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Text

What occurs when virus infection is spreading within a mixed plant species population? This question is important not only for environmentally significant mixed wild species populations but also for economically significant, mixed species managed systems. This contribution re-interprets examples of past research on mixed species managed pasture done over two decades on three continents that demonstrated plant species balance changes arising from virus infection. These examples showed that plants belonging to susceptible pasture cultivars sensitive to systemic virus infection are sufficiently weakened that their ability to withstand competition from non-host plants of other pasture species, or weed species, was decreased sufficiently to alter the plant species balance. Also, a similar alteration occurred when they were competing with virus-resistant or virus-tolerant host plants of the same or other pasture species, or a virus-resistant weed species. Such competition also diminished seed production, which decreased their ability to regenerate. Notably, when two different pasture species infected by the same virus compete with each other, growth of the more sensitive species is suppressed. Because managed mixed species pastures constitute an important component of regenerative agriculture, retaining an optimal balance of pasture species and delaying pasture decline from weed invasion both require effective management of virus diseases.

C4.4-3

VIROME RELEASE OF AN INVASIVE EXOTIC PLANT SPECIES IN SOUTHERN FRANCE

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Text

The increase in human-mediated introduction of plant species to new regions due to global travel and globalization has resulted in a rise of invasive exotic plants (IEPs) that can have significant effects on biodiversity, ecosystem processes, and food production. The introduction of IEPs to new regions often occurs through seed dispersal, and most pathogens

are not vertically transmitted, leading to low viral loads in these plants. Also, most pathogens are not evenly distributed across the Earth, meaning that IEPs colonizing a new territory are unlikely to encounter pathogens from their native range. This situation, referred to as the "enemy-release hypothesis" suggests that decreased pathogen-mediated selective pressures on IEPs in colonized territories will result in increased IEP populations, densities, and geographical distributions. To test the enemy-release hypothesis, the virome of an invasive cane bluestem (*Bothriochloa barbinodis*) was compared to that of four or more indigenous grass species in both naturalized and native ranges. The results showed that the IEPs had lower viral infection loads than the native grasses, providing evidence that supports the enemy release hypothesis. Novel viruses associated with *Bothriochloa barbinodis* were further partially or fully sequenced and the phylogenetic relationships of these viral sequences and representative sequences of corresponding virus families were analyzed.

C4.4-4

OCCURRENCE AND PREVALENCE OF SCHLUMBERGERA VIRUS X IN DRAGON FRUIT CROPS IN ECUADOR

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Text

Dragon fruit is a unique and highly sought-after fruit grown in many parts of the world, including Ecuador. In recent years, its cultivation has grown in popularity among farmers, as it is a highly profitable crop due to its domestic and international demand. Despite the growth in dragon fruit production, Ecuador faces challenges such as emerging pests and diseases and the lack of knowledge on their management and prevention. Emerging viruses are responsible for reductions in yields in many crops if they are not prevented and adequately managed. Cladodes exhibiting symptoms of irregular and ring-shaped chlorotic spots and mild chlorotic yellow spots were collected from farms in three coastal provinces and the main production area in the Amazon region of Ecuador. Schlumbergera virus X (SchVX), a potexvirus, was detected in more than 90% of tested cladodes, including symptomatic and asymptomatic samples of the two major dragon fruit species (*Hylocereus undatus* and *H. megalantus*) cultivated in the country. The symptoms presented differed among the species and were more severe on *H. undatus*. Phylogenetic inferences based on the partial nucleotide sequence of the RNA-dependent-RNA-polymerase (RdRp) showed that SchVX isolates found in *H. undatus* and *H. megalantus*, regardless of the field location, share a most recent ancestor with isolates from Spain and Portugal. Additional assays on the mechanical transmission of the virus are underway and will be further discussed.

C4.4-5

FACTORS INFLUENCING EPIDEMIOLOGY AND SPREAD OF WHITEFLY-TRANSMITTED CUCURBIT VIRUSES IN THE UNITED STATES VARY AMONG PRODUCTION REGIONS