GENETICS OF TWO INSECT PESTS INFESTATION, SEED YIELD AND EARLINESS OF SOME PEA CULTIVARS UNDER DIFFERENT CONDITIONS

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ABSTRACT

Gene action, maternal effects and some other quantitative genetic parameters as well as the population density and location effects on *Phytomyza atricornis* Mg. and *Thrips tabaci* (Lind) infestation were investigated in four pea crosses, i.e., "Master x Victory Freezer", "Victory Freezer x Master", "Master x Lincolen" and "Lincolen x Master". Genetic x environment interaction and earliness were found to be affecting the infestation. The results showed that the maximum abundance of the leafminer larvae took place towards the end of January in most of the studied genotypes. Both additive and non-additive genetic variances were involved in the genetic behaviour of all the studied traits. Therefore, it is demonstrated that there are variations among the parents involved and dominant effects are present. Different types of dominance were detected in the studied crosses.

The combined analyses of variance for infestation showed the significance of locations. Generally, genotypes sustained less infestation in El-Gemmeza than Behera location by *P. atricornis* and reverse results were obtained by *T. tabaci*. The cultivar Lincolen had the lowest and highest infestation by *P. atricornis* and *T. tabaci*, respectively in both locations. It is noted that the low and/or moderate values of infestation were associated with earliness.

INTRODUCTION

Pea (*Pisum sativum* L.) is one of the most important legume crops in Egypt. It is attacked by several insects such as *Phytomyza atricornis* Mg. which causes damage in pea yield as well as *Trips tabaci* (Lind) which causes considerable damage to pea plants. Thus, improvement of pea cultivars resistant to both insects resistance together with earliness is of a great importance to breeders and farmers. Fewer genetic studies have been made on pest resistance Prasad, *et al.* (1984); Rangaih and Sehgal (1986); Sheton and North (1987); Goyal, *et al.* (1992), El-Sayed, *et al.* (1993); Padmanabhan (1994); Abd-El-Aty (1997); Mishra, *et al.* (1998); Tunc *et al.* (1999) and Fadel (2001), they reported that both insects were the major insect pests infested pea plants at different stages of development. Moreover, Waly *et al.* (1983); Maxwell and Jennings (1980) and Faris *et al.* (1997) studied the inheritance of insect resistance on different crops. However, several authors made genetical studies on earliness (Arndt, 1980 and Zayed, 1988) reported the nature of gene effects, heterosis, inbreeding depression, estimates of heritibility and its relations with the expression of trait. Since breeder practice selection in one environment and evaluated selections in another one. Therefore, evaluation of breeding materials under different environments became necessary. It is important to understand more fully the nature of genotype x environment interaction to make tests and select the most efficient genotypes. Therefore, the objective of this investigation was to study the genetic system controlling both *P. atricornis* and *T. tabaci* infestations as well as the inheritance of the days to flowering.

MATERIALS AND METHODS

The present study was conducted in two regions; El-Gemmeza (Gharbia governorate) as location (A) and Behera Governorate as location (B). Three cultivars of pea (*Pisum sativum* L.) namely Master (P_1), Victory Freezer (P_2) and Lincolen (P_3) were used. Seeds of these parental cultivars were planted in hills, 25 cm apart, on 70 cm wide rows. In 1999/2000 and 2000/01, the following crosses were produced:

- Cross 1 : Master x Victory Freezer
- Cross 2 : Victory Freezer x Master
- Cross 3 : Master x Lincolen
- Cross 4 : Lincolen x Master

Seeds of the parents, F_1 and F_2 of the above crosses were sown at both locations (El-Gemmeza and Behera Research stations, Agriculture Research center) in a complete randomized blook design with three replications in 16th October during the winter season of 2001/02 to evaluate the populations of *P. atricornis* larvae and *T. tabaci* nymphs under natural conditions of infestation. Each plot consisted of four rows of parent, a single row of F_1 and 8 rows of F_2 progenies. The row was 70 cm wide and 5 meter long (about 20 plants / row). All cultural practices were applied according to the recommendations of the Ministry of Agriculture the experiment was kept free of insecticides:

Assessments:

A- Insects infestation:

On the 7^{th} week after planting date, samples of 10 random leaves from each plant in case of parents and their F_1 progeny and from each plant (at least 45plants) in case of F_2, populations in each replicate were collected and examined weekly over 8 weeks using a binocular microscope to estimate the number of *P. atricornis* larvae and *T. tabaci* nymphs.

B-1- Flowering date as the number of days from planting date to 50% flowering.

B- 2- Dry seed yield / plant : in g.

Statistical analysis:-

The genetic analyses were carried out on entry mean basis, using the following methods:

1- Mean, standard error, coefficient of variation among genotypes were calculated according to Senedecer (1956).
2- The combined analysis and the components of variation were calculated as outlined by Little and Hills (1975).
3- Estimates of arithmatic and geometric gene action as Powers and Lyon (1941).
4- Relative potence of gene set was determined according to Smith (1952).
5- Heterosis over mid-parent (MP), over the best parent (HP) including the cross and (HP) over the best parent over all parents were calculated.
6- Inbreeding depression according to Mather and Jinks (1971) as follows:-

$$I.D. = \frac{F_2 - F_1}{F_1} x100$$

7- Heritability values in broad sense were determined using the formula:

$$h^2 = \frac{S^2 F_2 - S^2 E}{S^2 F_2} x100$$

RESULTS AND DISCUSSION

***Phytomyza atricornis* Mg infestation:**

By examination data in Table 3, it is apparent that the number of larvae/leaf of different genotypes ranged from 1.08 to 1.62 and 0.89 to 1.82 for parents in the first and second locations, respectively and from 1.23 to 1.76 and 1.38 to 2.07 for F_1 in the 1st and 2nd locations respectively with a mean value (for all genotypes, parents and F_1 crosses) of 1.46 over the both locations of study.

The combined analysis of variance for this character showed significant locations mean squares (Table 1). The results obtained from single location indicated that most genotypes sustained less infestation in location A than location B, and parent 3 had the lowest infestation in both locations. In the F_1 crosses, 1x2 and 3x1 had the lowest and moderate infestation over both locations, respectively and both 1x2 and 2x1 had the lowest infestations in the locations B and A, respectively. It is noted that the low and/or moderate values of infestation, in these genotypes, were associated with earliness (Tables 2).

Table (1): Magnitude and significance of mean squares for combined analysis of variance for both infestations, seed yield and flowering date over two locations.

S.O.V.	d.F.	Mean squares			Dry seed yield g/plant
		P. atricornis	*T. tabaci*	Flowering date	
Location L	1	0.1142**	1.1336**	1633.1**	55.620
Error (Ea)	4	0.0016	0.046	0.186	0.711
Genotype (G)	6	0.3897**	1.1721**	468.1**	7.821
GxL	6	0.2183**	3.3236**	98.6**	2.241
Error (Eb)	24	0.0012	0.0157	0.143	0.658

** Significant at 0.01% probability

Again, the variation among the two locations of study was significant, the combined analysis revealed that the effects of genotype x location interaction was statistically significant, reflecting the drastic effect of varying environments besides the differential response of genotype, in rank performance in the two locations. In other words, genotypes responded differently in rank performance in the two tested locations and significant of the G x Y interaction effect emphasizes the necessity for evaluation in more diverse environments to select for tolerance. The relative magnitudes for of the variance components (Tables 2) indicate the relative importance of the corresponding sources of variation. The values of genotype variance (σ^2g) was high in magnitude compared to error one (σ^2e) reflecting the genetic difference, among the tested genotypes for this trait. Furthermore, the value of broad sense heritability was some what low, indicating a remarkable environmental effect on this character while confirm the above results.

Table (2): Variance components, PCV, GCV and heritability % from combined analysis of variance for studied traits.

Item	*P. atricornis*	*T. tabaci*	Flowering date	Dry seed yield g/plant
σ^2g	0.029	Zero	61.6	0.82
σ^2e	Zero	Zero	73.1	1.12
σ^2gL	0.072	1.103	32.8	0.61
σ^2e	0.001	0.016	0.14	0.66
PCV %	17.6	18.5	19.5	19.5
GCV %	11.7	Zero	17.3	16.7
Heritability %	44	Zero	78.9	6.7

Genetic studies:

As shown in Tables (3 and 4), the relative potency of gene set (Table 4) confirmed the over dominance of the tolerance in the following cases; in location A, the crosses 1x2 and 2x1 while the crosses 1 x 3 and 3 x 1 exhibited the over dominance in the susceptibility direction.

In location B, only the cross 1x3 gave over dominance of susceptibility over tolerance, while all the other crosses exhibited partial dominance. The arithmetic and geometric means of the F_1 and F_2 (Table 3) in both locations were close to each other for all crosses, revealing the existence of both additive and non additive gene effects. These results, are in general agreement with those obtained by Benepol and Hall (1967). On the other hand, the F_1 and F_2 means were higher than the mid or best parent, in most combinations. This figure suggests the preponderance of non-additive type of genetic variance in the expression of this trait.

The heterotic expression for number of larvae/leaf varied with crosses investigated. The important direction of heterosis for this trait, is negative. Estimates of the three types of heterosis (Table 4) varied between –1.6% and 141.3% in both locations. Only one out of four crosses showed significant negative MP heterosis, while non of the crosses exhibited negative HP or BP heterosis. In location A, all crosses exhibited heterosis in positive direction. On the other hand, the significant inbreeding depression values ranged from –28.1 (1x3) to 41.8% (2x1) in El-Gemmeza location while only 2x1 exhibited significant negative values in Behera location. This agree with that obtained by Arndt (1980); Faris *et al.* (1997) and Zayed and Faris (1998).

Table (3): Observed and expected means of infestation for four pea crosses by both insects in El-Gemmeza and Behera locations.

Character	Location	Crosses	Observed means				Expected means			
							Arithmetic		Geometric	
			Pa	Pb	F_1	F_2	F_1	F_2	F_1	F_2
P. latricornis	El-Gemmeza (A)	1x2	1.62	1.15	1.43	1.10	1.38	1.41	1.35	1.37
		2x1	1.15	1.62	1.23	1.53	1.38	1.31	1.35	1.23
		1x3	1.62	1.08	1.76	1.13	1.35	1.56	1.31	1.47
		3x1	1.08	1.62	1.56	0.96	1.35	1.46	1.31	1.42
	Behera (B)	1x2	1.82	1.44	1.38	1.21	1.63	1.51	1.61	1.46
		2x1	1.44	1.82	2.07	1.54	1.63	1.76	1.61	1.82
		1x3	1.82	0.89	1.49	1.54	1.36	1.42	1.26	1.36
		3x1	0.89	1.82	1.47	1.35	1.35	1.41	1.26	1.36
T. tabaci	El-Gemmeza (A)	1x2	2.9	2.3	3.5	2.5	2.6	3.1	2.6	3.0
		2x1	2.3	2.9	1.8	2.8	2.6	2.2	2.6	2.2
		1x3	2.9	3.2	2.3	2.3	3.05	2.7	3.05	2.7
		3x1	3.2	2.9	1.9	3.4	3.05	2.5	3.05	2.4
	Behera (B)	1x2	1.1	1.3	2.2	1.6	1.2	1.35	1.2	1.62
		2x1	1.3	1.1	3.4	1.7	1.2	2.45	1.2	2.02
		1x3	1.1	1.4	3.7	2.2	1.25	2.48	1.24	2.14
		3x1	1.4	1.1	2.5	1.4	1.25	1.38	1.24	1.76

LSD	El-Gem.	Beh.	El-Gem.	Beh.
0.05	0.06	0.03	0.09	0.10
0.01	0.08	0.04	0.09	0.16

Trips tabaci infestation :

It is apparent from data in Table (3), that the values of nymphs/pea leaf of different genotypes ranged from 2.3 to 3.2 and 1.1 to 1.4 for parents in the first and second locations, respectively, and from 1.8 to 3.5 and 2.2 to 3.7 for F_1 in the 1^{st} and 2^{nd} locations, respectively, with a mean value (for all genotypes, parents and F_1 crosses) of 2.4 over both locations of study.

The combined analysis of variance for this character showed the significance of locations (Table 1). Results of a single location for this character indicated that, genotypes, generally sustained less infestation in location B than location A parent 3 had the lowest infestation in location B whereas, parent 2 had the lowest infestation in the location A, over both locations. Among the F_1 crosses, 3 x 1 had the lowest infestation over both locations and both 2 x 1 and 1 x 2 had the lowest infestation in the locations A and B, respectively. It is, once more, noted that the low value of infestation in these genotypes, was associated with earliness (P_1 and P_3xP_1 in Behera and P_2xP_1 in El-Gemmeza locations. The combined analysis revealed that the effects of genotype x location interaction was significant reflecting the drastic effect of varying environments besides the differential response of genotypes in rank performance in both locations. Negative genotypes variance (σ^2 g)/and σ^2L were obtained for this trait. However σ^2gL and error variance (σ^2e) estimates were large in magnitude, reflecting the great effects of genotype x location interaction. On the other hand negative genotypes variance (σ^2g) was considered to be zero, resulted in negligible value for heritability estimate, then this trait was reviewed to be strongly affected by environment.

Genetic studies:

Relative potency of genes set (Table 4) confirmed the over dominance of the tolerance to this insect in all crosses at El-Gemmeza location except the cross 1x3 which exhibited the over dominance of the susceptibility as well as the complete dominance in Behera location. The arithmetic and geometric means of the F_1 and F_2 (Table 3) in both locations were close to each other for all crosses, revealing the existing of both additive and non-additive gene effects. The ranges of the three type of heterosis are given in Table (4). The heterotic expression for number of nymphs/ pea leaf varied with extreme values ranging from -37.07% to 236.4%. Three out of four crosses exhibited significant negative (important direction) MP heterosis as well as MP heterosis and two crosses showed significant negative BP heterosis in El-Gemmeza location.

The maximum significant true heterosis in desirable direction (-21.7) was recorded for 2x1. At location B, none of the crosses exhibited significant desirable heterosis. The significant inbreeding depression values ranged from - 44% (3x1 in Behera) to 78.9 (3 x1 in El-Gemmeza) at all crosses except 1x3 which was not exhibiting any value for inbreeding depression at El-Gemmeza location. This agree with that obtained by Arndt (1980) and Faris *et al* (1997).

Table (4): Genetic parameter for infestation of four pea crosses by both insects in El-Gemmeza and Behera locations.

Character	Location	Pasqb	Heterosis %			% I.D.	Potence ratio
			Mp	Hp	Bp		
P. atricornis	El- Gemmeza (A)	1x2	9.1*	42.2**	71.8**	18.8**	-2.4
		2x1	3.0*	42.1**	63.0**	41.8**	-6.6
		1x3	39.4**	81.1**	116.1**	-28.1**	3.0
		3x1	25.5**	41.7**	68**	-21.3**	1.4
	Behera (B)	1x2	-1.6	15.4**	73.2**	-5.0	0.1
		2x1	37.1**	56.4**	141.3**	-24.1**	0.3
		1x3	24.3**	81.3**	81.3**	1.4	1.6
		3x1	7.1*	65.6**	65.6**	2.4	0.6
T. tabaci	El- Gemmeza (A)	1x2	34.6**	52.2**	52.2**	-28.6**	3.0
		2x1	-30.8**	-21.7**	-21.7**	55.6**	-2.7
		1x3	-24.6**	-20.7**	zero	zero	-5.0
		3x1	-37.7**	-34.5**	-17.4**	78.9**	-7.7
	Behera (B)	1x2	83.3**	100.0**	100.0**	-27.3**	1.0
		2x1	183.3**	209.1**	209.1**	50.0**	2.2
		1x3	196**	236.4**	236.4**	-40.5**	16.3
		3x1	100**	127.3**	127.3**	-44.0**	8.3

Flowering date:

As illustrated in Table (5), this trait significantly differed among the tested genotypes in both locations of study. Master cv. held its level of superiority in earliness of flowering time at both locations. In both locations, the ranking of the genotypes for their potential flowering date is not consistent.

In general comparison between the two locations, on the whole, data obtained clearly confirmed the superiority of the location A over B one almost in all parents and F_1 crosses except Master cv. which gave the same value in both locations.

The combined analysis of variance (Table 1) revealed that the differences between locations and the effects of genotype x location interaction were statistically significant, indicating that some genotypes differed in their number of days to flowering from location to location. Estimates of the partitioning variance components, genotypic and phenotypic coefficients of variability are presented in Table 2. The relative magnitudes of these components indicate the relative importance of the corresponding sources of variation.

F_2 populations exhibited high values of the coefficients of variability indicating that the effects of both environment and genetics were involved in the inheritance of this trait. However, transgressive segregation was observed and a tendency towards the late parent in all F_2 crosses of both locations except both crosses 1x3 and 3x1 in location A was observed. The last two crosses were close to the late parent, respectively. The observed F_2 means (Tables 5) were slightly close to arithmetic mean to the geometric one in all crosses of both locations indicating that additive gene effects were mostly important than other types of gene action. In the mean time, F_2 mean values of the all F_2 crosses in location A were found to lie between the mid-parent and the high parent values, suggesting non-additive gene action for this character. It could be concluded that both additive and non-additive gene actions were involved in the inheritance of this trait. The relative potency of gene set confirmed the partial dominance of the earliest parent in all crosses of location A and of the latest one in location B.

Data obtained on heterosis types (Table 6) indicated that the heteretic expression for number of days to flowering varied with crosses and locations. The important direction of heterosis for this trait is negative. Estimates of the three types of heterosis, regarding location A, varied between – 21.17% to 20.13%. All crosses showed significant negative MP heterosis, while none of the crosses recorded HP or BP desirable heterosis in this location. However, in location B, none of the crosses exhibited significant negative heterosis for this trait. On the other hand, the significant inbreeding depression values ranged from 28.35% to 32.4% in the location A and none of the crosses recorded significant inbreeding depression values in the location B.

Estimates of heritability in broad sense (Table 6) were high for this trait in all crosses at both locations. This may give indication that selection can be used for improving this trait. These results are in agreement with the findings of Dobhal and Ram (1981), Gupta (1982), Faris *et al.* (1997) and Zayed (1988).

Table (5): Observed and expected means for flowering date of four pea crosses in El-Gemmeza and Behera locations.

Location	Crosses	Observed means				Expected means			
						Arithmetic		Geometric	
		Pa	Pb	F_1	F_2	F_1	F_2	F_1	F_2
El-Gemmeza (A)	1x2	30.8	49.1	33.4	44.2	39.9	36.6	38.8	36.0
	2x1	49.1	30.8	32.8	42.1	39.9	36.3	38.8	35.7
	1x3	30.8	56.3	34.3	45.1	43.5	38.9	41.6	37.8
	3x1	56.3	30.8	37.0	48.4	43.5	40.2	41.6	39.2
Behera (B)	1x2	30.8	60.0	52.8	61.1	45.4	49.1	42.9	47.6
	2x1	60.0	30.8	52.6	60.7	45.4	49.0	42.9	47.5
	1x3	30.8	59.4	52.9	61.0	45.0	48.9	42.7	47.5
	3x1	59.4	30.8	52.5	60.0	45.0	48.7	42.7	47.3

LSD	El-Gem.	Beh.
0.05	11.0	13.2

Table (6): Genetic parameter for both the flowering date and seed yield of four pea crosses in El-Gemmeza and Behera locations.

Character	Location	Paxpb	Heterosis %			% I.D.	Potence ratio	h^2
			Mp	Hp	Bp			
Flowering	El-Gemmeza (A)	1x2	-19.6**	8.4**	8.4**	32.4**	-0.7	96.7
		2x1	-17.9**	6.5*	6.5**	28.4**	-0.7	94.1
		1x3	-21.2**	11.5**	11.5**	31.3**	-0.7	96.1
		3x1	-15.0**	20.1**	20.1**	30.7**	-0.5	81.3
	Behera (B)	1x2	16.3**	71.4**	71.4**	15.7	0.5	94.1
		2x1	15.9**	70.8**	70.8**	15.3	0.4	95.8
		1x3	17.4**	71.8**	71.8**	15.2	0.5	97.3
		3x1	16.5	70.5**	70.5**	14.3	0.5	96.7
Dry seed yield	El-Gemmeza (A)	1x2	6.7**	-3.4**	-3.4**	35.2**	0.1	40.1
		2x1	12.9**	-4.3**	-4.3**	32.5**	-0.3	59.5
		1x3	67.3**	33.6**	-4.7**	25.1**	-0.2	41.1
		3x1	68.4**	38.5*	-2.8*	13.6	0.5	71.3
	Behera (B)	1x2	-12.6**	-47.2**	-47.2**	-108.3**	-0.1	96.3
		2x1	31.7**	-20.5	-20.5	-34.8**	0.4	91.7
		1x3	19.6**	-27.0**	-27.0**	-55.5**	0.3	88.4
		3x1	23.7**	-24.5**	-24.5	-20.2	0.3	87.7

Dry seed yield:

As illustrated in Table (1), this character significantly differed among the tested genotypes in both locations. The combined analysis of variance revealed that the difference between locations and the effects of gxL interactions were significant, indicating that some genotypes differed in their yield from location to location.

The range of variation for seed yield in the material studied was quite large. Seed yield per plant of parents varied from 17.2 to 39 g with the mean of 30.05 g. The F_1 hybrid means were 31.05 and

24.56g in both El-Gemmeza and Behera locations, respectively which confirmed the superiority F_1-seed yield of El-Gemmeza over Behera.

The data of the F_2 generation of studies crosses in both locations (Table 7), indicated that additive and non-additive genetic variances were involved in the genetic behaviour of this trait. The F_2 distributions and the values of coefficients of variability revealed that dry seed yield was inherited in a quantitative pattern. The relative potency of gene set (Table 6) confirmed the existence of the partial dominance in the inheritance of this trait in both locations. These results are in agreement with those of Gupta (1982), Loonig (1982) and Venkateswarlu and Sengh (1982). Heterosis value, for this trait in both locations indicated that all crosses exhibited significant positive heterosis relative to the mid-parent except the cross 1x2 which showed non-significant value in the first location and significant negative one in the other location. In the mean time all crosses exhibited significant negative heterosis relative to the best parent in both locations except the cross 2x1 in Behera which showed insignificant negative value.

Table (7): Observed and expected mean dry seed yield per plant for four pea crosses in El- Gemmeza and Behera locations.

Location	Cross	Observed means				Expected means			
						Arithmetic		Geometric	
		P_1	P_2	F_1	F_2	F_1	F_2	F_1	F_2
El-Gemmeza (A)	1x2	18.9	39.0	30.9	20.0	29.0	29.9	27.2	29.0
	2x1	39.0	18.9	32.7	22.1	29.0	30.8	27.2	29.8
	1x3	18.9	17.2	30.2	22.6	18.1	24.1	18.0	23.3
	3x1	17.2	18.9	30.4	26.3	18.1	24.2	18.0	23.4
Behera (B)	1x2	19.9	36.1	19.0	18.3	21.8	20.4	16.4	17.7
	2x1	36.1	19.9	28.7	18.0	21.8	25.3	16.4	21.7
	1x3	19.9	33.9	24.8	17.9	20.7	22.7	15.9	19.8
	3x1	33.9	19.9	25.6	14.8	20.7	23.2	15.9	20.2

LSD	El-Gem.	Beh.
0.05	9.3	5.61

The maximum heterosis value, over mid-parents being in the crosses 3x1 followed by 1 x3 in El-Gemmeza location whereas in the cross 2x1 followed by 3x1 in Behera location. On the other hand the inbreeding depression was ranged from 13.65% to 35.28% with mean of 26.67% for all crosses in the first location and from –20.27% to –108.31% with mean of 54.75% for all crosses in the second location.

Results are in accordance with those reported by Dhillor and chahal (1981); Hobbs and Mahan (1982) and Ranalli (1982).

As presented in the same previously (Table 6), heritability values in broad sense were found to range from 40.1 to 71.3% in location A and from 87.7% to 96.3% in location B. High heritability value is evident in agreement with that previously reported by Lonnig (1982) and Zayed (1988). On the contrary Escriban *et al.* (1994) in bean and Helal *et al.* (2000) in cowpea reported lower estimates of broad sense heritability for seed yield. This result revealed that there was a strong to moderate effect of the environment in location A for this character. Therefore, selection may be moderatly effective in breeding for higher values of this character under El-Gemmeza conditions in the crosses 2x1 and 3x1.

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الملخص العربى

وراثة الإصابة الحشرية والمحصول والتبكير فى البسلة بمناطق مختلفة

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أجريت هذه الدراسة بمحطتى بحوث الجميزة والبحيرة لدراسة النظم الوراثية التى يمكن أن تتحكم فى صفة الإصابة بصانعات الإنفاق (ذبابة البسلة) وكذلك التربس بالإضافة إلى صفة المحصول البذرى والتبكير فى الإزهار وذلك فى بعض الهجن الناتجة من ثلاثة أباء بسلة وهم ماستر وفيكتورى فريزر ولنكولن.

وكانت النتائج كالأتى :-

١- وجدت اختلافات وراثية واضحة بين التراكيب المختلفة لكل الصفات.
٢- أظهرت حسابات فعل الجين الهندسى والحسابى وجود كل من الفعل الإضافى وغير الإضافى للجينات فى وراثة الصفات.
٣- وجد أن التفاعل البيئى الوراثى وكذلك التبكير له علاقة كبيرة بالإصابة الحشرية.
٤- عامة وجد أن التراكيب الوراثية كانت أقل إصابة بصانعات الأنفاق فى الجميزة وأن سلوكها فى البحيرة كانت متأخرة بالإصابة ووجد العكس تماما فى حالة الإصابة بالتربس فنجد أن التراكيب الوراثية تحت الدراسة أظهرت إصابة أكبر فى الجميزة عن البحيرة.
٥- أظهر الصنف لنكولن أقل إصابة من غيرة فى المنطقتين على السواء.
٦- أظهرت قياسات درجة السيادة وجود أنواع مختلفة من السيادة فى صفتى الإصابة بصانعات الانفاق أو التربس. أما صفتى الأزهار والمحصول البذرى فقد ظهر بهما السيادة الجزئية باتجاهيها.
٧- كانت أعلى قوة هجين فى الجيل الأول لكمية المحصول والإصابة بالجميزة فى الهجين ماستر x لنكولن .
٨- وجد أن الهجين ماستر x لنكولن أقل إصابة بالحشرتين فى المنطقتين واعلى محصولا من الهجين لنكولن x ماستر فى المنطقتين.
٩- من هذه النتائج يمكن إستخدام الصنف ماستر والصنف لنكولن فى برامج التربية المتقدمة للمقاومة للتربس وصانعات الأنفاق (ذبابة الفاصوليا)
١٠- أظهر الهجين ماستر x فيكتورى سلوكا مقاوما للحشرتين فى الجميزة فقط وعلى العكس فقد كان الهجين فيكتورى x ماستر مقاوما فى البحيرة وهذا يرجع للتفاعل Genotype x Environment .