FABA BEAN SELECTION AND INHERITANCE OF *OROBANCHE* TOLERANCE

By

TAMER SALAMA ABD-ELSALAM EL-MARSAFAWY

B.Sc. (Agronomy) Faculty of Agriculture, Zagazig University, 1996
M.Sc. (Agronomy) Faculty of Agriculture, Cairo University, 2001

THESIS

Submitted in Partial Fulfillment of the
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الى أمي رحمها الله
الى أبى واخوتي
حفظهم الله
الى زوجتي وأبنائي
أهدي جهدي
المتواضع

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CONTENTS

1.INTRODUCTION

Faba bean (*Vicia faba* L.) is the most important food legume in Egypt .It is a primary source of protein in the diet of the masses. The crop is generally included in the crop rotation and has succeeded to keep the Egyptian soil fertile and productive through nitrogen fixation. It is widely cultivated for use in both food and feed. The acreage ,s and seed yields vary from season and location to another. This is attributed to various biotic and abiotic limiting stresses. These limiting stresses include *Orobanche*, disease, pests, less favorable environments…..etc.

Broomrape (*Orobanche crenata*) is an annual plant obligatory parasitic on faba bean and other susceptible hosts in Mediterranean Area. It causes severe losses to the host and in severe cases may result in a crop failure. *Orobanche* species lack chlorophyll and thus are unable to live independently. Losses of faba bean yield due to *Orobanche* parasitism may reach 100% **(Darwish 1987 and Zaitoun 1990)**. The degree of yield losses vary according to host genotype, level of parasitism, sowing date, soil moisture and many other factors **(Nassib *et al.* 1979 and 1982, Abdalla 1982, Darwish 1987, Zaitoun 1990, Darwish 1991a, b and c, Abdalla and Fischbeck 1992b and Abdalla and Darwish 1996a and 1999).** Therefore the control of broomrape will help to improve the production and stability of faba bean yield.

The control of this parasite is more difficult due to the production of huge amounts of tiny, long-lived seeds which are dispersed by wind and other means. Also, the seeds remain alive for several years in soils until germinated by secreted stimulant/s of proper host/s **(Kadry and Tewfic 1956, Edward 1972, Hiron 1973 and Whitney 1978)**. Different methods were suggested to control *Orobanche* and/or alleviate its effects. These include cultural practices such as deep plaughuing (**Nassib *et al.* 1984)** or zero tillage, hand pulling, irrigation/flooding, crop rotation including catch or trap crops, delayed sowing date **(Darwish 1992),** fertilizers (**Van Hezewijk *et al.* 1991)**, soil solarization (**Sauerborn and Saxena 1987)**, biological control (**Hammad *et al.* 1967 and Link *et al.*1990)**, chemical control (**Khalaf *et al.* 1994),** soil fumigation, use of suicidal germination stimulants (**Johanson *et al.* 1979 and Mangnus and Zwanenburg 1991),** using tolerant host/s (**Nassib *et al.* 1979, Ibrahim *et al.*1979, Abdalla 1982, Darwish 1982, Darwish and Abdalla 1994, Khalil *et al.*1994, Abdalla and Darwish 1996b and 1998**) and integrated control (**Link and Saxena 1991 and Pieterse *et al.* 1994)**.

Majority of these methods do not offer satisfactory results to control this parasitic weed and in some regions the problem tends to be catastrophic. Breeding resistant/tolerant genotypes may provide a reliable measure of production against *Orobanche* **(Nassib *et al.* 1982, Abdalla 1982, Darwish, 1987, Radwan, *et al.* 1988a and b, Abdalla and Fischbeck 1992b, Abdalla and Darwish 1994, 1996b and 1999, Khalil *et al.* 1994 and Saber *et al.* 1999).**

The improvement of faba bean yield could be achieved by reducing susceptibility to various limiting stresses such as *Orobanche* parasite. However, the most important drawback of using resistant/tolerant genotypes may be instability of reaction among seasons and locations. This may be due to the host, the parasite, the environments and /or all of them and their interactions.

Thus the present investigation dealt with the effects of selection within different twenty four *Orobanche*-tolerant faba bean genotypes under different locations for upgrading performance across these environments. On the other hand, different faba bean genotypes have been selected for *Orobanche* resistance/tolerance. Hybrids and segregating generations were obtained after crossing resistant/tolerant and susceptible genotypes. What will be the reaction of materials to the parasite in various locations when grown under infection and free soil? Would data provide information to assist breeders for planning *Orobanche* resistance/tolerance breeding programs?

3.MATERIALS AND METHODS

3.1.Selection of faba bean for *Orobanche* tolerance/resistance:

3.1.1.Materials:

Twenty-four faba bean genotypes selected for *Orobanche* tolerance/resistance along with the susceptible variety (Giza 2) were used. The tolerant/resistant genotypes included four recommended improved cultivars and 15 selections from these varieties in addition to 5 entries selected from Egyptian landraces by Cairo University **(Abdalla and Darwish, 1999)**. Code, pedigree, and *Orobanche* reaction are presented in Table (1).

Table (1): Code, pedigree and sources of the investigated genotypes.

N	Code	Pedigree	*Oro*. reaction
1	**Giza 843**	**561/2076/85 Sakha x 461/845/83***	**Tolerant**
2	**Misr 1**	**Giza 3 x 123A/45/76(667) ***	
3	**Giza 429**	**Selection from Giza 402***	
4	**Misr 2**	**Selected from Italian materials (Yousef El-Seddik,Y.S)***	
5	**Giza 2**	**Individual selection from landraces***	**Susceptible**
6	**843/27**	**Selected families from Giza 843 in 2000/2001 season***	**Tolerant**
7	**843/34**		
8	**843/41**		
9	**843/83**		
10	**843/103**		
11	**843/180**		
12	**667/85**	**Selected families from Misr 1 in 2000/2001 season***	
13	**667/88**		
14	**667/91**		
15	**667/121**		
16	**667/124**		
17	**667/129**		
18	**667/141**		
19	**L.377/4**	**Individual selection from (Y.S)***	
20	**L.377/2**		
21	**9 HYTO**	**Individual selection from Egyptian landraces****	**Tolerant**
22	**18 HYTO**		
23	**21 HYTO**		
24	**23 HYTO**		
25	**24 HYTO**		

***FCRI: Field Crop Research Institute, ARC** ****Cairo University, Faculty of Agriculture.**

3.1.2.Methods:

The experiments were conducted under the naturally *Orobanche* infested fields in Giza-Cairo University (G.CU), Giza-Agricultural Research Center (G.ARC) and Sids Research Station (Sids) during 2001/2002, 2002/2003 and 2003/2004 seasons.

The history of chosen fields indicated highly infestation of broomrape seeds. In the 1st and 2nd seasons, the 25 genotypes were evaluated under each of the three locations. In each location, a RCBD trail with 6 replications was conducted. To avoid heterogeneous distribution of the parasite seed, small plots with more replications were used. Thus, each genotype/ selection was represented in each replication by two ridges, each 1.5 m long and 60 cm apart. The seeds were hand planted in one side of the ridge using single-seed hills with 20cm distances. Normal recommendations of faba bean practices were followed.

At harvest, the bordered plants in each plot were considered for collecting data. The harvested hosts were classified into podless and pod-bearing two categories and the number of plants/each class was determined. The number and the weight of *Orobanche* spikes/host as well as seed yield/host were recorded individually. The plot base means were considered for statistical analysis. In this analysis proper transformation, arc sin for pod-bearing plants % and log (x +1) for parasite attributes were used **(Darwish, 1991b).**

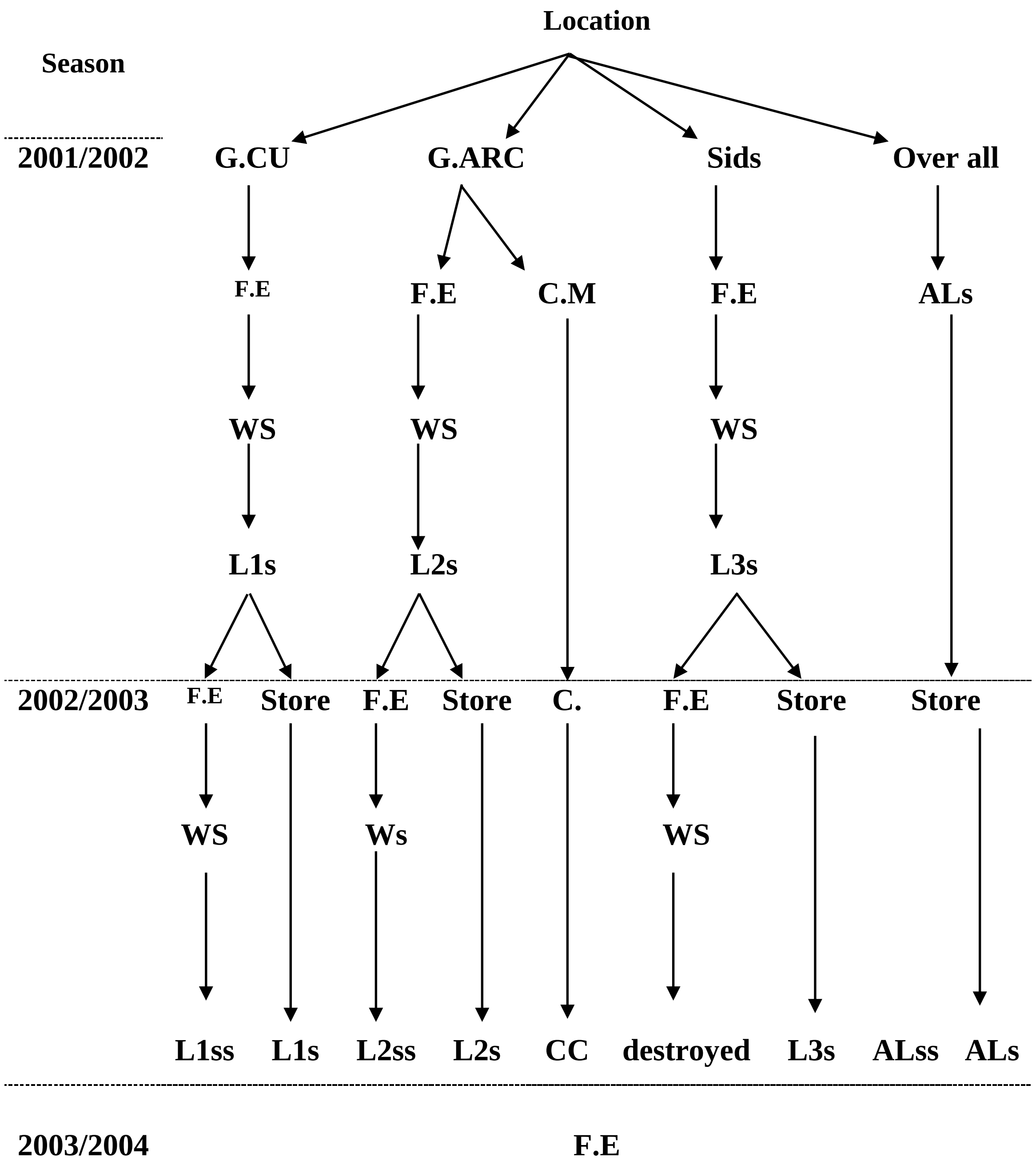
3.1.3.Selection and blending procedures

The best yield in two hosts of each genotype in each plot were considered for constructing the selected blends either in each location or across all locations in the given season (Fig.1). In this situation, under 1st season, two fixed numbers of seeds were taken from each selected plant belonged to the same genotype for composing two selected blends of the genotype for G.CU, G.ARC and Sids locations (L1s, L2s and L3s), respectively. One of these blends was used for field evaluation during the 2002/2003 season and the other one was stored for 2003/2004 evaluation season. Another 5 seeds represented each of selected plants belonged to the genotype in all locations were used for forming blend over all locations (ALs) was stored for evaluation during 2003/2004 season from G.CU (L1s) and G.ARC (L2s).

In the second season, the selected blend of each tolerant genotype harvested in each location were sown for field evaluation under the same location. The plants of Sids location were destroyed near harvest, thus selections from this trial couldn’t be obtained. Similar experimentation and selection procedures were repeated. but, the susceptible genotype (Giza 2) was sown from commercial seeds because all harvested seeds not allowed to construct any blend.

In 2003/2004 season, each single or all locations selections for one (L1s, L2s, L3s and ALs) or two (L1ss, L2ss and ALss) seasons along with the multiplicated counterparts under insect-free cage for two seasons (CC) of all investigated tolerant genotypes were evaluated under the three locations. In each location the RCBD with 3 replications in split plot arrangement was conducted. Faba bean tolerant genotypes were assigned to main plots and selected blends were distributed in sub-plots. Each sub-plot consisted of 2 ridges each 1.5 m long and 60 cm apart. Seeds were hand planted at one side of the ridge in single hills distanced 20 cm.

The sowing dates of all experiments during all seasons were during the second 10 days of November. Recommended cultural practices of faba bean production were adopted.



G.CU=Giza, Cairo University
G.ARC=Giza, Agricultural Research Center
F.E: Field evaluation
WS=Within selection
C.M=Cage multiplication
Als= All locations

Fig.(1):Sequences of experiments during 2001/2002, 2002/003 and 2003/2004 seasons

3.1.3.Data Collection

The following data were recorded:

2001/2002 and 2002/2003 seasons:

1-Number of *Orobanche* spikes /host (*Orobanche* /host):

Number of *Orobanche* spikes per plot divided on the number of plants per plot

2-*Orobanche* dry weight/host (g) (ODWT):

Dry weight of *Orobanche* spikes per plot divided on the number of hosts

3-Pod bearing hosts %(PBP):

The percentage of pod-bearing hosts to all harvested hosts per plot

4-Seed yield/host (g)

2003/2004 season:

1-Early counting of *Orobanche* /host after 95 days from sowing date (*Orobanche* /host after 95)

2-Late counting of *Orobanche* spikes/host at harvest (*Orobanche* at Harvest

3-Number of pods/host

4-Number of seeds /host

5-Seed yield/host (g)

3.1.4.Statistical analysis.

For statistical analysis number and weight of *Orobanche* spikes/plant and percentage of podded plants were transformed to log (x+1), and arc sin, respectively

In 2001/2002 and 2002/2003 seasons the recorded data of each location were statistically analyzed as randomized complete block design (RCBD). The combined analysis over locations in each season were performed.

The features of distribution of the tolerant and selected genotypes within each location and combined over locations were estimated or calculated

The genotypic and phenotypic variances (δ^2g and δ^2ph) each location and combined over locations were calculated from the pertinent mean squares expectation Table (2) as follows:

Table (2):Expectation of mean squares for the analysis of variance of data.

S.O.V	df	M.S	Expectation mean squares	
			Each location	Over locations
Genotypes(G)	(g-1)	Mg	$\delta^2_e + r\delta^2_g$	$\delta^2_e + r\delta^2_{g}l + rl\delta^2_g$
Genotype x Location	(g-1)(L-1)	Mgl	---------	$\delta^2_e + r\delta^2_g$
Error	g(r-1)(L-1)	Me	δ^2_e	δ^2_e/rl

$$\delta^2_g = (Mg - Mgl)/rl$$

$$\delta^2_{ph} = \delta^2_g + \delta^2_{gl}/r + \delta^2_e/rl$$

where:

$$\delta^2_{gl} = (Mg - Mgl)/r$$

$$\delta^2_e = Me/rl$$

Broad sense heritability **(h^2_B)** was calculated as follow:

$$h^2B = (\delta^2_g/\delta^2_{ph})$$

The genotypic **(G.C.V%)** and phenotypic **(P.C.V%)** coefficient of variability, of each location were calculated as **(δ_g/Mean) x 100** and **(δ_{ph}/Mean) x 100,**respectively.

Expected gain **(Gs)** in each location and combined over locations from selecting the top 20 % of the genotypes was computed as follow:

$Gs = K \times \delta_{ph} \times h^2$ Where:

K = standardized selection differential = 1.40

δ_{ph} = phenotypic standard deviation.

h^2 = broad sense heritability