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DISEASE NOTES

First Report of Taro bacilliform CH virus (TaBCHV) on Taro (*Colocasia esculenta*) in Hawaii, U.S.A

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Citation

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Taro (*Colocasia esculenta* L. Schott), family Araceae, is a traditional tropical root crop grown for its edible corms and leaves. The crop also has significant cultural and export importance, particularly in Pacific island communities (Revill et al. 2005). Taro bacilliform CH virus (TaBCHV) is a putative member of the genus *Badnavirus*, family *Caulimoviridae* that was recently described on taro in China (Kazmi et al. 2015). In May 2016, the leaves of a taro plant showing feather-like chlorosis and mosaic symptoms were collected from the University of Hawaii's Waimanalo Research Station (21°20′13.9″ N, 157°42′50.6″ W) on the island of Oahu, Hawaii. Total RNA was isolated using the RNeasy Plant Mini Kit (Qiagen, Redwood City, CA), according to manufacturer's instructions. Randomly primed cDNA was synthesized and served as template in PCR using three primer sets targeting TaBCHV: TB1009-F (5′-GGCTCTGAGAGAAGAGCTAGC-3′) and TB1619-R (5′-ATGTGTATGAACTGCACTCTG-3′), which amplify a 611-bp region between ORF2 and ORF3; TB 2790-F (5′-ACGAGTAATCCGACCCGAAG-3′) and TB 3401-R (5′-TCTTTGATCCTTGGACCGAG-3′), which amplify a 612-bp region of ORF3; and TB 4653-F (5′-GTATGGAAAAATGATCATTG-3′) and TB 5171-R (5′-GGCCTAATAGTGCCAAGTTTG-3′), which amplify a 519-bp portion of ORF3. The symptomatic sample yielded a fragment of the expected size for each primer set. No

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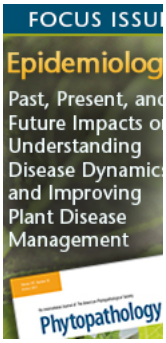

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amplification was observed in nontemplate control reaction. These amplicons were cloned using pGEM-T Easy (Promega, Madison, WI) and sequenced at the University of Hawaii's Advanced Studies in Genomics Proteomics and Bioinformatics laboratory. All sequences were most similar to the genomic sequence of TaBCHV. The 611-bp product (GenBank accession KY508687) shared 93% nucleotide (nt) sequence identity with the partial ORF2 and ORF3 of the published TaBCHV sequences (KP710177). The 612-bp product (KY508688) shared 98% nt sequence identity and 96% amino acid (aa) identity with the partial ORF3 of the published TaBCHV sequences (KP710177). The 519-bp product (KY508689) shared 91% nt sequence identity and 94% aa identity with the partial ORF3 of the published TaBCHV sequences (KP710177). To confirm the presence of TaBCHV in this sample, a DIG-labeled probe was generated using a PCR DIG Probe Synthesis Kit (Roche, Mannheim, Germany) spanning from position 324 to 1001 of the TaBCHV genome (NC_026819.1) for a dot-blot hybridization assay. Total RNA from the symptomatic plant sample tested positive using this assay, whereas total RNA samples from healthy controls tested negative. We conducted the RT-PCR assays on 12 additional randomly collected taro samples with or without clear symptoms from Oahu and confirmed the presence of TaBCHV in seven (58%) of these plants. However, there did not appear to be a correlation between the presence of TaBCHV and symptoms in the plants examined in this study. Kazmi et al. (2015) discovered TaBCHV in taro plants with leaves exhibiting a mild feathery mosaic and brown spots. There did not appear to be a correlation between the presence of TaBCHV and symptoms in the plants examined in this study. It is unclear how widespread TaBCHV is in Hawaii, if it is a recent introduction, or whether it arrived in the taro germplasm brought to Hawaii by Polynesian settlers. Studies examining the geographical and varietal distribution are needed to determine how widespread this virus is in Hawaii, whether this virus is integrated into the taro genome, and whether it is negatively impacting the local taro industry.

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