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DISEASE NOTES



# First Report of *Ralstonia pseudosolanacearum* Phylotype I Causing Bacterial Wilt in New Caledonia

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Bacterial wilt (BW), caused by the *Ralstonia solanacearum* species complex (RSSC), is a worldwide disease reported on a wide host range. RSSC strains belong to three species (Safni et al. 2014): *R. pseudosolanacearum* clusters in phylotypes I and III, *R. solanacearum* clusters in the phylotype II, and *R. syzygii* clusters in the phylotype IV. Each phylotype is subdivided into sequevars based on the endoglucanase gene (*egl*) partial sequencing (Fegan and Prior 2005). In New Caledonia, BW has been regularly encountered for decades around the island on solanaceous crops (*Solanum lycopersicum* L., *S. tuberosum* L., and *S. melongena* L.), but strains were never characterized except in 2015, when the quarantine IIB-1 (biovar 2 race 3) strains were reported from potato in La Foa and Bourail

(<https://www.ippc.int/en/countries/new-caledonia/pestreports/2015/08/ralstonia-solanacearum-bv2-race-3-in-new-caledonia/>). Quarantine and eradication measures were then ordered by the New Caledonian authorities. In July 2017, during the cool season, BW-like symptoms were observed in two potato and two tomato plots in the Western and Eastern coasts of New Caledonia, respectively. Samples were collected into the four plots, and macerates from processed stem sections were plated for RSSC isolation on SM-1 semiselective medium (Granada and Sequeira 1983). Typical RSSC-like colonies, obtained from eight wilted plants, were characterized through phylotype-specific multiplex PCR (PMX-PCR) (Fegan and Prior 2005) as belonging to *R. pseudosolanacearum* phylotype I. By including international strains covering the current phylogenetic diversity reported for the RSSC, the phylogenetic maximum-likelihood tree approach (PhyML version 3.3 [Guindon et al. 2010] under Geneious R10.2.6 <https://www.geneious.com>) from partial *egl* sequencing (Fegan and Prior 2005) assigned them all with high congruence to the phylotype I sequevar 18. Three strains (RUN5565, RUN5570, and RUN5571 [GenBank MH880857, MH880862, and MH880863]) were isolated from the two potato plots in Pouembout. Four strains (RUN5564, RUN5567, RUN5568, and RUN5569 [GenBank MH880856, MH880859, MH880860, and MH880861]) were isolated from one tomato plot in Ponerihouen. The remaining strain (RUN5566 [GenBank MH880858]) was isolated from a tomato plot in Canala. Koch's postulates were performed by inoculating the eight strains to the susceptible tomato accession L390 (Lebeau et al. 2011). Five plants per strain were inoculated by soil drenching with a Tris-buffer suspension of  $10^8$  CFU/ml, whereas negative control L390 plants were only drenched with sterile Tris-buffer. Plants were maintained at  $28 \pm 1^\circ\text{C}$  at 95% relative humidity. All the inoculated tomato plants wilted within 7 days, whereas the negative controls remained asymptomatic. RSSC colonies, confirmed by the PMX-PCR, were only reisolated on SM-1 medium from symptomatic plants. This is the first report of *R. pseudosolanacearum* phylotype I in New Caledonia. Interestingly, IIB-1 strains were not isolated, suggesting that implemented eradication measures were effective. An extensive survey during the warm season, when climatic conditions are optimal for phylotype I, should be established to infer the prevalence and distribution of strains in New Caledonia including Loyalty Islands and to implement adapted control measures against BW.

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The author(s) declare no conflict of interest.

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