

**MULTIPLY PRIMED ROLLING CIRCLE AMPLIFICATION (MPRCA)
OF YELLOW MOSAIC DISEASE FROM INFECTED SOYBEAN IN
CENTRAL DETECTED THE PRESENCE OF *MUNGBEAN YELLOW
MOSAIC INDIAN VIRUS*-[SB]**

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Genome characterization of the *yellow mosaic disease* wreaking damage on soybean in Indore-a focal point of soybean cultivation and processing in India- employing Multiply Primed Rolling Circle Amplification (MPRCA) resulted in amplification of complete genomic components of the virus. RCA, when coupled with restriction enzyme digestion investigation, revealed two components each of ~2.7 Kb unit length of genomic components of the virus. The study further revealed the absence of β - satellite DNA genomic component of the virus. The RCA derived partial genomic region on further restriction enzyme digestion investigation revealed that *Mungbean yellow mosaic Indian virus* (MYMIV) is the species of *begomovirus* causing damage on soybean in the central Indian region, Indore. The RCA together with restriction enzyme digestion has wider implications for obtaining RNAi mediated viral gene silencing via complete genome sequence characterization to identify conserved genomic regions along with the discovery of ORFs encoding for Viral Derived Suppressor Proteins (VSPs). The potent siRNA inducing regions identified, employing web based siRNA design algorithms, revealed plausible small RNA effectors to obtain RNAi based, broad spectrum resistance against *begomovirus* infection and trait stable transgenics in soybean. In addition, the RCA products followed by partial digestion and cloning in binary vector offers a prospect to develop MYMIV based virus induced knock-out vectors with a potential implication for functional genomics study on soybean.

Multiply Primed Rolling Circle Amplification (MPRCA) of *Begomovirus* genome from infected soybean in central Indian region divulges it as *Mungbean yellow mosaic Indian virus-[sb]* and its implications for RNAi mediated resistance

Ramesh S.V., Ramesh B., Nikita A., G.K.Gupta, Husain S.M.



Directorate of Soybean Research

(Formerly: National Research Centre for Soybean)



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भारतीय कृषि अनुसंधान परिषद

DSR Staff wishes you a very-very Happy New Year 2013!

Home	Director's Desk	Production Tech	IPR	Publication	RFD	Citizen charter	Statagic Plan	RTI	ICAR	FAQ	CeRA	Contact Us
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Hindi Version

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Welcome to
www.dsrindore.org

The institution is
located at Indore in
Madhya Pradesh.

News and Updates

DSR is selected for Rajarishi Tandon Award (First) for 2011-12.

Dr. H.S. Gupta, Director IARI, New Delhi visited DSR on 02nd January 2013.

DSR celebrated foundation day on 11th December 2012.

IMC meeting held on 16th November 2012.

Hindi workshop organized on 23rd November 2012.

Mandate

- Collection, evaluation and characterization of genetic resources of soybean.
- Basic, strategic and applied research to increase the productivity and oil content.
- Research on quality of oil and oilseed cake.
- Socio-economic research for assessing the sustainability of the technologies.
- Transfer of technology.
- Coordination of multilocation trials to develop varieties and technologies of national and regional importance through All India Coordinated Research.



News and Events



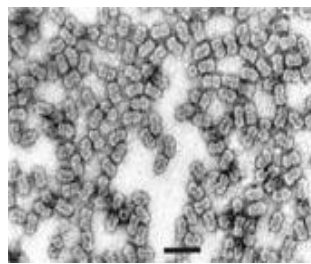
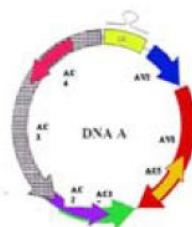
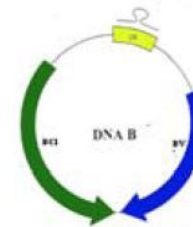
Growth Stages



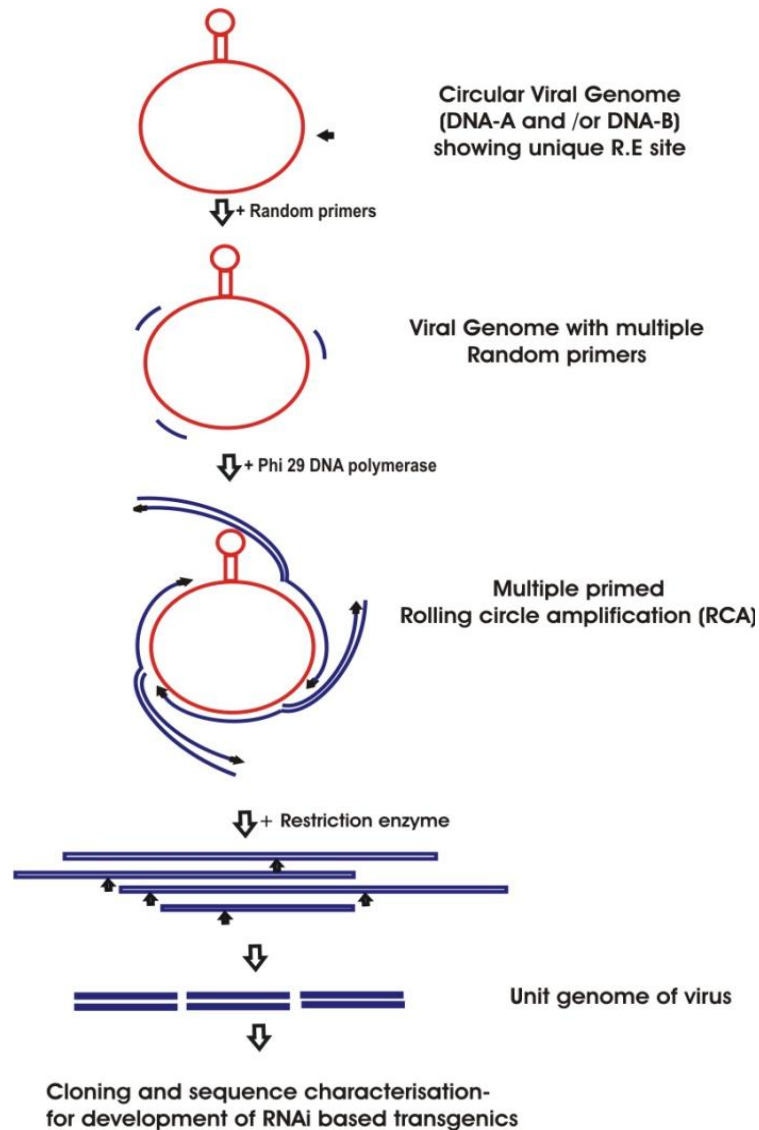
Pathogens

Background

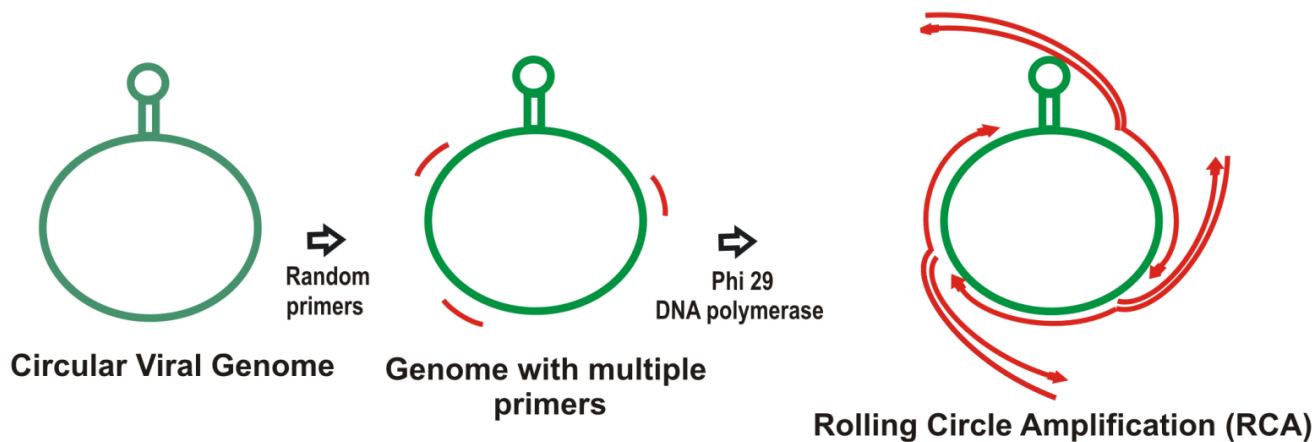
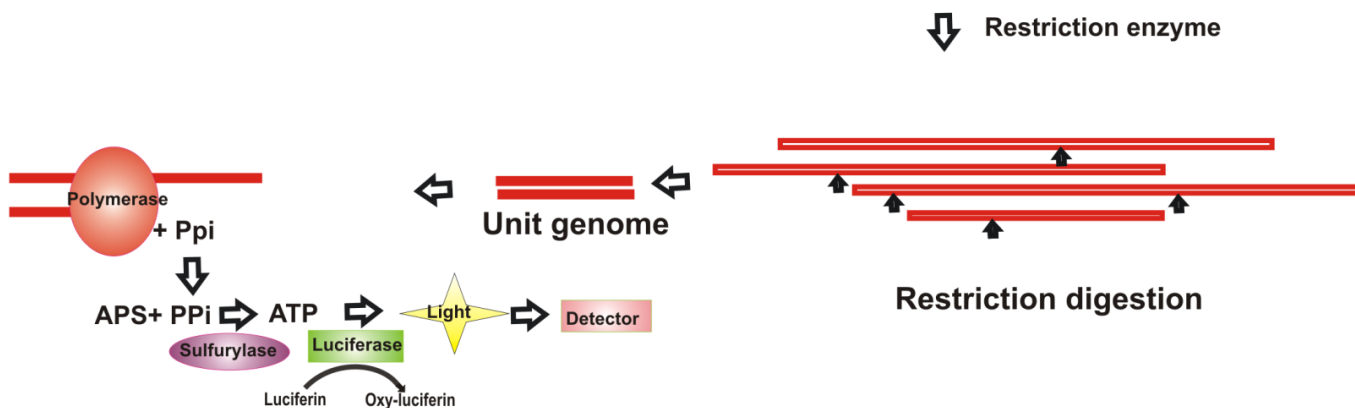
- Yellow mosaic disease (YMD) on soybean
Causative organism: *Yellow mosaic virus*
Family: Geminiviridae
Whitefly transmitted
- Yield loss due to YMD \$ 300 million/annum
- Spread of disease to hitherto uninfected regions
- Genome diversity



Multiply Primed Rolling circle amplification (Circomics)

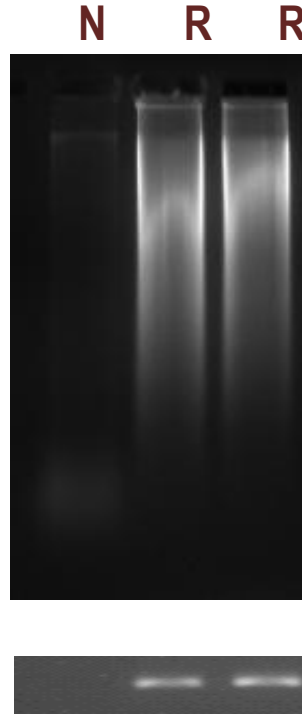


Multiply Primed Rolling circle amplification (Circomics)



Pyrosequencing

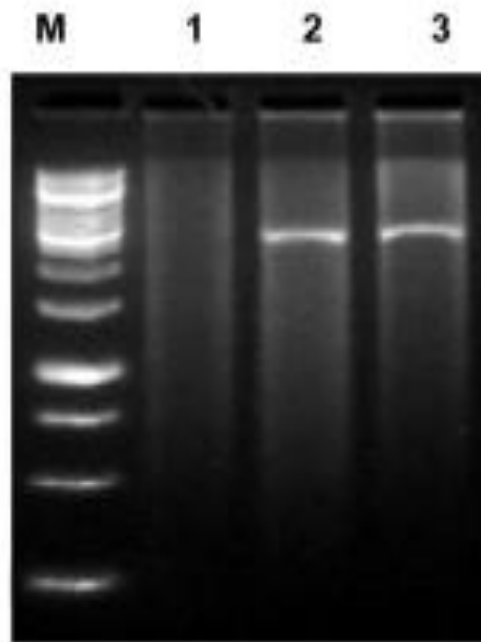
Multiply Primed Rolling circle amplification (Circomics)



N: Negative control

R: Partial AV-1 region amplicon

Restriction enzyme digestion of MPRCA Products



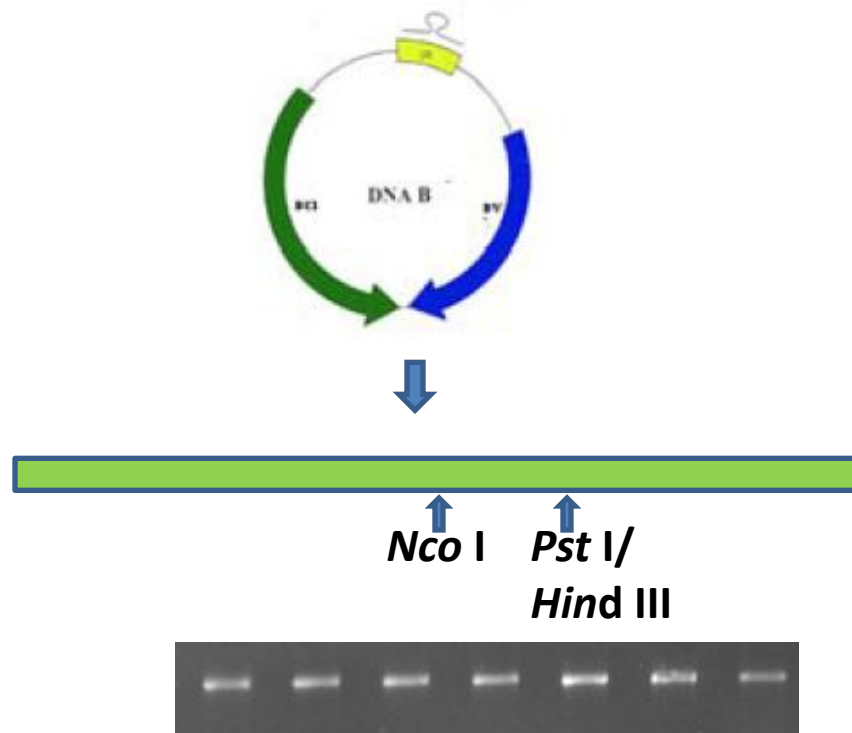
M: Molecular size marker

1- Negative control (- R.E.)

2- Restriction of RCA product with *Pst*-I

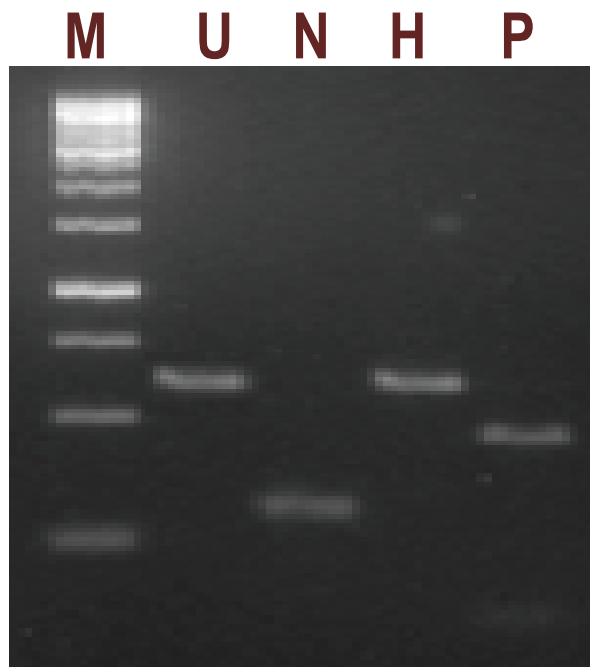
3- Restriction of RCA product with *Hind* III

RCA + RFLP Studies on Partial DNA-B region



Nco I is conserved in legume infecting *Begomoviruses*
Pst I- *Mungbean yellow mosaic Indian virus* (MYMIV)
Hind III-*Mungbean yellow mosaic virus* (MYMV)

RCA + RFLP Studies on Partial DNA-B region



M: 1Kb molecular size marker

U: Uncut DNA B genomic fragment

N: DNA B genomic fragment treated with *Nco* I

H: DNA B genomic fragment treated with *Hind* III

P: DNA B genomic fragment treated with *Pst* I

RCA Derived Complete Genome



Development of virus
induced knock-out vectors

Small non-coding RNAs
mediated antiviral resistance

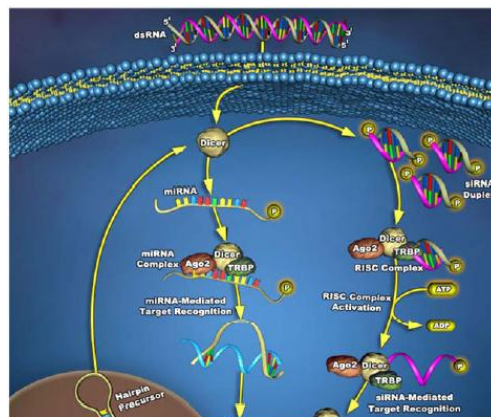


Host derived and artificial miRNAs

siRNAs mediated gene silencing

Small non coding RNAs based virus resistance

- ❑ RNA interference (RNAi)-hope for nucleotide sequence specific down-regulation of viral genes
- ❑ Successful deployment of RNAi in control of SS DNA viruses
African cassava mosaic virus,
Tomato leaf curl New Delhi virus etc.,



siRNAs mediated gene silencing

Concomitant silencing of AC1 and AC2 ORFs

- Replication initiator protein (rep)
and
- Transcriptional activator protein (TrAP) respectively

Prediction of miRNA cross silencing activity with viral genome

To support the psRNATarget, please cite: *Xinbin Dai and Patrick X. Zhao, psRNATarget: A Plant Small RNA Target Analysis Server, Nucleic Acids Research, 2011, W155-9. doi: 10.1093/nar/gkr319.*

THE SAMUEL ROBERTS
NOBLE
FOUNDATION

The Zhao Bioinformatics Laboratory

psRNATarget: A Plant Small RNA Target Analysis Server

[About](#)

[Citation](#)

[Analysis](#)

Location: Analysis

User-submitted small RNAs / preloaded transcripts

Preloaded small RNAs / user-submitted transcripts

User-submitted small RNAs / user-submitted transcripts

Upload target transcript candidates in FASTA format:

[\[Load demo data\]](#) ?

No file chosen

or paste sequences below:

- file / input sequence size limit: 200M. ?

Select published miRNAs (all or by species) ([miRBase](#) Release 19, August 2012):

All of miRNAs (from the following species)-----
 Acacia auriculiformis-----7 published miRNAs
 Acacia mangium-----3 published miRNAs
 Aegilops tauschii-----2 published miRNAs
 Amphimedon queenslandica-----16 published miRNAs
 Aquilegia caerulea-----45 published miRNAs
 Arabidopsis lyrata-----375 published miRNAs



Directorate of Soybean Research

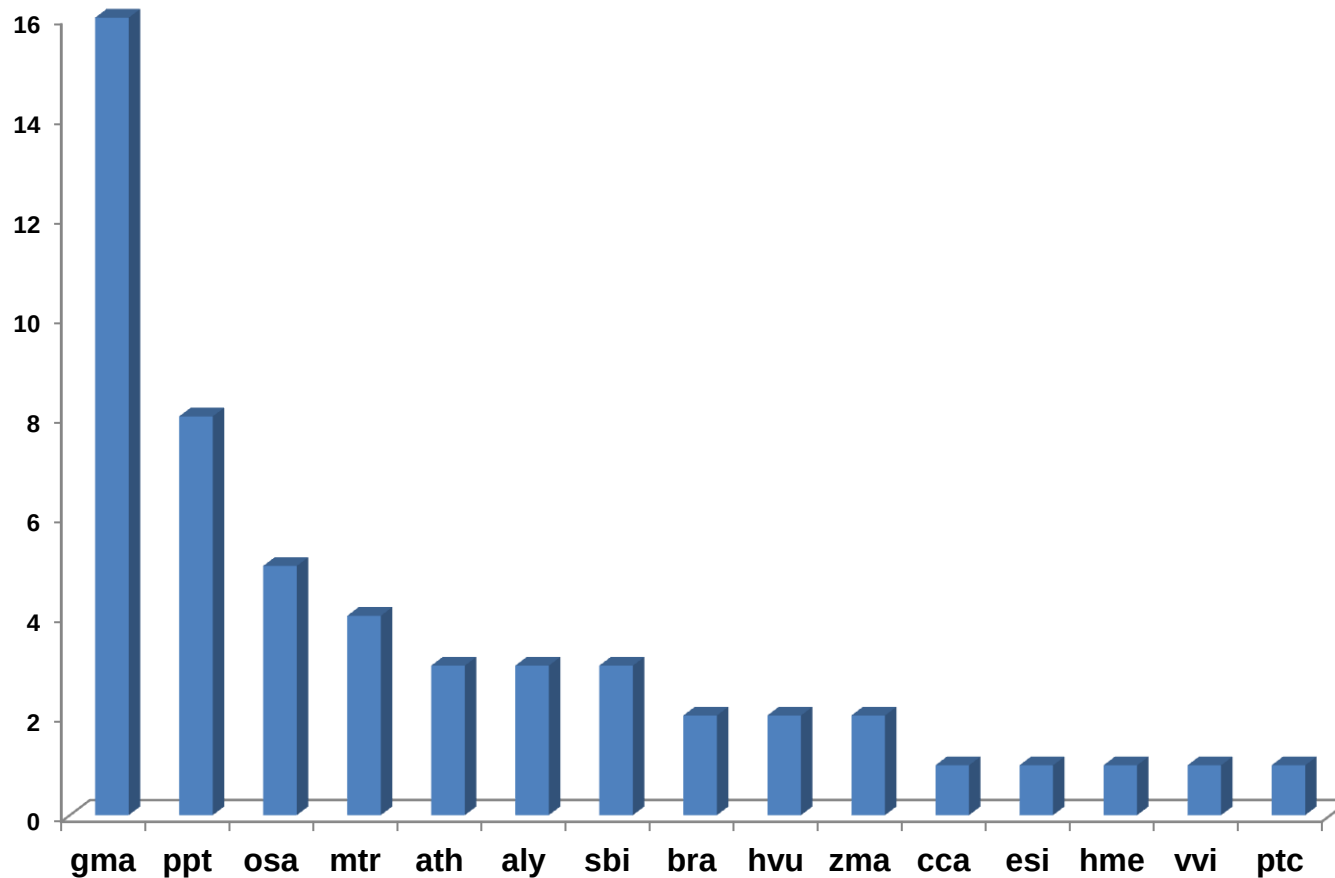
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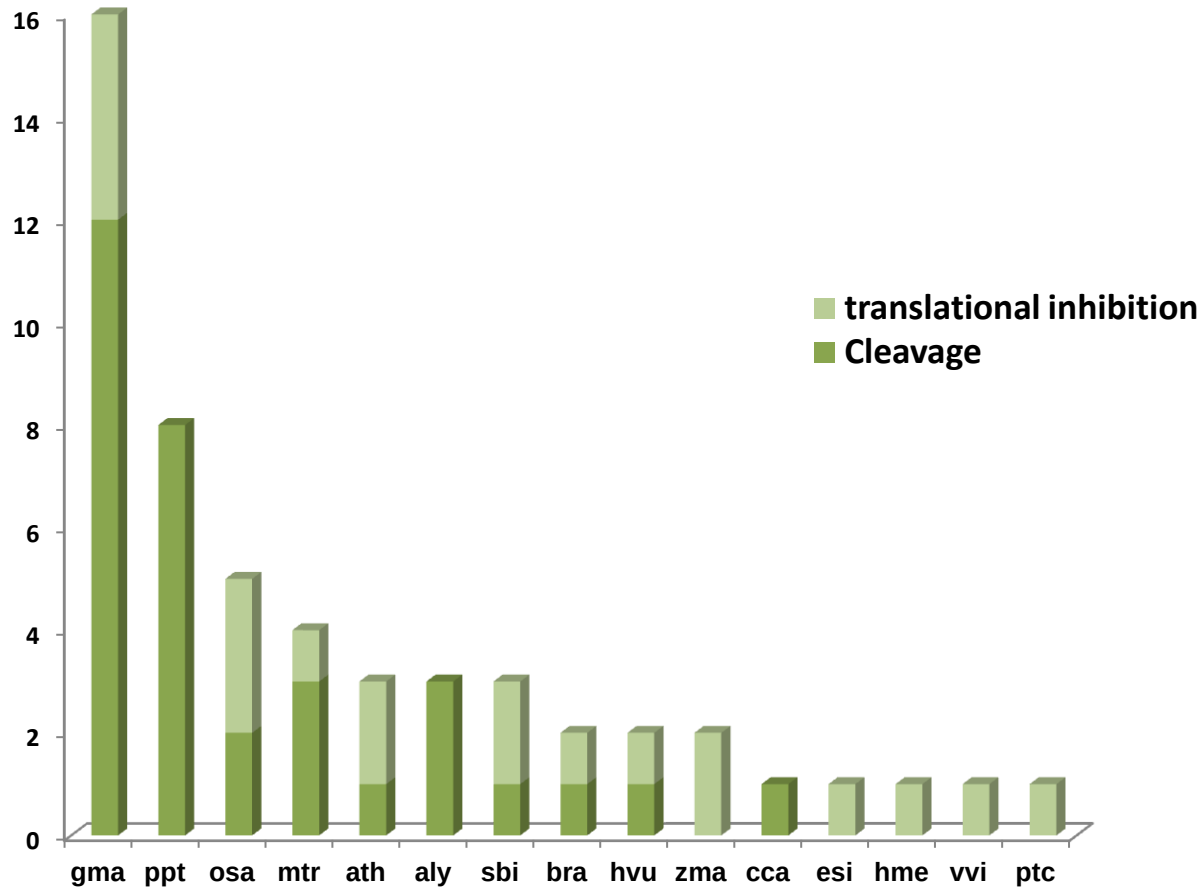
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Plant miRNAome targeting MYMIV-sb

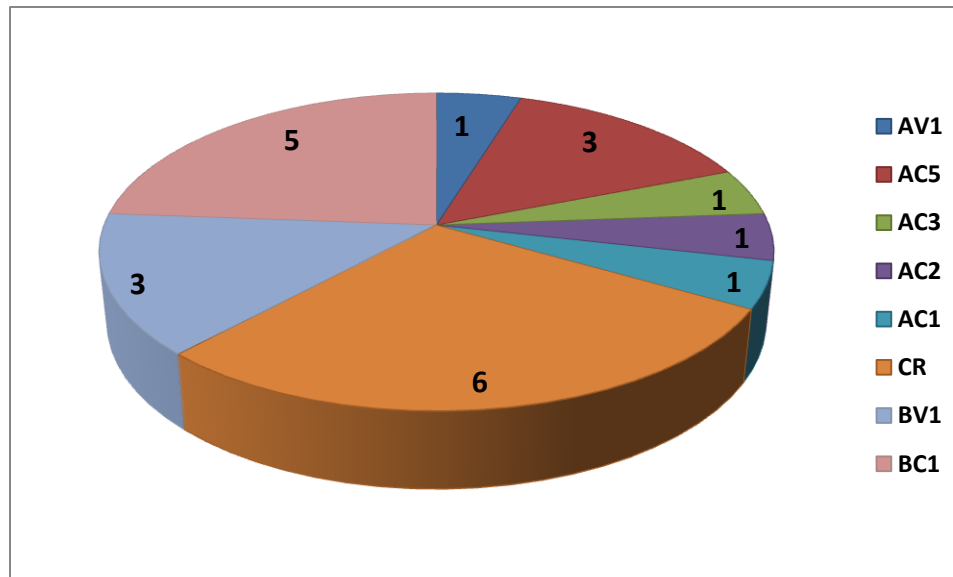
Number of miRNA Hits



Mode of action of Plant miRNAome against MYMIV-sb



Genomic regions targeted by plant miRNAome



***Glycine max* miRNAs repress MYMIV movement**

miRNA family	Viral genome Targets	Host transcriptome targets/functions
gmamiR482b	Common region	Root specific expression during nodulation
gmamiR1519	Non coding region	miRNA isolated from <i>B. japonicum</i> -inoculated soybean roots
gmamiR5764	BV 1 movement protein	Regulators of NB-LRR defense related genes
gmamiR1520	Non coding region	miRNA isolated from <i>B. japonicum</i> -inoculated soybean roots
gmamiR4371	AC 5	Non- annotated Protein targets in seed cotyledons
gmamiR5785	BC1 Nuclear shuttle protein	Regulators of NB-LRR defense related genes

Conclusions

- ❑ Complete Genome of soybean-infecting *Begomovirus* in central Indian region studied
- ❑ RCA-RFLP studies identifies it as MYMIV
- ❑ Small ncRNAs based gene silencing is explored to develop antiviral resistance
- ❑ Host derived miRNAs display propensity to repress virus movement

Acknowledgements

Co-workers

Scientists – Directorate of Soybean Research

Director -Directorate of Soybean Research

Asst. Director General -ADG (O&P)

Deputy Director General -DDG (Crop Science)

Director General -DG (ICAR)

&

WSRC-IX Organizers



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