Complete Genome Sequence of *Wohlfahrtiimonas chitiniclastica* Strain SH04, Isolated from *Chrysomya megacephala* Collected from Pudong International Airport in China

Xiao-Mei Cao, a Tu Chen, a Li-Zhi Xu, b Li-Si Yao, a Jun Qi, c Xiao-Long Zhang, a Qing-Li Yan, a Yao-Hua Deng, d Tian-Yu Guo, a Jing Wang, a

Institute of Health, Chinese Academy of Inspection and Quarantine, Beijing, China; Beijing Macro & Micro Test Biotech Company, Beijing, China; Tianjin Entry-Exit Inspection and Quarantine Bureau, Tianjin, China; Shanghai Entry-Exit Inspection and Quarantine Bureau, Shanghai, China

*Wohlfahrtiimonas chitiniclastica* bacilli that live in the larvae of a parasitic fly were recently isolated and are speculated to be the cause of fulminant sepsis. Here we report and analyze the complete genome sequence of *Wohlfahrtiimonas chitiniclastica* strain SH04. No complete genome sequence of a *Wohlfahrtiimonas chitiniclastica* isolate has been documented previously.

16S rRNA gene sequencing of *W. chitiniclastica* SH04 (GenBank accession no. JQ796717) showed 98.66% identity with the sequence corresponding to the *W. chitiniclastica* strain S5 (GenBank accession no. NR042554), which was isolated from third-stage larvae of *Wohlfahrtia magnifica* (Diptera: Sarcophagidae). However, the sequence similarity to the representatives of the *Ignatzschineria* larvae strain L1/68 was lower, at 93.57%. The availability of the genome sequence for *W. chitiniclastica* SH04 will be helpful for recognizing and analyzing this strain.

**Nucleotide sequence accession numbers.** The *Wohlfahrtiimonas chitiniclastica* SH04 Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AOBV0000000. The version described in this paper is the first version, AOBV01000000.

**ACKNOWLEDGMENTS**

This work was supported, in part, by the Fundamental Research Funds for the Public Research Institutes (No. 2011IK153) and the Science and Technology Planned Project of General Administration of Quality Supervision (No. 2011K153).

**REFERENCES**

1. Toth EM, Borsodi AK, Euzéby JP, Tindall BJ, Márialigeti K. 2007. Proposal to replace the illegitimate genus name *Schineria* Toth et al. 2001 with the genus name *Ignatzschineria* gen. nov. and to replace the illegitimate
combination Schineria larvae Toth et al. 2001 with Ignatzschineria larvae comb. nov. Int. J. Syst. Evol. Microbiol. 57:179–180.
2. Tóth EM, Kovács G, Schumann P, Kovács AL, Steiner U, Halbritter A, Márialigeti K. 2001. Schineria larvae gen. nov., sp. nov., isolated from the 1st and 2nd larval stages of Wohlfahrtia magnifica (Diptera: Sarcophagidae). Int. J. Syst. Evol. Microbiol. 51:401–407.
3. Tóth EM, Schumann P, Borsodi AK, Kéki Z, Kovács AL, Márialigeti K. 2008. Wohlfahrtiimonas chitiniclasticagen gen. nov., sp. nov., a new gamma-proteobacterium isolated from Wohlfahrtia magnifica (Diptera: Sarcophagidae). Int. J. Syst. Evol. Microbiol. 58:976–981.
4. Almuzara MN, Palombarani S, Tuduri A, Figueroa S, Gianecini A, Sabater L, Ramirez MS, Vay CA. 2011. First case of fulminant sepsis due to Wohlfahrtiimonas chitiniclasticabacteremia in homeless woman. Emerg. Infect. Dis. 15:985–987.
5. Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. 18:821–829.
6. Besemer J, Lomsadze A, Borodovsky M. 2001. GeneMarkS: a self-training method for prediction of gene starts in microbial genomes. Implications for finding sequence motifs in regulatory regions. Nucleic Acids Res. 29:2607–2618.
7. Lagesen K, Hallin P, Rødland EA, Staerfeldt H, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. 35:3100–3108.
8. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. 25:955–964.