



## 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.

**P**seudomonadaceae 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/opengene/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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**TABLE 1** Features of the *Pseudomonas* sp. isolates investigated in this study

Isolate	Yr of isolation	Sample source <sup>a</sup>	Market	Raw sequencing results <sup>b</sup>			Assembly results			Annotation results		
				Mean length (bp)	Total reads (M)	Total bases (M)	GC content (%)	No. of contigs	Genome size (bp)	N <sub>50</sub> contig size (bp)	WGS-based species	Total no. of genes
20-MC00609	2018	WA pygmy herring	Accra	146	4,800,810	704,385,343	66.54	91	6,279,602	212,748	<i>P. aeruginosa</i>	5,874
20-MC00610	2018	WA pygmy herring	Techiman	146	4,475,634	656,108,908	66.55	110	6,251,217	258,224	<i>P. aeruginosa</i>	5,827
20-MC00611	2018	WA pygmy herring	Techiman	146	4,226,370	619,125,989	66.58	106	6,250,467	281,521	<i>P. aeruginosa</i>	5,826
20-MC00612	2018	Round sardinella	Accra	146	3,396,300	498,454,028	61.79	80	4,576,278	161,651	<i>P. fulva</i>	4,149
20-MC00613	2018	African moonfish	Accra	146	3,187,654	468,509,732	61.71	78	4,577,142	170,695	<i>P. fulva</i>	4,153
20-MC00614	2018	Bigeye grunt	Techiman	146	3,245,274	475,860,409	61.75	63	4,595,530	197,085	<i>P. fulva</i>	4,166
20-MC00615	2018	African moonfish	Kumasi	146	2,604,412	381,622,970	61.75	85	4,927,608	331,604	<i>P. fulva</i>	4,493
20-MC00616	2018	African moonfish	Techiman	146	2,201,970	322,159,916	61.64	105	4,629,253	166,757	<i>P. fulva</i>	4,276
20-MC00617	2018	African moonfish	Techiman	146	3,256,114	476,576,303	61.85	71	4,596,202	193,568	<i>P. fulva</i>	4,172
20-MC00618	2018	Bigeye grunt	Kumasi	146	2,619,826	383,998,382	61.77	86	4,926,499	244,295	<i>P. fulva</i>	4,496
20-MC00619	2018	Bigeye grunt	Accra	146	3,702,502	543,679,923	63.54	118	5,065,018	119,512	<i>P. guariconensis</i>	4,606
20-MC00620	2018	WA pygmy herring	Accra	146	3,643,072	533,979,303	62.60	70	5,419,544	226,217	<i>P. guariconensis</i>	4,935
20-MC00621	2018	Anchovy	Kumasi	146	3,901,822	571,665,460	63.31	162	5,288,286	92,968	<i>P. guariconensis</i>	4,706
20-MC00622	2018	Anchovy	Kumasi	145	3,606,736	523,371,010	62.49	46	5,460,285	323,991	<i>P. guariconensis</i>	5,091
20-MC00623	2018	Anchovy	Kumasi	146	3,571,756	523,322,660	63.30	169	5,288,246	71,986	<i>P. guariconensis</i>	4,710
20-MC00624	2018	Tilapia	Tamale	146	3,367,602	493,079,541	55.40	57	5,387,473	305,993	<i>P. zeshuii</i>	5,041
20-MC00625	2018	Bigeye grunt	Accra	146	4,897,526	717,096,751	63.32	121	5,186,595	145,104	<i>P. montelli</i>	4,741
20-MC00626	2018	African moonfish	Accra	146	4,231,398	620,321,845	62.42	83	5,501,680	172,172	<i>P. montelli</i>	5,098
20-MC00627	2018	Anchovy	Accra	146	3,751,486	549,815,338	62.74	137	5,882,527	93,066	<i>P. putida</i>	5,357
20-MC00628	2018	Anchovy	Accra	146	4,076,876	597,221,091	62.83	131	5,882,156	110,679	<i>P. putida</i>	5,356
20-MC00629	2018	African moonfish	Accra	146	4,219,840	619,454,733	61.58	101	4,793,76	119,685	<i>P. putida</i>	4,355
20-MC00630	2018	WA pygmy herring	Bogatanga	146	2,832,042	415,657,437	61.60	99	4,710,419	191,328	<i>P. putida</i>	4,374
20-MC00631	2018	WA pygmy herring	Bogatanga	146	4,305,644	631,292,956	61.61	94	4,710,252	186,030	<i>P. putida</i>	4,375
20-MC00632	2018	Round sardinella	Tamale	146	3,363,110	493,604,577	61.78	96	4,868,050	213,857	<i>P. fulva</i>	4,432
20-MC00633	2018	Anchovy	Techiman	146	3,649,412	535,446,634	62.40	142	6,153,330	104,212	<i>P. putida</i>	5,775
20-MC00634	2018	Anchovy	Kumasi	146	4,021,018	589,80,2612	61.52	87	4,908,887	191,143	<i>P. putida</i>	4,482
20-MC00635	2018	Anchovy	Techiman	146	4,092,982	601,284,084	61.29	190	5,066,612	103,772	<i>P. putida</i>	4,754
20-MC00636	2018	Anchovy	Bogatanga	145	4,089,862	596,317,192	62.92	147	5,929,517	104,170	<i>P. putida</i>	5,394
20-MC00637	2018	Anchovy	Bogatanga	146	4,762,456	698,752,505	62.90	149	5,930,696	102,143	<i>P. putida</i>	5,387
20-MC00638	2018	Anchovy	Tamale	146	2,642,248	387,672,486	62.81	136	5,639,936	82,997	<i>P. asiatica</i>	5,171
20-MC00639	2018	Anchovy	Tamale	146	1,641,074	241,574,006	62.35	237	6,115,340	103,856	<i>P. asiatica</i>	5,726
20-MC00640	2018	Anchovy	Techiman	143	4,802,152	690,821,487	62.36	132	6,153,022	127,023	<i>P. putida</i>	5,787
20-MC00641	2018	Anchovy	Techiman	146	3,089,492	452,919,469	62.55	160	6,110,158	111,368	<i>P. putida</i>	5,695
20-MC00650	2018	Bigeye grunt	Techiman	146	3,610,254	529,495,604	61.81	49	4,583,286	211,866	<i>P. fulva</i>	4,164
20-MC00651	2018	Bigeye grunt	Techiman	146	3,641,184	533,486,812	63.77	59	4,505,983	206,201	<i>P. fulva</i>	4,123

<sup>a</sup> WA, West African.<sup>b</sup> M, million.

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. monteili* 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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