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Pantoea ananatis causing grain discoloration is widely distributed in the rice-growing fields of the Republic of Korea

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We collected local isolates of *Pantoea ananatis* causing bacterial grain discoloration from southern rice-growing fields in Korea and constructed phylogenetic tree to see the genetic variation of P. ananatis. In 2016, rice panicles showing symptoms of grain discoloration and grain abortion were collected and the inside of lemma and palea were streaked on the King's B agar plate for pathogen isolation. 63 regional isolates were randomly selected for avoiding selection bias and gDNA were extracted for gene-based species identification. Based on 16S rRNA gene, B. *glumae*, the major pathogen of grain rot, amounted for 49.2% and Pantoea spp. amounted for 22.2%, separately. Multilocus sequence analysis (MLSA) by four *gyrB*, *rpoB*, *infB*, and *atpD* identified *Pantoea* spp. as P. *ananatis*. The pathogenicity of collected P. *ananatis* isolators were tested and showed weak symptoms of stem rot by artificial injection and weak symptoms of grain discoloration by spraying to the panicles of rice. In this study, we show the incidence and the regional distribution of P. *ananatis*, and the phylogenetic relationship among P. *ananatis* regional isolates in Korea, 2016. As the risk of the grain rot and grain discoloration is increasing according to the climatic change, it would be the basic data for understanding P. *ananatis* in the Republic of Korea.

Biography

He is a researcher for plant pathology in the National Institute of Crop Science, RDA	A. Main works include diagnosis,	identification and control of	crop diseases on
the field and on the lab.			

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