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S2-P6

Pineapple is the third most cultivated tropical fruit crop in the world and the leading fruit production sector in Reunion Island, where Queen Victoria pineapple (*Ananas comosus*) is the flagship local fruit for export. However, pineapple plantations throughout Reunion have been affected by an upsurge of pineapple mealybug wilt disease (PMWD) for several years. Data available from the literature suggest that the etiology of PMWD involves a complex of viruses (1). We characterized the virome of symptomatic pineapple leaf samples collected from plantations throughout Reunion Island, using second (Illumina, HiSeq) and third generation (Oxford Nanopore Technologies, MinION) sequencing tools. Our results show the presence of up to nine distinct viruses in the analyzed samples. Seven viruses were characterized previously and belong to families *Closteroviridae* (PMWaV1, -2, -3, -5 and -6), *Caulimoviridae*, (PBCoV) and *Secoviridae* (PSVA). Two new viruses were characterized: pineapple mealybug wilt-associated virus 7 (PMWaV7) belong to genus *Ampelovirus* (family *Closteroviridae*) and pineapple vitivirus A (PinVA) to genus *Vitivirus* (family *Betaflexiviridae*). Our results underline the existence of an important viral community potentially associated with PMWD in Reunion. They stress out the importance of developing accurate diagnostic tools to assess the sanitary status of pineapple in Reunion and the need to implement the use of certified pineapple planting material to control the spread of PMWD.

Reference

(1) Dey, K., et al. (2018). Horticulturae, 4: 52.