

particles. Given the trade-offs between functional complementation and independence among the distinct components in viruses with divided genomes, it would be expected that the different components would be in an intimate process of co-evolution. The genus *Begomovirus* (family *Geminiviridae*) is comprised of viral species with one or two genomic components of circular, ssDNA. Thus, begomoviruses include viruses with non-segmented as well as divided (bipartite) genomes. The bipartite nature of these viruses has been little explored in evolutionary studies, and little is known about the evolutionary dynamics of the different components. Using a population genetics approach, we performed a parallel evolutionary analysis of the two components (DNA-A and DNA-B) of five well sampled begomoviruses that infect cultivated and non-cultivated plants. Our results demonstrate that the DNA-B, as well as the DNA-A, segregates based on geographical origin. In most datasets analyzed, the DNA-B was more variable than the DNA-A. The exception was *Macropodium yellow spot virus* (MaYSV), for which the DNA-A was more variable than the DNA-B due to a recombination event at the interface between the Rep gene 5' region and the intergenic region. The DNA-B was more prone to recombination than the DNA-A, with a higher number of events. Interestingly, we detected small ORFs in the complementary-sense strand of the DNA-B of several MaYSV isolates. These ORFs are homologous to the Rep gene located in the DNA-A, indicating occurrence of intercomponent recombination events. Together, our results indicate the two components evolve under different selection pressures, and thus display distinct evolutionary histories. The higher degree of genetic variability of the DNA-B may reflect weaker selection pressures due to the fact the functions encoded by its proteins can, to some extent, be provided by the proteins encoded by the DNA-A.

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Palavras-chaves: geminivirus, begomovirus, molecular evolution, reassortment, recombination

CULTURAL PRACTICES EFFECTS ON A SOIL-BORNE WHEAT MOSAIC DISEASE IN SOUTHERN BRAZIL

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Resumo

There are several diseases affecting wheat crops, including viral diseases such as the Soil-borne wheat mosaic disease (SBWMD), responsible for damages that can reach up to 85%. The viruses associated with SBWMD are transmitted by *Polymyxa graminis*, a soil microorganism known to infect grasses roots. The use of resistant cultivars is the main management strategy recommended for this disease. However, in Brazil, there are no virus-immune cultivars and given the constant evolution of plant viruses, genetic-only management becomes uncertain in the long run. In this way, we investigated the effect of nitrogen (N) fertilization and crop rotation on SBWMD incidence and wheat grain yield in two different field experiments conducted at Embrapa Wheat in 2017. Wheat cultivars Embrapa 16 (resistant) and BRS Guamirim (susceptible) were submitted to four nitrogen doses in the form of urea (0, 30, 60 and 90 kg ha⁻¹) divided into two ontogenetic stages: double-ring and terminal

spikelet. As environmental conditions influence viral infection, the experiment was sown in three periods. The study of the effects of crop rotation was performed in an experiment established in 1980 by Embrapa Wheat. The crop rotation schemes were monoculture of wheat, oats-wheat, vetch-oats-wheat and oats-barley-oats-turnip-wheat. Parcels (120 m²) were divided into three sub-plots, and sown with BRS Parrudo (resistant), BRS Reponte (moderately susceptible) and BRS Guamirim (susceptible) cultivars. Experimental areas has a history of the presence of the vector and the virus and was confirmed by molecular test. The effect of N on the incidence of SBWMD was not evident. The incidence ranged from 0.5 to 17% for cultivar Embrapa 16 and 1 to 95% for cultivar BRS Guamirim. Productivity for cultivar BRS Guamirim was positively influenced by N doses when the incidence were below the 50% threshold. The sowing period with higher rainfall showed higher incidence of the virus. The incidence in the crop rotation experiment was very low (0-0.12%). In wheat monoculture, the incidence was significantly higher in relation to crop rotation, although it showed a weak correlation with grain yield (-0.37) for BRS Reponte cultivar. Cultural practices may be used as complementary tools for managing soil-borne viruses in wheat in southern Brazil. Financial Support: EMBRAPA, UDESC, CAPES.

Palavras-chaves: Polymyxa graminis, Crop rotation, Fertilization, Grain yield

TOMATO SEVERE RUGOSE VIRUS: A PREVALENT BEGOMOVIRUS SPECIES INFECTING POTATO IN THE CENTRAL REGION OF BRAZIL

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Resumo

Deforming mosaic disease caused by *Begomovirus* species (Family *Geminiviridae*) transmitted by whitefly (*Bemisia tabaci* biotype B) is an emerging disease affecting potato crop (*Solanum tuberosum* L.) that has been more often detected over the last ten years in Brazil. Despite of been detected at low incidence (, table potatoes and potatoes for the processing industry of different varieties, 45-50 days after planting of tubers and showing yellow mosaic, and leaf deformation symptoms. High whitefly populations were observed in the production fields considered for sampling. Leaf samples were submitted to total DNA extraction using CTAB method, Rolling Circle Amplification (RCA) with Phi-29 DNA Polymerase, followed by polymerase chain reaction (PCR)-based methods for begomovirus detection. The first PCR was performed using degenerate primers (PAL1v1978/PAR1c496; Plant Dis. 77:340-347, 1993) that amplify a 1.1 kbp fragment of DNA-A component. The second PCR was done with ToSRV-specific primers (Phytopathol. 103:436-444, 2013) that amplify 820 pb amplicon also of the DNA-A component. Cloning and sequencing of 15 isolates was performed. Begomovirus detection occurred in 150 samples out of 200 [DF: 89; Goiás: 61 (Cristalina-20; Luziânia-41)] using the universal primers indicating that begomovirus presence is associated with leaf deformation and yellow mosaic symptoms observed in diseased plants in the field. ToSRV-detection was also identified in the same number of samples, 150. Sequencing data confirmed data obtained from PCR using specific primers, and ToSRV was the only *Begomovirus* species identified in all 15 isolates sequenced. These data indicate the prevalence of this *Begomovirus* species infecting potato in the Central region of Brazil.

Palavras-chaves: Begomovirus, potato, detection, PCR, ToSRV

THE PLANTING POTATO WITH SCIENCE PROJECT (PPWSP): A VOLUNTEER FUNDAMENTAL SCHOOL SCIENCE EDUCATIONAL PROJECT USING POTATO VIRUSES TO BUILD PLANT PROTECTION CONSCIENCE