

Genome Sequence of Mushroom Soft-Rot Pathogen *Janthinobacterium agaricidamnorum*

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***Janthinobacterium agaricidamnorum* causes soft-rot disease of the cultured button mushroom *Agaricus bisporus* and is thus responsible for agricultural losses. Here, we present the genome sequence of *J. agaricidamnorum* DSM 9628. The 5.9-Mb genome harbors several secondary metabolite biosynthesis gene clusters, which renders this neglected bacterium a promising source for genome mining approaches.**

Received 26 February 2015 Accepted 3 March 2015 Published 16 April 2015

Citation Graupner K, Lackner G, Hertweck C. 2015. Genome sequence of mushroom soft-rot pathogen *Janthinobacterium agaricidamnorum*. *Genome Announc* 3(2):e00277-15. doi:10.1128/genomeA.00277-15.

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The soft-rot disease of the cultured button mushroom *Agaricus bisporus* results from an infection with the Gram-negative bacterium *Janthinobacterium agaricidamnorum* (1). Despite its devastating disease outcome that accounts for substantial losses in agriculture, the pathobiology of the soft-rot disease has not been investigated in the past. Recently, we discovered that the cyclic lipopeptide jagaricin is involved in the soft-rot infection process (2). Moreover, jagaricin exhibits strong antifungal activity against major human pathogenic fungi (2).

The genome of *J. agaricidamnorum* DSM 9628 was sequenced using the 454 GS FLX Titanium system (282,254 reads) with an 8-kb paired-end library (405,849 reads) to a 24-fold coverage. The Newbler assembler (454 Life Science) was used for assembly of the sequencing reads. 167 contigs (N_{50} contig size 113,797 bp) were assembled into 9 scaffolds (N_{50} scaffold size 595,787 bp). Gene annotation was carried out by the IGS (Institute for Genome Science, University of Maryland, School of Medicine) prokaryotic annotation platform (3). The genome of *J. agaricidamnorum* has a total size of 5,949,001 bp, has an overall G+C content of 61%, and consists of 5,573 open reading frames, of which 4,327 (77.6%) were assigned a biological function.

In addition to the characterized jagaricin biosynthesis gene cluster (2), whole-genome sequencing of *J. agaricidamnorum* revealed a gene locus for violacein production (2, 4, 5) as well as several orphan natural product biosynthesis gene clusters: Three gene clusters coding for nonribosomal peptide synthetases (NRPSs), one hybrid NRPS-polyketide synthase (PKS) gene cluster, one putative siderophore biosynthesis gene cluster, and one bacteriocin biosynthesis gene cluster. This genome analysis highlights that such neglected bacteria can be a hidden source for novel secondary metabolites (6).

To date, seven genomes of *Janthinobacterium* spp. are accessible by the DDBJ/EMBL/GenBank databases, and five of them have been published (7–11). However, *J. agaricidamnorum* is the first pathogenic *Janthinobacterium* that has been sequenced. The other

Janthinobacterium spp. sequenced so far have been isolated from water, glaciers, soil, and rhizosphere.

Insight into the genome of *J. agaricidamnorum* not only reveals a high potential to produce secondary metabolites, but it could also aid in investigating the mechanism of soft-rot infection.

Nucleotide sequence accession number. The genome sequence of *J. agaricidamnorum* has been deposited in DDBJ/EMBL/GenBank under the accession no. [HG322949](https://www.ncbi.nlm.nih.gov/nuccore/HG322949). The version described in this paper is the first version.

ACKNOWLEDGMENTS

We thank the Institute for Genome Science (University of Maryland, School of Medicine) for kindly providing the IGS prokaryotic annotation service.

This research was supported by the International Leibniz Research School for Microbial and Biomolecular Interactions (ILRS) as part of the excellence graduate school Jena School for Microbial Communication (JSMC).

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