Gastrointestinal campylobacteriosis in industrialised countries: comparison of the disease situation with salmonellosis, and microbiological contamination assessment

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Summary
The science-based assessment of foodborne zoonotic risk is used to evaluate the public health impact of a hazard and to guide public decision-making on control measures. Key information for the hazard characterisation and microbiological contamination assessment phases of risk assessment may be obtained from the collection and structured statistical analysis of international data. This approach was used for the hazard characterisation phase of a risk assessment of gastrointestinal campylobacteriosis and salmonellosis in 30 industrialised countries over the period 2005–2009. The results showed an overall increase in the annual ratio campylobacteriosis/salmonellosis (R_moy > 2), despite significant differences among countries (P < 0.0001). For countries with complete data over 20 years, the results showed significantly higher exposure to campylobacteriosis among certain population segments (men, children under 5 years of age and adults aged between 20 and 30), as well as in summer. A number of paired factors (Campylobacter species/animal species–meat type) are observed in this consumer exposure. However, the overall rate of bacterial transfer in meat supply chains varies widely, with far lower values for cattle (0.16) and pigs (0.24) than for poultry (0.60) and chickens (1.17). A lack of harmonised epidemiological data on the contamination status of foodstuffs (frequency, level, site, and species) further hampers the accurate identification of critical points of contamination and of the spread of the hazard throughout the food chain.

Keywords

Introduction
Foodborne diseases (resulting from the ingestion of a foodstuff contaminated with a biological hazard) remain a leading cause of infectious diseases in the world today, with around 2.2 million cases per year, including 1.9 million child cases (1). Hazard characterisation – or, more generally, the provision of data describing the disease situation induced by the hazard – and quantitative microbiological contamination assessment, are two of the four steps defined by Codex Alimentarius for the science-based risk assessment of foodborne disease. Such a risk assessment is used to assess the public health impact of a hazard and, on this basis, to guide, as objectively as possible, decision-making on control measures and ways to implement them.

Such an objective assessment is clearly important for gastrointestinal campylobacteriosis, a foodborne bacterial disease that is often compared empirically with another foodborne bacterial disease: salmonellosis. Indeed,
salmonella is still frequently said to pose the greatest risk for foodborne diarrhoea. Yet Campylobacter spp., which are responsible for gastrointestinal campylobacteriosis, are also cited as the world’s leading cause of bacterial gastroenteritis. In Europe, even now, gastrointestinal campylobacteriosis appears to be twice as common as salmonellosis (2). Furthermore, the severity of the induced disease in industrialised countries, estimated using a score combining the average hospitalisation and fatality rates, places Campylobacter spp. in the group of foodborne biological hazards with moderately severe adverse effects, along with Shiga toxin-producing Escherichia coli and salmonellae (3).

While the natural reservoir of Campylobacter spp. is the intestinal contents of warm-blooded animals, the main route of transmission to humans is the ingestion of contaminated foods, eaten raw or undercooked (1, 4, 5, 6). Generally speaking, the clinical signs and symptoms of gastrointestinal campylobacteriosis are not pathognomonic, so differential diagnosis between campylobacteriosis and digestive disorders caused by other enteric pathogens is not easy. Indeed a range of symptoms may be observed, from a brief episode of gastroenteritis to severe enterocolitis lasting several weeks, accompanied by abdominal pain and bloody diarrhoea. When recovery is not spontaneous, the basic treatment consists of antibiotic therapy using mainly macrolides, supplemented by symptomatic treatment, the extent of which will depend on the intensity of the disease. Complications may arise, the best-known of which are the nerve diseases Guillain–Barré syndrome and Miller Fisher syndrome (7).

In general, the hazardousness of food for humans relates to the extent of its contamination, as well as to the physiological characteristics of the bacteria, their virulence and their resistance to drug treatment. From a bacterial systematics standpoint, data on the dangers posed by Campylobacter spp. can be found on the website of the French dictionary of veterinary bacteriology, Dictionnaire de Bactériologie Vétérinaire (8), but this article describes a few of its key characteristics. This thin, Gram-negative, spiral or helical, motile bacillus can be cultivated in vitro only in a microaerophilic atmosphere. A number of the 22 species referenced (May 2011) are thermophilic, that is to say, able to grow in vitro at 42°C. Four of these thermophilic species are involved in gastrointestinal campylobacteriosis: C. jejuni, C. coli, C. lari and C. upsaliensis. Owing to their highly specific growth requirements, it is not possible for these bacteria to grow on food. Their identification is time-consuming and insufficiently specific using conventional biochemical techniques (8). While identification is more reliable using molecular techniques (9, 10), their detection sensitivity is still insufficient in complex matrices like food (5, 11, 12). Finally, the infective dose able to induce gastrointestinal campylobacteriosis is low, with a consumer needing to ingest only 100 bacteria (13).

The dietary risk from Campylobacter spp. is therefore closely linked with the contamination status of food supply chains. The authors define contamination status as the frequency of hazard detection in the foodstuff produced, the observed level of contamination (amount of bacteria detected), the bacterial species involved and the site of contamination (surface or internal contamination of the foodstuff; at which stage in the chain, etc.). This contamination status emerges as a determinant of the risk of cross-contamination of foodstuffs and the level of consumer exposure. It is therefore important to ascertain its presence in the various food supply chains. However, by limiting the scope of its study to the chicken/Campylobacter jejuni pairing, the French food safety agency (AFSSA) report published in 2004 (14) unintentionally amplified a tendency to believe that only this bacterial species and only this foodstuff pose a risk of gastrointestinal campylobacteriosis. Clearly, other thermophilic species are involved (2, 15) and other foods can be contaminated (16, 17, 18), even though meat (from all species), by virtue of its processing method (5, 19), is the most commonly contaminated food (2). This contaminated meat introduces the hazard into the consumer’s kitchen where it causes secondary cross-contamination of other foods (20, 21).

Although there are already many reviews and syntheses on Campylobacter spp., most provide data that are qualitative or limited to: primary production in a single sector (mainly chicken [14, 22] but also pigs [23] and ruminants [4]); the biological characteristics of the hazard (24); study models of virulence (25); and prevalence data solely for France (15) or Europe (2). The current synthesis, which is based on the collection and statistical analysis of international data, aims to provide the key quantitative elements needed for a science-based risk assessment of gastrointestinal campylobacteriosis. To limit the impact of the choice of methodology for recording case incidence data, which are still highly specific to each country, the hazard characterisation phase is conducted by comparing gastrointestinal campylobacteriosis to salmonellosis, a foodborne zoonosis that has been under surveillance for many years. The quantitative microbiological contamination assessment phase focuses only on the Campylobacter hazard.

Disease situation caused by gastrointestinal campylobacteriosis

The authors start by considering variations in time series (prevalence and spatial and temporal variations) and go on to examine successively the distribution of cases by patient age and sex, season and bacterial species involved, limiting the analysis to the period 2000–2009.
The quantitative data were expressed as the number of cases or infection rates (number of reported cases per year per 100,000 inhabitants). The information, concerning 30 countries, was collected from official national or international websites accessible until early July 2011, directly from 18 national websites (26–45) and/or indirectly from two international websites (46, 2). A point of note is that the presentation or expression of data varies from one website to another, mainly because countries use different methods for obtaining data. Indeed, the number of ‘reported’ cases of a foodborne disease may correspond to different values from one country to another, ranging from the ‘estimated’ number of infected people in the general population to the fraction of the affected population in whom the presence of the pathogen is actually confirmed (29). Furthermore, the number of ‘reported’ cases within a single country may be estimated differently depending on the hazard being assessed. So a comparison between the two foodborne diseases, gastrointestinal campylobacteriosis and salmonellosis, will limit country-specific methodological effects. For their statistical analysis of factors of variation (age, sex, season, species involved, etc.), using the XLStat 2011 software (Adinsofi, Paris), the authors retained only countries for which data were presented as values. Indeed, a number of countries, including France (37), prefer to use graphic representations, which, while certainly more eloquent, are harder to incorporate into numerical analyses. Finally, the data analysed relate solely to industrialised countries, mainly European, both members and non-members of the European Union (EU), plus two countries in Oceania: Australia and New Zealand. For countries whose websites have been modified in recent years, the authors included in the list of websites only the address that was active the last time it was accessed. It is worth noting that no data from North American countries (the United States and Canada) could be incorporated into this analysis. In the case of the United States (47), the authors were unable to find any structured epidemiological data in the Foodborne Diseases Active Surveillance Network (FoodNet) of the Centers for Disease Control and Prevention (CDC), which covers only a few states. In Canada (31), the recording of cases and publication of statistics appear to have ceased in 2004, even though the website provided a wealth of numerical and graphical information.

**Prevalence and spatial and temporal variations: gastrointestinal campylobacteriosis is reported more often than foodborne salmonellosis**

For five countries (Australia [28], New Zealand [43], Switzerland [45], Denmark [32] and Norway [42]), the authors had time series, each of which covered a period of at least 20 years, expressed as rates (number of cases per year per 100,000 inhabitants), so the values were independent of the size of the population (Fig. 1). The rate of reported gastrointestinal campylobacteriosis increased markedly in New Zealand until 2006, whereas for the other countries considered, the increase seems to be especially marked in the 1990s (Fig. 1a). No explanation is given for the very high number of reported cases in New Zealand. Rates of salmonellosis (Fig. 1b) are relatively volatile over the same period and appear to have declined over the past decade. This decrease, which was echoed in the EU, is undoubtedly the result of introducing collective control measures (48).

The authors calculated, for 30 countries, the annual ratio of the number of reported cases of gastrointestinal campylobacteriosis to the number of reported cases of salmonellosis (represented as campylobacteriosis/salmonellosis or R) over the period 2005–2009. The average values of this ratio, shown in Figure 2, vary from a minimum of R < 0.02, observed in Poland, to a maximum of R = 8.6, observed in New Zealand, with the EU average being 1.36. For some countries (Poland, Cyprus, Italy, Lithuania, Estonia, Slovakia, France), the values of R < 0.5 could indicate that the reporting of gastrointestinal campylobacteriosis cases was introduced recently or else was anecdotal. In France, in particular (15), the surveillance programme for Campylobacter
infections was not established until 2002 and double the number of strains were isolated between 2005 and 2009. In contrast, countries that have systematically searched for *Campylobacter* spp. in diarrhoea cases for many years have the highest R moy values (Denmark: 1.77; Australia: 2.72; Switzerland: 3.83; R moy > 4 for Ireland, Scotland, England and Wales). In Canada, over the period 2000–2004, the average value of the ratio was 2. In New Zealand, values of more than 10 were observed over the period 2003–2007, while in 2008 and 2009 they ranged between 5 and 6. Without weighting values by the size of the population in these countries (Germany’s population is 200 times larger than that of Malta, for instance), the overall average annual ratio of these two foodborne diseases is around 2. While the analysis of variance on these data shows a highly significant country effect (P < 0.0001), the increase over time (by year) is not significant (P = 0.4).

The aggregate data for the EU are available in thousands of cases per year for the period 1995–2009 (2–49) and are shown in Figure 3. In the case of salmonellosis, the decrease in the number of cases of around 17,000 per year was linear with time ($r^2 = 0.987$) over the period in question. In the case of gastrointestinal campylobacteriosis, the values increased, also by about 17,000 per year between 1995 and 2001 ($r^2 = 0.961$), thereafter levelling off. Thus, the overall temporal variation of the ratio campylobacteriosis/salmonellosis is significant ($P = 0.02$ over the period 2005–2009, $P < 0.0001$ over the period 1995–2009).

Although, in 1995, salmonellosis was reported four times more often than gastrointestinal campylobacteriosis, since 2005 the latter has become the most frequently reported foodborne gastrointestinal bacterial disease in Europe, outstripping reported cases of salmonellosis (almost twice the number in 2009 [48]).

These initial observations confirm that the available data are highly dependent on variations specific to diagnostic and reporting systems. For example, in France, a case of campylobacteriosis, i.e. *Campylobacter* infection, is defined as the isolation of *Campylobacter* spp. from a biological sample, with no information on clinical signs. This means that the definition includes cases of both gastrointestinal campylobacteriosis and *C. fetus* septicemia. When analysing the different factors of variation (age, sex, etc.), it was therefore necessary to restrict the analysis to countries that had included only cases of gastrointestinal campylobacteriosis over a sufficient period.
Age distribution of reported cases: increased exposure in those under 5 and between 20 and 30 years of age

While the age distributions of reported cases are published by annual rate per 100,000 inhabitants or by number of cases, countries use different age groups. In some cases, different age groups are used for the two bacteria (27). For this reason, it was necessary to combine some age groups and break down others in order to obtain groups of identical size that could be used to make direct comparisons. The authors were forced to exclude from the analysis values for people over the age of 70, as data presentation for this group varied excessively from one website to another.

The authors used a series of values collected between 2000 and 2009 by Australia (28), Finland (36) and New Zealand (43), and values collected between 2001 and 2009 by Germany (26). The analysis of variance performed on the results, expressed as a rate per 100,000 inhabitants, shows an age group effect, apart from the country effect mentioned earlier, as well as country*age interactions with probability \( P < 0.0001 \) for both zoonoses. A year effect, which was more significant for foodborne salmonellosis \( (P < 0.0001) \) than for gastrointestinal campylobacteriosis \( (P = 0.03) \), provides further evidence of the impact of the preventive measures taken by these countries.

The country*age interactions, as mean values of the rates, are illustrated in Figure 4. Overall, in the case of campylobacteriosis, the highest rates are observed in those under 5 and between 20 and 30 years of age, and the lowest rates in those between 5 and 15 and over 60 years of age. In the case of salmonellosis, the rates are particularly high for the under-fives but variations are unclear as age increases.

The authors noted that the Finnish results were unusual for both gastrointestinal campylobacteriosis and salmonellosis, with lower values for children than for adults.

It appears that, in all countries, cases are generally reported more frequently among very young children and young adults. The particularly high rate in these age groups appears to be associated with greater exposure to the hazard. So far, no specific virulence factors of Campylobacter spp. (25) have been identified to explain the greater sensitivity of these age groups, especially the 20–30 age group. Among the under-fives, where the rates of both gastrointestinal campylobacteriosis and salmonellosis are high, a possible explanation is better detection and, therefore, better reporting in this age group because the greater severity of infection (risk of dehydration, etc.) systematically requires medical care.

Sex distribution of reported cases: more frequent exposure to the hazard among men

The available data on the number of reported cases for these two zoonoses by the sex of patients are usually published as an annual rate per 100,000 men or women or the number of cases by sex. For the latter data, it was not possible to calculate the annual rate per 100,000 men or women because the authors were unable to ascertain the sex ratios by country. Some country websites present data in both forms – rate and number of cases – which is useful for comparing the respective information value of this data. The authors therefore used the data from these countries, which number only four: Australia (28), Finland (36) and New Zealand (43) between 2000 and 2009; Germany (26) between 2001 and 2009. The results of the analysis of variance are shown in Figure 5.

![Figure 4](image_url)

Variations in the rates of gastrointestinal campylobacteriosis and foodborne salmonellosis per 100,000 inhabitants, by age group, in New Zealand, Germany, Australia and Finland
There is no year effect or country*sex interaction (data not shown). As regards rates, the gender effect is marked for gastrointestinal campylobacteriosis (P = 0.006), with a higher incidence of cases in men. In contrast, the gender effect is not apparent in the case of salmonellosis (P = 0.85). When considering the sex distribution of the number of cases, the highest proportion of gastrointestinal campylobacteriosis cases is always among men, but the reverse is true in salmonellosis cases. These differences are highly significant. A point of note is that the publication format of the data, rate or number of cases can mask or mitigate the gender effect, as mentioned above, because of the sex ratio of the population.

**Seasonal effect: a higher number of cases reported in summer**

Figure 6 shows the distribution of averages as a percentage of gastrointestinal campylobacteriosis and salmonellosis cases reported in each month of the year in six countries between 2000 and 2009: Iceland (39), Norway (42), Finland (36), England and Wales (1999–2008) (27), Australia (28) and New Zealand (43). The data for countries in the southern hemisphere were of course synchronised. The month effect and month*country interaction are highly significant for both zoonoses (P < 0.0001).

Variations over the year are more pronounced for gastrointestinal campylobacteriosis than for salmonellosis, particularly in Scandinavian countries. While cases of both these zoonoses peak in the summer months, the spike in salmonellosis cases is spread more evenly across countries. This average trend confirms the findings of Nylen et al. in 2002 (50) in an analysis of data expressed as the number of campylobacteriosis cases per week in nine European countries and New Zealand over the period 1993–1997. These authors also found slight differences between countries in the exact time at which this spike in cases occurs, but were unable to explain these variations.

Possible explanations for this rise in the number of cases of gastrointestinal campylobacteriosis in summer may be that there is a higher food contamination status (frequency and level) in the summer and/or that there is more consumer exposure owing to a change in culinary practices in the summer months, i.e. practices that encourage cross-contamination. Very little data is currently available on seasonal variations in the contamination status of different foods. The few data that exist refer to flocks of broiler chickens in Scandinavia (51), Lower Saxony (Germany [52]) and France (53), with the number of positive cases detected in chickens on the farm rising in summer. However, the number of human cases spikes earlier in the summer.
season than the spike in chicken infections! This makes it more likely that increased consumer exposure stems from changes in cooking practices in summer. Indeed it is a period when foodstuffs are often cut for eating raw (salads) or prepared for barbecuing. It is commonly believed that, when cooked on the barbecue, contaminated meat may not be heated to a high enough temperature to destroy the bacteria. However, Campylobacter spp. have little resistance to even moderate temperatures (54, 55); moreover, meat becomes contaminated mainly on the surface (56), where it is supposedly well cooked, so it is unlikely that the bacteria are not killed. Recontamination of barbecued food would provide a better explanation for this increased consumer exposure. Indeed, there is potential for secondary contamination or cross-contamination with Campylobacter spp. from contaminated inert surfaces (21, 22, 57, 58). Placing grilled meat on the same dish or chopping board used for raw food, without washing it first, therefore appears to be a risk factor. The assumption that it is mainly young adults who engage in such practices in the summer might explain the high incidence of campylobacteriosis in the 20–30 age group, as mentioned earlier. The authors found no reference to confirm or refute this hypothesis.

**Campylobacter species involved: clearly identifying the hazard to better target the risk**

Paradoxically, there is little data of interest on the identification of the Campylobacter species involved in reported cases of gastrointestinal campylobacteriosis. This lack of systematic identification poses two problems for risk assessment: the first is that cases associated with C. fetus, which is responsible for septicaemia and is not transmitted to humans by ingestion, might be amalgamated with the foodborne zoonosis group; the second is that the involvement of the C. jejuni species might be over-reported owing to the false analogy ‘gastrointestinal campylobacteriosis = C. jejuni’. Despite the fact that Australia and New Zealand have a highly active system for recording cases of gastrointestinal campylobacteriosis, they do not try to identify individual Campylobacter species. Other countries automatically associate all cases of gastrointestinal campylobacteriosis with C. jejuni. While estimates by Vaillant et al. (2004 [15]) confirm that the proportion of gastrointestinal campylobacteriosis in France is around 80% of all reported cases of campylobacteriosis and it is possible to make a differential medical diagnosis between the forms related to C. fetus and the thermophilic species, it is important to properly identify the four thermophilic species involved in gastrointestinal campylobacteriosis by individual species. This is because, first, the clinical picture of gastrointestinal campylobacteriosis is not enough in itself to make such a differential diagnosis between bacterial species and, second, this differential diagnosis will contribute to the sound management of animal reservoirs and characterisation of the contamination status of foodstuffs.

The useful data available are European data provided by the European Food Safety Authority (EFSA) and European Centre for Disease Prevention and Control (ECDC) (2, 49).

A point of note is that the distributions obtained, presented as more or less rounded percentages, vary slightly between these two sources even though, in principle, the percentages correspond to the same epidemiological unit. In 2009, barely half of the 198,252 confirmed cases of campylobacteriosis were identified to species level (Figure 7). Although C. jejuni is the species most frequently identified, its involvement is confirmed in only 36.4% of cases. The simplistic equation ‘gastrointestinal campylobacteriosis = C. jejuni’ is therefore unacceptable. Campylobacter coli is the second most common species involved (2.5% of identified strains), followed by C. lari (0.19%) and C. upsaliensis (0.01%). A full 10% of identified bacteria are associated with ‘other’ species, especially C. fetus.

France is where the widest diversity of Campylobacter species isolated in patients is reported. However, these identifications relate only to strains sent to the National Reference Centre in Bordeaux (59), which is a small proportion of all the strains involved in infections (7). Of the 20,000 strains isolated from patients suspected of campylobacteriosis and analysed over the period 2001–2009, 6% could not be identified, 0.42% were Arcobacter butzleri, and others belonged to the genera Arcobacter (cryaerophilta) or Helicobacter (canadensis, cinaedi, pullorum, pylori), which are very close to the Campylobacter genus. The confirmed Campylobacter species included: C. jejuni (74.0%), C. coli (14.7%), C. fetus (4.1%), C. lari (0.38%), C. upsaliensis (0.10%) and a few individuals of other species (C. concisus, C. hyointestinalis, C. sputorum).

**Fig. 7**

Distribution of confirmed campylobacteriosis cases by bacterial species, in 2009, for the European Union
Quantitative data on the bacterium

The data analysed by the authors on the incidence of animal and food contamination and the distribution among the main Campylobacter species was the weekly data recorded in Thomson Reuters Web of Knowledge (‘All Databases’, Topic=(campylobacter)). In order for data to be used, the results had to be presented in a digital form explicit enough to be integrated into a spreadsheet and must have been obtained from a minimum number of samples. For a description of the situation in terms of contamination frequency, the 350 selected references (1,118 lines in the database) were divided into homogeneous groups comprising a minimum of 20 samples. For the distribution among Campylobacter species (366 lines in the database, 190 references), the authors accepted batches of ten samples. Despite these constraints, the database used (as of July 2011) totalled more than 400 references.

In order to process aggregate data, it was necessary to form groups to limit the number of modalities. These groups, which depend on the characteristic studied, are the result of initial analyses not presented in this article.

Contamination frequency of animals, food and the environment: thermophilic Campylobacter, a bacterium of the gastrointestinal tract

Overall, the average detection frequency of Campylobacter is: 39% in the intestinal contents of animals; 32% in food and 22% in the environment. However, this level of analysis does not enable the food health risk to humans to be ascertained, nor does it allow the contamination status of different food supply chains to be characterised precisely. Therefore, the authors sought to separate the data on the intestinal carriage of Campylobacter by different farm animal species from the data on the detection frequency of the bacterium in foodstuffs. However, knowledge of the bacterium’s distribution in the ‘environment’ of humans, animals and foodstuffs is useful for identifying possible routes of cross-contamination. The data analysis was therefore split into different levels:

– The first level relates to the animal species and its role in society. So the authors separated farm animals (mammals and birds) from other mammals and birds, i.e. wildlife and companion and entertainment animals. Within the farm animals’ group, a distinction was made between mammals and birds because very different processes are used to produce and process these two types of animal, especially at the slaughter stage.

– The second level of data analysis relates to the foodstuff itself, with an initial distinction between meat and other food products. In ‘other food products’, two groups were formed: the SF group = Seafood (fish and shellfish) and the MF = Miscellaneous Foods group (fruit and vegetables, dairy products, egg products and ready meals). In the case of meat, it was necessary to distinguish between the animal species from which the meat was derived, as well as the stage in the supply chain at which the bacteria was detected (information gleaned from the type of sample). The authors therefore distinguished data on ‘Animal intestinal carriage’ obtained from samples of faeces or intestinal contents (A) from data on the detection of the bacterium at the ‘Consumer’ food (C) stage. The latter group includes detection data relating to the carcass and to food at the distribution stage;

– Lastly, the Env group corresponds to measurements performed in the Environment at large, from farm to fork, as well as in sand or recreational waters.

The authors were able to distribute the available data into five mammal groups:

C = Cattle
P = Pigs
F = other Farmed mammals
Pe = companion animals (or Pets, dogs and cats)
M = wild Mammals

and three bird groups:

Ch = Chickens
Po = Poultry (other than chicken)
W = Wild birds (avifauna);

The authors obtained a total of 16 groups identified by a letter code, e.g. SF = Seafood, CA = Animal intestinal carriage by Cattle and CC = detection on Consumer meat from Cattle (beef). The spread of results and the numbers in these 16 groups are shown in Figure 8. Given the technical difficulties of detecting and identifying Campylobacter mentioned earlier, it may be assumed that the spread of these data is to some extent related to differences in the conditions and methods (sensitivity) of studies. Nevertheless, given the numbers in the groups, the authors believed it was reasonable to base their analysis on mean values.

To clarify these results, the authors conducted an analysis of variance. The averages are shown in Figure 9. On average, beef and miscellaneous foods are the least frequently contaminated groups. However, individual intestinal carriage by pigs and the various poultry species is significantly more frequent (between 48% and 68%) than other animals, farmed or otherwise (< 33%). However, meat from poultry, especially broiler chickens, appears to become contaminated significantly more often than pork (57% compared with 17%). Lastly, seafood and the environment have the same average contamination
frequency of around 20%, showing that *Campylobacter* should not be considered an ‘environmental’ bacterium, even though it may be detected in the environment!

This level of paired analysis (hazard/foodstuff–animal species) is useful because it can provide an estimate of the bacterial transfer rate from a carrier animal to its carcass. This transfer rate quantifies both the carriage incidence of slaughtered animals and the control of good hygiene practices at the processing stage (60). Indeed, it is now recognised that the primary contamination of meat by *Campylobacter* occurs as a result of poor control of certain slaughter operations, by transferring bacteria from the intestinal reservoir of animals to the surface of the still-warm carcass muscle. Therefore, calculating the ratio of average prevalence between the animal stage and the consumer meat stage, for the four groups of farm animals considered, provides an estimate, albeit crude, of the degree of bacterial
transfer in these production sectors. The transfer rates of 0.16 and 0.24 for cattle and pigs respectively are much lower than for poultry (0.60), especially chickens, whose 1.17 rate would even indicate spread of contamination while processing the animal carcass.

**Thermophilic Campylobacter species detected in food supply chains, in wild or companion animals and in the environment**

As with the analysis of the species involved in gastrointestinal campylobacteriosis cases, the Campylobacter species detected are not systematically identified, especially in foodstuffs. The authors therefore considered separately the three species most often associated with cases: C. jejuni, C. coli and C. lari. The authors grouped the values found for C. upsaliensis with those for C. helveticus, as these species are very similar on a bacteriological level (61). Figure 10 shows the spread of results for each of the four thermophilic Campylobacter species, for the full set of 381 data collected.

Overall, the average detection frequencies of thermophilic Campylobacter species from all sources were found to be: 58.3% C. jejuni; 29.2% C. coli; 3% C. upsaliensis and C. helveticus; and 2.7% C. lari. For the four species considered, the reported results varied from practically 0% to 100%. The reason why the sum of averages is only 93.2% is that some bacteria were either not identified or belonged to species that were not selected for analysis.

In view of the high variability observed and the small number of available values, additional data groupings needed to be made in order to describe identification frequencies. As food contamination in animal production sectors usually occurs when bacteria are transferred from the main source (the gastrointestinal tract of animals) to the environment by cross-contamination, the authors collected the Campylobacter identification data obtained for each bacterial species relating to both the animal and the foodstuff, as well as the data obtained from samples taken from the environment of the animal species concerned. It is important to note that, to date, this data grouping rationale is somewhat imposed by the degree of characterisation of Campylobacter studies. As most studies seek to estimate the bacterium’s prevalence, they tend to define detection on the basis of the type of sample and/or stage in the foodstuff’s supply chain. In contrast, studies that identify bacterial species do so globally on all isolates, with a loss of information on their source (2, 62).

In the case of mammals, the authors retained the groups Pigs (P, n = 53) and companion animals, dogs and cats (Pe, n = 17) but combined the cattle and other farmed Mammals (M, n = 89) groups and excluded from the calculations data on wild mammals, as this group contained...
only four species. In the case of birds, the authors grouped together all consumer Poultry (Po, n = 162) and retained the Wild birds (W, n = 21) group. They formed a ‘Miscellaneous’ (Mi, n = 20) group by consolidating results for miscellaneous foods (n = 6), seafood (n = 3) and the environment (n = 11). The results of the corresponding analysis of variance are shown in Figure 11.

Except in the ‘pigs’ and ‘companion animals (Pe)’ groups, the leading species identified was C. jejuni, with a maximum of 72% in the ‘poultry’ supply chain. The species most frequently identified in the ‘pigs’ group was C. coli (80%) and, in the ‘companion animals (Pe)’ group, it was the species C. upsaliensis and C. helveticus (61% of cases, associated respectively with dogs and cats [61]). The identification frequency of C. lari was significant only in wild birds (18%) and other samples (15%). However, the authors hasten to point out that the high value (71%) identified in miscellaneous foods relates to a single result obtained from mussels and oysters (63) and that the results reported for wild birds relate primarily to waterfowl (64). In addition, one of the four data for ‘wild mammals’ refers to a population of seals (65) which, with 26% C. lari, confirms the ‘aquatic’ nature of this species.

Other specific associations can be observed: C. hyointestinalis in reindeer (66); C. laminae in cattle (67); C. insulaenigrae in marine mammals (68). Caution is required because this ‘Campylobacter species/host animal species’ association is not the only one! The development of molecular biology methods, which are more specific than conventional biochemical and bacteriological methods, has brought to light the animal intestinal carriage of several Campylobacter species (69, 70).

### Conclusions

It has become necessary to provide key quantitative data for the science-based risk assessment of gastrointestinal campylobacteriosis in industrialised countries, in order to develop sound measures for controlling this risk. Given the current difficulties in obtaining ‘standardised’ data on foodborne infectious diseases, for the hazard-characterisation phase the authors chose to carry out a comparative analysis between data on gastrointestinal campylobacteriosis and on salmonellosis, which has been the subject of surveillance and collective control measures for many years. In the five industrialised countries with complete data for these two hazards covering a period of 20 years, the annual number of reported cases of gastrointestinal campylobacteriosis per 100,000 inhabitants now outstrips that of salmonellosis. The higher incidence of cases would seem to be attributable to more frequent exposure to thermophilic Campylobacter species in young children (under 5 years of age) and men of between 20 and 30 years of age during the summer months. While the causes of this increased exposure are not always clearly identified, it does not appear to stem from more frequent primary contamination of foodstuffs, including meat. The magnitude of the animal intestinal reservoir means that meat from all species of farm animal has the highest likelihood of becoming contaminated when control of good hygiene practices at the processing stage is poor. Risk analysis should not be confined to the C. jejuni/poultry meat pairing because improvements in identification specificity have shown that the ‘Campylobacter species/host animal species’ association is not the only one. Unfortunately, to date, there is not enough data to accurately describe the contamination status of foodstuffs (taking into account frequency, level of contamination and bacterial species) in accordance with their specific supply chain. Better characterisation would make it possible to identify not only the critical points of contamination (primary and secondary) and the spread of the hazard through the food chain to the consumer’s plate, but also any specific capacities of survival, adherence and transfer in Campylobacter species.
References and websites accessed


