Disease Note

FIRST REPORT OF CROWN GALL ON *ASTER* sp. CAUSED BY *AGROBACTERIUM TUMEFACIENS* SPECIES COMPLEX GENOMOVAR G1 IN ITALY

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In June 2015, crown galls were observed in a 30 day-old greenhouse crop of *Aster* sp. in Lecce province (southern Italy). Symptoms occurred on *ca*. 20% of plants and consisted of stunting and, below the soil line, white-cream spherical galls which progressively darkened. Two representative isolates, producing 5 mm-circular convex colonies with reddish center and whitish border on selective agar medium 1A, were designated DiSSPA Ag26 and DiSSPA Ag27 and subjected to biochemical assays according to Schaad *et al.* (2001). They were Gram-negative, oxidase positive, able to grow in 2% NaCl and in ferric ammonium citrate and produced 3-ketolactose, acidity from melezitose but not from erythritol, alkalinity from litmus milk but no alkali from malonic, L-tartaric and mucic acids and utilized citrate but not L-tyrosine. Morphological and biochemical characters of our isolates were similar to those of *Agrobacterium tumefaciens* species complex, formerly called *A. tumefaciens* biovar 1 (Costechareyre *et al*., 2010). In a phylogenetic tree based on the sequence of DNA gyrase subunit B gene (*gyrB*), constructed as per Puławska and Kałużna (2012), DiSSPA Ag26 (accession No. MF000330) and DiSSPA Ag27 (MF000331) clustered within the genomovar G1 of *A. tumefaciens* species complex, with the best match (99%) with *Ch3* strain (HQ438217). Moreover, our isolates induced gall formation on stem of five week-old tomato cv. Marmande, tobacco cv. Samsun and on carrot disks after three weeks at room temperature from needle-inoculation of a bacterial cell suspension (10^8 CFU/ml). Re-isolated bacteria exhibited the same traits of the inoculated isolates. To the best of our knowledge, this is the first report of crown gall caused by *A. tumefaciens* species complex genomovar G1 on *Aster* sp. in Italy.

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Disease Note

FIRST REPORT OF A 16SRXI GROUP PHYTOPLASMA ('*CANDIDATUS* PHYTOPLASMA ORYZAE') ASSOCIATED WITH *CYPERUS* spp. WHITE LEAF DISEASE IN IRAN

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In 2014, *Cyperus* spp. (Cyperaceae) white leaf (CWL) disease was observed in lime orchards in Minab (Hormozgan province, Iran). Main disease symptoms were whitening of aerial plant parts and stunting. To investigate the phytoplasma presence, total DNAs extracted from five symptomatic and five symptomless *Cyperus* spp. plants were tested by nested PCR using primers P1/P7 followed by R16F2n/R16R2 (Lee *et al*., 1998). Amplicons of *ca.* 1.8 and 1.2 kb, were obtained from samples of symptomatic but not symptomless plants. All amplicons were cloned and sequenced. The obtained 16S rDNA sequences showed 100% identity with each other and a representative of the same sequences deposited in GenBank (accession No. MF136620). BLAST search using the full length 16S rRNA gene sequence revealed that the CWL sequence showed 99% identity with sugarcane white leaf and sugarcane grassy shoot phytoplasmas (AB646271 and KF908792, respectively), representatives of 16SrXI phytoplasma group. Computer-simulated restriction analysis using *i*PhyClassifier, showed that the RFLP profile of CWL phytoplasma was very similar to the reference pattern of the 16SrXI-B subgroup (X76432). Phylogenetic analysis using Mega software version 7 confirmed that the CWL phytoplasma clustered with16SrXI group phytoplasmas closest to 16SrXI-B subgroup. To our knowledge this is the first report of a 16SrXI group phytoplasma in Iran. Rice and sugarcane plants are two economically important hosts of 16SrXI group-related strains (Arocha and Jones, 2010), thus the CWL-associated phytoplasma could act as a source of inoculum for infecting rice and sugarcane crops in Iran.

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