Epidemiology and Infection

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Yersinia enterocolitica 2/O:9 outbreak in France linked to raw cow milk cheese, 2024

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Original Paper

Cite this article: Tessier S, Savin C, Terrien E, Remonnay J, Pamart P, Fredriksen N, Guichard L, Martins C, Houard E, Girardin C, Clinard F, Laurent E, Mossong J, Retel O, Denis M, Le Guern A-S and Chereau F (2026). *Yersinia enterocolitica* 2/O:9 outbreak in France linked to raw cow milk cheese, 2024. *Epidemiology and Infection*, **154**, e142, 1–6
https://doi.org/10.1017/S0950268826102209

Received: 19 December 2025 UTC
Revised: 12 August 2026 UTC
Accepted: 15 September 2026 UTC

Keywords:
Foodborne outbreak; *Yersinia enterocolitica* 2/O:9; cgMLST

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Abstract

Enteric yersiniosis represents the fourth most frequently reported bacterial foodborne zoonosis in Europe and has been responsible for several outbreaks. Infections are primarily caused by *Yersinia enterocolitica* and, to a lesser extent, by *Yersinia pseudotuberculosis*. Investigation of an outbreak caused by *Y. enterocolitica* bioserotype 2/O:9 with isolates belonging to a single genomic cluster (0–3 alleles distances mismatch between isolates) identified common exposure to a raw cow's milk cheese, leading to an international product recall. The outbreak affected 167 confirmed cases between 17 September 2024 and 07 March 2025 in France and 5 cross-border cases. *Y. enterocolitica* isolates belonging to the same genomic cluster were detected in the cheese at the cheese factory and in a milking machine filter of a milk producer. This investigation is a reminder of the risks associated with raw milk cheese consumption. We emphasize the need for producers of milk to identify and prevent critical contamination points for *Y. enterocolitica*.

Introduction

Enteric yersiniosis, primarily caused by *Yersinia enterocolitica* (*YE*), was the fourth most common zoonotic disease in European Union countries in 2023 with 8 738 confirmed cases and a notification rate of 2.4 per 100 000 population, with an increase of 13.5% compared to the rate in 2022 [1]. Germany accounted for the highest number of reported cases (n = 1 931), followed by France (n = 1 384) and Spain (n = 1 317).

In Europe, the most common type of *YE* reported in human infections is bioserotype 4/O:3 (87%), followed by 2/O:9 (11%) [1]. Pigs are an important reservoir of *YE*, especially bioserotype 4/O:3 [2, 3], whereas cattle seem to be associated with bioserotype 2/0:9 [4]. Most reported *YE* infections in Europe appear to be sporadic; yet, several foodborne outbreaks have been documented and linked to the consumption of pasteurized or unpasteurized milk [5–8], raw vegetables, and ready-to-eat products [9], as well as contaminated water [10]. The route of human contamination is mainly through the ingestion of contaminated food and more rarely through a direct or indirect contact with animals [10].

In France, microbiological surveillance of human yersiniosis is conducted by the National Reference Centre (NRC) for Plague and Other Yersiniosis. Since 2018, routine microbiological surveillance is based on the characterization of each isolate – species and lineage – and inclusion in a genomic cluster, using core genome multilocus sequence typing (cgMLST) schemes [11, 12]. Santé publique France (the French National Public Health Agency) is contacted for the assessment of clusters which meet the outbreak alert criteria: at least 5 isolates belonging to a same genomic cluster isolated within 8 weeks [12]. This method is useful for public health surveillance and has proven effective for outbreak detection [13].

Outbreak detection

On 22 October 2024, the NRC notified Santé publique France of a cluster consisting of 14 cases of isolates of *YE* belonging to a same genomic cluster (number 4452) isolated between 17 September and 07 October 2024. An outbreak investigation team with experts from Santé publique France, the NRC, the French Agency for Food, Environmental and Occupational Health and Safety

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(ANSES), and the French General Directorate of Food (DGAl) launched extensive epidemiological, microbiological, and food investigations to identify the vehicle of transmission and propose appropriate control measures.

Methods

Epidemiological investigation

Outbreak case definition and case finding

A French outbreak case was defined as a resident in mainland France with laboratory-confirmed *YE* infection whose isolate was isolated between 17 September 2024 and 07 March 2025, characterized as lineage 2/3-9b (corresponding to bioserotype 2/O:9) [11] and belonging to the genomic cluster 4452 using the 1 727-gene *Y. enterocolitica* cgMLST scheme followed by single-linkage clustering with a three-allele mismatch threshold [12]. French yersiniosis cases were identified by the routine microbiological surveillance conducted by the NRC on *Yersinia* isolates sent on a voluntary basis by the French clinical microbiology laboratories.

A cross-border case was defined as a laboratory-confirmed case residing in a European country other than France, with an isolate's genomic sequence belonging to cluster 4452 as identified for French isolates, with the isolation date between 17 September 2024 and 07 March 2025. Cross-border cases were identified from European countries through EpiPulse [14], the European surveillance portal for infectious diseases, run by the European Centre for Disease Prevention and Control (event 2024-FWD-00114), and genomic sequencing of raw data together with demographic and epidemiological data (when available) shared with France.

Data collection and analysis. Demographics (age, sex, and postal code of residence) of cases, as well as *YE* isolation dates, were available from medical laboratories' declaration forms. All French cases (or their legal representatives) with isolation dates between 17 September and 8 November were contacted by phone for interviews. Interviews took place between 22 October and 28 November and were temporarily suspended between 28 November and 16 December, following the implementation of control measures. Interviews were resumed between 16 and 24 December and targeted cases with isolation dates at least seven days after the start of the product recalls. Interviews were conducted by epidemiologists using a standardized trawling questionnaire, covering clinical aspects (symptoms and onset date), medical history, detailed food consumption, contact with other persons experiencing diarrhoea, travel history, and contact with animals during the seven days prior to symptom onset. Place of purchase and loyalty card information when available were also collected to trace back supermarket purchases.

Food product and environmental investigations. Food trace back investigations were conducted by the departmental direction in charge of the protection of populations (DDecPP) and by the DGAl. Suspected food products (30 cheeses with different ripening periods) and environmental samples (14 milk filters from 4 milk producers) were taken by DDecPP and sent to the ANSES Ploufragan Laboratory, France, for *YE* detection and characterization.

Microbiological investigation. Methods used, respectively, by the NRC and the ANSES, to isolate, characterize, and compare isolates for clinical, food, and environmental samples were described previously [13]. Relationships between genome isolates were visualized using a minimum spanning tree (Bionumerics v7.6.3), which was reconstructed by single linkage clustering based on allelic profiles obtained with the 1 727-gene *Y. enterocolitica* cgMLST. Phylogenetic inference was performed on the 1 727 loci that were first extracted with the 'Export' plugin available at https://bigsdb.pasteur.fr/yersinia, concatenated for each isolate, and subsequently aligned using MAFFT v7.467 [15]. The resulting alignment served as input for IQ-TREE2 [16], where the optimal nucleotide substitution model was identified with ModelFinder (integrated in IQ-TREE2), and a maximum-likelihood tree was constructed with 1 000 ultrafast bootstrap replicates.

Results

Epidemiological investigation

Description of the outbreak in France

As of 02 May 2025, 167 French cases had been identified with isolation dates between 17 September 2024 and 07 March 2025 (Figure 1a).

Median age was 50 years (range: 2–91), 4 cases were children under 5 years, 45 cases were aged over 65 years, and 84 (51%) were female. Cases originated from 11 of the 13 regions in mainland France, with 75 (45%) cases coming from the Bourgogne-Franche-Comté region (Figure 1b). Most isolates were collected from foecal samples ($n = 160$, 96%), four were isolated from blood samples, and two from other samples (dialysis fluid and pus).

All isolates were assigned to the cluster 4452 (Figure 2, Supplementary Figure S1) consisting of 229 clinical isolates identified between 01 August 2020 and 07 March 2025 (3 in 2020, 9 in 2021, 23 in 2022, 12 in 2023, 169 in 2024, and 13 in 2025).

Forty-five cases were interviewed: 39 cases between 22 October and 28 November 2024, and 6 cases between 16 and 24 December 2024 (Figure 1a). The cases were aged between 2 and 82 years old (mean age: 45), 25 (56%) were females, and 25 (56%) resided in the Bourgogne-Franche-Comté region. The onset dates of the symptoms ranged from 05 September to 26 November 2024. Most cases experienced abdominal pain ($n = 39$) and diarrhoea ($n = 33$) (28 cases presented both abdominal pain and diarrhoea). Fewer cases had fever ($n = 17$), nausea ($n = 17$), vomiting ($n = 6$), or bloody diarrhoea ($n = 2$). Three cases had been hospitalized (short stay: 3 to 5 days) and two patients had an emergency consultation. No death was reported.

Identification of the source of the outbreak

Food exposures of confirmed cases and trace back investigation

In total, 28 (72%) of the 39 cases interviewed between 22 October and 28 November reported consumption of a same cheese type: a soft cheese made in the Bourgogne-France-Comté region from raw cow's milk and wrapped in a wooden box. Cases reporting consumption of the suspected cheese type resided in 8 of the 11 affected regions and the symptom-onset dates ranged from 09 September to 28 October 2024. Among them, 20 had purchased the suspected cheese in cheese shops and 6 in supermarkets (2 could not specify the place of purchase). A cheese manufacturer in the Bourgogne-Franche-Comté region was identified as the suspected source. Three cases had bought the cheese directly from the suspected manufacturer's cheese shop and five additional cases reported purchasing the suspected cheese type produced by the suspected manufacturer, although the cheeses were bought in different places. No other food item was consumed by more than 50% of the cases. Among the six cases who mentioned purchase of the suspected cheese type in supermarkets, four cases had loyalty cards. Purchase of the cheese type could be confirmed for one case and trace back identified the suspected cheese manufacturer.

https://doi.org/10.1017/S0950268826102209 Published online by Cambridge University Press

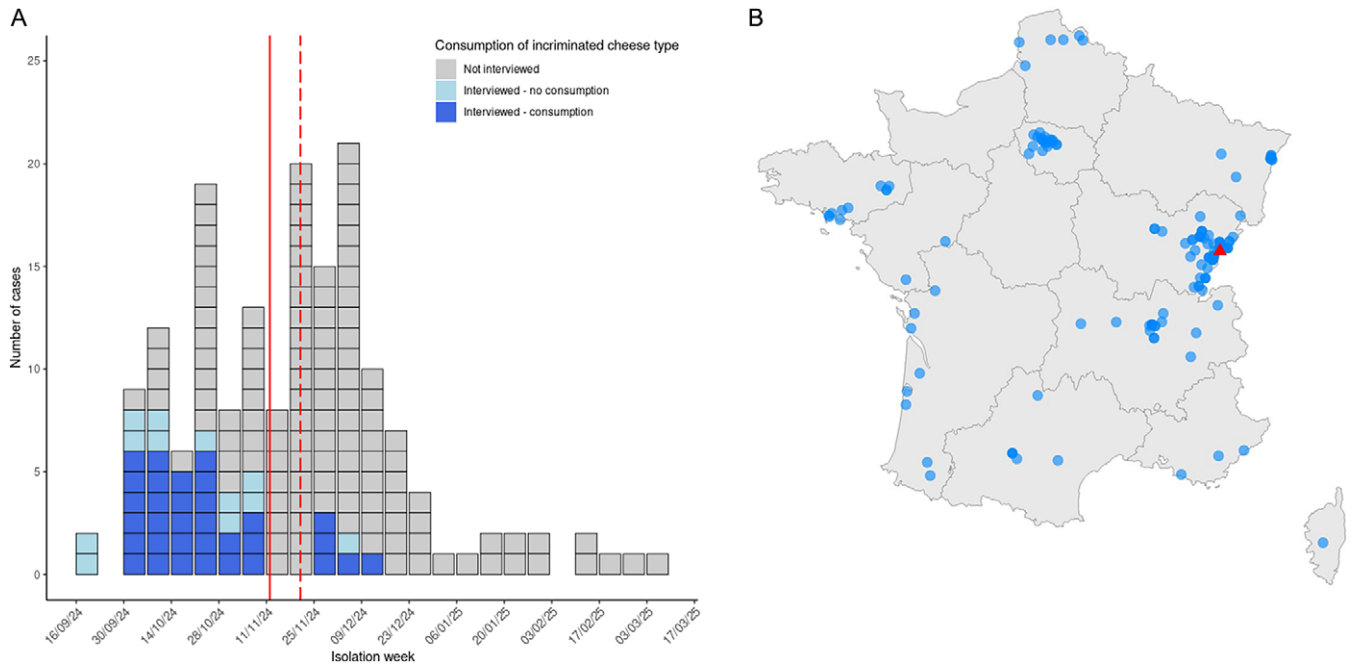


Figure 1. Distribution of French outbreak cases of *Yersinia enterocolitica* lineage 2/3–9b (bioserotype 2/O:9) (*n* = 167), France, September 2024–March 2025, by (a) sampling week, interview status, and reported consumption of the incriminated cheese type and (b) postal code of residence. (a) The solid vertical line marks the date of 12 November 2024, when an inspection was carried out at the cheese factory. The dotted vertical line marks the date of 21 November 2024, the initiation of the recall of products. (b) The red triangle marks the location of the cheese manufacturer from whom isolates were collected.

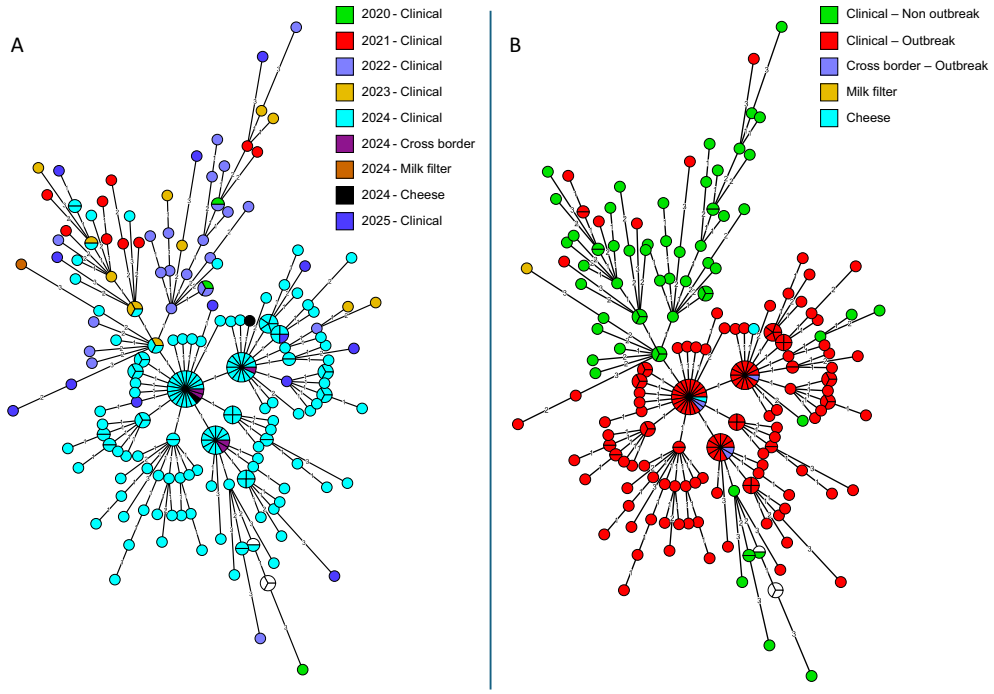


Figure 2. Minimum spanning tree of *Yersinia enterocolitica* lineage 2/3–9b cluster 4452 isolates (*n* = 232) from human cases (*n* = 229), including French outbreak cases (*n* = 167) and cross-border cases (*n* = 5), and from incriminated cheese (*n* = 2) and milk filter (*n* = 1), May 2020–March 2025, by (a) year of isolation and (b) outbreak case definition. cgMLST, core genome multilocus sequence typing. Numbers close to the branches correspond to the allelic distance between two nodes according to 1 727-gene *Y. enterocolitica* cgMLST [12].

Among the six cases interviewed in December, five reported consuming the suspected cheese type and trace back investigations identified the suspected cheese manufacturer for three cases. The three cheeses were purchased before the recalls.

Site inspections and food and environmental samples analysis. The DDecPP conducted a site inspection at the cheese manufacturer on 12 November 2024. The inspection did not reveal any hygiene deficiencies or non-conformities with regulations.

https://doi.org/10.1017/S0950268826102209 Published online by Cambridge University Press

Thirty samples were taken from 30 cheeses at the manufacturer and 14 milking machine filters at the 5 milk producers supplying the cheese manufacturer. On 20 November 2024, the ANSES isolated *YE* biotype 2 from two cheeses from different batches and one milking machine filter, sequenced their genomes, and shared the sequencing data with the NRC. On 28 November 2024, the NRC confirmed that the three isolates were *YE* lineage 2/3-9b (corresponding to bioserotype 2/O:9) and belonged to cluster 4452 (Figure 2). The two cheese isolates had 2 allelic distance (AD) between them and each was closely related to at least one outbreak case's isolates (0 and 1 AD). The milk filter isolate was 6 AD from the closest outbreak case's isolate (the closest isolate in the cluster was dated January 2025, 3 AD). On the phylogenetic tree (Supplementary Figure S1), the three food/environmental isolates were close to the outbreak cases' isolates.

Outbreak control measures. Following the inspection of the manufacturer, all stocks were blocked at the manufacturer from 14 November 2024, and the production was stopped on 15 November 2024. A withdrawal and a recall of all batches of different cheeses produced since September 2024 from the manufacturer were initiated on 21 November 2024. The milk producer, whose milking filter tested positive for *YE*, had sold all its production to the cheese manufacturer between October and November 2024. At the cheese manufacturer, raw milk cheese production was allowed to resume on 21 November, without the milk from the suspected farm. Sales were authorized once the ANSES conducted microbiological analyses on 29 November 2024 on all batches of cheese produced since 21 November, and the results came back negative.

Given the post-transfusion sepsis risk associated with *YE* [17], the French Blood Establishment included a two-month deferral criterion, from 20 November 2024 to 02 January 2025, for donors who reported having consumed the incriminated type of cheese during the seven days prior to donation.

Cross-border investigation. European health authorities were informed of the outbreak through EpiPulse (2024-FWD-00114), with genomic data for one outbreak isolate (BIGSdb id = 23297) on 15 November 2024, and a Rapid Alert System for Food and Feed (RASFF notification 2024.8664) on 22 November 2024. The cheese was exported to 16 European countries and 3 Asian countries. Five cross-border cases were identified between October and December 2024 in Luxemburg (n = 1) and Belgium (n = 4 cases, not interviewed). The case from Luxemburg (strain isolation date 30 October 2025), a 68-year-old male, had mild diarrhoea and mentioned no travel abroad. He reported a regular consumption of the incriminated type of cheese (no information on the manufacturer could be retrieved).

Discussion

The microbiological routine surveillance in place in France allowed the identification of an outbreak of *YE* 2/O:9 infections with isolates of the same genomic profile. Following the alert, prompt epidemiological and trace back investigations provided strong evidence pointing to a soft, cow raw milk cheese produced by one manufacturer as the source of the outbreak, which was reinforced by the identification of the outbreak strain from cheese samples and one milk filter. This same bioserotype (2/O:9) was identified in another large outbreak of *YE*, which occurred earlier in 2024 in France [13]. The peculiar feature of these outbreaks, beyond the serotype involved, was their association with the consumption of raw milk cheese. The implicated cheeses varied in manufacturing processes and milk source (cow versus goat); however, in both cases, the outbreak strains were isolated directly from cheese samples obtained at the manufacturer. A large number of cases occurred, especially in the region of production, and the outbreaks were ultimately contained through the withdrawal and recall of the contaminated cheese products. These two outbreaks highlighted the risk associated with raw milk products' consumption for French and international consumers.

Raw milk cheeses are part of the French dairy culture with 190 964 tons produced in 2023, with the leading region of production being Bourgogne-Franche-Comté with over 102 040 tons [18]. Their consumption has often been implicated in foodborne outbreaks worldwide [19, 20] caused by various pathogens such as *Salmonella*, enterohaemorrhagic *Escherichia coli*, *Listeria monocytogenes*, and less frequently *YE* [5–7]. In the French food industry, routine testing for the presence of *YE* is not compulsory. No precise data are available on the frequency of this microorganism in raw milk. Contamination of milk may be associated with poor hygienic practices and can occur at different stages (during milking, storage, transport, or cheese production). In this regard, control and prevention of contamination by pathogens are of primary importance to ensure public health. For several years, French health authorities [21] have recommended that vulnerable populations (young children <5 years, pregnant women, elderly over the age of 65, or immunosuppressed persons) avoid consuming raw milk or raw milk products.

In total, 167 outbreak cases were identified in France. This likely underestimates the true number of individuals who developed enteric yersiniosis after the consumption of the contaminated products as (1) only a portion of cases are identified from surveillance due to limitations in healthcare seeking and laboratory testing and (2) surveillance of enteric yersiniosis in France relies on a network of medical laboratories sending isolates on a voluntary basis. A second limitation is the small proportion of cases interviewed after the recall. Among those interviewed, the three who reported consumption of the incriminated cheese had purchased it prior to the recall. The observed delay in the decline in cases after implementation of control measures can likely be explained by several factors, including the delays between consumption and symptoms' onset, delays to healthcare seeking, and time required for cases to be integrated in surveillance data. It is also possible that some consumers who purchased the cheese before the recalls consumed it long time after without being aware of the recall notice. Nevertheless, as the number of new cases substantially decreased from January onwards, control measures were considered to be effective.

The genomic cluster 4452 had been identified as early as 2020 in the French microbiological surveillance, with 3 to 23 cases per year (2020–2023), without reaching the alert criteria (at least 5 isolates belonging to a genomic cluster isolated within 8 weeks). Furthermore, no seasonality, demographic, or geographic grouping could be observed. This outbreak was identified in October 2024 when the sudden increase across the country in the number of isolates belonging to this genomic cluster met the outbreak alert criteria. After control measures were implemented, the number of cases decreased but strains belonging to the genomic cluster are still being identified infrequently (after 07 March 2025, 17 isolates were identified in the cluster with isolation dates between 11 April and 29 August 2025). This suggests a continuous circulation of the strain at low levels. This continuous circulation is also supported by the fact that the cheese type which caused this outbreak is produced only between mid-August and mid-March and is sold

https://doi.org/10.1017/S0950268826102209 Published online by Cambridge University Press

over a limited period of time from mid-September to mid-May (even though consumption of frozen cheese cannot be excluded). Moreover, the close phylogenetic relatedness of all isolates in genomic cluster 4452, independently of the year of isolation, shows a slow diversification of this strain (as previously observed for the lineage [12]) and cannot reveal a clear genomic distinction between the cases/strains related to the outbreak and background noise.

In the case of genomic clusters that span over several months or even years, as for the present cluster, genomic analyses and epidemiological data may not be sufficient to understand the circulation of a strain. Although cgMLST is a powerful tool to identify clusters and improve investigation outcomes [22], the investigation of this cluster is an illustration of the necessity to interpret genomic data in the light of epidemiological and ecological information to comprehend the circulation of a strain and risk factors for human contamination [23].

A more comprehensive understanding of the epidemiology of bioserotype 2/O:9, including its prevalence in raw milk products and its distribution among different reservoirs, including wildlife and environment, is required. Elucidating the contamination pathways within herds through an integrated 'One Health' approach that links animal health, food safety, and public health could contribute to mitigating the public health risk posed by *YE*.

Conclusion and recommendations

Microbiological, epidemiological, and environmental evidence all pointed towards raw milk cheese as the vehicle of this *YE* 2/O:9 outbreak. Quick identification and withdrawal of incriminated cheese controlled this outbreak. Our study is a reminder of the risks associated with consumption of raw milk cheeses and highlights the importance of applying good hygiene practices on farms to minimize the risk of milk contamination.

Supplementary material. The supplementary material for this article can be found at http://doi.org/10.1017/S0950268826102209.

Data availability statement. Interviews' data that support the findings of this study cannot be shared with third parties because consent for this was not obtained from the participants. Genomic sequences and metadata of all isolates have been deposited and are freely accessible in the BIGSdb database at https://bigsdb.pasteur.fr/yersinia.

Acknowledgements. The authors would like to acknowledge all the people involved in the investigation including: Catherine Ragimbeau from Laboratoire National de Santé (Luxembourg), Wesley Mattheus and Elena Portell Buj from Sciensano, National Reference Centre for *Yersinia* (Belgium) for sharing genomic data, E. Fay from Direction départementale en charge de la protection des populations (DDecPP) du Doubs for technical participation in this investigation; Arnaud Felten from Anses for molecular analysis, Lauriane Szpakowski-Perrot, Laure-Marine Houel, and Marie Barba-Vasseur from Regional Health Authority Bourgogne-Franche-Comté for participation in this investigation; Syria Laperche from Etablissement Français du sang for participation in control measures implementation.

We would like to thank all cases who agreed to be interviewed.

Author contribution. Conceptualization: C.S., A-S.L.G., F.C.; Data curation: F.C.; Investigation: S.T., C.S., E.T., J.R., P.P., N.F., L.G., C.M., E.H., C.G., F.C., L.E., J.M., O.R., M.D., A-S.L.G., F.C.; Methodology: C.S., M.D., A-S.L.G.; Resources: J.R., L.G., C.M., E.H.; Software: C.S., A-S.L.G.; Supervision: A-S.L.G., F.C.; Validation: S.T., C.S., E.T., N.F., F.C., M.D., A-S.L.G., F.C.; Visualization: S.T., C.S.; Writing - original draft: S.T., C.S., A-S.L.G., F.C.; Writing - review & editing: S.T., C.S., E.T., J.R., P.P., N.F., L.G., C.M., E.H., C.G., F.C., L.E., J.M., O.R., M.D., A-S.L.G., F.C.

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