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Vol. 24(1) January-April, 2026

CONTENTS

Host response of diverse pulse genotypes to root-knot nematode (*Meloidogyne incognita*)

SAROJ YADAV, EKTA RATHORE* and ANIL KUMAR

Department of Nematology, Chaudhary Charan Singh Haryana Agricultural University, Haryana Agricultural University, Hisar
**Corresponding author's email id: rathoreekta311@gmail.com*

ABSTRACT: Root-knot nematodes (*Meloidogyne incognita*) are major constraints to pulse crop production, causing significant yield losses and affecting crop productivity. The present study was conducted to evaluate the reaction of different pulse genotypes against natural infestation of *M. incognita* under screen house conditions. The experiment was carried out during 2021–22 using 30 genotypes of moong bean, 18 genotypes of pigeon pea, and 33 genotypes of chickpea. After 45 days of nematode inoculation, roots of all genotypes were examined to assess gall indices using a 1-5 scale. The results revealed that two genotypes of moong bean (MH 1762 and MH 2-15 (C)), eight genotypes of pigeon pea (AH 16-02, AH 18-48, AH 19-03, AH 19-17, AH 19-22, AH 16-37, AH 17-28, and PAU 881), and six genotypes of chickpea (H 10-22, H 12-22, H 13-36, H 16-22, H 12-55, and H 19-40) were identified as moderately resistant to *M. incognita*. The remaining genotypes exhibited susceptible to highly susceptible reactions. The identified moderately resistant genotypes may serve as potential sources for breeding programs aimed at developing nematode-resistant varieties in pulse crops.

Key words: Genotype, Resistance, *Meloidogyne incognita,* Gall index, Pulse crops

Pulse crops (grain legumes) are integral to sustainable agricultural systems due to their ability to fix atmospheric nitrogen through symbiosis with rhizobia, thereby enhancing soil fertility and reducing reliance on synthetic fertilizers (Graham and Vance, 2003; Stagnari *et al.*, 2017). They are rich in high-quality plant protein, complex carbohydrates and essential micronutrients, contributing significantly to global nutritional security (Mudryj *et al.*, 2014). Pulse crops significantly contribute to sustainable agriculture by enhancing soil physicochemical properties, promoting beneficial microbial communities, and increasing soil carbon sequestration, thereby strengthening the resilience of cropping systems under changing climatic conditions (Varshney *et al.*, 2014). Pulses play a crucial role in global food and nutritional security, particularly in vegetarian populations where they serve as the primary source of plant-based protein. Leguminous crops are grown widely across diverse agro-ecological regions, covering nearly 28.78 million hectares globally and contributing approximately 27.75 million tonnes of grain annually (Singh, 2025).

Despite their substantial nutritional and economic value, pulse crops experience considerable yield reductions due to plant-parasitic nematodes, particularly root-knot nematodes (*Meloidogyne* spp.). These nematodes are among the most destructive groups, causing severe economic losses across a wide range of crops worldwide. *Meloidogyne incognita* is the most widespread and damaging species, inducing root galls, disrupting vascular tissues, impairing water and nutrient uptake (Zamarian *et al.*, 2025). In addition, species such as *M. javanica*, *M. arenaria*, and *M. artiellia* are widely distributed and pose serious constraints to the production of major pulses including chickpea, pigeon pea, mungbean, urdbean, pea, and lentil (Khan *et al.*, 2023; El-Nagdi and Youssef, 2019; Zwart *et al.*, 2019). The life cycle of *M. incognita* is relatively short and typically completed within 25–30 days under favorable conditions. It begins with eggs laid in a gelatinous matrix, from which second-stage juveniles (J2), the infective stage, hatch and penetrate host roots near the elongation zone. Inside the roots, juveniles migrate intercellularly and establish permanent feeding sites, where they develop into sedentary swollen females through successive molts (J3 and J4 stages), while males, if formed, become vermiform and non-feeding. Mature females lay eggs either inside or on the root surface, completing the cycle and enabling rapid population build-up in soil (Moens *et al*., 2009; Perry *et al*., 2018; Jones *et al*., 2013).

The pathogenic success of *M. incognita* is attributed to its ability to induce specialized feeding sites (giant cells) in host roots through complex host–parasite interactions, leading to physiological and biochemical modifications that favor nematode development and reproduction (Zamarian *et al*., 2025). The extent of damage varies with host genotype and nematode population density in soil, with reported yield losses reaching 19–22% in chickpea, 17–23% in urdbean, and 14–29% in mungbean (Chakraborty *et al*., 2016).

Management strategies such as crop rotation, biological control, organic amendments and chemical nematicides have been employed to suppress root-knot nematodes (Tanimola *et al*., 2017). However, reliance on chemical nematicides raises environmental and health concerns, and several products have been restricted. Therefore, the use of host plant resistance remains the most sustainable, economical and environmentally sound strategy for managing nematode infestations (Mattos *et al*., 2019). In this context, identifying resistant sources within pulse germplasm is essential for developing nematode-resilient cultivars and ensuring sustainable pulse production. Therefore, the present study aimed to evaluate a diverse collection of chickpea, pigeon pea, and mung bean genotypes for genetic resistance to the root-knot nematode, *M. incognita*, under controlled screen house conditions. Identified genetic resistant genotypes can be used further in breeding programmes.

MATERIALS AND METHODS

Experimental site

Experiments were conducted during 2021 and 2022 under *M. incognita* infested microplot conditions at Research Area, Nematology, CCS Haryana Agricultural University, Hisar, to screen chickpea, mungbean, and pigeon pea genotypes for resistance against *Meloidogyne incognita*. The experiment was laid out in a completely randomized design (CRD) with three replications. A total of 33 chickpea, 30 mungbean, and 18 pigeon pea genotypes were evaluated.

Culture of M. incognita

A pure population of *M. incognita* was cultured from a single egg mass handpicked from infected pulse roots using fine forceps. The egg mass was surface sterilized in 0.5% sodium hypochlorite for 5 minutes (Hussey and Barker, 1973), the eggs were collected on a 38 mm sieve and washed in a beaker. The egg suspension was poured onto an extraction tray and juveniles were collected (Whitehead and Hemming, 1965). The freshly hatched second stage juveniles were standardized and concentrated. The hatched juveniles were multiplied on susceptible host plants brinjal cv. Hisar Shyamal grown in sterilized soil to obtain a uniform inoculum (Sharma *et al*., 2006) under microplots.

Experimental procedure

Initial nematode population in three different moong bean, pigeon pea and chickpea microplots were 352 J_2 per 200 CC soil, 412 J_2 per 200 CC soil and 438 J_2 per 200 CC soil respectively. Seeds of each genotype were sown in infested microplots in different rows. Plants were watered and manured as per package and practices of CCS HAU, Hisar. Before sowing, soil samples were collected from infested microplots and mixed thoroughly to obtain a uniform composite sample. A representative sub-sample (200–250 g) was taken for nematode analysis. Nematodes were extracted using Cobb's sieving and decanting method followed by the modified Baermann funnel technique. The extracted juveniles were collected

Table 1: Gall index (Bhatti and Jain, 1994)

Gall Index	Disease Incidence (No. of galls per plant)	Disease Reaction
1	0.0	Highly Resistant (HR)
2	0.1–10.0	Resistant (R)
3	10.1–30.0	Moderately Resistant (MR)
4	30.1–100.0	Susceptible (S)
5	>100	Highly Susceptible (HS)

in water and counted under a stereomicroscope. The initial nematode population (Pi) was expressed as the number of second-stage juveniles (J2) per unit soil (Cobb, 1918; Baermann, 1917; Bridge and Starr, 2007). Roots were washed gently and processed separately for root-associated stages. Roots were fixed in 4% formalin, stained with lactophenol–acid fuchsin, and cleared in lactophenol for visualization. The number of galls per plant was recorded under a stereo-zoom microscope (Devi *et al.*, 2014). Genotypes were categorized based on root-knot index following standard rating scales to determine their reaction to *M. incognita*.

RESULTS AND DISCUSSION

Significant variability was observed among chickpea, mungbean, and pigeon pea genotypes in their response to *Meloidogyne incognita* under controlled screen house conditions; however, none exhibited complete resistance, indicating the absence of strong immunity.

In mungbean, screened at an initial nematode population of 352 J2 g^{-1} soil, only two genotypes (MH 1762 and MH 2-15) demonstrated a moderately resistant reaction. The majority of genotypes were categorized as susceptible, while several genotypes including MH 1740, MH 1772, MH 1871, MH 1890, MH 1908, MH 1911 and MH 2020-8 showed highly susceptible responses (Fig 5). The predominance of susceptible reactions suggests high vulnerability of mungbean genotypes to *M. incognita* (Table 2, Fig. 1). In pigeon pea (412 J2 g^{-1} soil), eight genotypes (AH 16-02, AH 18-48, AH 19-03, AH 19-17, AH 19-22, AH 16-37, AH 17-28 and PAU 881) were moderately resistant, whereas all others were susceptible, indicating only partial resistance (Table 3, Fig. 2). Similarly, in chickpea, only six genotypes (H 10-22, H 12-22, H 13-36, H 16-22, H 12-55 and H 19-40) exhibited moderate resistance, while most were susceptible or highly susceptible (Table 4, Fig. 3, Fig. 4). Overall, moderate resistance was the highest level detected and occurred at low frequency, particularly in mungbean and chickpea, highlighting the limited availability of effective resistance sources against root-knot nematodes in pulse crops.

Table 2: Evaluation of different mung bean genotypes against root-knot nematode

S. No.	Mung bean Genotype	No. of galls/plant	Root-knot index	Reaction
1.	MH 1314	40.75	4	S
2.	MH 1468	51.00	4	S
3.	MH 1703	49.25	4	S
4.	MH 1720	62.75	4	S
5.	MH 1740	105.75	5	HS
6.	MH 1762	16.00	3	MR
7.	MH 1767	71.00	4	S
8.	MH 1772	104.25	5	HS
9.	MH 1801	75.25	4	S
10.	MH 1830	68.00	4	S
11.	MH 1850	59.75	4	S
12.	MH 1857	39.00	4	S
13.	MH 1871	102.75	5	HS
14.	MH 1890	103.00	5	HS
15.	MH 18-100	45.25	4	S
16.	MH 18-172	81.00	4	S
17.	MH 18-181	102.00	5	HS
18.	MH 18-182	78.00	4	S
19.	MH 18-189	101.75	5	HS
20.	MH 1908	104.75	5	HS
21.	MH 1909	103.25	5	HS
22.	MH 1911	101.00	5	HS
23.	MH 1918	100.75	5	HS
24.	MH 1921	42.75	4	S
25.	MH 1923	70.00	4	S
26.	MH 2020-8	100.25	5	HS
27.	MH 2-15 (C)	21.50	3	MR
28.	MH 2-25 (C)	85.25	4	S
29.	MH 421 (C)	106.25	5	HS
30.	MH 1142 (C)	89.25	4	S
	C.D.	3.783		
	SE(m)	1.334		
	SE(d)	1.887		
	C.V.	3.038		

The present findings confirm that resistance to root-knot nematodes in pulse crops is limited and unevenly distributed, despite the presence of exploitable genetic variability. The predominance of susceptible and moderately resistant reactions highlights the scarcity of strong and stable resistance sources against *Meloidogyne incognita* and *M. javanica*.

Duggal *et al.* (2023) reported resistant pigeon pea genotypes (AH15-07, AH17-27, AH17-28 and AH15-01), while AH14-01, AH16-21, AH15-20, AH16-07, AH16-44, AH17-17, AH16-02, AH17-01,

Table 3: Evaluation of different pigeon pea genotypes against root-knot nematode

S. No.	Pigeon pea Genotype	No. of galls/plant	Root-knot index	Reaction
1.	AH 16-02	19.25	3	MR
2.	AH 16-07	46.00	4	S
3.	AH 18-18	62.75	4	S
4.	AH 18-48	22.00	3	MR
5.	AH 19-03	26.25	3	MR
6.	AH 19-04	84.25	4	S
7.	AH 19-17	28.00	3	MR
8.	AH 19-22	21.75	3	MR
9.	AH 19-37	81.00	4	S
10.	AH 16-37	25.25	3	MR
11.	AH 19-47	58.00	4	S
12.	AH 16-50	76.25	4	S
13.	AH 17-13	71.00	4	S
14.	AH 17-28	16.00	3	MR
15.	AH 14-01A	65.75	4	S
16.	Pusa 992	54.00	4	S
17.	Manak	61.25	4	S
18.	PAU 881	14.00	3	MR
	C.D.	2.689		
	SE(m)	0.934		
	SE(d)	1.320		
	C.V.	3.496		

AH16-36, AH16-40, AH16-49, AH17-03, AH16-38, VLA-1 and PADT16 exhibited moderately resistant reactions. Resistant chickpea genotypes (H-15-04, H-15-23 and H-15-25) and moderately resistant mungbean genotypes (MH 1762, MH-1767, MH 2-15 and MH-125) were also identified, indicating that resistance is largely quantitative and governed by multiple minor genes.

Table 4: Evaluation of different chick pea genotypes against root-knot nematode

S. No.	Chick pea Genotype	No. of galls/plant	Root-knot index	Reaction
1.	H 05-24	45.00	4	S
2.	H 07-120	51.25	4	S
3.	H 09-90	58.75	4	S
4.	H 10-22	21.00	3	MR
5.	H 12-22	14.25	3	MR
6.	H 12-63	71.00	4	S
7.	H 13-03	78.25	4	S
8.	H 13-36	18.00	3	MR
9.	H 16-05	62.00	4	S
10.	H 16-22	13.75	3	MR
11.	H 17-16	39.00	4	S
12.	H 12-55	20.00	3	MR
13.	HC-5	75.25	4	S
14.	GNG 1581	81.00	4	S
15.	GNG 2171	67.25	4	S
16.	H 16-04	71.00	4	S
17.	H 16-08	78.25	4	S
18.	H 16-17	101.25	5	HS
19.	H 16-21	63.00	4	S
20.	H 18-08	103.00	5	HS
21.	H 18-14	101.00	5	HS
22.	H 19-12	87.00	4	S
23.	H 19-15	102.75	5	HS
24.	H 19-16	44.00	4	S
25.	H 19-21	103.25	5	HS
26.	H 19-32	35.00	4	S
27.	H 19-36	51.00	4	S
28.	H 19-40	17.75	3	MR
29.	H 19-41	104.00	5	HS
30.	H 19-54	75.00	4	S
31.	H 08-18	103.75	5	HS
32.	GNG 2144	84.00	4	S
33.	GNG 2418	105.00	5	HS
	C.D.	2.954		
	SE(m)	1.044		
	SE(d)	1.476		
	C.V.	2.781		

Chakraborty *et al.* (2016) reported resistance variability across pulse crops, with resistant genotypes in chickpea (9/60), field pea (7/23), lentil (8/22), and pigeon pea (19/26, including one highly resistant), whereas only a few mungbean (3/14) and urdbean (2/12) lines showed moderate resistance. This reflects a comparatively narrow resistance base in mungbean and urdbean. Prasad *et al.* (2004) reported no highly resistant genotypes in mungbean and urdbean, but identified resistant lines in urdbean (AKU 9802, AKU 15, UG 1017, TPU 4, Phule U 9417-5, OBG 17 and USTD 102) and mungbean (ML 131, IPM 99-125 and Pusa 172), alongside highly susceptible cultivars such as TV 2000-28, OBG 15, ML 818, TM 99-47 and MH 98-1, indicating substantial but uneven genetic variability. Borah *et al.* (2020) observed limited resistance in chickpea, with only Vijay and ICC 313 showing moderate resistance, while most genotypes were susceptible, emphasizing the importance of moderately resistant lines as breeding resources. In contrast, Singh (2024) identified resistant mungbean genotypes (UPM 02-17, IPM 1620-6 and IPM 1718-1) against *M. javanica*, which showed reduced penetration, restricted development, and limited giant cell formation, indicating effective disruption of nematode feeding site establishment. Devindrappa

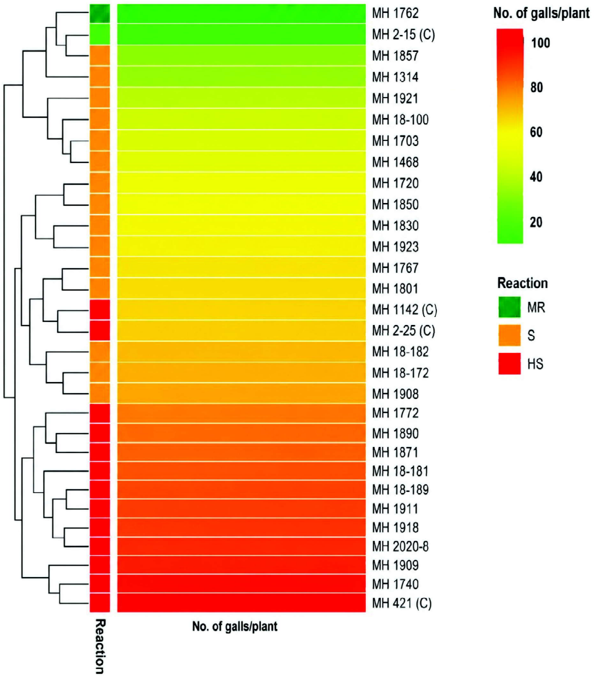

Fig. 1: Heatmap of mung bean genotypes reaction against root-knot nematode

et al. (2026) identified resistant mungbean genotypes (UPM 02-17, IPM 1620-6 and IPM 1718-1) with low galling index (≤2) and moderate resistance in five genotypes, indicating antibiosis-mediated resistance through reduced penetration, delayed development and impaired giant cell formation.

Overall, resistance in pulse crops is present but fragmented, particularly in mungbean. Strengthening breeding programs through the use of diverse germplasm, coupled with modern genomic tools and integrated management strategies, is essential for developing durable resistance to root-knot

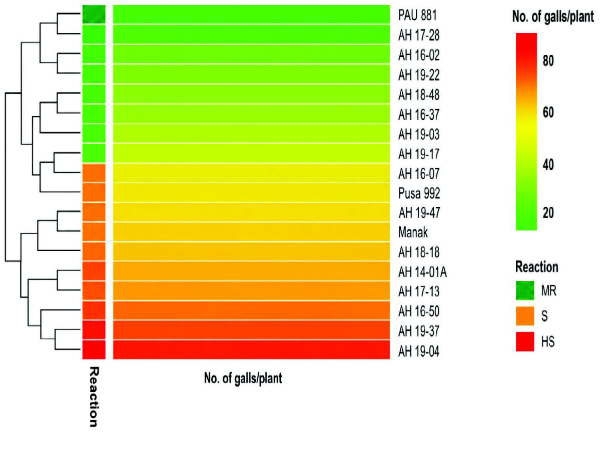

Fig. 2: Heatmap of pigeon pea genotypes Reaction against root-knot nematode

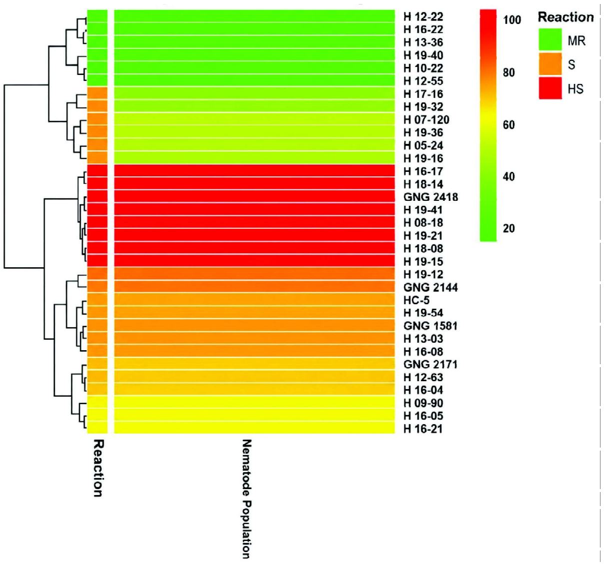

Fig. 3: Heatmap of chick pea genotypes reaction against root-knot nematode

Fig. 4: Chick pea genotype roots infected with root-knot nematode

Fig. 5: Mung bean genotype roots infected with root-knot nematode

nematodes.

CONCLUSION

Screening of pulse genotypes revealed predominantly susceptible reactions to *M. incognita*, with only a limited number exhibiting moderate resistance. The absence of strong resistance highlights the narrow genetic base against root-knot nematode in the evaluated material. The moderately resistant genotypes (particularly MH 1762 and MH 2-15 in mungbean, several pigeon pea lines including AH 16-02 and AH 17-28, and chickpea genotypes such as H 10-22 and H 12-22) identified in this study offer promising resources for resistance breeding and sustainable nematode management in pulse production systems.

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