Complete Genomic Data of *Pantoea ananatis* Strain TZ39 Associated with New Bacterial Blight of Rice in China

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Abstract

Pantoea ananatis is a phytopathogen infecting many economically important crops, including rice worldwide. Here, we report the complete genome of *P. ananatis* strain TZ39 identified as causative agent of a new bacterial blight of rice that emerged in China in 2020. The assembled genome consists of one circular chromosome of 4,483,976 bp and two plasmids of 135,135 and 276,579 bp. This complete genome of the first Chinese pathogenic *P. ananatis* strain will provide new insights into the traits of pathogenicity on genomic level from China and worldwide.

Genome Announcement

Pantoea ananatis is a gram-negative enterobacterium isolated from various environments, including soil, water, plant, animal, and human (De Maayer et al. 2014). As an enigmatic phytopathogen, *P. ananatis* have a broad host range and can infect pineapple, onion, eucalyptus, oyster mushroom, maize, wheat, rice, etc., where it causes varied disease symptoms such as stalk, fruit, and bulb rot, leaf spot, blight, and dieback (Alippi and Lopez 2010; Carr et al. 2010; De Maayer et al. 2010; Kim et al. 2007; Krawczyk et al. 2020; Mondal et al. 2011; Xue et al. 2021; Yu et al. 2021). Upon pathogenicity determinants, type II, type III, and type IV secretion systems and phytotoxins are absent, whereas type VI secretion system is shown to be present in *P. ananatis* (Coutinho and Venter 2009; De Maayer et al. 2014; Shyntum et al. 2015). In addition, the other recorded virulence factors including cell wall degrading enzymes, acyl-homoserine lactone mediated quorum sensing system, twitching motility, flagellar motility, exopolysaccharide, and endoglucanase have importance in pathogenicity (De Maayer et al. 2017; Ma et al. 2016; Miller et al. 2016). Rice is the staple food for over half of the world population. *P. ananatis* has been reported to cause rice leaf blight in India, Benin, Togo, and Russia (Egorova et al. 2015; Kini et al. 2017a, b, 2020; Mondal et al. 2011). In 2020, *P. ananatis* was identified as the causative agent for a new bacterial blight of rice emerged with 45 to 60% disease incidence in China (Xue et al. 2021; Yu et al. 2021). However, the complete genome sequences of pathogenic *P. ananatis* strains isolated from rice leaf in China remain to be determined and the genomic difference between strains from China and elsewhere is still unclear. Here, we present the whole-genome sequence of TZ39, the first identified pathogenic *P. ananatis* strain in China.

P. ananatis strain TZ39 was isolated from diseased rice leaves collected in Zhejiang Province, China, in 2020 by our group (Yu et al. 2021). Genomic DNA of TZ39 was extracted using the SDS method (Lim et al. 2016). SMRT Bell Template kit (version 1.0) and NEBNextUltra DNA Library Prep Kit for Illumina (NEB, U.S.A.) were used to construct

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Keywords

cereals and grains, vegetables, etiology, pathogen detection, pathogen diversity, viruses and viroids

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*The e-Xtra logo stands for “electronic extra” and indicates that one supplementary figure is published online.

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Table 1. Genome comparison between *Pantoea ananatis* TZ39 and LMG 2665^T

Strain ^a	Sequence state	Genomic type	Accession no.	Size (Mb)	GC (%)	Protein coding genes	ANI (%)
TZ39	complete	chromosome	CP081342	4,483,976	53.48	3,933	96.61
		plasmid 1	CP081343	135,135	50.25	106	
		plasmid 2	CP081344	276,579	52.08	243	
LMG 2665 ^T	draft	unplaced	JMJJ01	4,633,915	53.5	250	
		plasmid	JMJJ01000017	304,788	51.7	4,154	

^a LMG 2665^T is the type strain of *P. ananatis* that caused pineapple fruitlet rot (Adam et al. 2014).

sequencing library for PacBio Sequel and Illumina NovaSeq PE150 sequencing (Beijing Novogene Bioinformatics Technology Co., Ltd). In total, 150,626 reads from PacBio sequencing were obtained with mean concordance of 0.88, N50 value of 10,523 bp, and average read length of 9,053 bp, consisting of whole 1,363,583,566 bases. Quality filtered reads were assembled with SMRT Link (v5.0.1) (Ardui et al. 2018). Then, the Arrow algorithm was used for improving the genome assembly. Finally, circular chromosomes and plasmids were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (Tatusova et al. 2016). As a result, the assembly contains 4,518 genes, 123 pseudogenes, 22 rRNAs, and 78 tRNAs. Of 4,518 genes total, 299 were annotated to be secreted proteins by SignalP (Version 4.1) and TMHMM (Version 2.0c) (Eichinger et al. 2016; Petersen et al. 2011). Seven effectors belonging to type VI secretion system were detected, whereas the other secretion system effectors were absent. Otherwise, the genes encoding secondary metabolites (bacteriocin, siderophore, thiopeptide, terpene, and hserlactone) were predicted and annotated using antiSMASH 5.0 (Blin et al. 2019).

The genome of *P. ananatis* strain TZ39 was found to be composed of one unique circular chromosome and two unique circular plasmids (Table 1). The average nucleotide identity (ANI) of TZ39 is up to 96.61% with *P. ananatis* type strain LMG 2665^T calculated by NCBI, which suggests that TZ39 and LMG 2665^T belong to the same species. The chromosome was 4,483,976 bp in length, with 53.48% GC content, and was predicted to include 3,933 protein-coding genes. Plasmid 1 was 135,135 bp in length, with 50.25% GC content harboring 106 protein-encoding genes. Plasmid 2 was 276,579 bp in length, with 52.08% GC content covering 243 protein-encoding genes. The sequencing coverage of the genome was 278. The circular representation of the complete genome of *P. ananatis* strain TZ39 is shown in Supplementary Figure S1. Overall, the complete genome will provide a valuable resource for a better understanding of the functional analysis of genomic traits and the molecular pathogenesis of *P. ananatis* causing new bacterial blight of rice in China and worldwide.

Data Availability

The whole-genome sequences reported here have been deposited in GenBank (<https://www.ncbi.nlm.nih.gov/>) under the accession numbers CP081342 for chromosome, CP081343 for plasmid 1, and CP081344 for plasmid 2.

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