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Variability and genetic structure of emerging viruses in tomato crop in Cuba

Variabilidad y estructura genética de los virus emergentes en el cultivo del tomate en Cuba

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Climate changes, increasing mobility of humanity, indiscriminate use of pesticides, genetic resistance, crop rotation and cultural practices for reducing pests, have been combined to increase the risk of changes in ecosystems and the evolution of pathogens and their vectors causing the emergence of invasive pests. The aim of the present paper was to carry out a study on begomovirus populations present in tomato 20 years after the first detections of this pathogen. The results confirmed that *Tomato yellow leaf curl virus*, Israel strain (TYLCV-IL) was the predominant begomovirus in the cultivation of tomatoes and peppers in Cuba, with a distribution of 83.1% and 42.8%, respectively. Defective molecules of TYLCV-IL replication were characterized. Defective genomes associated with infection by TYLCV-IL (CU) were first described, with a complex structure including deletions, inversions, translocations and duplications of the viral genome fragments. Also, the appearance of new species of bipartite begomovirus in tomato and in associated weeds has caused high risk epidemiological situations for horticultural productions, increasing density and diversity of the vector populations. Mixed infection symptoms of more than one viral genus have been observed, coinciding with high vector populations. These studies will strengthen the phytosanitary surveillance and management programs being carried out in the country to control vector-borne diseases in crops of economic interest, mainly in tomato.