

DISEASE NOTE

FIRST REPORT OF *CLADOSPORIUM COLOCASIAE* AS A PATHOGEN CAUSING LEAF SPOT DISEASE ON TARO (*COLOCASIA ESCULENTA*) IN IRAN

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During the Summer 2013, a new foliar disease was observed on taro (*Colocasia esculenta*) in tropical areas of Iran, including Hormozgan, where many farmers were alarmed by complete destruction of their taro cultivation. Leaf spots, yellow to dark brown, were subglobose and oval. A fungus was consistently isolated from diseased tissues on Potato Dextrose Agar (PDA) at $23 \pm 2^\circ\text{C}$. Morphological observations were carried out on Synthetic Nutrient Agar (SNA) medium as described by Bensch *et al.* (2012). Conidiophores were macronematous, cylindrical-oblong with several nodes being quite apart from each other, very long, up to 350 μm or even longer. Conidia ellipsoid-subcylindrical to cylindrical, forming short, unbranched or branched chains. Terminal conidia were $9\text{-}16 \times 5\text{-}8 \mu\text{m}$ and aseptate or 1-septate. A portion of the translation elongation factor 1- α gene was amplified (Bensch *et al.*, 2012) and sequenced (GenBank Accession No. KP893386). A BLAST search showed 99% similarity with *Cladosporium colocasiae* sequences deposited in GenBank. To verify Koch's postulates, pathogenicity was tested by spraying a conidial suspension prepared from cultures on PDA (1×10^6 spores/ml) in sterile water on healthy leaves of four test plants (5-7 leaf stage, cv. Niue). Control plants were sprayed with sterile water. Plants were kept in a greenhouse (average minimum temp. 24°C , max. 37°C and relative humidity 64%). Symptoms appeared 2 weeks post-inoculation on inoculated plants, whereas control plants remained asymptomatic. Reisolation of the pathogen with the same morphological characters was achieved from symptomatic plants only, hence confirming the causal agent as *C. colocasiae*. To our knowledge, this is the first report of *C. colocasiae* on *C. esculenta* in Iran.

Bensch K., Braun U., Groenewald J.Z., Crous P.W., 2012. The genus *Cladosporium*. *Studies in Mycology* **72**: 1-401

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FIRST REPORT OF *LITTLE CHERRY VIRUS-1* IN SLOVAKIA

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Little cherry virus 1 (LChV-1) a member of the newly established genus *Velarivirus*, family *Closteroviridae* (Katsiani *et al.*, 2015) is associated with little cherry or shirofugen stunt diseases (Candresse *et al.*, 2013). As LChV-1 was recently detected in Czech Republic and Poland, a survey was undertaken to study its presence in Slovakia by sampling cherries (*Prunus avium* L.) in various sites (orchards, gardens, old local cherry plantations, botanical collections). Random primer-synthesized cDNA was used for amplification of the putative coat protein (CP) gene (449 bp) using primers 1LC_12776F: 5'TCAAGAAAAGTTCTGGTGTGC3' (sense) and 1LC_13223R: 5'CGAGCTAGACGTATCAGTATC3' (antisense), newly designed based on sequences from databases (www.ncbi.nlm.nih.gov, accessed on April, 2013). Five of ca. 60 cherry samples tested positive for LChV-1 using RT-PCR. LChV-1-infected samples originated from three distinct localities (Bratislava, Ivanka pri Dunaji, Brdarka) and, in all cases, they were recovered from local genotypes older than 20 years. No typical symptoms could be attributed to LChV-1 in cherries identified as infected, which remained in most of cases symptomless. The partial LChV-1 CP sequences obtained in this work and those retrieved from GenBank showed a substantial variability. Five Slovak isolates were genetically homogenous, showing a within group nucleotide divergence of 1.1% (GenBank accession Nos KP861749, KP861751, KP861755-57). However, these Slovak isolates formed a distinct phylogenetic cluster, divergent from the previously characterised European LChV-1 isolates (nucleotide identity with isolates NC_001836, EU715989 and JX669615 reached 82.3 – 84.2%). The detection of LChV-1 isolates in old local cherry genotypes and the extent of their molecular variability suggests a long-term establishment of this virus in the country. To our knowledge, this is the first report of LChV-1 in Slovakia.

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Candresse T., Marais A., Faure C., Gentil P., 2013. Association of *Little cherry virus 1* (LChV1) with the Shirofugen stunt disease and characterization of the genome of a divergent LChV1 isolate. *Phytopathology* **103**: 293-298.

Katsiani A.T., Maliogka V.I., Amoutzias G.D., Efthimiou K.E., Katis N.I., 2015. Insights into the genetic diversity and evolution of *Little cherry virus 1*. *Plant Pathology* **64**, doi: 10.1111/PPA.12309.

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