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REVIEW ARTICLE

Meta-analysis of the prevalence of thermotolerant *Campylobacter* in food-producing animals worldwide

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Abstract

The objective of this meta-analysis was to summarize available information on the prevalence of thermotolerant *Campylobacter* (TC) in different food-producing animals worldwide. Databases (i.e., PubMed, ScienceDirect, Scopus) were searched from 1980 to 2017 unrestricted by language. The inclusion criteria were as follows: prevalence or incidence studies, published in peer-reviewed journals, and they must have reported the total number of animal samples studied and the number of samples that were positive for the presence of TC. When the identification of *Campylobacter* species was available, this information was included in the analysis. Multilevel random-effect meta-analysis models were fitted to estimate mean occurrence rate of TC and to compare them among different factors potentially associated with the outcome. The mean occurrence rate of TC in food-producing animals was 0.424 (95% CI: 0.394–0.455), and the mean occurrence rate of *Campylobacter jejuni* and *Campylobacter coli* were 0.214 and 0.133, respectively. Pigs and poultry showed the highest prevalence of TC; however, there were differences in the prevalence of each *Campylobacter* species. *Campylobacter jejuni* was observed in broilers (0.322; 95% CI: 0.273–0.377) and hens (0.395; 95% CI: 0.265–0.542), while *C. coli* was restricted essentially in pigs (0.553; 95% CI: 0.541–0.650). The prevalence of *C. jejuni* in intensively bred cattle was higher (0.302; 95% CI: 0.227–0.389) than the prevalence in extensively bred cattle (0.172; 95% CI: 0.119–0.242) while the prevalence of *C. coli* was similar (0.051; 95% CI: 0.028–0.091 vs. 0.050; 95% CI: 0.027–0.091) in both production systems. Agar with or without blood used for the isolation of TC did not affect the prevalence observed. The method of species identification did not seem to generate differences in the prevalence of *Campylobacter* species. The prevalence of *Campylobacter* in primary food production has a strong impact on the entire agri-food chain. National authorities must monitor the situation with the aim to establish the appropriate risk management measures.

KEYWORDS
food-producing animals, meta-analysis, prevalence, thermotolerant *Campylobacter*

1 | INTRODUCTION

Thermotolerant *Campylobacter* (TC) is a common foodborne pathogen of humans worldwide (Epps et al., 2013). The incidence of campylobacteriosis has increased in recent years in many countries (Kaakoush, Castaño-Rodríguez, Mitchell, & Man, 2015). In addition, *Campylobacter* spp., and especially *Campylobacter jejuni* and *Campylobacter coli*, are the most important cause of acute gastroenteritis and traveller's diarrhoea in people all over the world (Jorgensen et al., 2011).

Campylobacter is normally found on farms without causing health problems or economic losses. Moreover, this pathogen is commonly found in the intestinal tract of food-producing animals, especially in broilers, and is transferred to the skin during slaughter and processing (Zbrun et al., 2013). Although the presence of TC has been associated primarily in broilers, other food-producing animals also contribute to the epidemiology of these pathogens and for that reason the study of their prevalence is important. Animal contamination by *Campylobacter* spp. begins at the farm level and human infections increase as the prevalence in animals increases (Humphrey, O'Brien, & Madsen, 2007; Signorini et al., 2013). The presence of TC in animal food products increases the spread to other foods through cross-contamination along the agro-food chain and inadequate hygienic manipulation by consumer mainly at home (Signorini et al., 2013). Food consumption and direct contact with farm animals have been reported as the most important sources of human campylobacteriosis (Studahl & Andersson, 2000).

To reduce the risk of human exposure to TC, it is essential to establish risk management measures to reduce contamination in food-producing animals. Therefore, it is essential to understand the epidemiology of infection in animals (Bull et al., 2006). In this sense, a meta-analysis is a highly valuable statistical tool whose objective is to synthesize, integrate and contrast the results of a large number of primary studies that investigate the same questions. In addition, when it is necessary that quantitative comparisons are made worldwide, meta-analysis becomes an essential tool. The objective of this study was to quantitatively summarize and compare the occurrence of TC in food-producing animals worldwide, which may be used as a basis for risk management measures in public health.

Impacts

- *Campylobacter* spp. and especially *Campylobacter jejuni* and *Campylobacter coli* are the most important cause of acute gastroenteritis and it is one of the main cause traveller's diarrhoea in people all over the world.
- The objective of this meta-analysis was to summarize available information on the prevalence of thermotolerant *Campylobacter* (TC) in different food-producing animals worldwide.
- Higher prevalence of TC was observed in different food-producing animals. *Campylobacter jejuni* was especially prevalent in poultry (broilers hens and other farm birds) while *C. coli* was isolated predominantly in pigs.

2 | MATERIALS AND METHODS

2.1 | Criteria for study selection

The scientific papers included in the meta-analysis were selected based on the following criteria: they should include at least one observational study (prevalence or incidence studies) and published in peer-reviewed journals, between 1980 and 2017. When different animal species have been included in one scientific paper, each animal species was included separately in the meta-analysis. Similarly, when a scientific paper reported the results derived from different conditions (i.e., systems of animal production, country of origin, prevalence estimation in different years), each condition was considered as an individual outcome. Therefore, each scientific article may contain more than one outcome.

Studies must have reported the total number of animal's samples studied (population) and the number of samples that were positive for the presence of *Campylobacter* spp. When the identification of *Campylobacter* species was available, this information was included in the analysis. Assorted reviews, duplicated reports, trials where the samples were artificially contaminated with *Campylobacter*, non-peer-reviewed articles (i.e., thesis, opinion articles, editor letters), assay where non-food-producing animals were included, and randomized controlled trials were excluded.

2.2 | Outcomes and definitions

The prevalence or incidence of TC and its species (*C. jejuni* and *C. coli*) was calculated from the number of positive samples over the total number of samples. The population of study was the type of food-producing animal investigated in each study.

2.3 | Data sources

Scopus, PubMed and ScienceDirect databases were searched for scientific papers unrestricted by language published from 1980 to 2017. Search terms included "prevalence" or "incidence" and "*Campylobacter*." The abstracts were assessed and the scientific papers that met the a priori inclusion criteria were selected. Preliminary screening of titles and abstracts was carried out for eligibility and relevance to this scientific paper according to the inclusion and exclusion criteria.

2.4 | Data extraction

Information on the study design, country, year in which the study was conducted, animal sampled, type of samples, origin of the samples,

methodology to isolate and confirm the *Campylobacter* identity and the outcomes (number of animals positive to TC and total animal sampled) were extracted from each scientific paper. However, no scores were used to exclude studies (Lean, Rabiee, Duffield, & Dohoo, 2009).

2.5 | Statistical analysis

Statistical analysis was performed used Comprehensive Meta-Analysis software version 2.2 (2011). Due to the measured outcome being binary (i.e., an animal tests either positive or negative for the pathogen) and is given only for single groups, the only possible parameter to measure effect size is the raw proportion *p* (with 95% confidence intervals—CIs) using a random effects model (Borenstein, Hedges, Higgins, & Rothstein, 2009). A cumulative meta-analysis was performed to display how the outcomes shift as a function of the year of publication. Meta-regression allows assessing the relationship between years of publication and TC prevalence. A priori subgroup analyses were planned depending on factors that could potentially influence the prevalence of TC: (a) Continent of origin; (b) Food-producing animal species; (c) Type of sample (faeces and liver); (d) Sampling site (slaughterhouse, feedlot and farms); (e) Method of isolation (medium with or without blood); and (f) Methodology to identify *Campylobacter* species (PCR and biochemical methods).

Heterogeneity among studies was assessed using the DerSimonian and the Laird test (*Q*-statistic). The degree of heterogeneity was quantified with the inconsistency index (I^2-statistic; Higgins & Thompson, 2002). A sensitivity analysis was completed to assess the robustness of the meta-analysis results. Sensitivity analyses have also been used to examine effects of studies identified as being aberrant or highly influential on the analysis outcome (Lean et al., 2009). This consisted of completing the same analysis, but dropping one study in each iteration.

An adjusted rank correlation test using the Egger method (Egger, Smith, Schneider, & Minder, 1997), Begg's test (Begg & Mazumdar, 1994) and the fail-safe N method (to calculate the number of studies that would have been needed to reverse the effect) were used to assess publication bias.

3 | RESULTS

3.1 | Excluded studies

The literature yielded 6,879 scientific papers using the terms "*Campylobacter*" and "Prevalence" or "Incidence." Reviews, prevalence studies in humans or in wild animals or pets, randomized controlled experiments, prevalence in animal foods, studies about laboratory techniques and studies without enough data to estimate the prevalence were excluded (*n* = 6,500; Figure 1).

3.2 | Overview of included prevalence studies

One-hundred and twenty-five of the 6,879 screened scientific papers met all inclusion criteria to estimate the *Campylobacter* spp. prevalence (with 268 prevalence or incidence outcomes), while 124 scientific papers (with 173 prevalence or incidence outcomes) and 125 scientific papers (with 165 prevalence or incidence outcomes) were included in the evaluation of *C. jejuni* and *C. coli*, respectively.

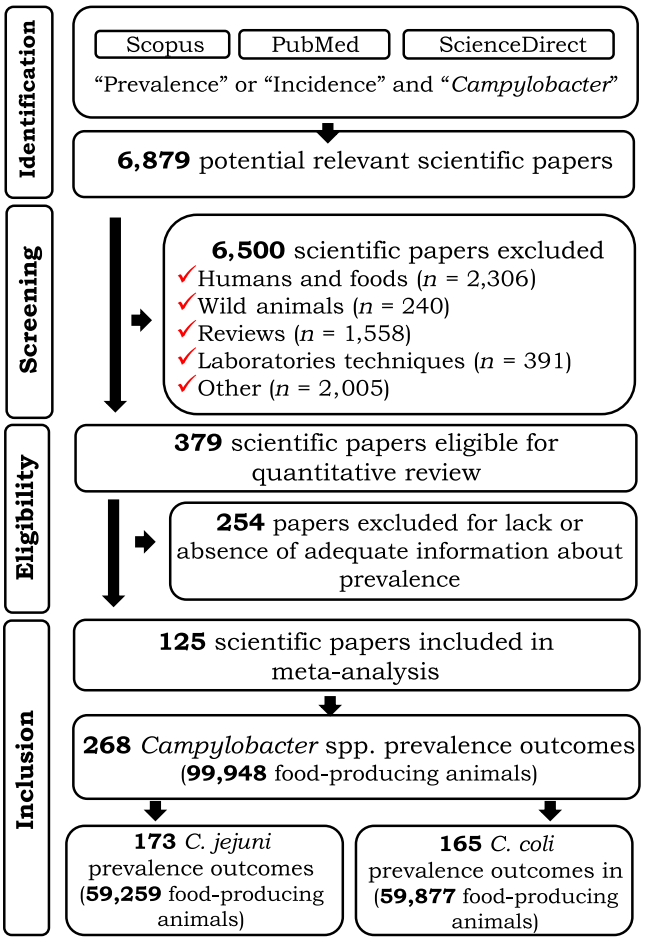

FIGURE 1 Flow diagram of selected studies included in the meta-analysis [Colour figure can be viewed at wileyonlinelibrary.com]

Of the outcomes, which estimated the prevalence of *Campylobacter* spp., 45 were conducted before 2000, 130 between 2000 and 2010, and the remaining 93 after 2010. The outcomes were conducted in 47 different countries from all the continents: Africa 17 outcomes, Asia 48 outcomes, Europa 116 outcomes, Latin America 12 outcomes, North America 55 outcomes and Oceania 13 outcomes. The other seven outcomes included information from more than one country and they were from different continents.

For *C. jejuni*, a total of 173 prevalence outcomes were included, with 51 outcomes conducted before 2010 (27 outcomes conducted before 2000) and 122 after 2010. Finally, a total of 165 *C. coli* prevalence outcomes were included, with 41 outcomes conducted before 2010 (22 outcomes conducted before 2000) and 124 after 2010.

3.2.1 | Thermotolerant *Campylobacter* prevalence

Of the 125 scientific papers that met the inclusion criteria, 268 outcomes of prevalence or incidence (99,948 food-producing

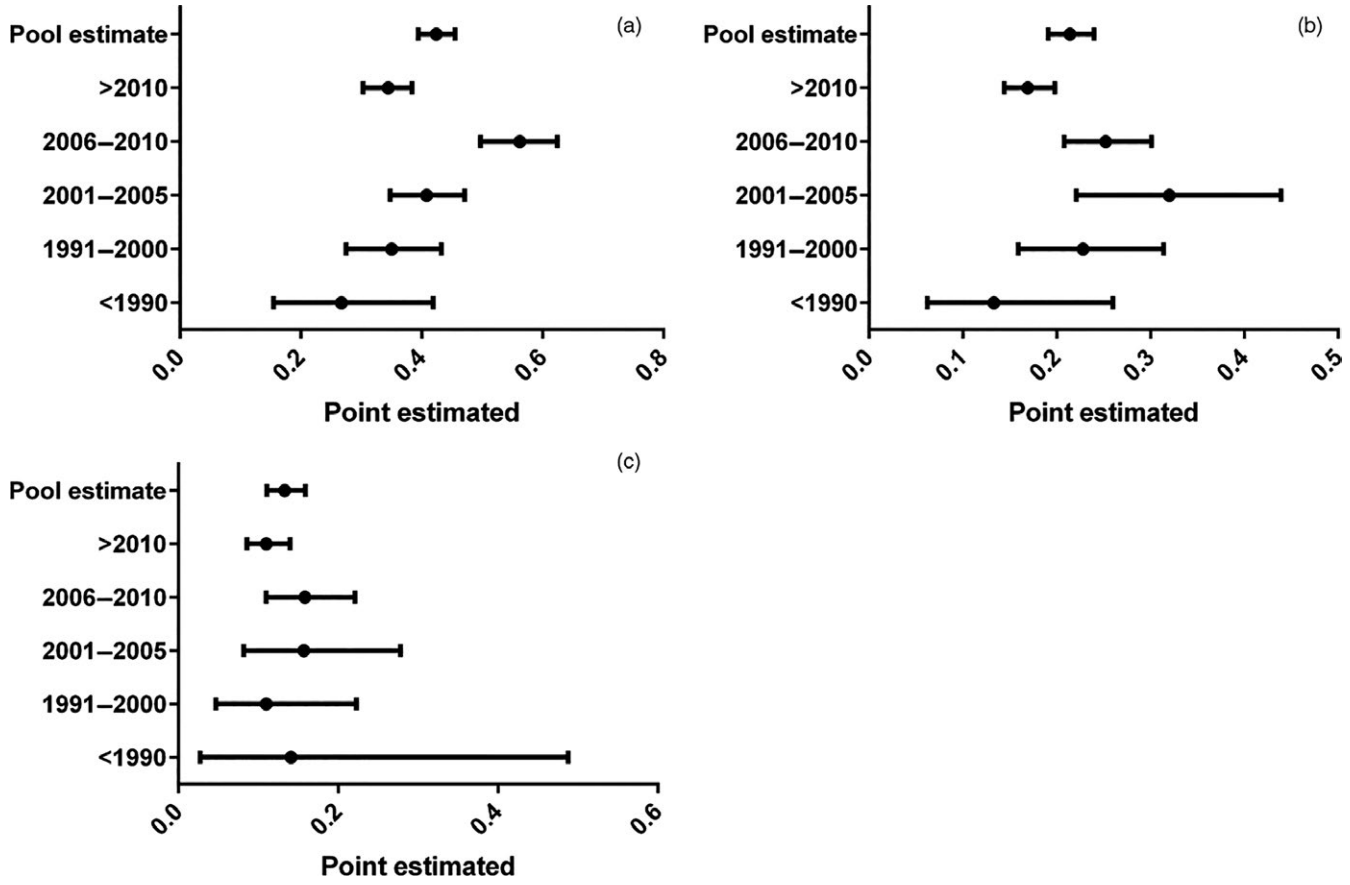

FIGURE 2 Subgroup analysis comparing the prevalence of thermotolerant *Campylobacter* over the years in food-producing animals. (a) *Campylobacter* spp.; (b) *Campylobacter jejuni*; (c) *Campylobacter coli*

animals included) were identified. The pooled prevalence estimate of *Campylobacter* spp. was 0.424 (95% CI: 0.394–0.455). Significant heterogeneity was observed across the 268 outcomes (Q-statistic: $p < 0.0001$; I^2-statistic = 98.28%).

A total of 124 scientific papers met the inclusion criteria, and 173 outcomes of prevalence or incidence of *C. jejuni* (59,259 food-producing animals included) were identified. The pooled prevalence estimate of *C. jejuni* was 0.214 (95% CI: 0.191 to 0.240). Significant heterogeneity was observed across the 173 studies (Q-statistic: $p < 0.0001$; I^2-statistic = 97.12%).

Finally, 125 scientific papers met the inclusion criteria and 165 outcomes of prevalence or incidence of *C. coli* (59,877 food-producing animals included) were identified. The pooled prevalence estimate of *C. coli* was 0.133 (95% CI: 0.111–0.159). Significant heterogeneity was observed across the 165 studies (Q-statistic: $p < 0.0001$; I^2-statistic = 98.19%).

3.2.2 | Evolution of thermotolerant *Campylobacter* prevalence throughout the period analysed

In this meta-analysis, we considered the year of publication instead of the year when the study was conducted. Normally, the year of publication of a scientific article is usually close (2 or 3 years) to the year in which the study was conducted.

The prevalence of *Campylobacter* spp. in all the food-producing animals including in this meta-analysis was different according to the year of publication (Figure 2a). The prevalence of *Campylobacter* varied from 0.267 to 0.562 in the period analysed. The highest prevalence was observed in the studies published in the period 2006–2010 (p-estimate 0.562; 95% CI: 0.497–0.624; $p < 0.001$). This pattern was observed when considered the prevalence among poultry and bovine, but the prevalence among pigs was the same throughout the years of published ($p = 0.479$). However, the cumulative analysis and meta-regression analysis did not show any evidence that the prevalence shifted over time (Table 1) for *Campylobacter* spp. or either subtype reviewed.The prevalence of *C. jejuni* in all the food-producing animals including in this meta-analysis was different

TABLE 1 Summary of random weighted meta-regression analysis for year of publication as independent variable and the prevalence of *Campylobacter* isolates from food-producing animals as outcome variable

Campylobacter specie	Intercept[a]	Slope	*p*-value
Campylobacter spp.	−13.68	0.0067	0.4227
Campylobacter jejuni	30.85	−0.0160	0.0852
Campylobacter coli	31.21	−0.0165	0.2687

[a]Intercept: constant in the model.

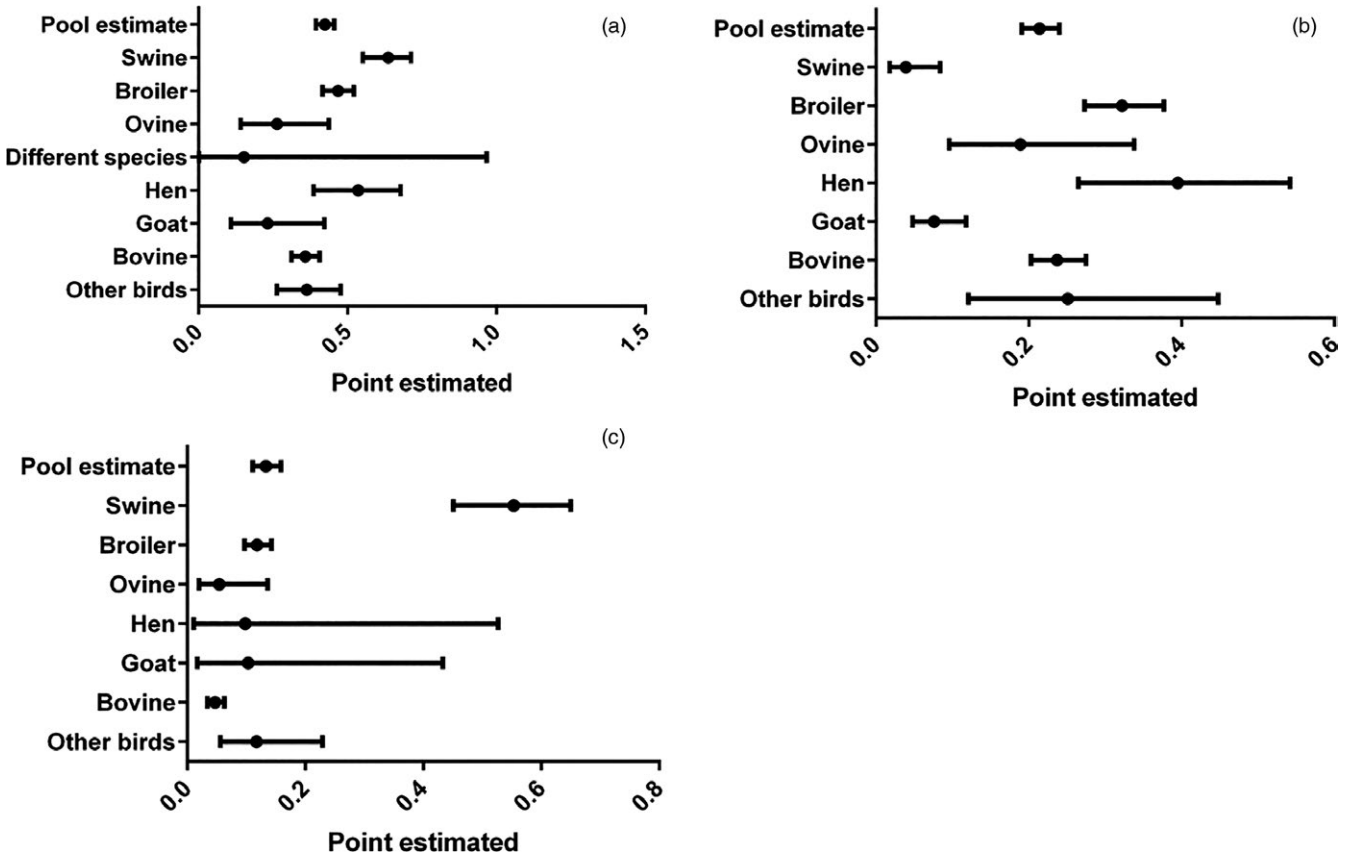

FIGURE 3 Subgroup analysis comparing the prevalence of thermotolerant *Campylobacter* across the food-producing animal's species. (a) *Campylobacter* spp.; (b) *Campylobacter jejuni*; (c) *Campylobacter coli*

according to the year of publication (Figure 2b). The highest prevalence was observed in the studies published in the period 2001–2005 (*p*-estimate 0.320; 95% CI: 0.221–0.439; $p < 0.001$), and the prevalence of *C. jejuni* varied from 0.133 to 0.320 throughout the years of published (Table 1). Contrary to the observed prevalence of *Campylobacter* spp. and *C. jejuni*, the prevalence of *C. coli* in all the food-producing animals included in this meta-analysis did not show differences according to the year of publication (Figure 2c; $p = 0.506$). The prevalence of *C. coli* varied from 0.110 to 0.158 throughout the years of published.

3.2.3 | Prevalence of thermotolerant *Campylobacter* in animal species

Pigs, hens and broiler samples showed the most important prevalence of *Campylobacter* spp. ($p < 0.001$). In contrast, ruminants (sheep, bovine and goats) were the food-producing animals sampled which presented the lowest prevalence (Figure 3a). Similar results were observed when the prevalence of *C. jejuni* was analysed. Hens and broilers samples showed the most important prevalence of *C. jejuni* ($p < 0.001$). In contrast, pigs and goats were the food-producing animals sampled which presented the lowest prevalence (Figure 3b). On the other hand, cattle showed the prevalence similar to the pooled prevalence.

Contrary, the most important prevalence of *C. coli* was observed in pigs ($p < 0.001$) for which the *p*-estimate was 0.553 (95% CI: 0.451–0.650). Additionally, the *C. coli* prevalence in the other food-producing animals presented pooled values lower than 0.118 (Figure 3c).

3.2.4 | Prevalence of thermotolerant *Campylobacter* across continents

Studies conducted in North America (*p*-estimate 0.557; 95% CI: 0.472–0.639) and Europe (*p*-estimate 0.457; 95% CI: 0.413–0.502) showed the highest prevalence of *Campylobacter* spp. ($p < 0.001$) while the lowest prevalence was showed in Oceania (*p*-estimate 0.294; 95% CI: 0.195–0.417; Figure 4a). However, the prevalence of *Campylobacter* spp. in broilers was the same in the different continents. Conversely, the prevalence of *Campylobacter* spp. in pigs was higher in the countries of North America (*p*-estimate 0.884; 95% CI: 0.788–0.939; $n = 9$), Asia (*p*-estimate 0.591; 95% CI: 0.340–0.802; $n = 8$) and Europe (*p*-estimate 0.564; 95% CI: 0.472–0.653; $n = 20$) in comparison with the countries of Africa (*p*-estimate 0.320; 95% CI: 0.163–0.532; $n = 3$). In the same way, the prevalence in bovines was higher in North America (*p*-estimate 0.596; 95% CI: 0.478–0.704; $n = 25$) and Europe (*p*-estimate 0.340; 95% CI: 0.295–0.389; $n = 26$) than in Oceania (*p*-estimate 0.190; 95% CI: 0.127–0.274; $n = 7$) and Asia (*p*-estimate 0.154; 95% CI: 0.088–0.255; $n = 10$).

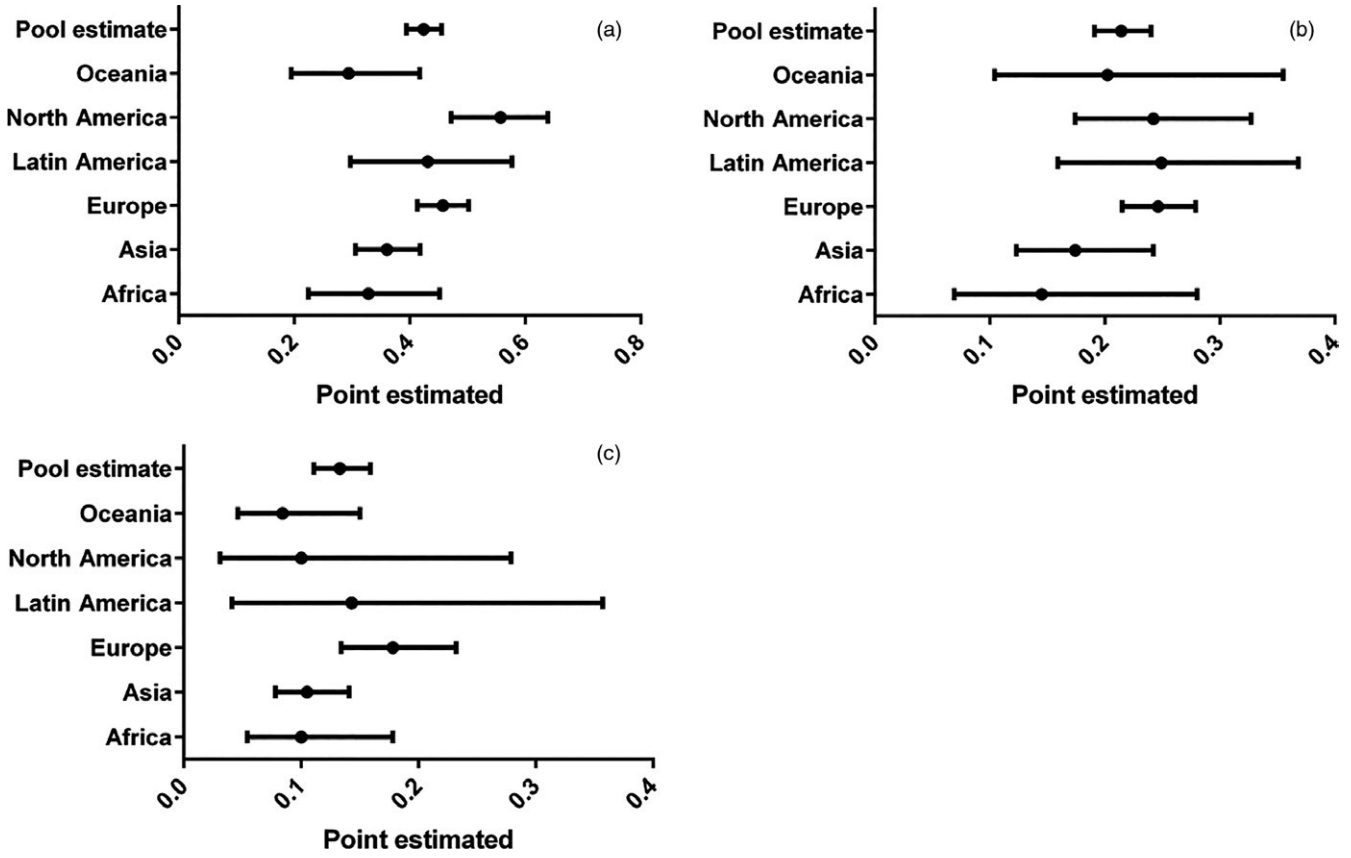

FIGURE 4 Subgroup analysis comparing the prevalence of thermotolerant *Campylobacter* across the continents in food-producing animals. (a) *Campylobacter* spp.; (b) *Campylobacter jejuni*; (c) *Campylobacter coli*

Studies conducted in Latin America, Europe and North America countries showed the highest prevalence of *C. jejuni* but they were not different compared with the prevalence estimated in the other continents ($p = 0.302$; Figure 4b). Similar results were observed when the prevalence of *C. coli* was analysed. Studies conducted in Latin America and in European countries showed the highest prevalence of this specie but they were not different compared with the prevalence estimated in the different continents ($p = 0.084$; Figure 4c).

3.2.5 | Prevalence of thermotolerant *Campylobacter* considering the site of sampling

Mostly, food-producing animals were sampled directly on farms. However, samples were also taken in slaughterhouses and in feedlot breeding systems (Intensive livestock system). The prevalence of TC in slaughterhouses was higher than the estimated average (p-estimate = 0.527; 95% CI: 0.452–0.601; $n = 35$). It was possible to identify differences ($p < 0.001$) in the *Campylobacter* spp. prevalence according to the site of sample being the highest prevalence in intensive systems like the feedlot (Figure 5a). For studies that included only bovines ($n = 76$), differences were examined by rearing extensive or intensively. The prevalence of TC in intensively bred cattle was higher (p-estimate = 0.500; 95% CI: 0.399–0.601; $n = 34$) than the prevalence in extensively bred cattle (p-estimate = 0.247; 95% CI: 0.188–0.317; $n = 21$; $p < 0.001$). In the remaining studies, it was not possible to obtain information to define the type of cattle rearing (p-estimate = 0.275; 95% CI: 0.227–0.328; $n = 21$).

On the other hand, the prevalence of *C. jejuni* was similar regardless of the site of sample ($p = 0.417$; Figure 5b). Considering only studies that included bovines ($n = 45$), the prevalence of *C. jejuni* in intensively bred cattle was higher (p-estimate = 0.302; 95% CI: 0.227–0.389; $n = 19$) than the prevalence in extensively bred cattle (p-estimate = 0.172; 95% CI: 0.119–0.242; $n = 14$; $p = 0.044$). In the remaining studies, it was not possible to obtain information to define the type of cattle rearing (p-estimate = 0.233; 95% CI: 0.190–0.282; $n = 12$).

Regarding *C. coli*, its prevalence was similar regardless of the site of sample ($p = 0.152$; Figure 5). Considering only studies that included bovines ($n = 37$), the prevalence of *C. coli* in intensively bred cattle was similar (p-estimate = 0.051; 95% CI: 0.028–0.091; $n = 15$) to the prevalence in extensively bred cattle (p-estimate = 0.050; 95% CI: 0.027–0.091; $n = 12$; $p = 0.354$). In the remaining studies, it was not possible to obtain information to define the type of cattle rearing (p-estimate = 0.035; 95% CI: 0.025–0.047; $n = 10$).

3.2.6 | Prevalence of thermotolerant *Campylobacter* considering identification method for species confirmation

There were not differences between the *Campylobacter* spp., *C. jejuni* and *C. coli* prevalence observed when the studies used the

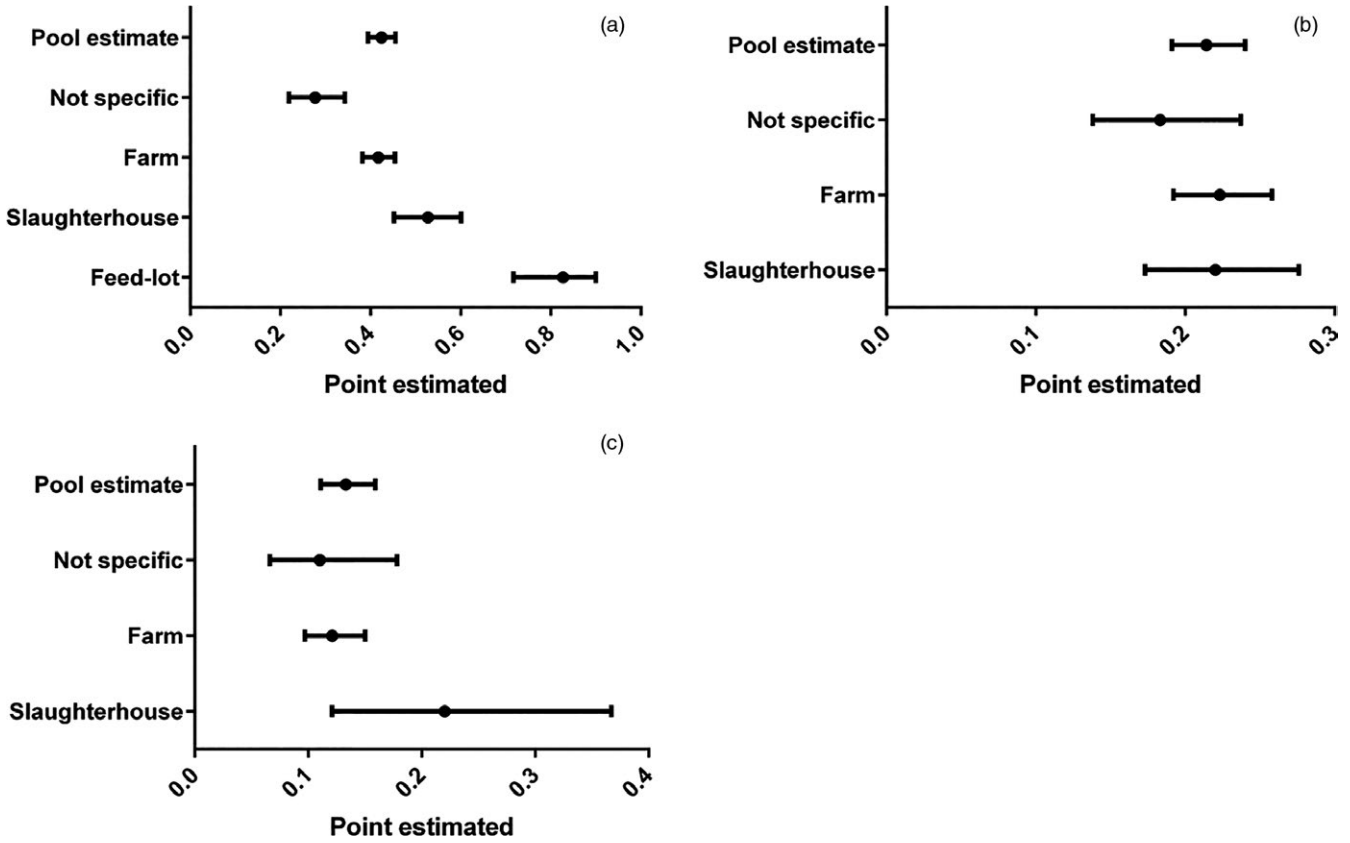

FIGURE 5 Subgroup analysis comparing the prevalence of thermotolerant *Campylobacter* in food-producing animals considering the site of sampling. (a) *Campylobacter* spp.; (b) *Campylobacter jejuni*; (c) *Campylobacter coli*

isolation agar with (i.e., Bolton, Skirrow Preston) or without blood (i.e., mCCDA; $p = 0.272$, $p = 0.716$ and $p = 0.163$, respectively).

The prevalence of TC was lower (p-estimate = 0.378) when biochemical methods were applied than prevalence based on PCR methods (p-estimate = 0.453; $p = 0.05$). Finally, the method of species identification did not seem to generate differences in the prevalence of *C. jejuni* ($p = 0.979$; Figure 6) and *C. coli* ($p = 0.403$; Figure 6).

3.2.7 | Publication bias

As part of this study, Egger´s regression test, Begg and Mazumdar rank correlation test and the fail-safe N method were used to detect publication bias in the included studies (Table 2). There was a general tendency in having few publication biases for most of the TC. However, the large number of scientific articles included in this meta-analysis provides valid results beyond the potential bias.

4 | DISCUSSION

The analysis of the available information in databases indicates that in the last decades, TC has become major foodborne pathogen in public health concern. Consequently, in the last 10 years there has been an increase in the studies focused on prevalence and incidence rates of TC in food-producing animals. Our meta-analysis showed that 42.4% of food-producing animals were colonized with TC. This result is important because the prevalence in live animals has a strong influence especially in the prevalence of meat products obtained from these animals (Zbrun et al., 2013). Thus, a high prevalence and wide range of animal reservoirs of TC were found.

Although in our study the prevalence of TC did not increase over the years, several reports indicate an increase in cases of human campylobacteriosis worldwide (EFSA, 2016; WHO, 2013). This could be due to the fact that data on human campylobacteriosis come from outbreaks or epidemiological studies which may present biases, especially the proportion of non-reported cases. An increase in the notification rate of cases could lead to a higher estimate of the prevalence without necessarily meaning a higher incidence of the disease. On the other hand, the increase in the incidence of human campylobacteriosis could also be due to improved surveillance and identification of the microbial agents causing foodborne diseases that were previously encompassed as acute gastroenteritis (Humphrey et al., 2007; Kaakoush et al., 2015).

Throughout the period analysed, it was not possible to identify a pattern in the prevalence of TC. This behaviour may be due to the application of inconsistent or sporadic (and often inappropriate) management measures in animal production systems (Economou et al., 2015). Interestingly, in recent years there has been an increase in the use of antimicrobials in animal breeding systems. The type of antimicrobial used, as well as the frequency and dose applied in animal

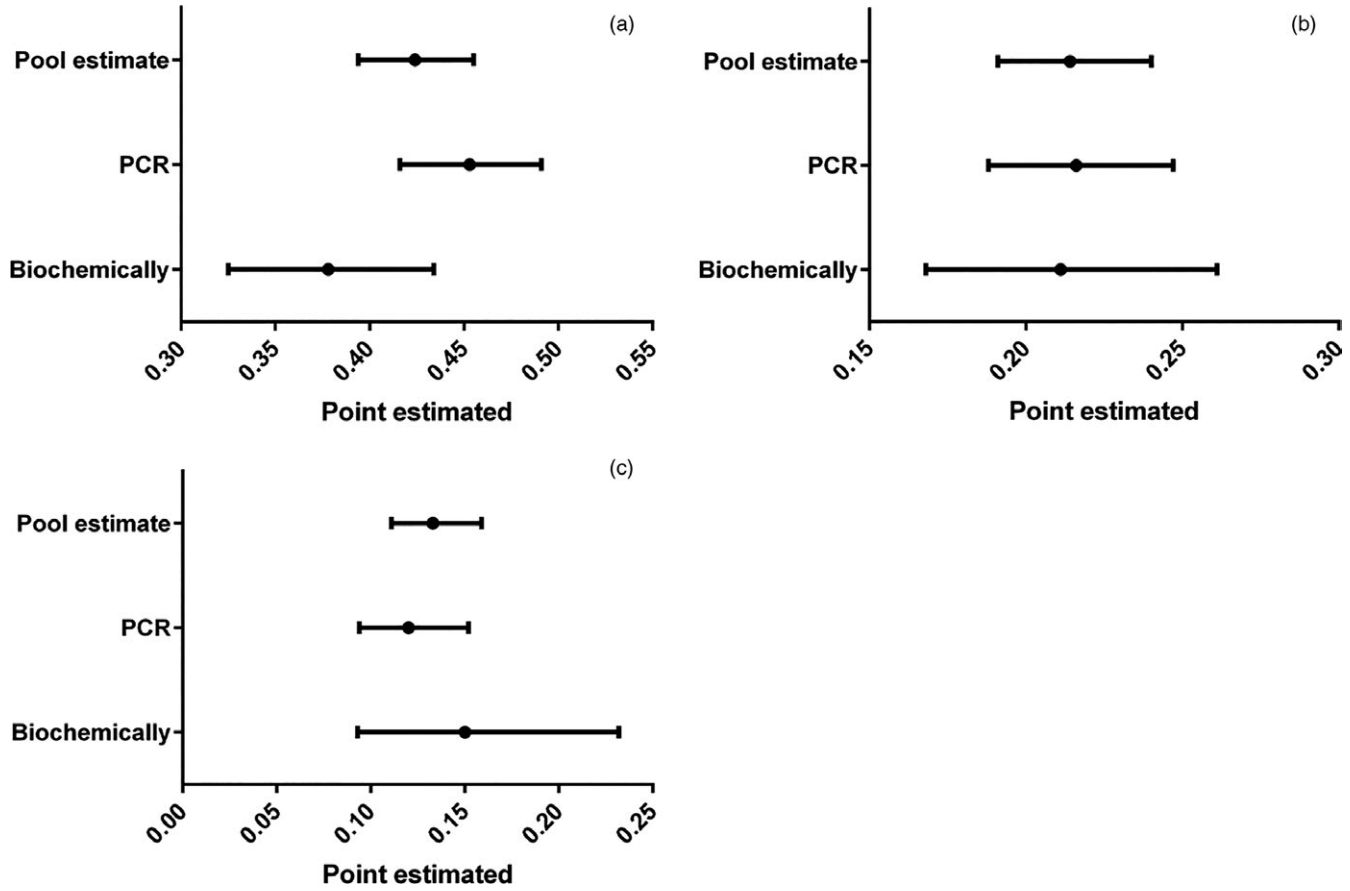

FIGURE 6 Subgroup analysis comparing the prevalence of thermotolerant Campylobacter considering the method. (a) *Campylobacter* spp.; (b) *Campylobacter jejuni*; (c) *Campylobacter coli*

TABLE 2 Results of publication bias detection

Response variable	Fail-safe N[a]	Begg and Mazumdar test	Egger's regression test	
			Intercept	*p*-value
Campylobacter spp	18	0.095	1.934	0.0034
Campylobacter jejuni	0	0.0019	−0.668	0.2883
Campylobacter coli	0	0.7394	−1.548	0.0469

[a]Number of studies required to reverse the effects are calculated on the condition of $p = 0.05$.

feed may explain, at least partially, the prevalence of Campylobacter in food-producing animals and the emergence of antimicrobial resistance in TC (Lévesque, Frost, & Michaud, 2007; Luber, Wagner, Hahn, & Bartelt, 2003; Signorini et al., 2018; Silbergeld, Graham, & Price, 2008; Wieczorek & Osek, 2015; Zbrun et al., 2015). The relatively stable prevalence of TC is accompanied by a gradual increase in the proportion of isolates resistant to antimicrobials, a phenomenon that became more evident in the last decade (Wieczorek & Osek, 2015).

The prevalence of TC was different according to the animal species analysed. In general, monogastric (mainly broilers and pigs) showed a higher prevalence than ruminants (cattle, sheep and goats). This may be because *Campylobacter* has a marked preference and adaptation to the colonization of certain animal species. Alternatively, it can be assumed that the prevalence is a reflection of the animal production system (Karesh et al., 2012). The intensification of animal production is observed mainly in broilers and pigs. It was observed that bovines reared in intensive systems tended to have a higher prevalence of TC than those reared extensively. Additionally, when cattle were bred in a feedlot, the prevalence was similar than the prevalence found in monogastric (which were reared mainly in intensive systems) (Horrocks, Anderson, Nisbet, & Ricke, 2009). Therefore, it is possible to consider that the prevalence of TC can be explained not only by a preference for specific hosts but also by the intensification of livestock production.

Another remarkable point is related to the higher prevalence of TC found in Europe and North America compared to the rest of the continents, especially in pigs. It is risky to propose a hypothesis to explain these results, although it is known that the intensification of livestock production systems have expanded throughout the world

and they are more common in developed countries than in those in development (Derner et al., 2017). Countries of North America, Asia and the European Union have the highest number of research studies related to the presence of *Campylobacter* along food chain and animal food products (CDC, 2014; EFSA, 2016). In the last 10 years, this increased number of studies due to campylobacteriosis has become the most often reported zoonotic foodborne disease in the world. These countries have developed surveillance programmes for TC and other enteropathogens that contaminate the food chain. These programmes provided epidemiological data and consequently show higher prevalence of *Campylobacter* (EFSA, 2016; Padungton & Kaneene, 2003). Available prevalence data of campylobacteriosis in Africa, Latin America and Oceania still remains incomplete and information about pathogens that cause diarrhoea is scarce. In addition, most diagnostic laboratories do not have adequate infrastructure, equipment and health workers for detection of TC.

In this meta-analysis, we observed that the prevalence of *Campylobacter* spp. in broilers was similar in all the continents (Figure 3). The pathogen/host relationship can explain this reported prevalence. A wide range of wild and domestic animals, especially poultry, have been recognized as reservoir of *Campylobacter* spp. (Newell, 2002). The gastrointestinal environment of the broiler is suitable for the colonization and multiplication of the TC and, consequently, it is a common source of the pathogen along the food chain (Han et al., 2017). Some virulence and survival determinants such as multidrug resistance, chemotaxis, flagella-mediated mobility, polysaccharide structures for invasion and adhesion allow colonization of the gastrointestinal tract (Bolton, 2015; Gao et al., 2017; Silva et al., 2011). In addition to the pathogen-specific characteristics, certain components of the animal cells and the intestinal environment contribute to multiplication and dissemination of TC species from the host animal.

Animals that arrived at the slaughterhouse had a higher prevalence (p-estimate = 0.527; 95% CI: 0.452–0.601; n = 35) of TC than the animals sampled on farms (p-estimate = 0.417; 95% CI: 0.382–0.454; n = 172; Figure 6). During animal transportation from farm to slaughterhouse, animal intestinal microbiota suffers changes due to the exposure to variety of stressors factors (Rostagno, 2009). These changes in the environment, such as feed withdrawal prior to transport and overcrowding of transport, may promote the growth of some intestinal microbial populations, to the detriment of others. In addition, a few weeks before slaughter, the antimicrobials used as growth promoters are removed from the feed to avoid residues in meats. TC would be favoured in these management practices, which would directly affect the prevalence found in the slaughterhouse prior to the slaughter. Consequently, the higher prevalence of *Campylobacter* in broilers in the slaughterhouse favours cross-contamination (Rostagno, 2009) during slaughter.

Regarding different isolation techniques, the method did not modify the prevalence of TC. The addition of blood in culture media seems to be not essential for *Campylobacter* isolation. Standardization of isolate methodology with the development of ISO-10272:2006 document and the massive use of PCR technique in last decades improved the detection of this pathogen and could explain the increase of *Campylobacter* prevalence.

However, results showed that the identification of the bacterial isolate (at the genus level) was more precise when PCR methods was applied but, the use of biochemical tests or PCR in the identification of TC species did not affect the prevalence estimation for *C. jejuni* and *C. coli*. In this way, biochemical tests for the identification of *Campylobacter* spp. are not standardized and each laboratory decides which biochemical test is more convenient to perform (Steinhauserova, Češkova, Fojtikova, & Obrovska, 2001). In addition, biochemical tests could underestimate the prevalence of this pathogen in domestic animals. Conversely, there are also no standardized genes for PCR determination and research select different DNA targets for the identification of TC. All of this makes the results variable which, added to the subjectivity in the interpretation of the biochemical tests, can explain the differences found.

Regarding the prevalence of TC species, half of the prevalence can be attributed to *C. jejuni*. Further, *C. jejuni* was the most prevalent species in poultry (broilers and chickens) and the least prevalent in pigs and goats. In contrast, our meta-analysis also showed that *C. coli* represented 30% of the prevalence found for *Campylobacter* spp. with the found in pigs. Beyond the influence of the production system, it is clear that each species of *Campylobacter* possesses a specificity to colonize certain hosts. The TC expresses different virulence genes that allow a selective colonization of each host (Bang et al., 2003). The difference in sensitivity to certain antibiotics used as growth promoters or for the treatment of diseases in the rearing of poultry or pigs could also explain why different species of *Campylobacter* are selected within the intestinal tract of domestic animals (Aarestrup, Nielsen, Madsen, & Engberg, 1997). Further studies should be conducted to evaluated how the prevalence of each species has changed in certain countries after the withdraw of antimicrobials growth promotion.

Although TC contamination can occur at any stage of the agri-food chain, the prevalence in food-producing animals in primary production has a strong impact on the rest of the food chain (Sahin et al., 2011; Signorini et al., 2013; Zorman, Heyndrickx, Uzunovic-Kamberovic, & Smole Mozina, 2006). Food-producing animals are the most important reservoirs and sources of TC, and the spread of this pathogen from primary production to the consumer's plate is a serious problem for public health (Damjanova et al., 2011; Ma, Wang, Shen, Zhang, & Congming, 2014). For all these reasons, many studies have been conducted regarding the application of different risk management technics aimed to reduce the prevalence of TC in primary production by interrupting the faecal–oral route. These control strategies could involve the use of bacteriophages, probiotic strains or vaccines (Annamalai et al., 2013; Connerton, Timms, & Connerton, 2011; Ganan, Silván, Carrascosa, & Martínez-Rodríguez, 2012; Rasschaert et al., 2013; Umaraw, Prajapati, Verma, Pathak, & Singh, 2017). In addition, an epidemiological surveillance system (including data from veterinary, food manufacture and human clinicians) should be established, at national and international with the aim to define the appropriate risk assessment measures to limit the prevalence of TC spp. in animals and the resulting emergence of campylobacteriosis in humans.

5 | CONCLUSIONS

Higher prevalence of TC was observed in different food-producing animals, especially in poultry (broiler, hens and other farm birds), pigs and bovine. *Campylobacter jejuni* was more prevalent in broiler and hens, and the least prevalent in pigs and goats. *Campylobacter coli* was found predominantly in pigs. Intensive production systems could facilitate the TC natural cycle, and this was clearly shown in the high prevalence rate in feedlot. Further, animals that arrived at the slaughterhouse had a higher prevalence of TC than the animals sampled on the farm. TC does not produce a decrease in the productive indicators of the livestock systems. However, the prevalence of *Campylobacter* in primary food production has a strong impact on the entire agri-food chain because is a public health issue. It is necessary that researchers quickly find tools aimed to reduce the prevalence in primary production stopping the faecal–oral cycle of TC, especially in intensive production systems.

CONFLICT OF INTEREST

There not conflict of interest.

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