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