

Genetic diversity of strains of *Acidovorax oryzae* causal agent of brown stripe of rice in Mazandaran province*

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Abstract

Brown stripe of rice is among the prevalent diseases of rice seedlings in Mazandaran and Guilan provinces. For assessment of genotypic diversity in populations of the causative bacterium samples were collected from rice seedbeds in the suburb of Sari, Mazandaran province in 2012. A total of 90 isolates were recovered and the phenotypic and genotypic characteristics of the causal bacterium were compared. The isolates were identified as *Acidovorax avenae* subsp. *avenae* (*Acidovorax oryzae*). The isolates were fairly homogeneous in their physiological and biochemical features. They were differentiated into two and five groups, at similarity levels of 45% and 68%, respectively, in the whole cell protein electrophoretic profiles. Genomic DNA of isolates was obtained and subjected to rep-PCR (with BOX and ERIC primers) fingerprinting. Dendrograms were constructed, using the jaccard coefficient, the UPGMA algorithm and NTSYS-PC program. Comparison of the genomic fingerprints demonstrated that, at 20%, 35% and 65% similarity levels isolates formed 2, 5 and 10 clusters with ERIC primer and at 20%, 50% and 80% similarity levels isolates formed 7, 16 and 23 clusters with BOX primer, respectively. The result indicates a high level of genetic diversity in *Ao* populations.

Keywords: *Acidovorax oryzae*, brown stripe of rice, genotypical diversity, rep-PCR

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