Disease Note

FIRST REPORT OF *ZUCCHINI YELLOW MOSAIC VIRUS* ON MUSKMELON IN INDIA

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Zucchini yellow mosaic virus (ZYMV, genus *Potyvirus* in the family *Potyviridae*) is the causal agent of diseases in a wide range of cucurbitaceae host species, causing important economic losses. During a 2014 survey of the main muskmelon (*Cucumis melo*) growing areas of Rajasthan in India, plants showing virus-like symptoms such as leaf curling, yellow vein mosaic, decreased leaf size and stunting were observed. Leaves from symptomatic plants were collected, total RNA was extracted from infected leaves using the TRIZOL (Sambrook and Russell, 2001) method and subjected to RT-PCR using potyvirus degenerate primers Pot1 and Pot2 (Colinet *et al*., 1997). A *ca.* 1.5 kb amplicon was partially sequenced and deposited in GenBank (Accession no. KJ425470) as *Zucchini yellow mosaic virus* isolate Rajasthan. BLASTn revealed 100% sequence identity with ZYMV-SG from China (AJ316228), 96% with ZYMV-NAT from Israel (EF062282) and 95% with ZYMV-fars from Iran (JN183062). In a phylogenetic analysis ZYMV-Rajasthan clustered with Asian ZYMV isolates. ZYMV was previously reported from cucurbitaceae species but, to our knowledge, this is the first report of ZYMV on muskmelon in India.

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Disease Note

FIRST REPORT OF GRAPEVINE RODITIS LEAF DISCOLORATION-ASSOCIATED VIRUS IN ITALY

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In 2014, some registered native grapevine cultivars from Apulia were analyzed to determine their "absolute" sanitary status (virome) i.e. the totality of virus, viroids and phytoplasmas, present in any single accession, using a high throughput sequencing (HTS) approach (Giampetruzzi *et al*., 2015). Small RNA libraries synthesized from a symptomless red-berried wine grapevine of cv. Bombino nero (accession D205), growing in a foundation block, showed the presence of 21 contigs (ranging from 329 to 56 nucleotides in length) which, upon BLASTX analysis (Altschul *et al*., 1997), were identified as badnavirus-like sequences. To confirm deep-sequencing findings, a set of PCR specific primers (11for-G: 5'CAAAGTAAGAGCAATCCTTGATACCGG3'; 13rev-G: 5' CCCAATGTTACAGATCACCATCTCCTG3') were designed, using the closest reference sequence, i.e. Fig badnavirus 1 (FBV-1, GenBank NC017830). A product of the expected size (410 bp) was amplified and custom-sequenced, showing *ca.* 91% identity at the nucleotide level with the sequence of a badnavirus recently discovered in Greece (Maliogka *et al*., 2015) and denoted Grapevine Roditis leaf discoloration-associated virus (GRLDaV, NC027131). For a preliminary assessment of the incidence of this virus in the field, a preliminary survey in the same foundation block was conducted. A total of 11 samples from different autochthonous cultivars were checked by PCR, but none of them tested positive. It is worth nothing that accession D205 is a registered clone, which has been inspected for years by laboratory testing and field indexing without revealing the presence of regulated viruses, nor showing symptoms. To our knowledge, this is the first report of GRLDaV in Italy.

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