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FIELD AND LABORATORY SCREENING OF IMPROVED GENOTYPES FOR RESISTANCE TO MAJOR INSECT PESTS IN PIGEONPEA

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ABSTRACT
Pigeonpea (Cajanus cajan L.) production is severely constrained by the pod borer complex, particularly Helicoverpa armigera, which causes substantial yield losses. This study evaluated 38 pigeonpea genotypes from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India, for resistance to the pod borer complex under natural field infestation and laboratory confirmation using detached-pod bioassays against H. armigera. Field screening was conducted during the Rabi 2025–26 season without insecticidal sprays; per cent pod damage (pod borer- and pod fly-damaged pods) and 100-seed weight were recorded at maturity. In parallel, detached-pod bioassays assessed pod damage rating (PDR) and larval weight gain per cent (LWG) for each genotype. Significant variation was observed among genotypes for all traits, with healthy pod percentage ranging from 30.67% (ICPL 11253) to 62.00% (ICPL 99094) and total pod damage ranging from 25.67% to 69.33%. In the bioassay, PDR ranged from 3.33 (ICPL 99102) to 6.33 (ICPL 11229), and LWG ranged from 48.77% (ICPL 94062) to 317.96% (ICPL 20135), with ICPL 94062 and ICPL 99102 showing the lowest larval weight gain. The Multi-trait Genotype–Ideotype Distance Index (MGIDI), integrating PDR and LWG, identified ICPL 99090, ICPL 90011, ICPL 17004, ICPL 17001, and ICPL 20123 as the genotypes closest to the ideotype, indicating superior combined resistance. These findings highlight substantial genetic variability for pod borer resistance among pigeonpea genotypes and identify promising resistant sources for future breeding programmes targeting pod borer complex resistance.
KEYWORDS: Cajanus cajan; Helicoverpa armigera; pod borer complex; host plant resistance; detached pod bioassay; MGIDI

1. INTRODUCTION

Pigeonpea (Cajanus cajan (L.) Millspaugh) is widely grown in tropical and subtropical Asia and Africa. Globally, it is a major grain legume crop, and in India it is the second most important legume after chickpea. The major share of pigeonpea global production comes from India and it is a vital source of dietary protein for resource-poor farming communities across the semi-arid tropics.

Among the various constraints limiting pigeonpea productivity, the major biotic factor is insect pests, mainly the pod borers, occurring in a complex, causing substantial economic losses each season. Substantial annual yield losses in pigeonpea occur due to damage to its reproductive parts caused by Helicoverpa armigera (25–70%), pod fly, Melanagromyza obtusa (10%), spotted borer, Maruca vitrata (5–25%), and pod-sucking bug, Clavigralla gibbosa (10–30%) (Volp et al., 2025). Economic losses attributable to H. armigera alone are estimated at USD 300 million annually, with pod fly causing a further USD 256 million in losses (Volp et al., 2025). Field-level screening studies have similarly reported wide variation among short-duration pigeonpea genotypes in their susceptibility to this pest complex (Chakravarty et al., 2016), and its management remains challenging despite considerable investment in insecticide-based control (Sharma et al., 2005a; Patange and Chiranjeevi, 2017). Under field conditions, farmers rely heavily on repeated insecticide applications to manage this pest complex; however, indiscriminate and injudicious pesticide use results in the development of insecticide resistance in target populations, pest resurgence, secondary outbreaks of previously minor pests, and negatively impacts on natural

enemies and the environment. These limitations necessitate the need to look into alternate pest management strategies.

Host plant resistance is the foundation for crop protection as a sustainable and economically viable component of integrated pest management, gives the long term solution by reducing dependence on chemical insecticides while offering compatibility with other control tactics (Halder et al., 2006; Shanower et al., 1999). Morphological and biochemical traits present in pigeonpea genotypes of both cultivated pigeonpea and its wild relatives offer resistance against the key pod borers complex (Kaur et al., 2014; Jat et al., 2018; Rana et al., 2017), by exhibiting antixenosis and antibiosis mechanisms (Sujana et al., 2008; Vishal et al., 2023; Sharma et al., 2005b) Genotypes vary considerably in their susceptibility depending on the combination of such traits they possess, and this variation can further shift with sowing time and prevailing pest pressure (Vishal et al., 2023). Identifying breeding lines with stable, multi-trait resistance is therefore central to developing pod borer–tolerant cultivars.

Screening germplasm for insect resistance requires assessment at two complementary levels: natural field incidence and controlled laboratory bioassays. Under field conditions, resistance is commonly evaluated by recording the proportion of healthy pods against pods damaged by individual components of the complex — namely pod borer- and pod fly-damaged pods — together with overall pod damage and yield-related traits such as test weight/seed index, since reduced seed weight is often a direct consequence of larval feeding on developing seeds. Under laboratory conditions, assessing pod damage rating (PDR) and larval weight gain (LWG) on excised pods of individual genotypes precisely quantifies antibiosis-based resistance through detached pod bioassays (Golla et al., 2018). However, genotypes superior for field-level pod damage are not always the same as those superior in bioassay-based antibiosis, complicating selection through either approach alone.

Trait variation among genotypes is generally assessed through analysis of variance, with Duncan's Multiple Range Test (DMRT) being used to separate genotype means (Duncan, 1955) into statistically distinct classes based on their pest incidence or resistance parameters and thereby aid in distinguishing significantly superior entries. The Multi-trait Genotype–Ideotype Distance Index (MGIDI) is used to combine information across traits into a single index, which ranks genotypes under test according to their overall closeness to an ideal genotype, allowing more efficient identification of lines with balanced resistance (Olivoto and Nardino, 2021).

The present study was undertaken to screen 38 pigeonpea breeding lines with prominent/resistance for diseases traits have taken consideration for testing for major insect pests under natural field incidence of the pod borer complex as well as for antibiosis-based resistance to H. armigera through detached pod bioassays for confirmative true resistance studies, and these traits further subjected for the MGIDI approach for identifying superior genotypes with combined reduced pod damage and suppressed larval growth as potential donor sourceswith having multiple pest & diseases resistance for future pigeonpea breeding programmes.

2. MATERIALS AND METHODS

2.1 Plant Material

Thirty-eight prominentpigeonpeagenotypes were obtained fromLegume Pathology, the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, India. In order to identify multiple resistance sources, these genotypes were evaluated during the Rabi 2025–26 season under field conditions for their response to the pod borer complex and associated insect pests under natural infestation. The same set of genotypes was also used for labdetached pod bioassays against H. armigera.

2.2 Field Screening for Insect Pest Incidence

At ICRISAT, Patancheru, a field screening study in a Randomized Block Design (RBD) with three replications was conducted. Each genotype was planted in a two-row plot following the recommended agronomic practices for pigeonpea cultivation. No insecticidal sprays were applied throughout the cropping season to facilitate natural infestation by insect pests.

Observations were recorded from representative plants in each replication for the infestation of the major insect pests associated with pigeonpea. These included damage by H. armigera, M. vitrata, M. obtusa, Exelastis atomosa (plume moth), and hymenopteran pod wasp (Tanaostigmodes cajaninae) pod damage. At crop maturity, the percentages of healthy pods, total pod damage, pod borer-damaged pods, pod fly-damaged pods, and 100-seed weight were recorded. Mean values for each trait were calculated across the three replications and used for statistical analysis.

2.3 Laboratory evaluation of pigeonpea improved lines

2.3.1 Insect Culture

A laboratory culture of H. armigera was maintained under controlled laboratory conditions (27 ± 2°C, 65–75% relative humidity, and a 16 h:8 h L:D photoperiod) at ICRISAT, Patancheru, India. We used a chickpea-based semi-synthetic diet for larval rearing [Sharma et al., 2014]. Healthy third-instar larvae of uniform age were used for detached pod bioassays (Karrem et al., 2025).

2.3.2 Detached Pod Bioassay

Resistance of pigeonpea disease-resistant lines to H. armigera was evaluated using a detached pod bioassay following the methodology of Golla et al. (2018) with suitable modifications.

Fresh, healthy green pods at the pod-filling stage (before complete maturity) were collected from genotypes raised in the fields, brought to the laboratory on ice and then placed in plastic cups containing a bottom layer of agar–agar medium (3%) to maintain pod freshness throughout the experiment. Two pods of each genotype were placed in individual cups. Before the experiment, 4 hours starved third-instar larvae were weighed individually and subsequently, one third-instar larva was released onto the pods in each container. The experiment was conducted with three replications.The final larval weight and the pod damage rating (PDR) for pods of each genotype at individual replications were recorded. Larval weight gain (LWG) was calculated using the following formula:

$$\text{Larval weight gain (\%)} = \frac{\text{Final larval weight} - \text{Initial larval weight}}{\text{Initial larval weight}} \times 100$$

2.3.4 Pod Damage Assessment

At crop maturity in the field experiment, pods were collected from representative plants from three replications to assess pod borer complex damage. The total number of pods and damaged pods were recorded for each genotype. Damaged pods were further categorized based on damage by individual pest species, viz., H. armigera, M. obtusa, M. vitrata, T. cajaninae, and E. atomosa, following the criteria of Sharma et al. (2022): pod borer-damaged pods (large circular holes without larval exuviae), pod fly-damaged pods (minute holes), pod wasp-damaged pods (minute holes at the pod tip with shortened pod length), and plume moth-damaged pods (2-3 medium circular holes). Healthy pods were also counted. Based on the observations made, healthy pods (%), pod borer-damaged pods (%), pod fly-damaged pods (%) and total pod damage (%) were calculated using the following formulas:

$$\text{Healthy pods (\%)} = \frac{[\text{Number of healthy pods}]}{[\text{Total number of pods}]} \times 100$$

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

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

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

In addition, the test weight/100-seed weight (g) was determined for each genotype by randomly selecting and weighing 100 healthy seeds using a high precision electronic balance. All observations were recorded from each replication and expressed as mean values for statistical analysis.

2.3.5 Statistical Analysis

Data obtained from the genotypes of the field screening experiment were subjected to analysis of variance (ANOVA) using a Randomized Block Design. Genotype means were separated using DMRT at the 5% level of significance ($P \leq 0.05$), using the agricolae package (de Mendiburu, 2021). The MGIDI analysis was performed using the metan package (Olivoto and Lúcio, 2020) to identify superior pigeonpea genotypes by simultaneously considering multiple resistance-related traits. The MGIDI index integrates information from all measured traits after factor analysis and ranks genotypes according to their Euclidean distance from an ideotype possessing the most desirable trait values. Genotypes with lower MGIDI values were considered more resistant and closer to the ideotype. R statistical software (version 4.4.0) was used for all statistical analyses (R Core Team, 2024). Of the 38 genotypes evaluated, complete data across all traits were available for 37 genotypes; one genotype (ICPL 11226) was excluded from the pod fly damage analysis due to missing observations.

3. RESULTS

3.1 Field screening

Significant variation was observed among the 38 pigeonpea genotypes for healthy pod %, total pod damage %, pod borer-damaged pods %, pod fly-damaged pods % and 100-seed weight under natural insect infestation **(Table 1)**.

The percentage of healthy pods ranged from 30.67% in ICPL 11253 to 62.00% in ICPL 99094. Higher proportions of healthy pods were also recorded in ICPL 20096-1 (59.33%), ICPL 11236 (54.00%) and ICPL 11229 (52.67%), indicating comparatively lower damage under field conditions.

Overall pod damage varied from 25.67% to 69.33%. The lowest pod damage was observed in ICPL 11226 (25.67%), followed by ICPL 99094 (38.00%) and ICPL 20096-1 (40.67%), whereas ICPL 11253 (69.33%), ICPL 20338 (68.33%) and ICPL 90011 (68.33%) recorded the highest pod damage.

The incidence of pod borer-damaged pods ranged from 7.33% to 41.00%. The lowest pod borer damage was recorded in ICPL 99102 (7.33%), followed by ICPL 99090 (8.00%), ICPL 99094 (11.33%), ICPL 11236 (12.00%) and ICPL 99099 (12.67%). In contrast, ICPL 11253 (41.00%) exhibited the highest pod borer damage, followed by ICPL 94062 (36.67%), ICPL 11215 (35.33%) and ICPL 11264 (34.42%).

Pod fly-damaged pods ranged from 24.00% to 53.33%. The lowest infestation was observed in ICPL 20096-1 (24.00%), followed by ICPL 11229 (24.67%), ICPL 2211228 (25.33%), ICPL 332 WR (25.33%) and ICPL 99094 (26.00%). The highest pod fly damage was recorded in ICPL 99102 (53.33%), followed by ICPL 20338 (42.67%), ICPL 99090 (41.67%), ICPL 99099 (38.00%) and ICPL 20124 (36.33%).

The 100-seed weight varied from 0.018 g in ICPL 11253 to 0.151 g in ICPL 20096-1. Higher seed weights were also observed in ICPL 11215 (0.147 g) and ICPL 15038 (0.141 g), whereas lower values were recorded for ICPL 20338 (0.026 g), ICPL 99010 (0.026 g), ICPL 11264 (0.027 g) and ICPL 99099 (0.033 g).

Overall, the field evaluation revealed considerable variability among the evaluated pigeonpea genotypes for resistance-related traits under natural insect infestation, indicating the availability of useful genetic variation for identifying promising sources of resistance for future breeding programmes.

Table 1. Mean performance of 37 pigeonpea genotypes for pod damage traits and 100-seed weight under natural field infestation by the pod borer complex during the Rabi 2025–26 season. Values are mean ± SE of three replications. Means followed by the same letter within a column are not significantly different according to Duncan's Multiple Range Test (DMRT) at P ≤ 0.05. Data for ICPL 11226 are incomplete; pod fly-damaged pods (%) were not recorded for this genotype due to missing observations.

Genotype	Healthy pods (%)	Pod damage (%)	Pod borer damaged pods (%)	Pod fly damaged pods (%)	100-seed weight (g)
ICPL 11215	35.00 ± 4.00 a	65.00 ± 4.00 a	35.33 ± 6.66 a	28.00 ± 1.73 a	0.147 ± 0.063 ab
ICPL 11226	51.00 ± 13.53 ab	25.67 ± 16.01 ab	25.33 ± 2.89 ab	0.108 ± 0.034 abcdefg	
ICPL 11227	47.33 ± 4.73 abc	52.67 ± 4.73 ab	22.67 ± 8.33 abc	29.00 ± 3.61 bc	0.088 ± 0.040 abcdefghi
ICPL 11229	52.67 ± 16.65 abc	47.33 ± 16.65 abc	22.33 ± 13.50 abcd	24.67 ± 4.51 bcd	0.083 ± 0.020 abcdefghi
ICPL 11236	54.00 ± 9.64 abcd	46.00 ± 9.64 abcd	12.00 ± 9.17 abcde	33.67 ± 1.53 bcde	0.079 ± 0.031 abcdefghi
ICPL 11253	30.67 ± 5.51 abcde	69.33 ± 5.51 abcd	41.00 ± 11.53 abcdef	27.00 ± 4.36 bcde	0.018 ± 0.021 i
ICPL 11264	33.12 ± 21.17 abcde	66.88 ± 21.17 abcd	34.42 ± 20.73 abcdefg	30.38 ± 4.01 bcde	0.027 ± 0.017 hi
ICPL 15014	47.00 ± 6.56 abcde	53.00 ± 6.56 abcde	24.33 ± 10.12 abcdefg	27.33 ± 5.03 bcde	0.082 ± 0.046 abcdefghi
ICPL 15018	50.67 ± 7.02 abcde	49.33 ± 7.02 abcdef	20.00 ± 10.58 abcdefg	29.33 ± 11.02 bcde	0.090 ± 0.016 abcdefghi
ICPL 15038	43.00 ± 10.39 abcde	57.00 ± 10.39 abcdef	26.33 ± 14.57 abcdefg	30.00 ± 5.00 bcde	0.141 ± 0.070 abc
ICPL 15061	42.00 ± 6.08 abcde	58.00 ± 6.08 abcdef	26.00 ± 8.72 abcdefgh	32.00 ± 3.00 bcde	0.115 ± 0.014 abcdef
ICPL 15079	46.33 ± 6.66 abcdef	53.67 ± 6.66 abcdef	26.33 ± 8.62 abcdefgh	26.33 ± 3.51 bcde	0.108 ± 0.012 abcdefg
ICPL 17001	40.67 ± 8.96 abcdef	59.33 ± 8.96 abcdef	23.33 ± 9.71 abcdefgh	35.67 ± 11.59 bcde	0.103 ± 0.028 abcdefgh
ICPL 17004	44.67 ± 3.51 abcdef	55.33 ± 3.51 abcdef	21.33 ± 10.07 abcdefgh	32.00 ± 8.00 bcde	0.065 ± 0.016 cdefghi
ICPL 20096-1	59.33 ± 9.71 abcdefg	40.67 ± 9.71 abcdef	15.67 ± 12.90 abcdefgh	24.00 ± 5.57 bcde	0.151 ± 0.055 a
ICPL 2011220	45.00 ± 4.58 abcdefg	55.00 ± 4.58 abcdefg	24.00 ± 8.72 abcdefgh	30.00 ± 6.00 bcde	0.111 ± 0.011 abcdefg
ICPL 20114	47.67 ± 10.21 abcdefg	52.33 ± 10.21 abcdefg	21.67 ± 10.41 abcdefghi	30.67 ± 11.15 bcde	0.125 ± 0.057 abcde
ICPL 20123	48.33 ± 6.51 bcdefg	51.33 ± 6.51 abcdefg	17.00 ± 1.00 abcdefghi	34.00 ± 6.00 bcde	0.116 ± 0.016 abcdef
ICPL 20124	48.33 ± 7.23 bcdefgh	51.67 ± 7.23 abcdefg	15.33 ± 9.45 bcdefghij	36.33 ± 3.21 bcde	0.064 ± 0.049 cdefghi
ICPL 20125	37.00 ± 10.58 bcdefgh	63.00 ± 10.58 bcdefg	32.33 ± 6.66 bcdefghij	28.67 ± 7.02 bcde	0.127 ± 0.093 abcd
ICPL 20135	44.33 ± 10.07 bcdefgh	55.67 ± 10.07 bcdefgh	25.00 ± 13.23 bcdefghij	29.67 ± 4.51 bcde	0.085 ± 0.013 abcdefghi
ICPL 20338	31.67 ± 6.51 bcdefgh	68.33 ± 6.51 bcdefgh	24.67 ± 11.55 bcdefghij	42.67 ± 13.01 bcde	0.026 ± 0.011 hi
ICPL 2211228	45.00 ± 7.94 cdefgh	55.00 ± 7.94 bcdefgh	29.00 ± 12.77 bcdefghij	25.33 ± 6.11 cde	0.071 ± 0.013 abcdefghi

ICPL 332 WR	47.00 ± 9.64 cdefgh	53.00 ± 9.64 cdefgh	27.00 ± 7.55 bcdefghij	25.33 ± 6.43 cde	0.094 ± 0.078 abcdefghi
ICPL 87	36.00 ± 5.20 cdefgh	64.00 ± 5.20 cdefgh	28.67 ± 8.39 bcdefghij	34.00 ± 8.00 cde	0.068 ± 0.015 bcdefghi
ICPL 90011	31.67 ± 8.74 cdefgh	68.33 ± 8.74 defgh	33.67 ± 13.65 cdefghij	32.67 ± 7.02 de	0.090 ± 0.006 abcdefghi
ICPL 94062	36.33 ± 6.11 cdefgh	63.67 ± 6.11 defgh	36.67 ± 4.93 defghij	27.00 ± 2.65 de	0.097 ± 0.056 abcdefghi
ICPL 99004	50.00 ± 10.00 cdefgh	50.00 ± 10.00 defgh	17.00 ± 6.56 efghij	32.33 ± 9.29 de	0.059 ± 0.011 defghi
ICPL 99008	41.00 ± 1.73 defgh	59.00 ± 1.73 defgh	29.00 ± 5.00 efghij	28.33 ± 2.89 de	0.044 ± 0.010 fghi
ICPL 99009	40.00 ± 4.00 efgh	60.00 ± 4.00 defgh	28.67 ± 11.02 fghij	30.67 ± 8.33 de	0.079 ± 0.019 abcdefghi
ICPL 99010	42.33 ± 9.87 efgh	57.67 ± 9.87 defgh	23.33 ± 13.80 fghij	33.67 ± 5.13 de	0.026 ± 0.015 hi
ICPL 99048	50.00 ± 14.00 efgh	50.00 ± 14.00 efgh	18.67 ± 7.02 ghij	30.00 ± 7.21 de	0.077 ± 0.071 abcdefghi
ICPL 99090	50.33 ± 10.07 fgh	49.67 ± 10.07 fgh	8.00 ± 3.61 ghij	41.67 ± 7.64 de	0.045 ± 0.018 fghi
ICPL 99094	62.00 ± 13.23 gh	38.00 ± 13.23 fgh	11.33 ± 5.77 hij	26.00 ± 10.15 de	0.094 ± 0.036 abcdefghi
ICPL 99099	49.33 ± 4.04 gh	50.67 ± 4.04 gh	12.67 ± 6.81 ij	38.00 ± 10.39 de	0.033 ± 0.016 ghi
ICPL 99102	39.33 ± 0.58 h	60.67 ± 0.58 h	7.33 ± 1.53 j	53.33 ± 1.53 e	0.047 ± 0.016 efghi

3.2 Detached Pod Bioassay against Helicoverpa armigera

Pigeonpea genotypes significantly varied in pod damage rating (PDR) and larval weight gain (LWG) in the detached pod bioassay **(Figure 1)**.

PDR varied from 3.33 to 6.33. The lowest PDR was recorded in ICPL 99102 (3.33), followed by ICPL 94062 (4.00), while ICPL 17004, ICPL 20338, ICPL 2211228, ICPL 99004 and ICPL 99099 each recorded a PDR of 4.33. In contrast, the highest PDR (6.33) was observed in ICPL 11229, followed by ICPL 15014 (6.00). Several genotypes, including ICPL 15018, ICPL 17001, ICPL 17016, ICPL 20123, ICPL 20125 and ICPL 99048, exhibited a PDR of 5.67, indicating relatively higher susceptibility.

LWG showed considerable variation among the evaluated genotypes (48.77% to 317.96%). The lowest LWG was recorded in ICPL 94062 (48.77%), followed by ICPL 99102 (65.05%), ICPL 17004 (81.97%), ICPL 11253 (95.81%) and ICPL 2211228 (99.21%), indicating reduced larval development on these genotypes. In contrast, the highest LWG was observed in ICPL 20135 (317.96%), ICPL 20114 (308.10%), ICPL 11236 (296.14%) and ICPL 20096-1 (293.62%), suggesting greater suitability for larval growth.

Overall, the detached pod bioassay revealed substantial variability among the pigeonpea genotypes for both pod damage rating and larval weight gain. Genotypes exhibiting lower values for both parameters were considered

to possess relatively greater resistance against H. armigera and were subsequently evaluated using the MGIDI.

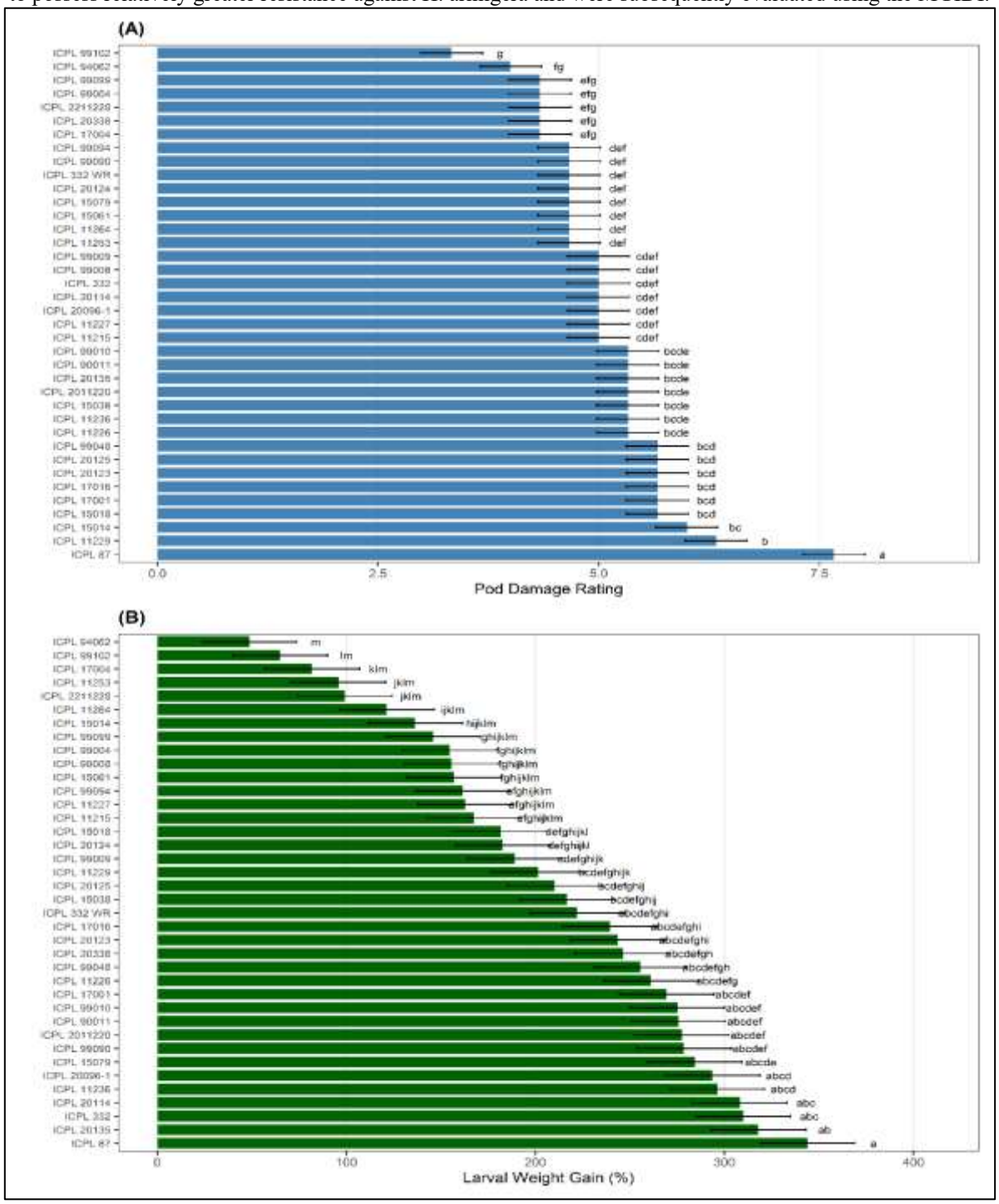


Figure 1. Mean pod damage rating (A) and larval weight gain (B) of Helicoverpa armigera on 38 pigeonpea genotypes using detached pod bioassay. Bars represent mean ± SE. Means followed by the same letter are not significantly different according to Duncan's Multiple Range Test (DMRT) at P ≤ 0.05.

3.3 Multi-trait Selection of Pigeonpea Genotypes Using MGIDI

The MGIDI values for all 38 genotypes ranged from 0.1188 to 5.4799 **(Figure 2)**. Among the evaluated genotypes, ICPL 99102 recorded the lowest MGIDI value (0.1188), indicating the closest proximity to the ideotype, followed by ICPL 94062 (0.5118), ICPL 17004 (1.0099), ICPL 2211228 (1.1356), and ICPL 11253 (1.3667). These genotypes exhibited superior overall performance by combining relatively lower pod damage ratings with reduced larval weight gain, suggesting enhanced resistance against H. armigera.

In contrast, the highest MGIDI values, indicating the greatest distance from the ideotype and comparatively lower resistance, were recorded in ICPL 87 (5.4799), ICPL 20135 (3.4991), ICPL 11229 (3.4169), ICPL 17001 (3.4012), and ICPL 11236 (3.3400) **(Figure 2)**.

Figure 2 illustrates the MGIDI ranking of the evaluated pigeonpea genotypes, where genotypes positioned closer to the ideotype possess lower MGIDI values and are therefore considered more desirable for resistance breeding.

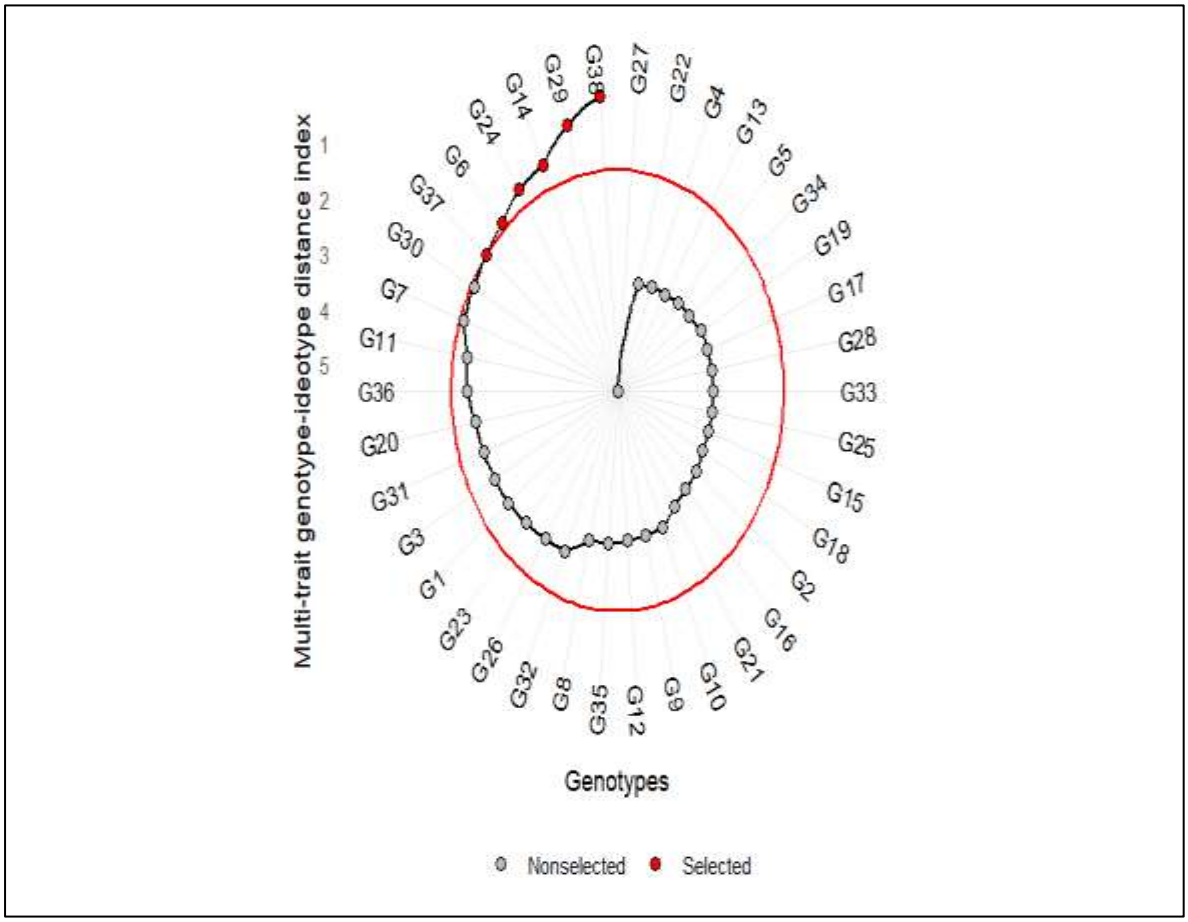
The analysis effectively integrated both resistance-related traits into a single index, facilitating simultaneous selection for reduced pod damage and lower larval weight gain.

Table 2. Multi-trait Genotype–Ideotype Distance Index (MGIDI) values and rankings for 38 pigeonpea genotypes based on pod damage rating (PDR) and larval weight gain (LWG) in the detached pod bioassay against Helicoverpa armigera. Genotypes are ranked in ascending order of MGIDI value; lower values indicate closer proximity to the ideotype and greater overall resistance.

Plot Code	Genotype	MGIDI
G1	ICPL 11215	2.1449
G2	ICPL 11226	3.0846
G3	ICPL 11227	2.1129
G4	ICPL 11229	3.4169
G5	ICPL 11236	3.3400
G6	ICPL 11253	**1.3667**
G7	ICPL 11264	1.5532
G8	ICPL 15014	2.6859
G9	ICPL 15018	2.7607
G10	ICPL 15038	2.7610
G11	ICPL 15061	1.8117
G12	ICPL 15079	2.7413
G13	ICPL 17001	3.4012
G14	ICPL 17004	**1.0099**
G15	ICPL 17016	3.1816
G16	ICPL 20096-1	3.0657
G17	ICPL 2011220	3.2033
G18	ICPL 20114	3.1713
G19	ICPL 20123	3.2120
G20	ICPL 20124	2.0011
G21	ICPL 20125	2.9695
G22	ICPL 20135	3.4991
G23	ICPL 20338	2.2081
G24	ICPL 2211228	**1.1356**
G25	ICPL 332	3.1841
G26	ICPL 332 WR	2.2880
G27	ICPL 87	**5.4799**
G28	ICPL 90011	3.1902
G29	ICPL 94062	**0.5118**
G30	ICPL 99004	1.5406
G31	ICPL 99008	2.0600
G32	ICPL 99009	2.3026
G33	ICPL 99010	3.1857
G34	ICPL 99048	3.2989
G35	ICPL 99090	2.6996
G36	ICPL 99094	1.8470
G37	ICPL 99099	1.4759
G38	ICPL 99102	**0.1188**

Figure 2. Ranking of 38 pigeonpea genotypes based on the Multi-trait Genotype–Ideotype Distance Index (MGIDI), integrating pod damage rating and larval weight gain from the detached pod bioassay against Helicoverpa armigera. Genotypes are arranged in ascending order of MGIDI value, with those closest to

the ideotype (lowest MGIDI) positioned at the top; these genotypes represent the most promising sources of resistance.



4. DISCUSSION

The MGIDI approach successfully integrated multiple resistance-related traits into a single selection criterion, thereby overcoming limitations in selecting genotypes based on individual characters. Conventional selection methods often identify different superior genotypes for separate traits, making simultaneous improvement difficult. In contrast, MGIDI ranks genotypes according to their overall proximity to an ideal genotype, allowing breeders to identify lines with balanced resistance (Olivoto and Nardino, 2021).

Principal component analysis reduced the two resistance-related bioassay variables — pod damage rating and larval weight gain — into a single factor (FA1). The first principal component (PC1), corresponding to the single retained factor (FA1), explained 78.3% of the total variation, with both pod damage rating and larval weight gain contributing nearly identical, strong loadings to this factor (0.885 each), indicating that both traits contributed substantially and comparably to genotype discrimination and justifying their combined, equally weighted use in the MGIDI index.

Among the evaluated genotypes, the lowest MGIDI value (0.1188) was in ICPL 99102, indicating the closest resemblance to the ideotype and therefore the greatest overall resistance based on the combined bioassay traits. The subsequent ranking of ICPL 94062 (0.5118), ICPL 17004 (1.0099), ICPL 2211228 (1.1356), and ICPL 11253 (1.3667) further demonstrates the ability of MGIDI to identify breeding lines with consistently desirable combinations of reduced PDR and suppressed LWG.

The superior performance of these five genotypes indicates that they possess favourable combinations of reduced pod damage and restricted larval development under detached pod bioassay conditions. Lower LWG generally reflects poor nutritional suitability or the presence of antibiosis mechanisms, whereas a lower PDR indicates effective physical or chemical resistance to larval feeding. Therefore, simultaneous improvement in both traits strengthens the reliability of genotype selection over single-trait approaches.

These antibiosis responses are consistent with larval feeding and selection behaviour reported for H. armigera larvae on wild and cultivated pigeonpea genotypes (Green et al., 2002). Physical resistance factors such as pod wall thickness and trichome density, and biochemical factors including phenolics and other defence compounds, have previously been shown to underlie antibiosis and antixenosis to the pod borer complex in pigeonpea and its wild relatives (Jat et al., 2018; Kaur et al., 2014; Shanower et al., 1997). The present bioassay results, obtained through direct evaluation of LWG and PDR, are broadly in agreement with these earlier antixenosis and antibiosis studies conducted on pigeonpea cultigens, hybrids, and wild relatives (Vishal et al., 2023; Karrem et al., 2025).

Field-based pod damage assessment provided a complementary line of evidence to the bioassay findings. Under natural infestation, the healthy pods % in genotypes such as ICPL 99094 (62.00)), ICPL 20096-1 (59.33), ICPL 11236 (54.00), ICPL 332 (53.33), and ICPL 11229 (52.67) sustained comparatively low pod damage and correspondingly higher 100-seed weight, consistent with reduced susceptibility to the pod borer complex under field conditions. In contrast, ICPL 11253 (30.67% healthy pods, 69.33% total damage, lowest seed weight of 0.018 g), ICPL 20338 (68.33% damage), and ICPL 90011 (68.33% damage) were among the most severely affected genotypes under field conditions, showing the characteristic reduction in seed weight associated with heavy larval feeding on developing seeds. Notably, ICPL 11253 combined severe field pod damage (69.33%) with a low MGIDI value (1.3667, ranked among the five most resistant genotypes in the bioassay), while ICPL 11236, despite comparatively low field pod damage (46.00%), recorded one of the highest MGIDI values (3.34) in the bioassay. This divergence suggests that antibiosis expressed against a single, confined larva under controlled bioassay conditions does not necessarily translate into equivalent protection under field conditions, where genotypes are exposed to multiple pest species, variable larval densities, and additional factors such as pod exposure and canopy architecture that influence oviposition and larval establishment (Halder et al., 2006). Such discrepancies between laboratory antibiosis and field performance have been noted in earlier pigeonpea resistance studies (Chakravarty et al., 2016; Rana et al., 2017) and underscore the value of combining both screening approaches, as adopted in the present study, rather than relying on either alone.The balanced contribution of traits observed in the bioassay-based MGIDI analysis further supports the usefulness of this index for host plant resistance studies. In crop improvement programmes, MGIDI has been efficiently used to identify superior genotypes, where several economically important traits are combined to converge into a single selection index (Olivoto and Nardino, 2021). These findings also complement previous host plant resistance work conducted on pod borer complex in pigeonpea, where morphological traits such as pod wall thickness and non-glandular trichome density, together with biochemical factors including phenols, tannins, and flavonoids, were similarly identified as key components underlying genotype resistance (Ambidi et al., 2021).

Overall, the bioassay-based MGIDI evaluation identified ICPL 99102, ICPL 94062, ICPL 17004, ICPL 2211228, and ICPL 11253 as the most promising genotypes for antibiosis resistance, while field screening additionally highlighted ICPL 99094, ICPL 20096-1, ICPL 11236, ICPL 332 WR, and ICPL 11229 as genotypes combining low natural pod damage with favourable seed weight. Together, these results indicate their potential as valuable resistant genotypes to the pigeonpea pod borer complex, including H. armigera, for future breeding programmes.

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DATA AVAILABILITY STATEMENT : The data that support the findings of this study are available in the supplementary material of this article.

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Author Contributions:

Arpita Mohanty: conceptualization, investigation, data curation, methodology, formal analysis, writing – original draft. Suraj Prashad Mishra: conceptualization, investigation, methodology, formal analysis, writing – review and editing. Karthiba Loganathan: investigation, data curation, formal analysis, writing – review and editing. Gopikrishan Ayyanar: supervision, writing – review and editing. Marimuthu Murugan: supervision, conceptualization, investigation, methodology, formal analysis, writing – review and editing. Jagdish Jaba: conceptualization, investigation, data curation, methodology, formal analysis, supervision, writing – original draft, funding acquisition.

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