

Draft Genome Sequence of *Pseudomonas* sp. Strain Ag1, Isolated from the Midgut of the Malaria Mosquito *Anopheles gambiae*

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A *Pseudomonas* sp. bacterium was isolated from the midguts of *Anopheles gambiae* mosquitoes. Here we present the annotated *Pseudomonas* sp. draft genome sequence as a contribution to the efforts of characterization of the mosquito gut microbiome.

The mosquito gut accommodates a complex microbial community comprising diverse microorganisms (2, 4, 9, 11–13), which are essential for various mosquito life traits, such as development, fecundity, and immunity against malaria (3, 5, 6, 8). Characterization of the structure and functionality of the mosquito gut microbiome would increase understanding of interactions between the mosquito and its associated gut microbes. We have initiated efforts to profile mosquito gut microbiota (13). Here we present the draft genome sequence of a *Pseudomonas* sp. isolate that was obtained from the gut of *Anopheles gambiae* (strain G3).

The midgut contents from blood-fed mosquitoes were cultured on tryptic soy agar plates. A *Pseudomonas* sp. isolate was selected based on its 16S rRNA gene sequence. The bacteria can also grow in Luria-Bertani broth. The genome was sequenced using Illumina pair-end technology from BGI America. Approximately 650 million reads were generated and assembled into 143 contigs, which totaled 7,259,712 bp. The contigs were annotated via the NCBI Prokaryotic Genome Automatic Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). The annotated genome contains 63 RNA genes and 6,570 protein-coding sequences. Among the protein coding sequences, 4,789 were assigned to 561 subsystems by the SEED subsystem database and the RAST server (1). The 16S rRNA comparison revealed that the isolate was closely related to *Pseudomonas fluorescens* strain SBW25 (10) and *P. fluorescens* strain A506 (GenBank accession number CP003041.1). Previously, we observed that blood meals drastically alter mosquito gut microbial composition; *Pseudomonas* spp. are among the taxa that are enriched in blood-fed guts (13). Blood digestion imposes strong oxidative stress upon blood-feeding insects (7). Besides the genetic adaptation that mosquitoes have developed throughout their evolution, the associated microbes in the blood-fed gut may provide the additional genetic capacity to cope with oxidative stress (13). Indeed, there are 42 genes in the oxidative stress-responsive category, including redox-sensitive transcriptional activators SoxR, OxyR, and Fcr/Fnr. Catalase, manganese superoxide dismutase, superoxide dismutase (Fe), heme oxygenase, alkyl hydroperoxide reductase (AhpC), and glutathione peroxidase are present as well. This supports the proposed correlation between a genetic tolerance and fitness in the stressful gut environment induced by a blood meal.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AKVH000000](https://doi.org/10.1093/nar/40/11/4000). The version described in this paper is the first version, AKVH01000000.

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