



**INDIAN INSTITUTE OF SCIENCE**  
**INSTITUTE COLLOQUIUM**  
(Biological Sciences)

**Prof. H.S. Savithri**  
**Department of Biochemistry**

*will deliver a lecture*

*on*

**VIRUSES-SMALL BUT NOT SIMPLE: TWO DECADES OF  
WORK ON PLANT VIRUSES**

**on Wednesday, October 31, 2007**  
**at 4.00 pm in the Faculty Hall**

**THE DIRECTOR**  
*will preside*

***All are cordially invited***

*Coffee/Tea: 5.00 pm*  
**Venue: Reception Hall**

**Abstract**

Viruses are obligate parasites that infect bacteria, plants, insects and animals alike. The viral genomes are small and code for a few proteins that interact with the host cell machinery and redirect it towards their own multiplication. A detailed study of the different steps involved in the life cycle of these viruses is necessary to unravel the molecular mechanisms of infection. Such studies will also enable design of suitable strategies for controlling the diseases. Single stranded RNA viruses such as Physalis mottle virus  
(p.t.o)



(PhMV), Sesbania mosaic virus (SeMV), Pepper vein banding virus (PVBV), Peanut bud necrosis virus infecting tomato (PBNV-K) and single stranded DNA viruses such as tomato leaf curl virus (ToLCV) and cotton leaf curl virus (CLCuV) have modular genomes and detailed studies on the structure and function of their gene products have been successfully carried out at IISc.

Viral genomes are protected by protein capsids made of one or more identical protein subunits. Disassembly and assembly of the capsid are two crucial steps in the life cycle of a virus. The pathway of assembly is difficult to establish, as polymerization of the subunits occurs rapidly. We have expressed the capsid proteins of PhMV, SeMV and PVBV in heterologous systems such as *E. coli* in which they form Virus-Like Particles (VLPs) and studied the molecular mechanisms of their assembly through mutational analysis. It was shown in PhMV that the N-terminal segment of the coat protein is dynamic and mediates an early step in the disassembly / assembly of the virus. The coat protein folding and assembly are concerted events in PhMV. In SeMV, metal-ion mediated inter-subunit interactions are not crucial for assembly but they increase the stability of virus particles. A positively charged arginine rich motif present at the N-terminal segment of the coat protein is essential for RNA encapsidation. VLPs of SeMV can be formed in the absence of the  $\beta$ -annulus, a motif, earlier believed to be crucial for the assembly. In PVBV, surface exposed amino- and carboxy- terminal residues are essential for the initiation of assembly.

The genomic analyses of these viruses have shown that PhMV, SeMV, and PVBV are distinct new members of the tymo, sobemo, and poty virus genus, respectively. Poly-protein processing is a common strategy exploited by these viruses to generate different functional products from a single large poly-protein. Viral proteases that play a crucial role in this maturation process are unique and are present within the poly-protein. The PVBV-N1a protease possesses a novel metal ion mediated DNase activity. The poly-protein processing by SeMV protease is modulated by the natively unfolded VPg polypeptide present at its C-terminus.

A distinguishing feature of plant viruses is that they code for movement proteins that are responsible for the cell to cell movement of the viral genome. Mechanism of viral movement has been investigated by heterologous expression of the SeMV and CLCuV movement proteins. The tospoviral NSS protein is multifunctional and can suppress host defense machinery.

Engineering resistance to viral infection is an attractive alternative to conventional breeding approaches for obtaining resistant plant varieties. Transgenic cotton with antisense CLCuV AV2 gene has been obtained and shown to be resistant to challenge inoculation in the R1 and R2 progeny plants.