First Report of Cucurbit Chlorotic Yellows Virus Infecting Watermelon and Zucchini in the Canary Islands, Spain

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Funding: This work was funded by grants from Spanish Ministerio de Economía, industria y competitividad (RTA2017-00061-C03-02) and from Instituto Valenciano de Investigaciones Agrarias (IVIA) (51912), both co-funded by the European Regional Development Fund (ERDF). Plant Dis. 106:2006, 2022; published online as <https://doi.org/10.1094/PDIS-10-21-2296-PDN>. Accepted for publication 16 December 2021.

In July 2019, 11 watermelon (*Citrullus lanatus*) plants (six ‘Augusta negra’ and five ‘Kasmira’) and seven zucchini (*Cucurbita pepo*) ‘Marcado’ plants showing yellowing and vein clearing on the leaves were collected in Arico on Tenerife Island of the Canary Islands. Analysis with enzyme-linked immunosorbent assay (ELISA) with polyclonal antibodies using kits from LOEWE Biochemica GmbH (Sauerlach, Germany) detected cucurbit chlorotic yellows virus (CCYV) in four watermelon (two ‘Augusta negra’ and two ‘Kasmira’) plants and one zucchini plant. Reverse transcription-polymerase chain reaction (RT-PCR) with primers CCYV-CPs (5′-ATGGAGAAGACTGACAATAAA CAA-3′) and CCYV-CPas (5′-TTTACTACAACCTCCCGGTG-3′) (Hamed et al. 2011) yielded 750-bp DNA fragments, which were purified and directly sequenced by Sanger sequencing. The four CCYV sequences obtained from watermelon plants were identical and showed a 99.6% nucleotide identity with the CCYV isolate from zucchini. The nucleotide sequences of CCYV isolates 351/19 from watermelon and 361/19 from zucchini were deposited in

GenBank under accessions OK562588 and OK562589, respectively. BLASTn analysis showed high nucleotide identity, being greater than 99% with most worldwide CCYV isolates (AB523789, HM581658, JF502222, JF807053, JN126045-6, JQ904629, JX014262, KC990503-5, KC990507, KJ735450, KJ149806, KT946809, KT946816, KU507602, KX118632, KY400632-4, KY618799, LT716000, LT716003-4, MH477612, MH806868, MH819191, MN529560, MN815012-3, MT396249, MT048669, MW033301, MW584337, MW251342, MW521380, MW521381, MW584335-6, MW629380, MZ325848-9, and MZ405664), about 98% with two Saudi Arabian isolates (KT946810 and KT946815), and about 95% with three Iranian isolates (KC577201-3). These genetic relationships were confirmed with a phylogenetic tree inferred with the maximum likelihood method with 500 bootstrap replicates and the nucleotide substitution model HKY+G implemented in the program MEGA-X (Kumar et al. 2018). There is no correlation between geographic distance and genetic distance. CCYV is related to viruses in the genus *Crinivirus*, family *Closteroviridae* (Okuda et al. 2010). It is widespread and causes high economic losses (yield reduction and unmarketable fruits) in cucurbit crops from East Asia: Japan, China, Taiwan, and South Korea; North America (the U.S. states of California, Texas, Georgia, and Alabama); the Middle East: Sudan, Saudi Arabia, and Iran; and the Mediterranean basin: Egypt, Israel, Lebanon, Turkey, Greece, Algeria, and peninsular Spain (Chynoweth et al. 2021; Jailani et al. 2021; Kheireddine et al. 2019; Kwak et al. 2021). This is the first report of CCYV infecting cucurbits in the Canary Islands. The emergence of this virus poses a threat to the cucurbit crops in the Canary Islands and requires control measures to prevent its spread in Tenerife and the other Canary Islands.

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The author(s) declare no conflict of interest.

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Keywords: CCYV, *Closteroviridae*, *Crinivirus*, cucurbits, viruses and viroids

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