

## SCHOOL III- OF CROP RESISTANCE SYSTEM RESEARCH

### Aim

- Utilizing modern frontier science-based plant resistance sourcing and its utilization

### Thrust areas:

1. Identification of novel host resistance and defense genes and their deployment
2. Understanding host resistance mechanisms against pests and disease of crops
3. Novel molecular approaches for understanding and stress mitigation of pests and diseases

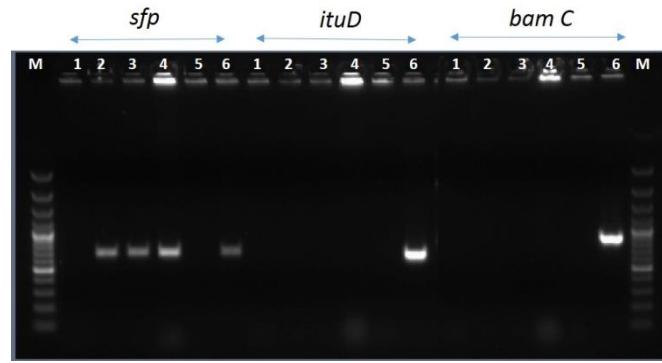
### Research Achievements:

- Surveys were conducted to generate the database on viral diseases affecting crop plants of Chhattisgarh. Information on the prevalence of virus and virus-like diseases and vectors were recorded by surveying in the farmer's fields of 22 districts of Chhattisgarh and prioritized. *Begomovirus* are the most important and causing huge economic losses to the growers in vegetable and pulse crops in Chhattisgarh.
- Molecular characterization of begomovirus infecting leaf curl disease in tomato, yellow mosaic and crinkle disease in cucurbits and identified as *Tomato leaf curl New Delhi virus*. Yellow mosaic disease of grain legume is identified to be caused by *Mungbean yellow mosaic India virus*.
- Standardized the methodology for yellow stem borer larval rearing in rice cv. Swarna, optimized the appropriate larval stage for infestation, Si dose and larval infestation and sampling time. Identification of differentially expressed transcript through transcriptome study is in progress.



### Standardized yellow stem borer infection for Si induced gene expression studies

- Isolated and functional characterized more than 200 bacterial and 25 fungal endophytes from rice and legume crops and their role in plant growth promotion and antagonistic activities against phytopathogens
- The presence of lipopeptide genes in the bacterial endophytes of rice having antagonistic activities against bacterial pathogen *Xanthomonas oryzae pv oryzae* (*Xoo*) and or soil borne fungal pathogens namely *Sclerotium rolfsii*, *Fusarium verticillioides* and *Rhizoctonia solani* were detected.



**PCR based detection of lipopeptide genes in the bacterial endophytes having antagonistic activities against bacterial and fungal pathogens**

( M, 100 bp ladder; amplification of lipopeptide genes Sfp- Surfactin; ituD-IturinD; BamD- BacilliomycinD)

- *In planta* validation of plant growth promoting activities of bacterial endophytes on chickpea

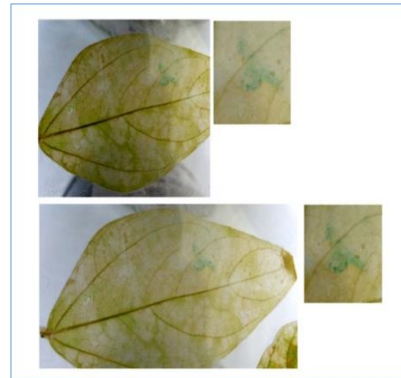
Bacterial endophytes isolated from pigeonpea (*Cajanus cajan L*) were tested for their plant growth promoting activities on chickpea plants. Bacterial endophyte recovered from pigeonpea showed significant increase in different parameters over the control plants. The bacterial endophyte inoculated plant produced root length (36.1%), fresh weight of root (206.3%) dry weight of root (125.3%) plant height (23.2) and fresh weight of shoot (42.3%) increase over the control (without endophyte treatment) plant (Figure 2).



**Morphological appearance of chickpea plants with and without treatment of bacterial endophyte**

- Collected of rice wild species and germplasm for development of super donor in rice having tolerance to multiple biotic stresses to develop rice line having resistance genes for important biotic stresses namely bacterial leaf blight, brown plant hopper and blast. IRBB lines containing *Xa* gene resistance to the bacterial leaf blight (BLB) disease (*Xanthomonas oryzae*). The presence of BLB resistance genes in the IRBB lines was confirmed using linked molecular markers. Crossing between MTU 1010 and rice line having five genes for BLB resistance and F<sub>1</sub>seeds were harvested. These seeds will be further tested for the presence of five BLB resistance genes and will be crossed with BPH and blast resistance lines.

- Plant genes associated with defence responses are activated by stress-factors are known to be regulated by promoters or the upstream elements. Promoters induced by abiotic stress factors in plants are fairly well studied compared to biotic stresses. This project has been initiated to identify promoters and regulatory elements involved in defence gene expression due to fungal, bacterial and viral infection in crop plants.
- The promoter of *IFS1* gene in soybean was characterized at molecular level from resistance and susceptible source and found to be involved in the induction of isoflavone synthesis against yellow mosaic disease in soybean, mungbean and other grain legumes upon inoculation of MYMIV through GUS assay.



#### **Activity of promoter of *IFS1* gene of soybean in soybean and mungbean upon inoculation of MYMIV**

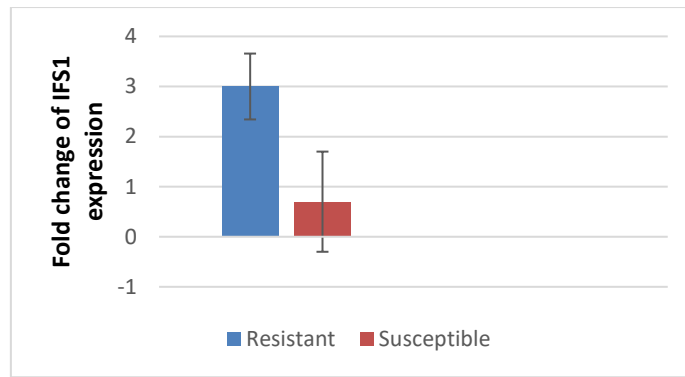
- Promoter region of *xa13* and *Xa21* from resistance and susceptible cultivars of rice against bacterial leaf blight have been cloned and sequencing of these clones is in process.
- Soybean mini core germplasm lines were screened for resistance/ susceptibility to MYMIV under natural conditions. Disease incidence was calculated and lines were grouped into various categories based on 1 to 9 scale according to All India Coordinated Project on MULLaRP.

<b>Susceptible</b>	<b>Resistance</b>
CAT-1809	CAT-1318
CAT-1921A	CAT-156
CAT-411B	CAT-1808
UPSM-57	CAT-411B
CAT-313A	EC-456647

- Functional activity of infectious clones of Sb-MYMIV DNA-A and DNA-B was demonstrated in mungbean.



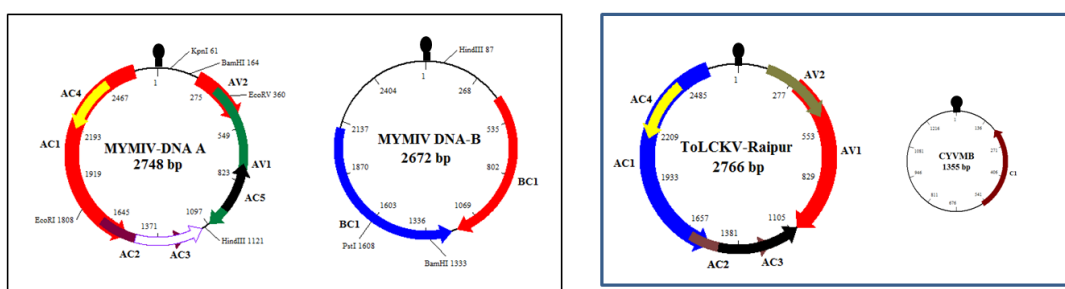
- Resistant and susceptible lines were subjected to expression analysis of *IFS1* gene. Higher expression of *IFS1* gene was observed in resistant (CAT-1808) compared to susceptible (CAT-313A)



- Genome editing for gene function validation has been initiated in soybean for mitigating biotic stress
- To understand the host factors responsible for infection and replication in the identified hosts (mungbean) and non-hosts (tomato) to begomoviruses, the infectious clones of MYMIV and *Tomato leaf curl Karnataka virus* (ToLCKV) developed. The new agroinoculation method and single whitefly transmission technique have been standardized. Using these techniques, the transcriptome data has been generated from the host and non-host to MYMIV infection. The differentially expressed transcripts/ genes are identified and their validation is being carried out.



Single whitefly transmission using micro-cage method for tomato and mungbean



**MYMIV** **ToLCKV**  
**Genome organization of MYMIV (DNA A and DNA B) and ToLCKV (DNA A and betasatellite)**



**Agroinoculated mungbean plants showing yellow mosaic symptoms (right side) and uninoculated control (left side)**