## Embrapa Hortalicas SIN -Biblioteca

#### ROUND TABLES

it was shown that coat protein and CoLV-associated RNAs were not present inside the chloroplasts.

### Financial support: FAPESP

2 - TECHNIQUES AND METHODS FOR ELUCIDATION OF PLANT VIRUS INSECT VECTOR RELATIONSHIPS: THE BRAZILIAN EXPERIENCE. Costa, C.L. (Departamento de Fitopatologia, Universidade de Brasília, CEP 70919-900 Brasília, DF)

Vectors, biological agents of dissemination, transmission and inoculation of plant viruses, participate in complex interactions with the viruses and are found in distinct group of organisms: insects and mites, aerial vectors, zoosporic fungi and plantparasitic nematodes, the soil-borne vectors. Thirty five percent of recognized plant virus groups have at least one of their members transmitted by a vector. The relationships between virus and insect vector are of two types: (a) noncirculative in which virions are carried in the insect feeding apparatus and can be inoculated into healthy plants immediately after been acquired from the infected ones, without any incubation period, but transmissibility is lost soon after insect makes the first inoculation probe (a no persistent mode of transmission); (b) circulative in which virions are acquired when the insects take-up sap from xylem tissues of infect plants, enter the homocoel, accumulate in the accessory salivary glands and are released into cells of the xylem tissues of healthy plants together with the secreted saliva, after an incubation period of hours or days. Once this is completed the insect can transmit the virus for life (a persistent mode of transmission). In the last years, the understanding of these two types of plant virus interactions with their insect vector experienced great progress due to introduction of new techniques and methods of studies such as PCR and ELISA tests, insect feeding through membranes, electrical penetration graphs (EPG), genome and point mutation analysis. New information on topics like the genetic determinants of the transmission, identification of cellular receptors for the virus in the insect vector and the involvement of proteins in processes like virus acquisition, retention, passage through gut wall to hemocoel and liberation for inoculation via salivary system of sucking insects is being made available constantly. The relationships of leaf beetle transmitted viruses with their vectors are now much better understood, as well. The Brazilian experience on these studies is faintly compared world widely, because of the lack of concern of the researchers on the subject.

### 3 - PRESENT STATE OF KNOWLEDGE ON PASSION FRUIT WOODINESS AND CUCUMBER MOSAIC VIRUSES IN PASSION FLOWER IN BRAZIL.

Rezende, J.A.M.; Novaes, Q.S. and Gioria, R. (Dept. Entomologia, Fitopatologia e Zoologia Agrícola, ESALQ/USP, Cx. P. 09, 13418-900 Piracicaba, SP, Brazil). <u>E-mail: jamrezen@esalq.usp.br</u> Seven viruses have been reported infecting passion flower (Passiflora edulis f. flavicarpa Deg.) crops in Brazil. Among them, Passion fruit woodiness virus (PWV) and Cucumber mosaic virus (CMV) are the most frequent, although PWV causes the greatest damage. Passion flower infected with PWV showed up to 50% reduction in leaf area and fresh and dry weight of upper part and root system. Yield loss and reduction on leaf area were directly related to the age that the plant was infected. Plants infected with PWV at 2, 4, 6 and 8 months after transplanting had average yield of 2.4, 3.4, 6.9 and 12.9 kg of fruits, respectively. Further more, the number of woody and industry fruits was drastically reduced on later infected plants. Attempts to control the disease by cross protection has failed. Selected mild strains of PWV did not protect passion flower against superinfection with severe strains of the virus. However, the same mild strains offered full protection in Crotalaria juncea L. Studies on virus concentration in these two hosts showed an even distribution of the mild strains in the leaf tissues of passion flower. Present recommendations to minimize the damage caused by PWV, specially in areas of high incidence of the virus, include elimination of old infected crops, planting in partially isolate area and systematic elimination of PWV infected plants, during the first 6 to 8 months after transplanting. Nucleotide sequence of the coat protein gene of mild and severe strains of PWV, collected in São Paulo State, showed 96% homology. Comparative analyzes with other potyviruses in the GenBank, showed 88 - 93% identity with the coat protein gene of Cawpea aphid borne mosaic virus, South African passiflora virus and Crotalaria mosaic virus. This result corroborates previous report (Santana et al. Virus Ver. Res. 47:153, 1999), suggesting that further studies are necessary for appropriate taxonomic placement of the Brazilian PWV. Infection with CMV is easily identified in the field based on the symptoms, which are characterized by bright yellow mottling on leaves, starting at random points on the vine and diminishing in intensity towards the tip, which becomes symptomless as it grows. Studies to determine whether symptomless portions of the vine are CMV free or represent latent infection were carried out by biological, serological, PCR and dot blot hybridization assays. Results showed that CMV was restricted to symptomatic portions of the vines. The mechanism responsible for remission of symptoms accompanied by CMV disappearance is still unknown. Whatever mechanism is involved, this apparent genetic trait should be maintained in any breeding program for this species. Any change in this trait, which would allow the virus complete and permanent invasion of passion flower plants, would certainly turn CMV into a very destructive pathogen for this crop.

### AINFO

**4 - FROM "VIRA-CABEÇA" TO TOSPOVIRUS: 66 YEARS OF TOSPOVIRUS RESEARCH IN BRAZIL.** Resende, R.O<sup>1\*</sup>; Ávila, A.C.<sup>1,2</sup>. Kitajima, E.W.<sup>3\*</sup> (<sup>1</sup>Universidade de Brasília, <u>rresende@unb.br</u>, <sup>2</sup> Embrapa Hortaliças; <sup>3</sup>ESALQ-USP). Originally described in 1930 in Australia, early reports of the tospoviruses in Brazil dates back to 1936 and the formal identification as tomato spotted wilt virus (TSWV) was made in 1941 by Costa & Forster. These diseases were commonly referred to as "vira-cabeça" (curved head) because of the apical shoot death. Subsequent works by Costa's group at the Instituto Agronomico, Campinas, demonstrated that TSWV is transmitted by thrips, being widespread in the country causing sometimes devastating diseases in crops as tomato, tobacco and lettuce; it also produced early works on he morphology and cytopathology of TSWV. In the last 15 years the knowledge on tospovirus has increased significantly. The establishment of new species, determination of genome organization as well as protein expression and function (virus polymerase, the movement protein, proteins involved in virus transmission) are examples of these contributions. More recently, the insights obtained on the mechanisms of virus transcription, virus pathway and receptors in the insect vector, generation of resistant plants by using pathogen derived resistance (PDR) and host genes as SW5, constitute remarkable advances on tospovirus research. On this context, Brazilian researches have been contributing with significant amount of data. The very fruitful cooperation with the Virology Group of the Wagenigen Agricultural University has provided expertise and facilities to produce high quality researches by the Brazilian Groups working with in Brasília. As the main contributions from these groups we can point out the characterization of several tospoviruses, particularly virus species (6 out the 13 species proposed were originated from Brazil), the elucidation of nucleotide and amino acid sequences of several N genes and NSm (movement protein) genes, the generation and biological role of virus defective RNAs, molecular and biological aspects of virus/vector relationship, cytopathology and virus assembly during infection, and the use of host resistance genes as SW5 to generate broad resistance against tospoviruses and to understand resistance mechanisms to virus infection. It is worthy to mention that the type species of tospovirus genus TSWV, BR-01 isolate, fully characterized, was isolated in Brasília. Among plant viruses, the research on tospoviruses carried out in Brazil can be considered as one of most significant examples of a Brazilian contribution to the plant virus research world.

### ROUND TABLE 6 – HTLV: BIOLOGY OF THE VIRUS AND CLINICAL ASPECTS

### 1 - NATURAL HISTORY OF HTLV-I/II: ACOHORT STUDY IN BELO HORIZONTE, MINAS GERAIS.

*Catalan Soares, B.C.* (Fundação Hemominas, Belo Horizonte, MG)

Little is known about the natural history of HTLV infection, which may be variable with viral and host factors, as well geographical origin of the infected subjects. The type I is associated to disabling and

#### ROUND TABLES

fatal diseases, yet there is no satisfactory treatment and the means of assess risk of diseases and prognosis are limited. Cohort studies are useful to address these questions, specially if they are multicentric. Although cohort studies are very expensive and of long duration, they provide answers that would not be feasible otherwise. Blood donors in Brazil have been routinely screening for the Human T-cell lymphotropic virus (HTLV-I/II) since 1993. The HTLV-I/II serostatus is confirmed using enzyme linked immunosorbent assay (Elisa), Western blot (WB) and polymerase chain reaction (PCR). In our experience with GIPH (Interdisciplinary HTLV-I/II Research Group), an open prevalent cohort started at Fundação Hemominas in March 1997, we are following up blood donors with positive or indeterminate serological results; a group of seronegative blood donors is part of our study too, as a control. The aim of this study is to determine and quantify epidemiological, clinical and laboratories features that may be associated with HTLV infection in a such low risk population. At least each two years the subjects are evaluated concerning these aspects and you intent follow these group for 20 years. After five years of follow up the population being studied consists of 662 subjects: seropositive (n = 298), seroindeterminate (n=245) and a negative control group (n=119). In multinomial logistic regression model seropositivity to HTLV was associated to age, sex, blood transfusion, education attainment and use of illegal drugs. Dermatological exam (biopsy) showed significant higher lesions frequency in HTLV positive subjects 49.2% (63/128) versus 12,0%(13/108) indeterminates subjects. Ophthalmologic examination (n=317) found two cases of HAU (0,63%). Keratoconjunctivitis sicca was not significantly associated with the infection. The phenotype and mRNA cytokine profile of peripheral blood leukocytes points toward the inability of the positive group to mount type 2 immune response. These results illustrate the benefits of cohort studies with the multidisciplinary approach of the infected individuals. We suggest the importance of other centers, specially those located in higher prevalence areas in South America to conduct such studies, to better understand the natural history of HTLV infection.

# 2 - HTLV-I AND SUPPRESSOR GENE P53 AND P16 IN ATL.

Pombo de Oliveira, M.S.\*; Cavalcanti Jr, G.B.; Fernandes, M.A.; Rios, M. (Instituto Nacional de Câncer, Rio de Janeiro, Brazil)

*P53* and *P16* genes are regulators of cell cycling. Mutation and/or deletion in these genes are associated with malignancies. The mechanisms of HTLV-I mediated cellular transformation into adult T-cell leukemia (ATL) are not clearly understood due to the multi-step process and the long latency time between infection and malignancy. However, events such as HTLV-I proviral deletions, loss of down regulation of viral transcription activators, and *p53* and/or *p16* genetic alterations have been implicated in ATL pathogenesis. HTLV-I encodes a 40kD