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COMPARATIVE EVALUATION OF PIGEONPEA GENOTYPES FOR THEIR RESPONSE TO POD BORER COMPLEX DURING *KHARIF*

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ABSTRACT

Pigeonpea (*Cajanus cajan* L.) is one of the most important pulse crops in India; however, its productivity is severely constrained by the pod borer complex, particularly *Helicoverpa armigera*, *Maruca vitrata* and *Melanagromyza obtusa*. The development and identification of resistant genotypes is considered one of the most economical and environmentally sustainable approaches for managing these insect pests. Keeping this in view, the present investigation was undertaken to evaluate the resistance of different pigeonpea genotypes against the pod borer complex under natural field conditions. The experiment was conducted at the Research-cum-Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, during the Kharif season of 2023–24. The trial was laid out in a Randomized Block Design (RBD) with three replications. The genotypes were screened under natural infestation and observations on pod damage caused by the major pod borers along with grain yield were recorded at crop maturity. The study revealed significant variability among the tested genotypes in their response to pod borer infestation. The minimum pod damage due to *Maruca vitrata* was recorded in genotype RP5-2016-16 (2.80%), while the maximum damage was observed in RP5-2017-7 (8.53%). In the case of *Helicoverpa armigera*, genotype RP5-2016-72 recorded the lowest pod damage (4.13%), whereas the highest damage (8.53%) was observed in RP5-2016-31. Similarly, for pigeonpea pod fly (*Melanagromyza obtusa*), the minimum pod damage was recorded in genotype RP5-2016-17 (3.66%), while the maximum damage (9.26%) was observed in RP5-2017-33. The resistant genotypes consistently exhibited lower levels of pod damage and superior yield performance compared with the susceptible genotypes, demonstrating their potential for cultivation under pod borer-prone conditions. The findings of the present study identify promising sources of resistance against the pod borer complex in pigeonpea. These genotypes can serve as valuable donor parents in resistance breeding programmes and may be effectively incorporated into integrated pest management (IPM) strategies to reduce dependence on chemical insecticides and enhance sustainable pigeonpea production.

Key words : Pigeonpea, *Cajanus cajan*, Pod borer complex, *Helicoverpa armigera*, *Maruca vitrata*, *Melanagromyza obtusa*, Host plant resistance, Genotype screening, Integrated Pest Management, Grain yield.

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millspaugh) (2n = 22) is one of the most important grain legume crops cultivated in tropical and subtropical regions of the world. It belongs to the family Fabaceae and is predominantly grown under rainfed conditions due to its wide adaptability, drought tolerance, and ability to perform well under diverse agro-climatic environments. Pigeonpea plays a vital role in global food and nutritional security, particularly in developing countries where it serves as an important source of dietary protein. The crop is popularly known by different names in various regions, such as arhar, red gram, tur, guandul, gungo pea, and Congo pea, reflecting its widespread cultivation and utilization across continents. The crop is believed to have originated in India, particularly the Peninsular region, where its wild relative *Cajanus cajanifolia* is naturally distributed (Van der Maesen, 1995).

Pigeonpea is cultivated in more than 25 tropical and subtropical countries of Asia, Africa, and Latin America, either as a sole crop or in intercropping systems with cereals and other legumes. Due to its multipurpose nature, pigeonpea contributes to food, fodder, fuelwood and sustainable agricultural systems. The grains are consumed as whole seeds, green vegetables, and split dhal, making it an indispensable component of vegetarian diets. The seeds contain approximately 20–22% protein along with essential amino acids, carbohydrates, minerals, vitamins, and dietary fibre, thereby contributing significantly to human nutrition. In several South Asian countries, pigeonpea provides a substantial proportion of dietary protein, particularly among vegetarian populations (Saxena *et al*., 2010).

India is the largest producer and consumer of pigeonpea globally and contributes significantly to world pulse production. The crop occupies an important position in Indian agriculture because of its role in nutritional security, soil improvement, and livelihood support for millions of farmers. However, despite its importance and wide cultivation, pigeonpea productivity remains considerably lower than its genetic potential due to several abiotic and biotic constraints. Among these constraints, insect pests are recognized as one of the major limiting factors responsible for reduced yield and economic losses (Nene *et al*., 1990).

Pigeonpea is attacked by a large number of insect species throughout its growth period. More than 250 insect species belonging to different orders and families have been reported to infest pigeonpea at various crop stages; however, only a few species cause significant economic damage (Lateef and Reed, 1990). Among these, the pod borer complex is considered the most destructive group of insect pests affecting pigeonpea production. The major members of this complex include gram pod borer, *Helicoverpa armigera* (Hübner), spotted pod borer, *Maruca vitrata* (Fabricius) and pigeonpea pod fly, *Melanagromyza obtusa* (Malloch). These pests directly attack reproductive structures such as flowers, pods, and developing seeds, resulting in severe yield reduction.

Among the pod borer complex, *Helicoverpa armigera* is considered the most important and destructive pest of pigeonpea due to its polyphagous nature, high reproductive capacity, mobility, overlapping generations, and ability to develop resistance against insecticides. The larvae feed on flower buds, flowers, and pods and cause direct damage to developing seeds by making holes in pods. A single larva can damage several pods during its larval period, resulting in substantial yield losses under severe infestation conditions (Sharma, 2016).

The spotted pod borer, *Maruca vitrata*, is another important pest of pigeonpea, particularly in short-duration and medium-duration cultivars. The larvae damage flowers, flower buds, and pods by webbing plant parts together and feeding within the protected web structure. This feeding behaviour reduces pod formation and adversely affects grain yield. The pest has also become increasingly difficult to manage due to limitations in chemical control and development of insecticide resistance (Sreelakshmi *et al*., 2015).

Similarly, pigeonpea pod fly, *Melanagromyza obtusa*, has emerged as a serious pest, particularly in central and southern regions of India. The maggots feed internally on developing seeds, causing shrivelling, discoloration, and reduction in seed quality. Since the insect remains concealed inside pods, its management through conventional insecticide applications is difficult. The combined infestation of pod borers may result in considerable yield losses, making them a major threat to sustainable pigeonpea production.

Therefore, systematic evaluation of pigeonpea genotypes against the pod borer complex is essential for identifying promising resistant materials suitable for cultivation and breeding purposes. Keeping these considerations in view, the present investigation entitled "Field Evaluation of Pigeonpea (*Cajanus cajan* L.) Genotypes against Pod Borer Complex under Natural Infestation during *Kharif* 2023–24" was undertaken at the Research-cum-Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, with the objective of identifying resistant genotypes against major pod borers, namely *H. armigera*, *M. vitrata* and *M. obtusa*, under natural field conditions.

Materials and Methods

The experiment was conducted during 2023-24 at the Research cum Instructional farm, College of Agriculture, (IGKV), Raipur by growing a total of twenty-two genotypes of pigeonpea in a Randomized Block Design (RBD). "Five plants were selected from each entry. Afterwards, the total number of pods and number of damaged pods by pod borer on each randomly plant were counted and converted into percentage. The percentage pod damage and yield of each tested entry was compared with check." The percentage of pod damage and grain yield Kg/ha was estimated with the help of the following formula:

$$\text{Pod damage (\%)} = \frac{\text{Number of damage pods}}{\text{Total number of pods (Healthy + Damage)}} \times 100$$

$$\text{Grain yield (Kg/ha)} = \frac{\text{Weight of grain in Kg/plot}}{\text{Plot area in m}^2} \times 10000$$

Pest resistance rating (PRR) for screening of pigeonpea genotypes against pod borer complex

The percentage of pod damage at maturity of test entry was compared with that of the check cultivar in the trial. The test entries were then graded using a formula derived from Abott (1925).

$$\text{Pest resistance (\%)} = \frac{\text{PD in check} - \text{PD of test genotypes}}{\text{PD in check}} \times 100$$

Where, PD = Mean of % Pod damage.

Based on this formula, the performance of each cultivar 1-9 scale as follow:

Table 1 : Pest resistance rating (1-9 rating scale) (IIPR Kanpur, 2023-24).

Pest Resistance (%)	Pest Resistance rating	Remarks
100	1	Immune
75 to 99	2	Highly resistant
50 to 75	3	Resistant
25 to 50	4	Moderately resistant
10 to 25	5	Tolerant
-10 to 10	6	Equal to check
-25 to -10	7	Moderately susceptible
-50 to -25	8	Susceptible
-50 or less	9	Highly susceptible

Statistical analysis : The data obtained were analyzed statistically after using appropriate transformation. The larval population of pod borer complex data obtained were converted into square root transformation, by using the formula ($\sqrt{x}$ +0.5). The data on pod and grain damage was first recorded from the plants and then converted into percentage. The percentage data were processed under arcsine transformation Sin-1 ($\sqrt{x}$ /100) before statistical analysis. This transformed data was then analyzed by the method of analysis of variance as described by Gomez and Gomez (1984). The "F" test was used at 5 per cent level of significance.

Results and Discussion

The incidence of insect pest was observed in terms of percent pod damage at harvesting stage of crop (Table 2). The per cent pod damage caused by *M. vitrata* in twenty two genotypes ranged between 2.80% to 8.53% with significant difference among different genotypes. The minimum per cent pod damage was recorded in RP5-2016-16genotype of 2.80 % followed by RP5-2016-42, RP5-2016-1 and RP5-2016-45genotypes of 3.53%, 3.60%, 4.13%. These were significantly lower than many of the other tested genotypes. The maximum per cent pod damage by *M. vitrata* was recorded in the genotype RP5-2017-7 (8.53%) followed by genotypes RP5-2016-31, RP5-2017-33 and RP5-2016-44 of 7.60%, 6.40% and 5.93%, respectively. These were significantly higher among many of the tested genotypes. In rest of the genotypes the per cent pod damage by *M. vitrata* were intermittent.

The current results are in agreement with the findings of Bhagat (2023), who screened genotypes of different durations of pigeonpea at the Instructional farm and Research Station, College of Agriculture, Raipur (C.G.), which also showed significant differences between each other. The percentage of pod damage by spotted pod borer (*Maruca vitrata*) in early genotypes ranged from 1.00 to 2.20 %, indicating significant variation between the genotypes. The examined genotypes IPAE 15-05 had the least amount of pod damage with 1.00% and highest per cent pod damage was observed in UPAS 120 (RC) with 2.20%. Similarly, during *Kharif* 2022-23, among the all tested genotypes, minimum pod damage by *Maruca vitrata* was observed in genotype of 1.42 % and maximum per cent pod damage was observed in UPAS 120 (RC) with 3.07%.

The per cent pod damage caused by *H. armigera* in the twenty two genotypes ranged between 4.13% to 8.53% with significant differences among them. The minimum per cent pod damage was recorded in the genotype RP5-2016-72 of 4.13% followed by RP5-2017-16, RP5-2017-33 and RP5-2016-62 genotypes of 5.00%, 5.00%, 5.13%, respectively (Table 2). These were significantly lower than many of the other tested genotypes. The maximum per cent pod damage by *H. armigera* was recorded in the genotype RP5-2016-31 of 8.53% followed by genotypes RP5-2016-3, RP5-2017-13 and RP5-2017-1of 7.86%, 7.60% and 7.40%, respectively. These were significantly higher among many of the tested genotypes. In rest of the genotype the per cent pod damage by *H. armigera* were intermittent.

The above results are in agreement with the findings of Sai *et al*. (2019), who revealed on the basis of per-cent pod damage and grain damage, five genotypes viz., LRG 30, LRG 41, ICPL 87119, ICP 8863 and BSMR 853 grouped under resistant category and nine genotypes *viz*., TDRG 33, Guliyal local, WRP 1, CO 6, LRG134, RVSA 9, SKNP 224, ICPL 4503 and WRG 79 under susceptible category against *H. armigera*.

Table 2 : Screening of pigeonpea genotypes against pod borer complex during *Kharif* (2023-24).

Genotypes	Pod Damage (%)					
	***M. vitrata* (A)**	***H. armigera* (B)**	***M. obtuse* (C)**	**Total % pod damage (A+B+C)**	**PRR**	**Yield**
RP5-2016-1	3.60 (10.90)	5.60 (13.67)	4.33 (11.90)	13.53	5	905.98
RP5-2016-3	4.46 (12.13)	7.86 (16.25)	5.33 (13.31)	17.66	6	513.58
RP5-2016-16	2.80 (9.61)	6.20 (14.40)	4.66 (12.44)	13.66	5	**1163.61**
RP5-2016-17	5.46 (13.46)	6.73 (14.96)	3.66 (10.99)	15.86	6	725.98
RP5-2016-25	5.73 (13.78)	6.40 (14.56)	8.66 (17.10)	20.08	7	578.81
RP5-2016-31	7.60 (15.97)	**8.53 (16.96)**	6.06 (14.20)	**22.20**	8	734.35
RP5-2016-37	4.66 (12.33)	5.60 (13.62)	7.93 (16.31)	18.20	6	589.65
RP5-2016-42	3.53 (10.74)	5.73 (13.77)	8.06 (16.48)	17.33	6	491.25
RP5-2016-44	5.93 (14.04)	5.53 (13.54)	5.60 (13.63)	17.06	6	635.05
RP5-2016-45	4.13 (11.72)	5.40 (13.42)	5.06 (12.99)	17.26	6	305.09
RP5-2016-50	4.53 (12.18)	6.00 (14.17)	5.20 (13.16)	16.33	6	736.14
RP5-2016-53	5.46 (13.47)	6.00 (14.16)	6.40 (14.61)	17.86	6	592.29
RP5-2016-62	5.40 (13.38)	5.13 (13.04)	7.40 (15.77)	17.93	6	649.52
RP5-2016-72	4.53 (12.22)	4.13 (11.67)	4.46 (12.16)	13.13	5	918.58
RP5-2017-1	5.93 (14.03)	7.40 (15.75)	7.93 (16.34)	21.26	7	754.74
RP5-2017-7	**8.53 (16.95)**	6.26 (14.43)	5.26 (13.24)	20.06	7	643.21
RP5-2017-13	5.86 (14.00)	7.60 (15.98)	7.26 (15.60)	20.73	7	594.51
RP5-2017-16	5.13 (12.88)	5.00 (12.90)	5.60 (13.62)	15.73	6	557.73
RP5-2017-21	4.26 (11.58)	5.60 (13.61)	6.06 (14.22)	15.93	6	962.40
RP5-2017-28	5.73 (13.80)	5.73 (13.81)	4.53 (12.23)	16.00	6	657.91

Table 2 continued...

Table 2 continued...

RP5-2017-33	6.40 (14.63)	5.00 (12.90)	**9.26 (17.70)**	20.66	7	730.12
RP5-2014-34 (RC)	4.60 (12.35)	5.40 (13.49)	7.00 (15.18)	16.93	6	662.17
C.D.	**2.72**	**2.12**	**1.91**	**-**	**-**	**287.11**
SE (m) ±	**0.95**	**0.73**	**0.66**	**-**	**-**	**100.24**
C.V.	**12.66**	**9.03**	**8.11**	**-**	**-**	**24.64**

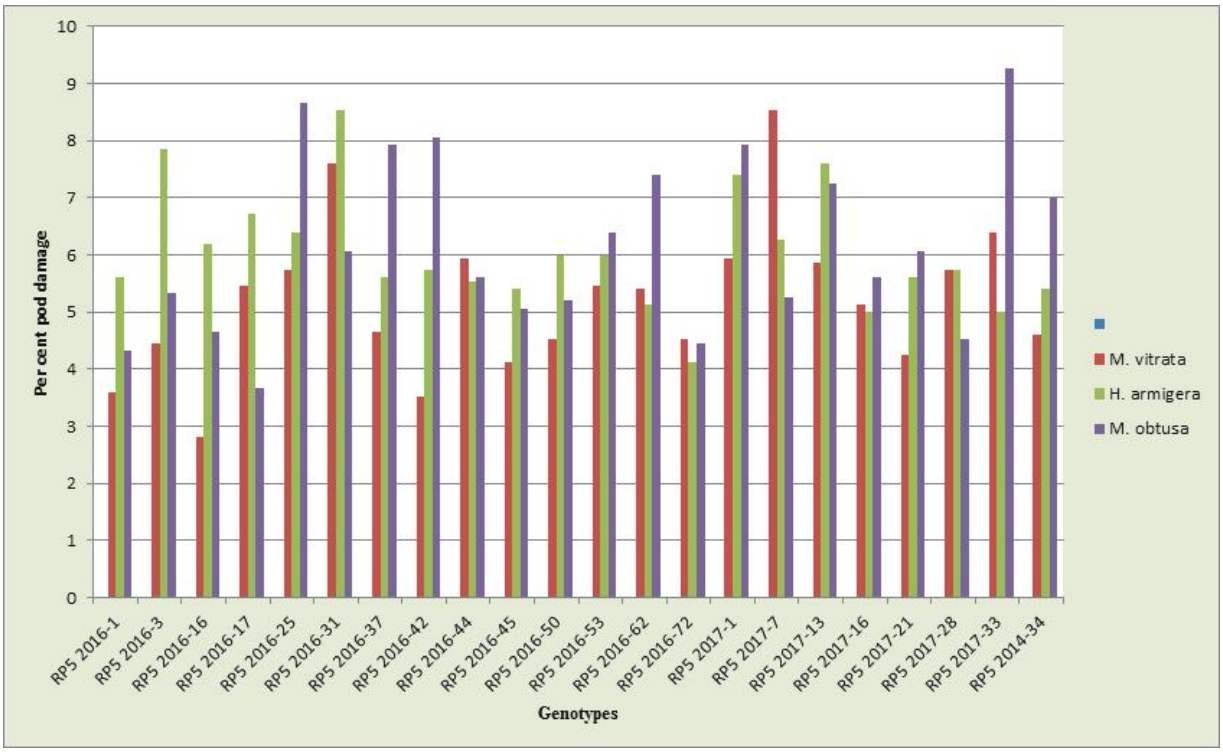

Fig. 1 : Per cent pod damage of different pigeon pea genotypes due to pod borer complex during (2023-24).

Plate 1 : Tur pod borer, *Helicoverpa armigera*.

Plate 2 : Spotted pod borer, *Maruca vitrata.*

The per cent pod damage caused by *M. obtusa* in the twenty-two genotypes ranged between 3.66% to 9.26% with significant differences among different genotypes. Minimum per cent pod damage was recorded in the genotype RP5-2016-17 of 3.66% followed by RP5-2016-1, RP5-2016-72 and RP5-2017-28 genotypes of 4.33%, 4.46%, 4.53%, respectively (Table 2). These were significantly lower than many of the other tested genotypes. Maximum per cent pod damage by *M. obtusa* was recorded in the genotype RP5-2017-33 of 9.26% followed by genotypes RP5-2016-25, RP5-2016-42 and

Plate 3 : Pod fly, *Melanagromyza obtusa.*

RP5-2016-37of 8.66%, 8.06% and 7.93%, respectively. These were significantly higher among the tested genotypes. In rest of the genotypes the per cent pod damage by *M. obtusa* were intermittent.

The current results are in agreement with the findings of Keval *et al*. (2017), who reported that the maximum pod damage due to pod fly were seen in KA-12-2 (49.97) followed by KA-12-3 (48.04) and NDA-1 (44.40) and lowest pod damage was observed in BAHAR (34.42) followed by MA-3 (34.43) and MAL13 (36.85).

Conclusion

The present investigation revealed significant variation among the evaluated pigeonpea (*Cajanus cajan* L.) genotypes for their response to the pod borer complex under natural field conditions during *Kharif* 2023–24. Genotypes showed considerable differences in pod damage caused by *Maruca vitrata*, *Helicoverpa armigera* and *Melanagromyza obtusa*. The lowest pod damage was recorded in RP5-2016-16 against *M. vitrata* (2.80%), RP5-2016-72 against *H. armigera* (4.13%), and RP5-2016-17 against *M. obtusa* (3.66%). The observed variability indicated the presence of resistance/tolerance among the tested genotypes. These promising genotypes can be utilized as valuable sources in pigeonpea breeding programmes for developing pod borer-resistant cultivars and can contribute to sustainable integrated pest management strategies.

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