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First Report of a Whole-Genome Shotgun Sequence of a Clinical *Enterococcus faecalis* Sequence Type 6 Strain from South Africa

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ABSTRACT *Enterococcus faecalis* is a lactic acid-producing Gram-positive bacterium commonly found in the intestinal tract of humans and animals; it is implicated in multidrug-resistant nosocomial infections. The draft genome of this *E. faecalis* sequence type 6 (ST6) strain consists of 3,215,228 bp, with 37.20% GC content, 3,048 predicted coding sequences, and 61 RNA genes.

Received 3 November 2017 **Accepted** 6 November 2017 **Published** 14 December 2017

Citation Mbelle NM, Maningi NE, Tshisevhe V, Modipane L, Amoako DG, Osei Sekyere J. 2017. First report of a whole-genome shotgun sequence of a clinical *Enterococcus faecalis* sequence type 6 strain from South Africa. Genome Announc 5:e01382-17. https://doi.org/10.1128/genomeA.01382-17.

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Enterococcus faecalis is part of the human microbiota and is implicated in several fatal clinical infections, such as bacteremia and infective endocarditis (1). To our knowledge, this is the first draft genome sequence of a clinical *E. faecalis* strain, ST-6:CF006, from South Africa and the rest of Africa. This vancomycin-susceptible sequence type 6 (ST6) strain was isolated from the urine of a 41-year-old male patient hospitalized in Kalafong Hospital in Pretoria, South Africa, in 2013.

The strain was grown overnight anaerobically at 37°C in brain heart infusion (BHI) broth (Oxoid, UK) and was catalase negative but esculin hydrolysis and pyrrolidonyl arylamidase (PYR) positive. The identification was confirmed with Vitek 2 (bioMérieux, France). Genomic DNA was sheared to 200-bp libraries; 280-bp fragments were selected using 2% agarose gels and Pippin Prep (Sage Science, USA). Individual libraries were pooled to 100 pM and sequenced on the Ion Proton (Thermo, Fisher, USA) at a coverage of 89.84×. The raw reads were *de novo* assembled using the SPAdes assembler (2).

The size, GC content, number of contigs, N_{50}, and L_{50} of the draft genome were 3,215,228 bp, 37.20%, 198, 104,004 bp, and 10 bp, respectively. Annotation with Rapid Annotations using Subsystems Technology (RAST) (3) and prokaryotic genome annotation pipeline (PGAP) (4) resulted in 3,048 protein-coding genes, 376 (10.98%) hypothetical proteins, 57 tRNAs, 3 rRNAs, and 4 noncoding RNAs. CRISPRFinder (5) predicted two clustered regularly interspaced short palindromic repeat 1 (CRISPR1) arrays each on nodes/contigs 3 and 59.

BLASTN analysis showed ST-6:CF006 to be closely related to the following *E. faecalis* strains with 99% nucleotide identity: V583 (GenBank accession no. AE016830), a clinical isolate from the United States; sorialis (accession no. CP015883), a fecal isolate from the United States; DD14 (accession no. CP021161), a meconium isolate from France; and L12 (accession no. CP018102) from swine in Brazil.

Resistome annotation with GoSeqIt and ResFinder (6, 7) showed aminoglycoside [*aph(3′)-III, ant(6)-Ia, aac(6′)-aph(2′′)*], macrolide-lincosamide-streptogramin (*isaA* and *mphD*), and tetracycline (*tetM*) resistance genes. ST-6:CF006 was resistant (R) to genta-

micin, streptomycin, erythromycin (R > 8 μg/ml), clindamycin (R > 8 μg/ml), tetracycline (R > 168 μg/ml), ciprofloxacin (R > 88 μg/ml), and moxifloxacin (R > 88 μg/ml) but susceptible to ampicillin (>2 μg/ml), teicoplanin (≤0.5 μg/ml), linezolid (2 μg/ml), tigecycline (≤0.12 μg/ml), and vancomycin (1 μg/ml), in agreement with the resistome annotation. As no fluoroquinolone resistance genes were identified, mutations in a chromosome-borne DNA gyrase gene (*gyrA*) (8, 9) were further investigated using tBLASTn; fluoroquinolone-susceptible *E. faecalis* ATCC 29212 (accession no. CP008816) was used as the reference/wild-type strain to call single-nucleotide polymorphisms (SNPs). A Ser84Ile mutation, previously implicated in fluoroquinolone resistance (8), was identified. Four plasmid replicon types, i.e., *rep2*, *rep6*, *rep9*, and *repUS11*, were identified with PlasmidFinder version 1.3 (10). The GoSeqIt VirulenceFinder database (6) discovered 19 virulence factor genes: collagen adhesion (*ace*), pheromone precursor lipoproteins (*cad, camE, cCF10*, and *cOB1*), cytolysin (*cylA, cylB, cylL,* and *cylM*), endocarditis- and biofilm-associated pili (*ebpA, ebpB,* and *ebpC*), endocarditis antigen A (*efaAfs*), enterococcal leucine-rich internalin-like protein A (*elrA*), gelatinase (*gelE*), hyaluronidase (*hylA* and *hylB*), sortase A (*srtA*), and thiolperoxidase (*tpx*), contributing to its ability to aggregate, adhere, lyse, and invade host tissues. Analysis of the genomes of *E. faecalis* will increase our insight into the factors that mediate its pathogenesis and antibiotic resistance, as well as establish a correlation between genomic and phenotypic data.

Accession number(s). This whole-genome shotgun project has been submitted to the National Center for Biotechnology Information GenBank database under the accession no. NXKG00000000. The version described in this paper is version NXKG01000000.

ACKNOWLEDGMENTS

We thank the staff of the Medical Microbiology Department of the Tshwane Academic Division of the National Health Laboratory Services.

This study was funded by grant 94445 from the NHLS.

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