Title: Complete genome sequences of African *Salmonella* Enteritidis clinical isolates associated with bloodstream infection

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# Running title: African *S.* Enteritidis Genome announcement

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# Abstract

We report the complete genome sequencing and annotation of four *Salmonella* Enteritidis isolates; two that are representative of the Central/Eastern African clade (CP255 and D7795) and two of the Global Epidemic clade (A1636 and P125109).

*Salmonella enterica* serovar Enteritidis (*S.* Enteritidis) typically causes gastroenteritis and is responsible for a global epidemic linked to poultry and egg production. Over recent decades, *S.* Enteritidis has become a leading cause of invasive non-typhoidal *Salmonella* (iNTS) disease in sub-Saharan Africa (1, 2), and novel clades of this serovar have been isolated from individuals with bloodstream infection (3). In contrast to the Global Epidemic clade, these novel African clades are associated with high mortality in immunocompromised individuals and are typically multidrug-resistant (MDR), representing an important public health challenge (4).

We used long-read sequencing to investigate the genome of two representative *S.* Enteritidis strains of the Central/Eastern African clade (CP255 and D7795) and two of the Global Epidemic clade (P125109 and A1636). CP255 was isolated in the Democratic Republic of Congo (the Zaire) in 1991, from the blood of a child at the Institut-Médical-Evangélique, Kimpese, and is phenotypically MDR (amoxicillin, tetracycline, chloramphenicol and streptomycin-resistant) (5, 6). D7795 (paediatric patient/MDR) and A1636 (adult patient/fully susceptible) were isolated in 1998 and 2000, respectively in Blantyre (Malawi) (3). *S.* Enteritidis P125109, a UK PT4 isolate from 1988, was used as a reference (7–10).

A single colony of each isolate was grown for 16 h in 5 mL of Lennox medium at 37˚C. Total DNA was extracted using the Quick-DNA™ Universal Kit (Zymo, D4069). DNA integrity was verified by 0.5% agarose gel electrophoresis at 90 V for 1.5 h. DNA purity/concentration were measured with a DeNovix DS-11FX spectrophotometer/fluorometer and Qubit dsDNA HS assay Kit. Long-read sequencing was performed by the Centre for Genomic Research (University of Liverpool, UK) in a PacBio SMRT (P6/C4 chemistry) using SMRTbell Template 1.0 (Pacific Biosciences, 100-259-100) library preparation with g-Tube (Covaris) fragmentation and size-selection of 15-50 kb with 0.75% agarose cassette (BluePippin, BMF7510). Illumina HiSeq sequencing was performed as part of the 10KSG project (11) and by MicrobesNG (UK) using Nextera XT Library Prep Kit (Illumina, USA) with modifications (2 ng DNA and 1 min PCR elongation) and 250 bp paired‑end protocol. Reads were adapter-trimmed using Trimmomatic v0.30, with a sliding window quality cut-off of Q15 (12).

Using Filtlong v0.2.0 (<https://github.com/rrwick/Filtlong>) and Illumina reads as a reference, we selected a subset of raw PacBio reads with best quality and length to yield an approximate 100x coverage for each genome. Selected long- and short-reads were assembled using Unicycler v0.4.4 in hybrid mode (13). Genomes were initially annotated using Prokka v1.13.7 (14) through Bacpipe v0.6 (<https://github.com/apredeus/multi-bacpipe>), and automatically re-annotated by GenBank with PGAP (15), and rotated to the origin at the *thrLABC* operon. Variant calling was done with Snippy v4.3.6 (<https://github.com/tseemann/snippy>) in contig mode.

Genome comparison revealed genomic degradation and differences in accessory genome (Table 1). P125109 and A1636 carried the virulence plasmid pSENV, whereas D7795 carried pSEN-BT (3) and CP255 pSEN-DRC, which both had a pSENV backbone with MDR-encoding genes. Other plasmids were identified in A1636, D7795, and CP255. The prophage repertoire of A1636 resembled P125109 (7). Both D7795 and CP255 lacked ΦSE20, and instead carried P88-like and Fels2-like prophages.

# Data Availability

The annotated complete genome assemblies of *S.* Enteritidis CP255, D7795, A1636 and P125109 have been deposited in NCBI. The BioProject accession number is [PRJNA671837](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA671837/), and the individual accession numbers are [SAMN16552338](https://www.ncbi.nlm.nih.gov/assembly/GCA_015241115.1) (A1636), [SAMN16552337](https://www.ncbi.nlm.nih.gov/assembly/GCA_015240995.1) (CP255), [SAMN16552336](https://www.ncbi.nlm.nih.gov/assembly/GCA_015240855.1) (D7795) and [SAMN16552335](https://www.ncbi.nlm.nih.gov/assembly/GCA_015240635.1) (P125109). The Bacpipe annotation pipeline can be accessed at <https://github.com/apredeus/multi-bacpipe>.

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**Table 1: Characteristics and accession numbers of genomes of four *S.* Enteritidis isolates**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Isolate | Year  | Assembly accession no. | Raw reads accession no.a | No. readsIllumina (2x250 bp) | Illumina coverage | No. readsPacBio | N50 PacBio reads | G+C content | Genome size (bp) | Total no. of genes | Virulence plasmidb | Other plasmidsc | SNPc P125109 | SNPc D7795 |
| **CP255** | 1991 | [GCA\_015240995](https://www.ncbi.nlm.nih.gov/assembly/GCA_015240995.1) | [SRR12953596](https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR12953596)[SRR12953597](https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR12953597) | 296,730 | 30.6 | 40,000 | 20,451 | 52.30% | 4,840,946 | 4,729 | pSEN-DRC (96 kb) | pRSF1010 (8.7 kb)(16) | 972 | 61 |
| **D7795** | 2000 | [GCA\_015240855](https://www.ncbi.nlm.nih.gov/assembly/GCA_015240855.1) | [SRR12953602](https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR12953602)[SRR12953603](https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR12953603) | 813,469 | 83.5 | 103,762 | 16,718 | 52.30% | 4,869,504 | 4,777 | pSEN-BT (116 kb)(3) | pRGI00316 (4.9 kb)(17) | 1,017 | 0 |
| **A1636** | 1998 | [GCA\_015241115](https://www.ncbi.nlm.nih.gov/assembly/GCA_015241115.1) | [SRR12953598](https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR12953598)[SRR12953599](https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR12953599) | 3,859,080 | 406.4 | 97,435 | 16,873 | 52.20% | 4,748,456 | 4,608 | pSENV (59 kb) | pSE-GC (3.2 kb) | 46 | 1,022 |
| **P125109** | 1988 | [GCA\_015240635](https://www.ncbi.nlm.nih.gov/assembly/GCA_015240635.1) | [SRR12953600](https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR12953600)[SRR12953601](https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR12953601) | 587,289 | 61.9 | 92,761 | 17,272 | 52.20% | 4,745,224 | 4,606 | pSENV (59 kb) |  | 0 | 1,022 |

aAccession numbers for raw short (Illumina) and long (PacBio) reads

bNumber in parenthesis indicates plasmid size in kb and reference

cSNP (single nucleotide polymorphisms) identified in whole genome-based sequence comparison against either *S.* Enteritidis P125109 or D7795