

PIV239 - IDENTIFICATION OF A POTATOINFECTING BEGOMOVIRUS IN THE CENTRAL REGION OF BRAZIL

Lima, M.F.; Ribeiro, S.G.; Inoue Nagata, A.K.; Nakasu, E.Y.T.

1. EMBRAPA RECURSOS GENÉTICOS
2. EMBRAPA HORTALIÇAS

Potato is one of the most important vegetable crops in Brazil. Production is concentrated mainly in three regions, South, Southeast, and CentralWest. Cristalina county, located in the state of Goiás, is considered as one of the major region for potato production in the country. In 2012, the production of potato reached 300,000 tons (10% of national share) in 6,000 hectares planted in Cristalina. Monitoring potato plants exhibiting begomoviruslike symptoms has been performed in potatogrowing areas since 2011. The incidence of symptoms in potato fields was generally low during 20132014 growing seasons. The objective of this work was to identify begomovirus species infecting potato plants in the central region of Brazil. Leaf samples were collected from 20 plants showing yellow mosaic and leaf deformation symptoms in potatogrowing fields, 50 to 60 days after planting, at Cristalina in 2014. Total DNA was extracted from samples and tested by polymerase chain reaction (PCR) using degenerate begomovirusgroup specific primers, which amplify a DNA fragment of ca. 1.1 kbp of the A component. Ten begomoviruspositive samples were selected to Rolling Circle Amplification (RCA) using Phi 29 DNA polymerase. RCA products were digested with restriction enzymes and Hind III was selected for cloning the genome. RCA digested products were electrophoresed on 1.2% agarose gel and a DNA fragment of ca. 2.6 kb was gelpurified, and cloned into pBluescript vector. Out of the 20 samples, 15 were positive by PCR, showing a ca. 1.1 kb DNA amplicon. Initial sequences of 750 bp, from DNAA of all ten selected samples, share from 94% to 98% nucleotide identity with Tomato severe rugose virus (ToSRV), a pathogen that primarily infects tomato. It is concluded that ToSRV is likely to be the predominant begomovirus in potatoes in the Cristalina region.

PIV240 - VIRAL BIODIVERSITY IN PLEBOTOMINAE CAPTURED IN PANTANAL AND CHAPADA DOS GUIMARÃES OF MATO GROSSO, BRAZIL

Carvalho, M.S.; de Lara Pinto, A.Z.; Rodrigues, J.S.V.; Ribeiro, A.L.M.; Melo, F.L.; Dezengrini Shlessarenko, R.

1. UNIVERSIDADE FEDERAL DE MATO GROSSO
2. SECRETARIA DE SAÚDE DE MATO GROSSO
3. UNIVERSIDADE FEDERAL DE BRASILIA

Arboviruses transmitted by phlebotominae present considerable medical importance, since many were isolated from these arthropods and humans in the Brazilian Amazon. This study was conducted to investigate the viral biodiversity in phlebotominae captured with CDC traps in two sylvatic areas of Cerrado of Mato Grosso containing RAPELD systems: the Chapada dos Guimarães National Park (PNCG, Rio Claro) and North Pantanal (Pirizal) during the rainy, intermediate and dry seasons of 20142015. After identification with a specific dichotomy key, 105 specimens (90 belonging to genus *Lutzomyia* [*L. witmani*, *L. evandroi*, *L. carmelina* and *L. sherloki wilsoni*], and 15 to genus *Brumptomyia*) were allocated 11 pools. These pools were minced and, subjected to viral RNA extraction, reverse transcription, synthesis of the second strand of cDNA and PCR amplification with viral randomic primers (random-KS). The purified and quantitated DNA product was sequenced by illumina HiSeq 2500 platform. Partial analysis of contigs obtained from five pools of *Lutzomyia* sp. revealed hits with sequences of vesiculovirus, pegivirus, flavivirus, phlebovirus, nairovirus and tospovirus. Since the whole arthropod was used in the experiment, is possible that some of these sequences originated from their gastrointestinal contents or either from their exterior parts in contact with plants and animals.