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Identification of *Ralstonia solanacearum* phylotypes causing bacterial wilt of potato in Badulla district of Sri Lanka

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Bacterial wilt is considered as one of the most destructive diseases of potato caused by *Ralstonia solanacearum* (E. F. Smith). More recently, a hierarchical classification scheme was proposed to distinguish the genetic variation within *R. solanacearum* species complex which is subdivided into four phylotypes: phylotype I from Asia; phylotype II from the America; phylotype III from Africa and surrounding islands; and phylotype IV from Indonesia, Japan, the Philippines, Korea and Australia. Thus, this study was aimed to identify phylotypes of *R. solanacearum*. Samples were collected from the potato-growing areas in Badulla district of Sri Lanka namely, Bandarawela, Boralanda, Koslanda, Passara and Welimada. A total of 32 bacterial isolates of *R. solanacearum* was isolated using triphenyl tetrazolium chloride agar medium. Genomic DNA extracted from those bacterial isolates was subjected to PCR with Rsol_*fliC* primers to confirm the identity of *R. solanacearum* and then subjected to the phylotype-specific multiplex PCR (Pmx-PCR) with *R. solanacearum* species-specific primers, 759/760, in combination with phylotype-specific primers, Nmult:21:1F, Nmult:21:2F, Nmult:23:AF, Nmult:22:InF and Nmult:22:RR. The Pmx-PCR revealed that 29 isolates (91%) belonged to the Asian phylotype I and the remaining 3 isolates (9%) belonged to the American phylotype II which were found only from Welimada area. These results indicate that the major causal agents of bacterial wilt of potato in Badulla district belonged to *R. solanacearum* phylotype I and in addition, *R. solanacearum* phylotype II were also responsible for the disease.

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