



First report of *Pineapple mealybug wilt associated virus-1* in Ecuador

R.A. Alvarez¹, R.R. Martin² and D.F. Quito-Avila^{1,3*}

¹ Centro de Investigaciones Biotecnológicas del Ecuador (CIBE), ESPOL Campus Gustavo Galindo Km 30.5 vía Perimetral, Guayaquil-Ecuador; ² USDA-ARS, Horticultural Crops Research Unit, Corvallis OR United States 97331; ³ Programa Prometeo-Senescyt, Quito-Ecuador

*E-mail: diego.quito.avila@gmail.com

Received: 27 Feb 2015. Published: 11 Apr 2015.

In Ecuador, where pineapple represents one of the most important export commodities, virus testing has been neglected. In July 2014, a total of twenty MD2 hybrid pineapple plants showing virus-like symptoms (Fig. 1) were collected from a commercial planting located at the border of Santo Domingo and Los Rios provinces, where most of the pineapple in Ecuador is grown. Double-stranded RNA (dsRNA) was extracted from 20 g batches of leaves as described by Morris & Dodds (1979). The dsRNA was heat-denatured and used as template to generate cDNA libraries using anchored-random primers. Sequencing of randomly amplified PCR products revealed the presence of *Pineapple mealybug wilt associated virus 1* (PMWaV-1). Partial sequences for the helicase (Hel) and the coat protein (CP) genes were re-sequenced using specific primers and deposited in GenBank under Accession Nos. KP728914 and KP728915, respectively. Diagnostic primers (PMWaV-1_EcF: 5'-CCAAGCGAGAGGAAGGAATGTAAG-3'; PMWaV-1_EcR: 5'-CTCTGAATAATTGCCGAAACTCGG-3') were designed to amplify a 217 nt fragment of the Hel gene. Upon confirmation of specificity, the primers were used to test 150 plants (75 symptomatic and 75 asymptomatic) collected from Santo Domingo and Los Rios provinces, where the MD2 hybrid is grown, and Guayas province, where 'Smooth Cayenne' is the cultivar of choice. Mealybugs (*Dysmicoccus* spp.) were prevalent in sampled fields. PMWaV-1 was detected in 33% and 77% of asymptomatic and symptomatic MD2 plants, respectively. In the cultivar

'Smooth Cayenne', the virus was detected in 37% and 65% of asymptomatic and symptomatic plants, respectively. These findings suggest the presence of additional virus(es) possibly associated with the observed symptoms, as has been reported elsewhere (Hernandez-Rodriguez *et al.*, 2014). Sequence alignments showed that PMWaV-1 from Ecuador is related most closely to Hainan isolate from China (KJ872494.1) with nucleotide identities of 99% and 98% for the CP and Hel genes, respectively. To the best of our knowledge, this is the first report of PMWaV-1 infecting pineapple in Ecuador.

Acknowledgements

The authors would like to thank the Ecuadorean Program PROMETEO-SENESCYT for financial support.

References

- Hernandez-Rodriguez L, Ramos-Gonzalez PL, Garcia-Garcia G, Zamora V, Peralta-Martin AM, Peña I, Perez JM, Ferriol X, 2014. Geographic distribution of mealybug wilt disease of pineapple and genetic diversity of viruses infecting pineapple in Cuba. *Crop Protection* **65**, 43-50. <http://dx.doi.org/10.1016/j.cropro.2014.07.003>
- TJ, Dodds JA, 1979. Isolation and analysis of double-stranded RNA from virus-infected plant and fungal tissue. *Phytopathology* **69**, 854-858.



Figure 1

To cite this report: Alvarez RA, Martin RR, Quito-Avila DF, 2015. First report of *Pineapple mealybug wilt associated virus-1* in Ecuador. *New Disease Reports* **31**, 15. <http://dx.doi.org/10.5197/j.2044-0588.2015.031.015>

©2015 The Authors

This report was published on-line at www.ndrs.org.uk where high quality versions of the figures can be found.