#132

Molecular profiling of the *Sclerotinia sclerotiorum* - Brassica pathosystem for controlling stem rot disease in mustard

Navin C Gupta[1]

Shaweta Arora[1]
Sunita Yadav[2]
Mahesh Rao[1]
Pankaj Sharma[3]
Dwijesh Chandra Mishra[2]

[1] ICAR-National Institute for Plant Biotechnology, New Delhi, India

[2] ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India

[3] ICAR-Directorate of Rapeseed & Mustard Research, Bharatpur, India

Background:

The sclerotinia stem rot disease in *Brassica* caused by *S. sclerotiorum* is one of the major phytopathogens that heavily affect yield and oil quality, especially in winter season mustard throughout the Asia Pacific region. The interaction between the *S. sclerotiorum* and Brassica species is being analysed through an integrated omics approach for deciphering the genes involved in infection and disease establishment pathways.

Objective:

To identify the genes and pathways for the *S. sclerotiorum-Brassica* pathosystem.

Methods:

The genome sequence of the *S. sclerotiorum* ESR-01 isolate was assembled and annotated. Secretome profiling predicted the genome-wide distributed effector candidates (Gupta *et al.*, 2022) and analysed them through their expression profiling in the mock and treated leaf samples after *S. sclerotiorum* infection at different time intervals. The comparative transcriptome profiling of the susceptible and tolerant *B. juncea* lines NRCHB 101, and RH1222-28 infected with *S. sclerotiorum* by stem inoculation screening methods (Gupta *et al.*, 2020) in the field has been done in two biological replicates on the Illumina 2500 sequencing platform. The *S. sclerotiorum*-specific transcript was recovered from the host transcriptomic datasets and analysed by quantitative expression analysis by qRT-PCR in the control and infected Brassica leaf samples with *S. sclerotiorum* ESR-01 isolate.

Results:

In the robust screening procedure of *S. sclerotiorum* infection in the field, one tolerant *B. juncea* (RH1222-28) and two resistant *B. napus* (Bnap 114) and *B. carinata* (Bcar 115) lines were identified to boost the resistance breeding program of Brassica against the Sclerotinia stem rot disease. The whole-genome sequencing and robust secretome analysis of an Indian isolate 'ESR-01'of *S. sclerotiorum* revealed 57 key effector molecules. Further, in expression studies, four of them were found significantly induced after 8- and 16 hours of infection in the *Brassica* leaves. The comparative transcriptome analysis in the identified tolerant and susceptible *B. juncea* lines has resulted in several candidate genes playing an important role during infection and disease development. From the recovered *S. sclerotiorum* transcripts from the host transcriptomic datasets, a few genes were identified would be important virulence factors of the pathogen.

Conclusions:

The combination of the genomics studies and secretome profiling of the *S. sclerotiorum* pathogen and the transcriptomic studies in the *S. sclerotiorum* infected *Brassica* lines has revealed several effectors, genes for the virulence of the pathogen and defence-responsive genes in the plants. The identified genes for the effectors and virulence factors will further be examined and utilized for deciphering the interacting target molecules in the host. Further, the identified tolerant/resistant *Brassica* lines and the genes would be useful in breeding or biotechnological interventions like gene editing/ silencing/overexpressing strategies for engineering *Sclerotinia* stem rot disease resistance in Indian mustard and other susceptible crop species.

References:

1. Gupta NC, Yadav S, Arora S, *et al*. (2022). Draft genome sequencing and secretome profiling of Sclerotinia sclerotiorum revealed effector repertoire diversity and allied broad-host range necrotrophy. *Scientific Reports* 12: 21855.
2. Gupta NC, Sharma, P, Rao, M *et al*. (2020). Evaluation of non-injury inoculation technique for assessing *Sclerotinia* stem rot (*Sclerotinia sclerotiorum*) in oilseed *Brassica*. JMIMT 175. 105983.