ABSTRACT

Ralstonia solanacearum is a pathogen causing bacterial wilt disease of potato, resulting in 70% potato production losses in Kenya. A study was conducted to determine the diversity of *R. solanacearum* species complex strains within the main potato-growing regions of Kenya. Potato tubers were collected in different potato-growing regions of Kenya from visibly wilted potato plants as well as samples of tomato, irrigation water, and cultures for pathogen isolation. Genomic DNA was isolated from 135 purified cultures of RSSC isolates and PCR-amplified using multiplex and sequevar primers targeting the endoglucanase (*egl*) partial gene sequences. Pathogenicity tests using *R. solanacearum* strain (phylotype II sequevar I) were done on the cultivars Kenya Karibu, Shangi, Chulu, Wanjiku, and MoneyMaker. Phylogenetic analysis of the partial *egl* gene identified two genospecies, *R. pseudosolanacearum* sp. nov. (1.5%) and *R. solanacearum* (98.5%). All *R. solanacearum* strains clustered in sequevar I and were distributed in all the potato-growing regions surveyed. The cultivars were grown in a greenhouse for two cycles in a randomized complete block design and inoculated with *R. solanacearum* strain. The severity scores were assessed and the area under the disease progress curve (AUDPC) was determined. All the cultivars tested for pathogenicity exhibited wilting symptoms at varying intervals after infection, with none showing complete resistance to *R. solanacearum*. Cultivar Shangi exhibited minimum disease severity and progression of 41.14% and AUDPC of 1041.7, respectively, while ‘Kenya Karibu’ was the most susceptible with a high progression rate of 68.24% and AUDPC of 1897.5, respectively. ‘MoneyMaker’, ‘Chulu’, and ‘Wanjiku’ showed no significant difference in disease severity, depicting a simultaneous rate of infection among them. These findings provide valuable information to better understand the pathogen genetic diversity in Kenya and how it spreads.