


Draft Genome Sequence of Triclosan-Degrading Bacterium *Sphingomonas* sp. Strain YL-JM2C, Isolated from a Wastewater Treatment Plant in China

Sikandar I. Mulla,  Anyi Hu, Haili Xu, Chang-Ping Yu

Key Laboratory of Urban Pollutant Conversion, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, China

S.I.M. and A.H. contributed equally to this work.

***Sphingomonas* sp. strain YL-JM2C was isolated from a wastewater treatment plant in Xiamen, China, by enrichment on triclosan. The bacterium is of special interest because of its ability to degrade triclosan. Here, we present a draft genome sequence of the microorganism and its functional annotation. To our best knowledge, this is the first report of a draft genome sequence of a triclosan-degrading bacterium**

Received 5 May 2015 Accepted 6 May 2015 Published 4 June 2015

Citation Mulla SI, Hu A, Xu H, Yu C-P. 2015. Draft genome sequence of triclosan-degrading bacterium *Sphingomonas* sp. strain YL-JM2C, isolated from a wastewater treatment plant in China. *Genome Announc* 3(3):e00603-15. doi:10.1128/genomeA.00603-15.

Copyright © 2015 Mulla et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Chang-Ping Yu, cpyu@iue.ac.cn.

Triclosan is an antimicrobial agent used in personal care products, textiles, and plastics (1). Studies demonstrate that triclosan has an acute toxicity to aquatic organisms (2). To date, most of the isolated microorganisms degrading triclosan belong to the sphingomonads (3–5). However, there are no reports available on a complete or draft genome sequence of a triclosan-degrading bacterium. Here, we report a draft genome sequence of the triclosan-degrading *Sphingomonas* sp. strain YL-JM2C, isolated from activated sludge of a wastewater treatment plant in Xiamen, China, through enrichment on triclosan (5 mg liter⁻¹). Phylogenetic analysis based on the 16S rRNA sequence showed that the percentage of similarity of YL-JM2C with related species, like *Sphingomonas wittichii* RW1, *Sphingomonas histidinilytica* UM2, and *Sphingomonas haloaromaticamans* A175, ranges from 99.93 to 99.06%.

The YL-JM2C genome was sequenced by an Illumina GAIIx instrument with one paired-end library (300 bp). A total of 594.6 Mb high-quality sequencing data were obtained, having approximately 100-fold coverage. Genome sequences were assembled *in silico* using SOAPdenovo version 1.05 (6), resulting in 273 contigs (>200 bp), with an N_{50} length of 45,887 bp. The gene-caller Glimmer 3.02 was used to predict coding sequences (CDSs), whereas for the identification of rRNA and tRNA, RNAmmer and tRNAscan-SE were used, respectively. For confirmation of the annotation sequence, the genome sequence was further uploaded into the Rapid Annotations using Subsystems Technology (RAST). Comparisons of the functions of predicted protein-coding genes using the NCBI-NR, COG, and KEGG databases were conducted during gene annotation (7).

The draft genome sequence of YL-JM2C consists of 5,923,019 bp, with 67.88% G+C content. From a total of 5,758 genes, 5,711 were protein-coding genes and 47 were RNAs. The majority of genes (69.28%) were assigned a putative function, whereas the remaining genes were either hypothetical proteins or

proteins with an unknown function. According to subsystem-based annotation generated by RAST, 44% of protein-coding genes were assigned to 401 metabolic subsystems. In comparison with other *Sphingomonas* strains, YL-JM2C has a bigger genome, with 5,711 protein-coding genes (8).

We performed an average nucleotide identity (ANI) and Genome-to-Genome Distance Calculator (GGDC) using JSpecies version 1.2 (9), and GGDC version 2.0 (10) was used to compare similarities among the genomic sequences of *Sphingomonas* strains YL-JM2C, RW1, DP58, KC8, and PR090111-T3T-6A (8, 11–13). ANI analysis showed YL-JM2C shared a low degree of similarity with other *Sphingomonas* species (<74% ANI), whereas relatively higher values were obtained for RW1 and DP58. The GGDC analysis showed similar results. We also compared orthologs of the genes of five *Sphingomonas* strains. Overall, strains YL-JM2C, RW1, and DP58 shared 3,957 orthologous genes, whereas relatively lower numbers of orthologous genes were identified between YL-JM2C and the other two strains, suggesting that strains YL-JM2C, RW1, and DP58 might belong to the same species. As for the annotation data (for YL-JM2C), the bacterium has 45 monooxygenase and 101 dioxygenase enzymes, which are probably involved in the degradation of diverse pollutants, including triclosan.

Nucleotide sequence accession numbers. The draft genome sequence of *Sphingomonas* sp. strain YL-JM2C was deposited in DDBJ/EMBL/GenBank under the accession no. [ASTM00000000](https://accession.ddbj.ac.jp/ASTM00000000/), and the version described here is the first version, [ASTM01000000](https://accession.ddbj.ac.jp/ASTM01000000/).

ACKNOWLEDGMENTS

This research was supported by the Natural Science Foundation of Fujian Province, China (grants 2013J05057 and 2013J06012), the National Natural Science Foundation of China for International Young Scientists (grant 31450110426), the Science and Technology Planning Project of

Xiamen, China (grant 3502Z20142021), and financial assistance (grant 2013FFZB0003) from the World Academy of Sciences-Chinese Academy of Sciences (TWAS-CAS) under its postdoctoral fellowships for Young International Scientists.

REFERENCES

- Rodricks JV, Swenberg JA, Borzelleca JF, Maronpot RR, Shipp AM. 2010. Triclosan: a critical review of the experimental data and development of margins of safety for consumer products. *Crit Rev Toxicol* 40: 422–484. <http://dx.doi.org/10.3109/10408441003667514>.
- Huang H, Du G, Zhang W, Hu J, Wu D, Song L, Xia Y, Wang X. 2014. The *in vitro* estrogenic activities of triclosan and triclocarban. *J Appl Toxicol* 34:1060–1067. <http://dx.doi.org/10.1002/jat.3012>.
- Hay AG, Dees PM, Saylor GS. 2001. Growth of a bacterial consortium on triclosan. *FEMS Microbiol Ecol* 36:105–112. <http://dx.doi.org/10.1111/j.1574-6941.2001.tb00830.x>.
- Lee do G, Zhao F, Rezenom YH, Russell DH, Chu KH. 2012. Biodegradation of triclosan by a wastewater microorganism. *Water Res* 46: 4226–4234. <http://dx.doi.org/10.1016/j.watres.2012.05.025>.
- Murugesan K, Bokare V, Jeon JR, Kim EJ, Kim JH, Chang YS. 2011. Effect of Fe-Pd bimetallic nanoparticles on *Sphingomonas* sp. PH-07 and a nano-bio hybrid process for triclosan degradation. *Bioresour Technol* 102:6019–6025. <http://dx.doi.org/10.1016/j.biortech.2011.02.099>.
- Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *Gigascience* 1:18. <http://dx.doi.org/10.1186/2047-217X-1-18>.
- Hu A, Lv M, Yu CP. 2013. Draft genome sequence of the bisphenol A-degrading bacterium *Sphingobium* sp. strain YL23. *Genome Announc* 1(4):e00549-13. <http://dx.doi.org/10.1128/genomeA.00549-13>.
- Aylward FO, McDonald BR, Adams SM, Valenzuela A, Schmidt RA, Goodwin LA, Woyke T, Currie CR, Suen G, Poulsen M. 2013. Comparison of 26 sphingomonad genomes reveals diverse environmental adaptations and biodegradative capabilities. *Appl Environ Microbiol* 79: 3724–3733. <http://dx.doi.org/10.1128/AEM.00518-13>.
- Richter M, Rosselló-Móra R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci U S A* 106: 19126–19131. <http://dx.doi.org/10.1073/pnas.0906412106>.
- Hothorn T, Bretz F, Westfall P. 2008. Simultaneous inference in general parametric models. *Biom J* 50:346–363. <http://dx.doi.org/10.1002/bimj.200810425>.
- Hu A, He J, Chu KH, Yu CP. 2011. Genome sequence of the 17beta-estradiol-utilizing bacterium *Sphingomonas* strain KC8. *J Bacteriol* 193: 4266–4267. <http://dx.doi.org/10.1128/JB.05356-11>.
- Ma Z, Shen X, Hu H, Wang W, Peng H, Xu P, Zhang X. 2012. Genome sequence of *Sphingomonas wittichii* DP58, the first reported phenazine-1-carboxylic acid-degrading strain. *J Bacteriol* 194:3535–3536. <http://dx.doi.org/10.1128/JB.00330-12>.
- Miller TR, Delcher AL, Salzberg SL, Saunders E, Detter JC, Halden RU. 2010. Genome sequence of the dioxin-mineralizing bacterium *Sphingomonas wittichii* RW1. *J Bacteriol* 192:6101–6102. <http://dx.doi.org/10.1128/JB.01030-10>.