Indian Journal of Ecology (2025) 52(6) (SI): 1727-1734
DOI: https://doi.org/10.55362/IJE/2025/4719

Manuscript Number: 4719
NAAS Rating: 5.38

Assessment of Resistance Linked Morpho-Physical and Biochemical Traits in Mungbean against Sucking Pests

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Abstract: Twenty-nine mungbean (*Vigna radiata* L.) genotypes were evaluated at the Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh, to identify susceptibility and tolerance to the sucking pest complex. Among them, the genotypes COGG-912, VGG 104 and VGG 17-106 recorded lowest population of whiteflies, aphids, and thrips, respectively. A significant positive correlation was observed between whitefly population and leaf length (r = 0.460 & 0.403), leaf width (r = 0.480 & 0.261), leaf area (r = 0.283 & 0.404), leaf thickness (r = 0.434 & 0.459), and protein content (r = 0.606 & 0.456) at 20 and 50 days after sowing (DAS), respectively. Conversely, a significant negative correlation was recorded between whitefly population and trichome density (r = –0.339 & –0.414), chlorophyll content (r = –0.345 & –0.387) and phenol content (r = –0.428 & –0.338). These findings suggest that higher trichome density and phenol content contribute to enhanced resistance against sucking pests. The identified morpho-physiological and biochemical traits can be effectively utilized in breeding programs aimed at developing pest-resistant mungbean varieties.

Keywords: Biophysical, Biochemical, Chlorophyll content, Mungbean genotypes, Proteins, Phenols, Resistance, Sucking pests, Trichome density

Mungbean (*Vigna radiata* L.) is one of the most important and nutritious pulse crops in India, ranking third in area and production after chickpea and pigeon pea. It contributes to total pulse production with 2.92 million tonnes, cultivated over an area of 5.01 million hectares with an average yield of 582 kg/ha (www.cacp.da.gov.in (Rabi price policy report 2025-26)). However, mungbean is highly susceptible to various sucking pests and the viral diseases they transmit. Among the sucking pests, whiteflies (*Bemisia tabaci* Gennadius), aphids (*Aphis craccivora*) and thrips (*Thrips palmi* Karny) are the major threats not only as direct feeders but also as vectors transmitting viral diseases like Mungbean Yellow Mosaic Virus (MYMV), bud necrosis, and leaf crinkle. Whiteflies, as efficient virus vectors, can cause 30–70% yield loss, while thrips can reduce yield up to 40% in greengram (Sujatha and Bharpoda 2016). The interaction between host plants and insect pests is a dynamic and co-evolutionary process, wherein plants develop defence mechanisms, and insect pests evolve strategies to overcome them. Leaf biophysical traits such as length, width, thickness, and trichome density, as well as physiological traits like chlorophyll content vary among genotypes and significantly influence insect feeding preferences. Trichomes, in particular, can deter insect oviposition and impede movement on the plant surface. Furthermore, biochemical constituents such as leaf protein and total phenol content play key roles in plant defence. These compounds, present in varying quantities and ratios in host plants, are known to profoundly affect the growth, development, survival, and reproduction of insect pests (Painter 1958). Hence, this study was conducted to assess biophysical and biochemical variability among mungbean genotypes and their role in conferring resistance to sucking pests.

MATERIAL AND METHODS

The study was conducted at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh, India during 2022 and 2023. Twenty-nine mungbean genotypes, including checks were evaluated under natural field conditions against major sucking insect pests. Observations on thrips, whitefly, and aphid incidence were recorded at weekly intervals from 10 to 50 days after sowing on five randomly selected plants per genotype per replication, using standard procedures. Population of whitefly adults were counted by using the magnifying lens (Salam et al., 2009) during the early hour of the day from fully formed trifoliate leaf of the plant and expressed as mean number per trifoliate leaf in individual genotypes (Men and Sarode 1999). Counted the number of apterous and winged aphids from the 10 cm terminal shoot portion of the plant from five randomly selected plants. Based on the aphid population which expressed as number of aphids per plant and the test genotypes were grouped into six categories based on a 5-point score (Souleymane et al., 2013). A score of 0 indicated very highly resistant (0–1 aphid), 1 denoted highly resistant (1–5 aphids), 2 of moderately resistant (5–20 aphids), 3 of moderately susceptible (20–100 aphids), 4 indicated susceptible (100–500 aphids), and 5 as highly susceptible (>500 aphids). The population of thrips (adults) were recorded early in the morning (6-8 A.M). by tapping the top, middle and bottom leaves on a white paper and expressed as number of thrips/three leaves per plant (Rathore and Tiwari 1999). The insect populations were identified based on taxonomic keys under microscope. Thrips samples were sent to National Bureau of Agricultural Insect Resources (NBAIR) for identification and further confirmation.

Various morpho-physical and biochemical traits were analysed to determine their role in resistance mechanisms against sucking pests. The influence of these traits on pest incidence was assessed through simple correlation and multiple linear regression analyses.

Morpho-Physical parameters: Leaf length and width was measured from tip to base from five leaves in a plant and average was calculated and expressed in cm. Total (infected and healthy) leaves from each plant of each genotype were cleaned properly and placed on the leaf area meter (LI-COR LI-3100C Area Meter) and measured the leaf area and expressed in cm^2. Leaf thickness was measured randomly from three areas of each leaf by using micrometre. Leaf was made into small bits with the help of blade and the small pieces were placed in the micro meter to recorded the readings (Witkowski and Lamont 1991). Number of trichomes per cm^2 of leaf was measured following Hasanuzzaman et al., 2016. Chlorophyll content of leaves was measured at 10 A.M by using a portable chlorophyll detector (Minolta SPAD-502 chlorophyll meter) from the third leaf of plant, like wise in five plants in each genotype and expressed in $\mu g/cm^2$ (Minolta 1989; Monje and Bugbee 1992).

Biochemical parameters: Total protein content was estimated by using Lowry's method (Lowry et al., 1951) and Phenol content in the leaf was estimated (Malik and Singh 1980) using folin's reagent. The data on the sucking pest infestation and morpho physical and bio chemical parameters at 20 and 50 days after sowing were subjected to correlation, regression and Multiple Linear Regression (MLR) analyses, and the computed results are presented.

RESULTS AND DISCUSSION

Sucking pest infestation: Significant variation was observed among the twenty-nine mungbean genotypes against the three major sucking pests under field conditions. Whitefly populations ranged from a low of 0.96 per trifoliate leaf in COGG-912, the least infested genotype, up to 10.70 in MH 18-181, the most susceptible. Other genotypes like Pusa 9072, IGKM 05-18-2, LGG 706, and LGG 686 also exhibited moderate to low whitefly infestations. For thrips, VGG 17-106 had the lowest mean population (2.54), followed by OBGG 59 and IPM 2, while MH 18-181 showed the highest infestation (26.00). COGG-8 and IPM 1603-1 recorded relatively high thrips populations. Aphid infestation was lowest in VGG 104 (0.53 aphids/10 cm shoot), indicating very high resistance, whereas IPM 1603-1 and PUSA M 2241 showed moderate susceptibility with high aphid counts. Genotypes such as OBGG 59, LGG 711, and VGG 17-009 demonstrated high resistance to aphids. Overall, COGG-912, VGG 104, and VGG 17-106 emerged as promising genotypes due to their consistently lower pest loads, whereas IPM 1603-1 and MH 18-181 were identified as susceptible. These results confirm considerable genetic variability among mungbean genotypes for resistance to sucking pests, providing valuable material for breeding programs aimed at developing pest-tolerant cultivars.

Morpho-physical observations and their association with insect pest infestation: The average leaf length across genotypes was 6.45 cm at 20 DAS, with MH 1762 having the longest leaves (7.78 cm) and LGG 711 the shortest (5.14 cm). At 50 DAS, MH 18-181 exhibited the longest leaves, while COGG-912 had the shortest. Leaf width increased from 4.70 cm at 20 DAS to 8.29 cm at 50 DAS; MH 18-181 had the broadest leaves (6.37 cm) at 20 DAS and MHBC 20-8 the widest (9.90 cm) at 50 DAS. Leaf area ranged from 99.03 cm^2 in LGG 574 at 20 DAS to 1042.52 cm^2 in SML 2016 at 50 DAS. Leaf thickness increased from 0.35 mm (20 DAS) to 0.51 mm (50 DAS), with VGG 17-009 and MH 1762 showing the highest values at respective stages. Trichome density averaged about 100/cm^2, peaking in OBGG 59, while chlorophyll content averaged ~41 $\mu g/cm^2$, highest in VGG 17-106 at 20 DAS and COGG-912 at 50 DAS. These morphological and physiological traits varied significantly across genotypes and growth stages, influencing pest resistance dynamics.

Correlation with insect pest infestation: Morpho-physical traits exhibited significant associations with sucking pest incidence in mungbean. Leaf length showed positive correlations with whitefly populations at both 20 and 50 DAS while its association with aphids and thrips was positive but non-significant. Leaf width was positively correlated with whiteflies and thrips at 20 DAS. Similarly, leaf area at 50 DAS exhibited significant positive correlations with whiteflies and aphids (indicating that larger leaf surfaces favor pest colonization. These findings align with earlier reports by Saini et al. (2017), Taggar and Gill (2012), Pal et al. (2021), Mulwa et al. (2023), and Javed et al. (2016). Leaf thickness showed significant positive correlations with whiteflies, aphids, and thrips at 20 DAS, and with whiteflies and) at 50 DAS, corroborating earlier observations (Lakshminarayan et al., 2008, Taggar and Gill 2012). In contrast, trichome density was negatively correlated with whiteflies and thrips at 20 and 50 DAS, suggesting its deterrent role against pest establishment, consistent with reports by Sanchez-Pena et al. (2006), Ramarao et al. (2021), Latha and Hanumanthraya (2018) and Javed et al. (2016). Chlorophyll content (SCMR values) exhibited significant negative correlations with whitefly populations at 20 DAS and 50 DAS, confirming earlier findings that higher chlorophyll indices are associated with reduced whitefly stress (Taggar et al., 2015, Mantesh and Pankaja 2020). The coefficient of determination (R^2) from multiple regression analysis indicated that biophysical traits contributed to sucking pest populations as follows: whiteflies: 29.5% at 20 DAS, and 30.4% at 50 DAS aphids: 31.4% at 20 DAS, and 19.3% at 50 DAS and thrips: 43.0% at 20 DAS and 29.4% at 50 DAS. Overall, leaf size and thickness were positively associated with pest incidence, while trichome density and chlorophyll content contributed to resistance, indicating their potential utility as morphological markers in resistance breeding programs.

Biochemical profiling of mungbean genotypes against sucking pests: Biochemical parameters such as phenol and protein contents were estimated at 20 and 50 DAS) to assess their potential role in imparting resistance to sucking pests in mungbean genotypes. Significant variations were observed

Table 1. Screening of mungbean genotypes to sucking pest incidence during *rabi*, 2022-23

Genotype	*Whitefly (Mean no./trifoliate leaf)	Thrips population (No./three leaves/plant)	*Aphid population (No./10 cm terminal shoot)	Reaction of genotypes to aphid population
COGG-912	0.96 (1.40)	5.00 (2.45)	28.13 (5.40)	MS
IGKM 05-18-2	1.06 (1.44)	8.99 (3.16)^{fg}	24.27 (5.03)^{de}	MS
LGG 706	1.10 (1.45)^{ij}	7.89 (2.98)^{ghi}	21.47 (4.74)^{ef}	MS
LGG 686	1.26 (1.50)	11.10 (3.48)^{d}	8.80 (3.13)^{hij}	MR
COGG-8	1.30 (1.52)	18.50 (4.42)^{b}	19.47 (4.52)^{f}	MR
LGG 574	2.32 (1.82)	5.06 (2.46)^{lm}	5.33 (2.52)^{klm}	MR
MH 18-189	1.48 (1.57)	8.52 (3.09)^{g}	26.40 (5.23)^{cd}	MS
Pusa 9072	1.00 (1.41)^{j}	9.89 (3.30)^{ef}	20.53 (4.64)^{f}	MS
LGG 609	1.30 (1.52)^{hij}	5.06 (2.46)^{lm}	6.13 (2.67)^{jkl}	MR
MH 1762	2.04 (1.74)	8.64 (3.10)^{g}	3.20 (2.05)	HR
LGG 711	1.12 (1.46)^{ij}	4.22 (2.28)^{mn}	2.40 (1.84)	HR
JLPM 707-27	3.02 (2.00)^{e}	8.76 (3.12)^{g}	23.73 (4.97)^{de}	MS
LGG 450 (SC)	4.80 (2.41)^{cd}	6.82 (2.80)^{ijk}	10.13 (3.34)^{hi}	MR
LGG 460 (TC)	1.68 (1.64)^{fghij}	3.42 (2.10)^{nop}	4.53 (2.35)^{lmn}	HR
VGG 16-045	2.38 (1.84)^{efg}	5.42 (2.53)^{l}	8.27 (3.04)^{ijk}	MR
VGG 17-009	1.56 (1.60)^{ghij}	7.16 (2.86)^{hij}	2.93 (1.98)^{mno}	HR
PMS-12	5.68 (2.58)^{bc}	7.97 (2.99)^{gh}	24.67 (5.07)^{d}	MS
OBGG 59	2.32 (1.82)^{efg}	2.78 (1.94)^{op}	1.60 (1.61)^{no}	HR
PM 2	2.64 (1.91)^{ef}	2.72 (1.93)^{op}	5.07 (2.46)^{lm}	MR
VGG 17-106	2.38 (1.84)^{efg}	2.54 (1.88)^{p}	4.53 (2.35)^{lmn}	HR
VGG 104	1.08 (1.44)^{ij}	6.58 (2.75)^{jk}	0.53 (1.24)^{o}	VHR
TMB 146	1.46 (1.57)^{ghij}	3.74 (2.18)^{mn}	3.20 (2.05)^{lmno}	HR
PUSA M 2141	2.16 (1.78)^{efgh}	5.90 (2.63)^{kl}	24.53 (5.05)^{de}	MS
IPM 1103-1	2.46 (1.86)^{efg}	4.04 (2.24)^{mn}	3.20 (2.05)^{lmno}	HR
MHBC 20-8	4.78 (2.40)^{cd}	10.56 (3.40)^{de}	3.73 (2.18)^{lmn}	HR
SML 2016	4.16 (2.27)^{d}	5.46 (2.54)^{l}	14.93 (3.99)^{g}	MR
PUSA M 2241	5.04 (2.46)^{cd}	5.06 (2.46)^{lm}	48.27 (7.02)^{b}	MS
IPM 1603-1	6.42 (2.72)^{b}	15.60 (4.07)^{c}	62.67 (7.98)^{a}	MS
MH 18-181	10.70 (3.42)^{a}	26.00 (5.20)^{a}	11.73 (3.57)^{h}	MR
CV (%)	6.42	3.12	6.71	

***Values in the parenthesis are square root transformed values**
DAS-Days After Sowing; S-Significant ; SC-Susceptible Check; TC-Tolerant Check;
VHR = Very Highly Resistant;, HR = Highly Resistant;, MR = Moderately Resistant and MS = Moderately Susceptible, SC- Susceptible Check TC- Tolerant Check

among the genotypes for both phenol and protein contents at both stages. Among the genotypes, COGG-912 recorded the highest phenol content at 50 DAS (26.89 mg/g FW), followed by LGG 711 (26.70 mg/g), LGG 609 (26.70 mg/g), and VGG 104 (26.42 mg/g), indicating a probable role of elevated phenolic levels in pest resistance. On the contrary, MH 18-181 (13.73 mg/g) and JLPM 707-27 (14.08 mg/g) exhibited lower phenol levels at 50 DAS, suggesting higher susceptibility. Protein content also varied considerably across genotypes. The highest protein content at 20 DAS was recorded in MHBC 20-8 (12.52 mg/g), PMS-12 (11.58 mg/g), and PUSA M 2241 (11.12 mg/g), whereas LGG 460 (TC) showed the lowest value (5.50 mg/g). At 50 DAS, the genotypes LGG 574 (16.83 mg/g) and PUSA M 2241 (16.37 mg/g) had the highest protein levels, which could be linked to improved pest tolerance. In contrast, COGG-912 (8.65 mg/g) and IPM 1103-1 (8.88 mg/g) showed lower protein accumulation at 50 DAS. The data indicate that genotypes with higher levels of phenols and proteins at later growth stages tend to exhibit greater resistance to sucking pests.

Correlation with sucking pest infestation: Biochemical parameters exhibited distinct associations with sucking pest

Table 2. Biophysical characteristics in leaves of mungbean genotypes

Genotype	Leaf length (cm)		Leaf width (cm)		Leaf area (cm^2/plant)		Leaf thickness (mm)		Trichomes (Number/cm^2 leaf area)		SCMR values ($\mu g/cm^2$)	
	20 DAS	50 DAS	20 DAS	50 DAS	20 DAS	50 DAS	20 DAS	50 DAS	20 DAS	50 DAS	20 DAS	50 DAS
COGG-912	5.72	7.47	4.12	5.68	123.75	397.94	0.2745	0.3505	126.70	130.00	54.75	56.53
IGKM 05-18-2	7.47	10.43	5.28	9.30	299.14	944.00	0.4057	0.6318	86.65	90.00	35.23	34.45
LGG 706	7.52	10.03	5.40	9.18	342.76	1014.09	0.4392	0.6038	88.35	98.33	35.88	36.67
LGG 686	5.18	8.37	4.07	8.55	161.90	487.12	0.4245	0.4360	113.00	114.01	46.65	46.37
COGG-8	5.22	7.80	4.33	5.84	160.95	382.63	0.2947	0.4768	88.00	90.00	45.95	48.19
LGG 574	6.32	9.97	3.88	8.78	99.03	256.21	0.2660	0.4237	110.00	108.33	33.22	46.53
MH 18-189	5.84	8.20	3.97	8.97	154.31	455.44	0.3075	0.4107	118.63	119.46	51.77	52.35
Pusa 9072	7.43	10.64	5.47	9.45	311.72	972.68	0.4657	0.6208	83.30	91.67	33.02	31.88
LGG 609	5.37	8.32	4.15	7.14	123.82	451.40	0.2447	0.4307	118.35	113.67	43.62	44.53
MH 1762	7.78	9.12	5.75	9.78	286.50	947.50	0.4640	0.7012	96.27	97.19	35.09	33.93
LGG 711	5.14	7.53	3.67	7.47	165.38	412.58	0.2860	0.3967	110.01	101.67	45.55	49.10
JLPM 707-27	7.35	10.69	5.20	9.80	304.89	978.00	0.4205	0.5997	73.30	90.00	37.77	34.92
LGG 450 (SC)	6.82	9.58	5.18	9.37	238.66	591.17	0.3392	0.3330	100.00	90.00	36.42	39.35
LGG 460 (TC)	6.23	9.20	5.28	8.90	136.78	390.28	0.3135	0.4217	110.00	101.67	49.90	49.77
VGG 16-045	5.68	7.50	3.95	7.72	109.03	324.12	0.2462	0.3459	100.00	100.00	46.58	32.95
VGG 17-009	7.37	10.50	5.65	9.43	406.76	1016.72	0.4880	0.6675	73.40	83.33	39.83	32.85
PMS-12	7.52	10.08	5.42	8.75	270.16	981.94	0.4425	0.6318	80.00	70.00	39.40	35.75
OBGG 59	6.02	9.25	3.88	7.07	231.76	577.50	0.2720	0.3025	130.00	140.00	32.98	36.13
PM 2	5.77	8.95	3.93	7.78	253.86	761.04	0.3332	0.4627	90.00	100.00	37.72	40.75
VGG 17-106	5.74	8.27	3.62	7.95	170.15	310.05	0.2973	0.4605	120.00	120.00	59.38	45.47
VGG 104	5.25	7.65	3.85	5.34	139.66	420.23	0.2650	0.4838	129.54	124.85	56.14	48.78
TMB 146	6.60	8.45	4.48	6.45	117.61	352.73	0.2402	0.3532	80.00	90.00	32.25	53.85
PUSA M 2141	5.98	9.35	4.07	8.92	257.78	644.26	0.1997	0.3037	73.35	70.00	46.35	33.45
IPM 1103-1	5.57	7.77	4.04	5.39	125.23	394.80	0.2653	0.4812	120.00	118.41	46.47	55.88
MHBC 20-8	7.23	10.32	5.47	9.90	342.86	957.62	0.4550	0.6574	90.00	90.00	33.48	32.78
SML 2016	7.26	10.45	5.07	9.55	336.53	1042.52	0.4535	0.6087	93.68	100.00	39.78	35.60
PUSA M 2241	7.38	10.70	6.05	8.79	325.06	1001.95	0.4695	0.6613	91.06	92.16	35.97	34.08
IPM 1603-1	6.97	8.68	4.40	6.90	132.80	735.27	0.4770	0.5835	118.30	110.00	36.75	42.60
MH 18-181	7.57	10.72	6.37	9.19	298.83	969.78	0.4410	0.6522	70.00	73.00	36.48	35.07
CD (p=0.05)	0.08	0.09	0.13	0.07	0.44	0.79	0.03	0.03	0.28	0.33	0.22	0.26

DAS-Days After Sowing; S-Significant, SC-Susceptible Check, TC-Tolerant Check incidence in mungbean. Protein content showed a significant positive correlation with whitefly and 50 DAS, respectively) and thrips populations. This indicates that higher protein content favoured greater pest colonization, corroborating earlier findings of Sameer and Singh (2021), Pal et al. (2021), and Joseph and Peter (2007). Although the correlation with

Table 3. Correlation between biophysical parameters of different mungbean genotypes and sucking pest infestation

Variable	Correlation coefficient	Regression equations	R^2 Value
Whitefly infestation			
Leaf length at 20 DAS (X) Vs Whitefly (Y)	0.460**	-4.5182+1.1247x	0.2115
Leaf length at 50 DAS (X) Vs Whitefly (Y)	0.403*	-4.2441+0.7535x	0.1621
Leaf width at 20 DAS (X) Vs Whitefly (Y)	0.480**	-3.4264+1.3115x	0.2305
Leaf width at 50 DAS (X) Vs Whitefly (Y)	0.261^{NS}	-0.5412+0.3956x	0.0681
Leaf area at 20 DAS (X) Vs Whitefly (Y)	0.283^{NS}	1.2163+0.0067x	0.0802
Leaf area at 50 DAS (X) Vs Whitefly (Y)	0.404*	0.6691+0.0032x	0.1635
Leaf thickness at 20 DAS (X) Vs Whitefly (Y)	0.434**	-0.7852+10.088x	0.1883
Leaf thickness at 50 DAS (X) Vs Whitefly (Y)	0.459**	-1.3574+8.1166x	0.2109
Trichomes at 20 DAS (X) Vs Whitefly (Y)	-0.339*	6.583-0.0384x	0.1149
Trichomes at 50 DAS (X) Vs Whitefly (Y)	-0.414*	7.8752-0.0515x	0.1717
SCMR Values at 20 DAS (X) Vs Whitefly (Y)	-0.345*	6.5426-0.0931x	0.1187
SCMR Values at 50 DAS (X) Vs Whitefly (Y)	-0.387*	6.8008-0.0988x	0.1499
Aphid incidence			
Leaf length at 20 DAS (X) Vs Aphids (Y)	0.311^{NS}	-60.316+15.564x	0.0968
Leaf length at 50 DAS (X) Vs Aphids (Y)	0.139^{NS}	-9.0534+5.3038x	0.0192
Leaf width at 20 DAS (X) Vs Aphids (Y)	0.203^{NS}	-13.194+11.337x	0.0412
Leaf width at 50 DAS (X) Vs Aphids (Y)	0.002^{NS}	39.64+0.0537x	3E-06
Leaf area at 20 DAS (X) Vs Aphids (Y)	0.065^{NS}	32.933+0.0316x	0.0042
Leaf area at 50 DAS (X) Vs Aphids (Y)	0.338*	4.7257+0.0542x	0.1143
Leaf thickness at 20 DAS (X) Vs Aphids (Y)	0.393*	-25.186+186.95x	0.1546
Leaf thickness at 50 DAS (X) Vs Aphids (Y)	0.253^{NS}	-6.0693+91.495x	0.0641
Trichomes at 20 DAS (X) Vs Aphids (Y)	-0.130^{NS}	70.252-0.3008x	0.0169
Trichomes at 50 DAS (X) Vs Aphids (Y)	-0.103^{NS}	66.331-0.2633x	0.0107
SCMR Values at 20 DAS (X) Vs Aphids (Y)	-0.043^{NS}	49.73-0.2361x	0.0018
SCMR Values at 50 DAS (X) Vs Aphids (Y)	-0.102^{NS}	61.93-0.5313x	0.0104
Thrips incidence			
Leaf length at 20 DAS (X) Vs Thrips (Y)	0.282^{NS}	-3.0518+1.6179x	0.0793
Leaf length at 50 DAS (X) Vs Thrips (Y)	0.169^{NS}	0.4894+0.7443x	0.0287
Leaf width at 20 DAS (X) Vs Thrips (Y)	0.412*	-5.0402+2.6439x	0.1698
Leaf width at 50 DAS (X) Vs Thrips (Y)	0.101^{NS}	4.4033+0.3598x	0.0102
Leaf area at 20 DAS (X) Vs Thrips (Y)	0.170^{NS}	5.2367+0.0095x	0.029
Leaf area at 50 DAS (X) Vs Thrips (Y)	0.323^{NS}	3.5039+0.0059x	0.1044
Leaf thickness at 20 DAS (X) Vs Thrips (Y)	0.460**	-1.3765+25.095x	0.2112
Leaf thickness at 50 DAS (X) Vs Thrips (Y)	0.445**	-1.9327+18.471x	0.198
Trichomes at 20 DAS (X) Vs Thrips (Y)	-0.388*	17.716-0.103x	0.1502
Trichomes at 50 DAS (X) Vs Thrips (Y)	-0.359*	17.837-0.1049x	0.1288
SCMR Values at 20 DAS (X) Vs Thrips (Y)	-0.161^{NS}	11.573-0.1025x	0.0261
SCMR Values at 50 DAS (X) Vs Thrips (Y)	-0.209^{NS}	12.534-0.1252x	0.0436

*Correlation is significant at 0.05 level (2 tailed); **Correlation is significant at 0.01 level (2 tailed); NS-non-significant

Table 4. Regression between sucking pest population and biophysical parameters during *rabi*, 2022-23

Variable	Regression equation	R^2 value (%)
Whitefly infestation at 20 DAS	$Y = -0.121+0.140x_1+0.977x_2-0.008x_3+5.542x_4-0.013x_5-0.038x_6$	29.5
Whitefly infestation at 50 DAS	$Y = 3.675+0.598x_1-0.483x_2-0.002x_3+6.546x_4-0.028x_5-0.049x_6$	30.4
Aphid population at 20 DAS	$Y = -131.356+32.501x_1-20.793x_2-0.229x_3+255.264x_4-0.296x_5+1.268x_6$	31.4
Aphid population at 50 DAS	$Y = 58.124-3.362x_1-7.824x_2+0.108x_3-19.422x_4-0.125x_5+0.719x_6$	19.3
Thrips population at 20 DAS	$Y = 16.891-2.993x_1+3.458x_2-0.029x_3+33.523x_4-0.108x_5-0.016x_6$	43.0
Thrips population at 50 DAS	$Y = 18.220-0.664x_1-0.781x_2-0.000x_3+20.728x_4-0.099x_5-0.024x_6$	29.4

DAS-Days after sowing
X_1 = leaf length, X_2 = leaf width, X_3 = leaf area, X_4 = leaf thickness,
X_5 = trichome density and X_6 = SCMR values

Table 5. Biochemical parameters in leaves of mungbean genotypes during *rabi*, 2022-23

Genotype	Phenols (mg/g FW of leaf)		Proteins (mg/g)	
	20 DAS	50 DAS	20 DAS	50 DAS
COGG-912	20.59	26.89	7.83	8.65
IGKM 05-18-2	18.53	22.53	7.39	10.68
LGG 706	13.42	14.77	10.16	14.09
LGG 686	12.52	14.50	7.73	13.45
COGG-8	16.90	22.33	7.75	12.52
LGG 574	18.23	25.08	10.06	16.83
MH 18-189	16.28	20.92	7.32	13.79
Pusa 9072	18.50	21.47	7.82	12.98
LGG 609	19.58	26.70	7.58	11.88
MH 1762	12.74	14.42	10.86	12.11
LGG 711	16.54	26.70	7.39	12.53
JLPM 707-27	12.72	14.08	10.99	14.52
LGG 450 (SC)	18.11	21.33	7.10	12.53
LGG 460 (TC)	20.11	23.55	5.50	11.09
VGG 16-045	15.22	23.95	7.44	11.43
VGG 17-009	12.50	14.75	10.83	12.98
PMS-12	12.15	17.48	11.58	15.61
OBGG 59	17.52	23.27	7.02	11.31
PM 2	13.38	17.38	7.80	12.82
VGG 17-106	16.23	25.93	7.03	10.31
VGG 104	16.67	26.42	7.28	11.87
TMB 146	13.20	16.47	7.76	13.76
PUSA M 2141	12.00	20.90	7.86	10.79
IPM 1103-1	20.19	24.63	7.66	8.88
MHBC 20-8	12.13	17.94	12.52	14.38
SML 2016	12.15	18.02	10.95	12.15
PUSA M 2241	12.19	15.45	11.12	16.37
IPM 1603-1	13.38	25.25	10.90	12.91
MH 18-181	12.05	13.73	11.29	15.75
CD (p=0.05)	0.16	0.18	0.09	0.13
CV (%)	1.99	1.85	1.36	1.66

DAS-Days After Sowing, FW-Fresh Weight, S-Significant, SC-Susceptible Check, TC-Tolerant Check

Table 6. Correlation between biochemical parameters and sucking pest infestation in mungbean genotypes

Variable	Correlation coefficient	Regression equation	R^2 Value
Whitefly infestation			
Phenols at 20 DAS (X) Vs Whitefly (Y)	-0.428*	7.3063-0.2889x	0.1831
Phenols at 50 DAS (X) Vs Whitefly (Y)	-0.338*	6.0813-0.1603x	0.1144
Proteins at 20 DAS (X) Vs Whitefly (Y)	0.606**	-3.2422+0.6803x	0.3667
Proteins at 50 DAS (X) Vs Whitefly (Y)	0.456**	-3.4811+0.4937x	0.2075
Aphid incidence			
Phenols at 20 DAS (X) Vs Aphids (Y)	-0.275^{NS}	100.19-3.7999x	0.0757
Phenols at 50 DAS (X) Vs Aphids (Y)	-0.091^{NS}	58.4-0.8778x	0.0082
Proteins at 20 DAS (X) Vs Aphids (Y)	0.287^{NS}	-17.973+6.6057x	0.0826
Proteins at 50 DAS (X) Vs Aphids (Y)	0.231^{NS}	-24.409+5.1203x	0.0534
Thrips incidence			
Phenols at 20 DAS (X) Vs Thrips (Y)	-0.347*	16.087-0.5501x	0.1204
Phenols at 50 DAS (X) Vs Thrips (Y)	-0.345*	15.395-0.3839x	0.119
Proteins at 20 DAS (X) Vs Thrips (Y)	0.400*	-1.8966+1.056x	0.1602
Proteins at 50 DAS (X) Vs Thrips (Y)	0.379*	-4.772+0.9652x	0.1438

Table 7. Regression between sucking pest population and biochemical parameters during *rabi*, 2022-23

Variable	Regression equation	R^2 value (%)
Whitefly infestation at 20 DAS	$Y = -1.906-0.053x_1+0.624x_2$	37.0
Whitefly infestation at 50 DAS	$Y = -1.415-0.055x_1+0.422x_2$	21.7
Aphid population at 20 DAS	$Y = 36.038-2.160x_1+4.349x_2$	9.7
Aphid population at 50 DAS	$Y = -46.157-0.584x_1+5.880x_2$	5.6
Thrips population at 20 DAS	$Y = 4.369-0.251x_1+0.794x_2$	17.5
Thrips population at 50 DAS	$Y = 3.150-0.213x_1+0.688x_2$	16.8

aphids was positive, it was not statistically significant. In contrast, phenol content displayed a significant negative correlation with whitefly and thrips populations at 20 and 50 DAS, suggesting its role in resistance through deterrent or toxic effects. No significant association was observed with aphids, though the trend remained negative. Similar findings were reported by Sameer and Singh (2021), Ramarao et al. (2021) and Anu et al. (2021) for whiteflies and aphids, and by Chaudhary and Pandya (2019) for thrips in chilli. Multiple linear regression (MLR) revealed that biochemical traits explained 37.0% of the variability in whitefly infestation at 20 DAS, declining to 21.7% at 50 DAS. For aphids, the explanatory power was much lower (9.7 and 5.6% at 20 and 50 DAS).

Between 20 days (DAS) and 50 days (DAS), significant differences were observed in both biophysical and biochemical parameters in mungbean genotypes. The average values for leaf length, leaf width, leaf area, and leaf thickness all showed a marked increase at 50 DAS compared to 20 DAS, signifying active vegetative growth. Trichome number and SCMR values also generally increased from 20 to 50 DAS. However, the magnitude of change in trichome number and SCMR was sometimes smaller or more variable depending on the genotype. Among biochemical traits, both phenol and protein contents increased from 20 to 50 DAS in most genotypes, often quite substantially for proteins. Overall, protein and phenol contents were identified as key determinants of susceptibility and resistance, respectively. While these traits significantly influenced pest dynamics, other physiological and environmental factors also contributed. Hence, protein and phenol levels m may serve as reliable biochemical markers for resistance screening in mungbean breeding programs.

CONCLUSIONS

The mungbean genotypes COGG-912, VGG 104 and VGG 17-106 were identified as resistant to whiteflies, aphids, and thrips. Among the biophysical traits, trichome density, chlorophyll content, and phenol content exhibited a significant negative correlation with pest incidence. On the other hand, leaf area, leaf thickness, and protein content were positively associated with pest populations. Among the biochemical parameters, protein content showed a significant positive correlation with whitefly and thrips populations, whereas phenol content was negatively correlated with all three pests. These morpho-physical and biochemical traits can serve as reliable indicators for screening large germplasm collections for resistance to the sucking pest complex. The resistant genotypes identified in this study may also be effectively utilized as donor parents in breeding programs to develop mungbean varieties with enhanced tolerance to sucking pests and their associated viral diseases.

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Received 15 September, 2025; Accepted 28 November, 2025