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The mosquito gut accommodates a diverse microbiota (1–4). Elizabethkingia sp. has been identified as a dominant resident in the gut of Anopheles gambiae (1, 5, 6) and Anopheles stephensi (3). Recently, Kämpfer and collaborators described the Elizabethkingia anophelis type strain R26, isolated from the midgut of the mosquito Anopheles gambiae, as a novel taxon in the genus Elizabethkingia (7). Another strain, designated Ag1, was isolated from the midgut of the mosquito Anopheles gambiae G3 strain in the Xu laboratory at New Mexico State University, and the strain was identified as Elizabethkingia anophelis based on the bacterial 16S rRNA gene sequence (99.8% homology). The genomes were sequenced using Illumina HiSeq 2000 paired-end technology at BGI, Hong Kong. The R26 genomic reads (652 Mbp) were de novo assembled using DNASTAR NGen v 10.0, which generated 66 contigs, totaling 4.03 Mbp with an average GC content of 35.4%. The Ag1 genomic reads (620 Mbp) were de novo assembled in CLC Genomics Workbench v.4.9, which yielded 51 contigs, totaling 4.05 Mbp. The draft genomes were annotated using the NCBI Prokaryotic Genome Automatic Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/), which predicted 3,687 protein coding sequences (CDS) and 44 RNA genes in R26 and 3,648 CDS and 38 RNA genes in Ag1. Strikingly, 112 protein features were identified in the category “Resistance to antibiotics and toxic compounds.” This included drug efflux/transport (36 features); resistance to β-lactam antibiotics, fluoroquinolones, and heavy metals (28, 4 and 25 features, respectively); and 19 additional features involved in resistance to a diverse set of antibiotics. The large genetic capacity against various antibiotics is consistent with the observation that E. anophelis has natural antibiotic resistance to several antibiotics (7). Recently, E. anophelis was reported as a human pathogen in Central Africa (8) and an outbreak was also seen in an intensive care unit in Singapore (9). In both clinical cases multidrug resistance was reported. Further analysis of the genomic background would improve our understanding of antibiotic resistance mechanisms and their significance in shaping a microbial community in natural environments and the host-associated metagenomic ecosystem (10, 11). Like some Bacteroides (12), E. anophelis possesses polysaccharide utilization loci (PUL), which suggests the genetic capability to utilize various plant polysaccharides. This implies an intriguing ecological connection with the nectar and plant sap feeding behavior of mosquitoes in nature. The genome of E. anophelis plus other bacterial genomes that Xu and collaborators isolated from the mosquito guts, Pseudomonas sp. (13) and Enterobacter sp. (14), will serve as references for subsequent characterization of the mosquito gut microbiome and its impact on Anopheles gambiae life traits. Additionally, the pathogenic and multiresistant nature of the bacteria prompts investigations of the vector potential of mosquitoes for E. anophelis transmission to humans.

Elizabethkingia anophelis is a species in the family Flavobacteriaceae. It is a dominant resident in the mosquito gut and also a human pathogen. We present the draft genome sequences of two strains of E. anophelis, R26 and Ag1, which were isolated from the midgut of the malaria mosquito Anopheles gambiae.

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