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Original article

GLOBAL SYSTEMATIC REVIEW AND META-ANALYSIS ON FOODBORNE THERMOTOLERANT *CAMPYLOBACTER* PREVALENCE IN DIFFERENT SPECIES OF POULTRY BIRDS AND ASSOCIATED SOURCES OF CONTAMINATION

M. M. MIA[1,2], M. HASAN[2*], F. S. PORY[1,2], M. T. A. KAKON[1,2], M. T. ISLAM[2,3], R. BARI[2,4], S. ROY[2,5] & M. IMRANUZZAMAN[2,6]

[1]Department of Poultry Science, Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Bangladesh; [2]Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Bangladesh; [3]Department of Physiology, Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Bangladesh; [4]Executive Veterinary Services, ACI Animal Health Limited; [5]Department of Livestock Production and Management, Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Bangladesh; [6]Department of Pharmacology and Toxicology, Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Bangladesh

Summary

Mia, M. M., M. Hasan, F. S. Pory, M. T. A. Kakon, M. T. Islam, R. Bari, S. Roy & M. Imranuzzaman, 2023. Global systematic review and meta-analysis on foodborne thermotolerant *Campylobacter* prevalence in different species of poultry birds and associated sources of contamination. *Bulg. J. Vet. Med.* (online first).

Campylobacteriosis is one of the most prevalent foodborne bacterial diseases. Infected chickens and poultry products are a possible source of this illness in people all over the world. Therefore, the objective of this current meta-analysis was to summarise the available data on the prevalence of thermotolerant *Campylobacter* species in poultry and their products. A systematic literature search was conducted to gather pertinent articles from 2000 to 2021, using globally recognised four electronic databases, including Google Scholar, PubMed, Science Direct, and Scopus. The mean prevalence of campylobacteriosis in poultry species and their products (meat, eggs, and offal) was 44% (95% CI: 39–50%) with the highest prevalence in Australia (67%). Among the European countries, France had the maximum prevalence rate of 76%, while Japan had recorded 61% as the peak among Asian countries. Prevalence rates of 43% and 56% were calculated in United States and Brazil representing the American region. In the species-wise results, the mean prevalence rates of *Campylobacter jejuni* and *Campylobacter coli* were 29% and 16%, correspondingly. In case of live birds, chickens and turkeys possessed maximum prevalence rates of 47% and 40%, whereas 46% and 63% were recorded from poultry meat and liver. Besides, categorising the difference sources of contamination, the maximum prevalence rate of 62% was found in the poultry processing plants followed by 54% from supermarkets and 38% from farms. According to the current meta-analysis, *Campylobacter jejuni* was the most common bacterium worldwide, and poultry meat – the most frequent source of human infection. The predominance of *Campylobacter* species is a threat for public health, and national authorities must undertake strategies to control this disease in each country with the goal of establishing adequate risk management measures.

Key words: *Campylobacter* species, foodborne bacterial gastroenteritis, meta-analysis, poultry products

INTRODUCTION

Campylobacteriosis, caused by the *Campylobacter* bacteria, has been identified as the most often reported foodborne illness in the European Union, having 246,158 confirmed human cases in 2017, and an incidence rate of 64.8 cases per 100,000 capita (EFSA, 2018). Although poultry meat may be the most common source of this infection in humans, it has also been connected to consuming other contaminated foods, environmental variables and exposure to contaminated carcass at work (Foddai *et al.*, 2021). A recent report projected that global consumption of poultry meat will arrive to 151.83 metric kilotons by 2030 (Shahadah, 2021). Thus, the vast majority of consumers are likely to be at risk due to the contamination of poultry with *Campylobacter*. Diarrhoea, stomach cramping, fever and vomiting are the most common signs of this infection, followed by severe chronic symptoms and acute paralysis due to an immunological reaction and a sluggish healing pace (Nyati & Nyati, 2013).

Campylobacter species are zoonotic, Gram-negative, non-spore-forming, microaerophilic, curved or spiral-shaped bacteria that employ polar flagella to move (Alfredson & Korolik, 2007). Although *C. jejuni* is considered the major species in terms of its influence on human health, three other *Campylobacter* species (*C. jejuni, C. coli,* and *C. lari*) are also associated with poultry digestive system and foodborne diseases (Ugarte-Ruiz *et al.*, 2018). *Campylobacter* infections are most commonly found in chicken and turkey products that contain giblets (Sallam, 2007; Suzuki & Yamamoto, 2009; Zhao *et al.*, 2010), and most infections are caused by inappropriate handling or eating of raw or undercooked meat (Perez-Arnedo & Gonzalez-Fandos, 2020). Contaminated chickens and their products are the main sources of human campylobacteriosis and are considered major sources of human infection (Young *et al.*, 2007).

Even though a thorough examination of *Campylobacter* species has been conducted over the past 20 years that involved novel approaches to farm and processing plant treatments, human health risk continued to rise in spite of these efforts (Sibanda *et al.*, 2018). To limit the danger of human exposure to thermotolerant *Campylobacter* species, risk management strategies to reduce contamination in food-producing animals must be implemented. As a result, understanding the epidemiology of thermotolerant *Campylobacter* in poultry bird is crucial (Bull *et al.*, 2006). In this regard, the meta-analysis is a highly supportive statistical method whose purpose is to integrate, synthesise and contrast the findings of a large number of primary research that address the same problems. Therefore, the meta-analysis provides a more precise estimate of the effect size of a specific event with better statistical power than a single study (Borenstein *et al.*, 2021).

Although previously a few numbers of studies have been conducted regarding meta-analysis of *Campylobacter* prevalence in broiler birds, only studies on different live poultry birds and their marketed products remain unexplored. Therefore, the objective of this study was to quantitatively summarise and compare the prevalence of *Campylobacter* species in different poultry species and their products worldwide. This information may be used as a basis for risk management measures in public health. Thus, the current meta-analysis regarding campylobacteriosis in poultry and poultry products compiled the last 21 years time series data

for analysis of the pooled prevalence with different factors that can serve as a baseline for policymakers before taking any mitigation strategy.

METHODS

Literature search

A systematic literature search was conducted for articles published between 2000 and 2021, using the combination of keywords such as '*Campylobacter*', 'poultry meat' and 'prevalence' in combination with '*Campylobacter*', 'poultry meat products and 'prevalence' in electronic databases Google Scholar, PubMed, Science Direct and Scopus; meanwhile, for obtaining the various country's studies, the database was scrutinised randomly. Besides, additional studies were gathered by manually searching the cross-references or bibliography section of eligible studies. However, the search criterion was limited to English-language studies; finally, the eligible studies were extracted by two reviewers for eliminating the bias. The PRISMA protocols were followed for searching and scrutinising procedures (http://www.prisma-statement. org).

Study selection criteria

Inclusion criteria. The scholarly articles in the meta-analysis were chosen based on the following criteria: at least one observational study (prevalence) and publication in peer-reviewed journals between 2000 and 2021. When multiple chicken species were included in a single scientific study, the meta-analysis looked at each one separately. Similarly, when a scientific study published data from various variables, such as sample origin, *Campylobacter* species, diagnostic methods, country of origin, and prevalence estimation in various years, each condition was treated as a separate outcome. As a result, any scientific paper may have multiple outcomes. The total number of bird samples studied (population) and the number of samples positive for *Campylobacter* species must have been recorded in studies. When information on *Campylobacter* species identification became available, it was incorporated into the analysis.

Exclusion criteria. Non-peer reviewed articles, theses, opinion articles, editor letters, investigations other than PCR, trials where the samples were artificially contaminated with *Campylobacter,* and randomised controlled trials were omitted from the study.

Data extraction

The information was gathered from qualified studies that included the name of the first author, published year, location of study, total sample size, detection or diagnostic test, and products type and sample variation. In this study, individual diseases from around the world were used to categorise as a parameter; besides, continent-by-continent and country-by-country stratification of studies was undertaken. Then, each selected study was double-checked to rule out any possible consensus, and all relevant data were extracted from the eligible studies.

Methodological quality assessment

Before including studies in the review, all eligible studies were subjected to a thorough, independent evaluation by the authors, who used standardised critical appraisal instruments from the Joanna Briggs Institute (JBI) (Munn *et al.*, 2015). Two authors assessed the methodological quality of the included studies, and any variations were discussed. A third researcher best resolved a consensual judg-

ment in the event of disagreement. The checklists focused on setting, sampling techniques and sample size determination, screening/diagnostic methods, measurement and data analysis, and validity with reliability. This meta-analysis included all relevant studies with an optimal score (7–9) (Table 1).

Statistical analysis

The statistical analysis was carried out using meta-analysis (Major) package of the Jamvoi software. For calculating the result, we considered the prevalence as the outcome, and used the restricted maximum-likelihood estimator for residual heterogeneity for the random effect model. The percentage of variation owing to heterogeneity among the numerous reports included in this study was calculated using the tau square, I^2 (Higgin's I^2), and P value (Higgins *et al.*, 2003). Furthermore, displaying the standard error of each study, the funnel plot was created with the y-axis and the x-axis used to show the bias of the selected studies. Consequently, representing the publication bias by presenting the nonsymmetrical shape of a funnel by dropping the points exterior to the funnel (Egger *et al.*, 1997). The standardised effect estimates were plotted as scattered points versus inverse standard error. The points indicating the study reports that are outside the confidence boundaries may contribute to the heterogeneity. When differences in results for the same exposure-pathogen association cannot be explained fully by sampling variance, there seems to be heterogeneity of effects between studies. Differences in study design as well as demographic variables might be sources of heterogeneity (Bueno-Notivol *et al.*, 2021). Besides, to investigate the sources of heterogeneity expected in meta-analyses of observational data, subgroup analyses were used (Thompson & Higgins, 2002). In the present meta-analysis, seven subgroup parameters (categorical covariates) were fitted for calculating the prevalence rate based on different continents, countries, source of samples, name of samples, verity of products, poultry species, and serotypes of *Campylobacter* species. Following the sequence, chi-square test among the categorised variables in each subgroup parameter was conducted (Odeniran & Ademola, 2019). Then, the Tukey's *post hoc* multiple pairwise comparison test of one-way ANOVA (Odeniran & Ademola, 2019) among the continuous variables (prevalence) of each subgroup, which showed significant P values was performed.

RESULTS

Studies that mentioned the prevalence rate were rigorously screened, and those that were irrelevant were removed. A total of 28,534 studies using the mentioned keywords were identified after customising the results on the basis of the published year range between 2000 and 2021.

After advance searching, 8,090 studies that contained the mentioned keywords in the title were retrieved. Then, reading the title, abstract and full text, we got 155 studies. After excluding 47 studies describing review article, case study and duplication, 108 studies were identified. Finally, 88 studies in total were chosen for systematic review and meta-analysis based on PCR diagnostic test (Table 1; Fig. 1[*]).

[*] All figures from this manuscript are available online; please click on respective hyperlink.

Table 1. Characteristics of included studies

Authors' name and year	Representativeness of the source of contamination (sample)	Country	Sample size	Quality assessment score
Adzitey *et al.*, 2012	Cloacal swab, feces, soil, drinking water, feed, egg shell swab, floor swab, intestinal content, carcass rinse table swab, transport crate swab, intestinal contents	Malaysia	643	8
Ahmed *et al.*, 2016	Cloacal swab, water	Germany	450	8
Alam *et al.*, 2020	Cloacal swab, feed, drinking water for poultry, attendants' hand rinsed, whole carcass	Bangladesh	352	8
Allain *et al.*, 2014	Caecal samples	France	121	8
Ammar *et al.*, 2021	Cloacal swabs, neck skin, thigh meat, breast meat, caecal parts, liver, and gizzard	Egypt	245	8
Ansari-Lari *et al.*, 2011a	Caecum	Iran	100	8
Baserisalehi *et al.*, 2007	Faecal sample	Iran	111	8
Communication *et al.*, 2008	Cloacal swabs	Italy	240	8
Dagnra *et al.*, 2000	Meat, caecal sample	Estonia	986	8
Deckert *et al.*, 2010	Meat	Canada	1256	8
Dekker *et al.*, 2019	Meat	Ghana	200	8
Desalegne & Adane, 2010	Meat	Ethiopia	2220	8
Furukawa *et al.*, 2017	Meat	Japan	100	8
García-Sánchez *et al.*, 2020	Faecal, environmental samples	Spain	1188	8
Garin *et al.*, 2012	Meat	Vietnam	750	8
Good *et al.*, 2019	Faecal sample	United States	672	8
Greige *et al.*, 2019	Caeca, neck skin	Lebanon	454	8
Guyard-Nicodème *et al.*, 2015	Carcasses and chicken legs	France	351	8
Han *et al.*, 2009b	Whole carcass	United States	194	8
Hue *et al.*, 2011	Caeca	France	849	8
Huneau-Salaün *et al.*, 2007	Faecal drooping's	France	219	8

Table 1 (cont'd). Characteristics of included studies

Authors' name and year	Representativeness of the source of contamination (sample)	Country	Sample size	Quality assessment score
Kagambèga *et al.*, 2018	Faecal sample and carcasses	Burkina Faso	123	8
Kashoma *et al.*, 2014	Faecal droppings and caeca	United States	810	8
Katzav *et al.*, 2008	Slices and barbecue sticks, breast fillet and fillet steaks, breasts and skin	Finland	194	8
Khan *et al.*, 2018	Chicken meat, intestine, feather, chopping boards and knives	India	400	8
Kim *et al.*, 2010	Meat	Korea	1342	8
Kim *et al.*, 2019	Raw chicken meat and duck meat	Korea	194	8
Kottawatta *et al.*, 2017	Caeca content and neck skin	Sri Lanka	164	8
Kovalenko, 2013	Faecal sample, neck skin and carcass	Latvia	720	8
Kwon *et al.*, 2021	Cloacal swabs	South Korea	1348	8
Lim *et al.*, 2017	breast meat, caeca, gizzard, intestines, liver, skin and thigh	Philippines	265	8
Logue *et al.*, 2003	Prechill swab, post chill swab and chill water	United States	2412	8
Ma *et al.*, 2017	Wing middle joints, wing roots, legs and breasts	China	227	8
Madden *et al.*, 2011	Meat	Ireland	510	8
Malik *et al.*, 2014	Caecal sample	India	100	8
McDowell *et al.*, 2008	Cloecloacal swabs	Ireland	388	8
Mdegela *et al.*, 2006	Cloacal swab	Tanzania	536	8
Menna *et al.*, 2005	Cloacal swab and environmental swab	Italy	440	8
Mohammed & Abdel Aziz, 2019	Cloacal samples environmental samples, Attendants' hand swabs	Egypt	220	8
Moore *et al.*, 2002	Ready to eat food, fresh meat and frozen meat	Ireland	2137	8
Morita *et al.*, 2004	Faecal drooping's	Japan	32	7
Nafarrate *et al.*, 2021	Meat/faeces	Spain	132	8

Table 1 (cont'd). Characteristics of included studies

Authors' name and year	Representativeness of the source of contamination (sample)	Country	Sample size	Quality assessment score
Natsos *et al.*, 2020	Caeca and carcasses	Greece	284	8
Ngulukun, 2010	Cloacal swabs	Nigeria	360	8
Noormohamed & Fakhr, 2012	Liver and gizzard	United States	202	8
Nouri Gharajalar *et al.*, 2020	Liver	Iran	100	8
Novoa Rama *et al.*, 2018b	Faecal sample and environmental swab	United States	425	8
Ohnishi & Hara-Kudo, 2021	Meat	Japan	20	8
Osaili *et al.*, 2012	Cloacal swabs, feathered skin, prescinding, skin after scalding, skin after evisceration and skin after washing-chilling	Jordan	700	8
Pallavi & Kumar, 2014	Meat	India	150	8
Parisi *et al.*, 2007	Faecal swab, meat	Italy	339	8
Perez-Arnedo & Gonzalez-Fandos, 2020	Meat	Spain	160	8
Perez-Sancho *et al.*, 2020	Breast meat and thigh meat	Italy	78	8
Pillay *et al.*, 2020	Meat, neck and thigh swabs and whole carcass rinsate	South Africa	191	8
Pires *et al.*, 2019b	Faecal sample	United States	451	8
Pointon *et al.*, 2008	Meat	Australia	859	8
Raeisi *et al.*, 2017	Meat	Iran	260	8
Ragimbeau *et al.*, 2008	Meat	Luxembourg	229	7
Rahimi *et al.*, 2010	Meat	Iran	336	8
Rahul *et al.*, 2016	Cloacal swab	India	370	8
Rajkumar *et al.*, 2010	Meat	India	300	8
Rejab *et al.*, 2011	Faecal droppings	Malaysia	450	8
Revenco, 2019	Meat	Latvia and Lithunia	249	8
Ristori *et al.*, 2017	Meat	Brazil	138	8

Table 1 (cont'd). Characteristics of included studies

Authors' name and year	Representativeness of the source of contamination (sample)	Country	Sample size	Quality assessment score
Rosenquist *et al.*, 2013	Carcasses	Denmark	436	7
Rozynek *et al.*, 2013	Meat and giblet	Poland	297	8
Rutledge *et al.*, 2013	Faecal droppings	United States	318	8
Salihu *et al.*, 2008	Faecal materials	Nigeria	866	8
Sammarco *et al.*, 2010	Meat	Italy	104	8
Schets *et al.*, 2017	Caecal materials, soil, air, dust, other animals, flies, wastewater and surface water	Netherlands	354	8
Shange *et al.*, 2020	Cloacal swab	South Africa	836	8
Sinulingga *et al.*, 2020	Cloacal swab and meat	Malaysia	319	8
Son *et al.*, 2007	Pre-scald carcass, pre-chill and post-chill	United States	325	8
Stoyanchev *et al.*, 2007	Frozen meat and chilled poultry products	Bulgaria	210	8
Szczepańska *et al.*, 2015	Rectal swab	Poland	398	7
Tenhagen *et al.*, 2020	Meat	Germany	990	8
Thorsness *et al.*, 2008	Faecal droppings	United States	2790	8
Tîrziu *et al.*, 2020	Meat	Romania	34	8
Torralbo *et al.*, 2014	Cloacal swab and environmental swab	Spain	2968	8
Walker *et al.*, 2019	Meat and offal	Australia	785	8
Wieczorek & Osek, 2015	Intact caeca and swab	Poland	256	8
Wieczorek *et al.*, 2013	Skin swab	Poland	802	8
Wong *et al.*, 2007	Meat	New Zealand	1011	8
Wright *et al.*, 2008	Environmental swab	United States	1512	8
Würfel *et al.*, 2019	Meat and liver	Brazil	36	7
Wysok *et al.*, 2020	Caecum and chilled skin sample	Poland	240	8
Yossapol *et al.*, 2015	Caeca	Thailand	510	8
Zhao *et al.*, 2001	Meat	United States	707	8

Meta-analysis of Campylobacter prevalence in poultry, meat and meat products

The selected 88 studies were obtained from Asia (27 studies), Europe (33 studies), North America (13 studies) and South America (2 studies), Africa (10 studies), and Australia (3 studies). The current meta-analysis analysed a total of 48,150 samples from the years 2000 to 2021, and revealed that the global prevalence of *Campylobacter* species was 44% (95% CI: 39–50%), H^2 value 231.509, P<.001) (Table 2).

The funnel plot of all studies was shown on Fig. 2. Then, analysing the continent-wise results (Fig. 3 and Fig. 4), the highest prevalence rate was found in Australia: 67% (95% CI: 26–100%) tailed by Europe 46% (95% CI: 38–54%), North America 44% (95% CI: 28–60%), Asia 40% (95% CI: 32–48%), and Africa 39% (95% CI: 24–55%). However, only two studies were reported from South America and the pooled prevalence was registered as 56% (Table 3).

Table 2. Pooled data regarding the 88 included studies

Parameters	Value
Total sample	48,150
Total outcome	18,804
Pooled prevalence (%) (Random effect mode)	44
Number of studies	88
95% CI:	39–50
H^2 value	231.509
Tau^2 value	0.0597
I^2 value	99.57
Z-test	16.9
P-value	<.001

Country wise prevalence

The analysis of results according to the countries (Fig. 5 and Fig. 6) showed that among the European countries, France had the highest prevalence rate, whereas Germany – the lowest percentage. In the case of European countries from multiple studies, prevalence rates of 76%, 56%, 46%, and 43% were found in France, Poland, Italy, and Ireland; whereas Germany and Spain reported 25.5% and 34% prevalence rates, respectively. In contrast, among the multiple studies from Asian countries, the pooled prevalence was found to be 61%, 51%, 41%, and 37% in Japan, Iran, Malaysia, and South Korea; meanwhile a 20% prevalence rate was reported from India. Likely, among the "North American countries" from multiple studies, the maximum 43% prevalence were found in United States, while Brazil reported a 56% prevalence rate among the "South American countries". Similarly, from African countries, Egypt and Nigeria reported 59.5% and 56%; whereas, 36% prevalence rate reported from South Africa. Moreover, in Australia 87.5% prevalence rate of *Campylobacter* species was reported (Table 3 and 4).

Analysing single studies from numerous countries, the highest (64–78%) prevalence rates were found in Philippines, Greece, Latvia, Bulgaria, Vietnam, Burkina Faso, and Tanzania. Rates of 40–60% were reported from Canada, Sri Lanka, and Lebanon, while 26–36% were found in Thailand, Denmark, Netherlands, Lithunia, Luxembourg, Romania, Estonia, Bangladesh, and New Zealand. Comparatively, the lowest range of prevalence (10–20%) was reported from China, Jordan, Finland, and Ghana (Fig. 7).

Prevalence rate according to different Campylobacter species

Among *Campylobacter* species, *Campylobacter jejuni, Campylobacter coli, Campylobacter lari,* and *Campylobacter upsaliensis* were highly circulating throughout

Table 3. Continent wise zoonotic *Campylobacter* species prevalence*

Region/continent with total prevalence	Heterogenicity	Country
Asia: 40% 95% CI: 32–48% Number of studies: 27	H^2 value: 84.7 Tau^2 value: 0.041 I^2 value: 98.8	China, Jordan, Bangladesh, India, Iran, Japan, South Korea, Lebanon, Malaysia, Philippines, Sri Lanka, Thailand, Vietnam
Europe: 46% 95% CI: 38–54% Number of studies: 33	H^2 value: 208.0 Tau^2 value: 0.056 I^2 value: 99.5	Bulgaria, Denmark, Estonia, Finland, France, Germany Greece, Ireland, Italy Latvia, Lithunia, Luxembourg, The Netherlands, Poland, Romania, Spain
Africa: 39% 95% CI: 24–55% Number of studies: 10	H^2 value: 214.4 Tau^2 value: 0.060 I^2 value: 99.5	Burkina Faso, Egypt, Ethiopia, Ghana, Nigeria, South Africa, Tanzania
North America: 44% 95% CI: 28–60% Number of studies: 13	H^2 value: 503.16 Tau^2 value: 0.0858 I^2 value: 99.8	United States, Canada
Australia: 67% 95% CI: 26–100% Number of studies: 3	H^2 value: 856.6 Tau^2 value: 0.127 I^2 value: 99.8	Australia, New Zealand

* Maximum reported infections – *Campylobacter jejuni, Campylobacter coli, Campylobacter lari, Campylobacter upsaliensis.*

the world. The maximum 77 studies reported infections caused by *Campylobacter jejuni,* followed by 70 studies reporting *Campylobacter coli.* The present study found prevalence rates of *Campylobacter jejuni* and *Campylobacter coli* of 29% and 16%, respectively. However, few studies reported infections caused by *Campylobacter lari* and *Campylobacter upsaliensis;* their prevalence rate was 2% for both species (Table 5).

Prevalence rate according to contamination sources

The sources of contamination were categorised into six groups including farms, grocery/retail shops, local areas, poultry processing plants, supermarkets/local markets, and slaughterhouses. Among them, the maximum (62%) prevalence rate of *Campylobacter* species was from poultry processing plants. Meanwhile, 54% prevalence rate was found from supermarkets/local market and slaughterhouses. However, the *Campylobacter* prevalence rates were comparatively lower (47% and 43%) in the sample from grocery/retail shops and local areas. In contrast, the lowest 38% prevalence rate was reported from the samples obtained from farms (Table 6).

Prevalence rate according to poultry species

Among the different poultry birds, *Campylobacter* species showed comparatively higher prevalence in chickens 47% vs 40% prevalence in turkeys (Fig. 8). Similarly, only three studies were found in ducks which reported a 25% pooled prevalence rate. Few studies were found in other species, including geese, pheasants, ostriches, storks with pooled prevalence rate of 29% (Table 7).

Prevalence rate according to poultry parts

Poultry parts were categorised as meat, faeces, caeca, carcass, skin, liver and in-

Table 4. Prevalence of *Campylobacter* species based on different country reporting more than two studies

Country	Number of studies	Random effect model			
		Prevalence (%) (95% CI)	I^2 (%)	Tau^2	P-value
Iran	5	51 (35–67)	95.9	0.177	<.001
India	5	20 (13–27)	90.6	0.005	<.001
Malaysia	3	41 (13–70)	99.3	0.069	<.001
Japan	3	61 (46–75)	60.9	0.099	0.066
South Korea	3	37 (13–61)	99.8	0.044	<.001
Poland	5	56 (32–81)	99.4	0.076	<.001
Italy	5	46 (25–66)	98.5	0.054	<.001
France	4	76 (73–78)	34.3	3e-04	0.198
Spain	4	34 (25–42)	95.8	0.006	<.001
Ireland	3	43 (-2–88)	99.8	0.156	<.001
United States	12	43 (26–60)	99.8	0.087	<.001

Table 5. Prevalence rate categorised by different *Campylobacter* species*

Causal agent	Random effect model				
	Number of studies	Prevalence (%) (95% CI)	I^2 (%)	H^2	Tau^2
Campylobacter jejuni	77	29 (24–33)	99.4	182.8	0.039
Campylobacter coli	70	16 (13–19)	99.4	185.8	0.016
Campylobacter lari	9	2 (0–4)	99.0	105.7	6e-04
Campylobacter upsaliensis	3	2 (0–3)	89.6	9.67	0.014

* Chi-square test/ANOVA: P<.001/P<.001.

Table 6. Prevalence of *Campylobacter* species from different poultry species based on the source of sample*

Sample source	Random effect model				
	Number of studies	Prevalence (%) (95% CI)	I^2 (%)	H^2	Tau^2
Farm	27	38 (30–47)	99.5	199.2	0.050
Grocery/retail shop	24	47 (36–57)	99.5	200.5	0.070
Local area	3	43 (-2–88)	99.8	647.3	0.160
Poultry processing plant	5	62 (47–76)	98.3	59.6	0.265
Supermarkets/ local market	7	54 (38–71)	98.8	86.1	0.029
Slaughterhouse	12	54 (41–67)	99.1	119.3	0.049

* Chi-square test/ANOVA: P<.001/P<.212.

testine; among them, the maximum *Campylobacter* prevalence rate of 63% was reported in liver and caeca, followed by 56% in carcass, 48% in faecal samples and 47% in intestine (Fig. 9). Flowing

Table 7. Prevalence of *Campylobacter* species categorised by poultry species*

Species	Random effect model				
	Number of studies	Prevalence (%) (95% CI)	I^2 (%)	H^2	Tau^2
Chicken	76	47 (41–52)	99.5	198.4	0.057
Duck	3	25 (13–37)	88.9	9.0	0.009
Turkey	8	40 (18–62)	99.9	1033.6	0.319
Others (geese, pheasant and ostrich, stork)	5	29 (6–52)	99.5	224.6	0.261

* Chi-square test/ANOVA: P<.001/P<.117.

Table 8. Prevalence of *Campylobacter* species from different poultry parts*

Type of product	Random effect model				
	Number of studies	Prevalence (%) (95% CI)	I^2 (%)	H^2	Tau^2
Meat	42	46 (48–53)	99.1	113.6	0.065
Faecal	17	48 (34–62)	99.7	358.1	0.082
Caeca	16	63 (52–72)	97.0	34.1	0.040
Carcass	10	56 (38–73)	98.8	89.3	0.077
Skin	9	38 (18–58)	99.5	209.6	0.089
Liver	4	63 (33–92)	98.2	56.3	0.089
Intestine	4	47 (13–81)	98.2	55.6	0.345

* Chi-square test/ANOVA: P<.001/P<.119.

42% prevalence rates were found in the poultry meat – the most edible part for human consumption (Table 8).

DISCUSSION

Campylobacter species are ubiquitous and classified as commensal microorganisms in the gastrointestinal tracts of humans and poultry. Human illness is usually caused by the intake of contaminated water and food, particularly chicken and its byproducts, which are the primarily *Campylobacter jejuni* reservoirs (Ugarte-Ruiz *et al.*, 2018). Moreover, people are exposed through retail poultry meat that has already been linked to 20 to 30% of the infections caused by processing and consumption of broiler meat and its products (Ammar *et al.*, 2021). However, establishing risk management methods to limit contamination in poultry meat and products is critical to reducing the danger of human exposure to *Campylobacter* species. Hence, it is crucial to understand the worldwide prevalence of thermotolerant *Campylobacter* species originating from poultry meat and products (Stella *et al.*, 2017).

According to the current meta-analysis, the mean prevalence of *Campylobacter* species was 44% in poultry meats and products. Because of inadequate and unclean farm management, several poultry houses, the presence of other animals on the same farm and antibiotic administration, there is a high incidence rate in chicken species (Ansari-Lari *et al.*,

2011). Following that, the conducted continent-by-continent analysis identified Australia as having the maximum prevalence rate, followed by Europe and North America. Likely, Asia and Africa had prevalence rates quite close to the average. According to a recent meta-analysis, European poultry products have a high incidence of *Campylobacter* species because retailers do not always adhere to stringent temperature controls, leaving the goods vulnerable to this disease through a number of different points of contamination (Gonçalves-Tenório *et al.*, 2018). Having access to quality drinking water sources and better hygiene standards can be credited for the low prevalence of *Campylobacter* in Indian continent (Vaishnavi *et al.*, 2015).

Following analysis of the country-wise statistics, France had the highest prevalence rate among European countries, while Germany – the lowest prevalence. The topmost prevalence was reported in Japan (61%), which is the most populous Asian country. India is most likely the country with the lowest prevalence. Similarly, the United States had the highest prevalence percentage of *Campylobacter* species in poultry species and their products among South American countries, which is consistent with the findings of a previous study conducted in the United States, reporting a prevalence rate of 11.3–87% (Han *et al.*, 2009; Noormohamed & Fakhr, 2012; Novoa Rama *et al.*, 2018; Pires *et al.*, 2019). Moreover, the present meta-analysis revealed a 56% prevalence rate in Brazil among the South American countries. Similarly, from African countries, 59.5% prevalence rate was reported in Egypt and 36% – from South Africa. However, a previous study showed that after accounting for the different types of samples analysed, Central African poultry species samples were considerably more likely to have *Campylobacter* isolated or identified than samples from other African locations (Thomas *et al.*, 2020). In addition, Australia as a whole reported a prevalence rate of 87.5%. These differences in prevalence rates may be the result of changes in the handling and management of poultry products sampled in each country, variations in the experience of *Campylobacter* isolation, or variations in the isolation procedure (Ammar *et al.*, 2021). Laboratory services play a major role in all key processes of pathogen detection and assessment. While developed nations are able to adapt their organised routine laboratory services and experienced lab technicians with ease, resource-limited nations require significant capacity building as many gaps still exist (Katz *et al.*, 2010), which could be a significant factor in the variation of *Campylobacter* prevalence in different nations.

According to the present meta-analysis results, among the four species, *Campylobacter jejuni* was more prevalent (29%), followed by *Campylobacter coli* (16%) and 2% for *Campylobacter lari* and *Campylobacter upsaliensis* in poultry species and poultry products. A previous study reported that the reason for the highest incidence might be the resistance of *Campylobacter jejuni* to ciprofloxacin, nalidixic acid, tetracycline and streptomycin, and its complete susceptibility to erythromycin and gentamicin (Popa *et al.*, 2022). Furthermore, due to the widespread and careless use of antibiotics in the poultry industry, bacterial foodborne pathogen resistance to antibiotics has steadily developed, raising severe concerns about worldwide public health (Rivera-Gomis *et al.*, 2021).

Furthermore, conferring on the present meta-analysis, chickens were the most

important *Campylobacter* source among all poultry species. It is well known that chickens are a natural host for *Campylobacter jejuni* and that colonised broiler chicks are the principal vector for spreading the infection to humans (Chatur *et al.*, 2014). Besides, the categorisation of the difference sources of contamination found that the maximum (62%) prevalence rate was at poultry processing plants followed by 54% from supermarkets and 38% from the farms. The apparent lower sensitivity of the farm sampling compared to the processing plant sampling may be caused by both late-term colonisation events and cross-contamination of birds in response to *Campylobacter* species during transit to slaughter (Berghaus *et al.*, 2013). Moreover, broiler flocks can be quickly colonised by *Campylobacter*, reaching a 95% within-flock prevalence 4 to 7 days after the first bird is colonised (van Gerwe *et al.*, 2009). *Campylobacter* prevalences and loads have previously been demonstrated to rise as a result of stress connected to catching and transportation; additionally, previously reported contamination of non-colonised birds exposed to infected shipping crates may be involved (Berghaus *et al.*, 2013).

Therefore, this high prevalence rate in poultry processing plants may be because of cross-contamination of poultry carcasses through evisceration, carcass chillers and unhygienic management (Keener *et al.*, 2004). Also, colonisation of *Campylobacter species* within poultry farms relies heavily on farm techniques. At the farm level, the prevalence can reach 100%, and colonisation duration varies greatly between flocks (Sibanda *et al.*, 2018).

Moreover, analysing the prevalence from different poultry parts, a significant (63%) prevalence rate of *Campylobacter* species in liver and caeca than in other samples was found out. Additionally, *Campylobacter* has been linked to chicken liver sold in stores, with prevalence rates ranging from 33 to 100% of livers analysed in the previous study (Berrang *et al.*, 2019). The variation in prevalence data of *Campylobacter* in the literature can be explained by variable processing facilities, locations, collection time of the year, and variable methodologies (Noormohamed & Fakhr, 2012).

This study contained the right approach of a literature search from an internationally known database, an overall sample size, subgroup analysis about epidemiological risk factors, the impact of climate variables, and a recognised methodology. However, our analysis has a few limitations, including a lack of sufficient data in some studies and the possibility of missing to include some studies. Our findings may differ slightly from the actual prevalence rate due to the constraints. As a result, we suggest that comprehensive molecular research should be conducted to obtain an exact global prevalence estimate.

CONCLUSION

The most frequent bacterial infections affecting poultry species are those belonging to the *Campylobacter* genus, particularly thermotolerant *Campylobacter* jejuni and *Campylobacter coli*. There is currently no viable treatment for these diseases due to drug resistance. Therefore, in order to further conduct any control initiatives, it is vital to shift the focus of concern in terms of the global prevalence of *Campylobacter* species. Thus, present study conducted a meta-analysis and found a mean prevalence of *Campylobacter* species in poultry products of 44% with the highest prevalence rate in Austra-

lia, followed by Europe, North America, Asia, and Africa. In the case of country-wise prevalence, the maximum prevalence rate was found in France, Poland, Italy, and Ireland, Japan, Iran, Malaysia, South Korea, United States and Brazil. Moreover, the present study revealed poultry processing plants as major sites of harbouring these pathogens. To reduce the high rate of contamination, it is advised to employ fundamental sanitary procedures in the poultry posing facility. Additionally, pre-harvest controls in farms can aid in reducing the spread of *Campylobacter* in the environment, on farms, and throughout the food industry. Furthermore, since *Campylobacter* contamination is not caused by a single vehicle or route, several cars and routes should be addressed concurrently. Finally, educating the people about illness reporting to their neighbourhood veterinarians and implementing biosecurity measures can greatly minimise the prevalence of *Campylobacter* species.

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Correspondence:

Mahamudul Hasan
Faculty of Veterinary, Animal and Biomedical Sciences, Sylhet Agricultural University, Sylhet-3100, Bangladesh,
mobile: +8801797735827,
e-mail: mhasan.student@sau.ac.bd,
ORCID ID: 0000-0002-5669-4684