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### Inheritance Studies on Productivity and Tolerance of some Genotypes for Infestation by some Insect Pests of Peas under Sohag Conditions

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#### ABSTRACT



The present study aims to assess the variability and to clarify genetic analysis of vegetative, yield and its components traits as well as infestation of three insect pests in peas through  $6 \times 6$  half-diallel mating design under Sohag conditions. All genotypes, apart from both Boogie and Snow Wind cultivars (which resistant to the three insects), showed moderately resistance to at least one insect, with varying degrees of severity, regardless of yield, could therefore be used as in breeding programs. Two crosses, i.e., (P4 x P5) and (P4 x P6) showed highly significant desirable SCA effects and heterosis for yield along with earliness, no. of branches, stem length, pod length, pod width, no. of seeds/pod, thrips and leafminer resistance, indicating the possibility of combine each of high yield, good qualities and insect pests' resistance. Genotypes P4 x P5, P1 x P4 and P4 x P6 along with the two semi-leafless cultivars, *i.e.*, Boogie and Snow Wind are particularly noteworthy as a leading candidate for breeding programs in regions or seasons where these insects are widespread, owing to its robust resistance. Conversely, genotype Progress 9 should probably be approached with caution or avoided in breeding programs because of its significant susceptibility.

Keywords: Half diallel, heterosis, aphid, thrips, leaf miner

#### **INTRODUCTION**

Peas are utilized as food crops; they are also used as green manuring, feed, and for the manufacture of hay, haylage, silage, grain fodder, and hay flour (Smýkal et al., 2012& Davletov and Gainullina, 2021). Peas, on the other hand, are a valuable high-protein crop that is crucial for solving the crop production problem of protein. Pea seeds include a high percentage of protein (up to 36%), carbohydrate, fiber, vitamins A, B, B2, and C, as well as mineral salts that are essential for both human and animal nutrition (Burstin et al., 2015). Adding peas to agricultural animals' feed increases livestock product production while lowering costs (Davletov and Gainullina, 2021). Pea plants are subjected to attack by many insect pests, among them, Aphis craccivora (Koch.) (Hemiptera: Aphididae), Thrips tabaci Lindeman (Thysanoptera: Thripidae) and Liriomyza trifolii (Burgess) (Diptera: Agromyzidae) which cause great yield reduction (El-Roby, 2016; Hassan et al., 2016; Shalaby et al., 2021 and Sadek, 2024). Plant resistance to insect infestation is one of the most important in the choice of the suited cultivar, so, many investigators evaluated pea genotypes for insect infestation (Khan et al., 2015; Krishna et al., 2019 and Chauhan et al., 2023). Climbing plants can attach to their higher neighbors thanks to their contactsensitive, filamentous tendrils. Tendrilled legume species are cultivated as field crops, with the tendrils helping to support the crop before it is harvested. Nearly a century ago, the homeotic tendril-less (tl) mutation in garden peas (Pisum sativum) was discovered. This mutation causes tendrils to change into leaflets (Hofer et al., 2009).

Peas' diverse leaf shape gives them a special place among economically significant legume taxa. Its well-

researched genetic base offers a variety of advantageous opportunities for breeding and other practical study. One may argue that the "semi-leafless" pea cultivars exhibited the greatest degree of agronomic value, contributing significantly to the preservation and advancement of dry pea production worldwide. Less research has been done on other pea leaf forms, but it should give them more consideration, particularly if they could produce fodder and be "semi leafless" for increased productivity (Mikić et al., 2011). When the "afila" pea cultivars (AF) mutation was introduced while retaining the wild type stipules, "semi-leafless" pea cultivars were created. These cultivars outperformed "leafless" in terms of photosynthetic capacity, matching that of the wild type. This is regarded as possibly pea breeding's best accomplishment (Duparque, 1996). Interest in growing peas as a high-quality food and feed in many European countries (Mikić et al., 2006) and around the world increased because of the "afila" pea cultivars (AF) significantly improved standing ability, which decreased grain yield losses and the severity of canopy disease (Banniza et al., 2005). Currently, over 95% of dry pea production in western Canada, over 80% in the EU, and over 30% in Russia comes from "semi-leafless" pea cultivars. Considering climate change, emphasis should be placed on hybridization to produce high-yielding, high-quality vegetables. Finding genetically superior parents is a crucial precondition for the formation of elite strains. The most crucial and effective method for selecting the ideal parents for hybridization programs is the combining ability analysis.

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Specific combining ability (SCA) describes instances where certain hybrid combinations exhibit performance levels that are significantly higher or lower than what would be anticipated based on the average performance of the parent

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lines involved. In contrast, general combining ability (GCA) refers to the overall average performance of a genotype across multiple hybrid combinations. SCA is largely influenced by non-additive genetic effects such as dominance, epistasis, and genotype-by-environment interactions, whereas GCA primarily results from additive genetic effects and additive × additive interactions. In plant breeding, the diallel cross method is widely employed to investigate the genetic behavior of parental genotypes, assess heritability, and evaluate combining ability. (El-Saadoown et al., 2017 and Muthoni and Shimelis, 2020). The diallel cross method also enables breeders to investigate the genetic behavior of traits in the first filial generation (F1). According to Ceyhan et al. (2014) and Gami et al. (2020), this approach is among the most efficient tools for identifying parental superiority and understanding the quantitative inheritance of various traits. Estimating the general combining ability (GCA) of each parent plays a crucial role in identifying superior genotypes with significant specific combining ability (SCA) effects, which are essential for evaluating hybrid performance in diallel crosses. Generally, successful breeding for insect resistance in host plants depends on effectively utilizing the genetic diversity available within cultivars, such as the leafless pea varieties. Accordingly, the current study aims to evaluate the genetic variability and conduct a comprehensive genetic analysis of vegetative growth, yield-related traits, and the degree of infestation by three insect pests in pea plants using a  $6 \times 6$  half-diallel mating design under the environmental conditions of Sohag.

#### **MATERIAL AND METHODS**

This study was carried out over two consecutive winter seasons, 2022/2023 and 2023/2024, at the Experimental Farm of the Shandweel Agricultural Research Station, located in Sohag Governorate, Egypt. During the 2022/2023 season, six parental lines (listed in Table 1) were used to generate a  $6 \times 6$  half-diallel set of crosses. The seeds of six parents and their 15 F<sub>1</sub>'s were sown on 15<sup>th</sup> November during winter season of 2023/2024 in a randomized complete block design (RCBD) with three replications. Each of the parents and their F1's hybrids were represented by three rows per plot. The long of the row was three meters, spaced 60 cm and plants spaced 20 cm within each row.

Table 1. Description for growth habit, seed texture, flower color and leaf shape of the six parental genotypes

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Parental	Stem	Dry seed	Flower	Leaf	Source
genotypes	length	texture	color	shape	Source
P1- On Ward	Tall	Smooth	White	Normal leaf	Hort.R.I*
P2- Progress 9	Tall	Wrinkled	White	Normal leaf	Hort.R.I
P3-Master Hindy	Short	Wrinkled	White	Normal leaf	Hort.R.I
P4- Balmoral	Medium	Wrinkled	White	Normal leaf	Hort.R.I
P5-Boogie	Medium	Wrinkled	White	Semi-leafless	Hort.R.I
P6- Snow Wind	Tall	Smooth	White	Semi-leafless	Hort.R.I
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Hort.R.I\*: Horticulture Research Institute, Giza, Egypt

All cultural practices were done as in the commercial production of pea with no insecticidal treatments during the whole study period. At the green harvesting time, samples of 10 random plants in one of the rows within plot were chosen to determine the studied characters.

#### Plant recorded traits

• Flowering date (FD): It was recorded as number of days from planting date to 50% of the plants had the first flower open in plot

- Number of branches/plant (NB/P): at the end of each season, samples consisted of 10 plants were randomly taken from each plot to determine them.
- Stem length (SL): it was the average of measurements taken from cotyledonary node to the top of the main stem (cm) of the randomly sampled plants per plot.
- **Pod length (PL)**: it was measured as the mean length (cm) of random ten pods/plot harvested at the suitable green consuming time.
- **Pod width (PW)**: it was measured as the mean width (cm) of random ten pods/plot harvested at the suitable green consuming time.
- Number of seeds per pod (NS/P): it was counted at fresh harvesting time, samples consisted of 20 pods were randomly taken from each plot.
- 100-Green seeds weight (100-GSW): it was calculated as an average weight (gm) of 100 green seeds/plot.
- Shellout percentage (SP): by dividing the weight of seeds per pods by the weight of the whole pods as average of randomly sampled pods multiplied by 100.
- Fresh pod yield/plant (FPY/P): it was estimated as an average weight (gm) at fresh harvesting time.

#### Insect recorded sampling:

The sampling was started after 15 days from sowing date (from first plant emergence) and continued at weekly interval to the harvesting time. Each sample was consisted of 10 leaves taken randomly per plot. In early morning, the chosen leaves were examined in the field and the number of adult and nymphs of thrips were recorded. After that, leaves were picked and transferred in polyethylene bags to laboratory in the same day, the numbers of mines due to leafminer and aphid individuals were counted. **Statistical Analysis:** 

The genetic analyses were based on the diallel Method 2, model 1 proposed by Griffing, (1956). The GCA and SCA mean squares' determination and their outcomes with significance were according to p values (P = 0.05 = significant, P = 0.01 = highly significant). The heterosis (H) was calculated as the percentage of difference between the  $F_1$  mean and the mean of mid parents (M.P) and mean of the

better parent (B.P), as follows. Heterosis M.P.  $\% = ((F_1 - M.P)/M.P) \times 100$ 

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Heterosis B.P. \% = ((F_1 - B.P) / B.P) \times 100
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Data of the three Insects infestation along with NB, SL, NSP, 100-SW and Fresh pod yield/plant (FPY/P) obtained were analyses using principal component analysis in Statistics Kingdom, 2017 (web-based, http://www.statskingdom.com).

To assess the genetic relationships among the genotypes, cluster analysis was performed using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA), based on Euclidean distance as a measure of similarity.

#### **RESULTS AND DISCUSSION**

#### Variances and means:

Table 2 showed the mean values for all studied traits and pests of parents and their fl hybrids. The highest values for fresh pod yield were found in the P4 x P5, P2 x P5, P3 x P4 and P3 x P5 genotypes (365.73, 364.79, 357.60 and 351.36 g), respectively. The earliest genotype was recorded by P3 P6 genotype (45 day), while Progress 9 (P2) was the latest genotype (66 day) in flowering date. Among the genotypes, P1 x P2 hybrid showed the highest values for no. of branshes and stem length while P2 x P3 hybrid was the longest pod (11.83 cm). The highest aphid infestation was observed in P1 x P3 (38.79 aphid/ 10 leaves) hybrid, followed by the crosses P1 x P4, P2 x P3, P1 x P2, and P1 x P5 as well as Master Hindy, Balmoral and On Ward cultivars with no significant differences between them. However, the lowest aphid number was recorded in the two semi-leafless cultivars, *i.e.*, Boogie (28.71 aphid/ 10 leaves), and Snow Wind (30.92 aphid/ 10 leaves) followed by both hybrids P3 x P5 and P5 x P6 with no significant differences between them. As for thrips infestation, the highest mean number was detected in P1 x P5 hybrid (29.96 thrips/ 10 leaves), followed insignificantly by P1 x P3, P3 x P5 and P1 x P4 hybrids, on opposite, the two semi-leafless cultivars, *i.e.*, Boogie (7.94 thrips/ 10 leaves) and Snow Wind (9.71 thrips/ 10 leaves) recorded the lowest infestation followed by both hybrids P4 x P6 and P 5x P6 with no significant differences between them. In regard of leafminer infestation, P1 x P3 (9.13 mines/ 10 leaves) showed the highest infestation rate, followed insignificantly by P2 x P4 and P1 x P4 hybrids as well as Balmoral and Progress 9 cultivars. While the two semi-leafless cultivars, Boogie (0.96 mines/ 10 leaves) and Snow Wind (1.09 mines/ 10 leaves) recorded the lowest infestation followed by the hybrid P5 x P6 with no significant differences between them. Therefore, the two semi-leafless cultivars, *i.e.*, Boogie and Snow Wind as well as the hybrid P5 x P6 appeared as the most resistant genotypes against the three insects' infestation.

Table 2. Mean performance of 6-parents genotypes and F1's hybrids of peas for studied traits and pests.

FD	NB/P	SL	PL	PW	NS/P	100-GSW	SP	FPY/P	Aphid	Thrips	Leaf miner
54	3.80	97.07	8.37	1.35	6.2	40.14	37.95	141.66	37.58	17.46	4.69
62	5.10	108.20	9.70	1.59	6.8	41.86	44.75	285.64	37.54	24.81	7.48
49	4.31	78.77	10.02	1.30	7.7	41.00	45.65	242.02	38.79	29.15	9.13
54	3.90	97.70	8.72	1.27	7.7	41.50	51.58	332.75	38.71	27.23	8.48
50	4.30	95.20	8.71	1.35	7.5	35.80	48.22	266.59	37.36	29.96	4.75
55	4.07	93.21	9.58	1.55	6.1	40.88	40.12	228.88	36.42	15.23	6.11
66	3.47	100.43	10.12	1.60	6.6	48.06	37.82	181.18	35.19	18.69	8.73
58	4.14	92.00	11.83	1.56	7.8	46.71	47.32	349.17	37.69	21.63	6.90
60	3.80	100.60	10.06	1.60	7.0	37.14	45.41	278.38	34.15	25.94	8.96
59	4.30	89.86	10.92	1.62	7.2	41.67	50.26	364.79	33.42	23.50	6.13
57	4.00	96.70	11.19	1.72	6.2	48.80	42.22	324.89	33.65	20.60	8.00
48	2.47	69.30	9.82	1.19	8.2	35.08	47.86	158.69	38.42	18.50	7.86
53	3.40	82.30	11.11	1.27	9.5	48.30	50.59	357.60	36.17	24.04	6.90
50	3.80	72.50	10.88	1.34	8.9	61.20	52.25	351.36	33.11	29.02	4.48
45	3.70	87.80	11.13	1.54	7.8	61.20	49.50	243.80	36.06	18.69	6.48
63	2.77	85.12	8.22	1.17	7.2	37.06	49.16	162.95	37.65	20.94	8.79
50	4.22	94.54	9.48	1.50	8.2	42.58	50.22	365.73	35.59	14.75	4.59
51	4.20	96.10	9.97	1.58	7.5	46.10	48.58	270.48	35.54	11.96	4.34
51	2.83	73.77	8.59	1.20	7.7	39.00	47.78	170.14	28.71	7.94	1.09
49	3.80	74.80	9.82	1.54	6.9	51.90	48.70	198.87	33.31	12.67	2.81
46	2.47	84.18	10.12	1.73	5.6	35.14	36.25	89.56	30.92	9.71	0.96
1.69	0.09	3.29	0.11	0.04	0.13	1.65	2.34	6.66	3.30	9.60	2.26
2.26	0.11	4.40	0.15	0.05	0.18	2.21	3.14	8.92	4.41	12.84	3.03
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$49.50$	54 $3.80$ $97.07$ $8.37$ $1.35$ $6.2$ $40.14$ $37.95$ $141.66$ $37.58$ $62$ $5.10$ $108.20$ $9.70$ $1.59$ $6.8$ $41.86$ $44.75$ $285.64$ $37.54$ $49$ $4.31$ $78.77$ $10.02$ $1.30$ $7.7$ $41.00$ $45.65$ $242.02$ $38.79$ $54$ $3.90$ $97.70$ $8.72$ $1.27$ $7.7$ $41.50$ $51.58$ $332.75$ $38.71$ $50$ $4.30$ $95.20$ $8.71$ $1.35$ $7.5$ $35.80$ $48.22$ $266.59$ $37.36$ $55$ $4.07$ $93.21$ $9.58$ $1.55$ $6.1$ $40.88$ $40.12$ $228.88$ $36.42$ $66$ $3.47$ $100.43$ $10.12$ $1.60$ $6.6$ $48.06$ $37.82$ $181.18$ $35.19$ $58$ $4.14$ $92.00$ $11.83$ $1.56$ $7.8$ $46.71$ $47.32$ $349.17$ $37.69$ $60$ $3.80$ $100.60$ $10.06$ $1.60$ $7.0$ $37.14$ $45.41$ $278.38$ $34.15$ $59$ $4.30$ $89.86$ $10.92$ $1.62$ $7.2$ $41.67$ $50.26$ $364.79$ $33.42$ $57$ $4.00$ $96.70$ $11.19$ $1.72$ $6.2$ $48.80$ $42.22$ $324.89$ $33.65$ $48$ $2.47$ $69.30$ $9.82$ $1.19$ $8.2$ $35.08$ $47.86$ $158.69$ $38.42$ $53$ $3.40$ $82.30$ $11.11$ $1.27$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

FD: Flowering date, NB/P: number of branches/plant, SL: stem length, PL: pod length, PW: pod width, NS/P: number of seeds/pod, 100-GSW: 100green seeds weight, PS: shellout percentage and FPY/P: fresh pod yield plant.

The results presented in Table (3) showed that the differences among pea genotypes were highly significant for all evaluated traits and for two of the three insect pests, with the exception of aphid infestation.

 Table 3. Mean squares 6-parent genotypes and F<sub>1</sub>'s hybrids of peas for all studied characters.

S.O.V.	Genotypes	GCA	SCA		GCA/SCA
DF	20	5	15	40	-
FD	100.99**	347.95**	18.66**	1.03	2.46
NB	1.32**	1.58**	1.24**	0.003	0.16
SL	339.55**	1,049.9**	102.73**	3.953	1.32
PL	3.08**	8.14**	1.40**	0.005	0.73
PW	0.093**	0.297**	0.025**	0.001	1.54
NSP	2.674**	8.578**	0.706**	0.006	1.53
100-GSW	168.37**	121.45**	184.02**	0.903	0.082
SP	67.69**	173.7**	32.35**	1.681	0.70
FPY/P	21,082.2**	15,463.2**	22,955.2**	15.879	0.084
No. of Aphid	20.992**	64.901**	6.356	3.144	2.40
No. of Thrips	125.925**	223.223**	93.493**	9.854	0.32
No. of Leafminer	18.211**	56.698**	5.382**	0.484	1.43

Furthermore, the mean squares attributed to general combining ability (GCA) and specific combining ability

(SCA) were also highly significant across all traits. This suggests that both additive and non-additive genetic effects play a crucial role in the inheritance of these characteristics. These findings are consistent with those previously reported by Abd-Elatty *et al.*, (2010) and Hamed *et al.*, (2015).

#### Combining ability effects

#### General combining ability effects

Table 4 showed the estimation a general combining ability effects (GCA) of the parental genotypes for all studied traits and pests on pea plants. Results revealed that the best desirable GCA effects for earliness and resistance to the three studied pests were found in Boogie and Snow wind parents. The parental cultivars Progress 9, Balmoral, Boogie and Master Hindy exhibited a positive high significant GCA effects for fresh pod yield. The parental cultivar Master Hindy showed a highest significant and positive GCA effects for pod length, no. of seeds/pod and 100 green seeds weight in addition to the earliness, while Progress 9, On Ward and Balmoral exhibited highly positive and significant GCA effects for stem length.

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Given that the general combining ability (GCA) effect reflects the inherent genetic potential of a parent, primarily governed by additive gene effects, which are heritable, parental genotypes identified as strong general combiners for yield and its related traits can serve as valuable resources in varietal improvement programs. However, it is important to note that parents exhibiting high GCA effects for specific yield components may not necessarily be effective combiners for total yield. Nonetheless, such genotypes can still be utilized to enhance particular traits through crosses with superior combining parents (Abd-Elatty *et al.*, 2010).

P1 0.5 1.128** 16.43** -2.247**	<b>P2</b> 19.25** 0.750** 24.30**	P3 -9.62** -0.747** -26.78**	P4 6.50** -0.462**	P5 -6.25** -0.078**	P6 -10.37** -0.591**	LSD0.05 1.15 0.055	LSD0.01 1.53
1.128** 16.43**	0.750** 24.30**	-0.747**	-0.462**				
16.43**	24.30**			-0.078**	-0 591**	0.055	0.072
		-26 78**			-0.571	0.055	0.073
-2.247**		-20.70	6.86**	-18.39**	-2.41*	2.24	3.0
	1.689**	1.932**	-1.380**	-0.921**	0.930**	0.079	0.105
-0.156**	0.417**	-0.300**	-0.231**	-0.162**	0.435**	0.03	0.04
-1.209**	-1.215**	2.508**	1.077**	1.005**	-2.163**	0.091	0.121
-9.678**	1.887**	8.112**	-6.435**	1.542**	4.572**	1.07	1.43
-6.696**	-6.927**	6.351**	7.725**	7.920**	-8.373**	1.47	1.96
-55.94**	66.33**	27.33**	53.36**	37.30**	-128.37**	4.50	6.02
5.748**	-0.687	3.75**	2.547*	-6.921**	-4.437**	2.0	2.67
7.686**	4.896**	7.023**	1.872	-5.634**	-15.84**	3.55	4.74
1.041*	4.641**	2.643**	3.114**	-6.606**	-4.833**	0.79	1.05
	-0.156** -1.209** -9.678** -6.696** -55.94** 5.748** 7.686** 1.041*	-0.156**         0.417**           -1.209**         -1.215**           -9.678**         1.887**           -6.696**         -6.927**           -55.94**         66.33**           5.748**         -0.687           7.686**         4.896**	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

Table 4. Estimates of the effects of general combining ability of 6 parental cultivars for all studied traits and pests.

\* Significant at 0.01 level, \*\* Significant at 0.05 level.

#### Specific combining ability effects

Tables 5 present the values of specific combining ability (SCA) effects of fifteen crosses for all studied traits and the infestation rate (IR) by three insects. Results revealed that P4 x P5 cross had a desirable highly significant value of specific combining ability effects for earliness (-11.68\*\*), stem length (27.97\*\*), pod width (0.53\*\*) and no. of thrips (-12.33\*\*), while P3 x P4 cross had best highly significant values of SCA effect for pod length (3.00\*\*) and number of seeds/pod (2.86\*\*). As for number of branches the hybrid P4 x P6 expressed the highest positive significant (2.39\*\*). The P1 x P4 cross showed the highest positive significant value for shellout percentage (14.73\*\*). The highest negative significant values of the SCA effect were found as desirable SCA value (-5.97\*\*) in the cross P2 x P4 for aphid and (- 4.83\*\*) in cross P2 x P3 for leafminer infestation. P2 x P6 cross had the best SCA effects for fresh pod yield (270.25\*\*) while the highest significant and positive SCA value for 100-green seeds weight (42.30\*\*) was displayed by cross P3 x P5. About of fresh pod yield/plant, all crosses had positive substantial (P < 0.01) SCA effects except three crosses (P1 x P3, P2 x P4 and P5 x P6). As for 100 green seeds weight, seven hybrids (P3 x P5, P3 x P6, P5 x P6, P3 x P4, P1 x P4, P4 x P6 and P2 x P6) expressed positive substantial (P < 0.01) SCA effects.

The investigation showed that the cross P4 x P6 had high significant SCA in the desired direction for all studied traits except for aphid infestation. Also, the cross P3 x P6 gave high significant for earliness and other traits except the infestation of the three studied pests.

Table 5. Estimates of s			

Tuble of Estimates of specific combining ubinty cheets of the crosses for studied traits in Fi generation of									ion of pe			
Crosses	FD	NB	SL	PL	PW	NSP	100-GSW	SP	FPY/P	Aphid	Thrips	Leafminer
P1xP2	4.82**	2.15**	16.69**	-0.12	0.15**	0.79**	1.65	8.99**	80.10**	1.00	1.52	-1.48
P1xP3	-5.30**	1.28**	-20.52**	0.60**	-0.01	-0.24**	-6.98**	-1.63	-11.78	0.30	12.38*	5.46**
P1xP4	-6.43**	-0.23**	2.64	0.02	-0.17**	1.19**	8.97**	14.73**	234.40**	1.27	11.78*	3.06**
P1xP5	-5.68**	0.59**	20.38**	-0.47**	0.01	0.66**	-16.08**	4.524*	51.95**	6.67*	27.48**	1.58
P1xP6	13.45**	0.41**	-1.55	0.29**	0.02	-0.37**	-3.92*	-3.26	104.51**	1.38	-6.50	3.87**
P2xP3	2.95	1.17**	11.29**	2.10**	0.21**	0.07	-1.52	3.65	187.40**	3.44	-7.38	-4.83**
P2xP4	-7.18**	-0.15	3.42	0.11	0.25**	-0.89**	-15.7**	-3.36	-50.98**	-5.97*	10.70*	0.89
P2xP5	2.57	0.96**	-3.53	2.28**	0.24**	-0.22	-10.09**	10.87**	224.29**	1.29	10.90*	2.11
P2xP6	0.70	0.58**	1.06	1.19**	-0.06	-0.07	8.38**	3.15	270.25**	-0.50	12.41*	5.96**
P3xP4	0.70	0.14	-0.21	3.00**	-0.04	2.86**	11.98**	-1.24	225.66**	-4.37	2.89	-3.30**
P3xP5	4.45**	0.96**	-4.52	1.85**	0.11**	1.15**	42.30**	3.60	223.20**	-4.08	25.33**	-0.83
P3xP6	-6.43**	1.18**	25.40**	0.77**	0.12**	1.01**	39.37**	11.64**	65.99**	2.31	4.54	3.39**
P4xP5	-11.68**	1.94**	27.97**	0.96**	0.53**	0.43**	1.00	-3.85	240.09**	4.57	-12.33*	-0.98
P4xP6	-4.55**	2.39**	16.66**	0.58**	0.17**	1.52**	8.62**	7.497**	120.01**	1.95	-10.49*	-3.51**
P5xP6	2.20	0.81**	-21.99**	-0.32**	-0.01	-0.18	18.14**	7.66**	-78.77**	4.73	-0.87	-1.64
LSD 0.05	3.15	0.16	6.16	0.21	0.07	0.24	2.95	4.02	12.36	5.50	9.73	2.16
LSD 0.01	4.20	0.21	8.24	0.28	0.10	0.32	3.94	5.38	16.52	7.35	13.01	2.88

The cross P3 x P5 showed high significant positive for all studied traits except shellout %, stem length, no. of aphid and no. of leafminer in which the effects were insignificant desirable values. While the cross P4 x P5 recorded desirable high significant for earliness, stem length, no. of branches, pod length, pod width, no. of seeds/pod, fresh pod yield and no. of thrips. The P2 x P3 cross had high significant for pod length, stem length, no. of branches, pod width, fresh pod yield/plant and tolerance of leafminer infestation. Even though, SCA effects do not contribute much to the improvement of self-pollinating crops like peas, but high SCA effects are of interest, if they are associated to complementary genes, instead of dominance effects (Zayed *et al.*, 2005; Mousa, 2010). Thus, best crosses with high SCA are expected to generate high frequency of transgressive segregants which could be used to isolate pure lines superior in yield (Zayed *et al.*, 1999a)

#### Genetical classification of insect pests:

Table 6 displays the severity ratings of 21 pea genotypes concerning their response to insects' infestation.

The genotypes were categorized into three distinct classifications: resistant (R), moderate (MT), and susceptible (S). The two semi-leafless cultivars, i.e., Boogie and Snow Wind exhibited resistance with a low infestation severity score, suggesting significant potential for application in breeding programs focused on insects' resistance (Elsolimany and Mousa, 2025). Among the genotypes, both hybrids P1 x P4, P2 x P4 demonstrated resistance for aphid infestation as well as each of P1 x P4, P4 x P5 and P4 x P6 for thrips, whereas both later genotypes (P4 x P5 and P4 x P6) in addition to P2 x P3, P3 x P4 exhibited resistance for leafminer, suggesting significant potential for application in selection breeding programs in segregation generations. Our results are similar with the finding of Omar et al., (2023) who screened 50 pea germplasm for resistance to pea leaf miner. The low infestation observed in semi-leafless cultivars may be due to increase in light penetration and air flow through the plant canopy and reducing the relative humidity. In semi-leafless cultivar the leaf area was reduced because the leaflets transformed into tendrils (Grevsen, 2003). All genotypes,

Table 6. Classifications of genotypes

apart from both Boogie (P5) and Snow Wind (P6) cultivars (which resistant to the three insects), showed moderatly resistance to at least one insect, with varying degrees of severity. This suggests that, although not highly resistant (regardless of yield), they exhibit a degree of tolerance to the insect and could therefore be used as in breeding programs. Both genotypes P2 x P6 and P1 x P6 as well as M.H, Balmoral and Progress 9 cultivars) were identified as susceptible for leafminer (Table 6), both P3 x P5 and P1 x P5 for thrips as well as both On Ward and Progress 9 for aphid. In contrast, genotype Progress 9 exhibited the greatest vulnerability to two insects, which categorizes it as highly susceptible. Genotypes P4 x P5, P1 x P4 and P4 x P6 along with the two semi-leafless cultivars, i.e., Boogie and Snow Wind are particularly noteworthy as a leading candidate for breeding programs in regions or seasons where these insects are widespread, owing to its robust resistance. Conversely, genotype Progress 9 should probably be approached with caution or avoided in breeding programs because of its significant susceptibility. This information is essential for directing future breeding initiatives focused on creating pea cultivars that are resistant to these insects.

tom	Infestat	tion rate and yie	ld	Sca,gca effects				Donco	ŀ	Resistance status		
Item	Low	Med	High	Aphid	Thrips	sL-M	Y	Per se	S†	MT	R	
P4 x P5 P4 x P6		Thr., LM	Aph., yield	NS	_*	-NS _**		365.7 270.5	-	Aph.	Thr., LM	
P3 x P5		Aph., LM	Thr., Yield	-NS	**	-NS		351.4	Thr.	Aph., LM	-	
P3 x P4 P2 x P3		Thr., LM	Aph., yield	-113	NS -NS	_**		357.6 349.2		Aph., Thr.	LM	
P1 x P4		-	Aph., Thr., LM, Yield	NS		**	**	332.8	-	LM	Aph., Thr	
P2 x P6	-	Aph., Thr.	LM, yield	-NS	*			324.9	LM	Aph., Thr.		
P2 x P5		Aph., Thr., LM	yield	NC		NS		364.8			_	
P1 x P2		Aph., Thr.	yield, LM	NS	NS	-NS		285.6	-	Aph., Thr., LM		
P1 x P3		yield	Aph., Thr., LM		*	**		242				
P2 x P4 P1 x P5		Aph., Thr. LM	LM, yield Aph., Thr., yield	_* *	**	NS	_** **	278.4 266.6	Thr.	Thr., LM Aph., LM	Aph.	
P3 x P6		Thr., LM, Yield	Aph.		NS	**	• •	243.8	-	Aph, Thr., LM		
P5 x P6 P1 x P6	yield -	Aph., Thr. Thr., LM, Yield	LM, Aph.	NS	-NS	NS	-***	198.8 228.8		1 / /		
M.H (P3)		Thr.	Aph., LM	-NS	**	*:	*	158.6	LM	Aph., Thr	-	
Balmoral (P4)	vield		-	*	*	*	ale ale	162.8				
On Ward (P1) Progress 9 (P2)	<i></i>	Thr., LM Thr.	Aph. Aph., LM	*	*	**	_** **	141.6 181.2	Aph. Aph., LM	Thr., LM Thr.		
Boogie (P5)	Aph., Thr., LM, Yield		• /		_**		• • •	170.2	• /		Aph.,	
	Aph., Thr., LM, Yield		-				_**	89.6	-	-	Thr., LM	

NS, \*\*: non-, significant, highly significant at 0.05 and 0.01 probability level, respectively; † S: susceptibility, MT: mediate tolerance, R: resistance, LM: leafminer, Aph: aphid, Thr: thrips

#### **Divergence Analysis**

# Contribution of the Component Characters to Genetic Diversity:

Multivariate analysis was performed on the data to examine and analyze the genetic correlations between genotypes. In addition to insect pests such as aphid, thrips, and leafminer, the quantitative parameters that made up the variance include NB, SL, NSP, 100-GSW, and FPY/P. Table 7 displays the percentage that each quantitative variable contributed to the overall variation within each Principal Component (PC) axis. Given that three of the components had Eigenvalues greater than 1.0, they were significant when considering the genetic diversity across all genotypes. According to reports, this method is crucial for choosing field pea genotypes that are resistant to infestation and have excellent yields (Ajmal *et al.*, 2017). The variations in the quantitative characters contributed significantly (Eigen vector  $\geq 0.2$ ) to the variation within each of the four PC-axes as 39.35, 23.15, 16.93 and 7.68% for PC1, PC2, PC3 and PC4, respectively. The cumulative proportion of variation explained by the first four PC-axes, 87.11% (Table 7) compared well with observations made by Campos *et al.* (2005) and Ogunbayo *et al.* (2005) that the PC-axes contributed 76.62 and 64.5% variations, respectively. In that order, the PC1 was associated with high positive loadings for thrips, FPY/P, leafminer, NB, and aphid. Regarding PC2, the variables with the most positive loading were NSP and 100-green seeds weight, in that order. On the other hand, this component showed negatively loaded leafminer and stem length. With NB and SL variables in their order and substantial positive loading, the third component (PC3) provided 16.93% of the variability, whereas aphid and

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leafminer variables contributed negatively. The fourth component (PC4), which accounted for just 7.68% of the overall variation, received polarized values from 100-GSW (0.781), leafminer (0.356), and FPY/P (-0.347), according to the dispersion graphic. These genotypes which are common in more than one PCs are indicated that selection of genotypes from these PCs is useful in further crop improvement program. These findings are also confirmation with Ojo *et al.*, (2012) and Amrita *et al.*, (2014).

Table 7. Principal component analysis (PCA) of 8 traits among pea genotypes, Eigen values, percentage variability explained by first four components

	Vector1	Vector2	Vector3	Vector4
NB	0.407*	-0.104	0.484*	-0.128
SL	0.269	(-0.497*	0.375*	0.008
NSP	0.198	0.591*	-0.255	-0.285
100-GSW	0.120	0.474*	0.341	0.781
FPY/P	0.418*	0.301	0.300	-0.347
Aphid	0.384	-0.206	(-0.407*	0.176
Thrips	0.465*	0.062	-0.223	-0.122
Leafminer	0.413*	-0.177	(-0.371*	0.356
Eigen value	3.1479	1.8519	1.3545	0.6147
% of Variance	39.3487	23.1491	16.9315	7.6839
Cumulative (%)	39.3487	62.4978	79.4294	87.1132

Interestingly, the variables in the first principal component that are closest to one and have the greatest values indicate that these axes basically quantify the qualities that are associated with infestation rates and fruit output. It is also advised that the criteria provided for the two primary components be employed as techniques of selecting parents in breeding programs because they would greatly boost plant resistance and productivity, as seen in the scatter plots (Figure 1). As a matter of fact, the variables identified for the two major components have proven to have a significant potential for genotype discrimination. However, the research and the genetic makeup of the materials employed determine how much each component contributes as well as the environmental conditions. The magnitudes for each associated eigen vector for the principal component that takes each vector's biggest element as unity are shown in Table 7.

These factors, according to Jeffers, (1967), could be interpreted as the proportional weight given to each major variable and component, including all of those with strong positive and negative values. The biplot shows how the traits being studied contribute to total variance and how genotypes are grouped according to their trait profiles. Traits with modest angles between dimension vectors in the same direction exhibit a high correlation when it comes to genotype differentiation (Mwadzingeni *et al.*, 2016).

The results of this study showed that FPY/P and each NB, 100-GSW, and NSP were positively and significantly correlated with leafminer, as were aphid and thrips. Genotypes with superior performance in each trait were plotted closer to the vector line and farther in the vector's direction; for example, 1x3 and 1x4 are heavily infested with the three pests-aphid, thrips, and leafminer; 3x6 has a high number of branches and a 100-green seeds weight; and 4x5 showed the highest FPY/P.

#### In general, Fig.1 illustrated that:

- First and second quadrants represent high yield, where above the line is highly infested with aphid and below the line are genotypes with average leafminer infestation.
- The third quadrant is moderately resistance to at least two pests along with low yield.

 Around the center is moderately resistance infestation for aphid with high yield, i.e., 2x5, 2x6, 4x5 and 4x6.

 The third and fourth quadrants also includes the two far points of the Boogie and Snow Wind varieties, which are low yielding and very low infested with all three insects.

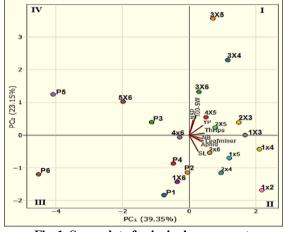


Fig. 1. Scree plot of principal components

Figure 2 presents the clustering diagram generated by cluster analysis. In general, it shows two large classes contain six groups were formed, interestingly, the distribution of genotypes by the clustering diagram was comparatively consistent with the aggregation of these genotypes obtained using the Cluster classification (Table 6) and along two axes in the PCA graph (Fig. 1).

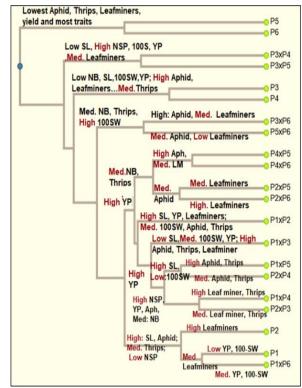


Fig. 2. Dendrogram of 21 pea genotypes based on 8 morpho-agronomic traits including three insect pest's relations using Euclidean distance matrix (The dendrogram represent clusters (1,2,3,4) =2 genotypes each, cluster 5=10 genotypes, cluster 6 =3 genotypes).

YP: Yield/plant, SL:stem length, NSP: no. of seeds/pod, NB: no. of branches, 100-SW: 100-green seeds weight, LM: leafminer, Aph: aphid, Thr: thrips

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Comparing the performance of the cross combinations based on mean yield and desirable heterotic response as well as SCA effects of crosses along with GCA effects of the parents were done to identify the most important 4 crosses yield, infestation resistance and other traits. The best crosses, which classified based on these parameters, are shown in Table 8. Again, as mentioned in Table 5, crossing potentiality between specific parents were detected by estimating SCA (specific combining ability) effects of each  $F_1$  cross combination for all studied traits. 12 out of 15 crosses exhibited significant positive SCA effects for fresh pod

yield/plant (FPY/P). Six out of these 12 crosses exhibited significant desirable heterosis effects for at least one pest (Table 9). Four out of these six crosses namely: (P3 x P4), (P3 x P5), (P4 x P5) and (P4 x P6) exhibited significant SCA effects for PL and NSP as well one or more of the three studied insect pests. Two out of these four crosses, i.e., (P4 x P5) and (P4 x P6) showed highly significant desirable SCA effects for FD, NB, SL, PL, PW, NSP, thrips and leafminer resistance, indicating the possibility of combine each of high yield, good qualities and insect pests' resistance.

Table 8. The best crosses chosen for fresh pod yield based on mean performance, heterosis and SCA along with GCA effects of the involved parents

Cross	Yield	Heterosis over	(	Combining abil	Desirable significant sca for	
Cross —	g/p	MP	sca	gca (i)	gca (j)	other traits
P4 x P5	365.73	119.6**	240.09**	53.36**	37.30**	(a-f), j
P3 x P4	357.60	122.5**	225.66**	27.33**	53.36**	d, f, g, i, k
P3 x P5	351.43	113.7**	223.20**	27.33**	37.30**	b, (d-g), i, j
P4 x P6	270.48	114.3**	120.01**	53.36**	-128.37**	(a-h), j, k

a: FD, b: NB, c: SL, d: PL, e: PW, f: NSP, g: 100-GSW, h: SP, i: Aphid, j: Thrips and k: Leafminer

#### **Heterosis:**

Heterosis was measured as the percentage increase or decrease in  $F_1$  hybrid performance relative to the mid-parent (MP) and the better parent (BP), also referred to as heterobeltiosis.

Table 9 presents the range of heterosis values and the number of superior crosses that exhibited significant and desirable heterotic effects for each trait studied. The findings revealed that the expression of heterosis varied depending on both the cross combinations and the traits under evaluation. For flowering date, heterosis ranged from -12.3% to 23.9% across both MP and BP comparisons. A desirable negative heterosis over the mid-parent was recorded in eight F1 crosses, while only one hybrid showed a favorable BP heterosis. Regarding the number of branches (NB), heterosis ranged from 2.5% to 60.5%, with 15 crosses demonstrating positive and desirable heterosis for both MP and BP. In the case of stem length (SL), heterosis over the mid-parent varied from -5.3% to 18.9%, and from -18.9% to 12.8% over the better parent. Desirable positive heterosis over the mid-parent was noted in 12 hybrids, while 4 crosses showed favorable heterosis over the better parent. The desirable direction of heterosis for plant length (PL)-whether positive or negative-depends on the breeder's objective, such as developing shorter or taller plant types. The data indicate that heterosis for PL ranged from -5.4% to 23.1% across both midparent and better-parent comparisons. Among the 15 F1 crosses evaluated, 15 showed highly significant positive heterosis over the mid-parent, while 10 displayed similar results over the better parent.

Regarding pod weight (PW), Table 9 shows that 15 crosses exhibited highly significant positive heterosis relative to the mid-parent, and 5 crosses did so relative to the better parent. For the number of seeds per pod (NSP), heterosis ranged from -10.5% to 23.1%, with 15 crosses showing significant positive heterosis over the mid-parent and 6 over the better parent. In the case of 100-green seed weight (100-GSW), 11 crosses showed highly significant positive heterosis over the mid-parent, and 10 showed similar heterosis over the better parent. As for fresh pod yield per plant (FPY/P), heterosis values ranged broadly from 53.1% to 140% over the mid-parent and from 16.8% to 119.6% over

the better parent. All 15  $F_1$  hybrids exhibited desirable and highly significant positive heterosis under both comparisons. Similar results were obtained by Abd-Elmonem *et al.*, 2010.

Heterosis for infestation of insect pests (Table 9) varied from - 6.2 % to 30.1% for aphid, -22 to 277.4% for thrips and -17.1 to 734.8% for leafminer when all the two types of heterosis are considered. Desirable negative MP heterosis was observed in 2, 1 and 4 F<sub>1</sub> crosses for resistance of aphid, thrips and leafminer, respectively. While 2 F<sub>1</sub> crosses exhibited desirable BP heterosis for resistance aphid and leafminer.

Table 9. Range of heterosis % for studied traits and number of superior crosses showing significant desirable heterosis.

Item		No signifi superior on the l	· crosses			
	Ν	1P	В	P	мп	DD
	Min	Max	Min	Max	- MP	BP
FD	-12.3	10.0	-4.8	23.9	8	1
NB	18.7	60.5	2.5	51.8	15	15
SL	-5.3	18.9	-18.9	12.8	12	4
PL	2.7	23.1	-5.4	16.9	15	10
PW	0.7	26.4	-9.6	25.0	15	5
NSP	0.7	23.1	-10.5	15.6	15	6
100-GSW	-12.8	74.3	-22.7	74.1	11	10
SP	3.6	18.4	-7.5	18.0	15	9
FPY/P	53.1	140.0	16.8	119.6	15	15
Aphid	-6.2	12.7	-3.9	30.1	2	2
Thrips	-22.0	135.9	16.9	277.4	1	0
Leafminer	-17.1	175.5	-12.2	734.8	4	2

#### **CONCLUSION**

The findings of this study demonstrate that the pea genotypes exhibited substantial genetic variability across the majority of the evaluated traits. Cluster analysis based on key characteristics facilitated the identification of promising parental lines, which can be strategically used to obtain superior recombinants. These genotypes hold significant potential for use in future breeding efforts aimed at developing high-yielding, insect-resistant pea varieties.

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# دراسات وراثية على انتاجية وتحمل بعض التراكيب الوراثية للاصابة ببعض الافات الحشرية بالبسلة تحت ظروف سوهاج

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#### الملخص

تهدف الدراسة الحالية إلى تقييم التباين وتوضيح التطيل الجيني للصفات الخضرية والمحصول ومكونته بالإضافة إلى الإصابة بثلاث أفات حشرية في البسلة من خلال تصميم تزاوج نصف تبادلي ٦ × ٦ في ظل ظروف سوهاج. أظهرت جميع الطرز الجينية، باستثناء صنفي Boogie و Boow Wind المقاومة للحشر ات الثلاث)، مقاومة متوسطة لحشرة واحدة على الأقل، بدرجات متفاوتة من الشدة. ويشير هذا إلى أنه على الرغم من أنها ليست شديدة المقاومة (بغض النظر عن المحصول)، فإنها تظهر درجة من التحل مع الحشرة واحدة استخدامها في بر امج التربية. أظهرت أربعة تهجينات وهي (Pa x P4) و (Pa x P5) و (Pa x P4) و (Pa x P5) تأثيرات SCA معنوية للمحصول وكذلك لصفات طول القرن و عد البذور بالقرن بالإضافة إلى واحدة أو أكثر من الأفات الحشرية الثلاث المدروسة. أظهر اثنان من هذه التهجينات الأربعة، أي (Pa x P5) و البذور بالقرن بالإضافة إلى واحدة أو أكثر من الأفات الحشرية الثلاث المدروسة. أظهر اثن من هذه التهجينات الأربعة، أي (Pa x P5) و الأهمية لتاريخ الإضافة إلى واحدة أو أكثر من الأفات الحشرية الثلاث المدروسة. أظهر اثنان من هذه التهجينات الأربعة، أي (Pa x P5) و (Pa x P5) و الأهمية لتاريخ الإز هار و عدد الفروع وطول الساق وطول القرون و عرض القرون و عدد البذور / القرون ومقاومة التربيق والعامي الى المحافي العمان على من المحصول العلى واصفات الجيدة ومقاومة الأفات الحشرية. تعتبر الأسط الجينية P5 و P4 x P4 و P6 إلى و P6 x P4 وال القروق، أي Boogie و Son و Sonow جنور العلى والمحاف الجيدة ومقاومة الأفات الحشرية والمواسم التي تنتشر فيها هذه الحشر الت على نظري الفريق، أي Boogie و Son المحصول العلى والمحاف الجذوع وطول المرام التربية القرون و عدد البذور / القرون و مقاومة التربيق، عمور القراق، أي العمور Boogie و Son والمحصول العلى والمات الحشرية. تعتبر الأنماط الجينية P4 x P6 و P4 x P6 و P4 x P6 و P4 x P5 و P4 المحصول العلى والمات الجذوع وطول الموات الحول المواسم التي تنتشر فيها هذه الحشر الم المن مقوامة القوية، القورة، أور قان والي مان والمحصول العلى والمات الجيدة ومقاومة المواسم التي تنتشر فيها هذه الحشر على نظرق واسع، نظرًا المقومتها القوية. على الم والمحصو المع منطرة بلمكر خاص كمرح راك لبر ماح البوما التي