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Management Strategies for Stem and Root Rot Disease of Sesame

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Sesame (Sesamum indicum L.), the queen of oilseeds is traditionally categorized as a health food. It contains 35–57% oils, 20–25% proteins, 20–25% carbohydrates and 5–6% essential minerals, high quantity of methionine and tryptophan, secondary metabolites such as lignans, saponins, flavonoids, and phenolic compounds. The seeds are a good source of calcium, phosphorus, and iron and are rich in vitamin B, E. In India, sesame is cultivated over an area of 16.27 lakh hectares with production of 7.89 lakh tonnes and productivity of 485 kg ha-1. In Telangana, it is grown over an area of 0.34 lakh hectares with an annual production of 0.260 lakh tonnes and productivity of 766 kg ha-1.

In addition to its inherently low yield potential and poor crop management, exposure to biotic stress is the major yield limiting factors in sesame production. Among the fungal diseases, macrophomina stem and root rot causes 5–100% yield loss when the crop faces water stress, high temperature at reproductive stage. Due to significant demand for sesame oil and seed for export, there is a demand of safer non-chemical and sustainable disease management approaches. Integrated management of diseases is a important strategy to mitigate the hazards associated with the intensive use of chemicals. Therefore, in this review, we seeks to summarize the current methodology used for management of stem and root rot of sesame including sanitation, legal methods, resistant cultivars/varieties and grafting, cropping system, soil solarization, biofumigants, soil amendments, anaerobic soil disinfestation, soil steam sterilization, soil fertility and plant nutrients, soilless culture, chemical control and biological control in a system based approach.

1. Sanitation

The resting structure like microsclerotia, produced by Macrophomina phaseolina, in the roots and stem tissues of its hosts can survive in the soil for a very long time of around 15 years even in the absence of a living host or plant debris and soil organic matter and primary source of inoculums. Therefore, it becomes very important to remove the plant debris away from growing areas whenever possible or accelerate residue breakdown. Sanitation includes any sort of activities which are aimed to prevent the spread of pathogens by removing diseased and infected plant parts, decontamination of tools and equipment and washing hands. Plowing under infected crop debris is also a good sanitation measure to control certain soil borne plant pathogens as tillage can expose the infected plant materials to the direct sunlight, which can kill some plant pathogens. The diseased plants and the immediate soil around its canopy should be removed to reduce the further spread of some diseases like lettuce drop or white mold caused by S. sclerotiorum. Tools that are used should be disinfected or cleaned at a minimum, when moving equipment between different plants or fields using different methods such as heat treatment, ultraviolet (UV) treatment and chlorine treatment. Thus, preventative measures should be adopted to avoid pathogen contamination. Field sanitation in combination with many other methods, can yield a desirable outcome. This is the first step for the management of macrophomina stem and root rot disease in sesame in an integrated system.

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2. Agronomic Practices

There is a relationship between pathogen inoculum density in soil and disease intensity, and between disease intensity and yield loss. Hence, some agricultural practices have intended to reduce the inoculum density. Irrigation maintains densities of microsclerotia relatively constant and did not prevent infection by M. phaseolina. However, high soil moisture (above 60%) reduced disease severity. The wide host range and high persistence of M. phaseolina microsclerotia make crop rotation, intercropping and lay period strategies less considered. Although crop rotation has not been effective in controlling this pathogen, reduced densities of inoculum occurred when soybean was less frequently used in rotations. For the particular case of sesame, grown as mixed or inter cropped with green gram, less incidence of Macrophomina stem and root rot and higher seed yield equivalent as compared to sole sesame was observed. Approaches intended to modify the soil environment, favouring antagonistic organisms interfering with the pathogen, like direct seeding, suppressed M. phaseolina favoured by the higher microbial abundance and activity, and the subsequent development of plants with healthier root systems. Application of Phosphorus fertilizer reduced while nitrogen increased disease severity.

3. Resistant Cultivars

One effective tool in disease management is the use of resistant cultivars/varieties. At the same time, the development of resistant cultivars/varieties through plant breeding is an industrious and time-consuming effort to combine resistance and desired commercial traits. Also, there is not any one plant cultivar/variety that is completely resistant to all disease threats. The cultivars/varieties having the marking of resistance against a disease have higher level of resistance than those labeled tolerant.

To the best of our knowledge, there is no known vertical resistance (R-gene based) to M. phaseolina inhibiting or limiting infection but rather, a partial resistance which do not limit infection but reduce or compensate the damages, and therefore the consequences on the fitness of plants. Cultivars of soybean and strawberry with varying degrees of resistance to M. phaseolina have been identified. Differences in fungal behaviour close to the roots and during infection of roots have been observed between resistant vs. susceptible varieties of sesame. The rhizosphere around the resistant variety had a reduced growth of M. phaseolina as compared to the susceptible variety. The identification and mapping of QTLs associated with resistance to M. phaseolina, revealed candidate genes with potential for further functional genomics analysis and it may facilitate breeding and molecular engineering progress against this pathogen.

4. Chemical Control

The chemical control of M. phaseolina is difficult because there are no systemic fungicides that move towards the root. As far as we know, no fungicides have been registered to control this pathogen. However, systemic and non-systemic fungicides like carbendazim, difenoconazole, benomyl, azoxystrobin, dazome at different concentration inhibited the mycelial growth and formation of sclerotia are highly sensitive to carbendazim. Carbendazim inactivates tubulin function, the building block of microtubules, necessary for the fungal growth. The nanoformulation (particle size < 100 nm) of the commercial fungicide Trifloxystrobin 25% + Tebuconazole 50% (75 WG), at 10 ppm, was better in comparison to the conventional one (micro sized) and it exerted hyphal abnormality, hyphal lysis and abnormality of sclerotial formation on M. phaseolina when tested under in vitro conditions.

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5. Biological Control

Biological control agents (BCAs) and elicitors of plant defenses have received increasing attention in the last few decades. Some BCAs impact the pathogens directly, inhibiting their growth, while others affect the pathogen indirectly by eliciting defense pathways in the host plant.

Trichoderma spp. are effective BCAs for several soil borne fungal plant pathogens including M. phaseolina. These saprotrophic fungi have evolved multiple antagonistic mechanisms such as nutrient competition, antibiotic production, and mycoparasitism. Moreover, some species are known for their effects on plant health, such as plant growth promotion effects or the abilities to enhance systemic resistance. M. phaseolina growth inhibitions during antagonism was positively correlated with the capacity of Trichoderma spp. to overgrowth and degrade the pathogen mycelia (coiling around the hyphae with appressoria and hook-like structure). The induction of chitinase, β-1, 3 glucanase and increase in total phenol content was also observed, suggesting their role in growth inhibition of pathogen during. In addition to inhibiting the growth of the pathogen during direct interaction, the antibiosis via microbial volatile organic compounds (mVOCs) produced by Trichoderma longibrachiatum reduced M. phaseolina mycelial growth by altering the mycelial structure. Interactions increased the level of terpenoids, which includes longifolene, caryophyllene, and cuprenene, but also resulted in newly expressed compound, which were not produced by none of the organisms before interaction, as limonene, azulene, 3-methyl-1-butanol, styrene, salicylaldehyde, undecane, and 3-methylphenol. These compounds might act as signaling molecules in microbe-microbe interactions and are potent antimicrobials.

Several rhizospheric and root-associated bacteria such as Bacillus, Pantoea, Pseudomonas, Stenotrophomonas, and Serratia genus reduced the growth of M. phaseolina. Bacillus amyloliquefaciens and B. siamensis have shown antifungal activities via the excretion of compounds of the lipopeptides-surfactin class, although further studies are required to understand the exact composition and molecular structure of the filtrates.

6. Innovative Genetic Tools:

Small interfering RNA (siRNA) molecules have been used as a tool for the management of many plant pathogens, like., Fusarium, Aspergillus, Verticillium, Sclerotinia). RNAi-mediated suppression of selected target genes, chosen based on their importance in growth and/or pathogenicity, can negatively affect the pathogen's ability to infect the host or minimizing host symptoms. Exogenous siRNAs were applied to target genes, β-1,3- glucan synthase and chitin synthase, in M. phaseolina. These targeting genes are important for the fungal cell wall synthesis. Interestingly, growth of siRNA-treated fungi has been suppressed, as indicated by smaller growth area and less dense mycelium. The siRNA treatments have also been reported to delay the maturation of the fungus since microsclerotia developed and melanized at a slower pace under multiple treatment conditions. Moreover, M. phaseolina growth suppression was correlated with a significant decreases in transcript abundances of target genes.