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Data in Brief

Complete genome sequence of *Erysipelothrix rhusiopathiae* strain GXBY-1 isolated from acute swine erysipelas outbreaks in south China

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ABSTRACT

Erysipelothrix rhusiopathiae (*E. rhusiopathiae*) is an important pathogenic microorganism affecting swine industry. Here, we report the finished annotated genome sequence of *E. rhusiopathiae* GXBY-1, isolated from acute swine erysipelas in Binyang County, Guangxi, China. The GXBY-1 strain, which exhibits high pathogenicity for swine, contains 1,876,490 bp with G + C content of 36.50%, and contains 1734 protein-coding genes, 57 tRNAs and 27 rRNAs. The nucleotide sequence of this genome was deposited into GenBank under the accession CP014861.

Specifications	
Organism/cell line/tissue	*Erysipelothrix rhusiopathiae*
Strain	GXBY-1
Sequencing Technology	Illumina
Data format	Genome Assembly
Experimental factors	Microbial strain
Experimental features	Genome sequencing
Consent	Data are publicly available
Sample source location	Binyang County, Guangxi, China

1. Direct link to deposited data

Deposited data can be found here: http://www.ncbi.nlm.nih.gov/nuccore/cp014861.

2. Experimental design, materials, and methods

Erysipelothrix rhusiopathiae is a gram-positive, non-sporeforming, slender and straight or slightly rod-shaped bacterium that causes erysipelas in swine and a wide spectrum of diseases in other animals, like sheep, birds, reptiles, amphibians, and some fishes [1]. This bacterium is ubiquitous in environment and in reservoir of asymptomatic carriers among both domestic and wild animals. Among the 23 serotypes of *E. rhusiopathiae*, serotypes 1a, 1b and 2 are the best known as the etiological agents affecting swine industry [2–5].

*E. rhusiopathiae*s vary widely in their morphology, host specificity and/or pathogenicity and little is known about the correlation of their proteins to virulence. *E. rhusiopathiae* GXBY-1, isolated from acute swine erysipelas in Binyang County, Guangxi Province, China, exhibits high pathogenic for mouse and swine. In order to elucidate the genetic background of this pathogenic strain and get deep insights into the virulence-associated proteins of this strain, we sequenced the complete genome of *E. rhusiopathiae* GXBY-1.

The genome of *E. rhusiopathiae* GXBY-1 was sequenced at Beijing Genomics Institute (BGI, Shenzhen, China) using Illumina Hiseq 2000 system. A total of 300 million high-quality base pairs were produced with 62-fold coverage of the genome, and then were assembled into 11 contigs by using SOAP denovo software [6–7], after which the contigs were joined into 2 scaffolds with paired-end information. Gene predictions and annotations were performed using the Glimmer software (version 3.02) [8] and tRNA and rRNA genes were identified by tRNAscan [9] and rRNAmmer [10], respectively. All genes were further categorized according to SwissProt, GO (Gene Ontology) and KEGG (Kyoto Ency-clopedia of Genes and Genomes).

The complete genome of *E. rhusiopathiae* GXBY-1 consists of one 1,876,490 bp circular chromosome with no plasmid. And its chromosome contains 1734 predicted open reading frames (ORFs) and the total length of genes is 1,668,564 bp, which makes up 88.36% of the

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Table 1
General features of *E. rhusiopathiae* GXBY-1 genome.

Attributes	Value
Genome size (bp)	1,876,490
G + C content (%)	36.50
Total predicted CDSs	1734
Plasmid	0
rRNAs	27
tRNAs	57

genome. The G + C content of the chromosome is 36.50% and encodes 57 tRNA and 27 rRNA operons (Table 1).

The GXBY-1 strain genome not only enriches the genome database of E. rhusiopathiae, but also supports and extends previous studies, and provides fundamental information for further studies.

3. Nucleotide sequence accession number

The genome sequence of *E. rhusiopathiae* GXBY-1 has been deposited in NCBI GenBank under accession number CP014861.

Conflict of interest

The authors declare that there is no conflict of interests with respect to the work published in this paper.

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