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Draft Genome Sequence of *Providencia stuartii* PS71, a Multidrug-Resistant Strain Associated with Nosocomial Infections in Greece

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ABSTRACT *Providencia stuartii* is frequently associated with nosocomial outbreaks and displays intrinsic resistance to many commonly used antimicrobials. We report here the draft genome sequence of a *P. stuartii* strain carrying acquired resistance genes conferring panresistance to cephalosporins (bla_{SHV-5} and bla_{VEB-1}), carbapenems (bla_{VIM-1}), and aminoglycosides (*rmtB*) involved in an outbreak in Greek hospitals.

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Providencia stuartii has emerged as an important nosocomial pathogen responsible for urinary tract infections in patients with indwelling urinary catheters, hospital-acquired pneumonia, bloodstream infections, and sepsis (1), with significant impact on patient morbidity, mortality, treatment, and management costs (2).

P. stuartii isolate PS71 was recovered in 2013 from the bloodstream of a patient during a cluster of *P. stuartii* infections in a critical care unit in a tertiary-care hospital in Athens, Greece (3). This outbreak-associated strain exhibited resistance to cephalosporins (first, second, third, and fourth generation), β-lactam–inhibitor combinations (amoxicillin-clavulanate and piperacillin-tazobactam), carbapenems (ertapenem and imipenem), aminoglycosides, fosfomycin, polymyxins (colistin and polymyxin B), quinolones, and tigecycline (3).

Genomic DNA was extracted and subjected to whole-genome sequencing with the Illumina MiSeq platform (Illumina, Inc., San Diego, CA), producing 2 × 250-bp paired-end reads, generating a total of 843,412 reads with a 475 bp average length. The Trimmomatic algorithm (version 0.36) (4) was used to trim all the generated reads and their quality assessed with in-house scripts using BedTools (version 2.25.0) (5), BWA-mem (version 2) (6), and SAMtools (version 1.3.1) (7) algorithms. High-quality filtered reads were subsequently assembled *de novo* using SPAdes algorithm (version 3.7.1) (8), resulting in 79 scaffolds with an N_{50} of 455,952 bp. The sequence coverage of the *de novo* assemblies was approximately 83 reads per assembled base. The draft genome sequence of PS71 consists of 4,411,042 bp with 41.75% average G+C content.

Provisional annotation carried out using the Prokka algorithm (version 1.11) (9) identified at least 4,026 coding sequences (CDSs), including 76 tRNAs and eight rRNAs. The assembled genome was used to predict the presence of acquired antibiotic resistance genes using ResFinder (10) and confirmed the presence of 24 genes conferring resistance to aminoglycosides [*aadA1*, *aadA2*, *aadB*, *aac(6′)-Ia*, *aph(3′)-Ia*, *strA*, *strB*, and *rmtB*], β-lactams (bla_{TEM-1b}, bla_{OXA-10}, bla_{SHV-5}, bla_{VEB-1}, and bla_{VIM-1}), macrolides, lincosamides, and streptogramin B [*mph*(*A*)] and phenicols (*cmlA1* and *catA3*), rifampin (*arr-2*), sulfonamides (*sul1* and *sul2*), tetracyclines [*tet*(A), *tet*(B), and *tet*(G)], and trimethoprim (*dfrA1* and *dfrA12*). The presence of multidrug efflux pump-mediated resis-

tance mechanisms was also inferred from the genome (i.e., *acrB*, *acrR*, *cmeB*, *mtrF*, *mfs*, *macA*, *macB*, and *tolC*), as well as resistance to toxic compounds, including arsenic (*arsA*, *arsB*, *arsC*, *arsD*, and *arsR*), cadmium, cobalt and zinc (*czcB*, *czcD*, *trcD*, and *trMer*), and mercury (*merA*, *merC*, *merD*, *merE*, and *merR*). PlasmidFinder (11) indicated that PS71 contains plasmids with ColE, A/C, and R replicon types, with the latter located on a multireplicon plasmid (3).

There are increasing reports of multiresistant strains of *Providencia* in the Mediterranean, and enhanced surveillance is needed to identify and track the epidemiology of resistant strains, their impact on human health, and the molecular epidemiology. This is the first draft genome sequence of such a multiresistant *P. stuartii* strain associated with a nosocomial outbreak in Greece.

Accession number(s). The draft genome sequence of *P. stuartii* PS71 has been deposited in the DDBJ/EMBL/GenBank databases under the accession number MSAA00000000. The version described in this paper is the first version, MSAA01000000.

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