First Draft Genome Sequence of *Salmonella enterica* subsp. *Enterica* Serovar Enteritidis Isolated from the Chicken Meat in Russia [†]

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Abstract: *Salmonella enterica* subsp. *enterica* serovar Enteritidis is one of the most common zoonotic pathogens. We report here the genome sequence of *Salmonella enterica* subsp. *enterica* serovar Enteritidis S-25048 isolated from chicken (*Gallus gallus domesticus*) meat in Artyom, Russia. The assembled genome size was 4,695,145 bp. A total of 4,565 coding genes, 4 rRNAs, 62 tRNAs, and 14 noncoding RNAs were predicted. To our knowledge, this is the first publically deposited annotated genome of this serovar isolated in Russia. The *Salmonella* Enteritidis S-25048 genome is suitable for use as a reference strain of *Salmonella* Enteritidis isolated in Russia.

Keywords: *Salmonella*; *Salmonella* Enteritidis; genome; whole-genome sequencing; Russia

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Salmonella spp. stand out as some of the most common causes of human bacterial food poisoning [1]. Specifically, *Salmonella enterica* subsp. *enterica* serovar Enteritidis (*S.* Enteritidis) represented 61.2% of all reported serovars of confirmed human cases in 2017 in the European Union [1] and about 70% of all reported serovars of confirmed human cases in 1988–2018 in Russia [2]. Chickens known to be the main reservoir for *S.* Enteritidis [1]. However, there is a lack of information on full-genome sequences of *S.* Enteritidis, isolated in Russia.

We announce here the draft genome sequence of *S.* Enteritidis strain S-25048, which was isolated from a local poultry farm in Artyom, Primorsky Krai of Russia from the chicken (*Gallus gallus domesticus*) meat in 2016. The strain was serotyped as *S.* Enteritidis (the seroformula is (1),9,12:g,m:-). Plasmid profile analysis showed that it contains two plasmids of size 59 kb and 2.1 kb. Genomic DNA was isolated from overnight culture using the AmpliSens DNA-sorb-B DNA extraction kit (AmpliSens Biotechnologies, Moscow, Russia), and libraries were constructed using the Nextera XT DNA library preparation kit (Illumina, CA, USA), both as per the manufacturers' directions. Whole-genome sequencing was performed on NextSeq 550 platform (Illumina, CA, USA), producing 2,316,265 paired-end reads with an average length of 300 bp and insert size of 500 bp, using High Output Kit v2.5 (300 cycles). Trimmed reads were assembled de novo by using SPAdes version 3.14.1 with default settings, which resulted in a coverage of 74× [3]. The draft genome assembly quality was assessed with QUAST version 5.0.2 [4]. All contigs with <500 bp were manually excluded. Contigs were manually oriented and ordered according to the reference genome *S.* Enteritidis P125109 (RefSeq Acc. No. NC_011294.1) by using Mauve version 26 February 2015 [5]. The draft genome sequence was annotated using the automated NCBI Prokaryotic Genome Annotation Pipeline

(PGAP) version 4.11 and subsequently deposited at GenBank [6]. Two plasmids were identified and placed as two last contigs of size 58,347 bp and 2173 bp.

The assembly size was 4,695,145 bp, with an N50 value of 371,562 bp, an average read depth of around 69×, and 52.14% GC content. The assembly size is comparable to that of recently announced *S.* Enteritidis genome sequences [7,8] and contains 4,565 coding sequences (CDSs), 4 rRNAs, 62 tRNAs, and 14 noncoding RNAs. *S.* Enteritidis S-25048 was confirmed to belong to serovar Enteritidis in silico by using both the SISTR Web service version 1.0 [9] and SeqSero2 version 1.1 [10]. The multilocus sequence typing (MLST) profile of the genome (sequence type 11 [ST11]) and the replicon typing of the plasmids (IncFII(S)/IncFIB(S) and ColpVC) was performed using MLST version 2.0 [11] and PlasmidFinder version 2.1 [12], respectively. Using ResFinder version 3.2 [13], only chromosomal-encoded *aac(6')-Iaa* gene, which confers aminoglycoside resistance, and *gyr*A S83Y point mutation, which confers resistance to nalidixic acid and ciprofloxacin, were found.

This sequence provides the first draft-quality reference for genome assemblies of *S.* Enteritidis, isolated in Russia, and for future virulence analyses or population structure studies of this epidemiologically and clinically relevant *S. enterica* serovar.

Data availability: This Whole Genome Shotgun project of *S.* Enteritidis isolate S-25048 has been deposited at DDBJ/ENA/GenBank under the accession JACEGM000000000 (BioProject, PRJNA638532; BioSample, SAMN15196029). The version described in this paper is version JACEGM010000000.

Conflicts of Interest: The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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