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Penetration behaviour of reniform nematode, *Rotylenchulus reniformis* on resistant and susceptible genotypes of Castor, *Ricinus communis*

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ABSTRACT

Penetration behavior of reniform nematode on nematode resistant (JC-12) and nematode susceptible (48-1) genotypes of castor was studied. Results showed that higher number of nematodes was attached to the roots of 48-1 than JC-12 as average root population of 48-1 and JC-12 were 60.3 and 9.8 respectively at four weeks after inoculation. Lowered nematode reproduction was observed on roots of resistant genotype (JC-12) as average number of eggmasses at 7, 14, 21 and 28 days after inoculation were 2.8, 5.0, 8.0 and 9.8. Corresponding values of susceptible genotype (48-1) were 38.3, 42.3, 46.3 and 60.3.

Keywords: Castor, Penetration, Reniform nematode, Resistance, Reproduction, Susceptibility

Castor is an economically important non-edible oilseed crop grown in tropical and sub-tropical regions of the world and India is the leading producer of castor sharing 65% of world castor growing area (0.75 million ha) with more than 85% of world's castor production (1.2 million tonnes) (FAOSTAT, 2019). Several biotic and abiotic factors account for our country's lower average productivity (1600kg/ha). Reniform nematode, *Rotylenchulus reniformis* is one among the major biotic factors affecting castor crop. This polyphagous, semi-endoparasite attacks numerous cultivated crops and yield loss estimates by Jain *et al* (2007) indicated that in castor, this nematode inflicts monetary loss to the tune of Rs. 180 million (13.93%). Interaction of the nematode with wilt pathogen, *Fusarium oxysporum* f. sp. *ricini* aggravates wilt incidence. Evaluation of various castor inbred lines, hybrids etc., under ICAR-AICRP on Castor, identified inbred line JC-12 developed by Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur as resistant to reniform nematode (Giribabu, 2014). Our objective is to study the penetration behavior of reniform nematode on resistant (JC-12) and susceptible (48-1) genotypes of castor.

MATERIALS AND METHOD

Plant materials: JC-12, reniform nematode resistant inbred line, and 48-1, susceptible line were selected for this study based on these genotypes' response under pot experiment conditions.

Methodology: Seeds of JC-12 and 48-1 were sown in plastic pots (500ml) filled with sterilized red soil, sand and vermicompost in the ratio of 2:1:1. Two weeks after sowing the seedlings were inoculated with freshly hatched second stage juveniles (J_2s) of reniform nematode @ circa 1000 J_2s / plant. Plants were harvested at 7, 14, 21 and 28 days after inoculation and the root nematode population was enumerated. Each treatment was replicated five times and the experiment was arranged in completely randomized design.

RESULTS AND DISCUSSION

Results showed that infective young females preferred to infect and penetrate the roots of susceptible genotype, 48-1. This was evident as average number of nematodes attached to the roots of 48-1was 60.3, which was six folds higher when compared to its counterpart, JC-12 (9.8) at four weeks after inoculation. At one week after inoculation, average number of nematodes attached to the roots of resistant and susceptible genotypes was 2.8 and 38.3 respectively. The same trend was observed in subsequent weeks. At two weeks after inoculation, the values were 5.0 and 42.3 respectively. At three and four weeks after inoculation, number of eggmasses attached to the roots of JC-12 and 48-1 were 8.0 and 46.8 and 9.8 and 60.3 respectively. Thus, it was concluded that JC-12 supports only 10% of population supported by its susceptible counterpart, 48-1. Nature of nematode resistance in JC-12 was governed by many genes, as QTL mapping using a linkage map consisting of 1,090 SNP markers resulted in the identification one QTL each on chromosome-6 and chromosome-8, linked to resistance (Poornima Kumari *et al*., 2022).

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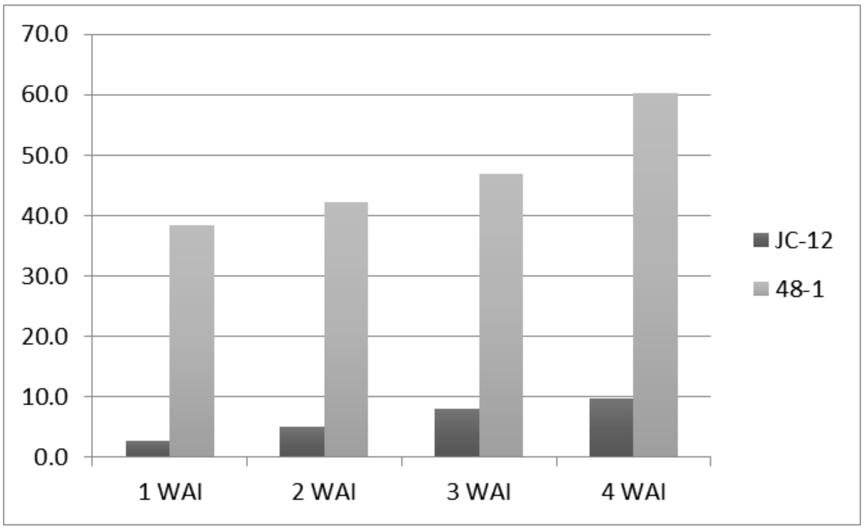

WAI – Weeks after inoculation

Fig.1. Number of eggmasses attached to the roots of resistant and susceptible genotypes of castor inoculated with reniform nematode, *Rotylenchulus reniformis*

Geographic specificity of infestation of phytoplasma in weeds and sesame as revealed *by 16S rRNA* gene based detection

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ABSTRACT

Nested PCR based study and analysis of the sequences of 16SrRNA fragment clones derived from the DNA isolated phyllody affected as well as healthy leaves of sesame crop and the weeds growing in the same fields showed that the prevalent strain of phytoplasma belonged to *Candidatus Phytoplasma aurantifolia* of 16SrII-D group. This study showed that the phytoplasma causing phyllody infects other weed plants and thus provides a hint to the continuum in the availability of the pathogen infecting sesame crop.

Keywords: Nested PCR, Phyllody, 16SrRNA, Sequence analysis

Bacteria without cell walls known as phytoplasmas are known to spread illness among hundreds of plant species around the world and are pathogens of both insects and plants (Liefting et al., 2004). While not all phytoplasma-infected plant species exhibit disease symptoms, infected plants typically exhibit signs including virescence, phyllody, yellowing, witches broom, leaf roll, and generalised decline (Bertaccini et al., 2022) in hosts including commercially significant food, fibre, forage, fruit, and ornamental plant species. Phytoplasmas have been recently assigned to a novel candidate taxon, 'Candidatus Phytoplasma' (IRPCM Phytoplasma/ Spiroplasma Working Team – Phytoplasma Taxonomy Group, 2004). 'Candidatus Phytoplasma' are delineated primarily on the basis that strains within a candidate species share at least 97.5 % sequence identity within their 16S rRNA gene, with new branches being constantly identified (Wei et al., 2007). An initial identification of the