ORIGINAL ARTICLE 10.1002/2052-2975.35

# A severe case of persistent diarrhoea associated with *Arcobacter cryaerophilus* but attributed to *Campylobacter* sp. and a review of the clinical incidence of *Arcobacter* spp.

**M. J. Figueras[1], A. Levican[1,2], I. Pujol[1,3], F. Ballester[1,3], M. J. Rabada Quilez[4] and F. Gomez-Bertomeu[5]**

1) *Unitat de Microbiologia, Departament de Cièancies Mediques Básiques, Facultad de Medicina i Ciencias de la Salud, IISPV, Universidad Rovira i Virgili, Sant Lorenzo 21, 43201, Reus, Spain,* 2) *Laboratorio de Patología de Organismos Acuáticos y Biotecnología Acuícola, Facultad de Ciencias Biológicasl, Facultad de Ciencias Biológicas, Universidad Andrés Bello, Viña del Mar, Chile,* 3) *Servei de Microbiologia, Hospital Universitari Sant Joan de Reus, Reus, Spain* 4) *ABS de La Selva del Camp, Tarragona, Spain and* 5) *Servei de Microbiologia, Hospital Universitari Joan XXII, Tarragona, Spain*

## Abstract

Although rarely, *Arcobacter* spp. have been associated with diarrhoea and bacteraemia. We report a persistent case in a healthy 26-year-old Spanish male of bloody diarrhoea, which was attributed to *Campylobacter* but in fact was caused by *Arcobacter cryaerophilus*, as determined by sequencing of the *rpoB* gene. The isolate was re-identified by matrix-assisted laser desorption ionization time of flight (MALDI-TOF) and genotyped for five putative virulence genes and for seven genes included in the *Arcobacter* multilocus sequence typing database. The low score obtained by MALDI-TOF indicates the need to complement the database with more isolates. Only the *ciaB* gene, which encodes for an invasin, was detected. Despite the isolate belonging to a new sequence type, three of the alleles (*glnA*, *pgm* and *tkt*) had been found previously in isolates from faeces of patients with diarrhoea. This study, together with the reviewed literature, indicates that *Arcobacter* can produce bacteraemia and that the isolation from patients with diarrhoea range from 0.11% to 1.25%. This study also demonstrates that *Arcobacter* species are confused with *Campylobacter* spp., as previously suggested. This is one of the factors that leads to underestimation of their incidence together with the use of inappropriate detection and identification methods.

**Keywords:** *Arcobacter*, emerging or re-emerging diseases, gastrointestinal disease, persistent diarrhoea
**Original Submission:** 3 November 2013; **Revised Submission:** 16 December 2013; **Accepted:** 19 December 2013
**Article published online:** 5 February 2014
*New Microbe New Infect* 2014; **2:** 31–37

**Corresponding author:** M. J. Figueras, Departament de Ciències Mèdiques Bàsiques, Facultat de Medicina i Ciències de la Salut, IISPV, Universitat Rovira i Virgili, Sant Llorenç 21, 43201 Reus, Spain.
**E-mail: mariajose.figueras@urv.cat**

## Introduction

Bacteria of the genus *Arcobacter*, which was created with aerotolerant species previously included in the genus *Campylobacter*, are considered emergent enteropathogens and potential zoonotic agents [1]. The genus currently includes 17 species and some of these species produce abortions, mastitis and gastrointestinal disorders in animals [2–5] and bacteraemia, endocarditis, peritonitis and diarrhoea in humans [6–12]. So far there have been very few human diarrhoea cases reported despite it having been found that *Arcobacter butzleri* was the fourth most common *Campylobacter*-like organism isolated from human stools [1,13,14]. Persistent watery diarrhoea was the main symptom associated with *Arcobacter* species, in contrast to the bloody diarrhoea produced by *Campylobacter jejuni* [1,13]. It has been suggested that *Campylobacter* isolates cover *Arcobacter* spp. [13], which are not routinely studied with the *ad hoc* methods in clinical laboratories. However, the true impact of this confusion is unknown [1].

This study describes in detail the clinical characteristics of an acute case of diarrhoea produced by *A. cryaerophilus*, which was recognized after sequencing of the *rpoB* gene from an isolate biochemically identified as *Campylobacter* sp. The isolate was re-identified with matrix-assisted laser desorption ionization time of flight (MALDI-TOF) and genotyped by multilocus

sequence typing; its putative virulence genotype was screened by PCR. The study intends to alert clinicians to the possible role that this poorly known bacteria genus plays in the development of human disease by showing all known clinical cases.

## Case Report

A 26-year-old male with no previous history of disease visited the doctor complaining of bloody watery diarrhoea of 3 weeks duration (with about three liquid depositions a day), with abdominal pain but without fever, nausea or vomiting. The patient had been seen with similar symptoms 4 months before and was diagnosed with acute gastroenteritis. A stringent diet was the recommended treatment but no laboratory testing was made at that time. Considering this previous history, a blood and stool analysis was carried out. The stool sample was examined for parasites and cultured for *Escherichia coli*, *Salmonella* spp., *Shigella* spp., *Yersinia enterocolitica*, *Aeromonas* spp., *Plesiomonas* spp., *Vibrio* spp. and *Campylobacter* spp. Complete blood count was performed and searches were made for hepatitis B antigen, anti-hepatitis C virus antibody and other antibodies against human immunodeficiency virus, cytomegalovirus, adenoviruses and parvovirus B19. The patient was diagnosed with acute gastroenteritis and an empirical antibiotic treatment was initiated with amoxicillin/clavulanic acid.

The laboratory evaluation showed an almost normal complete blood count, except for a slight relative reduction in neutrophils (37%) and an increase in lymphocytes (51.2%). The blood culture was negative but the stool sample showed a positive culture in Campylosel medium (BioMérieux, Marcy l'Etoile, France) after 3 days of incubation at 42°C, under microaerobic conditions. The colonies were identified as *Campylobacter* sp. based on phenotypic tests (Gram stain, hippurate hydrolysis and resistance to cephalothin). By disc diffusion, the isolate was susceptible to amoxicillin/clavulanic acid and to gentamicin, but was resistant to ciprofloxacin and erythromycin. Considering these results and the good evolution of the patient, the empirical treatment was maintained for 8 days, after which time he had recovered completely with no more diarrhoea episodes. The isolate was sent to the Unit of Microbiology at the University Rovira i Virgili for re-identification using the sequences of the *rpoB*, as was done routinely for all isolates identified as *Campylobacter* at the hospital. The DNA extraction, amplification and sequencing were performed using primers and conditions previously described [15]. A BlastN analysis with the obtained *rpoB* sequence revealed a 99% similarity with the strain of *A. cryaerophilus* (Strain of subgroup 1B, LMG 10229, accession number EU669900), followed by a 95% similarity with the sequence of the type strain of *A. cryaerophilus* (Strain of subgroup 1A, LMG 9904$^T$, accession number EU669899), and only 90% similarity with a strain of the next most similar species, *A. butzleri* (Strain ED-1, accession number AP012047). Therefore, the isolate was identified as being *A. cryaerophilus*.

Considering the rarity of the recovered bacterium, the patient was contacted again to obtain additional information. He indicated that he regularly eats raw meat and fish, and also had a dog at home and a group of laying hens fenced in the garden. Despite the patient indicating that he had not had any other episodes of diarrhoea, a new stool sample was taken to evaluate his possible carrier state. Rectal samples from the dog and cloacal swab samples from three of the six laying hens he had at that time, as well as two samples of their faeces collected from the ground, were taken for microbiological examination using molecular detection and culture, as described in a previous study [16]. However, all of these samples were negative for *Arcobacter*.

To our knowledge, only three cases of *A. cryaerophilus* infection have so far been reported [6,17,18]. Those cases, together with the few available for the other species of the genus, are summarized in Tables 1 and 2. The first and only case of diarrhoea due to *A. cryaerophilus* dates back to 1988 when it was still included in the genus *Campylobacter* with the name *Campylobacter cryaerophila*. The 35-year-old homosexual man with this infection showed intermittent diarrhoea of 4–6 months duration with abdominal pain [17]. The other two are cases of bacteraemia, one in Taiwan that involved an immunocompromised 72-year-old woman with uraemia who showed a haematogenous pneumonia [18], and the other in a 7-year-old boy from China who had fallen into a mud pool while driving a mini motorcycle and suffocated [6]. As seen in Tables 1 and 2, a few other cases of diarrhoea and bacteraemia have been linked to *A. butzleri* [4,7,19–23] and, more rarely, to *Arcobacter skirrowii* [24]. For instance, a case of acute diarrhoea caused by *A. butzleri* in a 30-year-old healthy man was reported from Turkey; it was cured with treatment with ciprofloxacin [23]. A recent case of peritonitis due to *Arcobacter* sp. has been reported in a peritoneal dialysis patient whose catheter was repositioned [25]. Despite intravenous cefazolin and oral levofloxacin being given as a prophylaxis, the patient only responded after intravenous ticarcillin–clavulanate treatment for 2 weeks, with no need for the catheter to be removed.

The majority of these case studies underline the difficulty in recognizing or identifying these bacteria because they grew slowly and their identification required sequencing of the 16S rRNA gene [6,7,21] or the use of specific multiplex PCR methods [22–24,26]. Considering that several hospitals

**TABLE 1. Cases of intestinal infections associated with *Arcobacter* spp.**

| Patients' sex/age | Country | Presentation | Species | Outcome | Underlying conditions | Reference |
|---|---|---|---|---|---|---|
| M/35 years | Australia | Chronic diarrhoea (6 months) | *A. cryaerophilus*[1] | NS | Homosexual with history of anxiety and repeated sexual exposure | [17] |
| 3–7 years[2] | Italy | No diarrhoea, abdominal pain, occasional vomiting or fever | *A. butzleri* | Recovered 7–10 days after no specific treatment | None | [4] |
| 1. M/48 years<br>2. F/52 years | Germany | 1. Acute watery diarrhoea (15 days) and abdominal cramps<br>2. Chronic diarrhoea (3 weeks) and abdominal cramps | *A. butzleri* | 1. Recovered 3 days after treatment with ofloxacin<br>2. Recovered 2 days after treatment with doxycycline | 1. Type 1 diabetes mellitus<br>2. Hyperuricaemia and alcohol abuse | [19] |
| 1. M/2 years<br>2. F/1 years | Chile | 1. Acute mucous diarrhoea and vomiting<br>2. Chronic diarrhoea (4 months) with abdominal cramps and pain | *A. butzleri* | 1. Recovered in 2 days with parenteral fluid therapy, restricted diet but without antimicrobial treatment<br>2. Recovered 10 days after treatment with erythromycin | None | [22] |
| M/73 years | Belgium | Chronic diarrhoea (2 months) | *A. skirrowii* | Recovered 10 days after no specific treatment | Prosthetic aortic heart valve | [24] |
| M/30 years | Turkey | Acute watery diarrhoea, abdominal pain, nausea and sweating | *A. butzleri* | Recovered 2 days after treatment with ciprofloxacin | None | [23] |
| M/26 years | Spain | Persistent bloody and watery diarrhoea (3 weeks) | *A. cryaerophilus* | Recovered 8 days after treatment with amoxicillin/clavulanic acid | Acute gastroenteritis 4 months earlier | Current study |

NS, not specified.
[1]Originally described as *Campylobacter cryaerophila*.
[2]Four males and six females between 3 and 7 years old.

**TABLE 2. Extra-intestinal infections associated with *Arcobacter* spp.**

| Patients sex/age | Country | Presentation | Species | Outcome | Underlying disease | Reference |
|---|---|---|---|---|---|---|
| Neonate | UK | Bacteraemia with hypotension, hypothermia and hypoglycaemia | *A. butzleri* | Recovered 6 days after penicillin and cefotaxime treatment | Mother had prenatal bleeding due to placenta praevia. Delivery at 26 weeks of gestation | [20] |
| M/72 years | Taiwan | Bacteraemia and haematogenous pneumonia | *A. cryaerophilus* | Recovered 2 weeks after ceftizoxime and tobramycin treatment | Chronic renal failure, haemodialysis with arteriovenous fistula. Two months of fever and progressive cough with purulent sputum. She also had a 1-month history of anorexia and frequent loose stool 2 months before admission | [18] |
| M/60 years | Taiwan | Bacteraemia with fever and haematemesis | *A. butzleri* | Recovered 4 days after cefuroxime treatment | Chronic hepatitis B carrier, liver cirrhosis | [21] |
| F/69 years | Hong Kong | Bacteraemia with fever and lower quadrant pain | *A. butzleri* | Recovered 3 days after cefuroxime and metronidazole treatment | Gangrenous appendicitis | [7] |
| F/63 years | China | Peritonitis after repositioning of catheter with fever and abdominal pain | *Arcobacter* sp. | Recovered 2 weeks after treatment with ticarcillin-clavulanate | End-stage renal failure of unknown cause | [25] |

NS, not specified.

now use the MALDI-TOF identification technique for such fastidious, slow-growing microbes, we have re-identified our *A. cryaerophilus* isolate using that method [27]. The isolate was studied with the Ultraflex TOF/TOF MALDI-TOF instrument, that uses the MALDI Biotyper 2.0 software (Bruker Daltonics, Bremen, Germany) after spotting a fresh colony directly on to the target plate and the addition of 1 μL of the matrix, cinaminic acid, as described by the manufacturer. The type strain of *A. cryaerophilus* (LMG 9904$^T$) was used in parallel as a control. The MALDI Biotyper output for our clinical strain scored 1.493 with the strain *A. cryaerophilus* T277 CPB. A score of <1.7 normally indicates an unconfident identification, between 1.7 and 1.99 indicates a genus-level identification, and a score ≥2 indicates a species-level identification. The second higher score was only 1.42 with a strain of the species *Pseudomonas proteolytica*. Despite the unconfident identification the first match was with an *A. cryaerophilus* and among the following bacteria listed there was no *Campylobacter* spp. The type strain of *A. cryaerophilus* (LMG 9904$^T$) used as control was correctly identified despite it showing a low score (1.885). Clinicians should be aware that in the case of a strain showing this behaviour with MALDI-TOF it is worth confirming its identity by sequencing the *rpoB* gene, so that the true incidence of these bacteria can be established. The inconclusive results obtained with MALDI-TOF could be explained by the fact that a correct identification with this method depends on the number of bacteria strains included in the database [27]. The Biotyper database has only 13 *Arcobacter* strains and only four of them belong to the species *A. cryaerophilus*. However, the capacity of this method to separate strains belonging to all

*Arcobacter* spp. has been recently demonstrated [2,28], therefore, it is possible that the inclusion of more strains in the BIOTYPER database will allow their correct identification, and this will contribute to clarify the clinical importance of this genus.

The seven housekeeping genes (*aspA*, *atpA*, *glnA*, *gltA*, *glyA*, *pgm* and *tkt*) included in the *Arcobacter* multilocus sequence typing database created by Miller *et al.* [29] were sequenced from our isolate of *A. cryaerophilus* using the primers described by these authors. New alleles were obtained for four genes (i.e. *aspA-215*, *atpA-152*, *gltA-149* and *glyA-473*), while the sequences of the *glnA* (codifying for glutamine synthetase), *pgm* (phosphoglucomutase) and *tkt* (transketolase) genes corresponded to the already known alleles 59, 133 and 115, respectively. Therefore, this new clinical isolate (strain 609) belonged to a new sequence type (ST) named ST-392. Interestingly, the allele glnA-59 and the pgm-133 had been obtained from strain 276, which was isolated from the faeces of a patient with gastroenteritis in France in 2004, while the allele tkt-115 had been obtained from strain 305, which was also obtained from faeces of a patient with gastroenteritis in the USA in 2009. Apart from strains 276 and 305, the database includes only two other isolates of *A. cryaerophilus* recovered from human samples, i.e. strains 281 (from gastroenteritis) and 285 (from human blood), and both isolates share the ST-201. The few available human pathogenic strains in the database do not allow a relationship to be established between the presence of certain alleles, or STs, and virulence. Therefore, it is important that more strains isolated from human infections are included in the

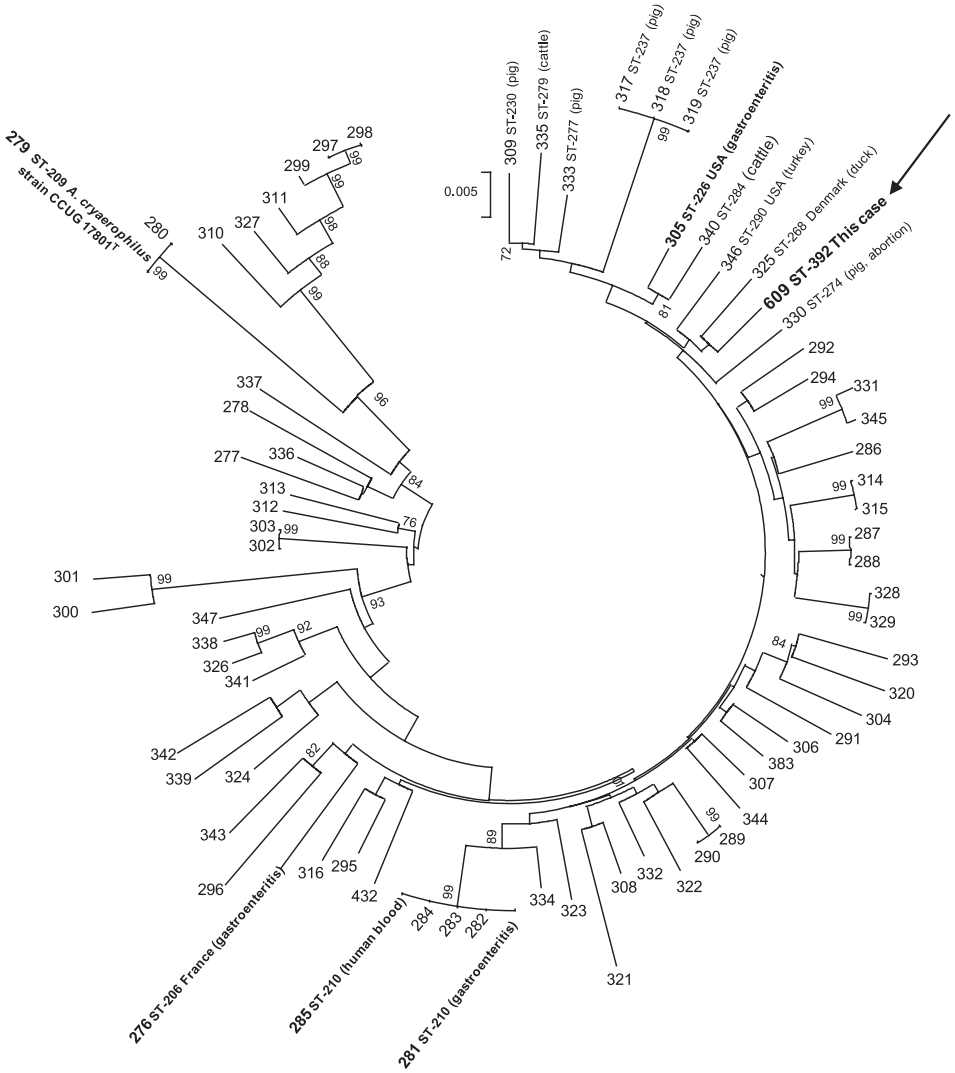


**FIG. 1.** Neighbour joining tree based on the concatenated sequences of *aspA*, *atpA*, *glnA*, *gltA*, *glyA*, *pgm* and *tkt* (3339 bp) showing the position of strain 609 (ST-392) among the 75 strains of *Arcobacter cryaerophilus* included in the *Arcobacter* multilocus sequence typing database. Bootstrap values (≥70%) based on 1000 replications are shown at the nodes.

database as we did. In the tree constructed with the concatenated sequences of the seven genes from each of the 75 *A. cryaerophilus* strains that are currently included in the database (Fig. 1), our strain grouped with two others obtained in Europe from poultry (strain 346, ST-290 and strain 325, ST-268), being therefore the most related strains. However, whether the *A. cryaerophilus* strain was acquired in our patient through consumption of poultry meat could not be demonstrated.

Five putative *Arcobacter* virulence genes (*ciaB*, *cadF*, *cj1349*, *hecA* and *irgA*) were also searched for in our strain using the primers designed by Douidah *et al.* [30]. However, only the presence of the *ciaB* gene was detected, which encodes for an invasion protein in *C. jejuni*. The same result was obtained for five strains of *A. cryaerophilus* recovered from shellfish and from animal faeces in our laboratory [31]. In the study of Douidah *et al.* [30], which included 99 *A. cryaerophilus* strains isolated from human, chicken, pig, cattle, sheep, horse and dog, the *ciaB* gene was present in the majority (92.9%) of the strains, followed by *cj1349* (51.5%), *cadF* (34.3%), *hecA* (4%) and *irgA* (3%).

Among the faecal samples at the *Hospital Universitari Sant Joan de Reus,* where the isolate of *A. cryaerophilus* was obtained, *Campylobacter* was the most commonly isolated enteropathogen, representing 41.4% (65/157) of the positive stools in the last year, followed by *Salmonella* spp. (36.3%), *Aeromonas* spp. (14.6%), *Shigella* spp. (4.4%), *Hafnia alvei* (3.2%) and *Yersinia enterocolitica* (1.3%). Among the *Campylobacter* and *Campylobacter*-like organisms, *C. jejuni* was the most prevalent species (82.7%), followed by *Campylobacter coli* (16.4%), while *A. cryaerophilus* was in third place (0.9%), which agrees with previous studies [13,14].

A summarized revision of studies on *Arcobacter*, including those comparing patients with and without diarrhoea, is provided in Table 3. The prevalence of *Arcobacter* species in human stools ranged from 0.1% to 1.25% in studies that derived the information from culturing, whereas the detection from faeces by PCR ranged from 0.4% to 13% [9,10,12–14,32–37]. In one study, performed in Belgium and France where the prevalence was determined by culture [13], *A. butzleri* occupied the fourth place (3.5%) among *Campylobacter*-like organisms, while *A. cryaerophilus* occupied the seventh place (0.5%). In another study performed in South Africa using multiplex PCR detection, *A. butzleri* showed a higher prevalence (6.2%) after *C. jejuni* (10.2%) [10]. In the same study, *A. cryaerophilus* and *A. skirrowii* showed lower incidences (2.8% and 1.9%, respectively). In two other studies that detected *Arcobacter* using the same multiplex PCR method a higher incidence was also observed [12,38]. One was a case–control study of faeces from diabetic patients in Italy [38]. In that study there was 78.9%

**TABLE 3. Characteristics of the patients from different diarrhoea surveys in which *Arcobacter* spp. were detected by culture or PCR-based methods**

| Number of patients | Country | Age (range or mean) | M/F ratio | Prevalence of *Arcobacter* spp. (%) among diarrhoeic patients | | Type of diarrhoea and symptoms (%) | | | | | | Monomicrobial infection (%) | Underlying disease (%) | Antimicrobial treatment (%) | Relapse (%) | Asymptomatic (%) | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Culture | PCR | Acute | Chronic | Watery | Blood | Nausea/ Vomiting | Abdominal pain | Fever >38°C | | | | | |
| 19 535 | South Africa | Paediatric (NS) | NS | 0.4 | ND | 100 | 0 | NS | NS | NS | NS | NS | NS | NS | NS | 49.7 | [34] |
| 67 599 | Belgium and France | 30 days to 90 years | NS | 0.11 | ND | 50.8 | 16.4 | 50.8 | 6.0 | 27.9 | 29.5 | 32.8 | 82.0 | 16.4 | 26.2 | 6.6 | 19.7 | [13] |
| 2855[1] | France | 54 years | 1.44 | 1.0 | ND | 59.0 | 3.4 | NS | 21.1 | 10.5 | 57.9 | 26.3 | 93.3 | 15.8 | 26.3 | 5.3 | NS | [14] |
| 322 | South Africa | 1 month to 88 years | 0.77 | ND | 13.0 | 47.8 | NS | NS | 3.1 | NS | NS | NS | 83.1 | 13.7 | NS | NS | 20.8 | [10] |
| 400[2] | India | ≥18 years (NS) | 1.4 | 1.25 | ND | 100 | 0 | NS | NS | NS | NS | NS | NS | 50.0 | NS | NS | 0 | [9] |
| 345 | France | 41.4 years | 0.56 | 0 | 1.2 | 100 | NS | NS | NS | NS | NS | NS | NS | NS | NS | NS | 0 | [35] |
| 201[3] | USA/ Europe | NS | NS | ND | 8.0 | 100 | NS | NS | NS | NS | NS | NS | 78.6 | NS | NS | NS | 0 | [12] |
| 1380 | New Zealand | 49 y | 1.0 | 0.9 | ND | 100 | 0 | NS | NS | 8.3 | NS | NS | 75.0 | NS | NS | NS | 0 | [32] |
| 3287 | Turkey | 26.6 years | 1.25 | 0.3 | ND | 100 | 0 | 33.3 | 0 | 22.2 | 100 | 11.1 | NS | NS | NS | NS | 0 | [33] |
| 140 | Chile | <5 years to >50 years | 0.96 | 0.7 | 1.4 | 100 | 0 | NS | NS | NS | NS | NS | 50.0 | NS | NS | NS | 45.3 | [36] |
| 493 | The Netherlands | 35 years | 0.88 | 0 | 0.4 | 100 | NS | NS | NS | NS | NS | NS | 0.4 | NS | NS | NS | NS | [37] |

NS, not specified; ND, not done.
[1]Surveillance study including only patients with diarrhoea due to *Campylobacter*-like microorganisms.
[2]Case–control study that included 200 human immunodeficiency virus type 1 infected patients and 200 non-infected controls.
[3]US or European travellers that suffered acute diarrhoea after returning from Mexico, Guatemala or India.
Reference 6 is not included, because despite *A. cryaerophilus* was isolated from the blood, the infection was not proven. The patient had a motorcycle accident and died 24 hours after hospitalization.

on-diarrhoeic faeces of patients with type 2 diabetes, versus the 26.2% found for the controls (non-diabetic non-diarrhoea subjects). In the second study, an 8.0% incidence was reported among US/European travellers who suffered acute diarrhoea while visiting Mexico, Guatemala and India [12]. Other recent studies compared the ability to detect *Arcobacter* using in parallel molecular and culture methods [36,37]. Collado *et al.* [36] detected the species *A. butzleri* in 1.4% of stool samples of patients with diarrhoea, using a genus-specific PCR and a species-specific multiplex PCR method, whereas it was isolated from only 0.7% of samples by culture. In the other study, de Boer *et al.* [37] developed a multiplex real-time PCR able to detect *A. butzleri* and campylobacters from the faeces of patients with diarrhoea; testing this method in parallel with culture. Using this method, *A. butzleri* was detected in 0.4% of samples but was not recovered by culture. The higher prevalence obtained using molecular methods supports the statement that *Arcobacter* spp. could be underestimated as enteropathogens because of limitations in the current culturing methods, and demonstrates the importance of routinely screening stool samples for the species of this genus using molecular methods in parallel.

The isolation in our patient of *A. cryaerophilus* in the absence of other enteropathogens and the remission of the diarrhoea symptoms after treatment with amoxicillin/clavulanic acid, to which the bacteria was sensitive, seems to indicate that this bacterium could be considered the aetiological agent of the diarrhoea process. Despite not being able to find the contagious source of *Arcobacter* in the environment of our patient, we were able to speculate that, in this case, it could have been acquired through the consumption of poorly cooked poultry meat or fish. Interestingly, the patient showed recurrent episodes with abdominal pain, which seems to be a typical clinical presentation for this genus.

## Acknowledgements

This work was supported in part by the project AGL2011-30461-C02-02 of the Ministerio de Ciencia e Innovación (MICINN), Spain and by funding from the European Union Seventh Framework Programme (FP7/2007-2013) under grant agreement no. 311846. The authors are solely responsible for the content of this publication. It does not represent the opinion of the European Commission. The European Commission is not responsible for any use that might be made of data appearing therein. AL is indebted to the Universitat Rovira i Virgili for a doctoral grant and to CONICYT, Chile, for financial support through Becas Chile.

## Conflict of Interest

None declared.

## References

1. Collado L, Figueras MJ. Taxonomy, epidemiology and clinical relevance of the genus *Arcobacter*. *Clin Microbiol Rev* 2011; 24: 174–192.
2. Levican A, Collado L, Figueras MJ. *Arcobacter cloacae* sp. nov. and *Arcobacter suis* sp. nov., new species isolated from food and sewage. *Syst Appl Microbiol* 2013; 36: 22–27.
3. Schroeder-Tucker L, Wesley IV, Kiehlbauch JA, Larson DJ, Thomas LA, Erickson GA. Phenotypic and ribosomal RNA characterization of *Arcobacter* species isolated from porcine aborted fetuses. *J Vet Diagn Invest* 1996; 8: 186–195.
4. Vandamme P, Pugina P, Benzi G *et al.* Outbreak of recurrent abdominal cramps associated with *Arcobacter butzleri* in an Italian school. *J Clin Microbiol* 1992; 30: 2335–2337.
5. Anderson KF, Kiehlbauch JA, Anderson DC, McClure HM, Wachsmuth IK. *Arcobacter* (*Campylobacter*) *butzleri*-associated diarrheal illness in a nonhuman primate population. *Infect Immun* 1993; 61: 2220–2223.
6. Woo PC, Chong KT, Leung K, Que T, Yuen K. Identification of *Arcobacter cryaerophilus* isolated from a traffic accident victim with bacteremia by 16S ribosomal RNA gene sequencing. *Diagn Microbiol Infect Dis* 2001; 40: 125–127.
7. Lau SK, Woo PC, Teng JL, Leung KW, Yuen KY. Identification by 16S ribosomal RNA gene sequencing of *Arcobacter butzleri* bacteraemia in a patient with acute gangrenous appendicitis. *Mol Pathol* 2002; 55: 182–185.
8. Ho HTK, Lipman LJ, Gaastra W. *Arcobacter*, what is known and unknown about a potential foodborne zoonotic agent!. *Vet Microbiol* 2006; 115: 1–13.
9. Kownhar H, Shankar EM, Rajan R, Vengatesan A, Rao UA. Prevalence of *Campylobacter jejuni* and enteric bacterial pathogens among hospitalized HIV infected versus non-HIV infected patients with diarrhoea in southern India. *Scand J Infect Dis* 2007; 39: 862–866.
10. Samie A, Obi CL, Barrett LJ, Powell SM, Guerrant RL. Prevalence of *Campylobacter* species, *Helicobacter pylori* and *Arcobacter* species in stool samples from the Venda region, Limpopo, South Africa: studies using molecular diagnostic methods. *J Infect* 2007; 54: 558–566.
11. Kopilovic B, Ucakar V, Koren N, Krek M, Kraigher A. Waterborne outbreak of acute gastroenteritis in a coastal area in Slovenia in June and July 2008. *Euro Surveill* 2008; 13: 1–3.
12. Jiang ZD, Dupont HL, Brown EL *et al.* Microbial etiology of travelers' diarrhea in Mexico, Guatemala and India importance of enterotoxigenic *Bacteroides fragilis* and *Arcobacter* species. *J Clin Microbiol* 2010; 48: 1417–1419.
13. Vandenberg O, Dediste A, Houf K *et al. Arcobacter* species in humans. *Emerg Infect Dis* 2004; 10: 1863–1867.
14. Prouzet-Mauleon V, Labadi L, Bouges N, Menard A, Megraud F. *Arcobacter butzleri*: underestimated enteropathogen. *Emerg Infect Dis* 2006; 12: 307–309.
15. Collado L, Guarro J, Figueras MJ. Prevalence of *Arcobacter* in meat and shellfish. *J Food Prot* 2009; 72: 1102–1106.
16. Collado L, Inza I, Guarro J, Figueras MJ. Presence of *Arcobacter* spp. in environmental waters correlates with high levels of fecal pollution. *Environ Microbiol* 2008; 10: 1635–1640.
17. Tee W, Baird R, Dyall-Smith M, Dwyer B. *Campylobacter cryaerophila* isolated from a human. *J Clin Microbiol* 1988; 26: 2469–2473.
18. Hsueh PR, Teng LJ, Yang PC *et al.* Bacteremia caused by *Arcobacter cryaerophilus* 1B. *J Clin Microbiol* 1997; 35: 489–491.

19. Lerner J, Brumberger V, Preac-Mursic V. Severe diarrhea associated with *Arcobacter butzleri*. *Eur J Clin Microbiol Infect Dis* 1994; 13: 660–662.
20. On SL, Stacey A, Smyth J. Isolation of *Arcobacter butzleri* from a neonate with bacteraemia. *J Infect* 1995; 31: 225–227.
21. Yan JJ, Ko WC, Huang AH, Chen HM, Jin Y, Wu JJ. *Arcobacter butzleri* bacteremia in a patient with liver cirrhosis. *J Formos Med Assoc* 2000; 99: 166–169.
22. Fernandez H, Krause S, Villanueva MP. *Arcobacter butzleri* an emerging enteropathogen: communication of two cases with chronic diarrhea. *Braz J Microbiol* 2004; 35: 216–218.
23. Kayman T, Atabay HI, Secil A, Hizlisoy H, Celenk M, Fuat A. Human acute gastroenteritis with *Arcobacter butzleri*. *Clin Microbiol Newsletter* 2012; 34: 197–199.
24. Wybo I, Breynaert J, Lauwers S, Lindenburg F, Houf K. Isolation of *Arcobacter skirrowii* from a patient with chronic diarrhea. *J Clin Microbiol* 2004; 42: 1851–1852.
25. Yap DY, Kwan LP, To KK, Chan TM. *Arcobacter* peritonitis after fluoroscopic repositioning of a Tenckhoff catheter. *Perit Dial Int* 2013; 33: 222–223.
26. Houf K, Tutenel A, De Zutter L, Van Hoof J, Vandamme P. Development of a multiplex PCR assay for the simultaneous detection and identification of *Arcobacter butzleri*, *Arcobacter cryaerophilus* and *Arcobacter skirrowii*. *FEMS Microbiol Lett* 2000; 193: 89–94.
27. Welker M, Moore ERB. Applications of whole-cell matrix-assisted laser-desorption/ionization time-of-flight mass spectrometry in systematic microbiology. *Syst Appl Microbiol* 2011; 34: 2–11.
28. Levican A, Collado L, Aguilar C *et al.* *Arcobacter bivalviorum* sp. nov. and *Arcobacter venerupis* sp. nov., new species isolated from shellfish. *Syst Appl Microbiol* 2012; 35: 133–138.
29. Miller WG, Wesley IV, On SL *et al.* First multilocus sequence typing scheme for *Arcobacter* spp. *BMC Microbiol* 2009; 9: 196.
30. Douidah L, de Zutter L, Baré J *et al.* Occurrence of putative virulence genes in *Arcobacter* species isolated from humans and animals. *J Clin Microbiol* 2012; 50: 735–741.
31. Levican A, Alkeskas A, Günter C, Forsythe SJ, Figueras MJ. The adherence and invasion of human intestinal cells by *Arcobacter* species and their virulence genotype. *Appl Environ Microbiol* 2013; 79: 4951–4957.
32. Mandidodza O, Burrows E, Nulsen M. *Arcobacter* species in diarrhoeal faeces from humans in New Zealand. *N Z Med J* 2012; 125: 40–46.
33. Kayman T, Secil A, Hizlisoy H, Atabay HI, Diker KS, Aydin F. Emerging pathogen *Arcobacter* spp. in acute gastroenteritis: molecular identification, antibiotic susceptibilities and genotyping of the isolated arcobacters. *J Med Microbiol* 2012; 61: 1439–1444.
34. Lastovica AJ, Le Roux E. Efficient isolation of campylobacteria from stools. *J Clin Microbiol* 2000; 38: 2798–2799.
35. Abdelbaqi K, Buissonniere A, Prouzet-Mauleon V *et al.* Development of a real-time fluorescence resonance energy transfer PCR to detect *Arcobacter* species. *J Clin Microbiol* 2007; 45: 3015–3021.
36. Collado L, Gutierrez M, González M, Fernandez H. Assessment of the prevalence and diversity of emergent campylobacteria in human stool samples using a combination of traditional and molecular methods. *Diagn Microbiol Infect Dis* 2013; 75: 434–436.
37. de Boer RF, Ott A, Güren P, van Zanten E, van Belkum A. Detection of *Campylobacter* species and *Arcobacter butzleri* in stool samples by use of real-time multiplex PCR. *J Clin Microbiol* 2013; 51: 253–259.
38. Fera MT, Russo GT, Di Benedetto A *et al.* High prevalence of *Arcobacter* carriage in older subjects with type 2 diabetes. *J Biomed Biotechnol* 2010; 489784. doi: 10.1155/2010/489784