Draft Genome Sequence of *Ralstonia pickettii* AU12-08, Isolated from an Intravascular Catheter in Australia

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**Ralstonia pickettii** is a nonfermenting Gram-negative bacillus that creates a significant problem in clinical settings, as it is a widespread cause of nosocomial infections. Here, we report the draft genome sequence of *R. pickettii* AU12-08, isolated from an intravascular catheter tip.

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**ACKNOWLEDGMENT**

L.Z. is supported by an NHMRC training clinical research fellowship (Australian Government grant no. 597491).

**REFERENCES**


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*Ralstonia pickettii* was previously known as *Pseudomonas pickettii* and *Burkholderia pickettii* (1). *R. pickettii* is an aerobic Gram-negative, oxidase-positive, nonfermenting rod that has been isolated from a wide variety of clinical specimens, including blood, urine, and cerebrospinal fluid (2). *R. pickettii* is not considered to be a major pathogen, and its virulence level is thought to be low (3). However, a wide range of *R. pickettii* infections have been reported recently (4). This demonstrates that this organism might be a more widespread pathogen than was thought. In addition, the types of infections are more invasive and severe than what was thought (4).

*R. pickettii* AU12-08 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. (5). DNA was prepared and the genome sequence of *R. pickettii* AU12-08 was determined on a 454 GS FLX system using Titanium chemistry (Roche) (6). The sequence data consist of 135,359,388 bp of DNA sequence at 22× coverage. A total of 78 contigs (>500 bp) were de novo assembled using the Roche GS de novo assembler (version 2.3). The contig N50 is 178,545 bp, and the largest contig assembled is 592,110 bp. The contigs were then ordered and oriented into 14 scaffolds using paired-end information. The average length of the scaffolds is 446,804 bp.

The draft genome of *R. pickettii* AU12-08 consists of a circular 6,229,152-bp chromosome, with a G+C content of 63.6%. The genome was automatically annotated using the RAST server (7). 6,229,152-bp chromosome, with a G+C content of 63.6%. The genome was automatically annotated using the RAST server (7).

The genome consists of 22 putative resistance-nodulation-cell division multidrug resistance efflux pumps, and 13 genes code for multidrug resistance. Four genes code for resistance to fluoroquinolones and 10 genes code for β-lactam antibiotics. In addition, 170 genes code for resistance to toxic compounds, including cobalt-zinc-cadmium resistance, copper homeostasis, mercury resistance, and arsenic and bile hydrolysis.

The sequence of the *R. pickettii* AU12-08 genome will greatly improve our understanding of the drug resistance and pathogenicity of this organism.

**Nucleotide sequence accession number.** The genome sequence of *R. pickettii* AU12-08 has been deposited in NCBI GenBank under the accession no. ASZV00000000.

