34**	-0.34
SCA L ₈ ×T ₁	0.58	-0.90	0.53	0.13	-2.22*	-12.58**	-7.17**	0.60	0.32*	0.49**
SCA L ₁ ×T ₂	-0.08	4.23**	2.69	-0.18	0.30	-4.75*	-0.0003	7.75**	-0.07	-0.07
SCA L ₂ ×T ₂	0.58	0.40	-0.36	-0.10	-1.45	-6.75**	-4.33*	-1.21	0.01	0.18
SCA L ₃ ×T ₂	-0.92	-3.27**	-2.19	-0.04	0.89	1.42	0.33	-0.94	-0.16	-0.16
SCA L ₄ ×T ₂	-0.08	1.73*	-4.69*	0.25	2.72**	5.75*	3.67*	-1.39*	-0.16	-0.16
SCA L ₅ ×T ₂	-0.08	-2.44*	1.97	0.37	-0.95	-5.08*	-3.50*	-0.06	0.18	0.18
SCA L ₆ ×T ₂	1.08	-0.77	1.14	-0.14	-0.78	-1.08	-1.50	-2.18**	0.18	0.18
SCA L ₇ ×T ₂	0.08	-0.77	1.97	-0.02	-2.95**	-2.08	-1.83	-1.37*	0.34**	0.34
SCA L ₈ ×T ₂	-0.58	0.90	-0.53	-0.13	2.22*	12.58**	7.17**	-0.60	-0.32*	-0.49**
S.E. (sij-sil)	1.15	1.19	2.19	0.32	0.92	2.32	1.65	0.68	0.24	0.25

*and ** significant and highly significant at 0.05 and 0.01 respectively

These findings validated that non-additive effects predominate in the inheritance of the aforementioned traits. For the majority of the characters under study *i.e.* maturity date, plant height, seeds number /plant, seeds yield/plant (g), and 100-seed weight(g), Abd El-Aty *et al.* (2018) found that both general (GCA) and specific (SCA) combining abilities were significant. This suggests that both additive and dominant components play a significant role in the inheritance of these characters. According to Abdalla *et al.*, (2021), results showed high variability among genotypes (parents and their crosses) in the majority of the characters, all characters were impacted by inbreeding showed highly significant SCA effects in all characters particularly the positive significance of resistance to chocolate spot disease. Both additive and non-additive effects of genes control maturation date, plant height, number of seeds/plants, number of seeds yield/plant, and 100-seed weight.

3.2.3. Gene action type

Table (8) displays estimates of the variance components of general and specific combining abilities (σ^2 GCA and σ^2 SCA) for each trait under study. Results revealed that σ^2 GCA played a major role in determining the performance of crosses for most traits. σ^2 GCA's magnitude was greater than σ^2 SCA's., suggesting that the inheritance of these traits was significantly influenced by the additive type of gene expression. On the other hand, the inheritance of the number of pods per plant revealed both additive and non-additive gene effects.

Ibrahim (2010) and Premlatha *et al.* (2011) reported similar findings, concluding that non-additive gene action was more significant for seed yield and its constituents than additive gene action. Furthermore, for every trait under study, the magnitude of σ^2 A was greater than σ^2 D, suggesting that the environment had a greater impact on additive gene expression than non-additive gene action. *These findings concur with those of Gnanasambandam et al.* (2012), Awaad et al. (2005), and Sillero et al. (2009).

Broad sense heritability % (h^2 b) gradient from 71.67 % for branches number to 89.8 % for

plant height (cm). High heritability estimates indicate show that these traits were less impacted by environment and demonstrate that either they were simply inherited characters governed by a few major genes or additive gene effect, even if, they were under polygenic control. Therefore, the selection of these traits would be more effective for yield improvement. All of the traits had high broad sense heritability scores. High broad-sense heritability does not always imply high genetic gain. Hence, high heritability coupled with a low degree of genetic advance point out that these characters were more affected by the environment and the non-additive gene effects (dominance and epistasis) are controlling these traits.

3.3. h^2 b and h^2 n: heritability in broad and narrow sense, respectively

For 100-seed weight (g), chocolate spot, and rust disease, estimates of narrow sense heritability (h^2 ns) were found to be high, suggesting that additive gene effects accounted for the majority of the genetic variance associated with these traits. Therefore, these traits would be successfully improved by selection based on the accumulation of additive genes. Moreover, the narrow sense heritability (h^2 n) estimates for plant height and days to blooming were moderate. Selection will be challenging and should be postponed to later segregating generations because the h^2 n values for the number of branches, number of pods, number of seeds, and seed production were low. Symmetric results were reported by Ibrahim *et al.* (2010 and 2019).

3.4. Lines, testers and their interaction, contribution to the overall variance

The sum of squares of the crosses was divided into the sum of squares resulting from lines, testers and their interaction presented in Table 8 and Fig.2. With the exception of days to maturity, plant height, and response to foliar diseases, lines' percentage contribution was greater than testers' for each characteristic.

Table 8. Additive (σ^2A), dominance (σ^2D) variances, σ^2A/ σ^2D ratio and heritabilities as well as the Contribution of lines, testers, and their interaction on the studied traits

Item	Flowering date	Maturity date	Plant height/ plant(cm)	Branches No. / plant	Pods No. /plant	Seeds No./plant	Seed yield/ plant(g)	100-seed weight/plant (g)	Disease's reaction	
									Chocolate spot	Rust
Genetic component										
Additive (σ^2A)	103.9	626.06	693.27	1.35	9.09	253.19	100.1	380.99	5.28	5.23
Dominance (σ^2D)	0.49	11.26	11.99	0.06	7.11	83.33	28.8	19.24	0.07	0.10
σ^2A/ σ^2D	211.3	55.62	508.30	23.38	1.28	3.04	3.5	19.80	73.90	52.98
h^2b	74.2	79.69	89.80	71.67	87.10	88.13	86.4	83.43	88.93	81.73
h^2ns	32.7	29.7	40.3	15.9	13.8	20	10.6	70.8	64.2	73.4
Contribution (%)										
Line	75.38	23.75	1.49	59.09	47.60	57.92	79.9	63.91	33.21	29.94
Tester	23.43	69.98	97.58	30.15	0.21	8.68	0.4	26.83	61.13	61.56
LxT	1.19	6.27	0.93	10.76	52.19	33.41	19.7	9.26	5.66	8.50

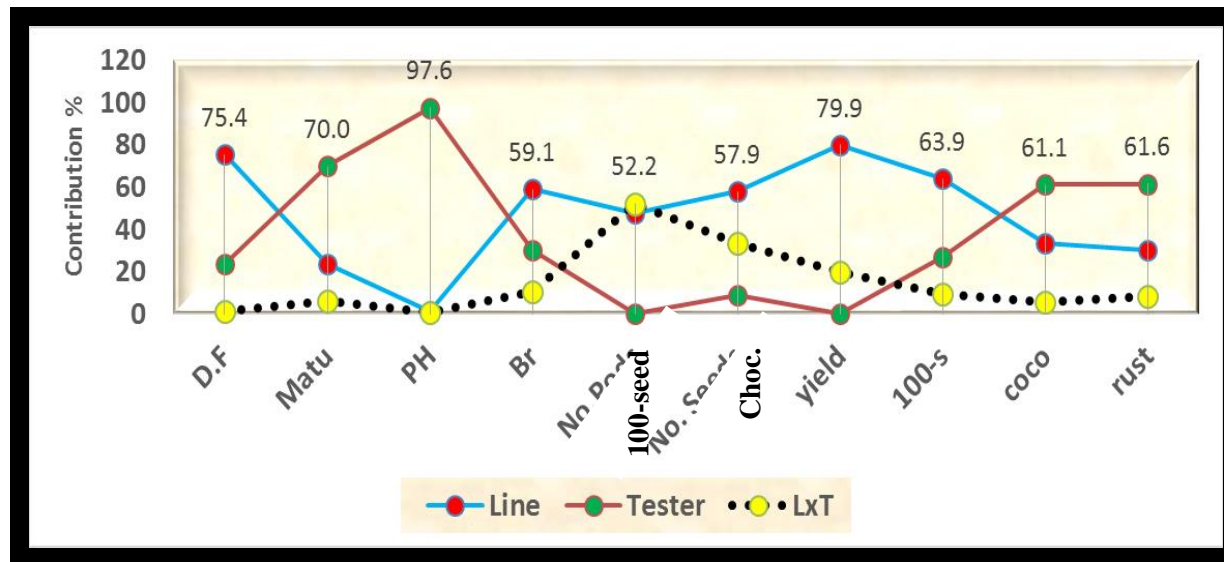


Figure 2. Lines, testers and their interaction, contribution on the studied traits

Additionally, in all traits except the number of pods, the contribution of lines was greater than the interaction of lines x testers, highlighting the significance of line selection for hybridization. Approximately 50% of the pods illustrating the significance of non-additive gene action were contributed by the line x tester. These findings are consistent with those published by Toker (2009) & Abd EL-Aty et al. (2018).

These results imply that these genotypes possess genes that confer resistance to chocolate spot disease, which may have originated from their parents who, based on their pedigree (Tables 1 and 9), are resistant to *B. fabae*. El-Absawy *et al.* (2012), Abdellatif *et al.* (2012), Abo-Mostafa *et al.* (2014), Beyene *et al.* (2016), and Eldemery *et al.* (2016) have reported similar findings for faba bean growth-related traits and yield and its components, as well as for disease resistance traits.

3.5. Genetic distance and cluster analysis

The results of the principal component analysis (PCA) of the genotypes are presented in Table 9. There were four main components identified by the PCA. 94.59% of the entire cumulative variability among genotypes has been explained by PC1 and PC2, which have eigenvalues of 2.89 and 0.89, respectively (Fig.3). The first principal component PC1 (72.33%) showed eigenvalues of more than one, *i.e.*, the maximum variance when correlating the most relevant components. The finding indicated that Rust & SY in PC1 and SY & maturity in PC2 followed by the chocolate spot in both PCs had the maximum loading value. According to Pradhan *et al.* (2011) who reported that PCA for 12 traits out of these only the first two components in the PCA analysis had Eigen values up to 1.0, exhibiting cumulative variance of 84.1%.

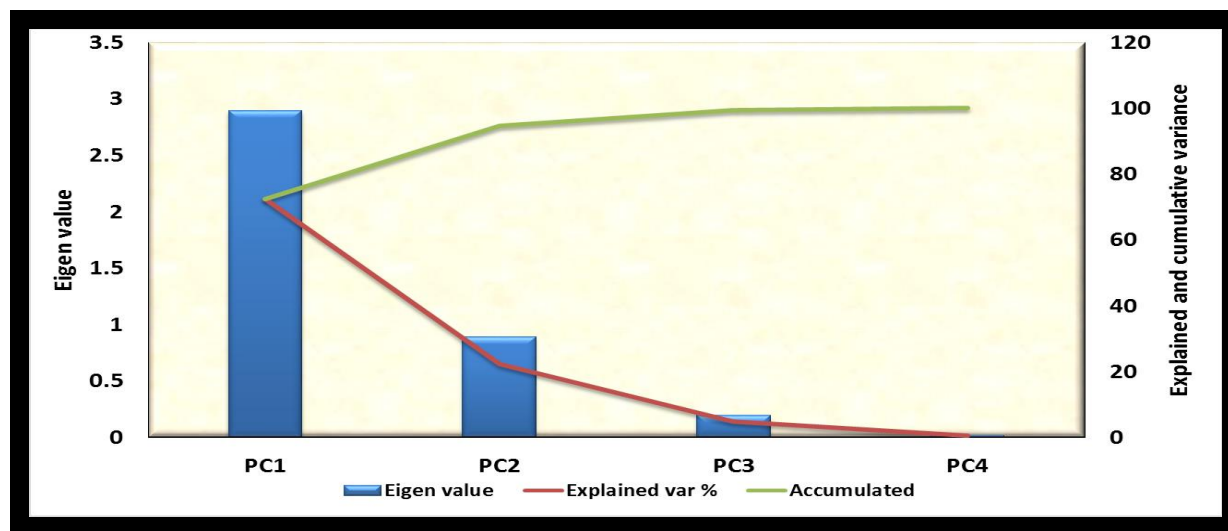


Figure 3. Eigen values, variability proportion, and cumulative variability (%) for the attributes of the genotypes of faba beans under study are plotted in a scree plot.

Table 9. Principal component analysis for some faba bean traits in studied genotype

Traits	PC ₁	PC ₂	PC ₃	PC ₄
Seed yield	0.5132	-0.5452	-0.5039	0.4307
Chocolate spot	-0.3674	-0.3763	-0.5333	-0.6625
Rust	-0.7736	-0.1295	-0.1292	0.6067
Maturity date	-0.056	-0.7378	0.667	-0.0867

According to Table 9 and Figure 4, PC1 exhibits a negative correlation with the other three traits and a positive correlation with seed yield. PC₂ has a negative association with the four studied traits. The third PC exhibited a positive correlation with maturity date and a

negative association with seed yield, chocolate spot, and rust diseases. The fourth PC has a positive association with rust and seed yield and a negative correlation with chocolate spot and maturity.

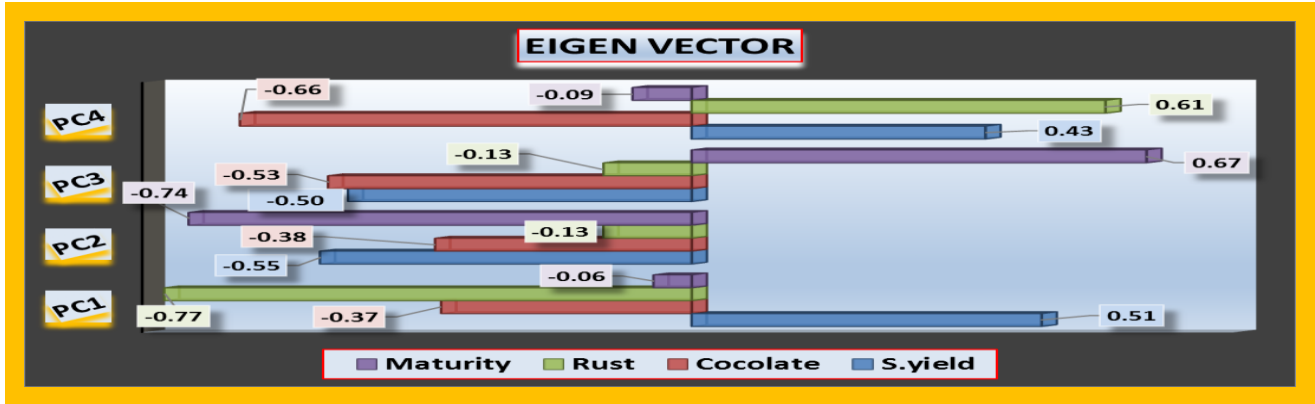


Figure 4. Eigen vector screen diagram for 16 faba bean genotypes' examined traits

The distance between the genotypes was interpreted using a principal component analysis. Once more, a scattered diagram of the genotypic distribution pattern on the axis was shown in Fig. 5. Remarkably, the PCA plot's genotype distribution along the two axes matched the cluster analysis's classification of these

genotypes. The Scree plot shows that the first and second components of the genotype data's Eigen-value account for the majority of the variation. Based on the data of the four variables under study, the biplot-PCA results showed that there were significant genetic variances among genotypes.

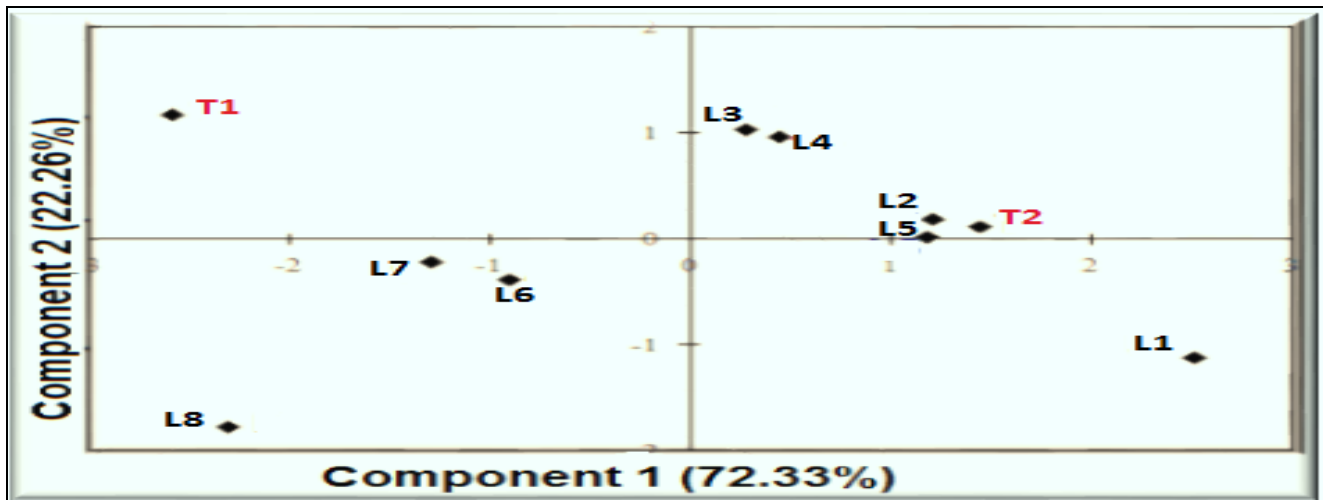


Figure 5. Scattered diagram: Principal component analysis based on first and second components for the 10 faba bean genotypes

GROUP1 (Y1 >= 0, Y2 >= 0)
 GROUP2 (Y1 >= 0, Y2 < 0)
 GROUP3 (Y1 < 0, Y2 < 0)
 GROUP4 (Y1 < 0, Y2 >= 0)

L2, L3, L4, L5 and T2
 L1
 L6, L7 and L8
 T1

In addition, two further clusters with one genotype each, five and three genotypes, representing 50 and 30% of the total genotypes, respectively, were categorized in the first and third clusters.

All genotypes were compared pairwise, and the mean dissimilarity values were computed using the four faba bean characteristics (seed yield, chocolate spot, rust, and maturity date). The distance between all ten genotypes was measured. As can be seen in Table 10, the distance matrix based on the Pearson coefficient showed a reasonable variance across the genotypes under biotic stress, with a mean distance between groups ranging from 0.024

(between L6 and L8) to 6.92 (between L7 and T1).

In order to obtain higher values of important characteristics, as well as to mitigate the speed of primitive extinction and adaptive genes between genotypes, the hybridization program would make sense if it were conducted between L7 and L3 or L4 and with RV tester 1 c.v. in combination with any other genotypes that have been studied (Govindaraj *et al.*, 2015). Slight differences between L8 and L6 (0.024 DC) or L3 and L4 (0.043) could indicate that they came from a similar progenitor or that some genetic material was swapped between these genotypes' ancestral roots, combining them into a single major group. (Tahir *et al.*, 2021).

Table 10. Distance matrix based on Pearson coefficient for studied faba bean genotypes

	L ₁	L ₂	L ₃	L ₄	L ₅	L ₆	L ₇	L ₈	T ₁	T ₂
L ₁	0	2.68	0.891	1.109	2.236	3.678	4.311	3.229	5.827	2.63
L ₂		0	0.525	0.445	0.175	0.212	0.206	0.136	6.032	0.265
L ₃			0	0.043	0.401	1.095	1.376	0.83	4.927	0.514
L ₄				0	0.42	0.895	1.198	0.661	4.552	0.38
L ₅					0	0.765	0.615	0.598	6.862	0.355
L ₆						0	0.138	0.024	5.422	0.519
L ₇							0	0.186	6.92	0.613
L ₈								0	5.057	0.344
T ₁									0	4.466
T ₂										0

3.6. Clustering dendrogram (UPGMA)

The UPGMA dendrogram produced by the cluster analysis based on four phenotypic parameters of faba bean genotypes is shown in Figure 6. Generally speaking, it displays two sizable classes: class 1 comprises the RV genotype (T1) sensitive to foliar diseases, and class 2 comprises the medium or high resistance genotypes (other genotypes). Overwhelmingly,

the dendrogram's genotype distribution was in line with the cluster analysis's results of these genotypes' grouping along the two axes of the PCA graph (Fig. 5). Once more, the RV genotype created a single cluster that was significantly different from the other clusters, suggesting that it might be crossed with other genotypes to add the desired traits.



Figure 6. Dendrogram, using average linkage (Between Groups), for ten faba bean genotypes based on four studied traits

3.7. Types of heterosis

Heterosis percentage relative to mid-parents (MP) and better parents (BP) given in Table 11. The range of the types of heterosis and the number of superior crosses show significant desirable heterosis for each studied trait are given in Table 12. The results illustrated that the expression of heterosis varied with crosses and studied traits. Presented data in Tables 11 and 12, revealed that heterosis for days to flowering varied from 55.34% to -7.41% when both MP and BP types of heterosis are considered. Data also, show that two and five out of 16 crosses exhibited significant and highly significant negative heterosis values over the mid-parents for flowering and maturity dates, respectively. However, over-dominance for earliness was indicated by two crosses for the blooming date and only one cross for the maturity date out of 16 ones that displayed extremely significant negative values of heterosis over the superior parent. According to the data in Table 12, three and one crosses of the 16 crossings showed highly significant negative heterosis over the mid-parent in terms of resistance or tolerance to foliar diseases. The highest values (-20.00 & -17.91 %) for both chocolate spot and rust disease were found in the cross $L_8 \times T_2$, respectively. On the contrary, the non-crosses displayed significant negative values of heterosis over the better parent for chocolate spot and rust disease.

For yield, data in Tables 11 and 12 showed that seven crosses out of 16 exhibited highly significant positive heterosis over the mid parent and three crosses showed highly significant positive values of heterosis over the better parent, indicating over-dominance for yield/plant. as per the findings, seven out of 16 crosses showed highly significant positive heterosis over the mid-parent for pod number/plant. In terms of heterosis over the better parent, five of the 16 crosses displayed highly significant positive values, suggesting over-dominance for a large number of pods per plant. According to data in Table 12, there is over-dominance for numerous seeds, with eight out of 16 crossings exhibiting high significant positive heterosis over the mid parent and two crosses having high significant positive heterosis over the better parent. El-Hady *et al.* (2006), Abd El-Aty *et al.* (2018), Ibrahim (2010), Ibrahim *et al.* (2018), and Abou Zied *et al.* (2019) all reported identical heterosis results to the ones in this study.

4. CONCLUSION

For all traits, the σ^2A/σ^2D ratio was greater than unity, suggesting that additive effects played a more significant role in the inheritance of these traits than dominant effects. Each feature has a different good combiner of parental lines and particular combiners.

Table 11. Heterosis (%) over mid and better parents for faba bean studied traits

Cross	Flowering date		Maturity date		Plant height/ plant (cm)		Branches No. / plant		Pods No. /plant	
	MP%	BP%	MP%	BP%	MP%	BP%	MP%	BP%	MP%	BP%
L ₁ ×T ₁	-4.19	55.34**	-5.79**	11.26**	-16.11**	-36.79**	-1.47	-39.65**	26.26**	25.00**
L ₂ ×T ₁	3.20	9.71*	1.89	8.58**	-9.91**	-33.59**	24.89	- 6.05	37.86**	31.48**
L ₃ ×T ₁	1.21	21.36**	8.72**	21.98**	-7.96**	-31.58**	30.07	-2.44	0.00	-7.02
L ₄ ×T ₁	0.78	26.21**	1.19	13.94**	-6.55*	-30.53**	12.07	-18.75	22.92**	20.41**
L ₅ ×T ₁	5.02	11.65*	8.72**	15.28**	-13.79**	-36.71**	-5.28	-26.00	8.26	-1.67
L ₆ ×T ₁	4.42	14.56*	1.61**	9.92**	-13.04**	-35.90**	32.00	3.13	46.94**	46.94**
L ₇ ×T ₁	2.52	18.45**	-0.36	9.92**	-15.20**	-39.77**	8.99	-18.25	27.62**	19.64**
L ₈ ×T ₁	4.42	14.56**	-0.61	9.92**	-9.40**	-33.75**	32.96*	3.88	0.00	-5.45
L ₁ ×T ₂	-7.41**	19.05**	-3.19**	-1.82**	-1.27	-8.24**	-14.29	-35.71**	7.44	-8.45
L ₂ ×T ₂	0.38	13.79**	-1.31	7.11**	-1.84	-5.88**	9.07	3.20	0.80	-11.27*
L ₃ ×T ₂	-7.22*	-6.25*	0.21	3.45**	-3.11	-8.24**	7.47	2.10	-7.81	-16.90**
L ₄ ×T ₂	-3.97	-1.36	-0.10	2.78**	-5.84**	-10.82**	15.00	15.00	28.81**	7.04
L ₅ ×T ₂	-1.14	12.07*	0.88	10.05**	-1.22	-4.71*	11.11	0.00	-17.56**	-23.94**
L ₆ ×T ₂	3.70	13.82**	-3.02**	3.69**	-1.84	-5.88**	3.11	-7.20	13.33**	-4.23
L ₇ ×T ₂	-2.13	2.22	-4.66**	0.00	-2.89	-4.55*	-4.17	-8.97	-21.26**	-29.58**
L ₈ ×T ₂	-3.70	5.69	-2.75**	1.77	-1.82	-4.71*	4.44	-6.00	4.76	-7.04

*and ** significant and highly significant at 0.05 and 0.01 respectively

Table 11. Cont.

Cross	Seeds No./plant		Seed yield/ plant (g)		100-Seed weight/plant (g)		Disease's Reaction			
	MP%	BP%	MP%	BP%	MP%	BP%	Chocolate spot		Rust	
							MP%	BP%	MP%	BP%
L1×T1	21.82**	-3.11	2.17	-40.55**	-3.93**	-38.64**	1.96	52.94**	20.93*	52.94**
L2×T1	93.13**	70.95**	123.35**	48.37**	21.67**	-13.21**	0.00	44.44**	18.18*	44.44**
L3×T1	5.19	-13.14**	9.57	-32.20**	14.41**	-21.92**	0.00	44.44**	18.18*	44.44**
L4×T1	18.34**	-2.29	35.71**	-14.55**	25.11**	-12.55**	-5.88	41.18**	20.93*	52.94**
L5×T1	28.67**	6.98	41.68**	-9.56	19.18**	-15.45**	0.00	44.44**	18.18*	44.44**
L6×T1	51.67**	44.44**	83.68**	30.96**	23.21**	-9.17**	-6.25	0.00	11.11	15.38
L7×T1	20.77**	7.53	37.59**	-4.16	18.57**	-10.85**	-12.50*	-6.67	7.69	7.69
L8×T1	1.19	-7.91	1.33	-29.91**	3.25*	-24.22**	-8.11	0.00	12.50*	38.46**
L1×T2	-28.39**	-29.29**	-19.37**	-39.18**	12.11**	-16.15**	6.25	13.33	4.29	8.97
L2×T2	12.14**	-2.02	26.18**	24.94**	10.32**	-2.77*	9.09	20.00	19.05**	28.21*
L3×T2	-23.86**	-28.28**	-18.17**	-28.91**	6.08**	-12.38**	-3.03	6.67	-4.76	2.56
L4×T2	0.27	-5.56	14.59**	3.40	13.07**	-3.26**	-12.50*	-6.67	-1.84	2.56
L5×T2	-27.03**	-31.82**	-17.53**	-23.35**	12.23**	-2.21	21.21**	33.33*	19.05**	28.21*
L6×T2	-3.09	-20.71**	6.70	-6.29	8.02**	-0.54	6.67	60.00**	10.09	53.85**
L7×T2	-26.74**	-36.36**	-21.52**	-28.60**	6.28**	0.97	6.67	60.00**	15.38**	53.85**
L8×T2	9.79**	-6.57	8.62	-0.04	-2.62*	-10.88**	-20.00**	46.67**	-17.91**	41.03**

*and ** significant and highly significant at 0.05 and 0.01 respectively

Table 12. Range of heterosis % for studied traits and the number of superior crosses showing significant desirable heterosis.

Trait	Heterosis % over		No. of superior crosses based on	
	MP	BP	MP	BP
Flowering date	5.02 to -7.41	55.34 to -6.25	2	1
Maturity date	8.72 to -5.79	21.98 to -1.82	5	1
plant height (cm)	-16.11 to 1.61	-39.77 to zero	0	0
Branches No.	-14.29 to 34.84	-39.65 to 15	1	0
Pods No.	-21.26 to 46.94	-29.58 to 46.94	7	5
Seeds No.	-28.39 to 93.13	-36.36 to 70.95	8	2
Seed yield (g)	-21.52 to 123.35	-40.55 to 48.37	7	3
100 Seeds weight (g)	-3.93 to 25.11	-38.64 to 0.97	14	0
Chocolate spot	21.21 to -20	60 to -6.67	3	0
Rust disease	20.93 to -17.91	2.56 to 53.85	1	0

With the exception of number of branches/plant, the lines' contribution was greater than the testers', and lines x testers interaction was more significant in all characters, highlighting the significance of line selection for hybridization. The distance between the genotypes was interpreted using a principal component analysis. The distribution of genotypes along the two axes in the PCA plot aligned with both the classification of genotypes' response to diseases and the grouping of these genotypes derived from cluster analysis. The Scree plot shows that the first and second components in the genotype data's Eigen-value account for the majority of the variation. Biplot-PCA results showed that there were significant genetic differences between genotypes based on seed yield, chocolate spot, rust, and maturity date data.

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الملخص العربي

التحليل الوراثي لبعض الصفات المورفولوجية والمحصولية للفلول البلدي

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أجريت هذه الدراسة في محطة بحوث سخا بمحافظة كفر الشيخ والتابعة لمركز البحوث الزراعية بمصر خلال ٢٠٢١/٢٠٢٢ و ٢٠٢٢/٢٠٢٣. لتقييم ٨ سلالات من الفول البلدي و٢ كشاف بالإضافة إلى ١٦ هجين ناتجة من نظام السلالة X الكشاف وذلك تحت ظروف الإصابة الطبيعية بأمراض المجموع الخضري لتقدير الفعل الجيني والقدرة العامة والخاصة على الإئتلاف وقوة الهجين لعشرة من الصفات الهامة.

- تم تهجين ثمانية اصناف من الفول البلدي كسلالات مع اثنين كمختبر كشاف لإنتاج ١٦ هجيناً F₁.
 - تم زراعة الستة عشر هجيناً والاباء العشرة تحت ظروف الاصابات الطبيعية بالامراض الفطرية.
 - تم تقييم شدة الإصابة بمرض التبقع البني والصدأ على الآباء ونباتات الجيل الأول F₁ باستخدام مقياس تصنيف ١-٩
 - تم تسجيل الصفات التالية الأيام حتى الزهرة الأولى (اليوم)، الأيام حتى النضج (اليوم)، ارتفاع النبات (سم)، عدد الأفرع / نبات، عدد القرون / نبات، عدد البذور / نبات، وزن ١٠٠ بذرة (جم) ، محصول البذور / نبات (جم).
 - تم اجراء جميع العمليات الزراعية بشكل موحد على منطقة التجربة بأكملها مع عدم استخدام اي مقاومة للأمراض
 - تم إجراء تحليل التباين واختبارات المعنوية مع إجراء التحليل العنقودي الهرمي (شجرة وراثية) كما تم إجراء تحليل المكون الرئيسي (Principal component analysis, PCA) لتحديد مدى الاختلاف.
 - تم الحصول على قيم PCA، والتي تم استخدامها لتحديد القوة التمييزية النسبية للمحاور والصفات المرتبطة بها.
- واسفرت النتائج على الاتي:

كان الهجينان سخا ١ × ٣٢٢ RV وجيزة ٤٢٩ × مارينا أفضل الهجن لمعظم الصفات المدروسة ويجب أخذها في الاعتبار في برنامج التربية، وظهرت الاصناف الأبوية سخا ١ ونوبارية ١ ومارينا وسخا ٣ قدرة ائتلافية جيدة. كانت النسبة σ^2A / σ^2D أكبر من الوحدة لجميع الصفات مما يشير إلى أن دور الفعل المضيف للجينات كان أكثر أهمية من التأثيرات غير المضافة في وراثية هذه الصفات.

كانت مساهمة السلالات أكبر من تلك الخاصة بالكشاف وتفاعل السلالة × الكشاف في حوالي نصف الصفات مما تشير إلى أهمية اختيار السلالات للتهجين، ويجب تأجيل الانتخاب للأجيال اللاحقة.

لوحظت قوة الهجين على اساس متوسط الابوين (%MP) لجميع الصفات المدروسة، بينما لوحظت على اساس الاب الافضل (%BP) في بعض التهجينات لمعظم الصفات.

بناءً على قوة الهجين (%BP) وجد ان الهجن سخا ١ × ٣٢٢ RV، جيزة ٨٤٣ × ٣٢٢ RV، سخا ١ × مارينا كانت الأفضل من حيث المحصول والصفات ذات الصلة.