



Aalborg Universitet

AALBORG UNIVERSITY  
DENMARK

## High-quality draft genome sequence of *Sphaerisporangium cinnabarinum* ATCC 31213

Christensen, Line Friis Bakmann; Otzen, Daniel; Dueholm, Morten Simonsen

*Published in:*  
Genome Announcements

*DOI (link to publication from Publisher):*  
[10.1128/genomeA.00456-18](https://doi.org/10.1128/genomeA.00456-18)

*Creative Commons License*  
CC BY 4.0

*Publication date:*  
2018

*Document Version*  
Publisher's PDF, also known as Version of record

[Link to publication from Aalborg University](#)

*Citation for published version (APA):*  
Christensen, L. F. B., Otzen, D., & Dueholm, M. S. (2018). High-quality draft genome sequence of *Sphaerisporangium cinnabarinum* ATCC 31213. *Genome Announcements*, 6(21), [e00456-18].  
<https://doi.org/10.1128/genomeA.00456-18>

### General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- ? Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- ? You may not further distribute the material or use it for any profit-making activity or commercial gain
- ? You may freely distribute the URL identifying the publication in the public portal ?

### Take down policy

If you believe that this document breaches copyright please contact us at [vbn@aub.aau.dk](mailto:vbn@aub.aau.dk) providing details, and we will remove access to the work immediately and investigate your claim.



# High-Quality Draft Genome Sequence of *Sphaerisporangium cinnabarinum* ATCC 31213

Line Friis Bakmann Christensen,<sup>a</sup> Daniel Otzen,<sup>a</sup>  Morten Simonsen Dueholm<sup>b</sup>

<sup>a</sup>Department of Molecular Biology, Interdisciplinary Nanoscience Center (iNANO), Aarhus University, Aarhus, Denmark

<sup>b</sup>Department of Chemistry and Bioscience, Center for Microbial Communities, Aalborg University, Aalborg, Denmark

**ABSTRACT** A high-quality draft genome sequence of *Sphaerisporangium cinnabarinum* ATCC 31213 is presented here. This bacterium produces several important bioactive compounds and may also produce functional amyloids. This is the first sequenced genome from the genus *Sphaerisporangium*, and it will be essential in determining the nature of the potential amyloid protein.

Members of the genus *Sphaerisporangium* are aerobic Gram-positive bacteria that form mycelia and spherical sporangia (1). They are primarily found in soils (2, 3), often in association with the rhizosphere (4–7). Many members of the genus produce bioactive secondary metabolites (8–12) and can also be used for the biotransformation of antimicrobials (13).

*Sphaerisporangium cinnabarinum* (previously referred to as *Streptosporangium cinnabarinum*) strain ATCC 31213 was originally isolated in 1977 from soil in the Philippines and was shown to produce two different antibiotics effective against strains of *Staphylococcus aureus*, *Mycobacterium smegmatis*, and *Bacillus subtilis* (14). Another antibiotic produced by *S. cinnabarinum*, the secondary metabolite GE82832, specifically inhibits translation in bacteria (10–12). *S. cinnabarinum* also produces 1-hydroxy-4-methoxy-2-naphthoic acid, which is an effective herbicide against the freshwater plant *Lemna minor* (15). Recently, *S. cinnabarinum* was proposed to form functional amyloids, as the mycelia showed strong binding to conformation-specific antibodies that recognize a generic amyloid fibril epitope (16, 17). Further studies of *S. cinnabarinum*, including identification of the proposed amyloid protein and identification of pathways for antibiotic synthesis, would benefit from this genome announcement.

Genomic DNA was isolated using a FastDNA spin kit (MP Biomedicals). A paired-end library was prepared with the NEBNext Ultra II DNA library prep kit for Illumina (New England BioLabs). All procedures were carried out as recommended by the manufacturer. Sequencing of the libraries was performed using a MiSeq sequencer (Illumina, Germany). The paired-end reads were trimmed for adapters and quality using the built-in tool of CLC Genomics Workbench version 9.5.5 (Qiagen, USA). The genome was *de novo* assembled from the paired-end data in CLC Genomics Workbench using the default settings. The average coverage of the assembly was 60×. Annotation was done using the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (18).

The draft genome sequence of *S. cinnabarinum* strain ATCC 31213 is composed of 134 contigs and has a predicted size of ~4.39 Mbp. The overall G+C content is 74.7%. Annotation by the NCBI PGAAP identified 3,988 coding sequences (CDSs), as well as 3 rRNA (5S, 16S, or 23S) and 51 tRNA genes.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [QAPD00000000](https://doi.org/10.1128/genomeA.00456-18). The version described in this paper is the first version, QAPD01000000.

Received 18 April 2018 Accepted 18 April 2018 Published 24 May 2018

**Citation** Christensen LFB, Otzen D, Dueholm MS. 2018. High-quality draft genome sequence of *Sphaerisporangium cinnabarinum* ATCC 31213. *Genome Announc* 6:e00456-18. <https://doi.org/10.1128/genomeA.00456-18>.

**Copyright** © 2018 Christensen et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Morten Simonsen Dueholm, [md@bio.aau.dk](mailto:md@bio.aau.dk).

## ACKNOWLEDGMENT

This study was supported by the EU Joint Programme–Neurodegenerative Disease Research (JPND).

## REFERENCES

1. Ara I, Kudo T. 2007. *Sphaerosporangium* gen. nov., a new member of the family Streptosporangiaceae, with descriptions of three new species as *Sphaerosporangium melleum* sp. nov., *Sphaerosporangium rubeum* sp. nov. and *Sphaerosporangium cinnabarinum* sp. nov., and transfer of *Streptosporangium viridialbum* Nonomura and Ohara 1960 to *Sphaerosporangium viridialbum* comb. nov. Actinomycetologica 21:11–21. <https://doi.org/10.3209/saj.SAJ210102>.
2. Guo L, Zhao J, Liu C, Bai L, Sun P, Han C, Li J, Guo X, Xiang W, Wang X. 2015. *Sphaerisporangium aureirubrum* sp. nov., an actinomycete isolated from soil. Int J Syst Evol Microbiol 65:4157–4162. <https://doi.org/10.1099/ijsem.0.000554>.
3. Suriyachadkun C, Chunhametha S, Ngaemthao W, Tamura T, Kirtikara K, Sanglier J-J, Kitpreechavanich V. 2011. *Sphaerisporangium krabiense* sp. nov., isolated from soil. Int J Syst Evol Microbiol 61:2890–2894. <https://doi.org/10.1099/ijms.0.027151-0>.
4. Wang X, Liu C, Cheng J, Zhang Y, Ma Z, Li L, Wang X, Xiang W. 2015. *Sphaerisporangium corydalis* sp. nov., isolated from the root of *Corydalis yanhusuo* L. Antonie van Leeuwenhoek 108:133–139. <https://doi.org/10.1007/s10482-015-0471-x>.
5. Xing J, Liu C, Zhang Y, He H, Zhou Y, Li L, Zhao J, Liu S, Wang X, Xiang W. 2015. *Sphaerisporangium dianthi* sp. nov., an endophytic actinomycete isolated from a root of *Dianthus chinensis* L. Antonie van Leeuwenhoek 107:9–14. <https://doi.org/10.1007/s10482-014-0298-x>.
6. Mingma R, Duangmal K, Trakulnaleamsai S, Thamchaipenet A, Matsumoto A, Takahashi Y. 2014. *Sphaerisporangium rufum* sp. nov., an endophytic actinomycete from roots of *Oryza sativa* L. Int J Syst Evol Microbiol 64:1077–1082. <https://doi.org/10.1099/ijms.0.057885-0>.
7. Duangmal K, Mingma R, Pathom-Aree W, Inahashi Y, Matsumoto A, Thamchaipenet A, Takahashi Y. 2011. *Sphaerisporangium siamense* sp. nov., an actinomycete isolated from rubber-tree rhizospheric soil. J Antibiot 64:293–296. <https://doi.org/10.1038/ja.2011.17>.
8. Kawahara T, Itoh M, Izumikawa M, Hashimoto J, Sakata N, Tsuchida T, Shin-Ya K. 2015. MBJ-0086 and MBJ-0087, new bicyclic depsipeptides, from *Sphaerisporangium* sp. 33226. J Antibiot (Tokyo) 68:67–70. <https://doi.org/10.1038/ja.2014.98>.
9. Janso JE, Carter GT. 2010. Biosynthetic potential of phylogenetically unique endophytic actinomycetes from tropical plants. Appl Environ Microbiol 76:4377–4386. <https://doi.org/10.1128/AEM.02959-09>.
10. Brandi L, Fabbretti A, Di Stefano M, Lazzarini A, Abbondi M, Gualerzi CO. 2006. Characterization of GE82832, a peptide inhibitor of translocation interacting with bacterial 30S ribosomal subunits. RNA 12:1262–1270. <https://doi.org/10.1261/rna.61206>.
11. Brandi L, Maffioli S, Donadio S, Quaglia F, Sette M, Milón P, Gualerzi CO, Fabbretti A. 2012. Structural and functional characterization of the bacterial translocation inhibitor GE82832. FEBS Lett 586:3373–3378. <https://doi.org/10.1016/j.febslet.2012.07.040>.
12. Bulkley D, Brandi L, Polikanov YS, Fabbretti A, O'Connor M, Gualerzi CO, Steitz TA. 2014. The antibiotics dityromycin and GE82832 bind protein S12 and block EF-G-catalyzed translocation. Cell Rep 6:357–365. <https://doi.org/10.1016/j.celrep.2013.12.024>.
13. Sasamura S, Muramatsu H, Takase S, Fujie A, Fujii T, Hino M, Sakamoto K, Hashimoto M. 2010. Bioconversion of AS1387392: screening and characterization of actinomycetes that convert AS1387392 to AS1429716. J Antibiot 63:637–642. <https://doi.org/10.1038/ja.2010.89>.
14. Celmer WD, Cullen WP, Moppett CE, Routien JB, Jefferson MT, Shibakawa R, Tone J. June 1977. Mixture of antibiotics produced by new species of *Streptosporangium*. US patent US4,032,632A.
15. Pfefferle C, Breinholt J, Gürtler H, Fiedler H-P. 1997. 1-Hydroxy-4-methoxy-2-naphthoic acid, a herbicidal compound produced by *Streptosporangium cinnabarinum* ATCC 31213. J Antibiot (Tokyo) 50:1067–1068. <https://doi.org/10.7164/antibiotics.50.1067>.
16. O'Nuallain B, Wetzel R. 2002. Conformational Abs recognizing a generic amyloid fibril epitope. Proc Natl Acad Sci U S A 99:1485–1490. <https://doi.org/10.1073/pnas.022662599>.
17. Jordal PB, Dueholm MS, Larsen P, Petersen SV, Enghild JJ, Christiansen G, Højrup P, Nielsen PH, Otzen DE. 2009. Widespread abundance of functional bacterial amyloid in mycolata and other Gram-positive bacteria. Appl Environ Microbiol 75:4101–4110. <https://doi.org/10.1128/AEM.02107-08>.
18. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity GM, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta) genomic annotation. OMICS 12:137–141. <https://doi.org/10.1089/omi.2008.0017>.