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# Comparative Genomics of Subspecies of Pantoea Stewartii

**James Tambong**
*Agriculture and Agri-Food, Canada*

## Abstract

Stewart's Wilt is a serious bacterial disease of corn caused by the bacterium Pantoea stewartii. Therefore, identifying the disease-causing Pantoea stewartii became important for economical purposes. The identification could be achieved by spotting a bar code DNA sequence that uniquely identifies the bacterium, thus assembling the genome of Pantoea stewartii became our research project. Since no Pantoea stewartii's genome has been assembled yet, we decided to de novo assemble it. The genome was sequenced using Illumina HiSeq technology, which resulted in 8465016 paired-end reads; the length of reads is 150 bp each; the insert length is 360 bp; and the average coverage is 253x. The assembly process started by checking the quality of reads using FastQC, followed by optimally assembling the genome based on kmer values and using multiple assemblers including Velvet and Abyss, then scaffolding the contigs resulting from the best run using SSPACE, and filling gaps between contigs within scaffolds using GapFiller. The resulting draft assembly consists of 37 scaffolds; the N50 is 550610 bp; the size of longest scaffold is 2376083 bp; and the total length is 5392784 bp. The expected genome size was 5 Mbp. The number of copies of ribosomal RNA genes 5S, 23S, and 16S found in the draft assembly were 10, 2, and 7 copies respectively. Pantoea stewartii's genome closing and finishing as well as genome annotation are going on. Once finished, this first assembled Pantoea stewartii will serve as a reference genome for four other P. stewartii subspecies that we already de novo assembled, which will allow for phylogenetic and comparative genomics analysis.

**Biography**

Dr. James Tambon (Ph. D. Ghent University) is a research scientist in Agriculture and Agri-Food Canada. His research focuses on the development and validation of array and real-time PCR tools for rapid detection, identification and quantification of plant pathogenic bacteria. He is also interested in the identification and evaluation of potential bacterial biological control agents against major soil-borne pathogens such as Pythium, Phytophthora, Fusarium and Sclerotinia. Currently, he is developing PCR-based techniques for the detection of the Stewartii's wilt pathogen (Pantoea stewartii subsp. stewartii) of corn and for screening of corn seeds.

Dr. Zaky Adam (Ph. D. University of Ottawa) is a Visiting Research Fellow in Agriculture and Agri-Food Canada focusing on genome assembly of bacterial genomes.