



Genome announcement

Whole genome sequence of *Pantoea ananatis* R100, an antagonistic bacterium isolated from rice seedLiwen Wu^{a,1}, Ruifang Liu^{a,b,1}, Yaofang Niu^{a,1}, Haiyan Lin^{a,b,1}, Weijun Ye^{a,1}, Longbiao Guo^{a,*,1}, Xingming Hu^{a,*,1}^a State Key Lab for Rice Biology, China National Rice Research Institute, Hangzhou 310006, PR China^b Agricultural Genomes Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen 518120, PR China

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ABSTRACT

Pantoea ananatis is a group of bacteria, which was first reported as plant pathogen. Recently, several papers also described its biocontrol ability. In 2003, *P. ananatis* R100, which showed strong antagonism against several plant pathogens, was isolated from rice seeds. In this study, whole genome sequence of this strain was determined by SMRT Cell technology. The total genome size of R100 is 4,857,861 bp with 4659 coding genes (CDS), 82 tRNAs and 22 rRNAs. The genome sequence of R100 may shed a light on the research of antagonism *P. ananatis*.

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Pantoea ananatis has long been recognized as phytopathogen, which can cause diseases in a wide range of economically important crops and forest tree (Coutinho and Venter, 2009). Except that, some *P. ananatis* has also been reported to show antagonism ability against some plant pathogens (Enya et al., 2007; Smits et al., 2010). In 2003, former colleagues in our institute isolated R100 from rice seed samples (Xie et al., 2003). Inhibition analysis indicated its biocontrol ability against *Acidovorax avenae* subsp. *avenae*, which is the causal agent of brown blight stripe on rice (Liu et al., 2014). Also, plant inoculation confirmed that this strain is non-pathogenic to rice, indicating its application potential on biocontrol. To further understand the details about this strain, whole genome sequencing was carried out in this study.

The culture of strain R100 used to prepare genomic DNA for sequencing was a laboratory stock and grown on LB (Luria Broth, BD, USA) at 30 °C with vigorous shaking. 2 ml of culture broth was used to isolate the genomic DNA. DNA was isolated by Wizard Genomic DNA Purification Kit (Promega, Madison, WI, USA). The genome of R100 was done by Guhe info by using the PacBio RS II platform. Around 2Gb data was obtained with 350X average coverage. After quality control, genome assembly was done by SMRT

Analysis 2.2.1 and the annotation of protein coding genes, tRNA and rRNA was done by RAST pipeline (Aziz et al., 2008).

The total size of the genome is 4,857,861 bp and has a GC content of 53.62%. A total of 4,659 CDSs were predicted. Of these, 3784 could be assigned to a COG number. The most abundant COG category was “General function prediction only” (471 proteins) followed by “Amino acid transport and metabolism” (451 proteins), “Carbohydrate transport and metabolism” (437 proteins), “Transcription” (373 proteins), and “Signal transduction mechanisms” (304 proteins). In addition, 104 RNAs including rRNA and tRNA were identified. All the genomic information was shown in Table 1.

Antagonistic bacteria usually compete with other bacteria by using secondary metabolism such as pantocin A and dapidamide E, which has been reported in previous *P. ananatis* strain (Smits et al., 2010). In R100, we found integrated oxazolomycin and chalcocyanin biosynthesis gene clusters. Oxazolomycin is a β-lactone antibiotic, which was first reported in 1985 (Mori et al., 1985). Oxazolomycin also showed its antiviral activity based on previous research (Tonew et al., 1992). Calicheamicin, which showed antibacterial activity against a spectrum of Gram-positive and Gram-negative bacteria, was first reported in 1980s (Maiese et al., 1989). These results indicate that R100 can be used as biocontrol agent.

Last, we compared R100 to the *P. ananatis* reference genome LMG 5342, which was isolated from human wound (De Maayer et al., 2012). Generally, more than 92% of the coding genes have homologs in R100, indicating the low diversity among the *P. ana-*

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Table 1
Genome statistics.

Features	Value
Genome size (bp)	4,857,861
Chromosome numbers	1
Plasmid number	1
G + C%	53.62
Protein-coding genes	4659
Protein with function	3738
tRNA number	82
rRNA operon number	7
ncRNA number	89
Genes with signal peptides	1026

natis species. Strikingly, we found only one type III secretion system coding gene exists in R100, indicating its non-pathogenicity on plant and human. Also, genomic islands (GIs) prediction by IslandViewer revealed that no GIs exist in R100 genome (Langille and Brinkman, 2009). This result indicated that the secondary metabolism in R100 was not horizontally transferred from other organisms, which is different from some previous researches (Shi et al., 2015).

In conclusion, we sequenced the genome of *P. ananatis* strain R100, which was isolated from rice seed. Genomic analysis found it contains a lot of secondary metabolism associated genes including oxazolomycin and chalcomycin biosynthesis gene clusters. By comparison with model strain LMG 5342, we found only one type III secretion system coding gene is exist in R100, indicating its non-pathogenicity on plant and human. Overall, the genome of this stain gives us the new insight of biocontrol bacteria.

Strain and nucleotide sequence accession numbers

This strain has been deposited in CGMCC with deposit number as CGMCC 1.15633. Nucleotide sequence accession numbers: This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank. The BioProject designation for this project is PRJNA310041 and the accession number is CP014207 for chromosome and CP014208 for plasmid.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.jbiotec.2016.03.007>.

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