Stenotrophomonas maltophilia is an opportunistic nosocomial pathogen that is characterized by its high-level intrinsic resistance to a variety of antibiotics and its ability to form biofilms. Here, we report the draft genome sequence of Stenotrophomonas maltophilia strain AU12-09, isolated from an intravascular catheter.

Stenotrophomonas maltophilia was first isolated in 1943 as Bacillus bookeri and was then named Pseudomonas maltophilia (1). Later, however, investigators using 16S rRNA cistron analysis determined that this microorganism was more appropriately named Xanthomonas maltophilia. More recently, DNA-rRNA hybridization studies and sequencing and mapping of PCR-amplified 16S rRNA genes have resulted in the classification and naming of X. maltophilia as Stenotrophomonas maltophilia (2). S. maltophilia is predominantly found in an aquatic or humid environment, and in hospitals, S. maltophilia is found as a contaminant of numerous medical devices, edetic acid anticoagulant in vacuum tubes for blood collection, chlorhexidine-cetrimide disinfectant, and sterile water (3).

S. maltophilia is the third most common nosocomial non-fermenting Gram-negative bacillus (4). A recent study shows that 4.3% of almost 75,000 Gram-negative infections were caused by S. maltophilia in intensive care units in the United States (5). The two most common diseases caused by S. maltophilia are bacteremia and pneumonia, with infection being via an intravascular catheter or ventilator, respectively (5). In addition, S. maltophilia is intrinsically resistant to a variety of clinically prescribed antibiotics (3). Also, S. maltophilia can form biofilms, which further increases its resistance to phagocytes and antibiotics (3).

S. maltophilia strain AU12-09 was isolated from an intravascular catheter tip by rolling the tip back and forth on the surface of a Columbia agar plate supplemented with 5% sheep blood, essentially as described by Maki et al. (6). DNA was prepared and the genome sequence of S. maltophilia AU12-09 was determined on a 454 GS FLX system using titanium chemistry (Roche) (7). The sequence data consist of 129,784,052 bp of DNA sequence at 29× coverage. A total of 125 contigs (>500 bp) were de novo assembled using the Roche GS de novo assembler (version 2.3). The contig N50 was 69,081 bp, and the largest contig assembled was 345,473 bp. The contigs were then ordered and oriented into four scaffolds using paired-end information. The average length of the scaffolds was 1,145,290 bp.

The draft genome of S. maltophilia AU12-09 consists of a circular 4,547,300-bp chromosome with a G+C content of 66.5%. The genome was automatically annotated using the RAST server (8). The genome contains 70 tRNA genes coding for all amino acids and 4,004 predicted protein-coding genes, consistent with other sequenced Stenotrophomonas spp. (5, 9). We identified numerous putative virulence factors, including those involved in quorum sensing, biofilm formation, and the production of bacteriocins and invasins. The S. maltophilia AU12-09 genome contains 24 genes coding for multidrug resistance efflux pumps, 11 genes coding for resistance to beta-lactam antibiotics, 5 genes coding for multidrug resistance tripartite systems, and 4 genes coding for resistance to fluoroquinolones.

This sequence information for the S. maltophilia genome will greatly improve our understanding of the drug resistance and pathogenicity of this organism.

Nucleotide sequence accession number. The genome sequence of S. maltophilia AU12-09 has been deposited in NCBI GenBank under accession no APIT00000000.

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REFERENCES


