Mosaic Virus. The virus is graft transmitted on *Jasminium simplicifolium*, *J. sambac* and *J. pubescens*. Destruction of the infected material and use of healthy stock is recommended. *J. auriculatum* is found relatively tolerant to the mosaic virus.

PLANT DISEASE MANAGEMENT

18457

71. Diseases of Flax and its Management

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Flaxseed is emerging as an important functional food ingredient because of its rich contents of α-linolenic acid (ALA, omega-3 fatty acid), lignans, and fiber. Flax is adversely affected by different diseases of Fusarium wilt and Rust has been considered major limiting factors in flax production in India.

1. Fusarium Wilt

Causal organism: *Fusarium oxysporum* f.sp. lini.

Symptoms

- In early infections seedlings may killed shortly after emergence, while delayed infections cause yellowing and wilting of leaves, followed by browning and death of plants
- The tops of wilted plants often turn downward and form a "shepherd's crook".
- Roots of dead plants turn ashy grey and show brownish vascular discoloration near collar region when stem is split open longitudinally

Disease Cycle

Primary inoculum: Soil borne chlamydospores and dormant mycelia on seeds

Secondary inoculum: Wind-blown and water run-off soil may spread the fungus from one field to another.

Management

- Use of resistant varieties like JRF-2 (released by ICAR- CRIJAF, Barracpore)
- Crop rotation of at least three years with Sorghum
- Seed treatment Trichoderma harzianum @ 4-6g or Carbendazim + Mancozeb @ 2g/Kg seed
- soil application of T. viride @4g/kg with 40 kg/ha well rotten FYM

2. Rust

Causal organism: *Melampsora lini*

Symptoms

Bright orange and powdery pustules appear on leaves, stems and also on bolls.

As the season progresses, the orange pustules turn black and produce over wintering telia and teliospores.

Disease Cycle

Primary inoculum: Teliospores on flax debris

Secondary inoculum: Windborne uredospores

Management

Growing resistant varieties like Jeevan (DPL-21), Him Alsi-I (KL-187)

Spraying Carbendazim or thiophenate methyl @ 1ml /lit

3. Phyllody

In India the disease was first reported by Biswas et al. (2014) Central Research Institute for Jute and Allied Fibres (CRIJAF) research farm, Barrackpore

Causal organism: Phytoplasma

Symptoms

- Floral virescence, phyllody, and stem fasciation (flattened stem).
- Floral malformation replaces normal flowers with green small hair like leaf structures.

Transmission

Transmitted by the leafhopper *Orosius albicinctus*, Akhtar et al. (2013)

4. Powdery Mildew

Causal organism: *Oidium lini*

Symptoms

- White powdery mass of mycelia that start as small spots and rapidly spread to cover the entire leaf surface
- Heavily infected leaves dry up wither and die.

Disease Cycle

Primary inoculum: Dormant mycelia on crop debris

Secondary inoculum: Windborne oidiospores

Management

- Field sanitation

- Use of resistant varieties like Jeevan (DPL-21), Him Alsi-I (KL-187)
- Spray of Hexaconazole or Propiconazole @ 1ml/lit twice at 15 days interval

References

Akhtar, K. P., Dickinson, M. P., Shah, T. M. and Sarwar, N, 2013, Natural occurrence, identification and transmission of the phytoplasma associated with flax phyllody and stem fasciation in Pakistan. *Phytoparasitica.*, DOI 10.1007/s12600-013-0299-8.

Biswas, C., Dey, P., Mandal, K., Mitra, J., Satpathy, S. and Karmakar, P. G., 2014, First report of a 16Sr I-B Phytoplasma associated with Phyllody and Stem Fasciation of Flax (*Linum usitatissimum*) in India. *Pl. Dis.*, **(98)**9: 1267.

NEMATOLOGY

18441

72. The Necessity of Omics in The Field of Nematology and their Role in Nematode's Management

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INTRODUCTION: The phytonematodes are responsible for the huge crop yield losses worldwide. Even in many cases, these losses are unpredictable and uncountable. Because the characteristic visible symptoms are lacking in case of nematode infestation. The losses are attributed to both in the quantitative and qualitative term, for an example, reduced fruit size or malformation in grounded edible arts due to infestation will lead to an overall reduction in final yield. Even though the number and species of nematodes infecting host are numerous but they can be categorized into two genera based on their threat potential on crops, namely major genera which includes root-knot nematodes, cyst nematodes, foliar nematodes, citrus nematodes, burrowing nematodes etc. and minor genera which include mostly ectoparasites.

What do these Nematodes do?

Majority of nematodes infesting on the host, modify their cells and alter their physiology which helps in their survival by developing a successful interaction. The genes, guiding the interactions need to identify and a successful understanding of the mechanism of these interactions is the only way to develop a new type of management strategies. Throughout the world, the scientific communities are involved in creating the omics databases of various nematodes, which will help in understating and predicting the biology of another unknown species by sequence analysis. Today huge databases of genomic sequences and their functions of the model nematode *Caenorhabditis elegans* is available on the internet, namely Wormatlas and Wormbook. These data help in predicting similar genes in their functions in another nematode

Genomics in the Field of Nematology

The whole genomes sequencing of an organism helps in identifying the total gene pool of that species and in later stages, the work functions of those genes can also be predicted by bioinformatics analysis. In recent the next generation sequencing technologies are making the whole genome sequencing economic and feasible. The sequencing platform like Illumina, 454 sequencings, SOLiD, and Nanopore, all have certain advantages and limitations over one another and highly used today by the researchers. In the late 1990s, the whole genome sequencing of free-living model nematode *Caenorhabditis elegans* boosted the research for future nematode genomics. Today the sequences of economically important sedentary endoparasitic nematode *Meloidogyne incoginita*, *Meloidogyne hapla* and migratory endoparasite pine wilt nematode and *Bursaphelenchus xylophilus* is available. Many other sequencing projects of other important plant-parasitic nematodes in under progress in various part of the world.

The Necessities of the Whole Genome Sequences

These available whole genome sequences help in documentation of novel proteins involved in parasitism, reproduction, feeding behaviour, and various other aspects of biology. Upon identification of these functional genes and protein, some of them can be chosen as effective targets for drawing management perspectives.

Role of Transcriptomics in the Field of Nematology

The overall RNA profile on an organism is called as