



Draft Genome Sequences of *Pseudomonas* sp. Isolates Recovered from Ghanaian Fish Food Samples in 2018

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ABSTRACT The genus *Pseudomonas* represents a broad diversity of opportunistic and pathogenic species that are able to colonize a wide range of ecological niches. Here, we report on draft genome sequences of 35 *Pseudomonas* sp. isolates that were recovered from small processed Ghanaian fishes offered at food markets in 2018.

Pseudomonadaceae are Gram-negative bacteria, of which some species are associated with animal, plant, and human diseases (1). Besides broad intrinsic resistance to different beta-lactams (2), many *Pseudomonas* species also produce exopolysaccharides involved in the formation of biofilms (3). These traits make them hard to treat, i.e., in food production, where they are involved in food spoilage (4). While detailed information on the diversity of *Pseudomonadaceae* exists (5), genomic data for food-associated isolates from middle income countries are rare.

Within the LEAP AGRI program-funded project SmallFishFood (<https://smallfishfood.org>), 104 samples of processed small fish were taken from five Ghanaian markets in November 2018 to assess the food safety and nutritional quality. For microbiological investigation, individual samples were pooled into batches for each fish species and market, prepared, and subjected to cultivation as previously described (6). *Pseudomonas* isolates were recovered from Brilliance *Escherichia coli*/coliform agar (Oxoid, Wesel, Germany) after incubation at 37°C for 20 to 24 h. Species confirmation was conducted using the direct transfer method on a matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) Biotyper (Bruker Daltonik, Bremen, Germany) (7). Information on isolates, sources, and sampled markets is summarized in Table 1.

Isolates were further subjected to cultivation in lysogeny broth (LB) for 24 h at 37°C for the preparation of genomic DNA with the PureLink genomic DNA kit (Invitrogen, Karlsruhe, Germany). For library preparation and whole-genome sequencing (WGS), the Nextera DNA Flex library prep kit with the IDT for Illumina Nextera DNA unique dual indexes set B and the NextSeq 500/550 midoutput kit v2.5 (300 cycles) for paired-end sequence determination (2 × 151-bp), respectively, were used on a NextSeq 500 device, as recommended by the manufacturer (Illumina, Inc., San Diego, CA, USA). The raw reads were trimmed using fastp v0.19.5 (<https://github.com/openscience/fastp>; parameters: base limit, 50; required length, 15) and checked with FastQC v1.0.4 (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc>). SPAdes *de novo* assembly and genome annotation were performed using the Pathosystems Resource Integration Center (PATRIC) release 3.6.7 (8) and the Prokaryotic Genome Annotation Pipeline (PGAP; National Center for Biotechnology Information) (9), respectively. If not otherwise indicated, default parameters were used for bioinformatics analysis.

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WGS provided insight into the genetic basis of fish-associated *Pseudomonas* sp. isolates from Ghana, Africa (Table 1). In addition to a reliable assignment to a *Pseudomonas* species (WGS based), which is often challenging using mass spectrometry due to their close relationship, the genome sequence data also provide an overview of the diversity of the *Pseudomonas* species occurring within Ghanaian fish products. Here, the sequences of 12 *P. putida* isolates, 10 *P. fulva* isolates, 5 *P. guariconensis* isolates, 3 *P. aeruginosa* isolates, 2 *P. montellii* isolates, 2 *P. asiatica* isolates, and 1 *P. zeshuii* isolate are announced. On the basis of the sequences' intrinsic/acquired resistance, information on the occurrence of genes involved in biocide tolerances as well as genes involved in the potential pathogenicity of the isolates for humans, animals, and plants can be used to assess if Ghanaian fish products might pose a potential health risk to the local public.

Data availability. The accession numbers of the whole-genome sequences and the raw sequencing read data are given in Table 1.

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