Ecofarming (e-Magazine)

Agriculture

Ecofarming
e-Magazine for Agriculture and Allied Sciences
http://www.ecofarming.rdagriculture.in
e-ISSN: 2583-0791

MOLECULAR CROSS-TALK BETWEEN OILSEED CROPS AND PATHOGENS

Dr. R. K. Kalaria[1], Dr. S. S. Patil[2] and Dr Vijay Vekariya[3]
[1]Bioinformatics section, Aspee Shakilam Biotechnology Institute, Navsari Agricultural University, Surat
[2]Dept. of Genetics and Plant Breeding, College of Agriculture, Navsari Agricultural University, Bharuch
[3]Main Cotton Research Station, Navsari Agricultural University, Surat
Corresponding author: risheekal@nau.in

Received: November, 2025; Accepted: December, 2025; Published: January, 2026

Introduction

Molecular crosstalk refers to the complex communication and interaction at the molecular level between plants and the various pathogens that can infect. This intricate dialogue involves the exchange of signaling molecules, biochemical process and genetic responses between the host plants such as mustard, groundnut, sunflower and soybean and their pathogenic invaders including fungi, bacteria and viruses. This phenomenon involves the complex network that determine whether a plant successfully resists or survive to a pathogen's attack. Understanding this crosstalk is crucial for developing effective strategies to enhance crop resistance and mitigate the impact of diseases ultimately contributing to food security and sustainable agriculture.

Threat of pathogens to oilseed crop yield and quality:

- The threat of pathogens to oilseed crop yield and quality is a specific concern within agriculture, particularly for crops like mustard, groundnut, sunflowers, and soybeans. Pathogens, including fungi, bacteria, viruses, and nematodes, can have a significant impact on these oilseed crops, affecting both their quantity and quality of crop production.
- Plant pathogens can attack in a number of different ways. Some colonize the tissue in the plant, others settle on the surface of the plant, and others may go for specific areas such as the roots, stems, and leaves.
- Pathogens commonly cause problems like tissue death, browning, a decrease in fruiting, problems with setting flowers. In extreme cases, they can kill the host plant.

Plant Immune System: It consist of two main branches :

1. PTI (Pattern Triggered Immunity)
2. ETI (Effector Triggered Immunity)

Plant Disease Resistance: Plant disease resistance protects plants from pathogens in two ways:

1. Pre-formed structures and chemicals
2. By infection-induced responses of the immune system

Signal Transduction Pathway: The transmission of molecular signals from the exterior of the cell to the interior is called Signal transduction.

Key signaling pathways are involved in plant-pathogen interactions are,

- Salicylic acid signaling pathway
- Jasmonic acid signaling pathway

Case studies

Ali *et al.*, (2017) analyzed that full-length cDNA sequences of pathogenesis-related proteins (PRs) in Brassica juncea were characterized, focusing on SA (PR1, PR2, PR5) and JA (PR3, PR12, PR13) marker genes, termed *BjPR* proteins. Expression profiling revealed that after abscisic acid (ABA) treatment, SA genes were downregulated while JA genes were upregulated. During *Erysiphe cruciferarum* infection, distinct expression patterns emerged for SA and JA dependent *BjPR* genes, with SA gene expression decreasing and JA gene expression increasing during drought stress. Notably, *BjPR*

genes exhibited ABA-independent expression patterns during abiotic stresses, indicating SA/JA cross-talk.

Wang *et al.*, (2020) observed that *Sclerotinia sclerotiorum* causes significant disease in oilseed rape (*Brassica napus*), leading to major economic losses. This study reveals that the *NPR1* genes of *Arabidopsis thaliana*, which regulate salicylic acid signaling, are crucial for plant defense against pathogens. The newly identified *NPR1* homolog *BnaNPR1* from *Brassica napus* shows 68.35% protein identity to *AtNPR1* and is significantly activated by salicylic acid treatment. Transgenic *Nicotiana benthamiana* and *Brassica napus* overexpressing *BnaNPR1* exhibited enhanced resistance to *Sclerotinia sclerotiorum*, highlighting *BnaNPR1* role in improving resistance in *Brassica napus*.

Nayak *et al.*, (2024) studied that groundnut trade is impacted by aflatoxin contamination from *Aspergillus flavus*. This study used RNA sequencing to analyze differentially expressed genes in groundnut genotypes J11(resistant) and JL24(susceptible), creating sixteen libraries and resulting in approximately 1,344.04 million reads. A total of 4,445 differentially expressed genes were identified, including those related to defense mechanisms. The results suggest potential for using these genes in breeding aflatoxin-resistant groundnut varieties.

Conclusion

- Understanding molecular crosstalk is essential for sustainable oilseed crop production.
- Oilseed crops resist pathogens through molecular cross-talk involving PTI, ETI, PR proteins and hormone signaling pathways understanding these mechanisms helps in developing disease resistant and sustainable high yield oilseed varieties.
- *PR* genes may serve as potential candidates for developing transgenic crops resistant to multiple stresses.
- *BnaNPR1* overexpression may serve as an important candidate gene for improving disease resistance by genetic engineering.
- Identified key defense genes and pathway involved in resistance against *Aspergillus flavus* in groundnut, which help to development of aflatoxin resistant varieties and ensure better food safety.

Future thrust

- Explore stable overexpression lines and evaluate their long term resistance against *Sclerotinia sclerotiorum* in field condition.
- Future research should be focus on detailed functional validation of identified *PR* genes under field condition to confirm their role in long term and multi stress resistance in plant.
- Integration of transcriptomics with proteomics and metabolomics will provide deeper understanding of the host-pathogen interaction.

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