First Draft Genome Sequences of *Neisseria* sp. Strain 83E34 and *Neisseria* sp. Strain 74A18, Previously Identified as CDC Eugonic Fermenter 4b Species

Alexander L. Greninger, Jessica Streithorst, © Charles Y. Chiu, Steve Miller

Department of Laboratory Medicine, UCSF, San Francisco, California, USA

We report the first draft genome sequences of two isolates previously classified as CDC EF-4b species, *Neisseria* sp. 83E34 and *Neisseria* sp. 74A18. Both strains were isolated from patients with animal bites and likely constitute novel genomospecies with average nucleotide identities of <95% to other sequenced strains.

C DC eugonic fermenter 4b (EF-4b) is a designation of Gram-negative bacteria that are members of animal oral flora and are typically isolated from animal bite wounds in humans (1). In 2006, this group was identified as *Neisseria zoodegmatensis* based on 16S sequence and biochemical testing (1–3). Only five isolates from human infections have been reported since the taxonomic classification of *Neisseria zoodegmatensis*, while >30 isolates have been collected from CDC EF-4b bacteria (1, 4, 5). CDC EF-4b has also been cultured from a case of infectious tenosynovitis due to a Siberian tiger bite (6). To date, the 16S sequence is the only available nucleotide sequence for *Neisseria zoodegmatensis*.

We sequenced the first draft genomes of two bacterial isolates that had been identified as CDC group EF-4b from the University of California, San Francisco (UCSF) microbiology lab. Isolate 74A18 was isolated from a right-hand index finger culture of a patient with flexor tenosynovitis following a dog bite. Isolate 83E34 was isolated from a left-lateral-hand culture of a patient with cellulitis following a cat bite. Both patients also had Pasteurella multocida isolated concurrently from the wound cultures.

DNA was extracted using the Qiagen EZ1 DNA tissue kit. Nextera XT paired-end and Nextera mate-pair libraries were sequenced at 250/350 bp and 2 tera XT paired-end and Nextera mate-pair libraries were sequenced at 250/350 bp and 2 tera XT paired-end and Nextera mate-pair libraries were sequenced at 250/350 bp. DNA was extracted using the Qiagen EZ1 DNA tissue kit. Nextera XT paired-end and Nextera mate-pair libraries were sequenced at 250/350 bp and 2 tera XT paired-end and Nextera mate-pair libraries were sequenced at 250/350 bp.

**REFERENCES**


