genomeA
Journals.ASM.org

Draft Genome Sequence of *Kitasatospora griseola* Strain MF730-N6, a Bafilomycin, Terpentecin, and Satosporin Producer

Jennifer C. Arens,[a] Brad Haltli,[a,b] Russell G. Kerr[a,b]

Department of Biomedical Sciences, University of Prince Edward Island, Charlottetown, Prince Edward Island, Canada[a]; Department of Chemistry, University of Prince Edward Island, Charlottetown, Prince Edward Island, Canada[b]

We report here the draft genome sequence of *Kitasatospora griseola* strain MF730-N6, a known producer of bafilomycin, terpentecin, and satosporins. The current assembly comprises 8 contigs covering 7.97 Mb. Genome annotation revealed 7,225 protein coding sequences, 100 tRNAs, 40 rRNA genes, and 23 secondary metabolite biosynthetic gene clusters.

Received 12 February 2015 **Accepted** 20 February 2015 **Published** 26 March 2015

Citation Arens JC, Haltli B, Kerr RG. 2015. Draft genome sequence of *Kitasatospora griseola* strain MF730-N6, a bafilomycin, terpentecin, and satosporin producer. Genome Announc 3(2):e00208-15. doi:10.1128/genomeA.00208-15.

Address correspondence to Russell G. Kerr, rkerr@upei.ca.

The presence of numerous secondary metabolite gene clusters within a single genome is a common feature in actinomycetes and has resulted in the sequencing of genomes from numerous organisms within this order, including streptomycetes (1) and the closely related kitasatosporae (2). Four kitasatosporae genome sequences are currently published (3–5), and an additional 8 genomes are in various phases of completion (JOGH00000000.1, JQMO00000000.1, JQLN00000000.1. JNYV00000000.1, JNWZ00000000.1, JNYE00000000.1, JNYQ00000000.1, and JNWY00000000.1). Given the large number of secondary metabolite biosynthetic gene clusters within their genomes and the relative lack of genome data in comparison to other actinomycete genera, there is a possibility of discovering new natural products with therapeutic potential from the underexplored genomes of kitasatosporae.

K. griseola strain MF730-N6 was isolated from Japanese soil and is responsible for the production of the diterpene terpentecin (6) and polyketides belonging to the bafilomycin (7) and satosporin (8) families. *K. griseola* MF730-N6 was obtained from the International Patent Organism Depositary (Nashihara, Japan) under the accession number FERM BP-1045. Genomic DNA was isolated using the Qiagen genomic tip 100/G kit. Library preparation (long insert ~20 kb) and sequencing using the Pacific Biosciences RS II platform was performed by the McGill University and Génome Québec Innovation Centre. Sequencing of 8 SMRT cells generated 1,377,430 subreads (2,920,331,552 bases) and 77,677 circular consensus sequences (175,515,662 bases), resulting in 324- and 18-fold coverage, respectively (assuming a 9-Mb genome). *De novo* assembly of corrected reads was performed by the sequencing facility using the hierarchical genome assembly process 2 analysis pipeline (9). The assembly consisted of 15 contigs; however, closure of 5 gaps was achieved by performing a *de novo* assembly using the Geneious assembler version 7.0.6 and sequencing amplicons spanning overlapping regions. The resulting assembly contained 8 contigs ranging in size from 5.9 kb to 3.5 Mb with a contig N_{50} of 2,590,787 bp.

The *K. griseola* draft genome comprised 7,966,157 bp with an overall G+C content of 72.7%. The genome was annotated using the RAST server (10) and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (NCBI annotation submitted to GenBank). Annotation identified a total of 7,225 protein-coding sequences, 100 tRNA genes, and 40 rRNA genes forming 9 complete and 5 incomplete rRNA operons. Orthologs of almost all developmental regulatory genes (11), with the exception of *bldB* and *whiJ*, as well as orthologs of *ram* cluster genes involved in aerial mycelia formation, were located within the *K. griseola* genome (12).

AntiSMASH analysis of the *K. griseola* MF730-N6 genome revealed 23 putative secondary metabolite biosynthetic gene clusters (13). Although gene clusters for known metabolites, such as hopanoids, germacradienol/geosmin, bafilomycin, spore pigment, a valanimycin-like compound, terpentecin, satosporin, and a spore-associated protein, were identified within the genome, 15 of the 23 gene clusters had unknown products; the isolation of other putatively novel natural products from this organism is thus promising and will be the subject of future studies.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JXZB00000000. The version described in this paper is version JXZB01000000.

ACKNOWLEDGMENTS

This work was supported by the Natural Sciences and Engineering Council of Canada (NSERC), the Canada Research Chair Program, the Atlantic Innovation Fund, and the Lévesque Foundation.

We acknowledge the contributions of Alfredo Staffa, Philippe Daoust, and Geneviève Geneau of the McGill University and Génome Québec Innovation Centre, Montréal, Canada, for PacBio sequencing services.

REFERENCES

1. **Rebets Y, Brötz E, Tokovenko B, Luzhetskyy A.** 2014. Actinomycetes biosynthetic potential: how to bridge *in silico* and *in vivo*? J Ind Microbiol Biotechnol **41**:387–402. http://dx.doi.org/10.1007/s10295-013-1352-9.
2. **Kämpfer P.** 2012. Genus *Incertae sedis* I. *Kitasatospora*, p 1768–1777. *In* Whitman WB, Goodfellow M, Kämpfer P, Busse H-J, Trujillo ME, Ludwig W, Suzuki K-i, Parte AE (ed), Bergey's manual of systematic bacteriology, vol. 5. Springer, New York, NY.

3. **Ichikawa N, Oguchi A, Ikeda H, Ishikawa J, Kitani S, Watanabe Y, Nakamura S, Katano Y, Kishi E, Sasagawa M, Ankai A, Fukui S, Hashimoto Y, Kamata S, Otoguro M, Tanikawa S, Nihira T, Horinouchi S, Ohnishi Y, Hayakawa M, Kuzuyama T, Arisawa A, Nomoto F, Miura H, Takahashi Y, Fujita N.** 2010. Genome sequence of *Kitasatospora setae* NBRC 14216T: an evolutionary snapshot of the family *Streptomycetaceae*. DNA Res **17:**393–406. http://dx.doi.org/10.1093/dnares/dsq026.
4. **Girard G, Willemse J, Zhu H, Claessen D, Bukarasam K, Goodfellow M, van Wezel GP.** 2014. Analysis of novel kitasatosporae reveals significant evolutionary changes in conserved developmental genes between *Kitasatospora* and *Streptomyces*. Antonie Van Leeuwenhoek **106:**365–380. http://dx.doi.org/10.1007/s10482-014-0209-1.
5. **Hwang JY, Kim SH, Oh HR, Cho Y-J, Chun J, Chung YR, Nam DH.** 2014. Draft genome sequence of *Kitasatospora cheerisanensis* KCTC 2395, which produces plecomacrolide against phytopathogenic fungi. Genome Announc **2**(3):e00604-00614. http://dx.doi.org/10.1128/genomeA.00604-14.
6. **Tamamura T, Sawa T, Isshiki K, Masuda T, Homma Y, Inuma H, Naganawa H, Hamada M, Takeuchi T, Umezawa H.** 1985. Isolation and characterization of terpentecin, a new antitumor antibiotic. J Antibiot **38:**1664–1669. http://dx.doi.org/10.7164/antibiotics.38.1664.
7. **Omura S, Otoguro K, Nishikiori T, Oiwa R, Iwai Y.** 1981. Setamycin, a new antibiotic. J Antibiot Tokyo **34:**1253–1256. http://dx.doi.org/10.7164/antibiotics.34.1253.
8. **Arens JC, Berrué F, Pearson JK, Kerr RG.** 2013. Isolation and structure elucidation of satosporin A and B: new polyketides from *Kitasatospora griseola*. Org Lett **15:**3864–3867. http://dx.doi.org/10.1021/ol401598f.
9. **Chin C-S, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J.** 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nat Methods **10:**563–569. http://dx.doi.org/10.1038/nmeth.2474.
10. **Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R.** 2014. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). Nucleic Acids Res **42:**D206–D214. http://dx.doi.org/10.1093/nar/gkt1226.
11. **Chater KF, Chandra G.** 2006. The evolution of development in *Streptomyces* analysed by genome comparisons. FEMS Microbiol Rev **30:**651–672. http://dx.doi.org/10.1111/j.1574-6976.2006.00033.x.
12. **Krawczyk B, Krawczyk JM, Sussmuth RD.** 2012. Class III lantibiotics—an emergining family of thioether-containing peptides, p 42–57. *In* Genilloud O, Vicente F (ed), Drug discovery from natural products. Royal Society of Chemistry, Dorchester, United Kingdom.
13. **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.