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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).

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The draft genome of the strain M009 isolate contained 1,065,952 quality reads. The trimmed reads were 4,831,705 paired-end reads, and a trimming of the sequences provided 2,23,175 were generated. The draft genome of the strain M009 isolate contained 1,065,952 quality reads. The trimmed reads were 4,831,705 paired-end reads, and a trimming of the sequences provided 2,23,175 were generated.

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