

designed on identified RNA virus sequences. As result, the metagenomic data analysis revealed mainly the presence of sequences matching RNA viruses including viral species that infects arthropods. Financial Support: CAPES, EMBRAPA.

PIV48 - BEGOMOVIRUS DIVERSITY IN RESISTANT AND SUSCEPTIBLE TOMATO PLANTS

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Tomato (*Solanum lycopersicum*) is one of the main vegetables grown in the world, but the occurrence of plant diseases can cause substantial production losses in this crop. Begomovirus infections (family *Geminiviridae*) generally occur at high frequency in tomatoes, posing serious constraints to its production in Brazil. Currently, the use of resistant cultivars is the most effective method for controlling begomovirus diseases, even though these plants are only moderately resistant and thus not immune. Our aim was to perform a preliminary assessment of the diversity of begomoviruses in resistant (cv. BRS Sena) and susceptible (cv. H-9553) tomato cultivars. Therefore, 117 symptomatic leaf samples from both cultivars were collected in the same field at the municipality of Luziânia-GO. A total of 45 samples were collected from symptomatic plants of the hybrid H-9553, and 72 samples for the hybrid BRS Sena, since begomovirus infection symptoms in resistant plants are milder and more difficult to identify than in susceptible cultivars. Viral infection was confirmed by PCR using universal begomovirus degenerate primers. Fifty-six resistant (77% tested positive) and 44 susceptible (97%) tomato samples were PCR-positive for the presence of begomoviruses. The viral DNA from these samples was further amplified by rolling circle amplification and subsequently digested with *MspI* restriction enzyme, in order to visualize the polymorphism in the viral genome restriction profiles. Seven different profiles were observed, being the pattern of *Tomato severe rugose virus* the predominant. This begomovirus species is considered to be the most prevalent in the tomato crop in Brazil. Variations in the restriction profiles indicate the presence of different viral species/strains/variants in the collected tomato plants. Additionally, two profiles appeared exclusively in resistant plants, while two

others only in susceptible plants. These results suggest the existence of differences between viral populations present in resistant and susceptible plants. Subsequent cloning and complete genomic sequencing of these viruses will allow the species identification, unravel their genetic diversity, and determine if the expansion of the use of resistant cultivars may result in changes in the virus population composition in the field. Further characterization of the variants present in resistant plants may provide insights to the durability and efficiency of the resistance genes in tomatoes. Financial Support: CNPq, FAPDF, EMBRAPA Hortaliças.

PIV58 - MYCOVIRUS DETECTION AND IDENTIFICATION IN *Hevea brasiliensis*

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Hevea brasiliensis is the best producing plant of latex and natural rubber in the world. This plant species is susceptible to several diseases caused by fungi and viruses. In plant tissue, there are many symbiotic organisms that can interact and help in plant protection against pathogens, as the endophytic fungi. Mycoviruses commonly occur in endophytic fungi and they can play an important role in mutualistic interactions between the fungus and the host plant. The main mycovirus families are those with genome composed by double-stranded RNA: *Hypoviridae*, *Chrysoviridae*, *Totiviridae*, *Partitiviridae*, and *Reoviridae*. However, nothing is known about the impact of mycoviruses in *H. brasiliensis*. Thus, the study of the mycovirus diversity is an important and required scientific investigation. For this reason, the following approach is proposed: First, the endophytic fungi will be isolated from native rubber tree individuals