

**Draft genome sequencing data of a pathogenic *Pantoea stewartii* subspecies *stewartii* strain SQT1 causing bronzing disease of jackfruit in Malaysia**

**ABSTRACT**

A Gram-negative bacterium, *Pantoea stewartii* subspecies *stewartii* (*P. stewartii* subsp. *stewartii*) has been recognized as the causative agent for jackfruit bronzing disease in Malaysia. Here, we report the whole genome sequencing dataset of *P. stewartii* subsp. *stewartii* strain SQT1 isolated from local infected jackfruit. The paired-end libraries with an insert size of 350 bp was subjected to the Illumina HiSeq 4000, generating a genome size of 4,783,993 bp with a G+C content of 53.7%. A total protein of 4,671 was identified including virulence factors, resistance factors and secretion systems. *Pantoea stewartii* subsp. *stewartii* strain DC283 (NCBI accession no. CP017581.1) was used as a reference genome, where the query hit 72% coverage and average sequencing depth of 68. In total, 28,717 nucleotide polymorphisms, 520 small insertion/deletions and 142 structure variants were identified. The complete genome was deposited at the European Nucleotide Archive under the sample accession number ERP119356 and study accession number PRJEB36196.

**Keyword:** Malaysia; Bronzing disease; Jackfruit; *Pantoea stewartii* subspecies *stewartii*; Genome sequencing; Illumina HiSeq; Virulence factors; T6SS