



Whole-Genome Shotgun Sequence of *Salmonella bongori*, First Isolated in Northwestern Italy

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ABSTRACT This study describes the whole-genome shotgun sequence of *Salmonella bongori* 48:z35:–, originally isolated from a 1-year-old symptomatic patient in northwest Italy, a typically nonendemic area. The draft genome sequence contained 4.56 Mbp and the G+C content was 51.27%.

Salmonella bongori 48:z35:– is considered endemic in Sicily, Italy but has not been reported as a clinical isolate responsible for human infection in mainland Italy (1). Phylogenetic analysis and comprehensive *Salmonella* evolution studies have suggested the genomic relationship between *S. bongori* and an ancestral *Salmonella* virulence gene set, which has been adapted by incorporating virulence determinants highly similar to those found in enteropathogenic *Escherichia coli* (2). Symptoms, in human cases, include nausea, fever, vomiting, abdominal pain, diarrhea, and acute enteritis (3).

Here, we report the whole-genome shotgun sequence of *S. bongori*, a fecal isolate from a 1-year old symptomatic patient in Piedmont in northwestern of Italy. The genomic content of the isolates was analyzed for potential genes that may be involved in virulence and antibiotic resistance. Bacterial genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, USA), the genomic libraries were prepared using the Nextera XT library prep kit, and 250-bp paired-end sequencing was performed using the Illumina MiSeq platform (Illumina, San Diego, CA). Raw reads were preprocessed to remove adapter sequences and low-quality reads using Trimmomatic (v0.36) software (4). *De novo* assembly was performed using the SPAdes genome assembler (v3.9.1) (5). Assembly resulted in the generation of 85 contigs with a total size of 4.57 Mb, a G+C content of 51.3%, and an N_{50} of 179,074 bp. After assembly, gene prediction was performed using Prodigal (6). As a result, a total number of 4,242 genes were predicted. The draft genome sequence was annotated using the NCBI GenBank annotation pipeline and RAST genome annotation server (7). A total of 4,446 coding sequences were annotated in various functional categories, including biological processes and metabolism (1,836 genes), cellular components (431 genes), and molecular functions (828 genes). The number of virulence, disease and defense features generated was 91, including adhesion (6.6%), bacteriocins, and ribosomally synthesized antibacterial peptides (13.2%), resistance to antibiotics and toxic compounds (70.3%), and invasion and intracellular resistance (9.9%).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [NAPQ00000000](https://doi.org/10.1128/JCM.40.9.3502-3505.2002). The version described in this paper is version NAPQ01000000.

REFERENCES

- Giammanco GM, Pignato S, Mammina C, Grimont F, Grimont PAD, Nastasi A, Giammanco G. 2002. Persistent endemicity of *Salmonella bongori* 48:z35:– in southern Italy: molecular characterization of human, animal, and environmental isolates. *J Clin Microbiol* 40:3502–3505. <https://doi.org/10.1128/JCM.40.9.3502-3505.2002>.
- Fookes M, Schroeder GN, Langridge GC, Blondel CJ, Mammina C, Connor

Received 10 May 2017 Accepted 15 May 2017 Published 6 July 2017

Citation Romano A, Bellio A, Macori G, Cotter PD, Bianchi DM, Gallina S, Decastelli L. 2017. Whole-genome shotgun sequence of *Salmonella bongori*, first isolated in northwestern Italy. *Genome Announc* 5:e00560-17. <https://doi.org/10.1128/genomeA.00560-17>.

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- TR, Seth-Smith H, Vernikos GS, Robinson KS, Sanders M, Petty NK, Kingsley RA, Bäumlér AJ, Nuccio SP, Contreras I, Santiviago CA, Maskell D, Barrow P, Humphrey T, Nastasi A, Roberts M, Frankel G, Parkhill J, Dougan G, Thomson NR. 2011. Salmonella bongori provides insights into the evolution of the salmonellae. *PLoS Pathog* 7:e1002191. <https://doi.org/10.1371/journal.ppat.1002191>.
3. Woodward DL, Khakhria R, Johnson WM. 1997. Human salmonellosis associated with exotic pets. *J Clin Microbiol* 35:2786–2790.
 4. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
 5. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
 6. Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119. <https://doi.org/10.1186/1471-2105-11-119>.
 7. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST Server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.