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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Providencia stuartii* Clinical Isolate MRSN 2154

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Here we present the complete genome sequence of *Providencia stuartii* MRSN 2154, isolated from an Afghan national. *P. stuartii* is a Gram-negative bacillus capable of causing infections in a wide variety of human tissues. Because *Providencia* readily acquires plasmids bearing drug resistance loci, it is of growing clinical significance.

Bacteria of the genus *Providencia* are Gram-negative urea-metabolizing bacilli (6) that naturally occur in soil, water, and sewage. In the clinical setting *P. stuartii* is most commonly seen in patients with indwelling urinary catheters, where it causes urinary tract infections (14). These infections may progress to bacteremia (15). Diarrhea (16), peritonitis (13), meningitis (10), and infections of burn wounds (7), the endocardium (2) and the brain (5) attributed to *P. stuartii* have also been reported.

Providencia readily incorporates DNA from other bacteria, enabling it to acquire resistance to a broad spectrum of antibiotics. *P. stuartii* clinical isolates have been observed to carry plasmids with the extended-spectrum β-lactamases TEM (12), CTX-M (9), VEB (1), VIM-1 (4), and NDM-1 (3, 8).

The *P. stuartii* strain that is the subject of our project, MRSN 2154, was isolated in 2011 from a burn patient treated in the intensive care unit of a U.S./coalition military medical facility in Afghanistan (11). The isolate tested positive for the New Delhi metallo-β-lactamase-1 gene, which was subsequently shown to reside on a plasmid bearing numerous other drug resistance loci (3).

The genome of MRSN 2154 was sequenced using the Roche GS FLX Titanium system (Roche 454 Life Sciences, Branford, CT) with a shotgun rapid ligation library. A total of 274,932 filtered reads, totaling 82 Mb of sequence, were subjected to *de novo* assembling using GSAssembler software (Newbler), version 2.5.3. A whole-genome NcoI restriction map generated by optical genome mapping using the Argus whole-genome mapping system (OpGen, Gaithersburg, MD) was used to guide assembly of the contigs into a complete genome sequence and to verify the final assembly. Sanger sequencing was used to determine the structure and organization of the multiple *rrn* operons. The average sequence coverage of the completed genome assembly is 17.5-fold. *P. stuartii* MRSN 2154 has a circular genome of 4,402,109 nucleotides and a G/C content of 41.27%. It has several genome structural rearrangements relative to *P. stuartii* strain ATCC 25827, whose genome was sequenced and assembled into 52 contigs (http://www.ncbi.nlm.nih.gov/bioproject/54899).

Whole-genome annotation was generated using the NCBI prokaryotic genomes automatic annotation pipeline (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). The *P. stuartii* MRSN 2154 genome has 4,194 predicted genes, including 4,099 protein-encoding genes, 75 tRNA genes, and seven *rrn* operons.

We have provided the first complete *Providencia stuartii* genome sequence, as well as the first genomic sequence of a multidrug-resistant *P. stuartii* isolate. Further studies on *P. stuartii* genomes may provide important insights into factors underlying *P. stuartii* virulence and pathogenicity.

Nucleotide sequence accession numbers. The nucleotide sequence of *P. stuartii* strain MRSN 2154 has been deposited in GenBank under accession number CP003488 and in the NCBI BioProject repository under accession number PRJNA88059.

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