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PATHOGEN DIVERSITY OF *Ralstonia solanacearum* THAT CAUSES BACTERIAL WILT DISEASE IN TOMATO

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Bacterial wilt, caused by *Ralstonia solanacearum*, is a highly destructive disease affecting tomatoes worldwide. The objective of this study was to investigate the pathogen diversity of *R. solanacearum* in selected high tomato cultivation areas in Sri Lanka. Disease samples were collected from fields in Wattegama, Matale, Dambulla and Marassna. Stems of tomato plants showing wilt symptoms were tested for bacterial oozing. Causative bacteria were isolated on nutrient agar, and pathogenicity was confirmed through Koch's postulates. Pathogens were characterised using colony morphology, micromorphology, and biochemical tests including gram staining and the sugar metabolization test. For molecular characterization, bacterial DNA was extracted and amplified by PCR using specific primers. Altogether, 13 bacterial strains were isolated from the four field sites. All 13 strains showed positive results for the ooze test and Koch's postulates. The study identified two main bacterial types. Type 1 was dirty white, circular, smooth, raised, shiny colonies with entire margins and was gram-negative. Type 2 was white, circular, smooth, raised, shiny colonies with entire margins and was gram-positive. Type 1 bacteria showed typical characteristics of *R. solanacearum*. In the biovar testing, Dambulla strains D1, D2, and D4 metabolized maltose, glucose, mannitol, and sorbitol. Matale strain M3 and Wattegama strain P3_1 metabolized only glucose. A single strain C from Wattegama was amplified in PCR using Nmult 21: 1F forward primer with the primer sequence of 5′-CGTTGATGAGGCGCGCAATTT-3′. According to the standard biovar test, Dambulla strains D1, D2, and D4 were classified as biovar 3, while Matale strain M3 was classified as biovar 1. According to the PCR analysis, Wattegama strain C was classified as biovar 3, 4 or 5. Further, Type 2 bacteria may represent a different bacterial species that caused similar disease symptoms, such as wilting. Strain typing is useful for accurate disease diagnosis and the development of more effective, region-specific tomato varieties.

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