PL 2 - ANALYSIS OF AN ISOLATE OF *CUCUMBER MOSAIC VIRUS* (CMV) FROM SWEET PEPPER.

Boari, A.J.*; Figueira, A.R.; Oliveira, F.A.; Moraes, F.H.; Santos, R.C.; Silva, O.A. (Dep. de Fitopatologia/ UFLA, Lavras, MG) *E-mail: ajb@ufla.br

One plant of sweet pepper was sampled from Pará de Minas, Minas Gerais State, to be analyzed for the presence of yellow mosaic and leaf deformation. When tested by DAS-ELISA method, using Agdia polyclonal anti-serum, extract of sweet-pepper leaves reacted positively to CMV. In addition, when mechanically inoculated on leaves of pumpkin "Caserta", *Chenopodium quinoa* and *Nicotiana tabacum* TNN induced the typical symptoms of CMV, being called CMV-CA21. The molecular characterization was done by RT-PCR and nucleotide sequencing. Fragments of DNA of about 0.5 kb, which correspond to approximately 2/3 of the capside protein of the gene (N) and part of the region 3' – non translated of RNA3' from isolates of CMV-CA21 and control isolates of CMV-I (Agr) and CMV-II (S), were amplified by RT-PCR technique. Digestion of PCR product by the *Eco*-RI and *Hind*-III enzymes caused no change on the restriction pattern, which was identical to the control (CMV-I). However, restriction with *Msp* I caused a different pattern as compared to CMV-I and CMV-II controls. Differences on the restriction pattern of the isolate CMV were also found by Boari et al. (Fitopatologia bras. 26:49-58, 2000) on isolates of sweet-pepper plants, considered as CA-8 using Eco-RI enzyme. Despite the differences in restriction pattern, CMV-CA21 was classified as sub-group I, based on nucleotide sequencing of the fragment from PCR. Between 91 and 93% nucleotide homology was observed for several isolates from sub-group I. Phylogenetic analysis showed that this isolate is far way from the other isolates of sub-group I, showing the great variability in this sub-group.

Financial support: CBP&D-Café, CNPq and FAPEMIG

PL 3 - CHARACTERIZATION OF BRAZILIAN POTYVIRUS ISOLATES FROM TOMATO AND SWEETPEPPER.

Cunha, L.C.V.[1,4], Resende, R.O.[1,5]; Nagata, T.[2] and Inoue-Nagata, A.K.[3]* ([1]Dep. Fitopatologia, UnB, Brasília, DF; [2]Biotecnologia Genômica, Universidade Católica de Brasília, Brasília, DF; [3]Embrapa Hortaliças, Brasília, DF). *E-mail: alicenag@cnph.embrapa.br

Information on virus variability in the field is extremely important to support breeding programs. Based on this demand of information, the present study aimed to characterize four field potyvirus isolates found naturally infecting sweetpepper (Sa66 and Sa115) and tomato (IAC3 and Sa21). Their biological characteristics, such as: 1) IAC3 did not infect *Capsicum annuum* 'Magali' and 'Serrano Vera Cruz'; 2) Sa21 was not able to infect 'Magda' cultivar and it showed high infectivity on tomato genotypes; and 3) the severe symptoms of sweetpepper genotypes with Sa66, showed to be significantly distinct from the ones observed for *Pepper yellow mosaic virus* (PepYMV) and *Potato virus Y* (PVY), both found in Brazil. These characteristic enabled the rough splitting into two groups. The first group comprised the sweetpepper isolates, which were more severe to sweetpepper cultivars and less infective to tomato genotypes. The second group with tomato isolates appeared to be more adapted to tomato plants. Serological studies showed absence of reaction of the isolates studied with PVY antiserum. However, all isolates reacted positively, in different reaction intensities, with antiserum against PepYMV. Nucleotide and amino acid (aa) sequences of the coat protein (CP) and the 3' untranslated region (3'-UTR) were determined and compared. All isolates showed high identity percentage (97 to 99%) of the CP aa with PepYMV (accession AF48610) and low (69 to 80%) with other potyvirus species. The high homology found indicated that the four isolates studied belonged to PepYMV species. The comparison of the 3'-UTR also confirmed this finding (homology of 97 to 98% identity with PepYMV and of 47 to 71% with other potyviruses). The phylogenetic tree obtained based on CP aa sequences showed that the isolates were grouped according to the original host. These results suggested that the tomato isolates might form a different group within PepYMV, possibly a distinct strain from pepper isolates.

Financial support: Embrapa and CNPq; [4]CAPES fellowship; [5]CNPq fellow

PL 4 - CHARACTERIZATION OF THE COAT PROTEIN GENE OF *GRAPEVINE VIRUS* A FROM KOBER STEM GROOVING-AFFECTED GRAPEVINES IN SÃO PAULO STATE, BRAZIL.

Moreira, A.E.[1]*, Gaspar, J.O.[1], Kuniyuki H.[2] and Camargo, L.E.A.[3] ([1]IBILCE/UNESP, São José do Rio Preto, SP; [2]IAC, Centro de Fitossanidade, Campinas, SP; [3]ESALQ/USP, Piracicaba, SP). E-mail: gaspar@bot.ibilce.unesp.br

The Kober stem grooving disease ("acanaladura do lenho de Kober") of grapevines has been associated with the *Grapevine virus A* (GVA). In Brazil, the disease was first recognized in 1992 in plantations of 'Niagara Rosada' in Jundiaí, São Paulo State, and, more recently, the presence of GVA in grapevines affected by the Kober stem grooving was further confirmed by ELISA (Kuniyuki et al., Summa Phytopatol. 27: 117, 2001). The virus, a type species of the Vitivirus genus, has filamentous particles about 800 nm in length and contains a single stranded, positive sense RNA genome with five open reading frames. Here we report the characterization of the coat protein gene of a Brazilian isolate of GVA (GVA-SP). RNAs were extracted from leaves and petioles by using the Qiagen RNeasy plant extraction kit. Primers were designed to amplify a fragment between positions 6409 and 7175 of the