

this knowledge gap, we used high-throughput sequencing (HTS) to examine the diversity and distribution of YDVs in cereals and grasses in south-eastern Australia. Our results show that Australian YDV isolates are much more complex and diverse than is currently suggested in the literature, both between and within species. Based on these results, new diagnostic tests are being designed to further examine the distribution of different YDV species in Australia, which will help us better understand this complex group of viruses. The information obtained in this study is critical for the more targeted development of virus-resistant cultivars.

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STRONGER TOGETHER: SYNERGY BETWEEN AN EMERGING MONOPARTITE BEGOMOVIRUS AND A DNA?B COMPONENT

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Text

In recent decades, a legion of monopartite begomoviruses transmitted by the whitefly has emerged as serious threats to vegetable crops in Africa. Recent studies in Burkina Faso reported the predominance of pepper yellow vein Mali virus (PepYVMLV) and its frequent association with a previously unknown DNA?B component. To understand the role of this DNA?B component in the emergence of PepYVMLV, we assessed biological traits related to virulence, virus accumulation, location in the tissue and transmission. We demonstrate that the DNA?B component is not required for systemic movement and symptom development of PepYVMLV, but that its association produces more severe symptoms including growth arrest and plant death. The increased virulence is associated with a higher viral DNA accumulation in plant tissues, an increase in the number of contaminated nuclei of the phloem parenchyma and in the transmission rate by *B. tabaci*. Our results suggest that the association of a DNA?B component with the otherwise monopartite PepYVMLV is a key factor of its emergence. To assess the impact of this DNA-B component on the structure of the geminivirus community, grid-based sampling and the use of metagenomic protocols allowed obtaining of complex networks. Further analysis of our networks using genome sequences showed the presence of nestedness and modularity. This support the need to continue studies of the virus-plant system.

Keywords: Begomovirus,disease, etiology, Tomato, Burkina Faso.

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IMPACT OF PLANT IMMUNITY ON VIRUS ADAPTATION: WHAT EVOLUTIONARY FORCES SHOULD WE RELY UPON IN PLANT BREEDING?