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Draft Genome Sequence of *Serratia* sp. Strain ATCC 39006, a Model Bacterium for Analysis of the Biosynthesis and Regulation of Prodigiosin, a Carbapenem, and Gas Vesicles

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***Serratia* sp. strain ATCC 39006 is a Gram-negative bacterium and a member of the *Enterobacteriaceae* that produces various bioactive secondary metabolites, including the tripyrrole red pigment prodigiosin and the β-lactam antibiotic 1-carbapenen-2-em-3-carboxylic acid (a carbapenem). This strain is the only member of the *Enterobacteriaceae* known to naturally produce gas vesicles, as flotation organelles. Here we present the genome sequence of this strain, which has served as a model for analysis of the biosynthesis and regulation of antibiotic production.**

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Serratia sp. strain ATCC 39006 was originally isolated from *Salicornia alterniflora* and in channel water from a salt marsh in Cheesequake, NJ, in a search by the Squibb Chemical Company for bacteria producing new antibiotics (1). In addition to the β-lactam produced, identified as 1-carbapen-2-em-3-carboxylic acid (a carbapenem) (2), this strain synthesizes the red, linear tripyrrole pigment prodigiosin (2-methyl-3-pentyl-6-methoxyprodigiosin). Prodigiosin is a secondary metabolite with antimicrobial, anticancer, and immunosuppressant properties with derivatives in clinical trials (3, 4). *Serratia* sp. strain ATCC 39006 was used to determine the prodigiosin biosynthetic pathway, with implications for biosynthesis of the related compound, undecylprodigiosin, produced by *Streptomyces coelicolor* (4, 5). Furthermore, *Serratia* sp. strain ATCC 39006 has provided an excellent model for investigating the regulation of antibiotic biosynthesis in Gram-negative enterobacteria (4). The control of these secondary metabolites is complex and responds to quorum sensing (6–8), cyclic di-GMP signaling (9, 10), phosphate availability (7, 11), carbon source (12), Hfq (13), stationary phase (14), and drug efflux pump activity (15), among other factors. In addition, due to the ease of prodigiosin detection, this strain has been used to analyze conserved uncharacterized genes and gene products (16–18). For example, SdhE was recently investigated in this strain. SdhE is widely conserved in eukaryotes and *Alpha-*, *Beta-*, and *Gammaproteobacteria* and is essential for flavinylation and activation of succinate dehydrogenase, an enzyme central to the electron transport chain and the tricarboxylic acid cycle (17, 19, 20).

Serratia sp. strain ATCC 39006 is motile by means of flagella and can swarm over surfaces aided by the production of a biosurfactant (10). Surprisingly, this strain also produces gas vesicles, which are hollow intracellular proteinaceous organelles that control bacterial buoyancy and allow flotation toward air-liquid interfaces (21). This is the only known enterobacterium to utilize this form of taxis naturally (21). The secretion of plant cell wall-degrading enzymes is also a feature of this bacterium, and plant pathogenicity has been confirmed in potato tuber-rotting assays (6, 9). Furthermore, this strain is virulent in a *Caenorhabditis elegans* infection model (22). The genetic analysis of *Serratia* sp. strain ATCC 39006 has been greatly facilitated by the isolation of an efficient broad-host-range generalized transducing phage (23).

Genomic DNA of *Serratia* sp. strain ATCC 39006 was sequenced using the 454 GS FLX Titanium platform (Roche) (~18× coverage single-end data) and 36-bp Illumina single-end reads (GAIIx) (~439× coverage). The 454 data were *de novo* assembled (Newbler v2.3), giving 53 large contigs (99.9% of sequence) from 94 total contigs. These were assembled into 5 scaffolds using PCR and Sanger sequencing (3 contigs between 200 and 1,000 bp remained). Illumina reads were mapped using BWA 0.5.8, indels were detected using GATK (24), and the sequence was polished using a custom perl script.

The *Serratia* sp. strain ATCC 39006 genome is ~4.94 Mb (G+C content of 49.2%), with 4,413 protein-encoding genes, 7 rRNA operons, and 72 tRNAs (predicted using Prodigal [25]). This sequence will now enable further analysis of the diverse and interesting biological traits that have been defined in this unusual enterobacterium.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AWXH00000000. The version described in this paper is version AWXH01000000.

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