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The microbiological and clinical characteristics of 1,204 human cases of *Aliarcobacter* spp. infections that occurred in France between 2002 and 2024

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Abstract
Aliarcobacter spp. bacteria are human enteropathogens, as are *Campylobacter* spp. However, the epidemiology of the former infections is not well described. Here, we present microbiological and clinical data on 1,204 *Aliarcobacter* spp. infections that occurred in France between 2002 and 2024. *Aliarcobacter butzleri* was the principal species identified, followed by *A. cryaerophilus*. *Aliarcobacter* spp. infections affected patients principally over 60 years of age, mostly men, particularly during autumn. Analysis of 253 clinical information sheets highlighted both diarrhea and abdominal pain that were only rarely associated with fever or blood in the stool. Many isolates of both main species were resistant to group A penicillins and ciprofloxacin.

Background

Aliarcobacter spp. are Gram-negative bacteria closely related to *Campylobacter* spp. but that grow at lower temperatures than the latter in the presence of oxygen. *Aliarcobacter* genus currently includes 17 species (https://lpsn.dsmz.de/search?word=aliarcobacter) [1–3]. *Aliarcobacter* spp. tolerate high sodium concentrations, multiply during refrigeration, resist desiccation, and adhere to many surfaces. The most significant human pathogen, *Aliarcobacter butzleri*, can grow at low temperatures (4–10 °C) and survive under various storage conditions [4].

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Aliarcobacter spp. are potentially present in farm animals; poultry; reptiles; animal-derived foods (meat, dairy products, and seafood); vegetables; and water [5–12]. Most transmission may involve contaminated food and water. Animals, including pets, may play roles in fecal-oral transmission. Infections caused by contaminated food (plants, chicken, pork) or water have been described [9, 13–17].

A. butzleri, *A. cryaerophilus*, *A. skirrowii*, and *A. cibarius* have been isolated from the stools of both healthy animals and those with mastitis, and pigs with gastric ulcers or reproductive abnormalities [18, 19]. The three main species associated with human infections are *A. butzleri*, *A. cryaerophilus*, and *A. skirrowii* [14, 20, 21]. Arguello et al., proposed that men over 85 years of age were the primary human target of *Aliarcobacter* spp. *A. butzleri* has been associated with enteritis, as have *A. cryaerophilus* and *A. skirrowii*, but rarely with bacteremia [22, 23]. In the past, *Aliarcobacter* spp. were described as causative agents of travel diarrhea [24]. Although *A. butzleri* shares

microbiological and clinical features with *Campylobacter jejuni*, the former is more often associated with persistent, watery, but less bloody diarrhea than *Campylobacter* [25, 26].

Aliarcobacter spp. from stool samples can be isolated using the selective agar plates employed for *Campylobacter* spp. cultivation. Identification of such bacteria by matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry is possible, as is the case for *Campylobacter* spp [20, 27, 28]. However, the pathogenicity of *Aliarcobacter* spp. remains poorly understood [29, 30]. The bacteria adhere to intestinal epithelial cells. The pathogenic mechanisms include host cell invasion and cytotoxicity [2, 16, 25, 31].

Here, we prospectively study the clinical and microbiological characteristics of *Aliarcobacter* spp. identified by the French medical biology laboratories of the surveillance network of the National Reference Center for Campylobacters and Helicobacters (NRCCH) between 2002 and 2024.

Materials and methods

Data Collection: We included all strains received at the NRCCH from any medical biology laboratory (private or hospital), from 2002 to 2024. Prior to 2016, a supplementary clinical information sheet was systematically sent to all correspondents. The clinical data requested in anonymized form included patient age, sex, date and type of collection, any travel information, and any grouped cases. Cases were described as isolated or grouped. Any travel abroad in the previous 15 days was noted. Any suspected source of food contamination was described, as was the presence/absence of another simultaneously isolated enteropathogen. Any change in general condition was noted, as was diarrhea, abdominal pain, blood in the stool, vomiting, fever, any antibiotic treatment initiated, the duration of symptoms, and progress under treatment. All data were entered into an Excel spreadsheet and manually analyzed.

Strain culture, identification, and antibiograms: All strains were cultured on receipt at the NRCCH using blood agar plates under microaerobic conditions at 36 ± 1 °C in an Anoxomat microprocessor (Mart Microbiology BV, Lichtenvoorde, the Netherlands). The microaerobic atmosphere was 79.7% N_2, 7.1% CO_2, 7.1% H_2 and 6% O_2. All strains was retrospectively identified from 2002 to 2013, but systematically classified from 2013 via MALDI-TOF mass spectrometry (Bruker, 2023 library), as previously described [27]. All the isolates since 2002 were stored at −80 °C in brucella broth with 25% glycerol.

Antibiograms were obtained via disc diffusion (Biorad) for 48 h on Mueller Hinton containing defibrinated sheep blood and read by a SIRcan Orion instrument (I2A, Montpellier, France). Resistance to ampicillin, amoxicillin-clavulanic acid and ciprofloxacin was determined using the 2022 cutoffs published by Jehanne et al. [32]: for ampicillin resistant (R) < 17 mm, amoxicillin-clavulanic acid $R < 17$ mm, and ciprofloxacin $R < 16$ mm.

Statistical analyzes were performed using an on-line tool available https://www.medcalc.org/. Patients were grouped into four age categories (0–14, 15–49, 50–74, and 75–103 years) to ensure sufficient sample sizes in each group for statistical analysis. These analyses were performed using chi-square goodness-of-fit tests to assess deviations from uniform distributions (age groups and monthly case counts), and chi-square tests of independence to compare proportions between groups (species distribution and antibiotic resistance across age groups). For all tests, a p-value < 0.05 was considered statistically significant.

Results

Patient Description: A total of 1,204 unique strains were recovered from 2002 to 2024. The minimum number was 5 in 2002 and the maximum 105 in 2018; the average was 52 ± 31 strains/year. The laboratories were homogeneously distributed across France. Only 5 of the 96 French metropolitan departments were not covered (Fig. 1). Three overseas French departments also contributed: Reunion Island, Mayotte, and French Polynesia.

Totals of 609 men (54.4%) and 595 women (45.6%) were infected; the sex ratio was 1.2. Men dominated in all 10-year age group intervals except the 90–100-years group (Table 1). The age groups most affected were 0–9 years (174/1,204 strains, 14.5%) and (especially) 60–99 years (758/1,204, 63%) (Table 1) (Fig. 2). The distribution of cases among the 11 age groups was evaluated using a chi-square goodness-of-fit test, which demonstrated a significant deviation from a uniform distribution ($\chi^2(10) = 681.76$, $p < 0.0001$).

Of the 1,204 cases, 565 were seen as outpatients or during consultation, 461 were hospitalized, and no information was available for the remaining 178. Of the 1,026 cases for which data were available, 55.1% were not clinically severe.

-Epidemiological characteristics.

Most strains were isolated from stool samples (1,171, 97.3%) or blood cultures (17, 1.4%) (Table 2).

A. butzleri was the principal species (1,080, 89.70%), followed by *A. cryoaerophilus* (117, 9.72%), *A. skirrowii* (4, 0.33%), *A. lanthieri* (2, 0.17%), and (one) *Aliarcobacter sp* (1, 0.08%). *A. butzleri* predominated regardless of the sample type: stool (73.7%), blood (87.5%), and other (100%) (Table 2). A chi-square test of independence was performed to compare the proportions of the two main species, *A. butzleri* and *A. cryaerophilus*, across four groups of age (0–14, 15–49, 50–74 and 74–103). The

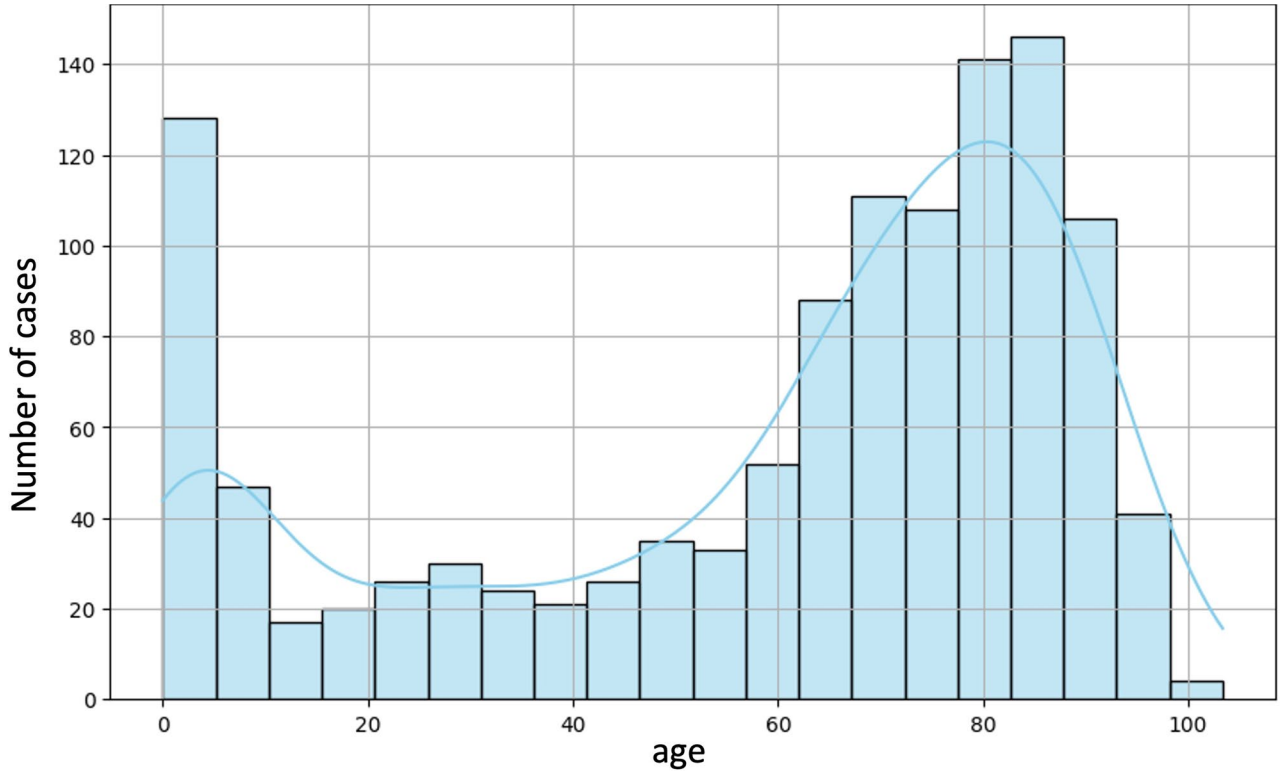

Fig. 1 The distribution of the 1,204 strains of *Aliarcobacter* spp. received between 2002 and 2024. The color intensity reflects the number of strains per department or overseas region

Table 1 Distribution of *Aliarcobacter* spp. Infections by age and sex

Age group (years)	*N* (%)	Male	Female	Sex ratio
0–9	174 (14.5%)	104	70	1.5
10–19	38 (3.2%)	23	15	1.5
20–29	55 (4.6%)	29	26	1.1
30–39	38 (3.2%)	22	16	1.4
40–49	60 (5%)	32	28	1.1
50–59	79 (6.6%)	41	38	1.1
60–69	166 (13.8%)	92	74	1.2
70–79	231 (19.2%)	128	103	1.2
80–89	265 (22%)	143	122	1.2
90–99	96 (8%)	41	55	0.7
100–109	2 (0.2%)	0	2	0.0
	1,204 (100%)	**655**	**549**	**1.2**

analysis was restricted to these species because sample sizes for *A. lanthieri* and *A. skirrowii* were insufficient for statistical testing. The test showed a highly significant difference between groups ($\chi^2 = 52.69$, df = 3, $p < 0.0001$), indicating that the species distribution is not uniform across the groups.

Strains were isolated throughout the year, but with a very clear peak in August-December (50.3% of cases) (Fig. 3). This differs from the annual peak in the French summer (May-September) of *Campylobacter* spp. infections. A chi-square goodness-of-fit test was conducted to assess the uniformity of case distribution throughout the year. The results showed a significant deviation from a uniform monthly distribution ($\chi^2 = 75.08$, df = 11, $p < 0.0001$), indicating substantial seasonal variation with elevated case counts observed in August, September, and October.

When information was available (696 cases out of 1,204), 95.4% of infections were isolated cases (664/696). Infectious clusters were rare (32, 4.6%). Travel abroad status was explored for 523 cases but not for the remaining 564. Of the 523 cases, 111 had been abroad (21.2%), principally to the Maghreb (38/111 cases (34.2%) or other African locations (18/111 cases, 16.2%).

Completed clinical information sheets were received for 253 of the 1,204 cases (21%). Only 19 intestinal co-infections (7.5%) were reported: four *Giardia intestinalis*, four unspecified, three *Salmonella* spp. two *C. jejuni*, two *Shigella sonnei*, one *Yersinia sp*, one *Aeromonas sp*, 1 toxinogenic *Clostridioides difficile*, and one adenovirus.

Diarrhea was reported by 195 of the 253 cases (77.1%), including 170 with *A. butzleri* infections (87.2%), abdominal pain by 137/253 (54.2%), blood in the stool by 31/253 (12.3%), and fever above 38 °C by 58/253 (9.9%). No symptoms were reported by only 15/253 patients (5.93%).

Antibiotics were prescribed for 118 of the 253 cases (46.6%): a macrolide (35/118 cases, 29.7%), a fluoroquinolone (26/118 cases, 22%), amoxicillin + clavulanic acid

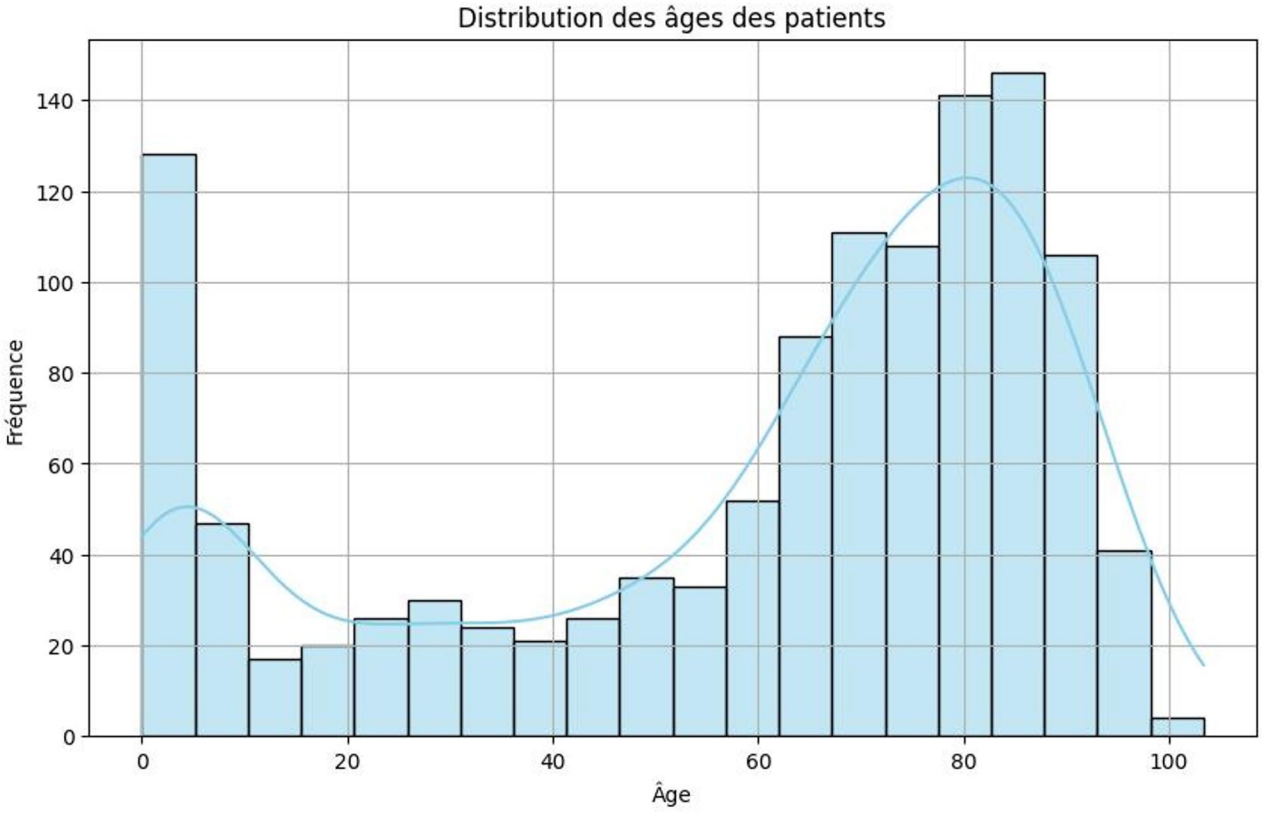

Fig. 2 The number of *Aliarcobacter* spp. infections by age group in 5-year increments

Table 2 Distribution by sample type

	N	%	A. butzleri	A. cryaerophilus	A. lanthieri	A. skirrowii	Aliarcobacter sp
Stool	1,171	97.26	1,048	116	4	2	1
Blood	17	1.41	16	1	0	0	0
Other*	16	1.33	16	0	0	0	0
	1,204	**100**	**1,080 (89.7%)**	**117 (0.7%)**	**4 (0.33%)**	**2 (0.17%)**	**1 0.08%)**

(14/118 cases, 11.9%), amoxicillin alone (8/118 cases, 6.8%), and other single agents or combinations (the remaining 35/118, 29.7%). The clinical evolutions under antibiotics were reported for 94/118 (79.7%): cures for 82, 6 deaths linked to comorbidities, no improvement in the clinical signs of 3, 1 relapse after stopping antibiotics, 1 chronic carriage, and 1 colopathy.

The duration of clinical signs was provided for 108 of the 253 cases: ≤ 7 days in 56 cases (51.8%), > 7 to ≤ 15 days in 28 (25.9%), > 15 days to < 1 month in 17 (15.7%), > 1 month to ≤ 2 months in 4 (3.7%), > 2 months to ≤ 3 months in 2 (1.8%), and > 3 months to ≤ 4 months in 1 (0.9%).

A. butzleri ampicillin susceptibility was assessed for 798 cases (582 resistant, 72.9%), amoxicillin-clavulanic acid susceptibility for 724 (274 resistant, 37.8%), and ciprofloxacin susceptibility for 640 (64 resistant, 10%). *A. cryaerophilus* ampicillin susceptibility was assessed for 90 cases (44 resistant, 48.9%), amoxicillin-clavulanic acid susceptibility for 88 (6 resistant, 6.8%), and ciprofloxacin susceptibility for 84 (23 resistant, 27.4%). Contact-resistance to a 15-µg erythromycin disc was noted in only 19 of 503 strains tested (3.8% high-level resistance to macrolides): 15 *A. butzleri*, 3 *A. cryaerophilus* and 1 *A. skirrowii*. Given the small numbers of *A. lanthieri* and *A. skirrowii* reported, no assessment of antibiotic sensitivity is possible. The association between age groups and resistance status to amoxicillin-clavulanic acid and ampicillin was assessed using chi-square tests of independence. A statistically significant difference in resistance rates to amoxicillin-clavulanic acid was observed across age groups (χ^2 = 8.55, df = 3, p = 0.036), with patients older than 50 years of age being infected with strains that were more resistant to this antibiotic. In contrast, no significant variation in ampicillin resistance was found among

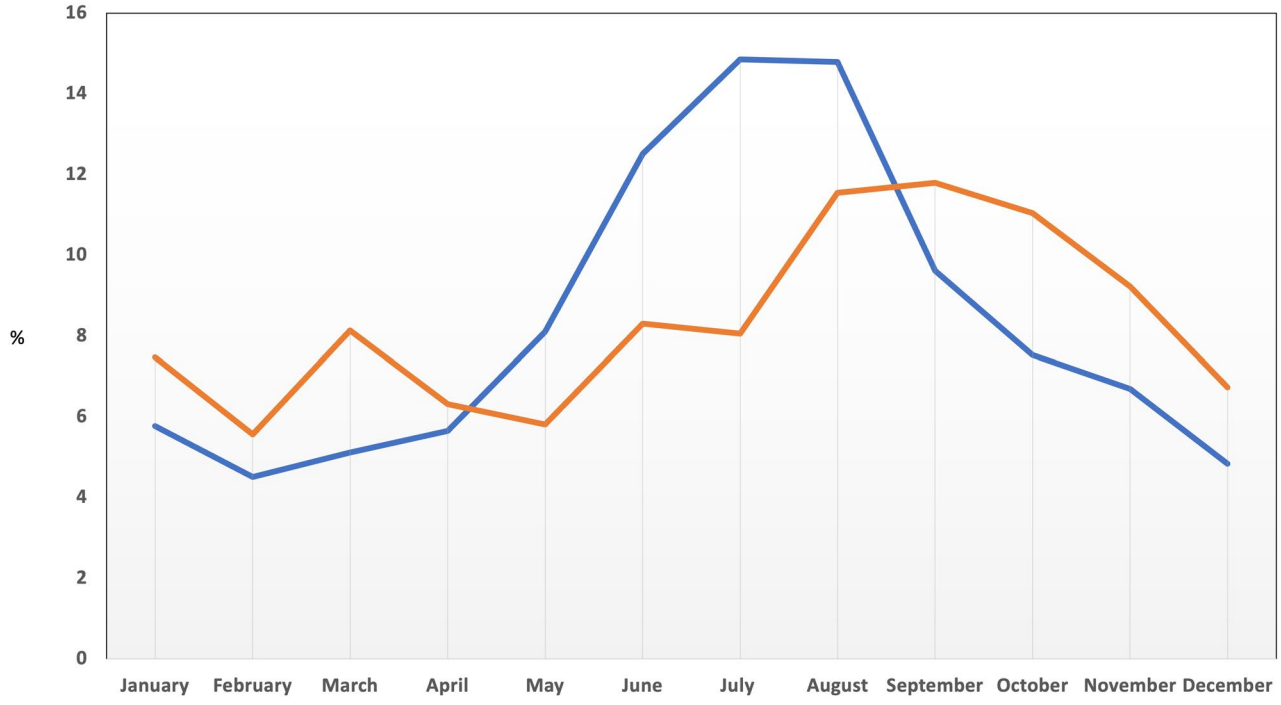

Fig. 3 The numbers of *Aliarcobacter* and *Campylobacter* spp. infections over the year. The data are percentages: blue for *Campylobacter* spp. and orange for *Aliarcobacter* spp. The *Campylobacter* data are derived from the strains collected by the NRCCH from 2017 to 2024 ($n = 76{,}370$)

age groups ($\chi^2 = 4.63$, df = 3, $p = 0.20$). These analyses were conducted on 844 and 934 tested strains, respectively.

Discussion

The epidemiology of *Aliarcobacter* spp. infections is less well described than that of *Campylobacter* spp. Our laboratory receives strains of *Campylobacter* spp. and related bacteria, including *Aliarcobacter* spp. associated with various pathologies, mainly infectious diarrhea, from a surveillance network of hospital and private medical biology laboratories. In this study, we describe the microbiological and clinical characteristics of such infections from 2002 to 2024.

Among the 1,204 cases included in the present study, only 253 (21%) had complete clinical information sheets, and data on travel history, infection clusters, and other epidemiological variables were largely missing. This may limit the reliability of the clinical and the epidemiological conclusions.

Human *A. butzleri* infections have been associated with diarrhea accompanied by abdominal pain, nausea, vomiting, and fever [13]. *A. skirrowii* has been associated with chronic diarrhea [33]. The clinical presentations are similar to those of *C. jejuni* campylobacteriosis, although some authors have reported more persistent watery diarrhea [16, 34]. Our data are in line with previous observations. However, the symptoms were of short duration (15 days in 77.8% of cases). We found that *A. butzleri* diarrhea was indeed often associated with abdominal pain. Unlike *Campylobacter* spp. infections, *Aliarcobacter* spp. infections were rarely accompanied by blood in the stool or a fever above 38 °C. This may differentiate such infections from those of *Campylobacter* spp. but this is not a differentially predictive clinical finding. Our data are in line with those of Vandenberg et al., who studied 67 patients infected with *A. butzleri* [34]. These more frequently presented with persistent and watery diarrhea, but less often with bloody diarrhea, than did those infected with *C. jejuni*. In the literature; *A. butzleri* infections have been associated with co-infections of other enteric pathogens. In our study, such co-infections were rare.

Some of our data differ from those of Vandenberg et al., who found no particular age or sex distribution of *Aliarcobacter* spp. infections, in contrast to 201 cases of Campylobacteriosis [34]. In our present study, the observed non-uniform distribution of cases across age groups suggests that susceptibility or exposure to infection differs by age. We observed a sex ratio favored men in all age groups (except those over 90 years of age, but this may reflect the small number of cases and the longer life expectancy of women). A favored male distribution is a common epidemiological feature of the annual French *Campylobacter* spp. infections, with the exception of a female predominance in the 20–40 age groups (https://www.santepubliquefrance.fr/recherche/#search=campylobacter). Van Den Abeele et al., found that the average age of *Aliarcobacter* spp. patients was 42 years, significantly

older than that of *Campylobacter spp.* patients [35]. Our findings are similar. Significant variation in species distribution across age groups were observed in particular, older patients exhibited more *A. butzleri* than *A. cryaerophilus* infections.

Vandenberg et al., reported that 20.9% of patients infected with *Aliarcobacter* spp. were hospitalized for more than 48 h [34]. We lacked hospitalization lengths, but 44.9% of infected patients for whom data were available were hospitalized. Without wishing to overinterpret such data, the bacteria may be markedly pathogenic. The pathogenicity of *A. cryaerophilus* has been debated in the past. In particular, Houf and Stephan sought *A. cryaerophilus* in stool samples from patients without gastrointestinal symptoms [20]. The fact that several *Aliarcobacter* spp. adhere to human cells suggests that *Aliarcobacter* spp. may produce virulence factors, but further research is needed [36–39]. Douidah et al., reported that *A. butzleri* induced apoptosis and inflammation of intestinal epithelial cells, and that the *cadF* gene encoded a fibronectin adhesin and *ciaB* an invasiveness gene [40]. Bacchus et al., found that *A. cryaerophilus* strains adhered to and invaded two cell lines, with strain-dependent differences in terms of their adhesion and invasion rates [31]. Some strains were cytotoxic to epithelial cell lines. The *Aliarcobacter* species reported here were rarely accompanied by another enteropathogen.

Grouped *Aliarcobacter* spp. infections are rare. This is consistent with our data; most were isolated, with a very clear peak in August-December, offset from the annual French spring-summer peak of *Campylobacter* spp. (May-September) (https://www.santepubliquefrance.fr/recherche/#search=campylobacter). This may reflect the travel habits of those aged 60 to 100 years (63% of cases in the present study), who preferentially choose the later period for international travel. Unknown individual susceptibility factors must also be considered.

Previous studies described increased *Aliarcobacter* spp. strain isolations from sheep in autumn and winter [41, 42]. Such data should be carefully considered when identifying potential sources of human foodborne contamination. Potential food sources of infections were identified for only 9 of the 1,204 cases. Poultry was mentioned only once, although this is the major source of *Campylobacter* spp. contamination. The French sources of *Aliarcobacter* spp. contamination remain unidentified, despite some international work on the topic [14, 16].

Aliarcobacter spp. are less susceptible to antibiotics than are thermophilic *Campylobacter* spp [43–46]. However, the available antibiogram data are limited and potentially biased because of the use of diverse methods and possibly inappropriate interpretative cutoffs [47]. Jehanne et al., used an next-generation sequencing-based approach to define interpretative cut-offs for group A penicillins ± clavulanic acid, and ciprofloxacin [32]. We employed these cutoffs. *A. butzleri* was more resistant to ampicillin and amoxicillin-clavulanic acid than was *A. cryaerophilus*, but the opposite was true for ciprofloxacin, in agreement with Van den Abeele et al., who also noted high rates of resistance to group-A penicillins, as did we in our study [43].

In general, as described by Jehanne et al., the beta-lactamase of *Aliarcobacter* spp. appears to be less active on clavulanic acid than the enzyme of of *Campylobacter* spp., explaining the high proportion of resistance to amoxicillin-clavulanic acid [32]. We do not discuss erythromycin sensitivity here because no validated cutoff is known. However, only 3.8% of our strains exhibited high-level resistance. Screening for mutations in *23 S rDNA* and *tetR* [48] might clarify the nature of such resistance mechanisms.

It would be very pertinent in futher studies to include a resistance trend analysis over time or discussing potential driving factors (e.g., antibiotic usage patterns).

Conclusion

Our study had certain limitations. We rely on laboratories that volunteer to participate in the surveillance network. Our data are therefore possibly unrepresentative of the national epidemiology. However, it is difficult to conceive of anything better. It is not mandatory in France to report either *Campylobacter* spp. or *Aliarcobacter* spp. infections.

Many laboratories use syndromic PCR as a first-line test; this detects the principal thermophilic *Campylobacter* spp. However, Houf and Stephan found that the selective media used to isolate *Campylobacter* spp. also grow *Aliarcobacter* spp. from stool samples [20]. We strongly recommend that, if clinical signs persist despite an initially negative PCR test, culture on selective media should explore the possible spectrum of enteropathogenic bacteria, in particular *Aliarcobacter* spp. and enterohepatic *Helicobacter* spp. (for example, *H. pullorum*) [49]. Despite the limitations, we believe that our data serve as an essential epidemiological basis for a better understanding (at least in France) of the epidemiology of *Aliarcobacter* spp. infections.

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Author contributions
PL supervised the study. PL, MJ, and MM drafted the manuscript. LB, JA, and AD performed the experiments. All authors interpreted the data and critically revised the manuscript in terms of important intellectual content.

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Data availability
The datasets generated and/or analyzed during the current study are not publicly available due to their confidentiality, but are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and consent to participate
All strains were sent to the NRCCH for research purposes only, any need for ethical approval and informed consent was waived by the ethics committee of the Bordeaux University Hospital because the scientific mission of this national reference center was mandated by Santé Publique France (www.spf). All strains were anonymized and sent from Bordeaux University Hospital to the Centre de Ressources Biologiques (CRB) (https://www.chu-bordeaux.fr/Professionnels-recherche/Centre-de-Ressources-Biologiques/). The CRB and the NRCCH entered into a Material Transfer Agreement. Data collected from 2002 to 2016 were also anonymized.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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