

MOLECULAR CHARACTERIZATION OF CTV ISOLATES IN URUGUAY: A PICTURE FROM THE PAST COMPARED TO PRESENT

María José Benítez Galeano¹, Leticia Rubio², Fernando Rivas², Ana Bertalmío², Diego Maeso², Rodney Colina¹.

¹ *Molecular Virology Lab, North Headquarters, University of the Republic, Uruguay.*

² *National Agricultural Research Institute (INIA), Salto Grande, Uruguay.*

Since its appearance two centuries ago, Tristeza has been classified as the most devastating viral disease which affects citrus worldwide. Its causative agent, Citrus Tristeza Virus (CTV), is transmitted by infected grafts or by insect vectors such as the aphid *Toxoptera citricida*. In all affected citrus growing areas, it has been reported the existence of genetic variants of the virus with different degrees of severity. Characterization of CTV isolates can provide epidemiological information and can be useful for disease control. The presence of CTV and its most efficient vector has been described in Uruguay since the 40s. However, there are no data, based on molecular biology, reflecting genetic variants circulating in the country. In the present study, using RT-PCR amplification of three regions of the CTV genome (p20, p23 and p25), we established phylogenetic relationships of the strains circulating in the country at present time and 20 years ago. The samples used were collected in 1990 and maintained *in planta* in free vector greenhouses, and also were compared with current field samples. This valuable historical collection provides a sample of past CTV occurrence in Uruguay. The results show that circulating strains in the country are severe and unsurprisingly resemble strains reported in Argentina. However, some of the strains under study are similar to reference strains of Israel or Hawaii. This may reflect the introduction of infected buds or trees in the past time of the country.