

presence of both components. The complete sequence of DNA-A was determined to be 2694 nucleotides, with a genome organization typical of New World bipartite begomoviruses. The full-length sequence of DNA-A had the highest identities of 85% to *Sida mosaic Alagoas virus*, a begomovirus previously reported in *Sida* sp. plants in Brazil. The DNA-B component was 2622 nucleotides and encoded two open reading frames (BV1 and BC1). It had 79% sequence identity with the DNA-B component of *Okra mottle virus*. In a recombination analysis, no significant recombination event was detected from the DNA-A component of this isolate. Thus, a novel bipartite begomovirus species was found infecting a *Sida* sp. plant in Brazil, and the implications of this finding in begomovirus evolution will be discussed. Financial Support: UNIVERSITY OF BRASÍLIA, UNIVERSITY OF DAVIS, EMBRAPA VEGETABLES

PIV408 - DETECTION AND WHOLE GENOME SEQUENCING OF CPMMV IN COMMON BEAN RESISTANT TO BGMV FROM PARANÁ STATE

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Cowpea mild mottle virus (CPMMV) is a *Carlavirus* from the family *Betaflexiviridae* which has a linear single stranded positive sense rna genome of approximately 8,200 nt and infects a wide range of cultivated plants from the *Fabaceae* family. It is transmitted by the whitefly *Bemisia tabaci*. During the field tests required for the release of a new common bean (*Phaseolus vulgaris*) cultivar resistant to bean golden mosaic virus by rna interference, some plants with mild mosaic and distortion in the leaves were tested for the presence of CPMMV by ELISA. These plants were collected in the cities of Cambará and Londrina, Paraná state. In order to confirm the etiology of the disease and compare the genome of these isolates with the CPMMV isolates from soybean which we had obtained a couple of years previously, the positive samples from ELISA were used for rna extraction and RT-PCR with primers previously used for sequencing of CPMMV in soybean. One of the samples was used for the sequencing of the whole genome of the virus, using also the race protocol for the amplification of the 5' end of the genome. Another four samples were confirmed as infected by CPMMV with

ELISA and RT-PCR of the 3' end portion of the genome. The complete genome showed 99% identity with some of the CPMMV isolates from soybean in Brazil and also with the complete genome of CPMMV obtained from whiteflies in Florida. The sequences also clustered with each other in the filogenetic analyses performed in mega v6.06. This work helps to elucidate the etiology of the virus causing disease in the newly developed common bean cultivar with resistance to BGMV by rna and goes further in the investigation of CPMMV distribution and potential impact in Brazil. Financial Support: CNPq.

PIV416 - HOMOLOGY MODELING OF TOSPOVIRUS NUCLEOPROTEIN: STRUCTURE AND FUNCTION

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The rapid progress in the understanding of protein folding mechanisms and the advances in the bioinformatics field have provided reliable tools to modeling and predict three dimensional structures of plant virus proteins. recently, the nucleoprotein (np) crystal structures of related rna virus families (arena/orthomyxo/bunyaviridae) were elucidated and despite having different sizes and distinct np-folding structures, these proteins share common features and architectural principles when forming np-np multimers and np-rna complexes. therefore, due to their genetic relationship, the la crosse virus (lacv-orthobunyavirus) crystal structure in complex with ssrna (pdb id 4bhh) was selected as template for a homology modeling approach to predict a three dimensional model for the np of the tospovirus groundnut ringspot virus (grsv). the grsv np monomer was predicted to possess thirteen helical segments and two small beta-sheets organized in a globular core domain (33-223 aa) containing a deep positively charged groove with the two terminal chains forming a n-terminus arm (1-32 aa) and a c-terminus arm (224-258 aa). both n- and c-arms extend outwards from the globular core domain and they interact with the globular core domain of neighboring monomers to mediate the multimerization, supporting the "head-to-tail" model. the rna is primarily bound at the central rna-binding groove and the key residues for this interaction are mainly located in this groove. rna is strongly bent at each np-np interface and is largely solvent-inaccessible in the tetramer structure. the