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Title of Ph.D. Thesis: *“Molecular Characterization and Phylogenetic Studies of Banana Bunchy Top Virus and Development of Diagnostic Method for its Detection”*

Keeping in view the huge losses attributed to BBTv infection it becomes necessary to characterize it at molecular level. Molecular characterization of the viruses and establishment of relationship among different isolates is also important for developing diagnostic methods for the management of virus. Beside, this would add data to existing pool of knowledge on BBTv. Characterized genes of virus can also be used in developing transgenic banana resistant to BBTv infection.

Important outcome drawn from overall study are as follows:

- Of the five states surveyed, BBTv symptoms were more prevalent in banana plantations of Karnataka followed by Bihar, Maharashtra, Delhi, and Uttar Pradesh. Symptoms in the field varied from mild to complete destruction of crop.
- Transmission electron microscopic studies revealed the presence of isometric particle of ~20 nm diameter in symptomatically infected banana leaf samples.
- Replicase and Coat protein gene of two isolates of Bhagalpur & Hajipur (Bihar) and one isolate from Jalgaon (Maharashtra) were successfully amplified by PCR, cloned and sequenced. These sequence data were submitted to EMBL database (DQ640741, EF584545, DQ640742, DQ996466, FJ168538 & EF584544).
- All six DNA components (DNA 1-6) of Bhagalpur (Bihar) isolate of BBTv were also amplified, cloned, sequenced. The sequence data were submitted to EMBL database (FJ605506, FJ605507, FJ605508, FJ609642, FJ609643 & FJ609644).
- Sequence data showed that clones of Rep (DNA-1 ORF) and CP (DNA-3 ORF) were 861 nt and 513 nt in length coding for 286 and 170 amino acids respectively. Complete DNA-1, DNA-2, DNA-3, DNA-4, DNA-5 and DNA-6 components were found to be 1111, 1061, 1075, 1046, 1018 and 1090 nucleotides respectively.
- The viral isolates under study were characterized to be BBTv on the basis of symptomatology, electron microscopic studies and sequence analysis of the amplified and cloned gene product.
- Sequence analysis revealed that each DNA component contain conserved Stem Loop Common Region (CR-SL), TATA Box, conserved Poly A signal, Major Common Region (CR-M) and potential ORF with initiation (ATG) and stop codon.
- DNA-3 ORF coding for Coat Protein share 98.6-100% & 99.4-100% identity with South Pacific isolates of BBTv at nucleotide and amino acid level respectively.