## New Disease Reports

## First report of 'Candidatus Phytoplasma australasia'-related strains associated with disease of Jasminum multiflorum in India

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Jasminum multiflorum (cv. Star Jasmine; family Oleaceae) is an important ornamental shrub native to South-East Asia. It is cultivated across the tropics for its ornamental value, in particular its fragrant, beautiful white flowers. During February 2020, symptoms of leaf yellowing and the premature decline of inflorescences were observed on 6.5% of plants grown in home gardens (Figs. 1-2) in the Uttara Kannada district of Karnataka state, India.

Four symptomatic and two symptomless plants were subjected to genomic DNA extraction using the CTAB method. Nested PCR was performed with universal phytoplasma 16S rRNA primers P1/P7 (Deng & Hiruki, 1991; Schneider et al., 1995) and R16F2n/R16R2 (Gundersen & Lee, 1996). A DNA extract from the periwinkle virescence phytoplasma of group 16SrI, 'Candidatus Phytoplasma asteris' (MN223677) was used as the positive control. Amplification of the 16S rRNA gene was obtained only from symptom-bearing jasmine and the positive control, but not from the symptomless plants. The nested PCR products (~1.25kb) were purified and sequenced directly. Sequences were compared to those of reference phytoplasmas and subjected to in silico RFLP with iPhyclassifier (Zhao et al., 2009) and phylogenetic analysis using the neighbour-joining method of MEGA X (Kumar et al., 2018). The R16F2n/R16R2 gene sequences of the phytoplasmas multiflorum (GenBank I Accession Nos. MW049328-MW049329) showed 99.9-100% sequence identity with those of the reference phytoplasmas of the former Peanut witches' broom (16SrII) group, 'Candidatus Phytoplasma aurantifolia', including 'Ca. P. australasia' (Y10097). The virtual RFLP profiles of both J. multiflorum phytoplasmas were identical to each other and to those of the 'Ca. P. australasia' related strain (Y10097) of the 16SrII-D subgroup with a similarity coefficient of 1.00. The phylogenetic tree confirmed that the J. multiflorum phytoplasmas were closely related to the 16SrII-D, 'Ca. P. australasia' strain cluster (Fig. 3). Based on the results of the 16S rDNA nucleotide sequence comparison, phylogenetic and RFLP analyses, the J. multiflorum phytoplasmas associated with inflorescence yellowing and premature decline were identified as strains of the 'Ca. P. australasia', 16SrII-D subgroup.

Phytoplasmas of 16SrII, 16SrXI ('Ca. P. oryzae') and 16SrI ('Ca. P. asteris') groups have been reported previously affecting J. sambac in Oman and India (Al-Zadjali et al., 2007; Madhupriya et al., 2015; Gopala & Rao, 2018). However, this is the first report of the association of 'Ca. P. australasia' affecting J. multiflorum in India. Considering the economic importance of jasmine for the ornamental industry, this report provides



Figure 1





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	Tagetes envise structure physiqueme strate (MEVIR2908) 165cE-D
	Western X-chaose mycophases-like organism (LOMR2) 18542 A
	Pipen pen wither-broom phytoplasma (AT248957) 1854X A
	Beamla grass white leaf phytopheses (AJ550904) 1056X27 A
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	20 Adi yilovi phytophana stala (AP092200) 1856/03-8
	Chrver plejkody plejtuplasma strain (AU222015) 165cf C
-	10 Countiers phytopheses (M20290.) 185nf. B
	Acheleslewa bidenii (M29912)

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significant information to support informed phytosanitary measures to prevent the spread of 'Ca. P. australasia' to nearby jasmine and other important members of the Oleaceae.

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Figure 3