

GRSV and TCSV isolates were completely sequenced by Illumina HiSeq 2000. The sequence reads obtained were assembled by CLC Genomic Workbench program and the final contigs were analysed by the GenBank® database. Extensive phylogenetic analysis made by the software PhyML showed that the genetic variability between GRSV and TCSV M RNA is less than in Tomato spotted wilt virus (TSWV) species, the virus type in the genus. The M RNA phylogeny does not separate GRSV and TCSV segments in different groups, signaling that probably they share the same M RNA. As result, the qPCR analysis showed that TCSV was more efficient in replication, even when mixed with a higher amount of GRSV.

PIV208 - A NEW CLOSTEROVIRUS FOUND IN ARRACACIA XANTHORRHIZA BY NEXT GENERATION SEQUENCING

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Arracacia xanthorrhiza, known as mandioquinhasalsa (MS) in Brazil, is a root vegetable originally from the Andes and belonging to family Apiaceae. It is a vegetatively propagated plant and viral infection symptoms are frequently observed. Next generation sequencing (NGS) has proven to be an efficient tool for viral metagenomic analysis, without the need of previous viral genome knowledge. Here we describe the identification and genome analysis of a novel closterovirus found in A. xanthorrhiza by NGS. RNA from viral enriched preparation after differential centrifugation of plant extracts were sequenced by Illumina HiSeq 2000 platform. Reads were analyzed, assembled, and submitted to blastx analysis against the RefSeq Viral database. The contig of 15.756 bp with coverage of 4464 reads share a high identity to closteroviruses, and similar genomic organization. The genus Closterovirus (family Closteroviridae) comprises species with monopartite positive singlestrand RNA genome whose size varies from 14.5 to 19.3kb. Based on the sequence information obtained by metagenomic analysis, specific primers that amplify overlapping regions of all genome were designed. Initially, the presence of this new closterovirus was confirmed in 21 MS plants from 47 total plants based on RTPCR. Then, one sample (MS#6)

was selected and used for complete genome sequence through Sanger sequencing. To determine the 5' and 3' terminals the RACE approach was successfully used. The complete genome of this closterovirus encodes 9 potential open reading frames and shows the typical organization of closteroviruses. The putative heat shock protein 70 homolog (HSP70h), RNA dependent RNA polymerase, and coat protein genes showed 3744, 2633, and 1835% amino acid sequence identities with other closteroviruses genome, respectively. A phylogenetic tree based on HSP70h gene showed that Beet yellows virus and Grapevine leafroll associated virus 2 are their closest relative to this virus. In conclusion, this study shows evidence of the presence of a putative new species in genus Closterovirus in Arracacia xanthorrhiza of Brazil. Considering that the sequence similarities of all taxonomically relevant proteins between this new Arracacia virus and recognized closteroviruses are far below the species demarcation threshold proposed by the Closteroviridae Study Group, we propose this virus to be representative of a new species in the genus, for which we propose the name "Arracacha virus 1".

PIV210 - IDENTIFICATION BRUGMANSIA SUAVEOLENS MOTTLE VIRUS IN BRUGMANSIA SP

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Plants of the genus Brugmansia (Solanaceae) are bushy-like trees that can reach up to 4.6 metres high. In Brazil, plants of this genus are popularly known as 'trombeteira' (trumpet) or 'saia branca' (white skirt). They are used as ornamental plants, because of their beautiful, large and tubular shape flowers. A leaf sample of Brugmansia sp. with mosaic and vein clearing symptoms was collected in 2015, in Curitiba - PR (Parque do Papa, S 25°24'40" W 49°16'13"). There is a report of the infection of the potyvirus Brugmansia suaveolens mottle virus (BsMoV) in a B. suaveolens plant, observed in Campinas SP (isolate BsCampinas). As the symptoms observed in this 'trombeteira' plant was distinct from the one collected in Campinas, it was supposed that a different virus could be causing the viruslike symptom in this plant.