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## High throughput evaluation of *Cajanus scarabaeoides* pigeonpea progenies for identifying gram pod borer tolerance

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**Abstract**

The pigeonpea pods of 89 genotypes, derived from Early 3 X ICP 15685 (*Cajanus scarabaeoides*) and UPAS120 X ICP15761 were subjected to detached pod assay against pod borer, *Helicoverpa armigera* larva under no-choice condition for assessing their tolerance in four batches of experiment. The highest pod consumption (0.320g/larva, 0.257g/larva, 0.160g/larva and 0.270g/larva) was recorded from the genotypes viz., WD22-1-5, WD 24-1-5 & WDBCE 2-1-1, WDBCE 3-3-1 and WD 5-5-3. The lowest pod consumption and consumption index (CI) is noticed from the following 4 genotypes, WD22-3-3 (0.060g/larva & 0.085), WD 24-1-6 (0.070g/larva & 1.18), WDBCE 3-4-2 (0.080g/larva & 1.15) and WD 5-3-2 (0.087g/larva & 0.89). Out of 89 pigeonpea genotypes screened, 16 were moderately tolerant to pod borer (RFDP: 61 to 80) while a single genotype, WD22-3-3 was found to be tolerant with highest RFDP (81.25). These 17 pigeonpea genotypes are being stabilized and can be exploited further in the pigeonpea improvement programme for incorporating pod borer resistance.

**Keywords:** pigeonpea, consumption index, host plant resistance and *Helicoverpa armigera*

**1. Introduction**

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is one of the important grain legumes in India and the world. It has a production of 4.87 million tonnes from an area of 5.38 million hectares during 2017<sup>[1]</sup>. Due to biotic and abiotic factors the productivity of pigeonpea in India is still low. More than 200 insect pests belonging to 8 orders were known to infest pigeonpea at various growth stages<sup>[2]</sup>. The pod borer, *Helicoverpa armigera* Hubner (Lepidoptera: Noctuidae), is an important key pest that inflicts a yield loss up to US\$ 2 billion annually<sup>[3, 4]</sup>. Pod borer damage alone causes 70-80% yield loss in pigeonpea<sup>[5, 6]</sup>. By virtue of pod borer's polyphagous nature, high fecundity, migrating ability and insecticide resistance, it can survive throughout the year in one or another crop and inflicts heavy yield loss. Synthetic insecticides like chlorpyrifos 20EC (0.1%), cypermethrin 25EC (0.0175%) and profenophos + cypermethrin (0.044%) were widely used for managing the pod borer. The over use of synthetic insecticides had destabilized the agro-ecosystem and led to development of insecticide resistance in pod borer<sup>[7]</sup>. The pod borer resistance to pyrethroids, organophosphorus and carbamates has been reported in many Asian countries<sup>[8-10]</sup> Africa<sup>[11]</sup> and Australia<sup>[12, 13]</sup>. Hence, alternate sustainable strategies like host plant resistance in pigeonpea has to be explored. Sharma *et al.* (2005)<sup>[4]</sup> had screened more than 15000 pigeonpea accessions none of them possess a high level of resistance to pod borer. The main reason for the lack of high resistance in cultivated accessions is because of the narrow genetic diversity. Most of the modern cultivated accessions were derived from *Cajanus cajan*. Some of the wild pigeonpea accessions belonging to *C. scarabaeoides*, *C. lineatus*, *C. sericeus*, *C. platycarpus*, *R. aurea*, *Flemingia bracteata* and *C. acutifolius* were reported to possess high levels of resistance to *H. armigera*<sup>[14-17]</sup>. This resistance can be exploited through interspecific crossing with wild progenitors and subsequent back crossing. There is a lack of technique for high throughput screening of pigeonpea genotypes under uniform pod borer infestation. Hence, in the present investigation, 89 wild derivatives of pigeonpea from 2 different crosses were screened in laboratory against *H. armigera* larvae to identify tolerant genotypes.

## 2. Materials and Methods

### 2.1 Pigeonpea cultivation and pod borer screening:

Eighty nine wild derivatives of pigeonpea emanated from pre-breeding programme involving *C. scarabaeoides* – accession number ICP 15685 & ICP 15761 were screened against *Helicoverpa armigera* larva under laboratory condition for identifying their pod borer resistance. Among the 89 genotypes, 27 genotypes (stage: BC<sub>1</sub>F<sub>5</sub>) were progenies of Early 3 X ICP 15685 while 62 (stage: F<sub>6</sub>) were derived from UPAS120 X ICP15761. All the genotypes were sown in cemented pots (119cm X 119cm X 80cm) with a spacing of 20cm X 15cm at ICAR-Indian Institute of Pulses Research, Kanpur (U.P.), India during *Kharif* 2015-2016. Standard agronomic practices like two hand weeding and periodical irrigation were given to raise a healthy crop. The plants were raised without any insecticidal spray. At the time of pod formation, green pods having fully developed seed (20 days after flowering *vis-a-vis* pod length  $\geq 35$ mm) were collected for conducting no choice assay with detached pods. The detached pod assay was conducted in completely randomized design (CRD) with 3 replications for each genotype. The 89 genotypes were screened in 4 batches having 24 genotypes in each batch except the 4<sup>th</sup> batch according to pod

availability/maturation. In the 4<sup>th</sup> batch 17 genotypes were screened. The pods from each genotype were collected along with the pedicel in a separate sample bag and it was washed twice with tap water to remove adhering inert material. The pods were dipped in 0.5% sodium hypochlorite for 30 seconds and then it was gently washed with sterile water and kept under a fan for 3 minutes. The sterilised pods were inserted into 2% water agar after recording initial pod weight using a precision balance (Citizen) in 50ml sample container. After 3 days, the final pod weight was recorded. The pod consumption by *H. armigera* larva in each genotype was calculated by detecting the final pod weight from the initial pod weight. Further the average pod consumption of each genotype was calculated. The number of bore holes present in each pod was counted and recorded on the 3<sup>rd</sup> day and each genotype's average was calculated. Relative Feeding Deterrence Percentage (RFDP) for each genotype was calculated based on the pod weight consumption by *H. armigera* larvae. The RFDP scores were grouped into 5 different categories (Table 1), higher values indicate less preference while lower values indicate higher preference by the larvae for feeding. Thus based on the pod consumption host plant reaction is identified with the help of RFDP.

$$\text{RFDP} = \left[ \frac{\text{Genotype having highest average pod consumption (g) in that batch} - \text{Average pod weight consumed in test genotype}}{\text{Genotype having highest average pod consumption (g) in that batch}} \right] \times 100$$

**Table 1:** Pigeonpea scoring based on relative feeding deterrence percentage (RFDP)

S. No.	RFDP Range	Pest susceptibility category
1.	0-20	Highly susceptible
2.	21-40	Susceptible
3.	41-60	Intermediate
4.	61-80	Moderately tolerant
5.	81-94	Tolerant
6.	95-100	Immune

### 2.2 *Helicoverpa armigera* maintenance and its consumption index:

The pod borer, *Helicoverpa armigera* larvae were maintained on artificial diet placed in 25 ml sample containers at a temperature of 25±1°C, 75±5% RH with a photoperiod of 16:8 in Remi environmental chamber [18]. Pre-starved *H. armigera* larva (ten days old) was deployed for detached pod assay under no choice condition. The initial and final larval weights were recorded before and after pod consumption for 3 days. The mean weight of *H. armigera* larva was calculated for computing the consumption index (CI). CI is a very useful parameter to access the palatability of the test genotype for *H. armigera* larva and it is calculated as given below [19],

$$\text{CI} = \frac{\text{Weight of pod consumed (g)}}{\text{Time (days)} \times \text{Mean weight of insect (g)}}$$

The pod weight consumption, larval weight gain and average number of bore holes per pod were subjected to Proc ANOVA and grouping was done based on DMRT in SAS 9.2 version. The average number of bore holes per pod was subjected to square root transformation before analysis in SAS 9.2.

## 3. Results and Discussion

### 3.1 Pod borer screening based on pod consumption:

In the first batch (Table 2) pigeonpea pods from 24 genotypes (progenies of UPAS120 X ICP15761) were screened against *H. armigera* larva under no choice condition. The minimum pod consumption was 0.06g (WD 22-3-3) followed by 0.077g (WD 22-1-1). These two genotypes recorded significantly less damage than WD22-1-5 (0.320g) genotype. Concurrently, the above two genotypes recorded highest RFDP (81.25 & 76.04). A total of 4 genotypes (WD 5-3-3, WD 5-6-3, WD 9-1-2, WD 22-1-1 and WD 24-1-1) were found to be moderately tolerant and 1 genotype viz., WD 22-3-3 was found to be tolerant to pod borer based on the RFDP value (Table 1 & 6). The higher level of tolerance might be imparted from the *C. scarabaeoides* (ICP15761). The present finding is in accordance with Mallikarjuna *et al.* (2007) [20], Mallikarjuna *et al.* (2011) [21], Green *et al.* (2006) [17] and Sharma *et al.* (2009) [15]. They also had reported that interspecific derivatives of *C. scarabaeoides*, *C. platycarpus* and *C. acutifolius* showed high level of resistance against *H. armigera*.

**Table 2:** No-choice assay for wild derivatives of pigeonpea against *Helicoverpa armigera* (batch 1)

Wild derivatives	Average pod weight consumed (g)/larva	Average larval weight gain (g)/larva	RFDP	CI	Average number of bore holes /pod*
WD5-3-3	0.107 <sup>a,b</sup>	0.020 <sup>a,b,c</sup>	66.67	1.72	1.00 (1.22 <sup>a,b,c</sup> )
WD5-5-1	0.213 <sup>a,b</sup>	0.048 <sup>a,b,c</sup>	33.33	1.89	1.33 (1.34 <sup>a,b,c</sup> )
WD5-6-2	0.283 <sup>a,b</sup>	0.066 <sup>a,b</sup>	11.46	1.85	1.00 (1.17 <sup>b,c</sup> )
WD5-6-3	0.090 <sup>a,b</sup>	0.006 <sup>c</sup>	71.88	1.96	0.00 (0.71 <sup>c</sup> )
WD5-6-4	0.230 <sup>a,b</sup>	0.0427 <sup>a,b,c</sup>	28.13	2.02	1.33 (1.29 <sup>a,b,c</sup> )
WD5-6-5	0.203 <sup>a,b</sup>	0.030 <sup>a,b,c</sup>	36.46	2.10	1.67 (1.39 <sup>a,b,c</sup> )

WD5-10-2	0.243 <sup>a,b</sup>	0.0417 <sup>a,b,c</sup>	23.96	2.11	3.00 (1.86 <sup>a</sup> )
WD5-12-4	0.220 <sup>a,b</sup>	0.046 <sup>a,b,c</sup>	31.25	1.81	1.67(1.46 <sup>a,b</sup> )
WD9-1-1	0.133 <sup>a,b</sup>	0.022 <sup>a,b,c</sup>	58.33	1.61	1.00 (1.17 <sup>b,c</sup> )
WD9-1-2	0.090 <sup>a,b</sup>	0.014 <sup>b,c</sup>	71.88	1.46	0.33 (0.88 <sup>b,c</sup> )
WD22-1-1	0.077 <sup>b</sup>	0.0101 <sup>b,c</sup>	76.04	1.35	0.67 (1.05 <sup>b,c</sup> )
WD22-1-2	0.237 <sup>a,b</sup>	0.040 <sup>a,b,c</sup>	26.04	1.96	1.00 (1.17 <sup>b,c</sup> )
WD22-1-3	0.237 <sup>a,b</sup>	0.044 <sup>a,b,c</sup>	26.04	2.50	1.00 (1.17 <sup>b,c</sup> )
WD22-1-4	0.283 <sup>a,b</sup>	0.058 <sup>a,b,c</sup>	11.46	2.10	1.67 (1.46 <sup>a,b</sup> )
WD22-1-5	0.320 <sup>a</sup>	0.074 <sup>a</sup>	0.00	1.89	1.67 (1.46 <sup>a,b</sup> )
WD22-1-6	0.210 <sup>a,b</sup>	0.033 <sup>a,b,c</sup>	36.46	2.64	2.00 (1.56 <sup>a,b</sup> )
WD22-2-1	0.173 <sup>a,b</sup>	0.042 <sup>a,b,c</sup>	45.83	2.15	1.67 (1.46 <sup>a,b</sup> )
WD22-2-2	0.146 <sup>a,b</sup>	0.035 <sup>a,b,c</sup>	54.17	1.96	1.67 (1.46 <sup>a,b</sup> )
WD22-2-3	0.177 <sup>a,b</sup>	0.039 <sup>a,b,c</sup>	44.79	2.22	1.33 (1.34 <sup>a,b,c</sup> )
WD22-2-5	0.163 <sup>a,b</sup>	0.0197 <sup>a,b,c</sup>	48.96	3.11	1.00(1.10 <sup>b,c</sup> )
WD22-3-1	0.133 <sup>a,b</sup>	0.031 <sup>a,b,c</sup>	58.33	1.55	0.67 (1.05 <sup>b,c</sup> )
WD22-3-2	0.163 <sup>a,b</sup>	0.037 <sup>a,b,c</sup>	48.96	1.62	1.00 (1.22 <sup>a,b,c</sup> )
WD22-3-3	0.060 <sup>b</sup>	0.0187 <sup>a,b,c</sup>	81.25	0.85	0.67 (1.05 <sup>b,c</sup> )
WD24-1-1	0.103 <sup>a,b</sup>	0.006 <sup>c</sup>	67.71	3.18	0.67 (1.05 <sup>b,c</sup> )

\* Values inside parentheses are square root transformed

Twelve progenies from both the crosses (UPAS120 X ICP15761 and Early 3 X ICP 15685) were screened in the second batch (Table 3). Among the 24 genotypes, the lowest pod consumption was recorded from WD 24-1-6 (0.070g) and it was on par with WD 22-2-4 (0.083g) whereas it was significantly lower than WD 24-1-5 (0.257g), WDBCE 2-1-1 (0.257g), WDBCE 2-1-2 (0.250g) and WDBCE 2-1-3 (0.253g). Among the 12 progenies of Early 3 cross, lowest pod consumption was recorded from WDBCE 2-3-4 (0.097g). The RFDP score indicates that 2 progenies of UPAS 120 X ICP15761 [WD 24-1-6 (73.08), WD 22-2-4 (67.95)] and 1

progeny of Early 3 X ICP 15685 [WDBCE 2-3-4 (62.82)] were moderately tolerant to pod borer. Eventhough, 3 genotypes were found to be moderately pod borer tolerant, there is variation in degree of tolerance that is reflected in the RFDP of WD 24-1-6 and WDBCE 2-3-4. The present finding corroborates with Choudhary *et al.* (2013) [22] wherein they had reported variation in degree of resistance among the accessions of *C. scarabaeoides*. Thus RFDP helps in differentiating the degree of pod borer resistance very efficiently based on the physico-chemical characters of pod.

**Table 3:** No-choice assay for wild derivatives of pigeonpea against *Helicoverpa armigera* (batch 2)

Wild derivatives	Average pod weight consumed (g)/larva	Average larval weight gain (g)/larva	RFDP	CI	Average number of bore holes /pod*
WD 24-1-2	0.187 <sup>a,b,c</sup>	0.031 <sup>a,b</sup>	28.21	2.16	3.33 (1.94 <sup>a,b,c</sup> )
WD 24-1-3	0.153 <sup>a,b,c</sup>	0.033 <sup>a,b</sup>	41.03	1.46	0.67 (1.05 <sup>d,e</sup> )
WD 24-1-4	0.217 <sup>a,b,c</sup>	0.052 <sup>a,b</sup>	16.67	1.71	1.67 (1.46 <sup>b,c,d,e</sup> )
WD 24-1-5	0.257 <sup>a</sup>	0.049 <sup>a,b</sup>	1.28	2.07	3.67 (2.00 <sup>a,b</sup> )
WD 24-1-6	0.070 <sup>c</sup>	0.014 <sup>b</sup>	73.08	1.18	0.66 (1.00 <sup>e</sup> )
WD 24-2-1	0.140 <sup>a,b,c</sup>	0.023 <sup>a,b</sup>	46.15	1.57	1.33 (1.27 <sup>b,c,d,e</sup> )
WD 24-2-2	0.153 <sup>a,b,c</sup>	0.026 <sup>a,b</sup>	41.03	1.47	1.00 (1.17 <sup>c,d,e</sup> )
WD 22-2-3	0.237 <sup>a,b,c</sup>	0.043 <sup>a,b</sup>	8.97	1.79	0.67 (1.05 <sup>d,e</sup> )
WD 22-2-4	0.083 <sup>b,c</sup>	0.015 <sup>b</sup>	67.95	1.31	0.67 (1.05 <sup>d,e</sup> )
WD 22-2-5	0.230 <sup>a,b,c</sup>	0.029 <sup>a,b</sup>	11.54	2.19	5.33 (2.42 <sup>a</sup> )
WD 22-2-6	0.233 <sup>a,b,c</sup>	0.044 <sup>a,b</sup>	10.26	1.89	3.33 (1.95 <sup>a,b,c</sup> )
WD 22-2-7	0.157 <sup>a,b,c</sup>	0.028 <sup>a,b</sup>	39.74	1.46	1.33 (1.27 <sup>b,c,d,e</sup> )
WDBCE 3-3-8	0.163 <sup>a,b,c</sup>	0.028 <sup>a,b</sup>	37.18	1.67	1.67 (1.39 <sup>b,c,d,e</sup> )
WDBCE 2-1-1	0.257 <sup>a</sup>	0.061 <sup>a</sup>	1.28	1.65	1.67 (1.46 <sup>b,c,d,e</sup> )
WDBCE 2-1-2	0.250 <sup>a,b</sup>	0.052 <sup>a,b</sup>	3.85	1.82	1.67 (1.46 <sup>b,c,d,e</sup> )
WDBCE 2-1-3	0.253 <sup>a</sup>	0.060 <sup>a</sup>	2.56	1.74	1.33 (1.34 <sup>b,c,d,e</sup> )
WDBCE 2-2-1	0.180 <sup>a,b,c</sup>	0.046 <sup>a,b</sup>	30.77	1.45	1.67 (1.46 <sup>b,c,d,e</sup> )
WDBCE 2-2-2	0.110 <sup>a,b,c</sup>	0.013 <sup>b</sup>	57.69	1.50	0.67 (1.05 <sup>d,e</sup> )
WDBCE 2-3-1	0.177 <sup>a,b,c</sup>	0.035 <sup>a,b</sup>	32.05	1.54	1.33 (1.29 <sup>b,c,d,e</sup> )
WDBCE 2-3-2	0.197 <sup>a,b,c</sup>	0.049 <sup>a,b</sup>	24.36	1.57	1.67 (1.46 <sup>b,c,d,e</sup> )
WDBCE 2-3-3	0.197 <sup>a,b,c</sup>	0.039 <sup>a,b</sup>	24.36	1.72	1.67 (1.46 <sup>b,c,d,e</sup> )
WDBCE 2-3-4	0.097 <sup>a,b,c</sup>	0.021 <sup>a,b</sup>	62.82	1.37	1.33 (1.27 <sup>b,c,d,e</sup> )
WDBCE 2-3-5	0.147 <sup>a,b,c</sup>	0.015 <sup>b</sup>	43.59	2.24	1.33 (1.29 <sup>b,c,d,e</sup> )
WDBCE 3-2-3	0.120 <sup>a,b,c</sup>	0.020 <sup>a,b</sup>	53.85	1.78	3.00 (1.81 <sup>a,b,c,d</sup> )

\* Values inside parentheses are square root transformed

In third batch, 14 progenies of Early 3 X ICP 15685 and 10 progenies of UPAS120 X ICP15761 were screened (Table 4). The lowest pod weight consumption was 0.043g (WDBCE3-3-5 and WDBCE 3-3-6) and it was on par with WDBCE 3-3-1 which had recorded highest pod weight consumption (0.160g). Four genotypes (WDBCE3-3-5, WDBCE 3-3-6,

WDBCE 3-3-7 and WDBCE 3-2-1) of Early 3 X ICP 15685 and a single genotype (WD 24-2-4) of UPAS120 X ICP15761 were found to be moderately tolerant based on RFDP score. The genotypes WDBCE3-3-5, WDBCE 3-3-6 had scored highest RFDP of 72.92 and lowest pod consumption (0.043g). The lowest pod consumption indicates the less preference of

Pods of above mentioned genotypes by *H. armigera* larva due to the pod morphology. This is supported by reports of Shanower *et al.* (1997)<sup>[23]</sup> and Sharma *et al.* (2009)<sup>[15]</sup>. They had documented the role of pod toughness, structure of pod

wall, trichomes on the pod surface in *H. armigera* resistance. The nature (Non glandular Type C) and density of pod trichomes imparts *H. armigera* resistance in *C. scarabaeoides*.

**Table 4:** No-choice assay for wild derivatives of pigeonpea against *Helicoverpa armigera* (batch 3)

Wild derivatives	Average pod weight consumed (g)/larva	Average larval weight gain (g)/larva	RFDP	CI	Average number of bore holes/pod*
WDBCE 3-2-4	0.060 <sup>a</sup>	0.015 <sup>a,b,c,d</sup>	62.50	1.07	1.00 (1.22 <sup>a,b</sup> )
WDBCE 3-3-1	0.160 <sup>a</sup>	0.033 <sup>a</sup>	0.00	2.11	1.67 (1.46 <sup>a,b</sup> )
WDBCE 3-3-2	0.080 <sup>a</sup>	0.009 <sup>b,c,d</sup>	50.00	2.22	0.33 (0.88 <sup>b</sup> )
WDBCE 3-3-3	0.103 <sup>a</sup>	0.019 <sup>a,b,c,d</sup>	35.42	1.97	1.00 (1.22 <sup>a,b</sup> )
WDBCE 3-3-4	0.053 <sup>a</sup>	0.003 <sup>c,d</sup>	66.67	1.72	1.00 (1.22 <sup>a,b</sup> )
WDBCE3-3-5	0.043 <sup>a</sup>	0.002 <sup>d</sup>	72.92	2.41	0.33 (0.88 <sup>b</sup> )
WDBCE 3-3-6	0.043 <sup>a</sup>	0.007 <sup>b,c,d</sup>	72.92	1.38	1.00 (1.22 <sup>a,b</sup> )
WDBCE 3-3-7	0.057 <sup>a</sup>	0.009 <sup>b,c,d</sup>	64.58	1.95	1.00 (1.22 <sup>a,b</sup> )
WDBCE 3-4-2	0.080 <sup>a</sup>	0.018 <sup>a,b,c,d</sup>	50.00	1.55	1.33 (1.34 <sup>a,b</sup> )
WDBCE 3-4-3	0.063 <sup>a</sup>	0.008 <sup>b,c,d</sup>	60.42	2.18	0.33 (0.88 <sup>b</sup> )
WDBCE 3-4-4	0.093 <sup>a</sup>	0.011 <sup>a,b,c,d</sup>	41.67	2.46	1.33 (1.34 <sup>a,b</sup> )
WD5-6-1	0.090 <sup>a</sup>	0.018 <sup>a,b,c,d</sup>	43.75	1.73	2.00 (1.56 <sup>a,b</sup> )
WD 5-6-6	0.067 <sup>a</sup>	0.013 <sup>a,b,c,d</sup>	58.33	1.52	1.33 (1.34 <sup>a,b</sup> )
WD 5-11-3	0.077 <sup>a</sup>	0.007 <sup>b,c,d</sup>	52.08	1.97	1.33 (1.18 <sup>a,b</sup> )
WD 5-12-1	0.083 <sup>a</sup>	0.016 <sup>a,b,c,d</sup>	47.92	1.45	2.33 (1.55 <sup>a,b</sup> )
WD 9-1-3	0.080 <sup>a</sup>	0.012 <sup>a,b,c,d</sup>	50.00	1.98	2.00 (1.56 <sup>a,b</sup> )
WD 24-2-4	0.057 <sup>a</sup>	0.012 <sup>a,b,c,d</sup>	64.58	1.60	0.67 (1.05 <sup>a,b</sup> )
WDBCE 3-2-3	0.100 <sup>a</sup>	0.009 <sup>b,c,d</sup>	37.50	3.03	1.00 (1.17 <sup>a,b</sup> )
WDBCE3-3-10	0.140 <sup>a</sup>	0.029 <sup>a,b</sup>	25.00	1.83	1.67 (1.46 <sup>a,b</sup> )
WD 5-10-1	0.097 <sup>a</sup>	0.015 <sup>a,b,c,d</sup>	39.58	1.81	1.33 (1.29 <sup>a,b</sup> )
WD5-12-2	0.147 <sup>a</sup>	0.026 <sup>a,b,c</sup>	8.33	2.08	2.67 (1.74 <sup>a</sup> )
WD 5-11-1	0.067 <sup>a</sup>	0.011 <sup>a,b,c,d</sup>	58.33	1.47	1.00 (1.17 <sup>a,b</sup> )
WD5-11-2	0.157 <sup>a</sup>	0.022 <sup>a,b,c,d</sup>	2.08	2.47	1.33 (1.34 <sup>a,b</sup> )
WDBCE 3-2-1	0.057 <sup>a</sup>	0.009 <sup>b,c,d</sup>	64.58	1.30	1.00 (1.17 <sup>a,b</sup> )

\* Values inside parentheses are square root transformed

In the fourth batch, 17 genotypes were screened. Sixteen genotypes except WDBCE 3-3-11, were derivatives of UPAS120 X ICP15761. The pod weight consumption was lowest in WD 5-3-2 (0.087g) (Table 5) while it was highest in WD 5-5-3 (0.270g) both were statistically on par with each other. Out of 17 only, WD 5-3-2 is moderately tolerant to pod borer based on RFDP score (67.90) and it also has lowest pod

consumption. The low pod consumption indicates its less preference due to pod surface characters. The present finding corroborates with that of Green *et al.* (2003)<sup>[24]</sup>. The acetone extracts of *C. scarabaeoides* pod surface has resulted in feeding inhibition in *H. armigera* whereas the methanol extracts of *C. cajan* has acted as phagostimulant.

**Table 5:** No-choice assay for wild derivatives of pigeonpea against *Helicoverpa armigera* (batch 4)

Wild derivatives	Average pod weight consumed (g)/larva	Average larval weight gain (g)/larva	RFDP	CI	Average number of bore holes /pod*
WD 1-1	0.187 <sup>a</sup>	0.035 <sup>a</sup>	30.86	1.71	2.67 (1.77 <sup>a</sup> )
WD 1-2	0.170 <sup>a</sup>	0.025 <sup>a</sup>	37.04	1.93	1.67 (1.46 <sup>a</sup> )
WD 5-1-1	0.147 <sup>a</sup>	0.022 <sup>a</sup>	45.68	1.82	1.67 (1.35 <sup>a</sup> )
WD 5-1-2	0.190 <sup>a</sup>	0.019 <sup>a</sup>	29.63	1.70	2.33 (1.64 <sup>a</sup> )
WD 5-1-3	0.107 <sup>a</sup>	0.018 <sup>a</sup>	60.49	1.36	3.33 (1.95 <sup>a</sup> )
WD 5-2-1	0.267 <sup>a</sup>	0.019 <sup>a</sup>	1.23	2.31	3.67 (1.91 <sup>a</sup> )
WD 5-2-2	0.223 <sup>a</sup>	0.038 <sup>a</sup>	17.28	2.03	4.00 (2.11 <sup>a</sup> )
WD 5-3-1	0.113 <sup>a</sup>	0.018 <sup>a</sup>	58.02	1.21	2.00 (1.47 <sup>a</sup> )
WD 5-3-2	0.087 <sup>a</sup>	0.010 <sup>a</sup>	67.90	0.89	1.33 (1.34 <sup>a</sup> )
WD 5-4	0.143 <sup>a</sup>	0.014 <sup>a</sup>	46.91	1.42	2.67 (1.64 <sup>a</sup> )
WD 5-5-2	0.123 <sup>a</sup>	0.019 <sup>a</sup>	54.32	1.27	2.00 (1.52 <sup>a</sup> )
WD 5-5-3	0.270 <sup>a</sup>	0.029 <sup>a</sup>	0.00	2.21	1.33 (1.34 <sup>a</sup> )
WD 5-7-1	0.220 <sup>a</sup>	0.041 <sup>a</sup>	18.52	1.53	3.00 (1.81 <sup>a</sup> )
WD 5-7-2	0.167 <sup>a</sup>	0.008 <sup>a</sup>	38.27	1.23	1.00 (1.17 <sup>a</sup> )
WD 5-12-3	0.220 <sup>a</sup>	0.010 <sup>a</sup>	18.64	2.62	1.00 (1.17 <sup>a</sup> )
WD 114	0.210 <sup>a</sup>	0.036 <sup>a</sup>	22.22	1.94	2.67 (1.72 <sup>a</sup> )
WDBCE 3-3-11	0.237 <sup>a</sup>	0.031 <sup>a</sup>	12.35	1.52	4.00 (2.11 <sup>a</sup> )

\* Values inside parentheses are square root transformed

Among the 89 wild pigeonpea derivatives tested under no choice condition, the relative feeding deterrence percentage varied from 0.00 to 81.25. Sixteen genotypes had shown

moderate tolerance, 24 entries were susceptible, 28 were intermediate, 20 were highly susceptible and 1 entry (WD22-3-3) was tolerant among 89 wild derivatives (Table 6).

**Table 6:** Tolerance reaction of different pigeonpea genotypes based on RFDP.

Genotypes	Reaction category (no. of genotypes)	Percentage of genotypes	
		UPAS120 X ICP15761	Early 3 X ICP 15685
WD22-3-3	Tolerant(1)	2	0
WD5-3-3, WD5-6-3, WD9-1-2, WD22-1-1, WD24-1-1, WD 24-1-6, WD 22-2-4, WDBCE 2-3-4, WDBCE 3-2-4, WDBCE 3-3-4, WDBCE3-3-5, WDBCE 3-3-6, WDBCE 3-3-7, WD 24-2-4, WDBCE 3-2-1, WD 5-3-2	Moderately tolerant (16)	14	26
WD9-1-1, WD22-2-1, WD22-2-2, WD22-2-3, WD22-2-5, WD22-3-1, WD22-3-2, WD 24-1-3, WD 24-2-1, WD 24-2-2, WDBCE 2-2-2, WDBCE 2-3-5, WDBCE 3-2-3, WDBCE 3-3-2, WDBCE 3-4-2, WDBCE 3-4-3, WDBCE 3-4-4, WD5-6-1, WD 5-6-6, WD 5-11-3, WD 5-12-1, WD 9-1-3, WD 5-11-1, WD 5-1-1, WD 5-1-3, WD 5-3-1, WD 5-4, WD 5-5-2	Intermediate (28)	34	26
WD5-5-1, WD5-6-4, WD5-6-5, WD5-10-2, WD5-12-4, WD22-1-2, WD22-1-3, WD22-1-6, WD 24-1-2, WD 22-2-7, WDBCE 3-3-8, WDBCE 2-2-1, WDBCE 2-3-1, WDBCE 2-3-2, WDBCE 2-3-3, WDBCE 3-3-3, WDBCE 3-2-3, WDBCE3-3-10, WD 5-10-1, WD 1-1, WD 1-2, WD 5-1-2, WD 5-7-2, WD 114	Susceptible (24)	26	30
WD 24-1-4, WD 24-1-5, WD 22-2-3, WD 22-2-5, WD 22-2-6, WDBCE 2-1-1, WDBCE 2-1-2, WDBCE 2-1-3, WDBCE 3-3-1, WD5-12-2, WD5-11-2, WD 5-2-1, WD 5-2-2, WD 5-5-3, WD 5-7-1, WD 5-12-3, WDBCE 3-3-11, WD5-6-2, WD22-1-4, WD22-1-5	Highly susceptible (20)	24	18

### 3.2 Larval weight gain & Consumption index

The first batch of detached pod assay revealed that WD 5-6-3 & WD 24-1-1 (0.006g) has recorded lowest larval weight gain and it significantly lower than WD22-1-5 (0.074) (Table 2). The lowest (0.85) and highest (3.18) consumption Index (CI) is recorded from genotypes, WD 22-3-3 and WD 24-1-1 respectively. Even though the CI is higher for WD 24-1-1 but it had recorded a lowest larval weight gain due to antibiosis property of the pod. The present finding is that *C. scarabaeoides* (ICP15761) derivatives also exhibit antibiosis against *H. armigera*. This is similar to the findings of Deepak *et al.* (2012)<sup>[25]</sup> and Sujana *et al.* (2008)<sup>[16]</sup>. Wherein they had reported the existence of antixenosis and antibiosis mechanism of resistance against *H. armigera* in *C. acutifolius* and *C. scarabaeoides* accession ICPW 280. The presence of tolerance due to antibiosis was reflected in RFDP score (67.71) based on which it falls under moderate tolerance category. Hence RFDP parameter helps in identifying pod borer tolerance irrespective of mechanism of tolerance (Antixenosis or antibiosis) operating in the pods.

The lowest larval weight gain during second batch of detached pod assay was recorded in WDBCE 2-2-2 (0.013g) which was on par with WD 24-1-6 (0.014g), WD 22-2-4 and WDBCE 2-3-5(0.015g) (Table 3). These 4 genotypes were significantly lower weight gain than WDBCE 2-1-1 (0.061g) and WDBCE 2-1-3 (0.060g). The CI was lowest (1.18) and highest (2.24) for the genotype, WD 24-1-6 and WDBCE 2-3-5 respectively. The average number of bore holes per pod was lowest (0.66) in WD 24-1-6 which is significantly lower than WD 22-2-5 (5.33). The genotype WD 24-1-6 has registered lowest CI, larval weight gain and average number of bore hole per pod indicative of existence of antixenosis or non preference by *H. armigera*.

Among the 24 genotypes screened in 3<sup>rd</sup> batch, the highest larval weight gain is recorded from WDBCE 3-3-1 (0.033g) and it is significantly different from WDBCE 3-3-5 (0.002g), WDBCE 3-4-3 (0.008g) and WDBCE 3-2-1, WDBCE 3-3-2, WDBCE 3-3-7 & WDBCE 3-2-3 (0.009g) (Table 4). The CI ranged from 1.07 (WDBCE 3-2-4) to 3.03 (WDBCE 3-2-3). The average number of bore holes per pod varied from 0.33 (WDBCE3-3-5, WDBCE 3-3-2 and WDBCE 3-4-3) to 2.67 (WD5-12-2). The genotype, WDBCE 3-3-5 might have antixenosis mechanism of resistance as it had recorded lowest average number of bore holes per pod, larval weight gain and

lowest pod consumption. The antixenosis character of pods might have transferred from *C. scarabaeoides*. The present result corroborates with the findings of Aruna *et al.* (2005)<sup>[26]</sup>, they had reported that *C. scarabaeoides* harbours 5 times higher density of trichome C than *C. cajan* on calyx and pods and trichome C density exhibited a significant negative correlation with damage to flowers, buds and pods. They also concluded that selection of plants with pods bearing high density of type C and low density of type A trichome in pods will be useful for imparting pod borer resistance. Verulkar *et al.* (1997)<sup>[27]</sup> has also reported the existence of antixenosis in the progenies of interspecific cross between *C. scarabaeoides* (JM4147) X Pant A-3. Similarly another interspecific cross, *C. platycarpus* X *C. cajan* progenies had recorded pod damage ranged from 6.85% to 22.84%.

Among the 17 genotypes screened in 4<sup>th</sup> batch, the highest and lowest larval weight gain is recorded from WD 5-7-1 (0.041g) and WD 5-7-2 (0.008g) respectively (Table 5). The present finding is in corroboration with Sujana *et al.* (2008)<sup>[16]</sup>. They had reported that lowest larval weight gain (<50mg) of the *H. armigera* larvae reared on lyophilized pod powders of *C. scarabaeoides* (ICPW 83) and 5 other wild accessions. The lowest CI is 0.89 from the genotype WD 5-3-2. The average number of bore holes per pod varied from 1.00 (WD 5-7-2 and WD 5-12-3) to 4.00 (WDBCE 3-3-11). The genotype, WD 5-3-2 has recorded lowest CI and highest RFDP among 17 genotypes tested.

### 4. Conclusion

Wild progenitors are able to tolerate insect pest that inflicts heavy damage to cultivated varieties as they were selected by virtue of its antixenosis or antibiosis mechanism that assisted in their survival. The present cultivars had lost this defense mechanism during anthropogenic selection for higher yield and improved nutritional quality. The present study portrays the screening of 89 pigeonpea genotypes derived from UPAS 120 X ICP15761 and Early 3 X ICP 15685 under uniform insect pressure. One genotype (WD 22-3-3) is found to be tolerant based on the pod consumption, consumption index and relative feeding deterrence percentage. Another 16 genotypes were found to be moderately tolerant. Among the 16 genotypes, 9 genotypes (14 per cent of progenies) belong to UPAS 120 X ICP15761, whereas 7 genotypes (26 per cent of progenies) belong to Early 3 X ICP 15685. These 16

genotypes are in the process of fixation and can be further utilized in pigeonpea improvement programme for incorporating pod borer resistance. To conclude the wild accessions of *C. scarabaeoides* (ICP15761, ICP 15685) and its progenies can be used in pigeonpea improvement programmes for incorporating pod borer tolerance. Further the screening method, detached leaf assay coupled with relative feeding deterrence percentage and consumption index depicts a robust and precise screening protocol for evaluating large number of genotypes at a stretch.

## 5. Disclosure statement

Authors have no conflict of interest.

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