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## P1-14

## Virus Family: Geminiviridae

## Category: Genetic diversity/variability

Title: Pattern of recombinations in begomovirus

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Abstract: With the development of new and reliable recombination detection tools, many studies have reported the presence of recombination events in begomovirus isolates Recombination has therefore been identified as being of major importance in begomoviruses evolution. Recombination may allow viruses to evolve quicker by providing immediate direct access to many more areas of a sequence space than are accessible by mutation alone. The detailed characterization and analysis of begomoviruses recombination is of great importance for understanding their evolution. Until now, there have been no statistical studies analysing the characteristics of observable inter-begomovirus species recombination events and the distribution of these events within begomovirus genomes. In this study, we present an extensive description of recombination in monopartite and bipartite begomoviruses. All full length Begomovirus genome A-component-like sequences available in June 2006 from GenBank were obtained. Sequences were sorted to discard similar viruses and monopartite, bipartite and monopartite + bipartite aligned sequence datasets were analysed using RDP3 with the extensive set of detection methods implemented therein. The patterns of recombination were established for each dataset and with a statistical approach, the distribution of recombination hot- and cold-spots determined. The characteristics of begomovirus recombination and the influence of intra genome interactions on the types of begomovirus recombination observable in nature are discussed.

