

PIV241 - PRODUCTION OF INFECTIOUS CLONES OF WEEDINFECTING BEGOMOVIRUSES FOR PATHOGENICITY STUDIES

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The genus Begomovirus has the highest number of known viral species. Some of them are responsible for large agricultural losses such as Tomato severe rugose virus (ToSRV) in Brazil. *Euphorbia heterophylla* and *Sida* spp. are weeds frequently found in tomato production fields and act as hosts of ToSRV and other begomovirus species. The aim of this work was to obtain infectious clones of weedinfesting begomoviruses, *Euphorbia* yellow mosaic virus (EuYMV) and *Sida micrantha* mosaic virus (SiMMV), for studies of characterization, interaction between viruses and pathogenicity in tomato plants. EuYMV and SiMMV isolates were obtained from *E. heterophylla* and *S. santaremnensis* plants naturally infected in the field. Total DNA was extracted and the begomovirus species identified by PCR. Circular DNA was amplified by the rolling circle amplification (RCA) technique followed by digestion with restriction endonucleases and dimeric molecules (4.8 to 5.4 Kb) were recovered after electrophoresis. The inserts were cloned in the pCAMBIA0380 vector. Two clones were obtained for each viral component. The EuYMV DNA-A clones shared 97 to 99% to EuYMV DNAA accession JF56676; the EuYMV DNAB clones 98% to EuYMV DNAB accession JF756678; the SiMMV DNAA clones 99 to 100% to SiMMV DNAA accession JX415194; and SiMMV DNAB clones 96% to SiMMV DNAB AJ557452. The recombinant plasmids were transformed into *Agrobacterium tumefaciens* and inoculated in test plants. Inoculated plants are under analysis. These clones will be useful for studies on pathogenicity and virus-virus interaction in weeds and tomato plants.

PIV248 - RECOMBINATION EVENTS IN FULL GENOME SEQUENCES OF APPLE STEM GROOVING VIRUS

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Apple stem grooving virus (ASGV), type species of the genus Capillovirus, is disseminated worldwide. No vector is known and the virus is transmitted only by grafting, usually causing a latent infection in most commercial cultivars of apple trees. However, infected scions grafted onto sensitive material display reduction of yield, loss of fruit quality and tree decline. Currently twenty three complete nucleotide sequences of this virus species are available in the GenBank. Here we report recombination events along the complete genome sequences of ASGV using two Brazilian isolates (M2193 and M220) and sequences available in the GenBank database. Confidence values for the recombination events were evaluated by seven programs built in the RDP4 software package: RDP, GENECONV, BootScan, MaxChi, Chimaera, SiScan and 3Seq. Events detected by RDP with a pvalue under 1×10^6 were considered significant in this study. In a full-length genome analysis, six potential recombinants, not previously reported, were detected. Four recombinants apple isolates, NC_001749 (Japan), JQ308181 (China), KJ579253 (China) and M2193 (Brazil) showed as major parents, apple isolate M220 (Brazil), lily isolate D16681 (Japan), apple isolate M2193 (Brazil) and lily isolate AB004063 (Japan), respectively. JQ308181, M2193 and KJ579253 shared the same minor parent, M220. NC001749 showed as minor parent, JQ308181. One recombinant pear isolate (JN701424 from China) showed citrus isolate LC143387 (Japan) as major parent and apple isolate KF434636 (China) as minor while the recombinant LC143387 was originated from JN701424 (majorparent) and pear isolate AY596172 (Korea). Among recombinants shown we have observed recombination between isolates from different countries and different hosts species. Recombinant events were likely a result from exchange of propagation materials and vegetative propagation and could play a role in virus evolution, emergence and epidemiology. It likely contributes to virus survival, adaptability to environmental factors and new hosts, increase in virulence and genetic diversity.