



# Draft Genome Sequences of *Enterobacter* spp., *Lelliottia* spp., and *Serratia* spp., Coliform Bacteria from Drinking Water Reservoirs and Lakes

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**ABSTRACT** Surface waters are a major source for drinking water production. Therefore, it is essential to examine microbial processes within the water bodies, such as mass proliferations of coliform bacteria. Here, we report the draft genome sequences of *Enterobacter* spp., *Lelliottia* spp., and *Serratia* spp. isolated from drinking water reservoirs and lakes.

Worldwide, surface waters such as lakes and drinking water reservoirs are major sources for drinking water production. In recent years, high concentrations of coliform bacteria have been observed during the summer months, with *Enterobacter* spp. and *Lelliottia* spp. forming “coliform blooms,” whereas *Serratia* spp. dominate in winter (1–3). As coliform bacteria occasionally overcome treatment and reach drinking water, further research is needed with regard to their hygienic relevance and their capability to proliferate in these oligotrophic environments (3). Traditionally regarded as fecal indicator bacteria, coliform bacteria also occur naturally in water, plants, and soil (4–6). Toward this end, whole-genome shotgun sequencing of 21 coliform bacteria isolates was performed (Table 1).

Coliform bacteria were isolated from 2014 to 2019 during coliform mass proliferations from drinking water reservoirs and lakes in Germany using Colilert-18/Quantitray tests (IDEXX Laboratories, Westbrook, ME, USA) according to ISO 9308-2 (7). To obtain single colonies, liquid from wells was transferred onto heterotrophic plate count agar plates (Merck KGaA, Darmstadt, Germany), recommended by German regulations (Deutsches Einheitsverfahren), and incubated for 24 h at 36°C. Bacterial isolates were picked and transferred to fresh heterotrophic plate count agar plates, where they were incubated under the same conditions as before. Genomic DNA of pure cultures, grown on these agar plates, was extracted using a FastDNA spin kit for soil (MP Biomedicals, Santa Ana, CA, USA) and quantified using a Qubit fluorometer (Invitrogen, Carlsbad, CA, USA) according to the manufacturer’s instructions.

Preparation of sequencing libraries was performed using a DNA prep kit (Illumina). The draft genomes were sequenced by 150-bp paired-end sequencing on an Illumina NextSeq 1000 instrument using NovaGene (Illumina). Reads were trimmed using Cutadapt v1.16.6 (8) and quality controlled using FastQC v0.72 (<https://github.com/s-andrews/FastQC>). High-quality sequence reads were assembled *de novo* using Unicycler v0.4.6.0 (9), which includes SPAdes v3.12.0 (10). Annotation was carried out using RASTtk v2.0 (11, 12) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.0 (13, 14). Phylogeny for exact identification was conducted with the codon tree pipeline in PATRIC v3.6.9 (15, 16), which uses single-copy cross-genus protein families and analyzes aligned proteins and coding DNA from single-copy genes using RAXML v8.0.0 (17). Default parameters were used for all software unless otherwise noted. Genome size and further information are presented in Table 1.

Antibiotic resistance genes were analyzed using the Comprehensive Antibiotic Resistance Database (CARD) v3.0.3 within PATRIC’s specialty gene table (18). Several multidrug-resistant efflux pumps (e.g., AcrAB, AcrAD, EmrAB, MacAB, and MdtABC) and antibiotic resistance genes (e.g.,  $\beta$ -lactamase class C [*ampC*]) were found in all of the

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**TABLE 1** Characteristics and accession numbers of genomes from coliform bacteria isolated in drinking water reservoirs

Bacterial species <sup>a</sup>	Strain	Reservoir/lake	Read count (bp)	Genome coverage (x)	Genome size (bp)	No. of contigs	N <sub>50</sub> (bp)	G+C content (%)	No. of CDSs <sup>b</sup>	GenBank accession no.	SRA no.
<i>Enterobacter asburiae</i>	TZW01	Klingenberg	5,949,546	370	4,940,293	45	355,075	55.3	4,782	JAEEAT0000000000	SRRI4430924
<i>Enterobacter asburiae</i>	TZW02	Klingenberg	5,088,393	317	4,661,786	26	454,690	55.7	4,386	JAENNF0000000000	SRRI4430923
<i>Enterobacter asburiae</i>	TZW03	Lake Constance	4,858,338	302	4,631,365	40	336,147	55.9	4,284	JAENNE0000000000	SRRI4430912
<i>Enterobacter asburiae</i>	TZW04	Wahnbach	5,719,871	356	4,800,941	19	396,606	55.6	4,589	JAENND0000000000	SRRI4430910
<i>Enterobacter asburiae</i>	TZW05	Klingenberg	5,527,150	344	4,747,844	40	231,680	55.6	4,478	JAENNC0000000000	SRRI4430909
<i>Enterobacter asburiae</i>	TZW06	Lake Constance	5,064,247	315	4,684,044	45	311,897	55.6	4,417	JAENNB0000000000	SRRI4430908
<i>Enterobacter asburiae</i>	TZW07	Lake Constance	5,322,862	331	4,795,094	25	502,428	55.7	4,555	JAENNA0000000000	SRRI4430907
<i>Enterobacter asburiae</i>	TZW08	Rappbode	5,225,148	325	4,792,810	33	470,802	55.6	4,547	JAENMZ0000000000	SRRI4430906
<i>Enterobacter asburiae</i>	TZW09	Obersee	5,305,554	330	4,746,220	36	323,238	55.6	4,468	JAENMY0000000000	SRRI4430905
<i>Enterobacter asburiae</i>	TZW10	Breitenbach	5,797,166	361	4,879,403	23	502,282	55.6	4,669	JAENMX0000000000	SRRI4430904
<i>Enterobacter asburiae</i>	TZW11	Wahnbach	5,071,083	315	4,803,492	19	396,606	55.6	4,592	JAENMW0000000000	SRRI4430922
<i>Lelliottia amnigena</i>	TZW12	Kleine Kinzig	6,333,162	428	4,694,183	26	415,957	52.5	4,382	JAENMV0000000000	SRRI4430921
<i>Lelliottia amnigena</i>	TZW13	Kleine Kinzig	5,906,285	399	4,830,285	26	337,333	52.5	4,577	JAENMU0000000000	SRRI4430920
<i>Lelliottia amnigena</i>	TZW14	Klingenberg	5,488,494	371	4,516,381	17	731,232	52.8	4,198	JAENMT0000000000	SRRI4430919
<i>Lelliottia amnigena</i>	TZW15	Söse	5,085,780	344	4,756,711	36	346,396	52.6	4,473	JAENMS0000000000	SRRI4430918
<i>Lelliottia aquatilis</i>	TZW16	Söse	5,417,881	366	4,756,331	35	346,396	52.6	4,472	JAENMQ0000000000	SRRI4430917
<i>Lelliottia aquatilis</i>	TZW17	Kleine Kinzig	5,684,773	360	4,835,026	27	233,298	53.8	4,472	JAENMR0000000000	SRRI4430916
<i>Serratia fonticola</i>	TZW18	Kleine Kinzig	5,104,384	269	5,752,035	55	190,940	53.7	5,178	JAENMP0000000000	SRRI4430915
<i>Serratia fonticola</i>	TZW19	Kleine Kinzig	6,409,833	338	6,050,704	65	181,482	53.6	5,437	JAENMO0000000000	SRRI4430914
<i>Serratia fonticola</i>	TZW20	Schönbrunn	5,601,327	295	6,223,117	58	218,606	53.7	5,590	JAENMN0000000000	SRRI4430913
<i>Serratia marcescens</i>	TZW21	Kleine Kinzig	5,039,584	292	5,248,648	27	2,884,332	59.4	4,942	JAENMM0000000000	SRRI4430911

<sup>a</sup> Strain identification based on 1,000 single-copy genes using the Randomized Accelerated Maximum Likelihood (RAxML) tool in the codon tree pipeline at PATRIC.<sup>b</sup> CDSs, coding DNA sequences.

genomes. Homologues of the antimicrobial peptide resistance gene *dlt*, commonly known from Gram-positive bacteria (19), were present in the *Enterobacter* genomes.

Further analysis of the genomes of coliform bacteria from drinking water reservoirs will increase our knowledge about their hygienic relevance, their ecology, and their ability to proliferate in oligotrophic environments.

**Data availability.** The whole-genome shotgun projects and the raw sequence reads have been deposited at DDBJ/ENA/GenBank under the accession numbers listed in Table 1. They belong to BioProject [PRJNA680915](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA680915). For all sequences, the first versions are described in this paper.

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