DISEASE NOTE

First Report of *Tomato leaf curl New Delhi virus* infecting Zucchini in Morocco

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Tomato leaf curl New Delhi virus (ToLCNDV, genus *Begomovirus*, family *Geminiviridae*) is a devastating pathogen vectored by the whitefly *Bemisia tabaci,* causing significant yield losses to several crops. ToLCNDV is a bipartite begomovirus first reported on tomato (*Solanum lycopersicum* L.) in 1995 in India and soon after found in other Asian countries particularly on vegetables of the *Cucurbitaceae* and *Solanaceae* families (revised in Zaidi et al. 2017). Further spread of ToLCNDV occurred after 2012, with recent reports in Mediterranean countries, initially in Spain (Juárez et al. 2014) and more recently in Tunisia (Mnari-Hattab et al. 2015) and Italy (Panno et al. 2016) affecting mainly zucchini (*Cucurbita pepo* L.), melon (*Cucumis melo* L.) and cucumber (*Cucumis sativus* L.). During spring 2017, generalized leaf symptoms including yellowing and curling, as well as stunting of plants were observed in several zucchini fields of one of the commonest commercial Moroccan cultivar, 'Suha' F_1 (Sakata Vegetables Europe S.A.S.) in the region of Agadir, Morocco. Leaf samples from nine symptomatic and three asymptomatic plants were first tested for ToLCNDV infection with an ImmunoStrip® kit (Adgia, Inc, Elkhart, IN). Only the symptomatic samples were positive for ToLCNDV infection. Since the immune strip test kit can also react with other begomoviruses, to confirm the identity of the virus, DNA was isolated from the symptomatic leaf samples and analyzed by PCR with two primer pairs, To-A1F and To-A1R from the DNA-A, and To-B1F and To-B1R from the DNA-B (Sáez et al. 2016), to amplify 505 bp and 677 bp fragments of viral DNAs A

and B, respectively. Amplicons were obtained from all the samples that had tested positive for ToLCNDV with the ImmunoStrip® kit. PCR products were directly sequenced and BLAST analysis showed nucleotide identity higher than 99% with sequences from ToLCNDV isolates of Spain. DNA from two positive samples was also used for rolling-circle amplification and selected to clone the DNA-A and DNA-B genome components by using *Bam*HI restriction enzyme. Inserts of two clones from each sample, one corresponding to DNA-A and one to DNA-B, were completely sequenced. The sequence of the two clones of both segments shared >99% nucleotide identity and one sequence of each segment (isolate Agadir) was submitted to GenBank. These sequences were 2,738 nt long for DNA-A (GenBank Accession No. MG098230) and 2,684 nt long for DNA-B (MG098231) and shared >99% nucleotide identity, with the complete sequence from ToLCNDV isolates infecting tomato (KM977733 and KM977734) and zucchini (KF749223 and KF749226 for DNAs A and B) in Spain. Efforts to identify the presence of additional begomoviruses or DNA satellites by PCR, using universal primers were negative. This is the first report of the presence of ToLCNDV in Morocco, that could therefore represent a serious threat for valuable cucurbit crops in this and other countries of northern Africa. Thus, it is necessary to implement efficient control measures to prevent further spread of the virus and minimize yield losses.

***References*:**

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