

**O-31 (165)****GENETIC DIVERSITY OF BANANA BUNCHY TOP VIRUS POPULATION REVEALS HYPERVARIABLE SUBGENOMIC REGIONS**

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Rapid evolution in viruses is achieved by high rate of mutations due to quick replication associated with small generation times, which is further shaped by reassortment and recombination. *Banana bunchy top virus* (BBTV) with a multicomponent circulars single stranded genome causes a highly devastating disease of banana called Banana bunchy top disease. Interestingly, some parts in BBTV genome and some of its components exhibit very high genetic diversity which cannot be explained solely by higher mutation rates. To understand this phenomenon, a detailed analysis of genetic diversity associated with its different components and their functional parts was performed by calculating pair-wise average nucleotide diversity per sites and Watterson estimator for population mutation rates per site, on nucleotide sequences of BBTV components available in GenBank. In addition, comprehensive analyses of recombination by genetic networks and various other tools implemented in the recombination detection program were performed to understand the pattern of recombination. Our results not only established the existence of extensive recombination but also identified certain recombination hot spots present in different genomic components of BBTV. Among them, the stem-loop region is a common recombination hot spot identified in all the six genomic components. The component DNA-U3, which bears highest genetic diversity, is involved extensively in inter and intragenomic recombination. Analyses of the recombined genomic regions indicate that recombination is responsible for many fold increase in genetic diversity in destination population. Interestingly the gene conversion, a special recombination process responsible for concerted evolution at CR-M loci conserved in all the six genomic components, contrary to its role of decreasing genetic diversity by homogenization, is leading to increase in genetic diversity in BBTV population. This study has provided significant insights about the dynamics of evolution of BBTV and indicated that recombination is responsible for most of the higher diversity observed in BBTV population.

**Keywords:** BBTV; recombination; gene conversion; genetic diversity