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Growth and Biochemical Responses of Mungbean (*Vigna radiata* L.) Genotypes to *Meloidogyne javanica* and *Rhizoctonia solani*

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Abstract

Mungbean (*Vigna radiata* L.) is an important pulse crop valued for its high protein content and contribution to nutritional security, particularly in Asia. However, its productivity is severely constrained by soil-borne pathogens, especially *Rhizoctonia solani* and *Meloidogyne javanica*, which cause root rot and root-knot disease, respectively. The present study evaluated the response of eight mungbean genotypes to these pathogens under greenhouse conditions, together with an *in vitro* seed germination assay to assess the pathogenic effect of *Rhizoctonia solani*. Pathogen inoculation significantly reduced seed germination, plant growth, chlorophyll, carotenoid, and total soluble protein contents, whereas total phenolic content increased in all genotypes. Based on disease severity, IPM-02-03 and PDM-54 were classified as moderately resistant to *Meloidogyne javanica*, whereas no genotype exhibited resistance to *Rhizoctonia solani*. In contrast, PDM-139 and IPM-302-2 showed the greatest reductions in growth and biochemical traits, indicating high susceptibility to *M. javanica* and *Rhizoctonia solani*, respectively. The observed genotypic variation highlights the potential of moderately tolerant genotypes for resistance breeding and provides valuable information for developing integrated and sustainable management strategies for soil-borne diseases in mungbean.

***Key words*:** Biochemical responses, Disease resistance, *Meloidogyne javanica*, Mungbean, *Rhizoctonia solani*, Soil-borne pathogens

Mungbean (*Vigna radiata* L.), commonly known as green gram, is an important pulse crop widely cultivated across Asia, particularly in India, Bangladesh, Myanmar, and China. It is valued for its high protein content, short growth duration, and ability to fix atmospheric nitrogen, thereby enhancing soil fertility and supporting sustainable cropping systems [1-3]. Despite its agronomic importance, mungbean productivity is often constrained by various biotic stresses, among which soil-borne pathogens constitute a major constraint to plant health and productivity [3-4]. Among fungal pathogens, *Rhizoctonia solani* Kuhn is a major causal agent of wet root rot, characterized by seedling damping-off, hypocotyl lesions, yellowing, wilting, and eventual plant mortality, particularly under warm and moist soil conditions that favor pathogen proliferation [5-7]. *Rhizoctonia solani* belongs to the phylum Basidiomycota and is categorized into 14 anastomosis groups (AGs 1–13 and AG-BI), with its teleomorph designated as *Thanatephorus cucumeris* [8]. Recent studies have highlighted the increasing incidence and destructive impact of this pathogen in major mungbean-growing regions [9-10].

In addition to fungal pathogens, root-knot nematodes (RKN), particularly *Meloidogyne javanica* and *Meloidogyne incognita,* represent another major constraint to mungbean cultivation. Among these species, *Meloidogyne javanica* was selected for the present investigation because it was the predominant root-knot nematode species recovered from naturally infected mungbean plants during field surveys conducted in the major mungbean-growing areas of Aligarh district. Root-knot nematodes induce characteristic gall formation on roots, disrupting nutrient and water uptake and resulting in stunted growth, chlorosis, reduced pod set, and significant yield losses [11-14]. Although root-knot nematodes and *Rhizoctonia solani* frequently occur together under field conditions and may form a disease complex, the present study evaluated each pathogen separately to assess the independent effects of *Meloidogyne javanica* and *Rhizoctonia solani* on mungbean genotypes. Recent reports indicate that yield losses in mungbean due to root-knot nematodes may range from 20-60%, depending on cultivar susceptibility and nematode infestation levels [15-16]. Similarly, wet root rot caused by *Rhizoctonia solani* remains a serious constraint in major mungbean-growing regions of South Asia, often leading to significant plant mortality (33-40%) and reduced grain yield [17-18].

Considering the limitations and environmental risks associated with chemical control measures, the development and deployment of disease-tolerant cultivars represent a sustainable, eco-friendly, and economically viable strategy for disease management. Therefore, the present study was undertaken to evaluate the response of genetically diverse mungbean genotypes to *Meloidogyne javanica* and *Rhizoctonia solani* under controlled conditions through the assessment of

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disease severity, growth, and biochemical traits, with the objective of identifying tolerant genotypes that could serve as valuable genetic resources for resistance breeding programmes.

MATERIALS AND METHODS

Survey and collection of plant material

A preliminary survey was conducted across major mungbean-growing areas of Aligarh district, Uttar Pradesh, India, during the crop growing season (March-May 2023), to assess the incidence of root rot and root-knot diseases. The mungbean plants showing typical disease symptoms were collected along with their roots and brought to the laboratory for isolation and identification of the pathogens. The survey revealed a high incidence of root-knot and root-rot diseases, with *Rhizoctonia solani* and *Meloidogyne javanica* being the predominant fungal and nematode pathogens, respectively. Based on these observations, eight mungbean genotypes were selected for screening. Seeds were procured from ICAR-IARI, New Delhi, and certified local suppliers.

Soil preparation and pot filling

Sandy loam soil was sieved through a 20-mesh sieve and mixed with river sand and well-decomposed farmyard manure at a 3:1:1 (v/v) ratio. Approximately 1 kg of the mixture was filled into 15-cm (6-inch) diameter clay pots. The potting medium was sterilized by autoclaving at 121 °C under 20 psi pressure for 20 minutes to eliminate soil-borne microorganisms.

Isolation and maintenance of pathogens

Rhizoctonia solani

Diseased root tissues (4-5 mm) collected from the advancing margins of lesions were washed thoroughly under running tap water, surface sterilized in 1% sodium hypochlorite solution for 1 min, rinsed three times with sterile distilled water, blotted dry on sterile filter paper, and placed on potato dextrose agar (PDA) plates amended with streptomycin sulfate (50 mg L^{-1}) to suppress bacterial contamination. The plates were incubated at 25 ± 2°C for 3–5 days. Hyphal tips emerging from the infected tissues were transferred to fresh PDA plates to obtain pure cultures. The pathogen was identified on the basis of colony morphology and characteristic right-angled hyphal branching with constrictions at the branch point and septa near the origin of the branches following the descriptions of Sneh *et al*. [19].

The fungal isolate was further confirmed by molecular characterization. Genomic DNA was extracted from actively growing mycelium using the HiPurA™ Fungal DNA Purification Kit following the manufacturer's instructions. The internal transcribed spacer (ITS) region of rDNA was amplified using universal ITS primers. PCR products were purified using the FavorPrep™ GEL/PCR Purification Kit (Cat. No. FAGCK001) and sequenced by Sanger DNA sequencing using an ABI-3500 XL automated DNA sequencer [20]. The obtained ITS sequence was compared with sequences available in the NCBI GenBank database using BLAST for species confirmation. The sequence was deposited in GenBank under accession number PX487754. Amplification of the ITS region is shown in (Fig 1).

Pathogenicity was confirmed by fulfilling Koch's postulates. Healthy mungbean seedlings grown in sterilized potting mixture were inoculated by applying the fungal inoculum around the root zone, while uninoculated plants served as controls. Typical root-rot symptoms developed within 10–15 days after inoculation. The fungus was re-isolated from symptomatic roots following the same isolation procedure, and its cultural and microscopic characteristics were confirmed to be identical to those of the original isolate, thereby fulfilling Koch's postulates.

For inoculum production, the fungus was grown in potato dextrose broth at 25 ± 2°C for 15–20 days. The mycelial biomass was harvested by filtration, washed with sterile distilled water, homogenized, and adjusted to a concentration of 2.0 g fresh mycelial biomass per 10 mL sterile distilled water, which was uniformly applied around the root zone of each 15-day-old seedling.

Meloidogyne javanica

Root-knot nematodes were isolated from naturally infected mungbean roots collected during the survey. Egg masses were hand-picked from infected roots using sterilized forceps, and second-stage juveniles (J_2) were extracted using the modified Baermann funnel technique [21].

Species identification was initially carried out based on the perineal pattern morphology of adult females following Eisenback *et al*. [22]. Adult females were carefully dissected from infected root galls under a stereoscopic microscope. The posterior body region was excised, the internal body contents were removed in 45% lactic acid, and the cuticular patterns were mounted in glycerin for microscopic examination. Identification was based on the characteristic morphology of the dorsal arch, lateral field, and striae.

The nematode isolate was further confirmed by molecular characterization. Genomic DNA was extracted from adult females using the NaOH extraction method described by Floyd *et al*. [23]. The 18S SSU rRNA gene region was amplified using Nem-18S primers. PCR products were resolved on 1.5% agarose gel, purified, and sequenced using an ABI-3500 XL automated DNA sequences. The obtained sequence was compared with the NCBI GenBank database using BLAST, confirming the identity of *Meloidogyne javanica*. The sequence was deposited in GenBank under accession number PX658536. Representative PCR amplification is shown in (Fig 2).

Nematode population density was determined using a counting dish under a stereoscopic microscope, and the suspension was adjusted to 2000 ± 50 second-stage juveniles (J_2) per pot (approximately 200 ± 5 J_2 mL^{-1}). The suspension was inoculated 15 days after sowing by pipetting it into three to five holes (2-3 cm deep) made around the root zone of each seedling, which were subsequently covered with soil.

In vitro seed germination assay

The pathogenic effect of *R. solani* on seed germination and early seedling vigour was assessed following the method described by Dubey *et al*. [24]. Surface-sterilized seeds were placed on sterile cotton in Petri-plates and inoculated with 2 g of *R. solani* inoculum, while uninoculated plates served as control. The Petri-plates were incubated at 27 °C and germination was recorded when radicle emergence exceeded 5 mm. The experiment was carried out with three biological replications per treatment.

Greenhouse screening

Sterilized soil-filled pots were sown with mungbean seeds and maintained under natural daylight conditions in a greenhouse with temperatures ranging from 25–35 °C and relative humidity of 60–80%. Seedlings were allowed to establish for 15 days after sowing, after which inoculations were carried out. Three treatments were imposed: (i) uninoculated control ©, (ii) inoculation with *Meloidogyne*

javanica (N), and (iii) inoculation with *Rhizoctonia solani* (F). Plants were maintained under optimum moisture conditions and arranged in a completely randomized design (CRD). Harvesting was carried out 65 days after sowing, and roots were gently washed prior to observation. Each genotype × treatment combination was replicated three times.

Observation and data recording

Five randomly selected plants from each replication were used for recording growth, disease, and biochemical observations.

Growth parameters

Shoot length (cm), root length (cm), fresh weight (g), dry weight (g), number of pods, and number of nodules per plant were recorded following standard procedures [25].

Biochemical analysis

Chlorophyll estimation

Total chlorophyll content (mg g^{-1} FW) was estimated following Arnon [26]. Leaf tissue (1 g) was homogenized in 80% acetone and centrifuged to obtain the supernatant. Absorbance was measured at 645 and 663 nm using a UV–Vis spectrophotometer. Chlorophyll content was calculated using the standard formula:

$$\text{Total chlorophyll content (mg g}^{-1}\text{ FW)} = [20.2\ (A_{645}) + 8.02\ (A_{663})] \times V/1000 \times W$$

where A_{645} and A_{663} are absorbance values at respective wavelengths, V is the final volume (mL), and W is the fresh weight (g).

Carotenoid estimation

Total carotenoid content was estimated following MacLachlan and Zalik [27]. The extract was prepared as described for chlorophyll estimation. Absorbance was recorded at 480 and 510 nm, and carotenoid content was calculated using following formula:

$$\text{Total carotenoid content (mg g}^{-1}\text{ FW)} = 7.6\ (OD_{480}) - 1.49\ (OD_{510}) \times V/D \times W \times 1000$$

where OD_{480} and OD_{510} are optical densities, V is extract volume (mL), D is path length (cm), and W is fresh weight (g).

Total phenols (TPh)

Total phenolic content was estimated using the method of Swain and Hillis [28]. Leaf tissue (100 mg) was extracted twice in methanol containing 0.3 N HCl. The extract was centrifuged at 5000 rpm for 10 minutes. To the supernatant, 0.5 mL Folin–Ciocalteu reagent and 1 mL of 35% sodium bicarbonate were added, resulting in a blue-colored complex. Absorbance was recorded at 630 nm, and results were expressed as mg gallic acid equivalents (GAE) per g fresh weight.

Total soluble proteins (TSP)

Total soluble proteins were estimated following Lowry *et al*. [29]. 100 mg oven dried powder of seed was extracted in 5 mL of 0.1 N NaOH and centrifuged at 6000 rpm for 15 minutes at 4°C. An aliquot (0.2 mL) of the extract was mixed with equal volume of 20% trichloroacetic acid and refrigerated for 1 hr, followed by centrifugation at 6000 rpm for 15 minutes at 4°C. The residue obtained was mixed with 5 mL of reagent (prepared from sodium carbonate, copper sulfate, sodium potassium tartrate, and Folin–Ciocalteu reagent). Absorbance was recorded at 570 nm, and protein concentration was determined from standard curve prepared by using bovine serum albumin (BSA) and expressed as mg per g dry weight.

Disease rating and classification

Genotypes were classified into disease reaction categories based on the root-gall index scale of Taylor and Sasser [30] for *Meloidogyne javanica* and the root-rot severity scale described by Nene *et al*. [31] and Pandey *et al*. [32] for *R. solani*.

Experimental design and statistical analysis

The experiment was conducted in a completely randomized design (CRD) with three replications. Results are presented as mean ± standard error (SE) of three replications. Data were subjected to analysis of variance (ANOVA) using R software (version 2.14.1). Treatment means were compared using Duncan's Multiple Range Test (DMRT) at $P \leq 0.05$ [33] and means followed by different letters differ significantly according to DMRT.

RESULTS AND DISCUSSION

Molecular identification of the pathogens

The fungal isolate was identified as *Rhizoctonia solani* based on its cultural and microscopic characteristics and was further confirmed by amplification and sequencing of the ITS region of rDNA. BLAST analysis showed high sequence similarity with *R. solani* AG-1 IA isolates available in the NCBI GenBank database, and the sequence was deposited under GenBank accession number PX487754 (Fig 1). Similarly, *Meloidogyne javanica* was identified based on perineal pattern morphology and further confirmed by amplification and sequencing of the 18S SSU rRNA gene. BLAST analysis confirmed the species identity, and the sequence was deposited in GenBank under accession number PX658536 (Fig 2).

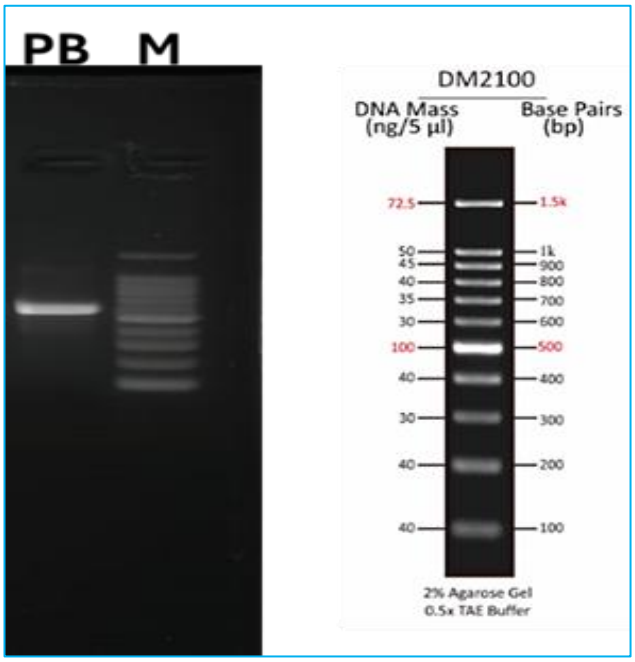


Fig 1 PCR amplification of the ITS region of *Rhizoctonia solani* genomic DNA on 1.5% agarose gel. M = 100 bp DNA ladder

In vitro response to Rhizoctonia solani

Inoculation with *Rhizoctonia solani* significantly ($P \leq 0.05$) reduced seed germination, seedling length, and seedling

vigour in all mungbean genotypes compared with the uninoculated control (Fig 3-4). Among the tested genotypes, SRPM-26 recorded the highest reduction in seed germination (62.96%) and seedling vigour (77.03%), with germination decreasing from 90.00% in the control to 33.33% under pathogen inoculation and vigour index declining from 1670.33 to 383.67. In contrast, IPM-205-7 showed the lowest reduction in seed germination (33.33%) and seedling vigour (45.01%), with germination decreasing from 80.00% to 53.33% and vigour index from 1339.67 to 736.67. The greatest reduction in seedling length was observed in IPM-2K14-9 (45.61%), whereas the lowest reduction was recorded in IPM-205-7 (17.33%).

Greenhouse evaluation of genotypes

Greenhouse evaluation demonstrated that inoculation with *M. javanica* and *R. solani* significantly ($P \leq 0.05$) affected growth and biochemical parameters of all mungbean genotypes compared with the uninoculated control (Fig 5-6). Reductions were observed in shoot length, root length, fresh weight, dry weight, pod number, nodulation, chlorophyll, carotenoid, and protein content. In contrast, total phenolic content increased following pathogen inoculation in all genotypes.

Reaction of Genotypes to Meloidogyne javanica

Disease reaction of mungbean genotypes to *M. javanica* is presented in (Table 1) and illustrated in (Fig 7-8). None of the tested genotypes exhibited immunity or high resistance to *M. javanica*. The highest gall number and egg mass production were recorded in PDM-139 (90.00 galls and 21.67 egg masses), followed by SRPM-26 (70.33 galls and 19.67 egg masses), SML-668 (68.67 galls and 19.00 egg masses), IPM-2K14-9 (65.33 galls and 18.33 egg masses), IPM-205-7 (56.33 galls and 18.00 egg masses) and IPM-302-2 (47.33 galls and 16.67 egg masses). These genotypes were classified as susceptible (gall index = 4.0). The lowest gall number and egg mass production were recorded in IPM-02-03 (15.33 galls and 6.33 egg masses) and PDM-54 (23.33 galls and 8.00 egg masses) and were categorized as moderately resistant, each with a gall index of 3.0.

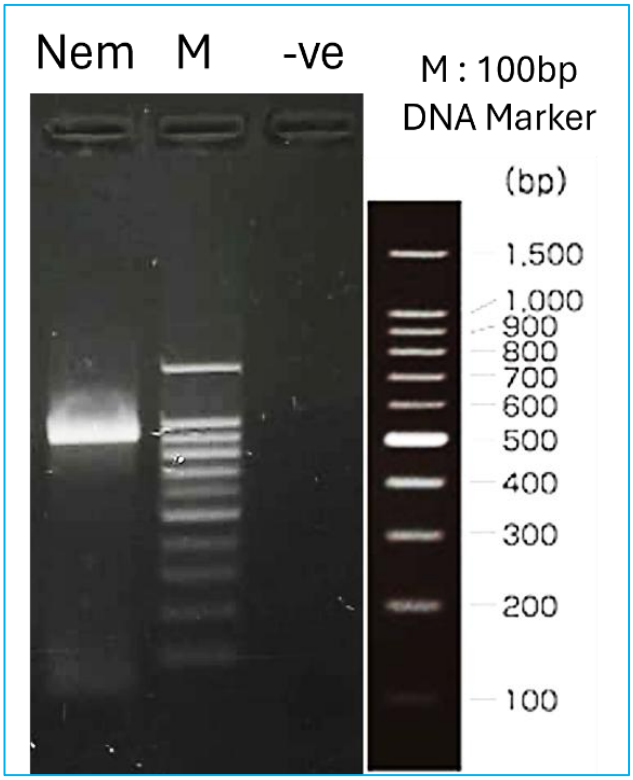


Fig 2 PCR amplification of the 18S SSU rRNA gene of *Meloidogyne javanica* genomic DNA on 1.5% agarose gel. M = 100 bp DNA ladder

Table 1 Reaction of mungbean genotypes to *Meloidogyne javanica* under greenhouse conditions

Genotypes	No. of galls per root system	Root gall index (RGI)	Reaction
IPM 02-03	15.33 ± 1.45^{f}	3.00 ± 0.00	MR
IPM 2K14-9	65.33 ± 2.19^{b}	4.00 ± 0.00	S
IPM 302-2	47.33 ± 2.73^{d}	4.00 ± 0.00	S
IPM 205-7	56.33 ± 1.20^{c}	4.00 ± 0.00	S
PDM-139	90.00 ± 2.08^{a}	4.00 ± 0.00	S
PDM-54	23.33 ± 1.20^{e}	3.00 ± 0.00	MR
SML-668	68.67 ± 0.88^{b}	4.00 ± 0.00	S
SRPM-26	70.33 ± 2.40^{b}	4.00 ± 0.00	S

*Values are expressed as mean ± standard error (SE) of three biological replications. Means followed by different letters differ significantly according to Duncan's Multiple Range Test (DMRT) at $P \leq 0.05$.

**Root gall index (RGI) was assessed on a 0–5 scale according to Taylor and Sasser [30]: 0 = no galls; 1 = 1–2 galls; 2 = 3–10 galls; 3 = 11–30 galls; 4 = 31–100 galls; and 5 = >100 galls. MR = moderately resistant; S = susceptible

Growth parameters under nematode stress

Among all genotypes, PDM-139 exhibited the maximum reduction in growth parameters following nematode inoculation. Significant reductions ($P \leq 0.05$) were observed in shoot length from 34.82 cm (control) to 28.56 cm (17.99%), root length from 15.17 cm (control) to 8.50 cm (43.95%), fresh weight from 25.55 g (control) to 18.05 g (29.35%), dry weight from 5.04 g (control) to 3.59 g (28.77%), number of pods from 8.00 (control) to 4.33 (45.88%), and nodules from 5.00 (control) to 3.00 (40.00%) (Fig 5).

Biochemical parameters under nematode stress

PDM-139 also showed the greatest reduction in biochemical parameters. There was a significant decrease in chlorophyll content from 2.01 mg g^{-1} FW (control) to 1.01 mg g^{-1} FW (49.75%), carotenoid content from 0.36 mg g^{-1} FW (control) to 0.23 mg g^{-1} FW (36.11%), and protein content from 190.65 mg g^{-1} DW (control) to 141.65 mg g^{-1} DW (25.70%). In contrast, total phenolic content increased from 14.27 mg g^{-1} FW (control) to 15.48 mg g^{-1} FW (8.47%) under nematode stress. Moderately resistant genotypes (IPM-02-03 and PDM-54) exhibited significantly greater accumulation of total phenolic content than susceptible genotypes, with increases of 54.32% and 53.31%, respectively (Fig 6).

Reaction of Genotypes to Rhizoctonia solani

Disease reaction of mungbean genotypes to *Rhizoctonia solani* is presented in (Table 2) and illustrated in (Fig 7-8).

Similar to the response observed following nematode inoculation, none of the genotypes exhibited immunity or high resistance to *Rhizoctonia solani*. The highest percentage of root-rot was observed in IPM-302-2 (86.30%), followed by PDM-139 (81.72%), SRPM-26 (80.44%) and IPM 02-03 (79.16%). Based on disease severity, they were classified as highly susceptible, with disease index values ranging from >8.0 to 9.0. The percentage of root-rot was lower in the remaining genotypes, i.e. IPM-205-7 (71.38%), IPM-2K14-9 (68.91%), PDM-54 (62.07%) and SML-668 (61.91%). These genotypes were categorized as susceptible, with disease scores ranging from > 6.0 to ≤8.0.

Table 2 Reaction of mungbean genotypes to *Rhizoctonia solani* under greenhouse conditions

Genotypes	Root-rot severity (%)	Root-rot index (RRI)	Reaction
IPM 02-03	79.16 ± 1.74^{b}	8.20 ± 0.06	HS
IPM 2K14-9	68.91 ± 1.30^{c}	7.53 ± 0.09	S
IPM 302-2	86.30 ± 1.28^{a}	8.50 ± 0.06	HS
IPM 205-7	71.38 ± 1.56^{c}	7.73 ± 0.12	S
PDM-139	81.72 ± 1.77^{b}	8.30 ± 0.06	HS
PDM-54	62.07 ± 1.07^{d}	6.97 ± 0.12	S
SML-668	61.91 ± 1.57^{d}	6.97 ± 0.15	S
SRPM-26	80.44 ± 1.56^{b}	8.30 ± 0.06	HS

*Values are expressed as mean ± standard error (SE) of three biological replications. Means followed by different letters differ significantly according to Duncan's Multiple Range Test (DMRT) at P ≤ 0.05.

**Root-rot index (1–9 scale: 1 = immune; >1 to ≤3 = resistant; >3 to ≤5 = moderately resistant; >5 to ≤6 = moderately susceptible; >6 to ≤8 = susceptible; >8 to 9 = highly susceptible) was determined according to Nene *et al*. [31] and Pandey *et al*. [32].

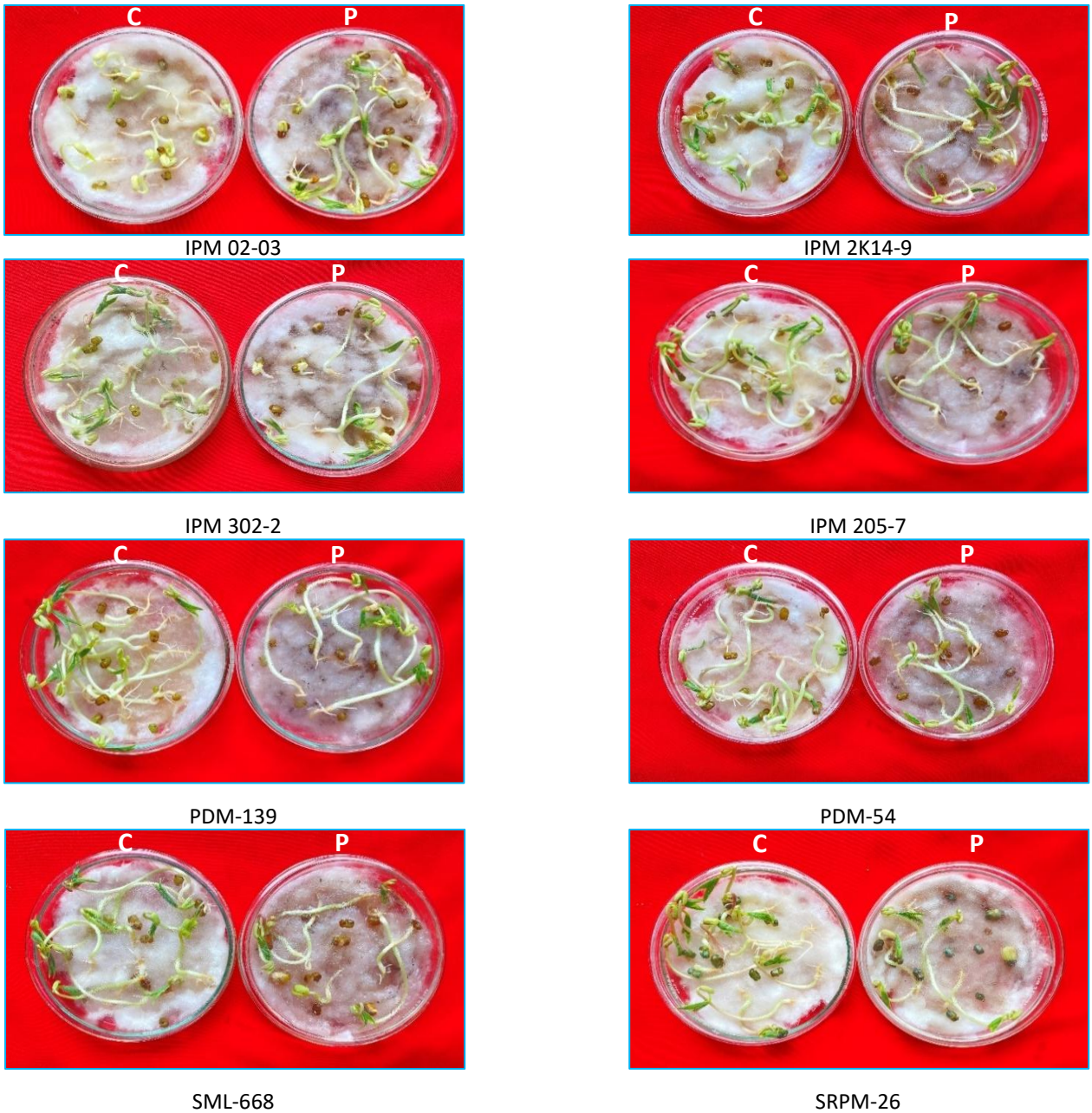


Fig 3 In vitro effect of *Rhizoctonia solani* on seed germination of mungbean genotypes (C = control; P = inoculated with *R. solani*)

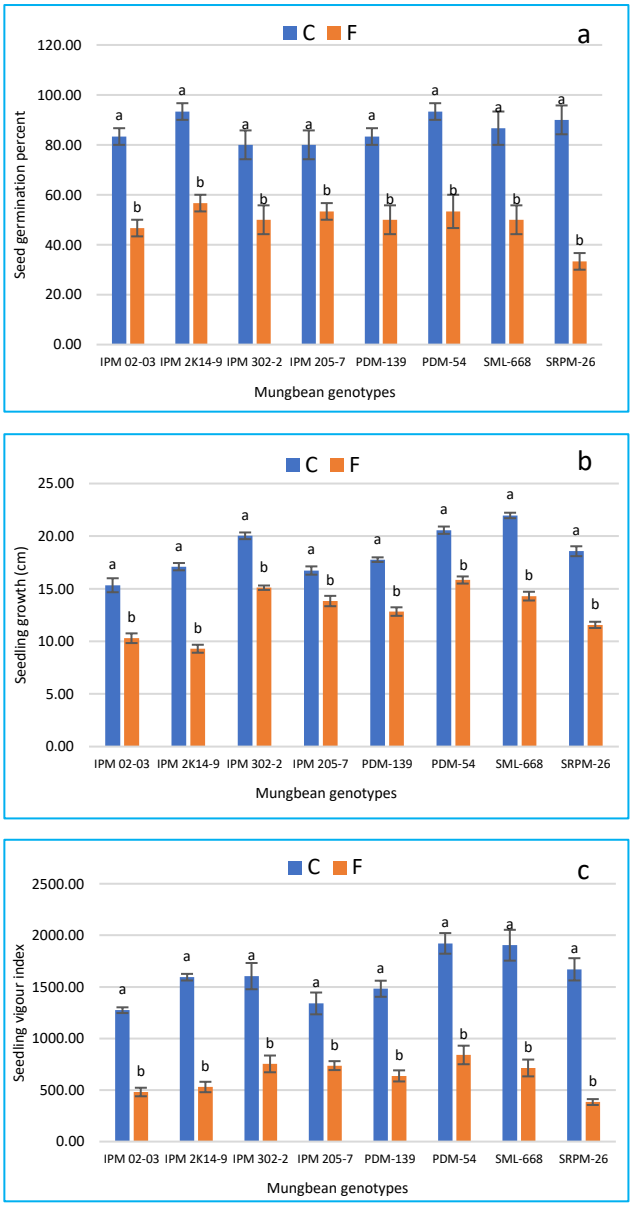


Fig 4 In vitro effect of *Rhizoctonia solani* on seed germination, seedling growth and vigour index of mungbean genotypes (C = control; F = inoculated with 2 g *R. solani*)

*Data represent mean ± standard error of three replicates. Means followed by different letters within a genotype differ significantly according to Duncan's Multiple Range Test (DMRT) at $p \leq 0.05$

Growth parameters under fungal stress

Among all genotypes, IPM-302-2 exhibited the greatest reduction in growth parameters under *R. solani* inoculation. Significant reductions ($P \leq 0.05$) were observed in shoot length from 35.15 cm (control) to 26.98 cm (23.24%), root length from 15.30 cm (control) to 8.09 cm (47.12%), fresh weight from 28.53 g (control) to 17.13 g (39.95%), dry weight from 5.34 g (control) to 3.43 g (35.76%), number of pods from 7.00 (control) to 3.67 (47.57%), and nodules from 4.33 (control) to 1.67 (61.43%) (Fig 5).

Biochemical parameters under fungal stress

Similarly, IPM-302-2 recorded the most pronounced reduction in biochemical constituents. There was a significant reduction in chlorophyll content from 1.90 mg g^{-1} FW (control) to 0.82 mg g^{-1} FW (56.84%), carotenoid content from 0.34 mg g^{-1} FW (control) to 0.22 mg g^{-1} FW (35.29%), and protein content from 173.03 mg g^{-1} DW (control) to 117.90 mg g^{-1} DW (31.86%). In contrast, total phenolic content increased from 12.49 mg g^{-1} FW (control) to 13.87 mg g^{-1} FW (11.04%) under fungal infection (Fig 6).

The present study revealed significant variation in the response of eight mungbean genotypes to *M. javanica* and *R. solani*, although none of the genotypes exhibited complete resistance to either pathogen. This indicates a limited availability of strong resistance within the evaluated germplasm. Similar findings have been reported in earlier studies, where most mungbean cultivars exhibited reactions ranging from susceptible to moderately resistant against root-knot nematodes and soil-borne fungal pathogens under controlled conditions [34-35].

The in vitro seed germination assay demonstrated a clear inhibitory effect of *R. solani* on seed germination and early seedling growth across all mungbean genotypes. None of the genotypes exhibited complete resistance under *in vitro* conditions. Pathogen inoculation significantly reduced germination percentage, radicle and plumule length, and seedling vigour index compared to the uninoculated control. Similar observations have been reported in *Solanum lycopersicum*, where *R. solani* significantly reduced seed germination, seedling growth, and biomass accumulation [36].

Under nematode stress, genotypes IPM-02-03 and PDM-54 were categorized as moderately resistant based on gall index, while the remaining genotypes were susceptible, with considerable variation in gall number and egg mass production. Notably, PDM-139 exhibited the highest galling intensity and greatest reduction in growth and biochemical parameters, indicating high susceptibility. These observations are consistent with previous reports highlighting that *Meloidogyne* spp. infection disrupts root architecture, impairs nutrient and water uptake, and interferes with physiological processes, ultimately reducing plant growth and productivity [30], [37]. The variability observed among susceptible genotypes further suggests differential levels of tolerance, even within similar disease rating classes.

In the case of *R. solani*, none of the genotypes exhibited resistance, and several genotypes, including IPM-302-2, PDM-139, and SRPM-26, were classified as highly susceptible based on disease severity. The pronounced reduction in growth and biochemical parameters in IPM-302-2 indicates its high sensitivity to fungal infection. These findings corroborate earlier reports that *R. solani* causes severe root damage, disrupts nodulation, and significantly reduces plant vigor and biomass in mungbean and other legumes [38]. However, the relatively better performance of IPM-205-7 during the in vitro assay suggests partial tolerance at the early seedling stage, which was not consistently maintained under greenhouse conditions, indicating that resistance expression may vary with plant developmental stage and environmental conditions.

Pathogen inoculation significantly reduced growth attributes, including shoot and root length, biomass, nodulation, and pod formation, across all genotypes. Similarly, key biochemical parameters such as chlorophyll, carotenoids, and total soluble protein content declined under both nematode and fungal stress. These reductions may be attributed to impaired photosynthetic efficiency, disruption of metabolic activities, diversion of assimilates towards defense mechanisms, and damage to vascular tissues, as reported previously [37-39].

In contrast to other biochemical parameters, total phenolic content increased following pathogen inoculation, with a markedly higher accumulation observed in moderately resistant genotypes such as IPM-02-03 and PDM-54. This enhanced phenolic response suggests activation of defense-related metabolic pathways. Phenolic compounds play a crucial

role in plant defense by contributing to cell wall strengthening, regulation of oxidative stress, and inhibition of pathogen development [9-10]. The comparatively lower increase in phenolic content in susceptible genotypes suggests a possible association between phenolic accumulation and enhanced tolerance to pathogen stress.

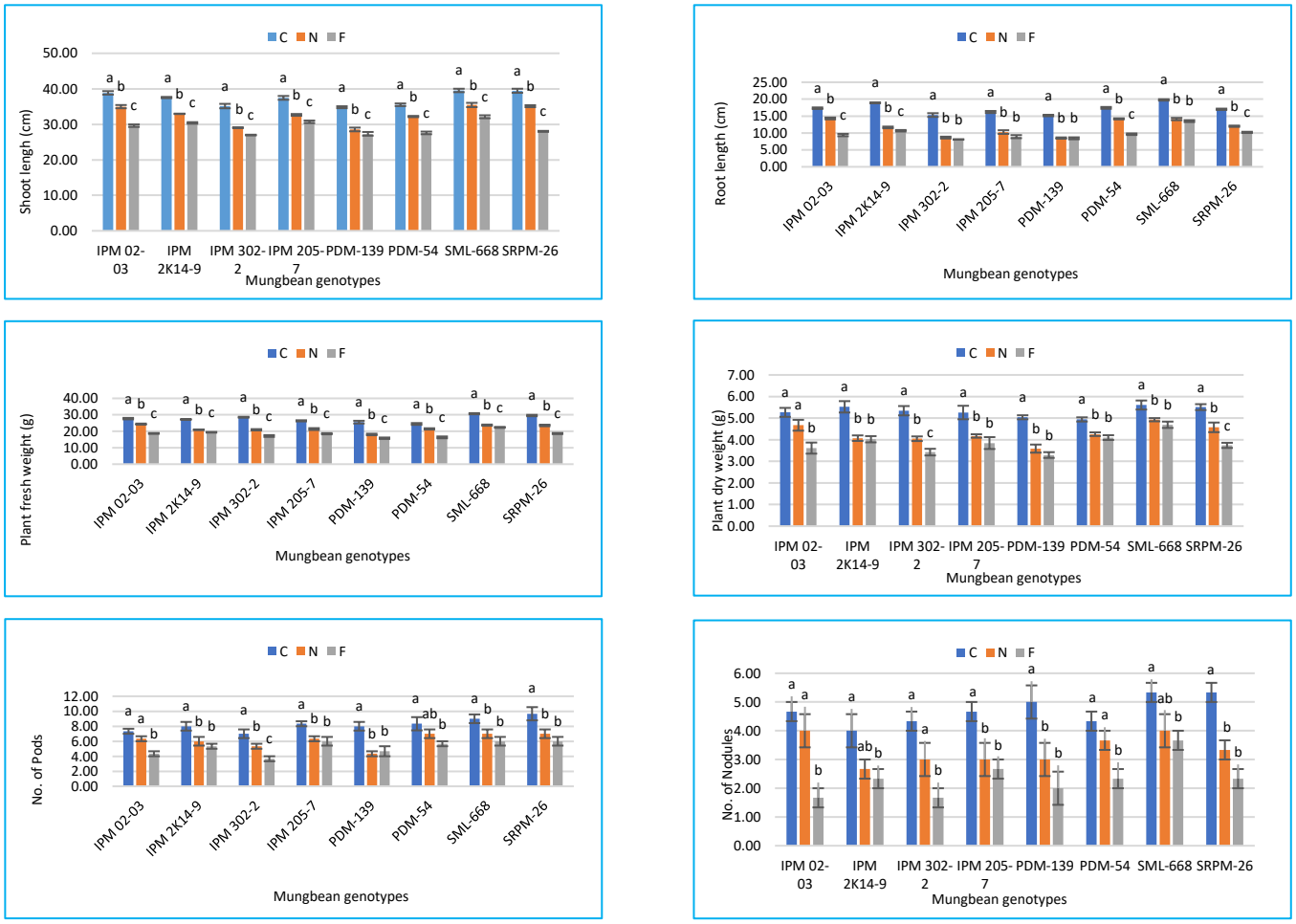


Fig 5 Effect of *Meloidogyne javanica* and *Rhizoctonia solani* on growth parameters of mungbean genotypes under greenhouse conditions (C = control; N = inoculated with 2000 J_2 of *M. javanica*; F = inoculated with 2 g *R. solani*).
*Data represent mean ± standard error of three replicates. Means followed by different letters within a genotype differ significantly according to Duncan's Multiple Range Test (DMRT) at $p \leq 0.05$

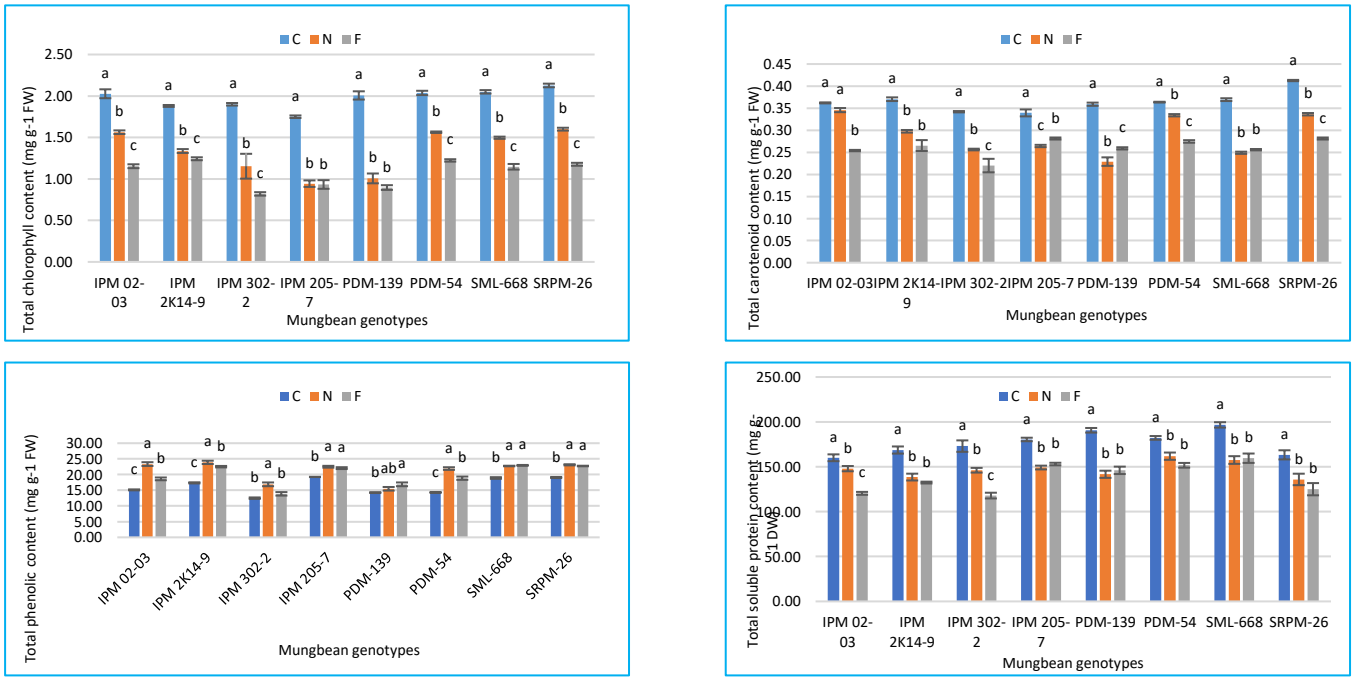


Fig 6 Effect of *Meloidogyne javanica* and *Rhizoctonia solani* on biochemical parameters of mungbean genotypes under greenhouse conditions (C = control; N = inoculated with 2000 J_2 of *M. javanica*; F = inoculated with 2 g *R. solani*).
*Data represent mean ± standard error of three replicates. Means followed by different letters within a genotype differ significantly according to Duncan's Multiple Range Test (DMRT) at $p \leq 0.05$

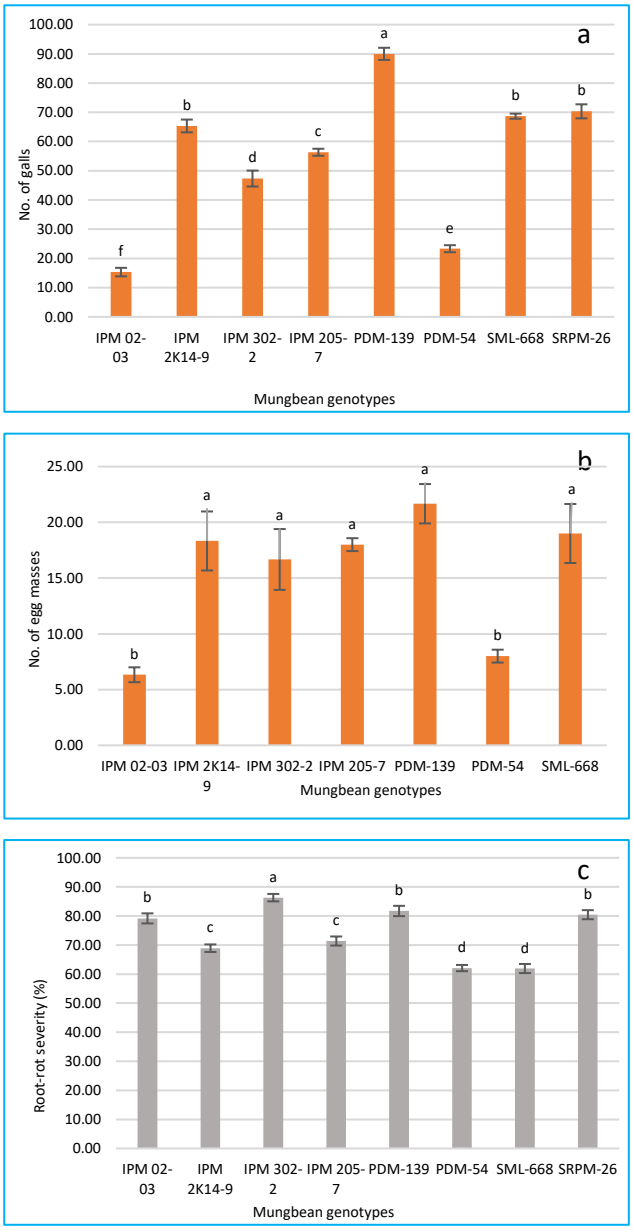


Fig 7 Reaction of mungbean genotypes to *Meloidogyne javanica* and *Rhizoctonia solani* under greenhouse conditions showing (a) number of galls per root system, (b) number of egg masses per root system, and (c) root-rot severity (%)

*Data represent mean ± SE of three replications. Means followed by different letters differ significantly according to DMRT ($P \leq 0.05$)

The predominance of susceptible reactions among the evaluated genotypes highlights the need for systematic identification and utilization of resistant genetic resources in mungbean breeding programs. The moderately resistant genotypes identified in this study, particularly IPM-02-03 and PDM-54, may serve as valuable donors for improving resistance against root-knot nematodes. Furthermore, integrating such genotypes with complementary disease management strategies, including biological control agents, organic amendments, and improved soil health practices, could enhance the effectiveness and sustainability of disease management in mungbean cultivation [16], [32].

The novelty of the present study lies in the comparative evaluation of diverse mungbean genotypes against two economically important soil-borne pathogens, *Meloidogyne javanica* and *Rhizoctonia solani*, under identical experimental conditions using both growth and biochemical parameters. The study identified genotypes exhibiting differential levels of tolerance and susceptibility, thereby providing useful information for resistance breeding and germplasm improvement programmes. In addition, the in vitro assay confirmed the detrimental effect of *R. solani* on seed germination and early seedling growth, complementing the greenhouse observations [40]. A limitation of the present study is that the responses of mungbean genotypes were evaluated separately against *M. javanica* and *R. solani*. Under field conditions, these pathogens may occur simultaneously and may interact synergistically, resulting in greater disease severity than infection by either pathogen alone. Therefore, future studies involving combined pathogen inoculation would be valuable for understanding genotype responses to the root-knot–root-rot disease complex and for developing integrated and environmentally sustainable disease-management strategies.

CONCLUSION

The present study demonstrated differential responses of mungbean genotypes to *Meloidogyne javanica* and *Rhizoctonia solani*, with none of the evaluated genotypes exhibiting complete resistance to either pathogen. The *in vitro* germination and seedling vigour assay proved to be a useful preliminary screening tool for assessing genotype responses to *R. solani* during the early stages of plant growth. Greenhouse evaluation further revealed that pathogen inoculation significantly reduced growth, nodulation, yield-related traits, and key biochemical parameters, while inducing an increase in total phenolic content, particularly in the moderately resistant genotypes. The differential responses observed among the tested genotypes provide a valuable basis for future biochemical and molecular investigations aimed at identifying resistance-associated traits and genes. The moderately resistant genotypes, particularly IPM-02-03 and PDM-54, may serve as promising genetic resources for resistance breeding programmes. However, the absence of highly resistant genotypes highlights the need for broader germplasm screening and the integration of host resistance with sustainable disease-management strategies for effective management of soil-borne pathogens in mungbean.

Data availability: The datasets generated and/or analysed during the current study are available from the corresponding author on reasonable request.

Conflict of interest: The authors declare that they have no conflict of interest.

Ethics declaration: Not applicable.

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Author contributions

Rose Rizvi conceived and designed the study, supervised the research, and critically reviewed and finalized the

manuscript. Noor Fatima conducted the experiments, collected and analyzed the data, and prepared the original draft of the manuscript. Both authors read and approved the final manuscript.

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Fig 8 Representative symptoms of root-knot disease caused by *Meloidogyne javanica* and root-rot disease caused by *Rhizoctonia solani* on different mungbean genotypes under greenhouse conditions

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