Diseases Caused by Viruses

First Report of Alfalfa Mosaic Virus in Chayote in Italy

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Chayote (*Sechium edule* [Jacq.] Sw.) is a vigorous perennial and climbing cucurbit, native to Mesoamerica, and cultivated for alimentary purposes in the American continent, Australia, New Zealand, South Europe, Asia, and Africa. During spring 2019, some chayote plants showing bright yellow vein banding, rings, and lines were observed in a private garden in South Italy (Campania region). Symptoms coalesced in some leaves, covering almost the whole foliar area. Double-stranded RNA was extracted from symptomatic leaves of a single chayote plant and reverse transcribed, randomly amplified, and submitted to Illumina sequencing (Marais et al. 2018). Reads were assembled using CLC Genomics Workbench 11.1 (<https://digitalinsights.qiagen.com/>). Contigs were then annotated by BLASTn and BLASTx comparison with the GenBank database, which allowed the identification of eight contigs of between 380 and 980 nucleotides (nt) sharing significant identity with alfalfa mosaic virus (AMV) genomic RNAs. No other viral contigs were identified. Mapping of reads on AMV genomic RNAs identified 4,209 AMV reads (1.26% of total reads) and allowed the scaffolding of the contigs into three scaffolds corresponding to the three AMV genomic RNAs. To complete the sequence of the AMV chayote isolate genome (named See-1), primers were designed from the contig

sequences and used to amplify rapid amplification of cDNA ends (RACE) polymerase chain reaction (PCR) products spanning the 5' and 3' terminal regions of the three genomic RNAs using the SMARTer RACE cDNA Amplification Kit (Clontech, China). All amplicons were cloned into the pGEM-T vector (Promega, U.S.A.) and sequenced (three clones for each amplicon) by Microsynth Seqlab (Microsynth, Switzerland). Finally, the complete genomic sequences of the three RNAs were assembled by MacVector 17.5 (MacVector, U.S.A.). The RNA1, RNA2, and RNA3 of See-1 are 3,643, 2,593, and 2,037 nt, respectively (GenBank accession nos. MT093209 to MT093211) and share the highest nt sequence identity with the RNA1 and RNA3 of AMV isolate (HZ) from tobacco (99.5% for RNA1, HQ316635; 98.7% for RNA3, HQ316637) and with the RNA2 of isolate AMV-Gym from *Gynostemma pentaphyllum* (98.1%, MH332898), both from China. AMV isolate See-1 was classified as belonging to subgroup I based on the presence of a *Bam*H I and two *Ava*II sites in the CP open reading frame (Parrella et al. 2000). Reverse transcription PCR, using primers targeting the CP gene (Parrella et al. 2000), confirmed AMV infection in three symptomatic chayote plants including that used for Illumina sequencing, with 100% of nt sequence identity of amplicons. Three plants each of *Chenopodium amaranticolor*, *Nicotiana benthamiana*, and *Solanum lycopersicon* were mechanically inoculated with sap from isolate See-1 infected plant, leading to the appearance of typical AMV symptoms in all three hosts 10 days postinoculation (Jaspars and Bos 1980). This note describes the first detection of AMV in chayote in Italy and, to the best of our knowledge, in the world. In some areas of Southern Italy, climatic conditions are favorable enough to allow chayote development in the wild. Further studies would be desirable to determine the distribution and incidence of AMV in chayote and to understand the possibility that this species may play a role in AMV epidemiology, representing a threat to other susceptible crops.

References:

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