Occurrence of potato yellowing virus in naranjilla (*Solanum quitoense* Lam.) in Ecuador

Karla Ramos¹ · Yeturu Sivaprasad² · Fiamma Guevara¹ · Francisco Ochoa-Corona³ · William Viera² · Francisco Flores^{1,4}

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Naranjilla (*Solanum quitoense* Lam.) is a fruit native to Ecuador and Colombia. It is consumed mainly as fresh fruit or juice. The cultivated area in Ecuador is *ca.* 2,342 ha and the average yield is 6.04 t ha⁻¹ (MAG 2017). Starting in 2015, generalized chlorosis, inter veins-space yellowing or chlorotic areas and young leaf curling symptoms were detected in plants of *S. quitoense* in Tumbaco, Pichincha, in plants of common origin at the INIAP Experimental Farm, Ecuador. The occurrence of potato yellowing virus (PYV) was confirmed in symptomatic leaves, from INIAP experimental farm, by DAS-ELISA with PYV specific antiserum (Sivaprasad et al. 2015), eight out of ten plants tested positive. High throughput sequencing (HTS) was carried out on a pool of RNA from leaves of three different symptomatic plants. Total RNA was isolated using the PureLink RNA mini kit (Invitrogen), libraries were prepared with the TruSeq Stranded Total RNA LT Kit (Illumina) and sequenced with the Illumina NovaSeq platform. A total of 92 million 150-bp reads were obtained. After cleaning, deduplication, and host genome sequence elimination, sequences were assembled with Spades-V3.13. From a total of 134 503 contigs, 24 mapped to the PYV ge-

nomes with an average coverage of 1500X. These contigs were used to assemble the complete PYV RNA1, RNA2 and nearly complete RNA3 using Geneious-R11. Sequences were deposited in GenBank with accession numbers (MN544549–MN544551). Tobacco virus 2, potato leafroll virus, tobacco vein clearing virus, and tomato torrado virus were also found with a lower coverage, therefore the observed symptoms cannot be attributed to PYV only. The RNA dependent RNA polymerase gene (RdRp) was used for a phylogenetic analysis using BEAST under the LG+G model and a strict molecular clock. The phylogeny showed that the PYV isolate from naranjilla clustered with an isolate described in pepper from the same location in Tumbaco (KP772263) (Sivaprasad et al. 2015), but was distantly related with isolates from *Solanum phureja* from other locations in Ecuador (Silvestre et al. 2011). Moreover, the PYV RNAs have 80.1, 78.1 and 73.5 identity with *Fragaria chiloensis* latent virus, (NC_006566, NC_006567, NC_006568) which confirms that PYV as a distinct *Ilavirus* (family *Bromoviridae*). To our knowledge, this is the first report of PYV infecting *S. quitoense* as a new host.

✉ William Viera
william.viera@iniap.gob.ec

- ¹ Departamento de Ciencias de la Vida y la Agricultura, Universidad de las Fuerzas Armadas (ESPE), Sangolquí 170501, Ecuador
- ² National Institute of Agricultural Research (INIAP), Fruit Program, Tumbaco, Quito 170184, Ecuador
- ³ National Institute for Microbial Forensics & Food and Agricultural Biosecurity, Oklahoma State University, Stillwater, OK 74078, USA
- ⁴ Centro de Investigación de Alimentos, Facultad de Ciencias de la Ingeniería e Industrias, Universidad UTE, 170147 Quito, Ecuador

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