THE ASSESSMENT OF GENETIC DIVERSITY OF STRAINS OF *Pseudomonas syringae* pv. *syringae* CAUSING BACTERIAL CANKER IN STONE FRUITS IN SOME NORTHERN PROVINCES OF IRAN*

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Abstract

*Pseudomonas syringae* pv. syringae (*Pss*) is the causative agent of several bacterial diseases on a range of agricultural and horticultural crops that causes canker, leafspot and necrosis of the bark of stone fruit trees (peach, nectarine, apricot, plum and cherry). In this research samples were collected from various areas in Ardebil, Guilan, Mazandaran and Khorasane-Razavi provinces during 2007-2009. Bacterial strains identified as *Pss*, on the basis of LOPAT and GATTA were selected. Number of 70 bacterial isolates were compared based on their physiological and biochemical characteristics and total cellular protein profiles (SDS-PAGE). *Pss* isolates showed slight differences in phenotypic characteristics and protein profiles. To assess genetic diversity among the strains, genomic DNA was extracted from strains and used in ERIC and REP-PCR analysis. Strains formed 8 and 5 clusters in the ERIC-PCR and REP-PCR, at 75% similarity level, respectively and by the combination data set of both ERIC and REP-PCR, strains formed 9 clusters. The results demonstrated the existence of a considerable genetic diversity among *Pss* strains causing canker of stone fruit trees in the northern provinces of Iran.

Keywords: Bacterial canker, *Pseudomonas syringae* pv. syringae, Genetic diversity, Stone fruit trees.

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