RADAR
Research Archive and Digital Asset Repository

OXFORD BROOKES UNIVERSITY

Kwun, M and Hong, H

Draft Genome Sequence of Amycolatopsis lurida NRRL 2430, Producer of the Glycopeptide Family Antibiotic Ristocetin

Kwun, M and Hong, H (2014) Draft Genome Sequence of Amycolatopsis lurida NRRL 2430, Producer of the Glycopeptide Family Antibiotic Ristocetin..*Genome Announcements*, 2 (5). pp. e01050-14.

doi: 10.1128/genomeA.01050-14

This version is available: https://radar.brookes.ac.uk/radar/items/7bd58ce1-a4e4-4da3-af32-ecc5e23d10ed/1/

Available on RADAR: July 2016
Copyright © and Moral Rights are retained by the author(s) and/ or other copyright owners. A copy can be downloaded for personal non-commercial research or study, without prior permission or charge. This item cannot be reproduced or quoted extensively from without first obtaining permission in writing from the copyright holder(s). The content must not be changed in any way or sold commercially in any format or medium without the formal permission of the copyright holders.

This document is the published version of the journal article.

WWW.BROOKES.AC.UK/GO/RADAR

genomeA
Journals.ASM.org

Draft Genome Sequence of *Amycolatopsis lurida* NRRL 2430, Producer of the Glycopeptide Family Antibiotic Ristocetin

Min Jung Kwun, Hee-Jeon Hong

Department of Biochemistry, University of Cambridge, Cambridge, United Kingdom

We report here the first draft genome sequence for *Amycolatopsis lurida* NRRL 2430, the producer of the glycopeptide antibiotic ristocetin. The 9-Mbp genome is predicted to harbor 8,143 genes, including those belonging to the ristocetin biosynthesis cluster and 31 additional predicted secondary metabolite gene clusters.

Received 9 September 2014 **Accepted** 10 September 2014 **Published** 16 October 2014

Citation Kwun MJ, Hong H-J. 2014. Draft genome sequence of *Amycolatopsis lurida* NRRL 2430, producer of the glycopeptide family antibiotic ristocetin. Genome Announc. 2(5):e01050-14. doi:10.1128/genomeA.01050-14.

Copyright © 2014 Kwun and Hong. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Hee-Jeon Hong, hh309@cam.ac.uk.

The glycopeptide family antibiotic ristocetin was originally used to treat Gram-positive pathogenic infections in humans, particularly staphylococcal infections. This use was soon discontinued, however, due to toxic side effects related to its ability to cause thrombocytopenia and platelet agglutination (1). Today, ristocetin is applied to the *in vitro* diagnosis of conditions, such as von Willebrand disease and Bernard-Soulier syndrome; blood from patients with the syndromes fail to exhibit a platelet agglutination response to ristocetin due to an absence of von Willebrand factor or its receptor (2). *Amycolatopsis lurida* is known to be the only producer of commercial ristocetin so far, but neither the whole-genome sequence information nor the sequence of its ristocetin synthetic gene cluster have been available. The sequence of the ristocetin biosynthesis gene cluster from *A. lurida* was recently published (GenBank accession no. KJ364518) (3).

The *A. lurida* NRRL 2430 genome was sequenced to 67-fold coverage using an Illumina MiSeq instrument, and it was assembled using the GS *de novo* Assembler (Newbler software version 2.9). A total of 1,993,479 reads were assembled into 101 contigs to produce a draft genome with an estimated size of 8,987,656 bp. The average contig size is 73,852 bp, and the largest single contig contains 424,186 bp. Annotation of the genome was performed using the NCBI Prokaryotic Genome Annotation Pipeline (4) with GeneMarkS+ (5). This annotation predicted 8,143 coding sequences (CDSs) with 109 pseudogenes, 54 tRNAs, two 5S rRNAs, one 23S rRNA, and an overall G+C content of 68.71%. The assembled draft genome sequence does not include any identifiable sequence for 16S rRNA, so we separately sequenced 16S rRNA in *A. lurida* NRRL 2430. Among several 16S rRNAs of different type strains of *A. lurida* available in the GenBank database, the 16S rRNA sequence from *A. lurida* NRRL 2430 perfectly matched one under the accession no. AJ577997 (6). According to the phylogenetic analysis of the 16S rRNA sequences, *A. lurida* NRRL 2430 is taxonomically most closely related to the strain *Amycolatopsis orientalis* HCCB10007, with 99% 16S rRNA identity. Analysis for secondary metabolite gene clusters using antiSMASH (7) identified 32 predicted clusters in the *A. lurida* NRRL 2430 genome, including the ristocetin synthetic gene cluster and clusters putatively responsible for producing terpenes, bacteriocins, type I, II, and III polyketide antibiotics, nonribosomal peptide synthetase (NRPS) compounds, ectoine, and several other unknown compounds

The genome information for *A. lurida* NRRL 2430 will help with understanding the mechanisms involved in the regulation of ristocetin biosynthesis, as well as assist the search for both new bioactive microbial metabolites and novel secondary metabolite-related enzyme activities.

Nucleotide sequence accession numbers. The draft genome sequence of *A. lurida* NRRL 2430 has been deposited in the DDBJ/EMBL/GenBank database under the accession no. JFBM00000000. The version described in this paper is the first version, JFBM01000000.

ACKNOWLEDGMENTS

This work was supported by the grants from the Royal Society (516002.K5877/ROG) and the Medical Research Council (G0700141).

REFERENCES

1. **Weiss HJ, Rogers J, Brand H.** 1973. Defective ristocetin-induced platelet aggregation in von Willebrand's disease and its correction by factor VIII. J. Clin. Invest. **52:**2697–2707. http://dx.doi.org/10.1172/JCI107464.
2. **Sarji KE, Stratton RD, Wagner RH, Brinkhous KM.** 1974. Nature of von Willebrand factor: a new assay and a specific inhibitor. Proc. Natl. Acad. Sci. U. S. A. **71:**2937–2941. http://dx.doi.org/10.1073/pnas.71.8.2937.
3. **Truman AW, Kwun MJ, Cheng J, Yang SH, Suh JW, Hong HJ.** 2014. Antibiotic resistance mechanisms inform discovery: identification and characterization of a novel *Amycolatopsis* strain producing ristocetin. Antimicrob. Agents Chemother., in press. http://dx.doi.org/10.1128/AAC.03349-14.
4. **Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, 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. http://dx.doi.org/10.1089/omi.2008.0017.
5. **Lukashin AV, Borodovsky M.** 1998. GeneMark.hmm: new solutions for gene finding. Nucleic Acids Res. **26:**1107–1115. http://dx.doi.org/10.1093/nar/26.4.1107.
6. **Wink J, Gandhi J, Kroppenstedt RM, Seibert G, Sträubler B, Schumann P, Stackebrandt E.** 2004. *Amycolatopsis decaplanina* sp. nov., a novel member of the genus with unusual morphology. Int. J. Syst. Evol. Microbiol. **54:**235–239. http://dx.doi.org/10.1099/ijs.0.02586-0.
7. **Blin K, Medema MH, Kazempour D, Fischbach MA, Breitling R, Takano E, Weber T.** 2013. antiSMASH 2.0—a versatile platform for genome mining of secondary metabolite producers. Nucleic Acids Res. **41:** W204–W212. http://dx.doi.org/10.1093/nar/gkt449.

Downloaded from http://genomea.asm.org/ on June 21, 2016 by guest