

occlusion bodies formation. Polyhedra production was observed after 72 h p.i in both BmNPV and AcMNPV infected cells. As expected no polyhedra was observed in cells infected with AgMNPV-2D, and the majority of the cells appear to be completely lysed due to apoptosis, as already described for this virus-cell interaction. The ultrastructure of the two virus isolates visualized by Transmission Electron Microscopy confirmed that they are single nucleopolyhedrovirus. Financial Support: FAP-DF.

PIV45 - A BEGOMOVIRUS IS A PUTATIVE CAUSAL AGENT OF INTERNERVAL CHLOROSIS AND CURLING IN SOYBEAN LEAVES

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Brazil is the world's largest soybean exporter, with a cultivated area of about 30 million hectares. Begomoviruses are whitefly-transmitted geminiviruses that cause a great impact in several economically important crops, such as tomatoes, cotton, cassava and beans. Although they are not economically important in soybean, four begomovirus species were reported infecting these plants: *Bean golden mosaic virus* (BGMV), *Sida micrantha mosaic virus* (SiMMV), *Sida mottle virus* (SiMoV) and *Soybean chlorotic spot virus* (SoCSV). The aim of this study was to identify the etiological agent of a novel soybean disease characterized by severe leaf curling of top leaves. Twenty-three symptomatic soybean leaf samples were collected in Luziânia (GO). Serological tests using antibodies against *Tomato spotted wilt virus* (TSWV), *Tomato chlorotic spot virus* (TCSV) and *Groundnut ringspot virus* (GRSV) were negative, indicating absence of these tospoviruses in the plants. Virus preparations from seven randomly selected samples were used for mechanical inoculation in two soybean varieties (Wehrmann - W79 / Rr and Nidera). However, inoculated plants did not present any symptoms after one month of incubation. Then, total DNA was extracted from each collected leaf and subjected to Rolling Circle Amplification (RCA), followed by digestion with the restriction enzyme *MspI*. DNA amplification was confirmed in all DNA samples, suggesting the presence of circular DNA viruses in the plants. The RCA

restriction profiles were similar in all samples, with *MspI* fragments of 1300bp, 1100bp (double band) and 400bp, which resembles those of bipartite begomoviruses. Direct sequencing of the RCA-amplified DNA, using a primer directed to the coat protein region in the DNA-A genome, indicated the presence of an isolate of *Euphorbia yellow mosaic virus*. In conclusion, the presence of a begomovirus was consistently observed in plants with severe symptoms, possibly a mechanically non-transmissible begomovirus. Characterization of this virus is being carried out to confirm the etiology of this disease. Financial Support: CNPq.

PIV46 - METAGENOMIC ANALYSIS OF VIRAL SPECIES IN NATIVE PLANTS FROM THE CERRADO BIOME

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The Brazilian Cerrado is the second largest biome in Brazil with a major diversity of native trees and shrubs, natural reservoirs of pathogenic microorganism including viruses. These are responsible for high economic losses especially in cultivated crops. Studies on viruses infecting Cerrado trees are rare. However using modern techniques of viral detection, metagenomics, and bioinformatics we expect to stretch our knowledge about our tree-associated viruses. The main objective of this work is to detect novel viral species infecting native plants from Cerrado with the aid of metagenomics. Thus, 71 seedlings from 29 tree species showing viral symptoms. were collected from a plant nursery at NOVACAP (Brasília, Distrito Federal). Plants were first subjected to half-purification process followed by nucleic acid extraction and then submitted Next-Generation Sequencing using NGS sequencing technology by Illumina platform HiSeq 2000. Sample analysis included the *de novo* assembly of sequences, consisting of 5.005.013 million reads generated by the joint data analysis. Assembled sequences produced 2.162 contigs that were subjected to BLASTX analysis (Basic Local Alignment Too Search). To validate the results, RT-PCR was employed using specific primers

designed on identified RNA virus sequences. As result, the metagenomic data analysis revealed mainly the presence of sequences matching RNA viruses including viral species that infects arthropods. Financial Support: CAPES, EMBRAPA.

PIV48 - BEGOMOVIRUS DIVERSITY IN RESISTANT AND SUSCEPTIBLE TOMATO PLANTS

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Tomato (*Solanum lycopersicum*) is one of the main vegetables grown in the world, but the occurrence of plant diseases can cause substantial production losses in this crop. Begomovirus infections (family *Geminiviridae*) generally occur at high frequency in tomatoes, posing serious constraints to its production in Brazil. Currently, the use of resistant cultivars is the most effective method for controlling begomovirus diseases, even though these plants are only moderately resistant and thus not immune. Our aim was to perform a preliminary assessment of the diversity of begomoviruses in resistant (cv. BRS Sena) and susceptible (cv. H-9553) tomato cultivars. Therefore, 117 symptomatic leaf samples from both cultivars were collected in the same field at the municipality of Luziânia-GO. A total of 45 samples were collected from symptomatic plants of the hybrid H-9553, and 72 samples for the hybrid BRS Sena, since begomovirus infection symptoms in resistant plants are milder and more difficult to identify than in susceptible cultivars. Viral infection was confirmed by PCR using universal begomovirus degenerate primers. Fifty-six resistant (77% tested positive) and 44 susceptible (97%) tomato samples were PCR-positive for the presence of begomoviruses. The viral DNA from these samples was further amplified by rolling circle amplification and subsequently digested with *MspI* restriction enzyme, in order to visualize the polymorphism in the viral genome restriction profiles. Seven different profiles were observed, being the pattern of *Tomato severe rugose virus* the predominant. This begomovirus species is considered to be the most prevalent in the tomato crop in Brazil. Variations in the restriction profiles indicate the presence of different viral species/strains/variants in the collected tomato plants. Additionally, two profiles appeared exclusively in resistant plants, while two

others only in susceptible plants. These results suggest the existence of differences between viral populations present in resistant and susceptible plants. Subsequent cloning and complete genomic sequencing of these viruses will allow the species identification, unravel their genetic diversity, and determine if the expansion of the use of resistant cultivars may result in changes in the virus population composition in the field. Further characterization of the variants present in resistant plants may provide insights to the durability and efficiency of the resistance genes in tomatoes. Financial Support: CNPq, FAPDF, EMBRAPA Hortaliças.

PIV58 - MYCOVIRUS DETECTION AND IDENTIFICATION IN *Hevea brasiliensis*

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Hevea brasiliensis is the best producing plant of latex and natural rubber in the world. This plant species is susceptible to several diseases caused by fungi and viruses. In plant tissue, there are many symbiotic organisms that can interact and help in plant protection against pathogens, as the endophytic fungi. Mycoviruses commonly occur in endophytic fungi and they can play an important role in mutualistic interactions between the fungus and the host plant. The main mycovirus families are those with genome composed by double-stranded RNA: *Hypoviridae*, *Chrysoviridae*, *Totiviridae*, *Partitiviridae*, and *Reoviridae*. However, nothing is known about the impact of mycoviruses in *H. brasiliensis*. Thus, the study of the mycovirus diversity is an important and required scientific investigation. For this reason, the following approach is proposed: First, the endophytic fungi will be isolated from native rubber tree individuals