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JOINT EVENT

10th International Virology Summit & 4th International Conference on Influenza & Zoonotic Diseases July 02-04, 2018 | Vienna, Austria

Phylogenetic analysis and characterization of a *Tomato spotted wilt orthotospovirus* isolate infecting Chrysanthemum (Dendranthema morifolium) in Zimbabwe

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T omato spotted wilt orthotospovirus (TSWV) is an economically important pathogen of many crops worldwide. However, prior to this study, only one complete genome sequence of an African TSWV isolate was available in public databases thus compromising pathogen phylogenetic studies on the continent. TSWV was detected in Zimbabwean chrysanthemums using tospovirus immunostrips and subsequently confirmed by double antibody sandwich enzyme-linked immunosorbent assay and reverse transcription-polymerase chain reaction. Next-generation sequencing was done to recover the full genome of the TSWV isolate. MEGA7 was used to construct phylogenetic trees while RDP4 was used to detect recombination events in the isolate. Protein molecular weights were calculated using the ExPasy online program while SIAS was used to calculate nucleotide sequence identities. The tripartite genome of Zimbabwe TSWV isolate consisted of L, M and S RNAs of 8914, 4824 and 2968 nucleotides, respectively. Phylogenetic analyses placed the respective Zimbabwe TSWV genomic segments in the same clades with the South African isolate respective segments. The Zimbabwe TSWV isolate was found to be a non-recombinant and non-resistance-breaking isolate. This study provides useful genome information about TSWV from Zimbabwe and reveals its phylogenetic position on a worldwide scale.

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