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Draft Genome Sequences of *Escherichia coli* Strains Isolated from Septic Patients

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We present the draft genome sequences of six strains of *Escherichia coli* isolated from blood cultures collected from patients with sepsis. The strains were collected from two patient sets, those with a high severity of illness, and those with a low severity of illness. Each genome was sequenced by both Illumina and PacBio for comparison.

**Sepsis** is a clinical syndrome defined as infection complicated by a systemic inflammatory response syndrome. Sepsis affects >1.6 million Americans each year and is the most costly reason for hospitalization in the United States (1, 2). The more severe subtypes of sepsis, known as severe sepsis and septic shock, are associated with acute end-organ dysfunction and a 30% risk of in-hospital mortality (3, 4). Mortality increases with increasing severity of end-organ dysfunction at the population level (5, 6); however, the clinical outcomes of individual patients vary significantly. The relative contributions of host susceptibility factors and pathogen virulence-associated factors to the severity of illness in sepsis are not well understood. In this study, we sequenced 3 pairs of uropathogenic *Escherichia coli* strains isolated from blood samples from patients with sepsis from a urinary tract infection who were admitted to the UC Davis Medical Center. Each pair of strains was selected from patients who were matched with regard to clinical characteristics, including age group, sex, site of infection within the urinary tract, and major comorbidities, but they differed significantly in sepsis severity of illness, as defined by scores on the Sequential Organ Failure Assessment (SOFA) (7). *E. coli* strains JA23, JA62, and JA65 were from patients with a high severity of illness, whereas strains JA03, JA17, and JA69 were from patients with a low severity of illness. All aspects of the study were approved by the institutional review board of the UC Davis Medical Center (protocol no. 247849).

Strains of *E. coli* were isolated from overnight-plated subcultures of initial liquid blood cultures obtained in the course of routine clinical practice and stored in a biorepository at -80°C. A single colony from each strain was grown in LB broth at 37°C and then used for genomic DNA extraction.

Illumina paired-end libraries were made from *E. coli* genomic DNA extracted using a Promega Wizard genomic DNA purification kit (Promega Corporation, Madison, WI). The libraries were prepared using an Illumina TruSeq kit (Illumina, San Diego, CA). The samples were pooled and then sequenced on an Illumina MiSeq for paired-end 250-bp reads. An average of 2,355,125 paired-end reads per sample were generated. Quality trimming and error correction resulted in an average of 2,040,300 high-quality reads. All sequence processing and assembly of the Illumina reads were performed using the a5 assembly pipeline (8). Automated annotation was performed using the RAST server (9). The assembly and annotation statistics are presented in Table 1.

PacBio sample prep and genomic DNA extraction were performed using a Mo Bio PowerSoil DNA isolation kit (Mo Bio, Carlsbad, CA). PacBio libraries were prepared via the PacBio standard 10-kb library prep and sequenced using Pacific Biosciences RS sequencing technology (Pacific Biosciences, Menlo Park, CA). *De novo* assembly of the read sequences was performed using the Hierarchical Genome Assembly Process (HGAP2) workflow (PacBio DevNet; Pacific Biosciences) as available in single-molecular real-time (SMRT) Analysis. Automated annotation was performed using the RAST annotation server (9). The assembly and annotation statistics are presented in Table 1.

**Nucleotide sequence accession numbers.** All 12 assemblies described in this paper have been deposited as whole-genome shotgun projects in DDBJ/EMBL/GenBank under the accession numbers provided in Table 1.

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