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Inheritance of Podborer (*Helicoverpa armigera*) Tolerance in Pigeonpea

M. Rizwana Banu, Ar. Muthiah and S. Ashok
Department of Plant Breeding and Genetics, Tamil Nadu Agricultural University,
Agricultural Research Station, Bhavani Sagar-638 451, India

Abstract: The legume pod borer, *Helicoverpa armigera* is one of the most devastating pests of pigeon pea. And it is an important biotic constraint to pigeon pea production worldwide. In recent years, development of *Helicoverpa armigera* populations resistant to insecticides has further hampered the control of measures. Therefore, identification and utilization of cultivars resistant to tolerant to *Helicoverpa armigera* would have a number of advantages, particularly for a relatively low value crop such as pigeon pea. Resistant/susceptible cultivars would provide an equitable, environmentally sound and sustainable pest management tool. High levels of resistance to pod borer have been reported in wild relatives and some of the cultivars of pigeon pea. The pod wall surface and their exudates play a major role in host selection process of insect herbivores. Based on this objective, in the present investigation, inheritance of resistance to pod borer in parents (*Cajanus cajan*) and their F₁, F₂, BC₁ and BC₂ generations have been studied. Single dominant gene was observed in F₂ and backcross generations. This can be incorporated in the adapted cultivar by the simple backcross method of breeding.

Key words: *Cajanus cajan*, *Helicoverpa armigera*, screening, inheritance, genetics, gene action

INTRODUCTION

Podborer (*Helicoverpa armigera*) is a major insect pest of pigeonpea. And it has been associated with the loss of 80-90% causing to an extent yield loss of 2, 50,000 tones of grains per annum worth more than 3750 million rupees per year. In pigeon pea more than 150 insect species feed on this crop of which *Helicoverpa armigera* is the most damaging pests of worldwide (Sharma *et al.*, 2001). The ability to feed on various plants enables *Helicoverpa armigera* populations to develop continuously during the entire cropping season (Bhatnagar *et al.*, 1982). Use of resistant cultivar is a practical and inexpensive method of controlling pest. Based on this objective the study was conducted at Tamilnadu Agricultural University, Coimbatore to determine the genetics of resistance to podborer in the eighteen entries of which 2 lines ICP13201 and ICP13208 proved to be tolerant. An efficient breeding programme for insect resistance requires not only the availability of sources of resistance, but also the knowledge of inheritance and genetic control systems. Therefore the reactions of F₁, F₂, BC₁ and BC₂ populations arising from the crosses of two resistance cultivars revealed in each of these cultivars was governed by single dominant and di genic, respectively.

MATERIALS AND METHODS

Field experiment was conducted during kharif (2001-02) and Rabi (2002-03) seasons. Randomized block design was followed with fifteen genotypes of pigeonpea. Each genotype was sown at 90 cm between rows and 30 cm between plants.

Redgram lines (ICP13201 and ICP13208) which showed consistent podborer resistant reaction and three susceptible lines (ICP7118, ICP7182 and Co5) formed the material for present study. They were crossed in line x tester model using susceptible as male parent.

F₁ plants of each cross were grown in open and F₂ were crossed with tolerant and susceptible plants to develop BC₁ and BC₂ generations. The remaining self pollinated pods on F₁ plants provided the F₂ generation seeds.

The parents, F₁, F₂s and backcross generations were evaluated to study the inheritance of podborer tolerance. The pods damaged by the podborer were recorded by the presence of large bored holes in pods and rated as tolerant and susceptible. A Chi-square test was used to determine goodness of fit to different genetic ratios.

RESULTS

In the cross ICP 13201 × ICP 7118 out of the total 200 F₂ plants screened. 145 were rated as tolerant and 55 as

susceptible. The data showed a good fit to a 3 (tolerant): 1 (susceptible) ratio. $\chi^2 = 0.60$ $p = 0.5-0.25$. The BC_2F_1 ($F_1 \times ICP 7118$) generation segregated into 55 (tolerant) and 45 (susceptible) plants with a good fit to 1: 1 ratio and as expected. All the BC_1F_1 ($F_1 \times ICP 13201$) plants were tolerant. The segregation pattern of the BC_1F_1 and BC_2F_1 generations confirmed the findings of the F_2 (Table 1).

In the cross $ICP 13201 \times CO5$ out of the total 200 F_2 plants screened. 185 were rated as tolerant and 15 as susceptible. The data showed a good fit to a 15(tolerant): 1 (susceptible) ratio. $\chi^2 = 0.53$ $p = 0.50-0.25$. The BC_2F_1 ($F_1 \times CO5$) generations segregated into 72 tolerant and 28 susceptible with a good fit of 3 (tolerant): 1 (susceptible) ratio and as expected. All the BC_1F_1 plants ($F_1 \times ICP 13201$) were tolerant. The segregation pattern of the BC_1F_1 and BC_2F_2 generations confirmed the findings of the F_2 .

In the cross $ICP 13201 \times ICP 7182$ out of the total 200 F_2 plants screened. 152 were rated as tolerant and 48 as susceptible. The data showed a good fit to a 3 (tolerant): 1 (susceptible) ratio $\chi^2 = 0.10$, $p = 0.95-0.75$. The BC_2F_1

($F_1 \times ICP 7182$) generations segregated into 52 tolerant and 48 susceptible with a good fit of 1: 1 ratio and as expected. All the BC_1F_1 ($F_1 \times ICP 13201$) plants were tolerant. The segregation pattern of the BC_1F_1 and BC_2F_2 generations confirmed the findings of the F_2 .

In the cross $ICP 13208 \times ICP 7118$ out of the total 200 F_2 plants screened. One hundred and sixty five were rated as tolerant and 35 as susceptible. The data showed a good fit to a 13 (tolerant): 3 (susceptible) ratio, $\chi^2 = 0.21$, $p = 0.75-0.50$. The BC_2F_1 ($F_1 \times ICP 7118$) generations segregated in to 74 tolerant and 26 susceptible with a good fit of 3 (tolerant): 1 (susceptible) ratio and as expected. All the BC_1F_1 plants ($F_1 \times ICP 13208$) were tolerant. The segregation pattern of the BC_1F_1 and BC_2F_1 generations confirmed the findings of the F_2 .

In the cross $ICP 13208 \times CO5$ out of the total 200 F_2 plants screened. 162 were rated as tolerant and 38 as susceptible. The data showed a good fit to a 3 (tolerant): 1 (susceptible) ratio, $\chi^2 = 0.13$, $p = 0.75-0.50$. The BC_2F_1 ($F_1 \times CO5$) generations segregated into 55 plants tolerant

Table 1: Inheritance of pod borer tolerance in pigeonpea

Cross and generation	Observed No. of plants		Total	Expected genetic ratio	χ^2	p-value
	Tolerant	Susceptible				
ICP 13201 × ICP 7118	40	-	40	All tolerant		
P ₁	-	40	40	All		
P ₂	40	-	40	Susceptible		
F ₁	145	55	200	All tolerant	0.60	0.5-0.25
F ₂	70	0	70	3:1	-	-
BC ₁ F ₁	55	45	100	All tolerant	1.00	0.5-0.25
BC ₂ F ₁				1:1		
ICP 13201 × CO5	40	-	40	All tolerant		
P ₁	-	40	40	All susceptible		
P ₂	40	-	40	All tolerant		
F ₁	185	15	200	All tolerant	0.53	0.50-0.25
F ₂	99	1	100	15:1	0.01	0.95-0.75
BC ₁ F ₁	72	28	100	All tolerant	0.04	0.95-0.50
BC ₂ F ₁				3:1		
ICP 13201 × ICP 7182	40	-	40	All tolerant		
P ₁	-	40	40	All susceptible		
P ₂	40	-	40	All tolerant		
F ₁	152	48	200	All tolerant	0.10	0.95-0.75
F ₂	70	-	70	3:1	-	-
F ₂	52	48	100	All tolerant	0.16	0.75-0.50
BC ₁ F ₁				1:1		
BC ₂ F ₁	40	-	40	All tolerant		
ICP 13208 × ICP 7118	-	40	40	All tolerant		
P ₁	40	-	40	All susceptible		
P ₂	165	35	200	All tolerant	0.21	0.75-0.50
F ₁	98	2	100	13:3	0.04	0.95-0.75
F ₂	74	26	100	All tolerant	0.05	0.95-0.75
F ₂				3:1		
BC ₁ F ₁	40	-	40	All tolerant		
BC ₂ F ₁	-	40	40	All tolerant		
ICP 13208 × CO5	40	-	40	All susceptible		
P ₁	162	38	200	All tolerant	0.13	0.75-0.50
P ₂	99	1	100	3:1	0.01	0.95-0.75
F ₁	55	45	100	All tolerant	1.00	0.50-0.25
F ₂				1:1		
BC ₁ F ₁						
BC ₂ F ₁						

and 45 plants susceptible with a good fit of 1:1 ratio and as expected. All the BC₁F₁ plants (F₁×ICP 13208) were tolerant. The segregation pattern of the BC₁F₁ and BC₂F₁ generations confirmed the findings of the F₂.

DISCUSSION

The segregation pattern in the backcross progenies further supported the F₂ data. In the cross ICP 13201×ICP 7118 out of the 200 F₂ plants screened. The data showed a good fit of 3:1 ratio. $\chi^2 = 0.60$, $p = 0.5-0.25$ indicating the single dominant gene is involved in the tolerance mechanism to *H. armigera*. While the BC₂F₁ generations showed a good fit of 1:1 ratio. $\chi^2 = 1.00$, $p = 0.5-0.25$ and the all BC₁F₁ plants are tolerant confirming the dominant gene action.

In the cross ICP 13201×ICP 7182 out of the 200 F₂ plants screened. The data showed a good fit of 3:1 ratio $\chi^2 = 0.10$, $p = 0.95-0.75$ indicating the single dominant gene is involved in the tolerance mechanism to *H. armigera*. While the BC₂F₁ generations showed a good fit of 1:1 ratio, $\chi^2 = 0.16$, $p = 0.75-0.50$ and all the BC₁F₁ plants are tolerant. Confirming the dominant gene action.

In the cross ICP 13208×CO5 out of the 200 F₂ plants screened. The data showed a good fit of 3:1 ratio $\chi^2 = 0.13$, $p = 0.75-0.50$. Thus indicating that single dominant gene is involved in the tolerance mechanism to *H. armigera*. While the BC₂F₁ generation showed a good fit of 1:1 ratio $\chi^2 = 0.01$, $p = 0.95-0.75$ and all the BC₁F₁ plants are tolerant. Confirming the dominant gene action.

The monogenic dominant and digenic duplicate was confirmed in backcross generation analysis also. All the backcross progenies involving tolerant parents (BC₁) were tolerant the BC₂ generation fits in a 3:1 ratio.

These results were in conformity with the findings of Aruna Rupakala *et al.* (2005) they used *Cajanus scarabaeoides* as a wild source in the inheritance of pod borer resistance in different generations of F₁, F₂, BC₁ and F₃ populations of pigeon pea. And the resistance is governed by single dominant gene.

The F₁, F₂ and backcross populations data thus obtained from the study indicated that, inheritance of podborer tolerance in pigeonpea is controlled by both single dominant gene and digenic. Single dominant gene inheritance for podborer tolerance makes it rather easy to manipulate this trait in breeding programmes.

The inheritance study from the podborer revealed that in the following three crosses ICP 13201×ICP 7118, ICP 13201×ICP 7182 and ICP 13208×CO5. The tolerance is governed by single dominant gene, where as, in two other crosses ICP 13201×CO5 and ICP 13208×ICP 7118 inheritance to tolerance is controlled by digenic duplicate and digenic inhibitory interaction, respectively.

Verulkar *et al.* (1997) observed their studies of inheritance of podborer in inter-specific crosses of pigeonpea, by using variety as female and *cajanus scarabaeoides* (JM 4147) as male parent and after studying the F₁, F₂ and back cross populations concluded that antixenosis controlled by single dominant gene.

Saxena *et al.* (2002) evaluated pigeonpea accessions and selected lines for reaction to *Maruca* in the Semi Arid Tropics. *Helicoverpa armigera* and *Melanagromyza obtusa* cause serious damage to pigeonpea, while under the humid tropical environment *Melanagromyza vitrata* is the major yield reducer of the tropical legumes.

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