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Understanding the Quorum-Sensing Bacterium *Pantoea stewartii* Strain M009 with Whole-Genome Sequencing Analysis

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*Pantoea stewartii* is known to be the causative agent of Stewart’s wilt, which usually affects sweet corn (*Zea mays*) with the corn flea beetle as the transmission vector. In this work, we present the whole-genome sequence of *Pantoea stewartii* strain M009, isolated from a Malaysian tropical rainforest waterfall.

Quorum sensing (QS) is a term coined to describe the ability of bacteria to communicate in order to form a unified response within a population (1). The communication occurs when small diffusible molecules in a given bacterial population synchronize and stimulate a series of gene expressions that could drive different responses, such as the production of virulence factors (2, 3). Since QS plays a vital role for bacteria, it is therefore important to study the freshwater-inhabiting bacteria that exhibit QS properties, because freshwater can serve as a reservoir for microorganisms (3, 4). *Pantoea stewartii* has long been known for causing Stewart’s wilt in sweet corn, and epidemics in the 1990s led to significant economic losses for the corn seed industry (5).

Stewart’s wilt in sweet corn, and epidemics in the 1990s led to significant economic losses for the corn seed industry (5). Since the 4 rRNAs (2 copies of 5S rRNA and one copy each of 23S RNA and 16S rRNA) and 70 tRNAs were predicted with RNAmer (7) and tRNAscan SE version 1.21 (8), respectively. Subsequently, the strain M009 sequence was annotated with RAST (9).

From the annotation results, the luxI and luxR homologues of strain M009 were predicted to be located at contig 5, where the luxR gene was located upstream of the contig. The whole-genome sequence allows deeper understanding of the genetic makeup of *P. stewartii* to determine the link between QS ability with plant pathogenicity and production of virulence factors (10, 11).

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JRW100000000. The version described in this paper is the first version, JRW101000000.

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