Genomics Data 10 (2016) 135–136

Contents lists available at ScienceDirect

Genomics Data

journal homepage: www.elsevier.com/locate/gdata

Data in Brief

Complete genome sequence of the biofilm-forming *Curtobacterium* sp. strain BH-2-1-1, isolated from lettuce (*Lactuca sativa*) originating from a conventional field in Norway

Merete Wiken Dees *, May Bente Brurberg, Erik Lysøe

NIBIO, The Norwegian Institute of Bioeconomy Research, N-1431, Ås, Norway

ARTICLE INFO

Article history:
Received 24 October 2016
Accepted 2 November 2016
Available online 5 November 2016

Keywords:
Epiphytic bacteria
Lettuce
Curtobacterium sp.
whole genome sequencing

ABSTRACT

Here, we present the 3,795,952 bp complete genome sequence of the biofilm-forming *Curtobacterium* sp. strain BH-2-1-1, isolated from conventionally grown lettuce (*Lactuca sativa*) from a field in Vestfold, Norway. The nucleotide sequence of this genome was deposited into NCBI GenBank under the accession CP017580.

© 2016 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

Specifications	
Organism/cell line/tissue	*Curtobacterium* sp.
Strain	BH-2-1-1
Sequencer or array type	PacBio RS II
Data format	Analyzed
Experimental factors	Bacterial strain
Experimental features	Whole genome analysis and gene annotation of BH-2-1-1
Sample source location	Lettuce (*Lactuca sativa*) from a conventional field in Vestfold, Norway

1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/CP017580

2. Experimental design, materials and methods

The phyllosphere is a habitat on the surface of plant leaves colonized by a variety of bacteria, yeasts, and fungi [1]. It harbors epiphytes, as well as plant-pathogenic bacteria. The Gram-positive genus *Curtobacterium* belongs to the family Microbacteriaceae, within the phylum Actinobacteria. The genus includes a wide range of species associated with plants as either epiphytes or pathogens [2–4]. A yellow-pigmented biofilm-forming *Curteobacterium* sp. strain BH-2-1-1 was isolated from the leaf surface of conventionally grown lettuce (*Lactuca sativa*) in Vestfold, Norway [5]. Genomic DNA was extracted using Genomic-tip 500/G kit (Qiagen GmbH, Hilden, Germany), a library was created using PacBio (Pacific Biosciences, California, USA) 20 kb library preparation protocol and whole genome sequencing was performed using PacBio RS II. The library was sequenced using P6-C4 chemistry with 360 min movie time on one single-molecule real-time (SMRT) cell. The reads were assembled using HGAP v3 (Pacific Biosciences, SMRT Analysis Software v2.3.0). The Minimus2 software of the Amos package was used to circularize the contig, which was confirmed by a dot plot to contain the same sequence at the beginning and end of the contig. RS_Resequencing.1 software (SMRT Analysis version v2.3.0) was used to map reads back to the assembled and circularized sequence in order to correct the sequence after circularization. The sequencing service was provided by the Norwegian Sequencing Centre (www.sequencing.uio.no), a national technology platform hosted by the University of Oslo and supported by the "Functional Genomics" and "Infrastructure" programs of the Research Council of Norway and the Southeastern Regional Health Authorities.

3. Data description

The genome of *Curtobacterium* sp. BH-2-1-1 was annotated using the NCBI Prokaryotic Genome Annotation Pipeline [6], GeneMarkS + v 3.3 and the Rapid Annotation System Technology (RAST) server [7]. Fig. 1 presents an overview of the count of each subsystem feature and the subsystem coverage. The circular chromosome has a GC content of 71.4%, consisted of 3,795,952 bp and contained 3515 coding sequences (CDSs), 9 rRNA genes, 47 tRNAs, and 4 noncoding RNA (ncRNA) genes.

* Corresponding author at: NIBIO, The Norwegian Institute of Bioeconomy Research, N-1431 Ås, Norway.
E-mail address: merete.wiken.dees@nibio.no (M.W. Dees).

http://dx.doi.org/10.1016/j.gdata.2016.11.003
2213-5960/© 2016 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

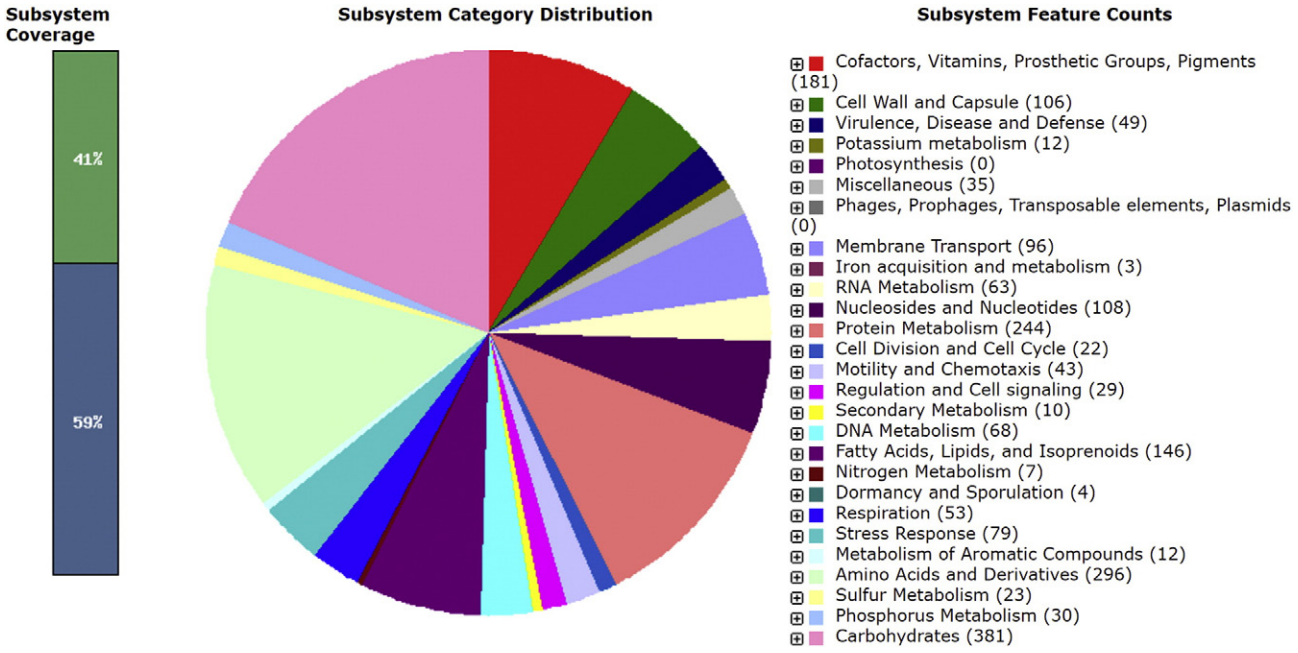

Fig. 1. Subsystem category distribution of major protein coding genes of *Curtobacterium* sp. strain BH-2-1-1 as annotated by the RAST annotation server. The bar chart shows the subsystem coverage in percentage (blue bar corresponds to percentage of proteins included). The pie chart shows percentage distribution of the 25 most abundant subsystem categories.

4. Nucleotide accession number

This whole genome project has been deposited at NCBI GenBank under the accession number CP017580.

Acknowledgements

We are grateful to Hege Særvold Steen for preparing the DNA. This study was supported by a grant from the Norwegian Research Council (221663/F40).

References

[1] S.E. Lindow, M.T. Brandl, Microbiology of the phyllosphere. Appl. Environ. Microbiol. 69 (2003) 1875–1883.
[2] F. Hedges, A bacterial wilt of the bean caused by *Bacterium flaccumfaciens* nov sp. Science 55 (1922) 433–434.
[3] K. Yamada, K. Komagata, Taxonomic studies on Coryneform bacteria. V. Classification of Coryneform bacteria. J. Gen. Appl. Microbiol. 18 (1972) 417–431.
[4] D.K. Zinniel, P. Lambrecht, N.B. Harris, Z. Feng, D. Kuczmarski, P. Higley, C.A. Ishimaru, A. Arunakumari, R.G. Barletta, A.K. Vidaver, Isolation and characterization of endophytic colonizing bacteria from agronomic crops and prairie plants. Appl. Environ. Microbiol. 68 (2002) 2198–2208.
[5] M.W. Dees, E. Lysoe, B. Nordskog, M.B. Brurberg, Bacterial communities associated with surfaces of leafy greens: Shift in composition and decrease in richness over time. Appl. Environ. Microbiol. 81 (2015) 1530–1539.
[6] T. Tatusova, M. DiCuccio, A. Badretdin, V. Chetvernin, S. Ciufo, W. Li, Prokaryotic Genome Annotation Pipeline, the NCBI Handbook. second ed. National Center for Biotechnology Information, Bethesda, MD, 2013.
[7] R.K. Aziz, D. Bartels, A.A. Best, M. DeJongh, T. Disz, R.A. Edwards, ... O. Zagnitko, The RAST server: Rapid annotations using subsystems technology. BMC Genomics 9 (2008) 75.