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Complete Genome Sequence of *Stenotrophomonas maltophilia* Type Strain 810-2 (ATCC 13637)

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An emerging nosocomial pathogen, *Stenotrophomonas maltophila* has a high mortality rate in those it infects. Here, we present the complete genome sequence of *Stenotrophomonas maltophilia* 810-2 (ATCC 13637), the type strain of the species. The 5-Mb (66.1% G+C content) genome has been deposited in NCBI under accession number CP008838.

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Stenotrophomonas maltophilia is a Gram-negative aerobic bacillus, generally found in aquatic environments, which causes occasional human disease in immunocompromised patients (1, 2). *Stenotrophomonas* is not highly virulent, but reported mortality rates range from 14% to 69%, likely due to a high repository of drug resistance genes (3–5). *S. maltophilia* 810-2 (ATCC 13637) is the type strain.

High-quality genomic DNA was extracted from a purified isolate using a Qiagen Genomic-tip 500 at the USAMRIID Diagnostic Systems Division (DSD). Specifically, a 100-mL bacterial culture was grown to stationary phase and nucleic was acid extracted per the manufacturer's recommendations. Sequences were obtained by use of both Illumina and 454 technologies (6, 7). We constructed and sequenced an Illumina standard library of 100-bp reads at 351-fold genome coverage and a separate long-insert paired-end library (67-fold genome coverage, 9,445- ± 2,361-bp insert) (Roche 454 Titanium platform). The two libraries were assembled together in Newbler (Roche) and the consensus sequences were computationally shredded into 2-kbp overlapping fake reads (shreds). The raw reads were also assembled in Velvet, and those consensus sequences were computationally shredded into 1.5-kbp overlapping shreds (8). Draft data from all platforms were then assembled together with Allpaths, and the consensus sequences were computationally shredded into 10-kbp overlapping shreds (9). We then integrated the Newbler consensus shreds, Velvet consensus shreds, Allpaths consensus shreds, and a subset of the long-insert read pairs using parallel Phrap (High Performance Software, LLC). Possible misassemblies were corrected, and some gap closure was accomplished with manual editing in Consed (10–12).

Automatic annotation for the *Stenotrophomonas maltophilia* 810-2 genome utilized an Ergatis-based workflow at LANL with minor manual curation. The annotated genome is available at NCBI (CP008838) and the raw data can be provided upon request. The annotated 4,989,212-bp circular genome (66.1% G+C content) contains 4,645 open reading frames (ORFs), 4,571 protein coding sequences, and 7 rRNA and 67 tRNA sequences. Four other complete genomes for this species are publicly available; a detailed comparison of isolation and genomic relatedness is planned.

Nucleotide sequence accession number. This genome has been deposited in GenBank under the accession number CP008838.

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REFERENCES

1. **Colin AA, Rabin HR.** 2011. *Stenotrophomonas maltophilia* in cystic fibrosis : guilty or innocent? Am. J. Respir. Crit. Care Med. **183:**564–566. http://dx.doi.org/10.1164/rccm.201010-1668ED.
2. **Denton M, Kerr KG.** 1998. Microbiological and clinical aspects of infection associated with *Stenotrophomonas maltophilia*. Clin. Microbiol. Rev. **11:**57–80.
3. **Crossman LC, Gould VC, Dow JM, Vernikos GS, Okazaki A, Sebaihia M, Saunders D, Arrowsmith C, Carver T, Peters N, Adlem E, Kerhornou A, Lord A, Murphy L, Seeger K, Squares R, Rutter S, Quail MA, Rajandream MA, Harris D, Churcher C, Bentley SD, Parkhill J, Thomson NR, Avison MB.** 2008. The complete genome, comparative and functional analysis of *Stenotrophomonas maltophilia* reveals an organism heavily shielded by drug resistance determinants. Genome Biol. **9:**R74. http://dx.doi.org/10.1186/gb-2008-9-4-r74.
4. **Brooke JS.** 2012. *Stenotrophomonas maltophilia*: an emerging global opportunistic pathogen. Clin. Microbiol. Rev. **25:**2–41. http://dx.doi.org/10.1128/CMR.00019-11.
5. **Falagas ME, Kastoris AC, Vouloumanou EK, Rafailidis PI, Kapaskelis AM, Dimopoulos G.** 2009. Attributable mortality of *Stenotrophomonas maltophilia* infections: a systematic review of the literature. Future Microbiol. **4:**1103–1109. http://dx.doi.org/10.2217/fmb.09.84.
6. **Bennett S.** 2004. Solexa Ltd. Pharmacogenomics **5:**433–438. http://dx.doi.org/10.1517/14622416.5.4.433.
7. **Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen Y-J, Chen Z, Dewell SB, Du L, Fierro JM,**

Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Irzyk GP, Jando SC, Alenquer MLI, Jarvie TP, Jirage KB, Kim J-B, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM. 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature **437:**376–380. http://dx.doi.org/10.1038/nature03959.

8. **Zerbino DR, Birney E.** 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. Genome Res. **18:**821–829. http://dx.doi.org/10.1101/gr.074492.107.
9. **Butler J, MacCallum I, Kleber M, Shlyakhter IA, Belmonte MK, Lander ES, Nusbaum C, Jaffe DB.** 2008. ALLPATHS: *de novo* assembly of whole-genome shotgun microreads. Genome Res. **18:**810–820. http://dx.doi.org/10.1101/gr.7337908.
10. **Ewing B, Hillier L, Wendl MC, Green P.** 1998. Base-calling of automated sequencer traces using phred. I. Accuracy assessment. Genome Res. **8:**175–185. http://dx.doi.org/10.1101/gr.8.3.175.
11. **Ewing B, Green P.** 1998. Base-calling of automated sequencer traces using phred. II. Error probabilities. Genome Res. **8:**186–194.
12. **Gordon D, Abajian C, Green P.** 1998. Consed: a graphical tool for sequence finishing. Genome Res. **8:**195–202. http://dx.doi.org/10.1101/gr.8.3.195.