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Identification of resistant genotypes against major podborers and diseases in pigeonpea (*Cajanus cajan* L.)

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Abstract

An experiment was conducted during Kharif, 2019 to identify the resistant genotypes towards major pod borers and diseases in pigeonpea. Observations on the larval population of *Helicoverpa armigera* (Hubner) at 50 per cent flowering stage ranged from 0.3 - 7.0 No.s / plant in all the pigeonpea genotypes tested with the lowest being obtained in Yelagiri local and the highest in ICP8840. The webcounts of *Maruca vitrata* (Geyer) ranged between 0.3-12.7 webs per plant. At the time of harvest, among the podborers, the pod damage caused due to *Melanagromyza obtusa* (Malloch) was comparatively high and recorded between 9.3-28.0 per cent. The pod damage caused by *M.vitrata* ranged from 1.3 – 30.5 per cent and *H. armigera* recorded 1.3-28.5 per cent. Out of seventy entries with ICP 8863 as check, sixty one entries were found to be highly susceptible, five entries were susceptible and three entries were moderately susceptible and AC9060 was moderately resistant to podborer complex. For sterility mosaic disease, fifteen entries were found to be susceptible expressing more than 30 per cent of infection. Thirty pigeonpea genotypes expressed 10-30% infection with moderately resistance and twenty four were found to be resistant. Zero wilt incidence was recorded in twenty one entries and the remaining entries tested also exhibited only 1.8 to 6.9 per cent wilt incidence which confers their resistance to wilt.

Keywords: Pigeonpea, screening, pod borer complex, wilt, sterility mosaic disease

Introduction

Pigeonpea, *Cajanus cajan*, L. is an important legume crop and is rich in protein source and ensures nutritional security to the country. The crop can be cultivated in areas of less rainfall due to its drought-resistant nature. The crop can also be able to fix atmospheric nitrogen and enriches the soil and also can be interplanted with other short term crops for higher productivity per land area and reduced risks associated with some crop failures (Dasbak *et al.*, 2012) [2]. In India, Pigeonpea is grown in 4.42 million ha with an annual production of 2.89 million tonnes with 655 kg ha⁻¹ of productivity. It is a predominant pulse crop in Vellore district next to groundnut, paddy and sugarcane. It is grown in an area of 13,584 ha which accounts for about 20% of Tamil Nadu state. Though the area under pigeonpea cultivation is more in this district, it is cultivated mainly under rainfed situation and many places it is grown as an intercrop in groundnut. There is a wide gap between potential and the actual yield obtained by the farmers. Among the various constraints, biotic constraints *viz.*, insects and diseases are the major ones that threatens pigeonpea production. Though approximately 200 insect and mite pests attack pigeonpea, the economic loss by attacking the crop at flowering and pod development stages, pod borers *viz.*, Spotted podborer, *Maruca vitrata* (Geyer), gram podborer, *Helicoverpa armigera* (Hubner) and podfly, *Melanagromyza obtusa* (Malloch) are the major insects determining the yield potential in pigeonpea crop (Saxena, 2012) [10]. Among the podborers, *M. vitrata* caused heavy losses in early, medium and late maturing genotypes (Shanower *et al.*, 1999) [12] as the larvae feed by remaining inside the webbed mass of leaves, flowers and pods. This concealed feeding complicates the management of this pest as pesticides and natural enemies have difficulty in penetrating the shelter to reach the target (Sharma, 1998) [13].

Among the various diseases, wilt and sterility mosaic diseases (SMD) are the major constraints limiting the pigeonpea production. Wilt, *Fusarium udum* is a major soil-borne disease in almost all pigeonpea growing areas (Carlos Popelka *et al.*, 2004) [1]. The pathogen enters the plant through roots, affect the vascular system and causes wilting within few days of entry. The loss in grain yield due to wilt disease depends on the stage of the crop at which the disease appears and loss is total if it occurs before pod formation (Kannaiyan and Nene, 1981 and Okiror, 2002) [4, 8]. SMD caused by pigeonpea sterility mosaic virus (PPSMV) is the economically important viral diseases in India, causing an estimate annual loss of more than

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US\$300 million. This was first reported in 1931 from Pusa (Mitra, 1931) [6] and is mostly endemic to India, Nepal, Bangladesh and Myanmar. The yield losses caused by SMD vary and depend on the genotype and stage of infection, infection before flowering less than 45 days after planting can lead to a yield loss from 95 to 100%, whereas infections more than 45 days after planting can lead to a yield loss of between 26 and 97% (Kannaiyan *et al.*, 1984) [3]. The disease is mainly controlled by using resistant cultivars. Seed treatment or soil and foliar application of a number of organophosphorus based insecticides or acaricides which are recommended for the management of vector mites are seldom practiced because of prohibitive costs and also their risks to human health and environment.

One of the ways in which these insects and diseases could be managed is by using integrated approaches which includes the integration of resistant cultivars as a first line of defense, there arises the immense need to develop pigeonpea cultivar with multiple resistance to insects and diseases. Hence it is imperative to identify stable sources of resistance and exploit them to develop resistant varieties of pigeonpea through breeding approaches. The study was aimed to identify the resistant cultivars under natural field conditions against insects and diseases.

Materials and methods

A field experiment was laid out at Agricultural Research Station, Virinjipuram, Vellore, Tamil Nadu during Kharif 2019. Seventy genotypes collected from IIPR, Kanpur, ICRISAT and from the national centers were grown each in plots of 4m length with a spacing of 90x30 cm. The crop was grown with normal agronomic practices in a randomized block design with two replications. The plots were grown without insecticides and fungicides to test their resistance / tolerance to podborer complex *viz.*, *H. armigera*, *M. vitrata* and *M. obtusa* and diseases *viz.* wilt and SMD with ICP 8863 as a national check. Observations on the larval population of *H. armigera* and number of webs per plant caused by *M. vitrata* was taken at flowering stage. At maturity, the number

of pods showing the damage caused by different podborers were distinguished based on the presence of big holes for *H. armigera*, relatively small holes and scrapped margins for *M. vitrata* and pin-sized holes for *M. obtusa* as described by Naresh and Singh, 1984 [7].

$$\text{Percent pod damage} = \frac{\text{Number of damaged pods}}{\text{Total number of pods}} \times 100$$

Based on the pod damage by individual insect in the entries with the national check, the pest susceptibility per cent (PSP) and Pest susceptibility index (PSI) were calculated for each entry. Based on the PSI, category of resistance was given for each entry for each insect. the susceptibility of different genotypes to insect pests will be calculated on the basis of per cent pod damage at the time of crop maturity. PSP was calculated by the following formula

$$\text{Pest Susceptibility (\%)} = \frac{\text{Per cent damage in check cultivar} - \text{per cent damage in test cultivar}}{\text{Per cent damage in check cultivar}} \times 100$$

Table 1: Based on the following scale with the PSP values obtained for each Entries tested, the categorization of resistance was classified as

Pest susceptibility (%)	Grade	Category
100	1	Highly Resistant
75 to 90	2	Resistant
50 to 75	3	Least susceptible
25 to 50	4	Least susceptible
10 to 25	5	Least susceptible
-10 to 10	6	Moderately susceptible
-10 to -25	7	Moderately susceptible
-25 to -50	8	Highly susceptible
<-50	9	Highly susceptible

For screening of wilt disease, the same entries were scored based on the 9 point scale divided in to five categories developed at ICRISAT and for SMD as per the standard scale (Singh *et al.*, 2003) [11].

Table 2: Wilt Scoring and SMD scoring Category

Wilt Scoring	Category	SMD scoring	Category
No symptoms on any plant	Resistant (R)	0-10% infected	Resistant (R)
10% or less mortality	Moderately resistant (MR)	10.1-30% infected	Moderately resistant (MR)
11-20% mortality	Tolerant (T)	30.1-100% infected	Susceptible (S)
21-50% mortality	Moderately susceptible (MS)		
51% or more mortality	Susceptible (S)		

Results and Discussion

The sources of resistant pigeonpea genotypes was presented in Table 3. Observations on the larval population of *H. armigera* at 50 per cent flowering stage ranged from 0.3 - 7.0 No.s / plant in all the pigeonpea genotypes tested with the lowest being obtained in Yelagiri local and the highest in ICP8840. The webcounts of *M. vitrata* ranged between 0.3-12.7 webs per plant. At the time of harvest, among the podborers, the pod damage caused due to *M. obtusa* was comparatively high and recorded between 9.3-28.0 per cent. The pod damage caused by *M. vitrata* ranged from 1.3 – 30.5 per cent and *H. armigera* recorded 1.3-28.5 per cent. Based on the total pod damage recorded in all the entries was worked out with ICP 8863 check variety to assess its resistance. All the entries tested were categorized based on the pest susceptibility index (PSI). Less PSI in test entry contributes high resistance levels. Out of seventy entries

which includes ICP 8863 as check, evaluated for its resistance / susceptibility towards pod borer complex, sixty one entries were found to be highly susceptible (86.9%), five entries comes under susceptible (7.24%) and three entries under moderately susceptible (4.34%) and single entry under moderately resistant (1.44%) (Table 4).

The same entries when tested for its resistance source against SMD, out of seventy entries, fifteen entries were found to be susceptible expressing more than 30 per cent of infection and contributed 21.7 per cent susceptibility. Thirty pigeonpea genotypes (43.47%) expressed between 10-30% infection of SMD and contributed their moderate resistance nature. However, twenty four pigeonpea genotypes (40.57%) expressed their infection between 0.0-9.3 per cent and contributed resistance behaviour towards SMD. The susceptible check towards SMD reported with 32.6 per cent disease infection. Among the tested pigeonpea genotypes,

zero wilt incidence was recorded in twenty one entries and the remaining entries tested also exhibited with the lowest being 1.8 to 6.9 per cent highest incidence and confers the pigeonpea genotypes tested towards resistance nature to wilt. The pigeonpea genotypes tested towards podborer complex contributes to susceptibility, whereas towards disease incidence contributes for resistance. The only entry which contributes for moderate resistance to podborer complex and resistant to wilt and SMD was AC9060 and should be evaluated for its contribution factor to multiple resistance nature.

Various research findings on screening of resistant genotypes are available and found only few entries contributes for resistant to many biotic factors. Zadda Kavitha and Vijayaraghavan, 2017 [14] reported that out of 145 pigeonpea entries, ICP 11007, H 23, DA332, GR 28, ICP 49114, ICP

11957 and BRG 10-02 were found to be resistant to pod borers. Similar findings were also reported by Ram Keval *et al.*, 2017 [9]. In case of wilt resistance studies, the infection per cent is very less under experimental period doesn't mean that the genotypes are resistance, because the incidence was dependant on abiotic factors *viz.*, sowing time, inoculum density, soil texture, soil pH, soil moisture, rainfall, soil temperature (Kumar, 2012) [5]. However, when there is a search for wider adaptation to biotic factors only one genotype contributed for resistance towards podborer complex, wilt and SMD and that resistance nature has also to be tested under field condition for consistent results and also tested for artificial screening to both insects and pathogen in order to identify that particular genotype to be included under future breeding programmes in pigeonpea.

Table 3: Identification of resistance pigeonpea genotypes towards pod borers and major diseases

S. No	Germplasm entries	Insect population (Nos./plant) and damage (%)					Disease incidence (%)		
		<i>H.armigera</i>	<i>M.vitrata</i>	Pod damage			Total pod damage	SMD	Wilt
				<i>H.armigera</i>	<i>M.vitrata</i>	<i>M.obtusa</i>			
1.	ICP 26	1.0	1.2	4.5	5.5	8.5	18.5	33.4	6.0
2.	ICP 377	2.0	3.7	13.5	16.5	15.5	45.5	24.0	4.4
3.	ICP 2431	2.3	7.0	5.5	2.3	10.5	18.3	8.0	4.0
4.	ICP 9922	1.7	3.3	5.5	3.3	13.3	22.1	9.3	2.1
5.	ICP 9162	2.0	7.7	2.3	5.3	7.3	14.9	6.4	2.7
6.	ICP 2446	2.3	7.7	13.5	20.5	22.5	56.5	17.2	0.0
7.	ICP 25534	2.7	12.7	1.3	9.3	7.3	17.9	13.7	0.0
8.	ICP 9562	3.7	10.0	7.3	5.3	10.3	22.9	14.0	2.2
9.	ICP 15049	4.0	10.7	20.5	18.5	13.5	52.5	59.1	2.3
10.	ICP 14832	1.0	7.0	10.5	13.5	14.5	38.5	40.1	0.0
11.	ICP 14701	1.3	3.3	12.5	16.5	15.5	44.5	43.6	2.1
12.	ICP 6974	1.2	11.7	19.5	13.5	18.5	51.5	11.4	0.0
13.	ICP 8860	2.7	3.3	18.5	22.5	23.5	64.5	47.7	2.2
14.	ICP 8840	7.0	10.0	22.5	26.5	26.5	75.5	68.3	0.0
15.	ICP6973	1.7	2.0	10.5	27	22	59.5	28.8	0.0
16.	ICP 8865	3.3	5.7	24.5	28.5	24	77	20.3	0.0
17.	ICP 7803	2.0	8.7	14	15.5	13.5	43	26.2	2.1
18.	ICP 3451	1.0	2.3	2.3	2.3	10.3	14.9	57.1	4.1
19.	ICP 7366	1.7	2.0	12.5	15.5	18.5	46.5	73.7	6.1
20.	ICP10654	1.3	3.3	13.5	14	18	45.5	55.0	4.3
21.	ICP 3046	2.0	3.3	15.5	16	18.5	50	43.8	6.9
22.	ICP11015	1.2	2.0	16.5	18	20.5	55	19.9	2.1
23.	ICP9174	1.0	1.7	11.5	13	17.5	42	36.6	2.4
24.	ICP11230	2.3	5.0	12.5	13.5	17	43	2.2	0.0
25.	ICP2577	5.3	9.0	28.5	30.5	28	87	17.5	2.1
26.	ICP9750	0.7	1.0	5.5	8	12	25.5	31.6	2.0
27.	ICP6128	2.7	6.0	15.5	10	12	37.5	8.7	4.4
28.	ICP1071	1.3	1.3	10.5	12.5	14.5	37.5	2.1	0.0
29.	ICP6859	1.0	2.0	12.5	13	15.5	41	0.0	0.0
30.	ICP8602	1.3	3.7	13.5	15	18.5	47	0.0	0.0
31.	ICP 13304	1.3	2.3	14.5	16	18	48.5	8.9	3.4
32.	ICP2454474	1.0	2.3	5.6	3.3	10	18.9	2.8	2.2
33.	IC525430	1.0	3.0	3.3	4.3	15	22.6	17.8	0.0
34.	IC525514	3.7	9.7	25.5	24	18	67.5	6.0	0.0
35.	IC73999	2.3	6.7	2.3	5.3	10.3	17.9	6.5	2.1
36.	IC525516	1.7	2.7	4.3	4.3	10.3	18.9	10.4	4.4
37.	IC 215535	2.3	3.0	4.3	2.3	13	19.6	26.0	3.8
38.	IC525558	1.3	2.7	3.3	2.3	10.3	15.9	19.0	6.0
39.	ICPR2441	1.0	6.0	14.5	18	12.5	45	18.9	4.8
40.	ICPR88034	3.0	7.0	13.5	15	16.5	45	9.1	0.0
41.	PYR-16-08	1.7	2.3	12.3	4.3	8.3	24.9	20.0	0.0
42.	PYR-16-15	1.3	1.0	5.3	6.3	6.3	17.9	16.7	0.0
43.	PYR16-12	1.3	1.7	1.3	1.6	16.3	19.2	13.0	0.0
44.	PYR 16-16	1.7	2.0	12.3	2.3	9.3	23.9	12.5	2.8
45.	KDL-46	1.0	1.7	13.5	14	16.5	44	45.5	6.5
46.	C11	2.7	7.0	1.3	10.3	12.3	23.9	18.2	2.0
47.	Bananapalar	1.7	2.0	20.5	22.5	20.5	63.5	10.0	4.2

48.	IAW 56-H	1.0	1.7	2.3	3.3	23.3	28.9	20.0	7.9
49.	BDH-1	1.0	2.0	10.5	22	18.5	51	5.6	2.8
50.	AC9060	1.7	4.3	3.3	2.3	2.3	7.9	8.5	2.2
51.	YH1	3.0	5.3	13.5	12.5	15.5	41.5	13.1	4.4
52.	KPI44	2.0	3.7	15.5	20	16.5	52	14.0	5.9
53.	Vathalmalai1	3.3	7.7	2.3	2.3	10.3	14.9	0.0	2.1
54.	Vathalmalai2	2.0	6.0	2.3	3.3	11.3	16.9	4.0	2.0
55.	Asha	2.0	1.0	5.3	10.3	11.3	26.9	10.7	2.0
56.	Yelagiri local	0.3	0.3	1.3	2.3	10.3	13.9	0.0	0.0
57.	APK1	1.7	1.7	11.5	13.5	10.5	35.5	2.3	2.1
58.	CORg7	2.7	7.3	12.5	18	16.5	47	3.9	2.0
59.	BRG1	1.0	2.3	1.3	2.3	12.3	15.9	2.8	0.0
60.	BRG2	1.3	2.3	5.3	2.3	10.3	17.9	2.3	2.0
61.	BRG3	1.0	1.7	5.5	10.5	8.5	24.5	2.8	1.8
62.	KPI 49	2.3	1.3	11.5	18.5	10.5	40.5	34.7	0.0
63.	VBN2	1.0	2.0	5.5	12.5	12.5	30.5	8.0	2.0
64.	BSR1	3.3	7.7	18.5	19.5	15.5	53.5	17.4	2.5
65.	VBN3	1.0	2.0	5.5	12.5	12.5	30.5	6.0	2.1
66.	LRG 41	2.3	4.3	22.5	24	15.5	62	12.5	4.8
67.	TTB 7	1.0	1.0	6.3	7.3	12.3	25.9	0.0	0.0
68.	PI39740	1.0	1.7	10.5	13.5	12.5	36.5	35.7	6.1
69.	Malaithuvarai	1.3	2.3	8.5	12.5	10.5	31.5	8.4	2.8
70.	ICP 8863 (Check)	0.5	1.2	2.3	1.3	9.3	12.9	32.6	2.3

Table 4: Classification of pigeonpea genotypes towards pod borers and major diseases

S. No	Germplasm entries	PSI	Germplasm nature			S.No	Germplasm entries	PSI	Germplasm nature		
			Pod borers	SMD	Wilt				Pod borers	SMD	Wilt
1.	ICP 26	8	HS	S	R	36.	IC525516	8	HS	MR	R
2.	ICP 377	9	HS	MR	R	37.	IC 215535	9	HS	MR	R
3.	ICP 2431	8	HS	R	R	38.	IC525558	7	S	MR	R
4.	ICP 9922	9	HS	R	R	39.	ICPR2441	9	HS	MR	R
5.	ICP 9162	7	S	R	R	40.	ICPR88034	9	HS	R	R
6.	ICP 2446	9	HS	MR	R	41.	PYR-16-08	9	HS	MR	R
7.	ICP 25534	8	HS	MR	R	42.	PYR-16-15	8	HS	MR	R
8.	ICP 9562	9	HS	MR	R	43.	PYR16-12	8	HS	MR	R
9.	ICP 15049	9	HS	S	R	44.	PYR 16-16	9	HS	MR	R
10.	ICP 14832	9	HS	S	R	45.	KDL-46	9	HS	S	R
11.	ICP 14701	9	HS	S	R	46.	C11	9	HS	MR	R
12.	ICP 6974	9	HS	MR	R	47.	Bananapalar	9	HS	R	R
13.	ICP 8860	9	HS	S	R	48.	IAW 56-H	9	HS	MR	R
14.	ICP 8840	9	HS	S	R	49.	BDH-1	9	HS	R	R
15.	ICP6973	9	HS	MR	R	50.	AC9060	4	MR	R	R
16.	ICP 8865	9	HS	MR	R	51.	YH1	9	HS	MR	R
17.	ICP 7803	9	HS	MR	R	52.	KPI44	9	HS	MR	R
18.	ICP 3451	7	S	S	R	53.	Vathalmalai1	6	MS	R	R
19.	ICP 7366	9	HS	S	R	54.	Vathalmalai2	6	MS	R	R
20.	ICP10654	9	HS	S	R	55.	Asha	7	S	MR	R
21.	ICP 3046	9	HS	S	R	56.	Yelagiri local	6	MS	R	R
22.	ICP11015	9	HS	MR	R	57.	APK1	9	HS	R	R
23.	ICP9174	9	HS	MR	R	58.	CORg7	9	HS	R	R
24.	ICP11230	9	HS	R	R	59.	BRG1	7	S	R	R
25.	ICP2577	9	HS	MR	R	60.	BRG2	8	HS	R	R
26.	ICP9750	9	HS	S	R	61.	BRG3	9	HS	R	R
27.	ICP6128	9	HS	R	R	62.	KPI 49	9	HS	S	R
28.	ICP1071	9	HS	R	R	63.	VBN2	9	HS	R	R
29.	ICP6859	9	HS	R	R	64.	BSR1	9	HS	MR	R
30.	ICP8602	9	HS	R	R	65.	VBN3	9	HS	R	R
31.	ICP 13304	9	HS	R	R	66.	LRG 41	9	HS	MR	R
32.	ICP2454474	8	HS	R	R	67.	TTB 7	9	HS	R	R
33.	IC525430	9	HS	MR	R	68.	PI39740	9	HS	S	R
34.	IC525514	9	HS	R	R	69.	Malaithuvarai	9	HS	R	R
35.	IC73999	8	HS	R	R	70.	ICP 8863 (Check)	0	-	S	R

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