

Draft Genome Sequences of *Enterobacter* sp. Isolate Ag1 from the Midgut of the Malaria Mosquito *Anopheles gambiae*

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An isolate of *Enterobacter* sp. was obtained from the microbial community within the gut of the *Anopheles gambiae* mosquito, a major malaria vector in Africa. This genome was sequenced and annotated. The genome sequences will facilitate subsequent efforts to characterize the mosquito gut microbiome.

The mosquito gut ecosystem harbors a complex microbiota with a dynamic taxonomic composition at different stages of the insect's life. Taxa from the family *Enterobacteriaceae* were selectively enriched by blood meals in adult mosquitoes (8). *Enterobacter* sp. is one of the abundant gut inhabitants and has been identified in various mosquitoes, such as *Anopheles gambiae*, *Anopheles stephensi*, *Anopheles funestus*, *Anopheles albimanus*, *Aedes triseriatus*, *Aedes aegypti*, *Culex pipiens*, and *Psorophora columbiae* (3, 5–8). Furthermore, an isolate of *Enterobacter* sp. from wild mosquitoes has demonstrated the ability to interfere with the development of *Plasmodium falciparum*, the causative agent of malaria, in the mosquito midgut (2). We have sequenced the genome of an isolate of *Enterobacter* sp. that was obtained from the midgut of *Anopheles gambiae*. Here we report the draft genome sequences.

The cultivatable bacteria from the midgut of mosquito *Anopheles gambiae* were grown on a BBL PC agar plate. Several colonies were identified as *Enterobacter* sp. based on the 16S rRNA gene sequences. The genome of one isolate, the *Enterobacter* sp. strain Ag1, was sequenced using Illumina paired-end technology at BGI America. The sequence reads (~650 Mbp) were *de novo* assembled with the DNASTar SeqMan NGen assembler (v.10.0), which generated 64 contigs totaling 4.75 Mbp. The genome was annotated using NCBI Prokaryotic Genome Automatic Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), which predicted 4,433 protein-coding features and 83 RNA genes. Among them, 3,614 protein features were assigned to 530 subsystems by the SEED subsystem at the RAST server (1). One thousand nine hundred seventy-one (54.5%) protein features belong to the following subsystems: carbohydrates, amino acids and derivatives, cofactors, vitamins, prosthetic groups, pigments, cell wall and capsule, and protein metabolism. In the blood-fed gut, blood digestion imposes acute oxidative stress (4). *Enterobacter* is among the bacteria that expand in the blood-fed gut (8). The presence of 179 stress response genes demonstrates the genetic capability of *Enterobacter* to live in the stressful blood-fed gut. This is consistent with the speculation that the gut-resident microbes may provide additional genetic capacity to cope with the blood meal-associated oxidative stress in the gut ecosystem (4, 8).

The draft genome sequences, in combination with other genomes of mosquito-associated bacteria, such as *Elizabethkingia*

sp. strain Ag1 (accession no. [AHHG01000000](#)) and *Pseudomonas* sp. strain Ag1 (accession no. [AKVH01000000](#)), will serve as references for functional characterization of the mosquito gut microbiome.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AKXM00000000](#). The version described in this paper is the first version, AKXM01000000.

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