

Genome Resources of Three West African Strains of *Pantoea ananatis* Causing Bacterial Blight and Grain Discoloration of Rice

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Abstract

Members of the genus *Pantoea* have been reported as pathogens for many economically important crops, including rice. Little is known about their host–pathogen interactions at the molecular level and the lack of comprehensive genome data impedes targeted breeding strategies toward resistant rice cultivars. Here, we describe the structural and functional annotation of the draft genome sequences of three rice-pathogenic *Pantoea ananatis* strains, ARC272, ARC310, and ARC311, which were isolated in Burkina Faso, Togo, and Benin, respectively. The genome sequences of these strains will help in developing molecular diagnostic tools and provide new insight into common traits that may enable *P. ananatis* to infect rice.

Resource Announcement

Bacteria of the species *Pantoea ananatis* are implicated in diseases of a wide range of economically important crops, such as rice, maize, sorghum, and onion (Achbani et al. 2015; Cortesi and Pizzatti 2007; Cota et al. 2010; Egorova et al. 2015; Gitaitis and Gay 1997; Mondal et al. 2011; Yan et al. 2010) and are a serious threat for crop production across the globe (Coutinho and Venter 2009; Walterson and Stavrinides 2015; Weller-Stuart et al. 2017). *P. ananatis* was recently reported as being responsible for bacterial leaf blight of rice in several countries of sub-Saharan Africa, such as Benin, Burkina Faso, Mali, Nigeria, Senegal, and Togo (Kini et al. 2017a, b, 2018). Comparative genome sequence analyses revealed candidate pathogenicity determinants of Asian and American strains of *P. ananatis* (Asselin et al. 2018; De Maayer et al. 2011, 2014; Stice et al. 2018). To complement these data, we report the first genome sequences of West African *P. ananatis* strains, which were isolated from rice leaves or seeds in Benin, Burkina Faso, and Togo.

Bacteria were isolated during surveys carried out from 2010 to 2013 in several rice fields in West Africa. Two strains were isolated from leaves with symptoms resembling bacterial blight and one strain was isolated from a discolored rice grain (Table 1). Pure cultures were obtained using the protocol described by Kini et al. (2017a). Genomic DNA was extracted from the cultures using the Wizard genomic DNA purification kit of Promega (Madison, WI, U.S.A.) according to the manufacturer instructions. The genomes were sequenced using the Illumina

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

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Keywords

bacteriology, *Erwiniaceae*, genome sequence, *Pantoea ananatis*, rice pathogen, West Africa

Table 1. Project information and genomic features of *Pantoea ananatis* strains ARC272, ARC310, and ARC311

Strain	ARC272	ARC310	ARC311
Sample	Rice leaf	Rice leaf	Rice seed
Origin of sample	Burkina Faso: Bobo-Dioulasso, Bama	Togo: Deve	Benin
Collection date	22 Oct 2013	29 Jun 2010	2013
GenBank BioProject	PRJNA399058	PRJNA399062	PRJNA399063
GenBank BioSample	SAMN07522540	SAMN07522547	SAMN07522548
GenBank WGS project	PUGD000000000	PUGC000000000	PUGB000000000
Coverage	62x	90x	73x
Contigs	128	216	166
N50	72,412	36,729	47,567
L50	21	40	32
G+C content (%)	53.50	53.59	53.58
Genome size (bp)	4,615,013	4,598,241	4,593,415
Predicted genes	4,471	4,470	4,420
Protein-coding genes	4,258	4,234	4,180
RNA genes	104	105	107
Pseudo genes	109	131	133

HiSeq 2500 platform (Fasteris SA, Geneva, Switzerland). Nextera-Xt libraries (Illumina) with an insert size of 250 bp to 1.5 kb were generated and 125 sequencing cycles were performed from both sides. The shotgun sequencing yielded paired-end reads for 1,827,519 clusters (457 Mb) for strain ARC272, 2,690,980 clusters (673 Mb) for strain ARC310, and 2,211,169 clusters (553 Mb) for strain ARC311. Upon adapter removal, reads were assembled using the Edena algorithm v3.131028 (Hernandez et al. 2013). Contigs were annotated with GeneMarkS+ (revision 4.4) (Borodovsky and Lomsadze 2014), as implemented in the NCBI Prokaryotic Genome Annotation Pipeline (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/). The three draft genome sequences were each 4.6 Mbp in size and had an average G+C content of about 53.5% (Table 1). Between 4,420 and 4,471 genes were predicted for the three genomes, among which 95% were predicted to encode proteins (Table 1).

Genome-wide average nucleotide identities were calculated at <http://enve-omics.ce.gatech.edu> (Rodriguez-R and Konstantinidis 2016) and confirmed the taxonomic position of the three strains (Goris et al. 2007). Genome sequences of all three strains were >99% identical to those from *P. ananatis* strains that were collected from rice in China (strains PaMB1, RSA47, and Sd-1), India (strains NS296, NS303, and NS311), or Spain (strains 1.38 and AMG521) (Megías et al. 2016, 2018; Midha et al. 2016), and clearly distinct from those of the two other major plant-pathogenic *Pantoea* species, *P. agglomerans* and *P. stewartii* (Supplementary Table S1). Interestingly, the species *P. ananatis* forms two major clades, one of which apparently consists only of isolates originating from rice-associated samples, such as leaves, seeds, or the rhizosphere whereas the other clade includes strains from diverse origin, such as plants (e.g., eucalyptus, grasses, maize, onion, pineapple, strawberry, and sugarcane), but also insects and environmental samples. The three West African strains from this study belong to the rice-associated clade of *P. ananatis*. With this expanded geographic coverage, our new data sets represent a valuable resource for the functional analysis of genomic traits that might be involved in host range adaptation of *P. ananatis*.

Draft genome sequences of the three strains ARC272, ARC310, and ARC311 were deposited at NCBI GenBank under BioProject accession numbers PRJNA399058, PRJNA399062, and PRJNA399063, respectively. The three bacterial strains described in this study are available from the Africa Rice Center (<http://www.africarice.org>).

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