



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2024; 13(4): 83-87

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www.thepharmajournal.com

Received: 09-02-2024

Accepted: 11-03-2024

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Screening of different duration pigeonpea genotypes against pod borers

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Abstract

The different duration pigeonpea genotypes were screened which showed significant difference between tested genotypes on different parameters viz., percent pod damage and grain yield. Genotypes UPAS 120 (RC), WRGE 124, and SKNP 1715 are early, mid-early, and medium duration genotypes respectively, showed least affected by pod borers. The highest grain yield was observed in UPAS 120 (RC), PT 0012, and PT 11-16 are early, mid-early, and medium duration genotypes respectively.

Keywords: Genotypes, pigeonpea, early, mid-early, medium

1. Introduction

Pulses are an important commodities group of crops that provide high-quality protein to the country's large vegetarian population, in addition to cereal proteins. Even though the nation cultivates the greatest amount of pulse crops worldwide, only 6-7% of the country's overall food grain output is derived from pulses. Pulses don't require much irrigation and are frequently cultivated in rainfed conditions. Furthermore, pulses offer several additional advantageous characteristics, including high protein content, improved soil fertility and structure, compatibility with crop rotation, mixed/intercropping systems, dry farming, and the ability to produce green vegetable pods and nutritious animal feed.

After chickpea, pigeonpea [*Cajanus cajan* (L.) Millsp.] Is regarded as one of India's most significant pulse crops. The annual/perennial legume known as pigeonpea (*Cajanus cajan*), often referred to as arhar or tur, is a member of the fabaceae family. Since at least 3500 years ago, when it was domesticated in the Indian subcontinent, its seeds have spread throughout Asia, Africa, and Latin America and are now a staple meal. It is widely consumed in South Asia and a significant source of protein for those living on the Indian subcontinent.

Globally, 60.96 million hectares are used to grow pigeonpeas, yielding 50.12 million tonnes with a productivity of 822.2 kg/ha (FAO STAT, 2020). With a yield of 887 kg/hectare in 2020-21, 42.8 lakh tonnes were grown on 48.24 lakh hectares. According to Agricoop (2021) India is the world's top producer of pigeonpeas. Over an area of 50.02 lakh hectares, the expected production of pigeonpea in Kharif 2021-2022 was 44.3 lakh tonnes.

Pigeonpea was linked to more than 350 insect pest species globally (Chhabra 2008) [2]. Approximately 66% of these bug species have only ever been discovered in India (Rolania *et al.*, 2021) [8]. A total of 250 bug species from 61 families and 8 orders are known to attack pigeonpea. Only a small number of lepidopteran species-including the Tur plume moth, *Exelastis atomosa* (Walsh), Tur pod borer, *Helicoverpa armigera* (Hubner), and Tur pod fly, *Melanagromyza obtusa* (Mall) are economically significant as pests. These species are known as the "Pod borer complex" (Lal, 1998; Patil *et al.*, 1990) [7, 12]. More than thirty species of lepidoptera feed on pigeonpea pods and seeds (Shanower *et al.*, 1999) [9].

2. Materials and Methods

The research was conducted during Kharif 2022-23 at the Research cum Instructional Farm, IGKV, Raipur (C.G.) by growing of different duration twenty-three pigeonpea genotypes viz., early, mid-early, and medium maturity groups.

Details of experiment

Next, on each plant that was marked, the total number of pods and the number of pods that had been damaged by pod borers were calculated and transformed into a percentage Each tested entry's yield and percentage of damaged pods were computed. Using the following formula, the proportion of pod damage and grain production (kg/ha) were determined.

Maturity type	Early	Mid-early	Medium
Total genotypes	06	11	06
Design	RBD	RBD	RBD
Replication	4	3	4
Plot size	3.60×4m	3.60×4m	3.60×4m

Observations recorded

Pod damage (%)	At harvest, 100 randomly selected pods were divided into percentages of pods injured by various pod borers according to the nature of damage. Nature of damage: <i>Helicoverpa armigera</i> : The pods have big, regular, circular holes. <i>Maruca vitrata</i> : Holes in the pods and irregular scraping. <i>Melanagromyza obtusa</i> : Holes the size of a pin near the outside edge of the pod.
Yield parameters	Grain yield was taken on whole plot basis

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

$$\text{Grain yields (Kg/ha)} = \frac{\text{weight of grains in kg/plot}}{\text{plot area in m}^2} \times 10000$$

The genotypes were grouped in to highly resistance, moderately susceptible, susceptible, and highly susceptible on the basis of Pest Resistance Rating (PRR) 1 to 9 rating scale as suggested by Abott, 1925 [1]

$$\text{PRR (\%)} = \frac{\text{P. D. of check} - \text{P. D. of tested genotype}}{\text{P. D. of check}} \times 100$$

Where,

P.D. = Mean of % pods damaged by pod borers

The pest resistance percentage is then converted to 1 to 9 rating adopting the following scale:

Pest resistance (%)	Score	Pest Resistance Rating (PRR)
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

Source: Technical program, IIPR, Kanpur, 2022

Statistical analysis: The acquired data were transformed appropriately before being statistically examined. The data collected from the pod borer complex larval population were transformed into square roots using the formula ($\sqrt{x + 0.5}$). Plant damage data on pod and grain damage was initially collected and then transformed to a percentage. Prior to statistical analysis, the percentage data were transformed using the arcsine transformation $\text{Sin}^{-1}(\sqrt{x}/100)$. Following the transformation of the data, Gomez and Gomez (1984) [5] described the analysis of variance method. The significance criterion for the "F" test was set at five percent.

Table 1: The skeleton of the analysis of variance

Source of variation	DF	SS	MSS	F cal	F tab	CD 5%
Replication (R)	(R-1)	RSS				
Treatment (T)	(T-1)	TrSS				
Error	(R-1)(T-1)	ESS				
Total	(R x T)-1	TSS				

The following formulae were used for standard error, critical difference and coefficient of variance estimations:

$$\text{C.D.} = \frac{\sqrt{2\text{EMSR}}}{R} \times t(\text{D.F. at } 5\%)$$

Where,

R=Number of Replications, D.F=Degrees of Freedom

T =Number of Treatments, SS=Sum of Square

CD=Critical Difference, EMS= Error Mean Square

M.S.S=Mean Sum of Square, GM=Grand Mean

3. Results and Discussion

3.1 Screening of different duration pigeonpea genotypes against pod borers

In the current study, 23 different duration pigeonpea genotypes viz., Early, mid-early, and medium were evaluated in the field against the tur pod borer (*Helicoverpa armigera*), spotted pod borer (*Maruca vitrata*), and podfly (*Melanagromyza obtusa*) under the field conditions. The infestation of pod borers was measured in terms of per cent pod damage during the harvesting stage of the crop.

3.2 Screening of early duration pigeonpea genotypes against pod borers

3.2.1 Tur pod borer, *Helicoverpa armigera* (Hubner)

Early genotypes were showed significantly difference with each other for per cent pod damage by tur pod borer (*H. armigera*) which varied from 4% to 8.25%. Among the all tested genotypes, minimum pod damage by *H. armigera* was observed in genotype of UPAS 120(RC) with 4 per cent, whereas the maximum pod damage was observed in Pusa Arhar-16 with 8.25 per cent.

3.2.2 Spotted pod borer, *Maruca vitrata* (Fabricius)

The percentage of pod damage by spotted pod borer (*Maruca vitrata*) in the early genotypes was ranged from 3% to 7%, indicated a significant variation between the genotypes. The examined genotype UPAS 120 (RC) had the least amount of pod damage with 4% and maximum per cent pod damage was observed in Pusa Arhar-16 with 7%.

3.2.3 Tur pod fly, *Melanagromyza obtusa* (Malloch)

Genotypes differed considerably from one another in terms of the percentage of pod damage caused by tur pod flies (*M. obtusa*), ranging from 3.25% to 7%. The genotype PA 662 showed the least amount of pod damage caused by *M. obtusa* among the examined genotypes with 3.25%, whereas Pusa Arhar-16 showed the most pod damage with 7%.

3.3 Screening of mid-early duration pigeonpea genotypes against pod borers

3.3.1 Tur pod borer, *Helicoverpa armigera* (Hubner)

During the crop's harvesting period, the percentage of pod damage caused by the pod borer infestation was calculated. When it came to the percentage of pod damage caused by the Turpod Borer (*H. armigera*), these mid-early genotypes differed significantly from one another, ranging from 2.33% to 6.33%. Of all the genotypes that were examined, WRGE-124 genotype showed the least amount of pod damage caused by *H. armigera* (2.33%), while PT 12-19-2 genotype showed the highest amount of pod damage (6.33%).

3.3.2 Spotted pod borer, *Maruca vitrata* (Fabricius)

The percentage of pod damage by spotted pod borer (*Maruca vitrata*) in the mid-early genotypes was ranged from 1.67% to 5.67%, indicated a significant variation between the genotypes. The examined genotype AKTE 19-05 had the least amount of pod damage with 1.67% and highest per cent pod damage was recorded in PT 2017-2 with 5.67%.

3.3.3 Tur pod fly, *Melanagromyza obtusa* (Malloch)

The percentage of pod damage caused by the tur pod fly (*M. obtusa*) varied between 1.33% and 7.33%, and genotypes exhibited a substantial difference with each other in this regard. The genotype BDN 711(RC) showed the least pod damage with 1.33% by *M. obtusa* among the examined genotypes, whereas the genotype PT 12-19-2 showed the most pod damage with 7.33%.

3.4 Screening of medium duration pigeonpea genotypes against pod borers

3.4.1 Tur pod borer, *Helicoverpa armigera* (Hubner)

The percentage of pod damage during the crop's harvesting stage was used to calculate the infestation of pod borers. When it came to the percentage of pod damage caused by the Tur Pod Borer (*H. armigera*), which ranged from 3.50% to 7.50%, these medium genotypes considerably differed from one another. AKTM 1914 showed the highest pod damage, at 7.50%, whereas the genotype of SKNP 1715 showed the least pod damage among all studied genotypes, at 3.50%.

3.4.2 Spotted pod borer, *Maruca vitrata* (Fabricius)

The percentage of pod damage by spotted pod borer (*Maruca vitrata*) in the medium genotypes was ranged from 1.75% to 4.25%, indicated a significant variation between the genotypes. The examined genotype BDN 716 (RC) had the least amount of pod damage with 1.75% and maximum per cent pod damage was recorded in AKTM 1914 with 4%.

3.4.3 Tur pod fly, *Melanagromyza obtusa* (Malloch)

During the harvesting stage of the crop, the infestation of pod fly was measured in terms of per cent pod damage. Genotypes were showed significantly difference with each other for per cent pod damage by tur pod fly (*M. obtusa*) which varied from 3.25% to 6.50%. Among the tested genotypes, minimum pod damage by *M. obtusa* was observed in genotype SKNP 1715 with 3.25%, whereas the maximum pod damage was observed in AKTM 1914 with 7.33 per cent.

Present observations were in confirmation with Srivastava and Mohapatra (2002) [11], at Varanasi (U. P.), India, observed fifteen medium-duration pigeonpea genotypes. This study examines the extent of pod damage in insecticide-free situations caused by lepidopterous pod borers (LPBs),

including the gramme pod borer (*Helicoverpa armigera*), legume pod borer (*Maruca vitrata*), plume moth (*Exelastis atomosa*), and pod fly (*Melanagromyza obtusa*). Pod fly and LPB-caused pod damage varied from 15.1 to 33.1% and 1.0 to 6.3%, respectively.

3.5 Reaction of pigeonpea different duration genotypes against pod borers during Kharif 2022-23.

The total of 23 different duration pigeonpea genotypes viz., early, mid-early, and medium were screened to check the resistance and susceptibility against pod borers (Tur pod borer, spotted pod borer, and Tur pod fly). The statistical analyzed data presented in Table 03.

Among all the 6 genotypes of early duration pigeonpea, no genotype was found to be immune, highly resistant, resistant, moderately resistant, and tolerant with respect to per cent pod damage against *H. armigera*, *Maruca vitrata*, and *M. obtusa*. Whereas, one genotype [UPAS 120 (RC)] registered as equal to check, three genotypes (Pusa Arhar 2018-4, Pusa Arhar 21-29, and PA 662) were noted as moderately susceptible. Likewise, NAAM 88 and Pusa Arhar-16 were noted as susceptible and highly susceptible, respectively.

Among all the 11 genotypes of mid-early duration pigeonpea, no genotype was found to be immune, highly resistant, resistant, and moderately resistant with respect to per cent pod damage against *H. armigera*, *Maruca vitrata*, and *M. obtusa*. Whereas, one genotype (WRGE 124) registered as tolerant, three genotypes (BDN 711 RC, TDRG 272, and AKTE 19-05) were noted as equal to check. Likewise, ICPL 17103 and Daftari Manik were noted as moderately susceptible and susceptible, respectively. Whereas, five genotypes namely, PT 2017-2, RVSA 14-2, PT 12-19-2, WRGE-134, and PT 0012 were screened as highly susceptible.

Among all the 6 genotypes of medium duration pigeonpea, no genotype was found to be immune, highly resistant, resistant, and moderately resistant with respect to per cent pod damage against *H. armigera*, *Maruca vitrata*, and *M. obtusa*. Whereas, one genotype (SKNP 1715) registered as tolerant, two genotypes (BDN 716 RC, PT 12-5-5-1) were noted as equal to check. Likewise, BDN 2013-5, PT 11-16, and AKTM 1914 were noted as moderately susceptible, susceptible, and highly susceptible, respectively.

Present findings were more or less related to Kavitha and Vijayaraghavan (2018) [6] when they screened 145 entries to identify the sources of resistance in pigeonpea to the *Maruca vitrata* and *Helicoverpa armigera*. Nine of the 145 entries-ICP 11007, H 23, BAHAR, DA 322, GR 28, ICP 49114, ICP 11957, SMR 1693158, and BRG-10-02 showed a stable resistant reaction to *M. vitrata*, making them promising. For the entire three years, 17 entrants continuously displayed resistance to *H. armigera*. *M. vitrata* was found to have a minimal pest susceptibility index (PSI) of 2.0 in ICP 11957, 2.3 in SMR 1693158, and 2.7 in BRG-10-02, Bahar, and H 23 records. Less PSI for *H. armigera* was seen in H 23, JKE 110, GR 28, WRG 42, ICP 11957, and ICPL 8719 (2.3).

3.6 Grain yield

Among the all screened pigeonpea genotypes of different duration, the highest grain yield of pigeonpea was recorded in UPAS 120(RC) as 532.29 kg/ha, PT 0012 as 1130 kg/ha, and PT 11-16 as 901.04 kg/ha are early, mid-early, and medium duration genotypes, respectively (Table 02). Whereas, the lowest grain yield was recorded in Pusa Arhar 2018-4 as 167.08 kg/ha, BDN 711 as 280.28 kg/ha, and SKNP 1715 as

456.25 kg/ha are early, mid-early, and medium duration genotypes, respectively (Table 02). Singh *et al.* (2017) [10] reported that there were considerable differences in the grain

yield across the genotypes, with IVT-510 exhibiting a yield of 479 kg/ha and IVT-520 exhibiting a yield of 3314 kg/ha.

Table 2: Screening of different duration pigeonpea genotypes against pod borers during Kharif (2022-23)

Genotypes	<i>Maruca vitrata</i>	% Pod Damage <i>Helicoverpa armigera</i>	<i>M. obtusa</i>	Yield (kg / ha)
Early Genotypes				
PA 662	6.50 (14.66)	4.50 (11.86)	3.25 (10.18)	371.25
Pusa Arhar 21-29	4.25 (11.80)	6.00 (14.15)	3.75 (11.10)	303.33
NAAM 88	4.75 (12.49)	5.50 (13.41)	5.75 (13.76)	309.79
Pusa Arhar-16	7.00 (15.24)	8.25 (16.65)	7.00 (15.32)	217.71
Pusa Arhar 2018-4	3.25 (10.25)	5.75 (13.80)	4.00 (11.37)	167.08
UPAS 120(RC)	3.00 (9.93)	4.00 (11.49)	4.50 (12.03)	532.29
CD @ 5%	3.71	3.07	2.99	112.02
CV Mid-early genotypes	19.71	14.88	16	23.24
ICPL 17103	2.67 (9.36)	4.33 (11.99)	3.67 (10.95)	1124.17
PT 2017-2	5.67 (13.68)	5.00 (12.87)	7.00 (15.31)	907.5
AKTE 19-05	1.67 (7.33)	3.33 (10.34)	3.33 (10.49)	809.44
Daftari Manik	5.00 (12.87)	3.67 (11.01)	4.00 (11.37)	851.11
WRGE 124	2.00 (7.95)	2.33 (8.74)	3.00 (9.88)	895
RVSA 14-2	3.67 (10.86)	5.33 (13.34)	5.00 (12.87)	1001.67
TDRG 272	2.67 (9.36)	4.00 (11.37)	2.67 (9.26)	958.89
PT 12-19-2	3.33 (10.40)	6.33 (14.50)	7.33 (15.65)	917.22
WRGE-134	4.67 (12.35)	6.00 (14.14)	5.67 (13.72)	841.67
BDN 711(RC)	2.67 (9.36)	4.67 (12.13)	1.33 (6.53)	280.28
PT 0012	3.00 (9.88)	5.67 (13.68)	5.33 (13.26)	1130
CD @ 5%	3.03	3.2	2.86	365.08
CV	17.15	15.33	14.2	24.09
Medium genotypes				
PT 11-16	2.75 (9.51)	5.50 (13.45)	5.50 (13.54)	901.04
SKNP 1715	2.25 (8.59)	3.50 (10.98)	3.25 (10.36)	456.25
BDN 2013-5	3.50 (10.52)	5.50 (13.45)	4.75 (12.46)	759.79
PT 12-5-5-1	2.50 (9.05)	3.75 (11.10)	4.50 (12.22)	882.08
AKTM 1914	4.25 (11.69)	7.50 (15.88)	6.50 (14.71)	774.58
BDN 716 (RC)	1.75 (7.39)	4.50 (11.98)	4.25 (11.80)	674.38
CD @ 5%	2.62	3.09	2.08	156.29
CV	18.25	15.89	10.93	13.86

Figure in the parenthesis are arc sine transformed values; RC = Resistant Check

Fig 1 Reaction of pigeonpea different duration genotypes against pod borers during Kharif 2022-23

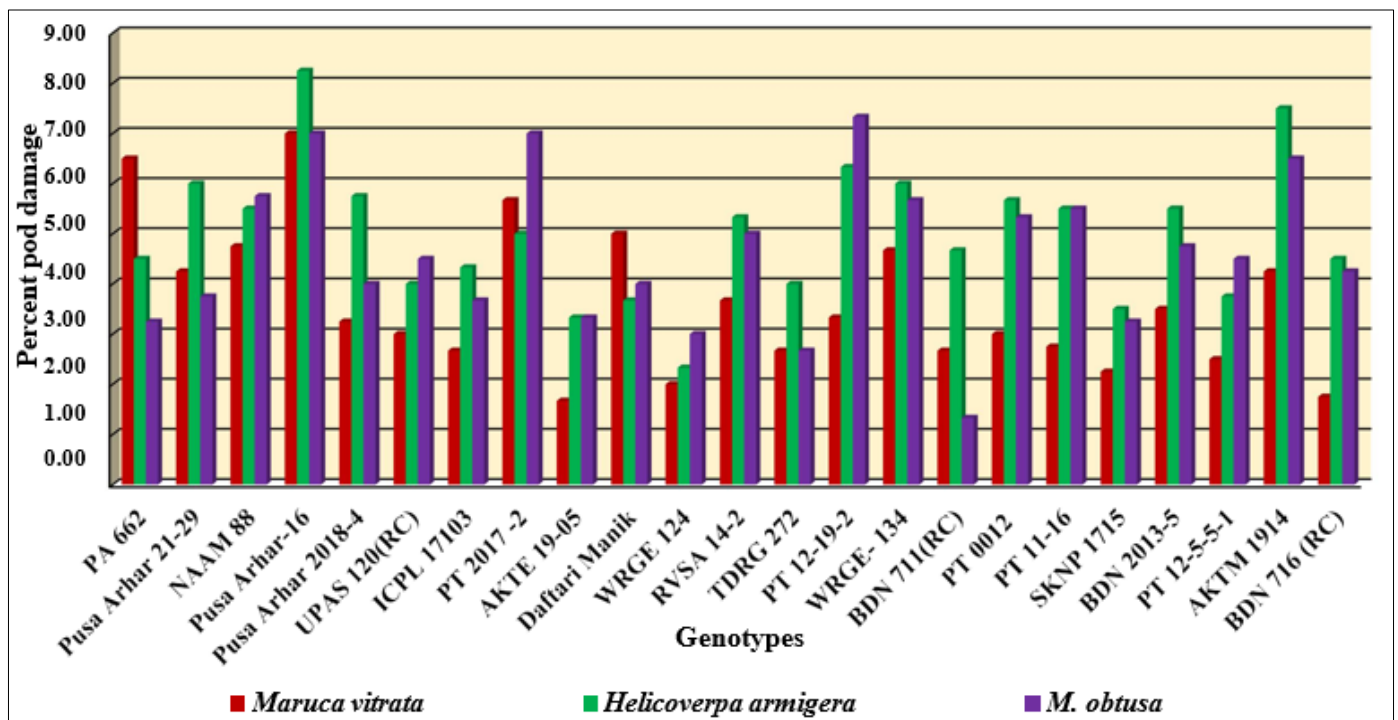


Fig 1: Percent pod damage due to different pod borers on different duration pigeonpea genotypes

4. Conclusion

The different duration pigeonpea genotypes were screened which showed significant difference between tested genotypes on different parameters *viz.*, percent pod damage and grain yield. Genotypes UPAS 120(RC), WRGE 124, and SKNP 1715 are early, mid-early, and medium duration genotypes respectively, showed least affected by pod borers. The highest grain yield was observed in UPAS 120(RC), PT 0012, and PT 11-16 are early, mid-early, and medium duration genotypes respectively.

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