



## Assessment of the genetic diversity of tomato yellow leaf curl virus

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**ABSTRACT.** The objective of the present study was to analyze the genetic diversity of tomato yellow leaf curl virus (TYLCV). Representative TYLCV sequences were searched in the National Center for Biotechnology Information database. Comprehensive analysis of TYLCV was performed using bioinformatics by examining gene structure, sequence alignments, phylogeny, GC content, and homology. Forty-eight representative TYLCV sequences were selected from 48 regions in 29 countries. The results showed that all TYLCV sequences were 2752-2794 nucleotides in length, which encoded 6 open reading frames (AV1, AV2, AC1, AC2, AC3, and AC4). GC content ranged from 0.41-0.42. Sequence alignment showed a number of insertions and deletions within these TYLCV sequences. Phylogenetic tree results revealed that the sequences were divided into 10 classes; homology of the sequences ranged from 72.8 to 98.6%. All 48 sequences contained the typical structure of TYLCV, including open reading frames and intergenic regions. These results provide a theoretical basis for the identification and evolution of the virus in the future.

**Key words:** Cluster analysis; Structural characteristics;  
Homology analysis; Tomato yellow leaf curl virus