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Letter to the Editor

Case report of a bloodstream infection due by *Salmonella strathcona* ST2559 in northeast Italy, 2025

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ABSTRACT

Not applicable.

Dear Editor,

Recently, a multi-country outbreak of *Salmonella strathcona* ST2559 has been reported in the European Union and the United Kingdom (UK) [1]. In particular, from January 2023 to November 2024, different countries reported a total of 232 confirmed cases of *S. strathcona* [2]. Epidemiological and traceback investigations demonstrated that the *S. strathcona* ST2559 widespread in different countries was vehiculated by small tomatoes originated from Sicily since 2011 [2–4]. Indeed, prior to 2010 no confirmed cases with *S. strathcona* were reported in the EU countries (https://atlas.ecdc.europa.eu/public/index.aspx). Here, we present the case of a bloodstream infection due to *S. strathcona* ST2559 isolated from a hospitalized patient in northeast Italy, 2025.

A young woman was admitted on November 2025 to the Azienda Sanitaria Universitaria Friuli Centrale for fever, vomiting, splenic abscess, and pleural effusion. During hospitalization patient developed fever and Blood culture yielded a positive result initially identified as *Salmonella* spp. by MALDI-TOF system (Bruker, Germany). Therefore, patient was initially treated with piperacillin-tazobactam, then switched to ceftriaxone 2 g once daily when the susceptibility test demonstrated a multi-susceptible Salmonella spp strain. The patient also had a positive stool sample for *Salmonella (molecular test)*, which became negative after antibiotic therapy. Both the pleural effusion and the splenic abscess were drained; microbiological cultures from these samples were negative for *Salmonella* as well as for other pathogens. To achieve complete defervescence, a short tapering course of corticosteroids was administered.

In order to characterize the serovar of *S. enterica*, a whole-genome DNA sequencing was performed as previously described [5]. Briefly, genomic DNA was extracted using QIASymphony instrument (Qiagen, Germany) and library preparation was performed using the FX DNA Library Preparation Kit (Qiagen, Germany) and the Nextera™ XT Index Kit (Illumina, USA). Sequencing was carried out on an Illumina MiSeq System using a 2 × 300-bp and paired-reads quality was evaluated with FastQC v0.12.1 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/). Genome assembly was carried out using SPAdes v3.15.5 (https://github.com/ablab/spades) and quality was evaluated with QUAST v.5.3.0. The final assembled genome of the *S. strathcona* object of this study, named strain SAL-UD, produced a draft with a total size of 4.698.491 bp, composed of 78 contigs ranging from 378.300 to 500 bp in length. The genome had a 52.15 % G + C content, 173.434 N50, 45.456 N90 and 20x mean coverage. Species identification was determined using SpeciesFinder v.2.0 (https://cge.food.dtu.dk/services/SpeciesFinder/) and results showed that strain SAL-UD belonged to the *Salmonella enterica* subsp. *enterica*. The MLST and antigenic profile identification were performed respectively using PubMLST (https://pubmlst.org/bigsdb) and SeqSero (https://cge.food.dtu.dk/services/SeqSero/). Genome-based typing revealed that the strain SUL-UD belonged to ST2559 (aroC→481,dnaN→18,hemD→10,hisD→124, purE→5,sucA→10,thrA→14), with the following antigenic profile: O-Antigen:O-7; H1-Antigen:l,z13,z28; H2-Antigen:1,7. Analysis of antimicrobial resistance determinants showed that SAL-UD carried gene related to the aminoglycoside-resistance (*aac(6′)-Iaa*). Clonal relatedness of the strain SAL-UD with the genomes of *S.strathcona* available in GenBank was performed as previously described [5]. Genome comparison among *S.strathcona* strains displayed a wide range of nucleotide homology value (ranging from 85.36 % to 99.85 %) among isolates isolated in Europe (Fig. 1).

To evaluate the role of prophages among *S.strathcona*, we performed a pro-phage regions analysis in the genome of the strain SAL-UD. Our analysis demonstrated that SAL-UD harboured 2 complete (ranging from 31.8 Kb to 36.5 Kb), 3 incomplete (ranging from 7.4 Kb to 21 Kb) and 2 questionable pro-phage regions (ranging from 10.2 Kb to 42.2 Kb) (Fig. S1 in the Supplementary material). Blast analysis demonstrated that the intact prophage regions exhibited high homology (nucleotide identity of 100 % with a coverage of 100 %) with chromosome of *S. strathcona* strain N22-0456 (Acc.no CP179910) isolated in 2022 from a patient recovered in Switzerland (Fig. S2 and S3 in the Supplementary material). At the same time, analysis of prophage regions demonstrated that several salmonella loci were found (Table S1 in the Supplementary material).

In conclusion, here we reported the case of a bloodstream infection occurred in northeast Italy, 2025. Also, we described the genome of *S. strathcona* ST2559 strain by enlarging the acknowledgment of the diffusion of this emerging pathogen in Europe and analysing the role of

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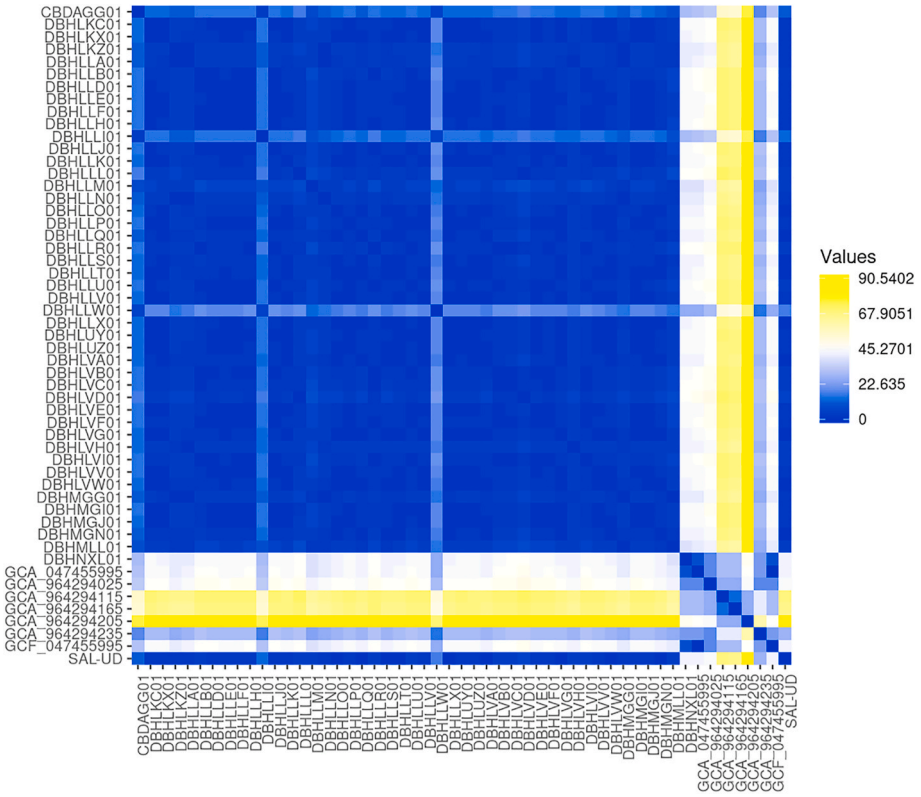

Fig. 1. *Heat map* based on a pair-wise *distance matrix* of *Salmonella strathcona* strains collected in Europe. ANI values were calculated for each pairwise comparison and the heat map visualization was performed by heatmapper tool and colours represent the ANI values ranging from low (yellow) to high identity (blue).

the prophage regions in the diversification of *S. strathcona*. Based on these findings, we highlighted the importance of monitoring emerging strains which could pose a significant risk for public health also recommending a more widespread use of genome sequencing.

Nucleotide sequence accession numbers

The draft genome assembly of the *Salmonella strathcona* strain SAL-UD as been deposited in the NCBI BioSample database under accession number SAMN53173069.

CRediT authorship contribution statement

Michela Bulfoni: Data curation, Formal analysis, Writing – original draft, Writing – review & editing. **Carlo Tascini:** Investigation, Writing – original draft, Writing – review & editing. **Paola Della Siega:** Investigation, Writing – original draft, Writing – review & editing. **Corrado Pipan:** Investigation, Writing – original draft, Writing – review & editing. **Silvio Brusaferro:** Investigation, Writing – original draft, Writing – review & editing. **Paolo Gaibani:** Conceptualization, Data curation, Formal analysis, Funding acquisition, Supervision, Writing – original draft, Writing – review & editing.

Ethical approval

Not required.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.nmni.2025.101679.

References

[1] Brait V, Böff L, Zmarlak-Feher NM, Jourdan-Da Silva N, Mazzilli S, Pardos de la Gandara M, et al. Insights into recurring multi-country outbreaks of *Salmonella strathcona* associated with tomatoes, Europe, 2011 to 2024. Euro Surveill 2025;30(41):2500224. 2025.
[2] European food safety authority (available at: https://www.efsa.europa.eu/en/supporting/pub/9740.
[3] Müller L, Kjelsø C, Frank C, Jensen T, Torpdahl M, Sorg B, et al. Outbreak of *Salmonella strathcona* caused by datterino tomatoes, Denmark, 2011. Epidemiol Infect 2016;144(13):2802–11.
[4] Møller FT, Mølbak K, Ethelberg S. Analysis of consumer food purchase data used for outbreak investigations, a review. Euro Surveill 2018;23(24):1700503.
[5] Gaibani P, Latorre R. Prophages in *Bacteroides fragilis*: distribution and genetic diversity. Heliyon 2025;11(4):e42755.

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