

## INVESTIGATIONS ON FABA BEANS, *Vicia faba* L.

### 23- GENETIC ANALYSIS OF *Orobanche* TOLERANCE/RESISTANCE

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#### ABSTRACT

*The F<sub>1</sub> & F<sub>2</sub> generations of diallel cross among variable six lines were evaluated under Orobanche -infested and free fields to explore the genetic inheritance of resistance/tolerance of faba beans to Orobanche.*

*The studied parents could be classified into four categories for general combining ability effects. The first category included Misr 1 that has favourable GCA effects for crossing either under Orobanche infestation or -free conditions. The second category comprised L.379 and L.388, which may be favourable for inclusion in the cross-program only under Orobanche infestation. The tolerant cv. (Misr 2) is favourable only for improving the percent of podded hosts and seed yield rather than the level of infestation as the third category. The fourth group included the two susceptible parents (Nubaria 1 and Giza 40), which seemed to be unfavourable for inclusion in cross program for improving varietal performance under broomrape conditions. Hybrids either F<sub>1</sub> or F<sub>2</sub> differed significantly from their reciprocals concerning broomrape level, seed yield under Orobanche-infested and -free fields and relative yield.*

*Both additive and dominance effects of genes were important in the inheritance of most studied traits. Over dominance effects of genes were obvious for the inheritance of SYPI and RY (in both generations), podded hosts% (in F<sub>1</sub>) and SYPF (in F<sub>2</sub>). Complete dominance seemed to control the level of broomrape infestation. The rest traits exhibited less dominance effects than additive one or may be inherited as partial dominance.*

*The studied parents appeared to have different proportions of negative (recessive) and positive (dominant) alleles. The frequencies of both positive and negative alleles over all loci are existed in parental genotypes equally only for SYPI and RY (in F<sub>1</sub>). In other traits the positive and negative alleles were not equally distributed among the parents. The positive estimates of F (the mean of covariance of additive and dominance effects over the array) that recorded in podded hosts% indicated the excess of dominant alleles. Whereas, the negative F value of No O means the excess of recessive alleles conditioning infestation level. The other traits may be possessed an excess of dominant genes than recessives.*

*The correlations of parental mean performance (rY) and their order of dominance (Wr+Yr) were highly significantly negative for all studied traits except SYPF in F<sub>2</sub> generation. This indicated that dominant alleles are negative in direction for SYPI, RY, podded hosts% and NoO.*

*Highly significant environmental variances were detected for all studied traits except SYPI and RY.*

*The genes or alleles that controlling the seed yield under both conditions of investigation may be different and the proportion and nature of such alleles varied due to*

*genotype. Therefore, both yielding attributes may be handled in the breeding program independently.*

Keywords. *Orobanche resistance, Orobanche tolerance, Inheritance, Faba beans, Components of variances.*

## INTRODUCTION

Many Egyptian scientists reported the variability among faba bean genotypes to *Orobanche crenata* parasitism as reviewed by Abdalla and Darwish (2002). This variability ranged from very severe susceptible hosts to relatively more tolerant to broomrape with more or less normal development and pod set, associated with poor and late parasite development, in addition to different intermediate reactions (similar to performance of reaction to quantitative characters).

Regarding the genetic backgrounds conditioning reactions of faba bean to *Orobanche* several arguments were suggested. Cubero (1973) suggested the existence of complete dominance for resistance of faba bean to *O. crenata* over susceptibility. So, F<sub>2</sub> crosses differed between resistant and susceptible lines according to the group of complementation to which the line belongs with dependence of resistance on environmental effects. However, Cubero and Martinez (1980) found strong additive effects of faba bean resistance to broomrape, with insignificant dominance effects. The results suggested that the genetic system controlling the number of broomrape per plant gave a rather low partial dominance, with resistance being recessive. Abdalla (1982) reported that tolerance (or resistance) to *Orobanche* seems to be a quantitative trait controlled by a complex genetic system. Hernandez *et al* (1984) detected no dominance of faba beans for *Orobanche* resistance. Cubero and Hernandez (1991) found also that the most important genetic components of *V. faba* resistance to *O. crenata* is additively and environmentally dependent. Hussein (1987) pointed out that the resistance/susceptibility of faba bean to *Orobanche* may be controlled by polygenic system and the resistance is controlled by recessive genes.

Darwish (1987), Radwan *et al* (1988) and Radwan and Darwish (1991) concluded that faba host parents have different sets of genes conditioning different tolerance expressions to broomrape and that different genes govern different patterns of host/parasite reactions. Abdalla and Darwish (1994) pointed out that the genetics of faba bean host tolerance to *Orobanche* and parasitism against the host may not be a simple one.

Abd El-Halim (1994) concluded that the number of factors affecting the faba bean resistance to *Orobanche* was 10.8 pairs of gene groups in the cross R 40 × G. 402 (susceptible × tolerant) and 23.6 pairs of genes (or gene groups) in the cross Rebaya 40 × Giza 2 (susceptible × susceptible). Zayed (1995) reported that additive, dominance, over dominance, major gene and

polygenes are operating in determining number of broomrapes per faba bean host plant.

The results of Attia (1998) and Darwish *et al* (1999) pointed out that the inheritance of parasitism was not simple and recessive quantitative genes conferring resistance/tolerance may be present in both tolerant and susceptible combinations. They may contribute directly or indirectly to the expression of the tolerance/ resistance. Similar results were obtained by Darwish *et al* (2007).

Roman *et al* (2002) used 196-F<sub>2</sub> plants derived from a cross between susceptible and resistant parent to identify and map the quantitative trait loci (QTLs) controlling *Orobanche* resistance. The materials were analyzed using isozymes, RAPD, seed protein genes and micro satellites. F<sub>3</sub> lines were studied for *Orobanche* resistance under field conditions. The results suggested that broomrape resistance in faba bean could be considered a polygenic trait with major effects of a few single genes.

The objectives of this work were to evaluate F<sub>1</sub> & F<sub>2</sub> generations of diallel cross among variable parental lines for *Orobanche* resistance/tolerance. The Obtained data were analyzed to determine the genetic and environmental components of variation for exploring the genetic nature conditioning faba beans reactions to *Orobanche*.

#### MATERIALS AND METHODS

Six faba bean lines developed by single seed descent for more than 2 generations under the insect-free cages were crossed in diallel cross mating design. These parents included 4 *Orobanche* tolerants [Misr 2 (P1), Misr 1 (P4), L.379 (P5) and L.388 (P6)] and two susceptible ones [Nubarial (P2) and Giza 40 (P3)]. Parents 5 and 6 belonged to the Agronomy Department, Cairo University, whereas parents 1, 2, 3 and 4 were kindly obtained from ARC.

During 2001/02 and 2002/003 seasons, all F<sub>1</sub> and F<sub>2</sub> seed combinations of diallel mating design (including reciprocals) among the six faba bean parents were obtained under the insect-free cages of the Food Legume Section, FCRI, ARC, Giza.

During 2003/2004 season, the obtained F<sub>1</sub> and F<sub>2</sub> seeds of the diallel cross combinations along with their parents were sown under each of *Orobanche*-free and infested fields at the Experimental Station of Fac. Agric., Cairo Univ., Giza. In each field a RCBD with 3 replications was used. Each parent, F<sub>1</sub> and F<sub>2</sub> was represented by one, one and two ridges, respectively. Each ridge was 3 m long and 60-cm apart and planted in one side using single-seed hills distanced 20 cm.

At harvest all plants/plot were harvested individually and the traits were recorded. At *Orobanche*-infested field, the percentages of podded hosts, the number of *Orobanche* spikes/host (No. O) and seed yield/plant, g (SYPI) were considered. Under the *Orobanche*-free trial the seed yield/plant (SYPF) was recorded individually. In both trials the means of plots were handled for statistical analysis. The relative seed yield (RY) of SYPI to SYPF was used as *Orobanche* tolerance. To nullify the effects of hybridity each group of genotypes (parents, F<sub>1</sub> and F<sub>2</sub>) was divided to corresponded means.

Arc sin and log (x +1) transformation were applied to the percentages of podded plants and the number of *Orobanche* spikes/plant, respectively prior the statistical analysis (Darwish 1991). Combining ability analyses were conducted according to Griffing (1956) method I model I (fixed model). The genetic parameters were estimated using Hayman s' approach as developed by Jinks and Hayman (1953). The notations of Mather and Jinks (1982) were used. Vr/Wr graphs were constructed according to Hayman (1954a and b) for all traits. The Vr and Wr values for each array were plotted against each other to construct the (Vr, Wr) graph.

## RESULTS AND DISCUSSION

### Analyses of combining ability

The mean squares due to GCA, SCA and reciprocals for studied traits using Method I Model I (Griffing 1956) are presented in Table (1). Highly significant differences due to each set of genotypes for all studied traits were recorded. This revealed the validity for analyzing the combining abilities. Highly significant mean squares of general combining ability (GCA) were recorded in both generations for all traits. However, the mean squares of specific combining ability (SCA) were significant for all characters except podded hosts % in F<sub>2</sub>s' and free seed yield (SYPF) in F<sub>1</sub>s'. These results proved that both additive and non-additive gene effects are operating in the heredity of most traits in both generations.

The ratio of additive ( $g_i^2$ ) to non-additive ( $s_i^2$ ) gene effects as an indication of the relative importance of both effects, exceeded the unity only for *Orobanche*-numbers in both generations (1.6 and 2.0, respectively) and SYPF (6.7) of F<sub>1</sub> hybrids. Thus, additive gene effects appeared to be predominant only for infestation levels and yield of F<sub>1</sub> under *Orobanche*-free conditions. However, the other tabulated host traits and relative yield may be more influenced by non-additive gene effects than additive ones. Consequently these traits could be upgraded by maintaining the heterozygosis among the plants of used varieties, which is useful for utilizing the non-additive effects of proper components.

**Table 1. Significance of mean squares due to genotypes, general (GCA) and specific (SCA) combining abilities and reciprocals as well as ratio of additive ( $g_i^2$ ) to non-additive ( $s_i^2$ ) gene effects for studied traits.**

| Trait   | Genotypes      |                | GCA            |                | SCA            |                | Reciprocal     |                | $g_i^2/s_i^2$  |                |
|---------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
|         | df = 35        |                | 5              |                | 15             |                | 15             |                |                |                |
|         | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> |
| Podded% | 85.3**         | 78.0*          | 49.6**         | 46.3**         | 33.8**         | 26.6ns         | 16.1ns         | 18.7ns         | 0.09           | 0.22           |
| NoO     | 0.65**         | 0.56**         | 0.96**         | 0.84**         | 0.10**         | 0.08**         | 0.09**         | 0.08**         | 1.64           | 2.03           |
| SYPI    | 611.6**        | 291.9**        | 545.4**        | 321.3**        | 246.6**        | 99.3**         | 47.3**         | 20.7ns         | 0.18           | 0.37           |
| SYPF    | 538.4**        | 568.8**        | 356.6**        | 213.4**        | 102.7ns        | 194.9**        | 197.2*         | 176.3**        | 6.67           | 0.009          |
| RY      | 0.29**         | 0.20**         | 0.22**         | 0.18**         | 0.09**         | 0.05**         | 0.06**         | 0.04**         | 0.20           | 0.67           |

Ns, \* and \*\* indicate insignificant, significant at 5% and significant at 1%, respectively.

The variances due to reciprocals were highly significant (or significant) for all traits in both generations except for podded hosts% (in F<sub>1s</sub>' and F<sub>2s</sub>') and SYPI (in F<sub>2s</sub>'). This indicated that hybrids either F<sub>1</sub> or F<sub>2</sub> differed significantly from their reciprocals concerning broomrape level, seed yield under free conditions and relative yield. The seed yield under *Orobanche*-infested field varied significantly only between both sets of F<sub>1</sub> hybrids.

General combining ability effects ( $g_i$ ) of parental genotypes in F<sub>1s</sub>' and F<sub>2s</sub>' are presented in Table (2). The studied genotypes could be classified into four categories. The first category included the parent Misr 1 which may be described as greatly favourable for improving the performance of crosses either under *Orobanche* infestation or -free conditions. The second category comprised L.379 and L.388. These lines may be favourable for inclusion in the cross-program for improving performance only under *Orobanche* infestation. The last tolerant genotype (Misr 2) is favourable only for improving the percent of podded hosts and seed yield as the third category. However, this variety may be violated to level of *Orobanche* tolerance. The fourth group included the two susceptible parents (Nubaria 1 and Giza 40), which seemed to be unfavourable for inclusion in cross programs for improving varietal performance under broomrape conditions.

**Table 2. Estimates of general combining ability effects of the parental genotypes in the F<sub>1</sub>'s and F<sub>2</sub>'s generations.**

|         | Misr 2<br>(P1) |                | Nubaria 1<br>(P2) |                | Giza 40<br>(P3) |                | Misr 1<br>(P4) |                | L.379<br>(P5)  |                | L.388<br>(P6)  |                |
|---------|----------------|----------------|-------------------|----------------|-----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
|         | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub>    | F <sub>2</sub> | F <sub>1</sub>  | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> |
| Podded% | 2.5*           | 2.0*           | -2.2**            | -2.5*          | -1.4ns          | -2.1*          | 0.1ns          | 0.8ns          | 1.6ns          | -0.2ns         | 0.4ns          | 2.0*           |
| NoO     | 0.01ns         | -0.02ns        | 0.34**            | 0.34**         | 0.35**          | 0.30**         | -0.22**        | -0.26**        | -0.18**        | -0.18**        | -0.29**        | -0.20**        |
| SYPI    | 2.6**          | -2.8ns         | -9.7**            | -1.9ns         | -7.3**          | -7.3**         | 6.4**          | 5.4**          | 3.6*           | 0.2ns          | 4.3**          | 6.4**          |
| SYPF    | 4.5ns          | 4.2*           | -4.4ns            | -1.6ns         | 5.7*            | 0.8ns          | 4.2ns          | 5.3**          | -7.0**         | -5.4**         | -3.1ns         | -3.4ns         |
| RY      | 0.00ns         | -0.09**        | 0.06*             | -0.13**        | -0.19**         | 0.15**         | 0.04*          | 0.06*          | 0.16**         | 0.05ns         | 0.12**         | 0.19**         |

Ns,\* and \*\* indicate insignificant, significant at 5% and significant at 1%, respectively.

### Components of variation in diallel

The estimates of genetic and environmental components of variation based on the analysis suggested by Jinks and Hayman (1953) for studied traits in F<sub>1</sub> and F<sub>2</sub> generations are presented in Table (3).

**Table 3. Estimates of genetic and environmental components of variation for studied traits.**

| Components and ratios                | Podded%        |                | No. O          |                | SYPI           |                | SYPF           |                | RY             |                |
|--------------------------------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
|                                      | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> | F <sub>1</sub> | F <sub>2</sub> |
| D                                    | 42.43**        | 40.08**        | 0.11**         | 0.11**         | 163.89**       | 165.26**       | 105.74**       | 148.27*        | 0.060**        | 0.050*         |
| H <sub>1</sub>                       | 51.82**        | 26.17**        | 0.10**         | 0.06**         | 451.56**       | 220.19**       | 16.10ns        | 332.12**       | 0.180**        | 0.084**        |
| H <sub>2</sub>                       | 41.35**        | 22.16ns        | 0.08**         | 0.05**         | 452.62**       | 138.96ns       | 9.58ns         | 279.19ns       | 0.180**        | 0.078ns        |
| F                                    | 40.87*         | 33.84*         | -0.07*         | -0.05**        | -12.19ns       | 135.69ns       | 26.01ns        | 148.57ns       | -0.010ns       | 0.002ns        |
| h <sup>2</sup>                       | 34.84**        | 36.54**        | 0.19**         | 0.14**         | 1461.13**      | 12.98ns        | 4.64ns         | 145.40ns       | 0.440**        | 0.044ns        |
| E                                    | 13.19**        | 15.54**        | 0.02**         | 0.02**         | 20.08ns        | 18.71ns        | 97.83**        | 55.30*         | 0.010ns        | 0.012ns        |
| H <sub>n</sub> <sup>2</sup>          | 20.36          | 41.65          | 70.63          | 76.83          | 39.65          | 68.24          | 30.09          | 37.48          | 42.23          | 60.24          |
| (H <sub>1</sub> /D) <sup>1/2</sup>   | 1.11           | 0.81           | 0.96           | 0.73           | 1.66           | 1.15           | 0.39           | 1.49           | 1.75           | 1.29           |
| K <sub>D</sub> /K <sub>R</sub>       | 2.55           | 3.19           | 0.45           | 0.50           | 0.96           | 2.10           | 1.92           | 2.01           | 0.88           | 1.03           |
| rY&(V <sub>r</sub> +W <sub>r</sub> ) | -0.96**        | -0.75**        | -0.69**        | -0.93**        | -0.99**        | -0.84**        | 0.06ns         | 0.75**         | -0.95**        | -0.64**        |
| r <sup>2</sup>                       | 0.92           | 0.56           | 0.50           | 0.86           | 0.99           | 0.70           | 0.004          | 0.57           | 0.90           | 0.41           |
| h <sup>2</sup> /H <sub>2</sub>       | 0.84           | 1.65           | 2.31           | 2.55           | 3.22           | 0.09           | 0.48           | 0.52           | 2.50           | 0.56           |
| H <sub>2</sub> /4H <sub>1</sub>      | 0.20           | 0.21           | 0.21           | 0.23           | 0.25           | 0.16           | 0.15           | 0.21           | 0.25           | 0.23           |

Ns,\* and \*\* indicate insignificant, significant at 5% and significant at 1%, respectively.

The additive genetic variance (D) was highly significant (or significant) in both hybrid sets for all studied traits. The component of variation due to the dominance effects of genes ( $H_1$ ) was highly significant for all traits in both generations, except SYPF in  $F_1$ . The component of variation arising from dominance phenotypic increment of all segregating genes ( $H_2$ ) was significant in  $F_1$  for all traits except SYPF. However, this variance ( $H_2$ ) in  $F_2$  reached to the level of significance only for NoO. This indicated that both additive and dominance effects of genes played an important role in the inheritance of most of studied traits.

The magnitude of both effects of genes varied greatly from trait to another and also among hybrid generations. The relationship between additive and dominance effects of genes could be elucidated by calculating the average degree of dominance  $[(H_1/D)^{1/2}]$ . This ratio is more than unity in both generations for SYPI and RY as well as in  $F_1$  for podded hosts% and in  $F_2$  for SYPF. This means that these traits showed over dominance. In other words, the dominance effects of genes were greater than additive ones in conditioning these traits in corresponding generations. The NoO in  $F_1$  recorded equal charging of both gene effects [or  $(H_1/D)^{1/2}=1$ ] that means complete dominance seemed to control the level of broomrape infestation. The rest cases exhibited less dominance effects than additive one, which reflected in lower degree of dominance than unity or may be inherited as partial dominance.

Comparing both dominance effects of genes:  $H_1$  and  $H_2$ , the  $H_2$  was smaller than  $H_1$  in  $F_1$  and  $F_2$  generations for all traits except SYPI in  $F_1$  (which recorded equal magnitude of both estimates). Theoretically,  $H_2$  should be equal or less than  $H_1$  (Hayman 1954b) that indicated unequal allele frequencies ( $U \neq V$ ) at all loci. This proved that the positive ( $U$ = the proportion of parents that are homozygous dominant) and negative ( $V$ = the proportion of parents that are homozygous recessive) alleles frequencies at the loci for studied attributes regarding *Orobanche* tolerance aren't equal in the studied parents. Therefore, studied parental genotypes appeared to have different proportions of negative and positive alleles.

The proportion of positive and negative genes frequencies could be explored via calculating the  $H_2/4H_1$  ratio. Such ratio measures the mean value of UV over all loci. The equal frequencies of both kinds of genes ( $U=V=0.5$ ) of all loci resulted in 0.25 of both frequencies. Results of Table (3) concerning  $H_2/4H_1$  reached the maximum value, i.e. (0.25) only in  $F_1$  for SYPI and RY. Thus the frequencies of both positive and negative alleles over all loci that are responsible of both traits existed in parental genotypes equally ( $=0.5$ ). The less obtained  $H_2/4H_1$  ratio than 0.25 in other traits indicating that the positive and negative alleles were not equally distributed

among the parents. However, the significance of  $h^2$  (dominance effects as algebraic sum over all loci in heterozygous phase in all crosses) for podded hosts%, number of *Orobanche* spikes/host in both generations and SYPI and RY in  $F_1$  generation confirmed that dominance is unidirectional.

On the other hand, the number of effective factors which showed dominance ( $h^2/H_2$ ) was estimated for  $F_1s'$  and  $F_2s'$  (Table 3). The values ranged from 0.09 to 3.22 for SYPI in  $F_2$  and  $F_1$ , respectively. It may be noted that this value is underestimated either when the dominance effects of all the genes concerned are not equal in number and direction or when the distribution of genes is correlated or when both two conditions are fulfilled (Jinks 1954).

The F letter denotes the mean of covariance of additive and dominance effects over the array. Such estimate is significant only for podded hosts% and NoO in both generations. The positive estimates of F that recorded in podded hosts% indicated the excess of dominant alleles controlling this trait. Whereas, the negative F value of NoO means the excess of recessive alleles conditioning infestation level.

The ratio of dominant to recessive genes in the parents could be explored by calculating the  $K_D/K_R$  ratio. Only the number of *Orobanche* was about 0.5, which means that the recessive genes are 2 folds as dominant ones. However, RY recorded about the unity of this ratio that means the dominant and recessive genes in the parents are equal in proportion. The other cases are greater than one which proved an excess of dominant genes than recessives.

The correlation of parental mean performance ( $r_Y$ ) and their order of dominance ( $W_r+V_r$ ) was highly significantly negative for all studied traits except SYPF in  $F_2$  generation. This indicated that dominant alleles are negative in direction for SYPI, RY, podded hosts% and NoO.

On the other hand, it is possible to predict the measurements of completely dominant and recessive parents by calculating  $r^2$ . The estimates of  $r^2$  ranged from 0.004 to 0.99 and when close to unity, the regression of  $r_Y$  on  $W_r+V_r$  exists, making it possible to predict the measurements of completely dominant and recessive parents. These predictions suggest the possible limits of selection among genes showing dominance.

Regarding to the environmental variance (E), the results showed highly significant values for all studied traits except SYPI and RY.

#### **Graphical analysis**

The graphical analysis was conducted based on the procedures suggested by Jinks (1954) and quoted from Mather and Jinks (1982).



The linear regression coefficients (b) for podded hosts% differed from zero in both generations (Fig. 1), which reflected the absence of epistasis in the inheritance of this character. The regression lines for podded hosts% determined in F<sub>1</sub>s' and F<sub>2</sub>s' being below and above the origin point, respectively. The position of array members showed that the parental genotypes rated as tolerant ones, i. e. Misr 2, Misr 1, L.379 and L.388 located nearest to the W<sub>r</sub> line, whereas the susceptible ones (Nubaria 1 and Giza 40) were far from this line. This indicates that high percentages of podded hosts are dominated over less ones.

The liner regression coefficient (b) of parasite level (NoO) differed from zero in both generations. This indicating that NoO showed over dominance in F<sub>1</sub> and partial dominance in F<sub>2</sub> generation. The position of array members on W<sub>r</sub>/V<sub>r</sub> graph varied among F<sub>1</sub> and F<sub>2</sub> generations. Such variation may be due to that F<sub>2</sub> populations comprised variable frequencies of homozygous and heterozygous combination of genes. However, the general view suggested that resistant parents, Misr 2, Misr 1 and L.379 (which parasitized by less number of broomrapes) contain recessive alleles. Whereas, the parental genotypes that possessed higher number of parasite per host: Nubaria 1, Giza 40 and L.388 may have dominant alleles. Therefore, the level of infestation distinguished the faba bean genotypes into resistant (less numbers and weak parasite per host) and susceptible parents (high numbers and vigour broomrape per host). The obtained W<sub>r</sub>/V<sub>r</sub> graph pointed out that the *Orobanche* susceptibility in faba bean may be dominant character over resistance.

The linear regression coefficient (b) of seed yield under *Orobanche* infestation (SYPI) differed from zero in both generations, which suggested the absence of epistasis. The W<sub>r</sub> intercept was below the origin, indicating over dominance in both generations. The position of the investigated faba bean genotypes on the graph indicated that both susceptible parents: Nubaria 1 and Giza 40 had recessive alleles for SYPI, while the tolerant ones, Misr 2, Misr 1, L.379 and L.388 may have principally dominant alleles for SYPI

Similar direction could be observed for seed yield under *Orobanche*-free field (SYPF) with different distribution of array members. The parents Nubaria 1, Giza 40, Misr 1 and L.379 fall near to the W<sub>r</sub> lines, but the remainders (Misr 2 and L.388) are in the recessive position (Fig. 2).

Regarding to relative yield (RY), W<sub>r</sub> intercept was below and above the origin in F<sub>1</sub> and F<sub>2</sub>, indicating over and partial dominance, respectively. The position of array members indicating Nubaria 1 and Giza 40 had recessive alleles but the tolerant parents i.e. Misr 2, Misr 1 and L.379 may have dominant alleles for RY (Fig.2).

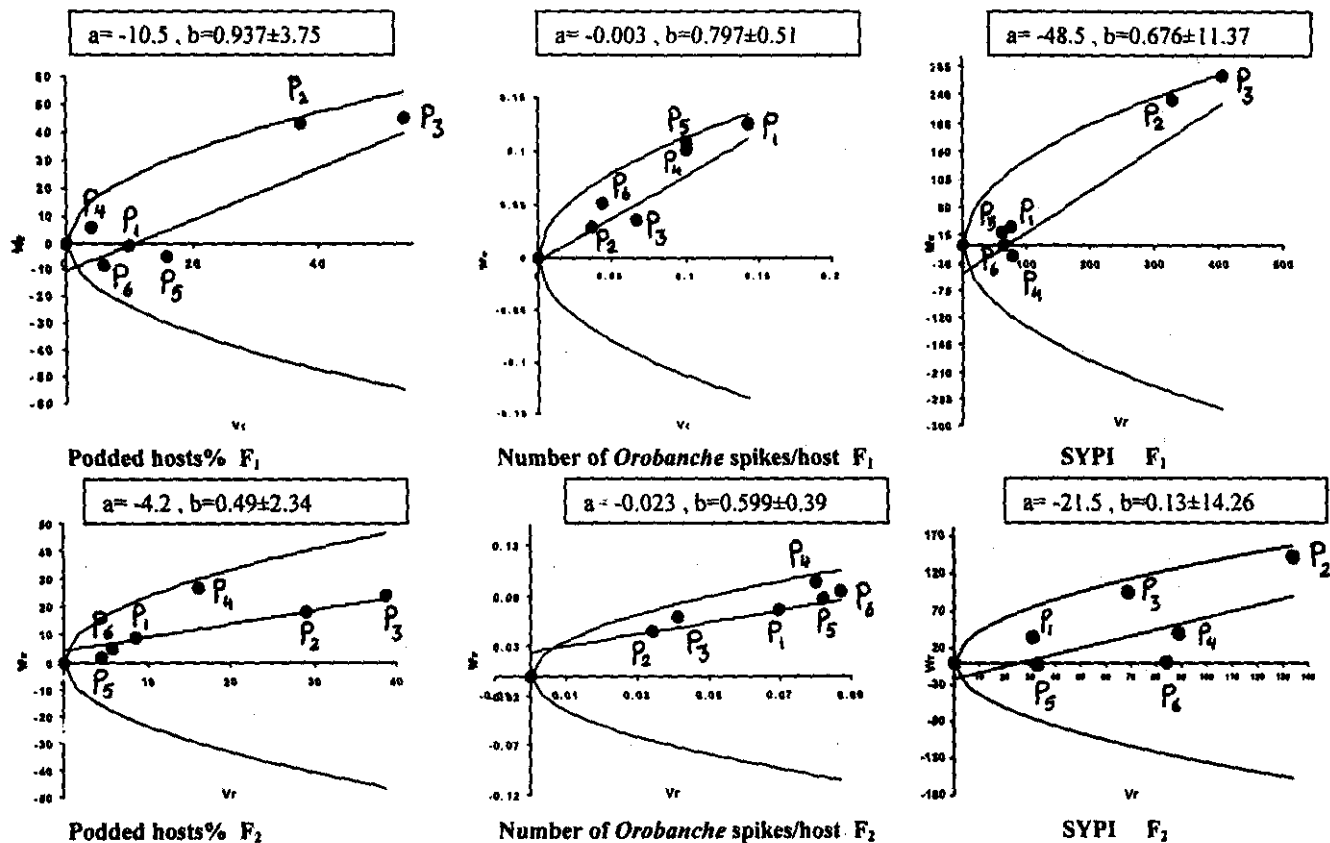
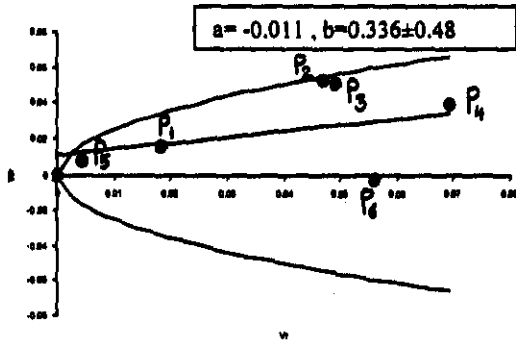
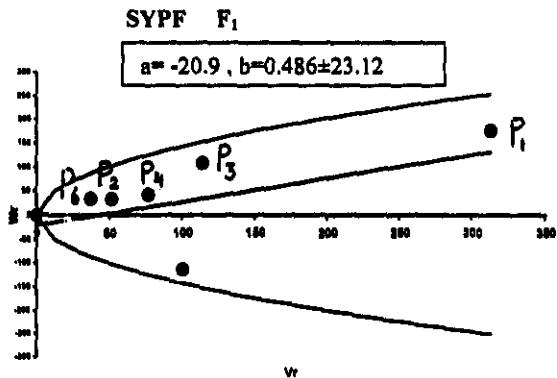
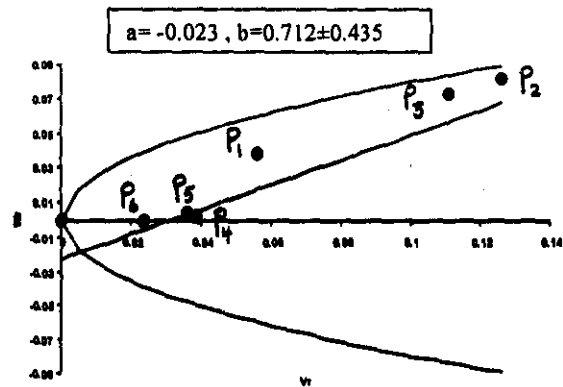
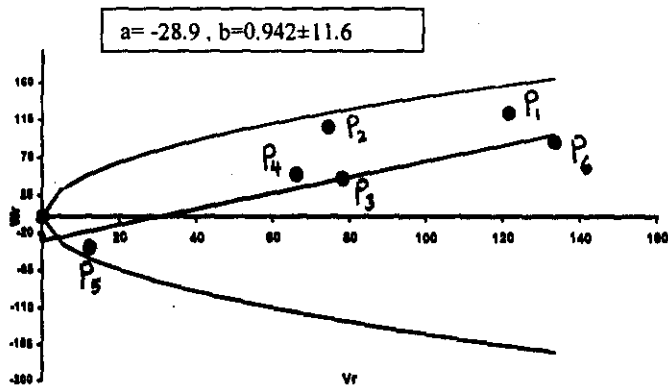


Fig. 1.  $W_r/V_r$  graph for podded plants%, number of *Orobanchae* spikes/host and plant seed yield under *Orobanchae*-infested field (SYPI) in  $F_1$  and  $F_2$  generations



**SYPF F<sub>2</sub>**

**RY F<sub>2</sub>**

Fig. 2.  $W_r/V_r$  graph for plant seed yield under *Orobanch*-free field and relative yield (RY) in F<sub>1</sub> and F<sub>2</sub> generations

The aforementioned results indicated that the genes or alleles controlling the seed yield under both conditions of investigation may be different and the proportion and nature of such alleles varied due to genotype. In other words, the parents classified as tolerant principally may contain dominant alleles for SYPI over susceptible ones. However, under the *Orobanche* conditions, Nubaria 1, Giza 40, Misr 1 and L.379 (susceptible and tolerant ones) may include dominant alleles over that existed in Misr 2 and L.388 (tolerant) for seed yield under *Orobanche*-free field (SYPF). Therefore, both yielding attributes may be handled in the breeding program independently. In other words, some parents may comprise different alleles that condition the yield ability under conditions of *Orobanche* infestations. However, the level of infestation expressing *Orobanche* resistance versus susceptibility are obviously determined in the investigated genotypes and consequently inherited and transmitted in the resultant offspring. The *Orobanche* tolerance versus sensitivity measured by yield and relative yield (RY) may be conflicted by the potential yield under free conditions which may be conditioned by different alleles that controlling seed yield under *Orobanche* infestation.

It could be concluded that crossing of different parental genotypes that having variable reactions to *Orobanche* widens the resultant combinations' performance. Generally, the *Orobanche* tolerance of faba bean was strengthened by crossing and the superior combinations enrolled in the breeding program.

The better cross combinations may be subjected to isolated intercrossing together for developing elite gene pool. Such gene pool may be used for recurrent selection program or used directly as a composite variety.

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## دراسات على الفول البلدي ٢٣- التحليل الوراثي للمقاومة/ للتحمل للهالوك

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استخدمت ستة أباء من الفول البلدي (مصر ٢، نوبلوية ١، جيزة ٤٠، مصر ١، سلالة ٣٧٩، سلالة ٣٨٨) للتهجين باستخدام الهجن الدائرية الكاملة بهدف دراسة وراثته للتحمل/المقاومة للهالوك وفي الموسم ٢٠٠٣/ ٢٠٠٤ زرعت الأباء وبنور الجيل الأول وبنور الجيل الثاني في حقل موبوء طبيعياً بالهالوك مقارنة بنظيرة الخالي من الهالوك بمحطة لتجارب الزراعية بكلية الزراعة - جامعة القاهرة .

أظهرت نتائج الجيل الأول والثاني أن الأباء المستخدمة يمكن تصنيفها إلى أربع مجموعات على حسب تأثيرات القدرة لعلمه على التآلف. والمجموعة الأولى شملت فقط الصنف مصر ١ حيث أظهر تأثيراً مرغوباً بدرجة كبيرة في تحسين إداء الهجن سواء في الأصباة بالهالوك أو عدم الأصباة به أما المجموعة الثانية (السلالة ٣٧٩ والسلالة ٣٨٨) فهي أظهرت تأثيرات مرغوبة على إداء الهجن فقط في حقل الأصباة بالهالوك أما المجموعة الثالثة فكان بها الصنف مصر ٢ الذي أظهر تأثيراً مرغوباً فقط على النسبة المنوية للنباتات المقرنه بالإضافة إلى غلة البنور في حقل الهالوك بينما الصنفان الحاصلان للهالوك نوبلوية ١ و جيزة ٤٠ فلم يكونا ذا تأثيرات مرغوبة في تحسين إداء الهجن عند الأصباة بالهالوك. كانت التأثيرات العكسية للتهجين في الجيلين معنوية لصفات مستوى الأصباة وغلة بنور النبات في الحقلين والغلة النسبية .

كانت تأثيرات الجينات المضيفة والمساعدة مهمة في وراثه غابية الصفات . إلا أن تلك التأثيرات أظهرت سيادة فاتقة لصفات غلة النبات في الهالوك والغلة النسبية (في الجيلين) والنسبة المنوية للنباتات المقرنة (في الجيل الأول فقط) وغلة النبات في عدم الأصباة (في الجيل الثاني فقط) . وأظهرت صفة مستوى الإصباة بالهالوك سيادة تامة لجينات تورثها . أما بقية الصفات فطى ما يبدو أن جينات تورثها أظهرت درجة سيادة أقل من الفعل المضيف أو سيادة جزئية .

ظهر من النتائج أن الأباء لكل المواقع لوراثته تحتوي نسب متباينة من الأليلات المساعدة والمنتحية . وكانت نسبة هذان للتوعان من الأليلات متساوية النسب فقط لصفات غلة النبات في الهالوك والغلة النسبية في الجيل الأول . أما صفة النسبة المنوية للنباتات المقرنة فأظهرت نسبة أعلى من الأليلات السائدة . بينما صفة عدد الهالوك فأظهرت إحتواء الأباء على نسبة أعلى من الأليلات المنتحية . أما بقية الصفات فربما تحتوي الأباء نسب أعلى من الأليلات المساعدة عن تلك المنتحية . كان معامل الارتباط بين إداء الأباء والسيدة على المعنوية وسالب لكل الصفات فيما عدا غلة النبات في عدم الهالوك في الجيل الثاني مما دل على أن الأليلات المساعدة كانت سلبية لإتجاه لصفات غلة بنور النبات في الهالوك والغلة النسبية والنسبة المنوية للنباتات المقرنة وعدد الهالوك .

كانت التباينات البيئية عالية للمعنوية في اداء كل الصفات فيما عدا غلة بذور الثبات في الهالوك والظلة النسبية وعلى ما يبدو فإن الاليات التي تحكم وراثه غلة الثبات في الإصابة بالهالوك وعدم الإصابة كانت مختلفة في نسب تولدها في الأباء وفي طبيعة تأثيرها وعلى ذلك فإن تداول هذه الصفة في برامج التربية تحت كلى البيئتين قد يكون مختلفاً .

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