

APPLICATIONS OF BIOINFORMATICS IN PLANT VIRUS RESEARCH

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Plant viruses cause enormous losses to crops worldwide. In order to devise strategies for disease control, it is essential to understand the sequences of the plant viral genomes and the proteins encoded by them. Currently there are about 9000 plant viral sequences in the databases. Bioinformatics plays an important role in mining valuable information from these data. The tools of bioinformatics are used right from the beginning, namely the design of PCR primers for the amplification of plant viral genomes. Determining the phylogenetic relationships between viruses, elucidating the recombination, molecular reassortment and mutations in plant viruses and finally the choice of viral genes for genetic engineering of plants for developing virus-resistant plants, are all processes, which rely on bioinformatics.

Examples for the applications of bioinformatics in plant virus research from our lab:

- Sequence analysis of the coat protein of *Cardamom mosaic virus* helped to classify it as a new member of the *Macluravirus* genus of the *Potyviridae* family.
- Design of universal primers led to the identification of a novel satellite DNA associated with Bhendi yellow vein mosaic disease.
- Phylogenetic relationships between the various isolates of *Cardamom mosaic virus* gave key information about the movement of virus along the cardamom tract.
- Recombination and molecular reassortment among the viruses causing yellow mosaic disease in legumes in South and South East Asia could be understood using multiple sequence alignment and recombination detection programs.

- Detection of motifs and domains in the coat protein, movement protein and the β C1 protein of the soybean and bhendi virus proteins has led to the elucidation of the functions of these proteins.
- Promoter regions in the bhendi virus could be analyzed.
- The sequences of candidate genes from the cardamom, bhendi and soybean viruses could be chosen for genetic engineering of plants for virus resistance.