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Data in Brief

Genome sequencing and annotation of *Stenotrophomonas* sp. SAM8

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ABSTRACT

We report draft genome sequence of *Stenotrophomonas* sp. strain SAM8, isolated from environmental water. The draft genome size is 3,665,538 bp with a G + C content of 67.2% and contains 6 rRNA sequence (single copies of 5S, 16S & 23S rRNA). The genome sequence can be accessed at DDBJ/EMBL/GenBank under the accession no. LDAV00000000.

Specifications	
Organism/cell line/tissue	*Stenotrophomonas* sp.
Strain(s)	SAM8
Sequencer or array type	Sequencer; Roche 454
Data format	Processed
Experimental factors	Microbial strains
Experimental features	Draft genome sequence of *Stenotrophomonas* sp. SAM8 assembly and annotation
Consent	N/A
Sample source location	Water spring in Aljouf, Saudi Arabia

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/bioproject/?term=LDAV00000000.

2. Experimental design, materials and methods

Stenotrophomonas sp. stain SAM8 is a Gram-negative obligate aerobe that is rod shaped and motile with a few polar flagella. The isolate is an environmental bacterium found in aqueous habitats, including plant rhizospheres, animals, foods, and water sources [1]. In addition, the isolate is an increasingly relevant human opportunistic pathogen that is involved in infections at hospitals and in patients with cystic fibrosis [1–2].The isolate is major opportunistic waterborne pathogens causing hospital-acquired infections [3]. Genomic DNA was extracted from pure culture of bacterial strain and subsequently sequenced using Roche 454 GS (FLX Titanium) pyrosequencing. All of the reads were assembled using GS De Novo Assembler version 2.8 (454 life science), which generated 529 contigs with *N*50 12,907 bp. The G + C content was calculated using the draft genome sequence. The G + C content for the draft genome is 67.2%. The genome contains 58 tRNA genes and 6 rRNA genes (5S–23S–16S) predicted by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP).

A total of 3448 protein coding sequences in 355 subsystems were functionally annotated by Rapid Annotation using the Subsystems Technology (RAST) [4] server (Fig. 1). Genome analysis revealed that the genome of *Stenotrophomonas* sp. stain SAM8 contains various gene clusters for biosynthesis of secondary metabolites and antimicrobial peptides. The genome information displays several antibiotic resistance genes encoding methicillin, efflux pumps, quinolone, fosmidomycin and acriflavine resistance protein [5].There also exist in the genome multiple genes encoding chitinase, xylanase, esterase and lipase enzymes. Overall, the strain demonstrates the potential for resistance to a wide range of antimicrobial and heavy metals.

Functional comparison of genome sequences in the RAST server revealed the closest neighbors of *Stenotrophomonas maltophilia* K279a (score 513) followed by *Stenotrophomonas* sp. SKA14 (score 513), *S. maltophilia* R551-3 (score 506), *S. maltophilia* D457 (score 339) and *Xanthomonas campestris* pv. *campestris* ATCC 33913 (score 333). On the other hand, the analysis of the complete 16S rRNA sequence in EzTaxon server (http://www.ezbiocloud.net/eztaxon; [6]) under default settings (with matches only against cultured

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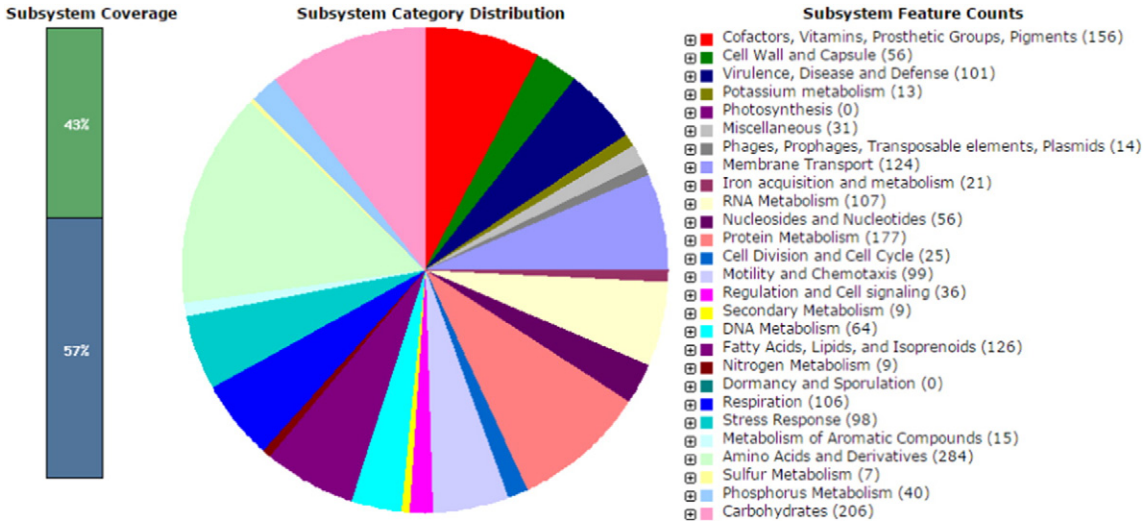

Fig. 1. Subsystem distribution of *Stenotrophomonas* strain SAM8 (based on RAST annotation server).

strains) identified *S. maltophilia*. Overall, the various in silico results confirmed that the present environmental isolate is a member of the genus *Stenotrophomonas*, though further characterization work is required to determine its species.

3. Nucleotide sequence accession number

The *Stenotrophomonas* sp. SAM8 whole genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no LDAV00000000.

Conflict of interest

The authors declare that there is no conflict of interests on the work published in this paper.

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