

mosaic, blistering in the leaves and floral abortion were collected in the province of Holguín (eastern region of Cuba). Rolling circle amplification and restriction fragment length polymorphism analyses evidenced that a begomovirus was associated with symptomatic plants. Sequences of six DNA-A clones were obtained, with 99.5% identity between each other. The full-length sequence of one DNA-A clone (GenBank acc. # KT192632), comprising 2581 nucleotides, showed highest identity (92%) with *Rhynchosia golden mosaic Yucatan virus* (RhGMYuV, EU021216). Based on its genome organization and according to ICTV guidelines, it corresponds to a distinct strain of this species. RhGMYuV has been reported in *Rhynchosia minima* in several Latin American countries, including Cuba, and also in soybean and tomato crops in Mexico and Ecuador, respectively. We have now reported its presence in soybeans in Cuba, which is also the first report of begomovirus infection in soybean crops in the country. Unusual for begomoviruses, RhGMYuV seems to be well adapted to infect both cultivated and non-cultivated hosts. Financial Support: CAPES, CNPq, FAPEMIG.

PIV286 - A NOVEL MYCOVIRUS ASSOCIATED TO SAPROPHYTE *Alternaria alternata* BELONGS TO A DISTINCT LINEAGE IN *Gammartitivirus*

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Mycoviruses are widely distributed in all major taxonomic groups of filamentous fungi and yeasts, and also in oomycetes, and their genomes are predominantly comprised of double-stranded RNA (dsRNA) molecules. The presence of dsRNA in an *Alternaria alternata* strain that displays phenotypic plasticity draw our interest, and the objective of this study was to perform the molecular and biological characterization of this putative mycovirus. The complete genome was sequenced and is comprised of two dsRNA molecules, the largest (dsRNA1) with approximately 1796 bp, encoding a putative RNA-dependent RNA polymerase (RdRp), and the smallest (dsRNA2) being 1624 bp in length, encoding the putative capsid protein (CP). BLASTp searches of the RdRp revealed low identity with partial RdRps of members of the family *Partitiviridae*, and similar low identity with polyproteins and NIB

proteins of plant and animal viruses in the families *Potyviridae* and *Caliciviridae*. However, alignment of the RdRp revealed the presence of six conserved motifs from members of the family *Partitiviridae*. Interestingly, BLASTp searches of the putative CP revealed identity only with the putative CP of *Botryosphaeria dothidea partitivirus 1* (BdPV1), a recently described divergent partitivirus. Phylogenetic analysis based on the RdRp grouped the virus, provisionally named *Alternaria partitivirus 1* (AtPV1), with BdPV1, comprising a distinct lineage in the genus *Gammartitivirus*. Vertical transmission tests showed that AtPV1 was transmitted to 100% of the conidial progeny, and standard curing was unable to eliminate it from the host, characterizing it as a persistent virus. On the other hand, horizontal transmission was not possible for the tested species. The absence of a virus-free isogenic strain prevented us from assessing details of the virus-host interaction, and therefore it remains unclear whether the phenotypic plasticity phenomenon is associated with AtPV1 infection. Keywords: Persistence, virus-host association and phenotypic plasticity. Financial Support: CNPq, CAPES, FAPEMIG.

PIV287 - TRANSFORMING LIFESTYLES: A VIRUS CONVERTS THE DESTRUCTIVE PLANT PATHOGEN *Ralstonia solanacearum* INTO A COMMENSAL MICROBE

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Filamentous bacterial viruses containing single-stranded DNA (ssDNA) genomes have a peculiar lifestyle compared to other bacterial viruses, because they do not cause cell lysis, but rather establish a persistent association with the host, often causing behavioral changes. For years, an intriguing phenomenon occurred in newly farmed deforested area in Brazil characterized by a downward trend in the incidence of the bacterial wilt caused by *Ralstonia solanacearum*, after a very high incidence during the first crop cycle in the area. In an attempt to elucidate the factors associated with this phenomenon, a strain of *R. solanacearum* (UB2014) obtained from one of these areas was investigated. Pathogenicity tests in tomato confirmed the loss of

virulence of this strain. To verify if the presence of viruses was related to the phenotype, we purified virus-like particles (VLPs) from a UB2014 colony. Total nucleic acids were extracted from DNase- and RNase-treated VLPs, and a 9-10 kb nucleic acid fragment was identified. Digestion of this VLP-purified nucleic acid with nucleases indicated its ssDNA nature. The putative ssDNA genome was amplified with the phi29 DNA polymerase, cloned and completely sequenced. The profile of structural proteins indicates that the UB2014-associated virus is related to species in the genus *Inovirus*. The virus was transmitted to the aggressive *R. solanacearum* strain GMI1000. Upon infection, GMI1000 showed abnormal culture characteristics such as frequent aggregation and the production of a brown pigment. Tomato plants inoculated with *Rs* UB2014 did not show any symptoms. Interestingly, virus-infected *Rs* GMI1000 caused only mild symptoms in tomato plants, which eventually reversed so that the plants developed normally, similar to negative controls. The presence of *Rs* UB2014 and virus-infected GMI1000 in the xylem vessels of plants without any symptoms after 3 months demonstrates the drastic change in lifestyle of the pathogen. Assays are under way to confirm the identity of the virus and to elucidate the mechanisms involved in the modulation of the parasitic plant-bacteria relationship. Keywords: Ecology, phage, viral infection. Financial Support: CNPq, CAPES, FAPEMIG.

PIV288 - MOLECULAR AND BIOLOGICAL CHARACTERIZATION OF A MYCOVIRUS INFECTING THE PHYTOPATHOGENIC FUNGUS *Sclerotinia sclerotiorum*

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The mycoviruses are distributed in all major taxonomic groups of fungi. The association established between mycoviruses and their hosts may occur in a latent form or can change the phenotype of the host causing hyper- or hypovirulence. Viruses that cause hypovirulence have been studied as potential agents for biocontrol of phytopathogenic fungi. *Sclerotinia sclerotiorum*, the causal agent of white mold, is a fungus adapted to several soil and climatic variations, and which develops resistance structures that confer the ability to survive

in soil even in the absence of a host plant. Several economically important crops are affected by this fungus worldwide. In this context, our objective was to detect and characterize mycoviruses in *S. sclerotiorum*. Double-stranded RNA (dsRNA) was purified from 12 isolates of *S. sclerotiorum*. In one of them, six dsRNA segments were detected, suggesting that this particular isolate is infected by a mycovirus. These dsRNA segments are being sequenced. We obtained an isogenic virus-free line to compare the physiological characteristics between the virus-infected and virus-free lines. Pronounced changes were observed in the virus-infected line, including delay in mycelial growth, changes in the shape and pigmentation of the colony, drastic reduction in the number of sclerotia and low production of oxalic acid. The virus-free line exhibits a typical phenotype of *S. sclerotiorum*. The virus infected line was not capable of inducing disease under controlled conditions, while plants inoculated with the virus-free line showed typical symptoms of white mold. These distinctive patterns observed between the virus-infected and virus-free lines suggest that the mycovirus modulates these characteristics of the host fungus. Together, these findings potentiate the use of this mycovirus as a tool for studies on the mechanisms of fungal pathogenicity as well as its use as a biocontrol agent. Keywords: Mycovirus, White mold disease, hypovirulence. Financial Support: CNPq, CAPES, FAPEMIG.

PIV304 - BIOLOGICAL AND MOLECULAR CHARACTERIZATION OF A BACTERIOPHAGE SPECIFIC TO *Xanthomonas scampestris* pv. *campestris*

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Viruses that infect phytopathogenic bacteria have gained increased interest due to their potential use as biocontrol agents. Black rot, caused by the Gram-negative bacterium *Xanthomonas campestris* pv. *campestris* (Xcc), is one of the most important diseases infecting all cultivated varieties of brassicas worldwide. This study aimed to isolate and characterize bacteriophages capable of infecting Xcc. To this, plants of the *Brassicaceae* family showing symptoms of black rot, as well as rhizospheric soil of these plants, were collected and screened for the presence of bacteriophages by lysis assay. One phage