Keerati Sindhavajiva 2011: Genome of *Citrus tristeza virus* (CTV) in Thailand and Detection of CTV by RT-PCR and Dot Blot Hybridization Techniques in Weeds.

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Genome of Citrus tristeza virus (CTV) causing stem pitting symptom on mandarin grown in Thailand (CTV-A18) was investigated. By reverse transcription-polymerase chain reaction (RT-PCR) technique with 22 specific primer pairs, cDNA fragment of CTV-A18 whole genome was synthesized and cloned into pCR[®]8/GW/TOPO vector. The research result revealed that whole genome of CTV-A18 isolate consisted of 19,302 nucleotides with 2 Untranslated Regions (UTRs) and 12 Open Reading Frames (ORFs) which at least 17 proteins could be produced. The whole genome of CTV-A18 was then analytical compared with other 24 CTV isolates from previous data in GenBank by Clustal W and MEGA 4 programs. Identity, Pairwise Distance and Phylogenetic tree analysis of CTV-A18 nucleotide sequence was the most similar to CTV NUagA isolate from Japan. From comparative amino acid sequences, the most conservative regions of CTV-A18 genome were cp gene (Coat protein, p25) and 3'UTR which exhibited 96-99% and 98-99%, respectively. On the other hand, the less conservative regions of CTV-A18 genome were 5'UTR, p349 and RdRp (p54) which exhibited 66-97%, 49-91% and 71-97%, orderly. Based on this work, the different of amino acid sequences of mentioned regions might be one important data used for classification or identification of CTV strains. RT-PCR technique with specific primer CPF/CPR [coat protein gene (cp) 672 bp] and result confirmation by Dot blot hybridization (DBH) with specific Biotin-CP-probe was demonstrated for CTV detection and lateral host study. Many kinds of plants including weeds, 45 samples in 11 Genera, 8 Families, established in CTV infected orchards were collected for research trials. The positive CTV-detection was recorded from infected mandarin and lime samples, but negative results were observed on all of those 45 plant samples.

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