Review

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Prevalence and Distribution of Thermotolerant *Campylobacter* Species in Poultry: A Comprehensive Review with a Focus on the Factors Affecting the Detection and Enumeration of *Campylobacter jejuni* and *Campylobacter coli* in Chicken Meat

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Prevalence and Distribution of Thermotolerant *Campylobacter* Species in Poultry: A Comprehensive Review with a Focus on the Factors Affecting the Detection and Enumeration of *Campylobacter jejuni* and *Campylobacter coli* in Chicken Meat

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Abstract: It is well known that the strong-evidence foodborne outbreaks of human campylobacteriosis are associated with the consumption of raw or incompletely thermally processed poultry meat, whereas broilers act as the main reservoir for *Campylobacter* species. *Campylobacter jejuni* and *Campylobacter coli* are the two main species of campylobacters detected in chicken meat, while they account for almost 90% of the reported cases of campylobacteriosis in humans. Over 80% of these cases are attributed to *C. jejuni* and about 10% of them are due to *C. coli*. Therefore, until recently the dominance of *C. jejuni* against all other *Campylobacter* spp. isolated from chicken meat samples was well established and unquestionable. Lately, however, *C. coli* has been increasingly recovered from chicken meat to such an extent that it is now evident that it often comprises the dominant species among the identified campylobacters in the meat samples. This work attempts for the first time a detailed review in the literature to deepen into this noteworthy epidemiological swift in the prevalence of *C. jejuni* and *C. coli*, along with the distribution of *Campylobacter* spp. in chicken meat. Factors such as the sampling method followed for screening campylobacters in broiler carcasses (e.g., swabs or carcass rinsates, skinned or skinless meat excised samples) and part of the animal carcass from which the sample is obtained (e.g., neck, breast, leg), seasonality of sampling (summer *vs.* winter) and environmental conditions (e.g., rainfall, relative humidity) at the farm level, the isolation procedure (enumeration or detection) and pathogen identification (biochemical or molecular), the enrichment and plating isolation media (e.g., Bolton *vs.* Preston broth, charcoal-based *vs.* chromogenic agars), as well as the biofilm-forming ability of different campylobacters, highlight the multivariate dimension of the phenomenon and are thoroughly discussed in the present review.

Keywords: *Campylobacter*; chicken; epidemiology; meat; poultry

1. Introduction

According to the latest scientific report of the European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC) on the trends and sources of zoonoses and foodborne outbreaks in the European Union (EU), campylobacteriosis is the most commonly reported foodborne gastrointestinal infection in humans in the EU and has been so since 2007 [1]. Estimates of the overall human health impact of bacterial agents transmitted commonly through food, place *Campylobacter* as the first or second most common agent after nontyphoidal *Salmonella* in Europe, North America, Australia, and Japan [2–4]. The notable absence of notified *Campylobacter* outbreaks in China and some other populous countries, like India, could be attributed to the lack of mandatory surveillance by the established foodborne disease surveillance system or to the

underreporting (e.g., mild symptoms and a smaller number of cases seeking health care) and/or underdiagnosis (e.g., lack of testing and diagnostic accuracy) of the disease, the lack of epidemiological surveillance data connecting causative agents of outbreaks, and the different dietary habits on those countries [5–7].

Major food categories of interest for *Campylobacter* occurrence include mostly meat and meat products (i.e., animal carcasses and fresh/ready-to-eat (RTE), cooked and fermented products), as well as milk and milk products (i.e., raw and pasteurized milk and dairy products including cheese) [1], although the prevalence of the disease-causing *Campylobacter* spp. is significantly increased in poultry meat samples compared to other types of meat or compared with milk and dairy products [8–11]. The strong-evidence foodborne association of campylobacteriosis outbreaks with the consumption of raw or incompletely thermally processed poultry meat is already well known and has been emphatically documented nowadays [8,10,12], while the foodborne illness due to the presence of *Campylobacter* spp. in poultry has been classified as the costliest pathogen-meat combination from an economic perspective [13]. Regardless the fact today poultry is considered the main reservoir for *Campylobacter* spp. (source of infection), latest epidemiological evidence suggests pathogen transmission to humans through a pathway implicating cattle as the primary reservoir of *Campylobacter* (source of contamination), infecting people via the fecal-oral route and the consumption of contaminated chickens [14].

World poultry meat consumption refers to the consumption of meat from chickens (broilers), turkey, and other avian species (e.g., ducks, geese). Available data compiled from the Food and Agriculture Organization (FAO) of the United Nations (UN) reveal an increase in worldwide annual poultry meat consumption per capita by more than 5.0 kg in the past 20 years; from 10.8 kg in 2000 to 16.2 kg in 2020 [15]. Chickens are by far the main protein source of animal origin for humans in terms of livestock animals reared and slaughtered for their meat [15], so the previous rates represent roughly the chicken meat being consumed on a global basis.

The different thermotolerant campylobacters validly described to date are summarized in Supplementary Table S1. Of these, *Campylobacter jejuni* and *C. coli* are the two most important species mainly detected in foods of animal origin [55], [56] (p. 1670). These two species account for almost 90% of the reported human campylobacteriosis cases, with over 80% of the occurring gastrointestinal infections being attributable to *C. jejuni* and the rest about 10% of infections attributed to *C. coli* [56] (pp. 1669–1670), [57]. Therefore, until recently it was well established and beyond any reasonable question that *C. jejuni* is the dominant species among all other *Campylobacter* spp. isolated from chicken meat samples. Lately, however, *C. coli* has been increasingly recovered from chicken samples to such an extent that it is now obvious it many times comprises the dominant species among the identified campylobacters in the meat samples [58–62]. To this end, in studies pertaining to the metropolitan area of Athens, Greece, and its suburbs in the Attica region, Andritsos et al. [63] reported isolation rates of 6% and 27% for *C. jejuni* and *C. coli*, respectively, during *Campylobacter* spp. detection in chicken meat samples, whereas the strict majority (87.5%) of the recovered campylobacters (16) from 830 fecal samples collected from five poultry farms by Marinou et al. [64] were identified as *C. coli*, without any of the strains being identified as *C. jejuni* whatsoever. Taking into account that in the latter case of *Campylobacter* presence in broilers' litter, the positive predictive value in terms of microorganism's occurrence in carcass skin samples is much greater, unless the pathogen cannot be detected in the intestinal content of the bird [65], *C. coli* dominance in the chicken flocks should be taken for granted.

Considering all the above, the present work attempts for the first time, to the best of the authors' knowledge, a detailed review in the literature in order to elucidate the underlying epidemiological transition from *C. jejuni* to *C. coli* in chicken meat, along with the distribution of campylobacters in poultry. Figure 1 outlines the factors affecting the occurrence of *Campylobacter* spp. in poultry meat samples, while those factors are thoroughly being discussed below.

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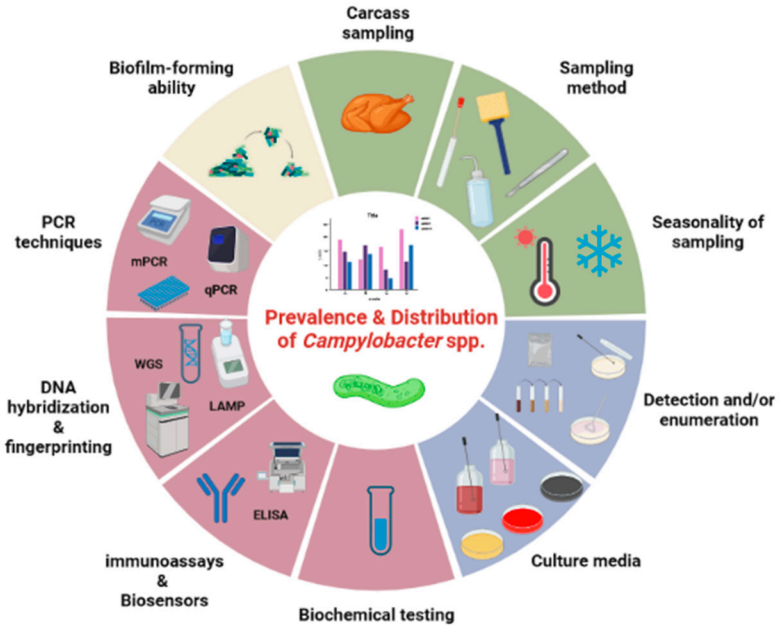

Figure 1. Factors affecting the prevalence and distribution of *Campylobacter* spp. in poultry meat. Factors that are related to each other are grouped together under the same color. As a result, distinct groups of factors referring to sampling (light green), isolation procedure (light blue), confirmation and/or identification (light purple), and biofilm production (light brown) for *Campylobacter* species are presented. Created with BioRender.com.

2. Sampling of Poultry

2.1. Carcass Sampling

Campylobacter which is originally associated with the bird's feathers and contaminates the exterior of the animal might be transferred to the poultry skin during mechanical defeathering of broiler carcasses in the slaughterhouse [66]. Thus, the meat sampled with skin from poultry is more likely to contain the pathogen when compared to animal tissue samples obtained from broiler carcasses without the skin. Furthermore, due to the favorable conditions of humidity and temperature in the wings of poultry, there is a high *Campylobacter* load in the wings which could also be attributed to imperfect scalding, post-scalding contamination or a combination of both [67]. Hence, there is an increased prevalence of *C. jejuni* in the wings of sampled poultry [65,68–70]. Besides, an initial high *Campylobacter* contamination of the neck skin may occur when water excess drips down the carcass dragging along the bacteria during the slaughter line hanging (upside down) of carcasses [71]. This may also explain the comparatively lower number of campylobacters found on the back, breast and leg skin samples and other parts of the carcass than in the neck and wing skin samples (Figure 2). Moreover, breast and wing skin sites when sampled show a higher correlation in *Campylobacter* populations with the neck skin samples [71]. The variations in *Campylobacter* concentrations between skin sites of individual carcasses are often reflected in the non-homogeneous distribution of carcass contamination after post-chilling of broiler carcasses [71] (Figure 2).

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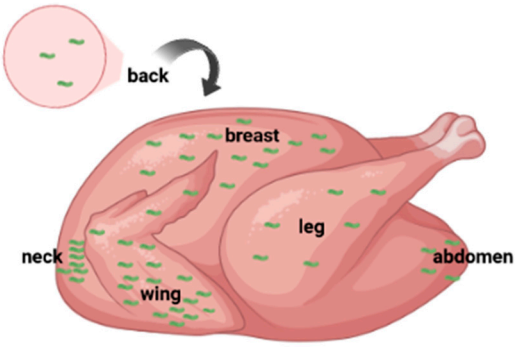

Figure 2. Sampling sites of a broiler carcass with variations in *Campylobacter* contamination depicted with the relative concentration of campylobacters (green curved bacteria). *Campylobacter* concentration in descending order from the more heavily contaminated site to the less contaminated one, when sampled with skin, is as follows: (neck ≥ wing ≥ breast ≥ leg) > (abdomen ≥ back). Parentheses designate the sites that are highly correlated to each other in terms of *Campylobacter* concentration. Created with BioRender.com.

2.2. Sampling Method, Type of Product and Refrigerated Storage

The method of sampling plays an important role in determining the microbiological quality of foods. Several non-destructive methods (e.g., surface swabs, contact plates, tissue excisions) are suitable for estimating bacterial populations anticipated in relatively high concentrations on the carcass, such as aerobic plate count (APC) and enterobacteria, while other –destructive in nature– methods (e.g., sampling/cutting of parts of the carcass, whole carcass rinses) are more suitable for detecting the presence of pathogens that may be more unevenly distributed and in low population on the carcass [72,73]. The former are fast and simple methods that can be used for comparative purposes, sanitation verification procedures, and shelf-life prediction, whereas the latter are time-consuming and labor-intensive methods preferable when the microbiological safety is of outmost importance. For instance, a sample area of at least 100 cm^2 is swabbed for APC and Enterobacteriaceae enumeration in a cattle carcass after dressing but before chilling and a pooled neck skin sample is recommended for detecting *Salmonella* and enumerating *Campylobacter* in poultry carcasses after chilling [74,75]. In the case of broiler carcasses, counts for APC and hygiene indicators (total coliforms, *Escherichia coli*) from the microbiological analysis of swabs were generally more than 0.5 log units lower than the smallest values obtained through tissue excisions and carcass rinses [76].

The type of product or its preparation also affect *Campylobacter* incidence. Statistical analysis in a survey of *Campylobacter* spp. contamination in chicken meat preparations in Belgium indicated that the odds of *Campylobacter* presence are lower in minced meat than in portioned or cut meat and an unpredicted bias into prevalence and enumeration results could be plausible, unless proper sampling and a balanced selection of product types takes place [67]. Progressive increase of product's surface through mincing, apart from increased levels of pathogen contamination, implies also increased microbial exposure to the air. For microaerophilic *Campylobacter* spp. this exposure to aerobic conditions could prove lethal since the degree of processing leads to an ever-increasing decrease in the number of campylobacters encountered in the products [55,68,77,78]. Finally, storage of product at refrigeration temperature may reduce *Campylobacter* count, as revealed by culturing methods during storage of refrigerated broiler breast and thigh meat at 4°C, packaged under aerobic, modified atmosphere packaging (MAP) or vacuum conditions [79,80]. Interestingly, the succession of *Campylobacter* species or strains, with a special emphasis on *C. jejuni* and *C. coli*, during refrigerated storage of artificially contaminated chicken meat packaged samples could be the subject of future research, as in the case of *Listeria monocytogenes* [81].

2.3. Seasonality of Sampling and Environmental Conditions

The seasonality of sampling and the effect environmental conditions may have on the recovery of *Campylobacter* spp. from broiler carcasses or chicken meat has been the subject of dozens of research papers, which present conflicting results as far as the effect of seasonality on *Campylobacter* prevalence is concerned and fail to reach an agreement on the matter. In this context, a large number of studies have indicated a significant seasonal increase in the prevalence of *Campylobacter* in broiler carcasses or in poultry meat during the hot summer months [10,68,82–85], even in tropical countries without marked seasons where other climatic conditions though, like increased rainfall and relative humidity, possibly reflect to the pathogen's potential to colonize its host (e.g., chicken broilers) [86,87]. The seasonal effect on *Campylobacter* prevalence is inferred either by the increased number of reported campylobacteriosis cases during the summer months [10,82] or the increased fly activity [88] and the presence of flies in the summer, which play the role of the bacterial vector (mechanical/transport host) in the warm months [83]. In addition, the aforementioned increase in prevalence could reflect the level of environmental contamination due to more regular ventilation of the poultry houses in summer, resulting in increased contact of birds with the external environment [89,90]. To this end, higher wind speeds and the geographical location of the farm, surrounded by a more agricultural landscape, may also contribute to the extent of contamination in the poultry flock [84,91]. Wind may introduce contaminated material (e.g., soil, dried fecal particles) to the poultry house, which is more likely to exist in the rural setting, exposing the flock to *Campylobacter* spp. among other fecal pathogens, if birds have access to the external environment [91]. Biosecurity measures at the farm level greatly contribute towards prevention of *Campylobacter* colonization and reduce prevalence of the pathogen in broiler flocks [90,92].

On the other hand, several papers highlight the non-statistically significant effect of seasonality on *Campylobacter* populations from broiler carcasses or chicken meat [61,63,90,93], where especially in the warmer countries of southern Europe, like the Mediterranean countries, a higher prevalence of *Campylobacter* spp. is reported in broiler flocks throughout the year compared to the colder northern European countries with the more pronounced and obvious seasonality in their bacterial recoveries of the pathogen [90,92]. Moreover, many times the inability to ascertain the degree of influence of the seasonality on the recovery rate of *Campylobacter* spp. is even related to the small number of samples analyzed which does not allow safe conclusions to be drawn [61,63].

Regarding the distribution of different *Campylobacter* species in poultry carcasses, Manfreda et al. [59] reported higher recovery rates for *C. jejuni* (75.2%) against *C. coli* (24.8%) in winter (i.e., December–March) for chicken carcasses sampled from a single slaughterhouse in Italy, which were processed from broilers coming from a dozen of different chicken farms, compared to other seasons where *C. jejuni* was either absent (in autumn), marginally (in spring) or slightly (in summer) dominant over *C. coli*. In contrast, in a retrospective study conducted in Poland for the five-year period 2014–2018, Wieczorek et al. [61] showed that the peak in the distribution of *C. coli* was clearly placed to the autumn-winter months (i.e., October–February).

3. Isolation of *Campylobacter* spp.

3.1. Detection and/or Enumeration Procedure

The choice of microbiological method that can be used to isolate campylobacters from a food commodity can significantly affect the prevalence or even the estimated concentration of the pathogen in food [73,94–101], and therefore the distribution of different *Campylobacter* species recovered from food during the microorganism's detection or enumeration procedure followed. *C. jejuni* was mainly isolated during pathogen enumeration procedure, while *C. coli* was the predominant species recovered from all plating culture media following enrichment in Bolton broth during the detection of *Campylobacter* in chicken meat [63,98].

The possibility of combining different enrichment broths (e.g., Bolton broth or Preston broth) with different selective and/or differential (i.e., chromogenic) solid culture media (i.e., agars) (e.g., modified charcoal-cefoperazone-deoxycholate agar; mCCDA, Preston agar) could be utilized as an

alternative to the standard ISO 10272-1 protocol [102] used for the detection of *Campylobacter* in food [103–105]. For pathogen enumeration, different agars than mCCDA proposed by ISO 10272-2 enumeration method [107], either selective (e.g., Preston agar or Karmali agar) or chromogenic (e.g., Campylobacter selective agar; CASA®, Brilliance™ Campy count agar, BCCA) which have been found to perform equally well to the recommended mCCDA in enumerating colonies of *Campylobacter* spp. [63,96,108–112], could be used after the initial dilution of the food sample. After all, the colored colonies of *Campylobacter* on chromogenic agars are easier to record and count than those on the charcoal-based agars, such as mCCDA.

Enrichment of chicken meat samples in Preston broth for 24 h followed by plating on mCCDA performed better than 48 h enrichment in Bolton broth and plating on mCCDA [96], while this alternative enrichment and plating combination was taken into account in the revised ISO method for *Campylobacter* spp. detection (i.e., procedure B in the ISO 10272-1 protocol) [102]. Furthermore, the parallel use of the detection and enumeration procedures improves the recovery of *Campylobacter* spp., whereas chromogenic agars, like CASA and BCCA, should be considered as secondary plating media for simultaneous or optional use together with the ISO recommended mCCDA and/or even as suitable alternatives to the latter selective agar [63]. In any case, it has been proved that the previously mentioned enrichment and/or plating alternatives can significantly affect the recovery of *Campylobacter* strains from food [73,94–101].

3.1.1. Composition of Culture Media for Detection/Enumeration

In food samples with an expected low number of *Campylobacter* spp. and low concentration levels of accompanying (background) microbiota and/or stressed campylobacters (e.g., cooked or frozen samples), the enrichment in Bolton broth is highly recommended for pathogen detection, whereas for samples with high concentration levels of background microbiota other than *Campylobacter* spp. (e.g., raw meats including poultry or raw milk), the use of Preston broth as a sample enrichment medium is suggested [96,102].

The reduced recovery of campylobacters from raw chicken meat after sample enrichment in Bolton broth compared to direct plating from the initial dilution of the food sample, is likely attributable to the presence of cefoperazone in the liquid medium. The latter is a third generation β-lactam antibiotic which is supplemented into Bolton enrichment broth, as well as in mCCDA plates utilized for pathogen isolation. Foods containing microbiota resistant to third generation β-lactams, including cefoperazone, such as raw chicken containing β-lactam-degrading *E. coli*, namely extended-spectrum β-lactamase-producing; ESBL-producing *E. coli*, may lead to the overgrowth of the accompanying flora during the enrichment procedure in Bolton broth, which in turns leads to the suppression of *Campylobacter* spp. rendering them non detectable following the subculturing on agar plates. Limited growth of *Campylobacter* co-cultured with ESBL-producing *E. coli* in Bolton broth is hypothesized to be due to oxygen availability during the growth of *Campylobacter* in the medium [113]. In such a case, different enrichment broth and plating agar combinations, based on different principles of selectivity (e.g., Preston broth combined with Preston agar), are considered more suitable for combating this type of resistant microbiota and allowing for better detection of *Campylobacter* spp. in chicken meat [96,102,103,105]. Alternatively, restoring the selectivity of Bolton broth and mCCDA can be achieved by supplementation of these media with β-lactamase inhibitors or inhibitory bacterial growth agents (e.g., antibiotics) to overcome the problem of ESBL-producing *E. coli* [114–121].

4. Confirmation and Identification of *Campylobacter* spp.

Using conventional microbiological methods and following the enrichment of food sample or direct plating from the initial dilution of the food sample and isolation of *Campylobacter* spp. on selective plating media, there is a need to confirm the presence of *Campylobacter* and then to proceed, if necessary, with the identification of *Campylobacter* species [102,107]. Biochemical tests are routinely used for confirmation and identification purposes, even though molecular methods, such as

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polymerase chain reaction (PCR) techniques (e.g., multiplex or quantitative PCR), are gaining more and more ground lately.

4.1. Biochemical Differentiation of Campylobacter species

Among the *Campylobacter* spp. present in food, the most frequently encountered species, as already highlighted, are *C. jejuni* and *C. coli*. However, other species have been described (e.g., *C. lari*, *C. upsaliensis*; Supplementary Table S1), some key characteristics of which permit their differentiation (Table 1) [102,107].

With a closer look, Table 1 reveals that the only biochemical test that can distinguish between *C. jejuni* and *C. coli* is hippurate hydrolysis, with the former species showing a positive reaction compared to the latter species which give a negative reaction to the presence of hippurate. Thence, this test is typically used to differentiate *C. jejuni* and *C. coli*. Nevertheless, given the fact that some hippurate-negative *C. jejuni* strains have been reported [122,123], hippurate hydrolysis is not a robust criterion for differentiating thermotolerant *Campylobacter* species.

Table 1. Key biochemical characteristics of *Campylobacter* species encountered in foods.

Characteristic	*C. jejuni*	*C. coli*	*C. lari*	*C. upsaliensis*
Catalase activity	+ [1]	+	+	- [2] or weak
Hippurate hydrolysis	+ [3]	-	-	-
Indoxyl acetate hydrolysis	+	+	-	+

[1] +: positive reaction. [2] -: negative reaction. [3] Some hippurate-negative *C. jejuni* strains have been reported [122,123].

4.2. Molecular Methods for Differentiating Campylobacter species

The inherent disadvantage that biochemical differentiation of *C. jejuni* and *C. coli* has because of the low specificity (*ca.* 20%) hippurate hydrolysis exhibits to some hippurate-negative strains of *C. jejuni* [122,123], together with the laborious and time-consuming character of biochemical identification tests, stimulated the development of molecular diagnostic methods and techniques as alternatives to the classical culture-dependent approach to differentiation of *Campylobacter* species.

Serological methods (i.e., immunoassays) (e.g., enzyme-linked immunosorbent assay; ELISA) [124–128], biosensors for the on-site detection of foodborne pathogens [129,130], DNA hybridization techniques (e.g., loop-mediated isothermal amplification; LAMP) [126,131,132], DNA fingerprinting techniques (e.g., multilocus sequence typing; MLST) [133–135] and above all PCR-based method and techniques (e.g., multiplex PCR; mPCR, quantitative or real time PCR; qPCR/rt-PCR), have been developed for the fastest and most efficient identification and differentiation of *Campylobacter* species among other foodborne pathogens. It should be noted though that some DNA fingerprinting techniques are more sophisticated (e.g., pulsed-field gel electrophoresis; PFGE, whole-genome sequencing; WGS) and require well-trained personnel with a know-how-to conduct the technique and interpret the data. Due to their enormous discriminatory power these molecular typing methods are preferable tools in outbreak investigations rather than the routine monitoring of pathogens [136–140]. For this reason, PCR techniques are the method of choice for *Campylobacter* differentiation during laboratory screening for the pathogen.

4.2.1. PCR-Based Methods and Techniques

The technique of mPRC has been widely studied by several researchers in an effort to find a fast and at the same time reliable means of identifying isolated *Campylobacter* species [141–143]. The combination of food sample enrichment with multiplex real-time PCR (mrt-PCR) results in a more rapid detection and identification of *Campylobacter* spp. isolated from food [144], compared to the standard ISO method utilizing the biochemical identification of the isolates [102]. Nevertheless, the enrichment of the food sample as well as the initial *Campylobacter* load in the matrix significantly affect the isolation frequency and the recovery rate of different subtypes of *C. jejuni* [145] and of many

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Campylobacter species. In such a case, combining mPCR with the pre-enrichment in Brucella broth and further enrichment in Preston broth of chicken meat samples led to the identification of the majority of isolated campylobacters as *C. coli* (53%) than *C. jejuni* (47%) [146].

The quantitative determination of *Campylobacter* spp. in contaminated foods and generally in the food chain is crucial, among others in order to comply with imposed EU microbiological criteria for *Campylobacter* in broiler carcasses [147]. Quantitative molecular PCR-based methods, such as rt-PCR techniques, have been developed for such quantification purposes [148–151], although currently only the culture-based ISO method is officially approved for pathogen enumeration [104]. Nonetheless, PCR-based methods suffer from the inability to differentiate between live and dead cells of the target microorganism and the apparent PCR signal that may occur from DNA originating from those dead cells. Therefore, quantitative viability rt-PCR assays have been proposed to normalize on the one hand the underestimation of *Campylobacter* spp. recovered from different food matrices, on the other to allow for reliable differentiation between live and dead *Campylobacter* and thus accurate estimations of pathogen concentration in foods [79,152–155].

5. Biofilm-forming ability of *Campylobacter* spp.

The survival of campylobacter in the food chain remains a paradox since the bacterium is a fastidious organism with characteristic special growth requirements for successful subculturing in the laboratory (e.g., heat-resistant, microaerophilic organism requiring the presence of blood in its culture medium). Recently, biofilm formation has been proposed as the main mechanism of maintenance and transmission for the pathogen from animals to humans [156]. In general, the biofilm-forming ability of *Campylobacter* is strain-dependent and varies among organism's isolated strains [157,158], as well as between different *Campylobacter* spp. [159–161], while it is also affected by the presence of other bacterial species [162–167]. Regarding the biofilm-forming ability of *C. jejuni* and *C. coli*, the latter isolates seem able to form biofilms significantly better compared to *C. jejuni* isolates ($p < 0.05$) [157,160] and that could be another reason for the increased prevalence of *C. coli* against *C. jejuni* in the chicken meat samples.

The ability of *C. jejuni* to form a biofilm is highly dependent on the strain and the type of abiotic surface on which it is found [159]. Teh et al. [165] concluded that *C. jejuni* exhibits a much weaker biofilm-forming ability compared to other bacteria, such as *Pseudomonas* spp., *Staphylococcus aureus*, *Salmonella* spp., and *E. coli*. However, in controlled mixed-microbial populations of a specific *C. jejuni* strain (sequence type; ST-474) with *Enterococcus faecalis* and/or *Staphylococcus* sp., optical intense biofilms for the two species were developed when they were grown with *C. jejuni*, while *C. jejuni* cells were recovered from most of the biofilms containing *E. faecalis* and/or *Staphylococcus* sp. [165]. That was the case and in the studies of Ica et al. [166] and Sterniša et al. [167], where the co-cultivation of *C. jejuni* with *P.aeruginosa* and *P. fragi*, respectively, resulted in the increased determined number of culturable biofilm *C. jejuni* cells. In contrast to monoculture biofilms, the mixed-culture biofilms of *C. jejuni* with pseudomonads had significantly enhanced mechanical strength [166]. Enhanced biofilm formation was also observed for *C. jejuni* and *C. coli* in the presence of *S. aureus*, with increased aerotolerance and survivability in parallel for the *Campylobacter* strains [162].

5. Conclusions

The prevalence and distribution of *Campylobacter* spp. in raw poultry meat from broiler carcasses depends on a variety of factors, such as the sampling method, part of the animal carcass from which the meat sample is obtained, seasonality of sampling, the isolation procedure followed with the different enrichment and plating media utilized for pathogen isolation along with the methods and techniques used for *Campylobacter* spp. differentiation, as well as the biofilm-forming ability of the isolated *Campylobacter* strains with regards to their co-culture with other bacterial species. All these factors should be considered when conducting field surveys or monitoring for *Campylobacter* presence in naturally contaminated poultry meat samples. At the same time, the indicated number of factors highlights the multifactorial dimension and complexity of the phenomenon when interpreting results for the recovery of *Campylobacter* spp. from poultry meat. Thus, the noticed epidemiological transition

from the established predominance of *C. jejuni* to the ever-increasing recovery of *C. coli* in raw chicken meat could be the result of such a versatile effect. The present review attempted for the first time to elucidate the causes of this noteworthy epidemiological swift in prevalence and distribution of *Campylobacter* species on the food matrix itself, without extending to the interaction between pathogen and human host.

Supplementary Materials: The following supporting information can be downloaded at: www.mdpi.com/xxx/s1, Table S1: List of thermotolerant *Campylobacter* species currently identified.

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References

1. EFSA (European Food Safety Authority); ECDC (European Centre for Disease Prevention and Control). The European Union one health 2021 zoonoses report. *ESFA J.* **2022**, *20*, e07666. https://doi.org/10.2903/j.efsa.2022.7666
2. Kumagai, Y.; Pires, S.M.; Kubota, K.; Asakura, H. Attributing human foodborne diseases to food sources and water in Japan using analysis of outbreak surveillance data. *J. Food Prot.* **2020**, *83*, 2087–2094. https://doi.org/10.4315/JFP-20-151
3. Scallan, E.; Hoekstra, R.M.; Angulo, F.J.; Tauxe, R.V.; Widdowson, M.-A.; Roy, S.L.; Jones, J.L.; Grifiin, P.M. Foodborne illness acquired in the United States – Major pathogens, *Emerg. Infect. Dis.* **2011**, *17*, 7–15. https://doi.org/10.3201/eid1701.P11101
4. Walter, E.J.S.; Griffin, P.M.; Bruce, B.B.; Hoekstra, R.M. Estimating the number of illnesses caused by agents transmitted commonly through food: A scoping review. *Foodborne Pathog. Dis.* **2021**, *18*, 841–858. http://doi.org/10.1089/fpd.2021.0038
5. Bisht, A.; Kamble, M.P.; Choudhary, P.; Chaturvedi, K.; Kohli, G.; Juneja, V.K.; Sehgal, S.; Taneja, N.K. A surveillance of food borne disease outbreaks in India: 2009–2018. *Food Control* **2021**, *121*, 107630. https://doi.org/10.1016/j.foodcont.2020.107630
6. Li, W.; Pires, S.M.; Liu, Z.; Ma, X.; Liang, J.; Jiang, Y.; Chen, J.; Liang, J.; Wang, S.; Wang, L.; Wang, Y.; Meng, C.; Huo, X.; Lan, Z.; Lai, S.; Liu, C.; Han, H.; Liu, J. Fu, P.; Guo, Y. Surveillance of foodborne disease outbreaks in China, 2003–2017. *Food Control* **2020**, *118*, 107359. https://doi.org/10.1016/j.foodcont.2020.107630
7. Zhao, J.; Cheng, H.; Wang, Z.; Fu, P.; Guo, Y.; Yang, S. Attribution analysis of foodborne disease outbreaks related to meat and meat products in China, 2002–2017. *Foodborne Pathog. Dis.* **2022**, *19*, 839–847. http://doi.org/10.1089/fpd.2022.0028
8. Batz, M.B.; Hoffmann, S.; Morris, Jr., J.G. Ranking the disease burden of 14 pathogens in food sources in the United States using attribution data from outbreak investigations and expert elicitation. *J. Food Prot.* **2012**, *75*, 1278–1291. https://doi.org/10.4315/0362-028X.JFP-11-418
9. Batz, M.B.; Richardson, L.C.; Bazaco, M.C.; Parker, C.C.; Chirtel, S.J.; Cole, D.; Golden, N.J.; Griffin, P.M.; Gu, W.; Schmitt, S.K.; Wolpert, B.J.; Kufel, J.S.Z.; Hoekstra, R.M. Recency-weighted statistical modeling approach to attribute illnesses caused by 4 pathogens to food sources using outbreak data, United States. *Emerg. Infect. Dis.* **2021**, *27*, 214–222. https://doi.org/10.3201/eid2701.203832
10. Silva, J.; Leite, D.; Fernandes, M.; Mena, C.; Gibbs, P.A.; Teixeira, P. *Campylobacter* spp. as a foodborne pathogen: a review. *Front. Microbiol.* **2011**, *2*, 200. https://doi.org/10.3389/fmicb.2011.00200
11. Stern, N.J.; Hernandez, M.P.; Blankenship, L.; Deibel, K.E.; Doores, S.; Doyle, M.P.; Ng, H.; Pierson, M.D.; Sofos, J.N.; Sveum, W.H.; Westhoff, D.C. Prevalence and distribution of *Campylobacter jejuni* and *Campylobacter coli* in retail meats. *J. Food Prot.* **1985**, *48*, 595–599. https://doi.org/10.4315/0362-028X-48.7.595

12. Mataragas, M.; Skandamis, P.N.; Drosinos, E.H. Risk profiles of pork and poultry meat and risk ratings of various pathogen/product combinations. *Int. J. Food. Microbiol.* **2008**, *126*, 1–12. https://doi.org/10.1016/j.ijfoodmicro.2008.05.014
13. Scharff, R.L. Food attribution and economic cost estimates for meat- and poultry-related illnesses. *J. Food Prot.* **2020**, *80*, 959–967. https://doi.org/10.4315/JFP-19-548
14. Teixeira, J.S.; Boras, V.F.; Hetman, B.J.; Taboada, E.N.; Inglis, G.D. Molecular epidemiological evidence implicates cattle as a primary reservoir of *Campylobacter jejuni* infecting people via contaminated chickens. *Pathogens* **2022**, *11*, 1366. https://doi.org/10.3390/pathogens11111366
15. Ritchie, H.; Rosado, P.; Roser, M. Our World in Data: Meat and Dairy Production. 2017, Available online: https://ourworldindata.org/meat-production#citation (accessed on 12 April 2023).
16. Parte, A.C.; Sardà Carbasse, J.; Meier-Kolthoff, J.P.; Reimer, L.C.; Göker, M. List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. *Int. J. Syst. Evol. Microbiol.* **2022**, *70*, 5607–5612. https://doi.org/10.1099/ijsem.0.004332
17. Genus *Campylobacter*. Available online: https://www.bacterio.net/genus/campylobacter (accessed on 7 May 2023).
18. Aydin, F.; Abay, S.; Kayman, T.; Karakaya, E.; Mustak, H.K.; Mustak, I.B.; Bilgen, N.; Goncuoglu, M.; Duzler, A.; Guran, O.; Sahin, O.; Saticioglu, I.B. *Campylobacter anatolicus* sp. nov., a novel member of the genus *Campylobacter* isolated from feces of Anatolian Ground Squirrel (*Spermophilus xanthoprymnus*) in Turkey. *Syst. Appl. Microbiol.* **2021**, *44*, 126265. https://doi.org/10.1016/j.syapm.2021.126265
19. Boukerb, A.M.; Penny, C.; Serghine, J.; Walczak, C.; Cauchie, H.M.; Miller, W.G.; Losch, S.; Ragimbeau, C.; Mossong, J.; Mégraud, F.; Lehours, P.; Bénéjat, L.; Gourmelot, M. *Campylobacter armoricus* sp. nov., a novel member of the *Campylobacter lari* group isolated from surface water and stools from humans with enteric infection. *Int. J. Syst. Evol. Microbiol.* **2019**, *69*, 3969–3979. https://doi.org/10.1099/ijsem.0.003836
20. Bryant, E.; Shen, Z.; Mannion, A.; Patterson, M.; Buczek, J.; Fox, J.G. *Campylobacter taeniopygiae* sp. nov., *Campylobacter aviculae* sp. nov., and *Campylobacter estrildidarum* sp. nov., novel species isolated from laboratory-maintained zebra finches. *Avian Dis.* **2020**, *64*, 457–466. https://doi.org/10.1637/aviandiseases-D-20-00019
21. Rossi, M.; Debruyne, L.; Zanoni, R.G.; Manfreda, G.; Revez, J.; Vandamme, P. *Campylobacter avium* sp. nov., a hippurate-positive species isolated from poultry. *Int. J. Syst. Evol. Microbiol.* **2009**, *59*, 2364–2369. https://doi.org/10.1099/ijs.0.007419-0
22. Phung, C.; Scott, P.C.; Dekiwadia, C.; Moore, R.J.; Van T.T.H. *Campylobacter bilis* sp. nov., isolated from chickens with spotty liver disease. *Int. J. Syst. Evol. Microbiol.* **2022**, *72*, 5314. https://doi.org/10.1099/ijsem.0.005314
23. Gilbert, M.J.; Zomer, A.L.; Timmerman, A.J.; Spaninks, M.P.; Rubio-Garcia, A.; Rossen, J.W.; Duim, B.; Wagenaar, J.A. *Campylobacter blaseri* sp. nov., isolated from common seals (*Phoca vitulina*). *Int. J. Syst. Evol. Microbiol.* **2018**, *68*, 1787–1794. https://doi.org/10.1099/ijsem.0.002742
24. Inglis, G.D.; Hoar, B.M.; Whiteside, D.P.; Morck, D.W. *Campylobacter canadensis* sp. nov., from captive whooping cranes in Canada. *Int. J. Syst. Evol. Microbiol.* **2007**, *57*, 2636–2644. https://doi.org/10.1099/ijs.0.65061-0
25. Véron, M.; Chatelain, R. Taxonomic study of the genus *Campylobacter* Sebald and Véron and designation of the neotype strain for the type species, *Campylobacter fetus* (Smith and Taylor) Sebald and Véron. *Int. J. Syst. Bact.* **1973**, *23*:122–134. https://doi.org/10.1099/00207713-23-2-122
26. Tanner, A.C.R.; Badger, S.; Lai, C.H.; Listgarten, M.A.; Visconti, R.A.; Socransky, S.S. *Wolinella* gen. nov., *Wolinella succinogenes* (*Vibrio succinogenes* Wolin et al.) comb. nov., and description of *Bacteroides gracilis* sp. nov., *Wolinella recta* sp. nov., *Campylobacter concisus* sp. nov., and *Eikenella corrodens* from humans with periodontal disease. *Int. J. Syst. Bacteriol.* **1981**, *31*, 432–445. https://doi.org/10.1099/00207713-31-4-432
27. Koziel, M.; O'Doherty, P.; Vandamme, P.; Corcoran, G.D.; Sleator R.D.; Lucey, B. *Campylobacter corcagiensis* sp. nov., isolated from faeces of captive lion-tailed macaques (Macaca silenus). *Int. J. Syst. Evol. Microbiol.* **2014**; *64*, 2878–2883. https://doi.org/10.1099/ijs.0.063867-0
28. Zanoni, R.G.; Debruyne, L.; Rossi, M.; Revez, J.; Vandamme, P. *Campylobacter cuniculorum* sp. nov., from rabbits. *Int. J. Syst. Evol. Microbiol.* **2009**, *59*, 1666–1671. https://doi.org/10.1099/ijs.0.007286-0
29. Vandamme, P.; Falsen, E.; Rossau, R.; Hoste, B.; Segers, P.; Tytgat, R.; De Ley, J. Revision of *Campylobacter*, *Helicobacter*, and *Wolinella* taxonomy: emendation of generic descriptions and proposal of *Arcobacter* gen. nov. *Int. J. Syst. Bacteriol.* **1991**, *41*, 88–103. https://doi.org/10.1099/00207713-41-1-88
30. Sebald, M.; Veron, M. [BASE DNA CONTENT AND CLASSIFICATION OF VIBRIOS]. *Ann. Inst. Pasteur (Paris)* **1963**, *105*, 897–910.
31. Piccirillo, A.; Nier,o G.; Calleros, L.; Perez, R.; Naya, H.; Iraola, G. *Campylobacter geochelonis* sp. nov. isolated from the western Hermann's tortoise (*Testudo hermanni hermanni*). *Int. J. Syst. Evol. Microbiol.* **2016** *66*, 3468–3476. https://doi.org/10.1099/ijsem.0.001219
32. Vandamme, P.; Daneshvar, M.I.; Dewhirst, F.E.; Paster, B.J.; Kersters, K.; Goossens, H.; Moss, C.W. Chemotaxonomic analyses of *Bacteroides gracilis* and *Bacteroides ureolyticus* and reclassification of *B. gracilis*

as *Campylobacter gracilis* comb. nov. *Int. J. Syst. Bacteriol.* **1995**, *45*, 145–152. https://doi.org/10.1099/00207713-45-1-145

33. Stanley, J.; Burnens, A.P.; Linton, D.; On, S.L.; Costas, M.; Owen, R.J. *Campylobacter helveticus* sp. nov., a new thermophilic species from domestic animals: characterization, and cloning of a species-specific DNA probe. *J. Gen. Microbiol.* **1992**, *138*, 2293–2303. https://doi.org/10.1099/00221287-138-11-2293
34. Van, T.T.; Elshagmani, E.; Gor, M.C.; Scott, P.C.; Moore, R.J. *Campylobacter hepaticus* sp. nov., isolated from chickens with spotty liver disease. *Int. J. Syst. Evol. Microbiol.* **2016**, *66*, 4518–4524. https://doi.org/10.1099/ijsem.0.001383
35. Lawson, A.J.; On, S.L.; Logan, J.M.; Stanley, J. *Campylobacter hominis* sp. nov., from the human gastrointestinal tract. *Int. J. Syst. Evol. Microbiol.* **2001**, *51*, 651–660. https://doi.org/10.1099/00207713-51-2-651
36. Gebhart, C.J.; Edmonds, P.; Ward, G.E.; Kurtz, H.J.; Brenner, D.J. "*Campylobacter hyointestinalis*" sp. nov.: a new species of *Campylobacter* found in the intestines of pigs and other animals. *J. Clin. Microbiol.* **1985**, *21*, 715–720. https://doi.org/10.1128/jcm.21.5.715-720.1985
37. Gilbert, M.J.; Kik, M.; Miller, W.G.; Duim, B.; Wagenaar, J.A. *Campylobacter iguaniorum* sp. nov., isolated from reptiles. *Int. J. Syst. Evol. Microbiol.* **2015**, *65*, 975–982. https://doi.org/10.1099/ijs.0.000048
38. Foster, G.; Holmes, B.; Steigerwalt, A.G.; Lawson, P.A.; Thorne, P.; Byrer, D.E.; Ross, H.M.; Xerry, J.; Thompson, P.M.; Collins, M.D. *Campylobacter insulaenigrae* sp. nov., isolated from marine mammals. *Int. J. Syst. Evol. Microbiol.* **2004**, *54*, 2369–2373. https://doi.org/10.1099/ijs.0.63147-0
39. Logan, J.M.; Burnens, A.; Linton, D.; Lawson, A.J.; Stanley, J. *Campylobacter lanienae* sp. nov., a new species isolated from workers in an abattoir. *Int. J. Syst. Evol. Microbiol.* **2000**, *50*, 865–872. https://doi.org/10.1099/00207713-50-2-865
40. Benjamin, J.; Leaper, S.; Owen, R.J.; Skirrow, M.B. Description of *Campylobacter laridis*, a new species comprising the nalidixic acid resistant thermophilic *Campylobacter* (NARTC) group. *Curr. Microbiol.* **1983**, *8*, 231–238. https://doi.org/10.1007/BF01579552
41. Lynch, C.; Peeters, C.; Walsh, N.; McCarthy, C.; Coffey, A.; Lucey, B.; Vandamme, P. *Campylobacter majalis* sp. nov. and *Campylobacter suis* sp. nov., novel *Campylobacter* species isolated from porcine gastrointestinal mucosa. *Int. J. Syst. Evol. Microbiol.* **2022**, *72*,5510. https://doi.org/10.1099/ijsem.0.005510
42. Antezack, A.; Boxberger, M.; Rolland, C.; Ben Khedher, M.; Monnet-Corti, V.; La Scola, B. Isolation and characterization of *Campylobacter massiliensis* sp. nov., a novel *Campylobacter* species detected in a gingivitis subject. *Int. J. Syst. Evol. Microbiol.* **2021**, *71*, 5039. https://doi.org/10.1099/ijsem.0.005039
43. Roop Ii, R.M.; Smibert, R.M.; Johnson, J.L.; Krieg, N.R. *Campylobacter mucosalis* (Lawson, Leaver, Pettigrew, and Rowland 1981) comb. nov.: emended description. *Int. J. Syst. Bacteriol.* **1985**, *35*, 189–192. https://doi.org/10.1099/00207713-35-2-189
44. Bloomfield, S.; Wilkinson, D.; Rogers, L.; Biggs, P.; French, N.; Mohan, V.; Savoian, M.; Venter, P.; Midwinter, A. *Campylobacter novaezeelandiae* sp. nov., isolated from birds and water in New Zealand. *Int. J. Syst. Evol. Microbiol.* **2020**, *70*, 3775–3784. https://doi.org/10.1099/ijsem.0.004231
45. Caceres, A.; Munoz, I.; Iraola, G.; Diaz-Viraque, F.; Collado, L. *Campylobacter ornithocola* sp. nov., a novel member of the *Campylobacter lari* group isolated from wild bird faecal samples. *Int. J. Syst. Evol. Microbiol.* **2017**, *67*, 1643–1649. https://doi.org/10.1099/ijsem.0.001822
46. Debruyne, L.; On, S.L.; De Brandt, E.; Vandamme, P. Novel *Campylobacter lari*-like bacteria from humans and molluscs: description of *Campylobacter peloridis* sp. nov., *Campylobacter lari* subsp. *concheus* subsp. nov. and *Campylobacter lari* subsp. *lari* subsp. nov. *Int. J. Syst. Evol. Microbiol.* **2009**, *59*, 1126–1132. https://doi.org/10.1099/ijs.0.000851-0
47. Gilbert, M.J.; Miller, W.G.; Leger, J.S.; Chapman, M.H.; Timmerman, A.J.; Duim, B.; Foster, G.; Wagenaar, J.A. *Campylobacter pinnipediorum* sp. nov., isolated from pinnipeds, comprising *Campylobacter pinnipediorum* subsp. *pinnipediorum* subsp. nov. and *Campylobacter pinnipediorum* subsp. *caledonicus* subsp. nov. *Int. J. Syst. Evol. Microbiol.* **2017**, *67*, 1961–1968. https://doi.org/10.1099/ijsem.0.001894
48. Silva, M.F.; Pereira, G.; Carneiro, C.; Hemphill, A.; Mateus, L.; Lopes-da-Costa, L.; Silva, E. *Campylobacter portucalensis* sp. nov., a new species of *Campylobacter* isolated from the preputial mucosa of bulls. *PLoS One* **2020**, *15*, e0227500. https://doi.org/10.1371/journal.pone.0227500
49. Etoh, Y.; Dewhirst, F.E.; Paster, B.J.; Yamamoto, A.; Goto, N. *Campylobacter showae* sp. nov., isolated from the human oral cavity. *Int. J. Syst. Bacteriol.* **1993**, *43*, 631–639. https://doi.org/10.1099/00207713-43-4-631
50. Debruyne, L.; Broman, T.; Bergstrom, S.; Olsen, B.; On, S.L.; Vandamme, P. *Campylobacter subantarcticus* sp. nov., isolated from birds in the sub-Antarctic region. *Int. J. Syst. Evol. Microbiol.* **2010**, *60*, 815–819. https://doi.org/10.1099/ijs.0.011056-0
51. Sandstedt, K.; Ursing, J. Description of *Campylobacter upsaliensis* sp. nov. previously known as the CNW group. *Syst. Appl. Microbiol.* **1991**, *14*, 39–45. https://doi.org/10.1016/S0723-2020(11)80359-0
52. Vandamme, P.; Debruyne, L.; De Brandt, E.; Falsen, E. Reclassification of *Bacteroides ureolyticus* as *Campylobacter ureolyticus* comb. nov., and emended description of the genus *Campylobacter*. *Int. J. Syst. Evol. Microbiol.* **2010**, *60*, 2016–2022. https://doi.org/10.1099/ijs.0.017152-0

53. Debruyne, L.; Broman, T.; Bergstrom, S.; Olsen, B.; On, S.L.; Vandamme, P. *Campylobacter volucris* sp. nov., isolated from black-headed gulls (Larus ridibundus). *Int. J. Syst. Evol. Microbiol.* **2010**, *60*, 1870–1875. https://doi.org/10.1099/ijs.0.013748-0
54. Parisi, A.; Chiara, M.; Caffara, M.; Mion, D.; Miller, W.G.; Caruso, M.; Manzari, C.; Florio, D.; Capozzi, L.; D'Erchia, A.M.; Manzulli, V.; Zanoni, R.G. *Campylobacter vulpis* sp. nov. isolated from wild red foxes. *Syst. Appl. Microbiol.* **2021**, *44*, 126204. https://doi.org/10.1016/j.syapm.2021.126204
55. Ghafir, Y.; China, B.; Dierick, K.; De Zutter, L.; Daube, G. A seven-year survey of *Campylobacter* contamination in meat at different production stages in Belgium. *Int. J. Food Microbiol.* **2007**, *116*, 111–120. https://doi.org/10.1016/j.ijfoodmicro.2006.12.012
56. Wagenaar, J.A.; van der Graaf-van Blools, L. Chapter 3.10.4. Infection with *Campylobacter jejuni* and *C. coli*. In *Manual of Diagnostic Tests and Vaccines for Terrestrial Animals*, OIE; World Organization for Animal Health, 2018; pp. 1669–1677. Available online: https://www.woah.org/en/what-we-do/standards/codes-and-manuals/terrestrial-manual-online-access/ (accessed on 11 April 2023).
57. Jorgensen, F.; Ellis-Iversen, J.; Rushton, S.; Bull, S.A.; Harris; S.A.; Bryan, S.J.; Gonzalez, A.; Humphrey, T.J. Influence of season and geography on *Campylobacter jejuni* and *C. coli* subtypes in housed broiler flocks reared in Great Britain. *Appl. Environ. Microbiol.* **2011**, *77*, 3741–3748. https://doi.org/10.1128%2FAEM.02444-10
58. Habib, I.; Mohamed, M.-Y.I.; Lakshmi, G.B.; Khan, M.; Li, D. Quantification of *Campylobacter* contamination on chicken carcasses sold in retail markets in the United Arab Emirates. *Int. J. Food Contam.* **2022**, *9*, 9. https://doi.org/10.1186/s40550-022-00095-4
59. Manfreda, G.; De Cesare, A.; Bondioli, V.; Stern, J.N.; Franchini, A. Enumeration and identity of *Campylobacter* spp. in Italian broilers. *Poult. Sci.* **2006**, *85*, 556–562. https://doi.org/10.1093/ps/85.3.556
60. Repérant, E.; Laisney, M.J.; Nagard, B.; Quesne, S.; Rouxel, S.; Le Gall, F.; Chemaly, M.; Denis, M. Influence of enrichment and isolation media on the detection of *Campylobacter* spp. in naturally contaminated chicken samples. *J. Microbiol. Methods* **2016**, *128*, 42–47. https://dx.doi.org/10.1016/j.mimet.2016.06.028
61. Wieczorek, K.; Bocian, Ł.; Osek, J. Prevalence and antimicrobial resistance of *Campylobacter* isolated from carcasses of chickens slaughtered in Poland – a retrospective study. *Food Control* **2020**, *112*, 107159. https://doi.org/10.1016/j.foodcont.2020.107159
62. Wieczorek, K.; Szewczyk, R.; Osek, J. Prevalence, antimicrobial resistance, and molecular characterization of *Campylobacter jejuni* and *C. coli* isolated from retail raw meat in Poland. *Vet. Med.* **2012**, *57*, 293–299.
63. Andritsos, N.D.; Tzimotoudis, N.; Mataragas, M. Estimating the performance of four culture media used for enumeration and detection of *Campylobacter* species in chicken meat. *LWT* **2020**, *118*, 108808. https://doi.org/10.1016/j.lwt.2019.108808
64. Marinou, I.; Bersimis, S.; Ioannidis, A.; Nicolau, C.; Mitroussia-Ziouva, A.; Legakis, N.J.; Chatzipanagiotou, S. Identification and antimicrobial resistance of *Campylobacter* species isolated from animal sources. *Front. Microbiol.* **2012**, *3*, 58. https://doi.org/10.3389/fmicb.2012.00058
65. Jeffrey, J.S.; Tonooka, K.H.; Lozano, J. (2001). Prevalence of *Campylobacter* spp. from skin, crop, and intestine of commercial broiler chicken carcasses at processing. *Poult. Sci.* **2001**, *80*, 1390–1392. https://doi.org/10.1093/ps/80.9.1390
66. Buhr, R.J.; Berrang, M.E.; Cason, J.A. Bacterial recovery from breast skin of genetically feathered and featherless broiler carcasses immediately following scalding and picking. *Poult. Sci.* **2003**, *82*, 1641–1647.
67. Cason, J.A.; Hinton, Jr., A.;Buhr, R.J. Impact of feathers and feather follicles on broiler carcass bacteria. *Poult. Sci.* **2004**, *83*, 1452–1455. https://doi.org/10.1093/ps/83.8.1452
68. Habib, I.; Sampers, I.; Uyttendaelle, M.; Berkvens, D.; De Zutter, L. Baseline data from a Belgium-wide survey of *Campylobacter* species contamination in chicken meat preparations and considerations for a reliable monitoring program. *Appl. Environ. Microbiol.* **2008**, *74*, 5483–5489. https://doi.org/10.1128/AEM.00161-08
69. Kinde, H.; Genigeorgis, C.A.; Pappaioanou, M. Prevalence of *Campylobacter jejuni* in chicken wings. *Appl. Environ. Microbiol.* **1983**, *45*, 1116–1118. https://doi.org/10.1128/aem.45.3.1116-1118.1983
70. Rayes, H.M.; Genigeorgis, C.A.; Farver, T.B. Prevalence of *Campylobacter jejuni* on turkey wings at the supermarket level. *J. Food Prot.* **1983**, *46*, 292–294. https://doi.org/10.4315/0362-028X-46.4.292
71. Baré, J.; Uyttendaele, M.; Depraetere, O.; Houf, K.; De Zutter, L. Variation in *Campylobacter* distribution on different sites of broiler carcasses. *Food Control* **2013**, *32*, 279–282. https://doi.org/10.1016/j.foodcont.2012.11.011
72. Russell, S.M.; Cox, N.A.; Bailey, J.S. Sampling poultry carcasses and parts to determine bacterial levels. *J. Appl. Poult. Res.* **1997**, *6*, 234–237. https://doi.org/10.1093/japr/6.2.234
73. Sproston, E.L.; Carrillo, C.D.; Boulter-Bitzer, J. The quantitative and qualitative recovery of *Campylobacter* from raw poultry using USDA and Health Canada methods. *Food Microbiol.* **2014**, *44*, 258–263. http://dx.doi.org/10.1016/j.fm.2014.06.003
74. Commission Regulation (EC) 2073/2005. Microbiological criteria for foodstuffs. Available online: https://eur-lex.europa.eu/legal-content/EN/ALL/?uri=CELEX%3A32005R2073 (accessed on 12 April 2023).

75. Commission Regulation (EU) 2017/1495. Amending Regulation (EC) No 2073/2005 as regards *Campylobacter* in broiler carcasses. Available online: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX%3A32017R1495 (accessed on 12 April 2023).
76. Gill, C.O.; Badoni, M.; Moza, L.F.; Barbut, S.; Griffiths, M.W. Microbiological sampling of poultry carcass portions by excision, rinsing, or swabbing. *J. Food Prot.* **2005**, *68*, 2718–2720. https://doi.org/10.4315/0362-028X-68.12.2718
77. Bishop. H.; Evans, J.; Eze, J.I.; Webster, C.; Humphry, R.W.; Beattie, R.; White, J.; Couper, J.; Allison, L.; Brown, D.; Tongue, S.C. Bacteriological survey of fresh minced beef on sale at retail outlets in Scotland in 2019: Three foodborne pathogens, hygiene process indicators, and phenotypic antimicrobial resistance. *J. Food Prot.* **2022**, *85*, 1370–1379. https://doi.org/10.4315/JFP-22-051
78. Stella, S.; Soncini, G.; Ziino, G.; Panebianco, A.; Pedonese, F.; Nuvoloni, R.; Di Giannatale, E.; Colavita, G.; Alberghini, L.; Giaccone, V. Prevalence and quantification of thermophilic *Campylobacter* spp. in Italian retail poultry meat: Analysis of influencing factors. *Food Microbiol.* **2017**, *62*, 232–238. http://dx.doi.org/10.1016/j.fm.2016.10.028
79. Beterams, A.; Tolksdorf, T.; Martin, A.; Stingl, K.; Bandick, N.; Reich, F. Change of *Campylobacter*, *Escherichia coli* and *Salmonella* counts in packaged broiler breast meat stored under modified atmosphere and vacuum conditions at 4 and 10 °C based on cultural and molecular biological quantification. *Food Control* **2023**, *145*, 109337. https://doi.org/10.1016/j.foodcont.2022.109337
80. Proietti, P.C.; Pergola, S.; Bellucci, S.; Menchetti, L.; Miraglia, D.; Franciosini, M.P. Occurrence and antimicrobial susceptibility of *Campylobacter* spp. on fresh and refrigerated chicken meat products in central Italy. *Poult. Sci.* **2018**, *97*, 2895–2901. http://dx.doi.org/10.3382/ps/pey147
81. Andritsos, N.D.; Paramithiotis, S.; Mataragas, M.; Drosinos, E.H. *Listeria monocytogenes* serogroup 1/2 strains have a competitive growth advantage over serotype 4b during refrigerated storage of an artificially contaminated ready-to-eat pork meat product. *Appl. Sci.* **2021**, *11*, 6096. http://dx.doi.org/10.3382/ps/pey147
82. Djennad, A.; Lo lacono, G.; Sarran, C.; Lane, C.; Elson, R.; Höser, C.; Lake, I.R.; Colón-González, F.J.; Kovats, S.; Semenza, J.C.; Bailey, T.C.; Kessel, A.; Fleming, L.E.; Nichols, G.L. Seasonality and the effects of weather on *Campylobacter* infections. *BMC Infect. Dis.* **2019**, *19*, 255. https://doi.org/10.1186/s12879-019-3840-7
83. Guerrin, M.T.; Sir, C.; Sargeant, J.M.; Wadell, L.; O'Connor, A.M.; Wills, R.M.; Bailey, R.H.; Byrd, J.A. The change in prevalence of *Campylobacter* on chicken carcasses during processing. *Poult. Sci.* **2010**, *89*, 1070–1084. https://doi.org/10.3382/ps.2009-00213
84. Jorgensen, F.; Ellis-Iversen, J.; Rushton, S.; Bull, S.A.; Harris, S.A.; Bryan, S.J.; Gonzalez, A.; Humphrey, T.J. Influence of season and geography on *Campylobacter jejuni* and *C. coli* subtypes in housed broiler flocks reared in Great Britain. *Appl. Environ. Microbiol.* **2011**, *77*, 3741–3748. https://doi.org/10.1128/AEM.02444-10
85. Mäesaar, M.; Praakle, K.; Meremäe, K.; Kramarenko, T.; Sõgel, J.; Viltrop, A.; Muutra, K.; Kovalenko, K.; Matt, D.; Hörman, A.; Hänninen, M.-L.; Roasto, M. Prevalence and counts of *Campylobacter* spp. in poultry meat at retail level in Estonia. *Food Control* **2014**, *44*, 72–77. http://dx.doi.org/10.1016/j.foodcont.2014.03.044
86. Kalupahana, R.S.; Mughini-Gras, L.; Kottawatta, S.A.; Somarathne, S.; Gamage, C.; Wagenaar, J.A. Weather correlates of *Campylobacter* prevalence in broilers at slaughter under tropical conditions in Sri Lanka. *Epidemiol. Infect.* **2018**, *146*, 972–979. https://doi.org/10.1017/S0950268818000894
87. Prachantasena, S.; Charununtakorn, P.; Muangnoicharoen, S.; Hankla, L.; Techawal, N.; Chaveerach, P.; Tuitemwong, P.; Chokesajjawatee, N.; Williams, N.; Humphrey, T.; Luangtongkum, T. Climatic factors and prevalence of *Campylobacter* in commercial broiler flocks in Thailand. *Poult. Sci.* **2017**, *96*, 980–985. http://dx.doi.org/10.3382/ps/pew364
88. Jonsson, M.E.; Chriél, M.; Norström, M.; Hofshagen, M. Effect of climate and farm environment on *Campylobacter* spp. colonization in Norwegian broiler flocks. *Prev. Vet. Med.* **2012**, *107*, 95–104. http://dx.doi.org/10.1016/j.prevetmed.2012.05.002
89. Nylen, G.; Dunstan, F.; Palmer, S.R.; Andersson, Y.; Bager, F.; Cowden, J.; Feierl, G.; Galloway, Y.; Kapperud, G.; Megraud, F.; Molbak, K.; Petersen, L.R.; Ruutu, P. The seasonal distribution of campylobacter infection in nine European countries and New Zealand. *Epidemiol. Infect.* **2002**, *128*, 383–390. https://doi.org/10.1017/S0950268802006830
90. Urdaneta, S.; Lorca-Oró, C.; Dolz, R.; López-Soria, S.; Cerdà-Cuéllar, M. In a warm climate, ventilation, indoor temperature and outdoor relative humidity have significant effects on *Campylobacter* spp. colonization in chicken broiler farms which can occur in only 2 days. *Food Microbiol.* **2023**, *109*, 104118. https://doi.org/10.1016/j.fm.2022.104118
91. Smith, O.M.; Cornell, K.A.; Crossley, M.S.; Crespo, R.; Jones, M.S.; Snyder, W.E.; Owen, J.P. Wind speed and landscape context mediate *Campylobacter* risk among poultry reared in open environments. *Animals* **2023**, *13*, 492. https://doi.org/10.3390/ani13030492
92. Sommer, H.M.; Borck Høg, B.; Larsen, L.S.; Sørensen, A.I.V.; Williams, N.; Merga, J.Y.; Cerdà-Cuéllae, M.; Urdaneta, S.; Dolz, R.; Wieczorek, K.; Osek, J.; David, B.; Hofshagen, M.; Jonsson, M.; Wagenaar, J.A.; Bolder, N.; Rosenquist, H. Analysis of farm specific risk factors for *Campylobacter* colonization of broilers in six European countries. *Microb. Risk Anal.* **2016**, *2–3*, 16–26. http://dx.doi.org/10.1016/j.mran.2016.06.002

93. Wong, T.L.; Hollis, L.; Cornelius, A.; Nicol, C.; Cook, R.; Hudson, J.A. Prevalence, numbers, and subtypes of *Campylobacter jejuni* and *Campylobacter coli* in uncooked retail meat samples. *J. Food. Prot.* **2007**, *70*, 566–573. https://doi.org/10.4315/0362-028X-70.3.566
94. Baylis, C.L.; MacPhee, S.; Martin, K.W.; Humphrey, T.J.; Betts, R.P. Comparison of three enrichment media for the isolation of *Campylobacter* spp. from foods. *J. Appl. Microbiol.* **2000**, *89*, 884–891. https://doi.org/10.1046/j.1365-2672.2000.01203.x
95. Carrillo, C.D.; Plante, D.; Iugovaz, I.; Kenwell, R.; Bélanger, G.; Boucher, F.; Poulin, N.; Trottier, Y.-L. Method-dependent variability in determination of prevalence of *Campylobacter jejuni* and *Campylobacter coli* in Canadian retail poultry. *J. Food Prot.* **2014**, *77*, 1682–1688. http://doi.org/10.4315/0362-028X.JFP-14-133
96. Habib, I.; Uyttendaele, M.; De Zutter, L. Evaluation of ISO 10272:2006 standard versus alternative enrichment and plating combinations for enumeration and detection of *Campylobacter* in chicken meat. *Food Microbiol.* **2011**, *28*, 1117–1123. https://doi.org/10.1016/j.fm.2011.03.001
97. Jasson, V.; Sampers, I.; Botteldoorn, N.; López-Gálvez, F.; Baert, L.; Denayer, S.; Rajkovic, A.; Habib, I.; De Zutter, L.; Debevere, J.; Uyttendaele, M. Characterization of *Escherichia coli* from raw poultry in Belgium and impact on the detection of *Campylobacter jejuni* using Bolton broth. *Int. J. Food Microbiol.* **2009**, *135*, 248–253. https://doi.org/10.1016/j.ijfoodmicro.2009.09.007
98. Repérant, E.; Laisney, M.J.; Nagard, B.; Quesne, S.; Rouxel, S.; Le Gall, F.; Chemaly, M.; Denis, M. Influence of enrichment and isolation media on the detection of *Campylobacter* spp. in naturally contaminated chicken meat samples. *J. Microbiol. Methods* **2016**, *128*, 42–47. http://dx.doi.org/10.1016/j.mimet.2016.06.028
99. Seliwiorstow, T.; De Zutter, L.; Houf, K.; Botteldoorn, N.; Baré, J.; Van Damme, I. Comparative performance of isolation methods using Preston broth, Bolton broth and their modifications for the detection of *Campylobacter* spp. from naturally contaminated fresh and frozen raw poultry meat. *Int. J. Food Microbiol.* **2016**, *234*, 60–64. http://dx.doi.org/10.1016/j.ijfoodmicro.2016.06.040
100. Stern, N.J.; Line, J.E. Comparison of three methods for recovery of *Campylobacter* spp. from broiler carcasses. *J. Food Prot.* **1992**, *55*, 663–666. https://doi.org/10.4315/0362-028x-55.9.663
101. Williams, L.K.; Jørgensen, F.; Grogono-Thomas, R.; Humphrey, T.J. Enrichment culture for the isolation of *Campylobacter* spp.: Effects of incubation conditions and the inclusion of blood in selective broths. *Int. J. Food Microbiol.* **2009**, *130*, 131–134. https://doi.org/10.1016/j.ijfoodmicro.2009.01.018
102. *ISO 10272-1*; Microbiology of the Food Chain–Horizontal Method for Detection and Enumeration of *Campylobacter* spp.–Part 1: Detection Method. ISO (International Organization for Standardization): Geneva, Switzerland, 2017.
103. Hayashi, M.; Kubota-Hayashi, S.; Natori, T.; Mizuno, T.; Miyata, M.; Yoshida, S.; Zhang, J.; Kawamoto, K.; Ohkusu, K.; Makino, S.; Ezaki, T. Use of blood-free enrichment broth in the development of a rapid protocol to detect *Campylobacter* in twenty-five grams of chicken meat. *Int. J. Food Microbiol.* **2013**, *163*, 41–46. https://doi.org/10.1016/j.ijfoodmicro.2013.02.007
104. Hinton, A.; Cox, N.A.; Selective medium for aerobic incubation of *Campylobacter*. *J. Food Microbiol. Saf. Hyg.* **2018**, *3*, 131. https://doi.org/10.4172/2476-2059.1000131
105. Seliwiorstow, T.; De Zutter, L.; Houf, K.; Botteldoorn, N.; Baré, J.; Van Damme, I. Comparative performance of isolation methods using Preston broth, Bolton broth and their modifications for the detection of *Campylobacter* spp. from naturally contaminated fresh and frozen raw poultry meat. *Int. J. Food Microbiol.* **2016**, *234*, 60–64. https://doi.org/10.1016/j.ijfoodmicro.2016.06.040
106. Yoo, J.-H.; Choi, N.-Y.; Bae, Y.-M.; Lee, J.-S.; Lee, S.-Y. Development of a selective agar plate for the detection of *Campylobacter* spp. in fresh produce. *Int. J. Food Microbiol.* **2014**, *189*, 67–74. https://doi.org/10.1016/j.ijfoodmicro.2014.07.032
107. *ISO 10272-2*; Microbiology of the Food Chain–Horizontal Method for Detection and Enumeration of *Campylobacter* spp.–Part 2: Enumeration Method. ISO (International Organization for Standardization): Geneva, Switzerland, 2017.
108. Ahmed, León-Velarde, C.G.; Odumeru, J.A. Evaluation of novel agars for the enumeration of *Campylobacter* spp. in poultry retail samples. *J. Microbiol. Methods* **2012**, *88*, 304–310. https://doi.org/10.1016/j.mimet.2011.12.011
109. Le Bars, H.; Kayal, S.; Bonnaure-Mallet, M.; Minet, J. CASA chromogenic medium for enteric *Campylobacter* species. *J. Clin. Microbiol.* **2011**, *49*, 3675–3677. https://doi.org/10.1128/jcm.00899-11
110. Levican, A.; Hinton, Jr., A. CAMPYAIR, a new selective, differential medium for *Campylobacter* spp. isolation without the need for microaerobic atmosphere. *Microorganisms* **2022**, *10*, 1403. https://doi.org/10.3390/microorganisms10071403
111. Seliwiorstow, T.; Baré, J.; Verhaegen, B.; Uyttendaele, M.; De Zutter, L. Evaluation of a new chromogenic medium for direct enumeration of *Campylobacter* in poultry meat samples. *J. Food Prot.* **2014**, *77*, 2111–2114. https://doi.org/10.4315/0362-028X.JFP-14-237
112. Teramura, H.; Iwasaki, M.; Ogihara, H. Development of a novel chromogenic medium for improved *Campylobacter* detection from poultry samples. *J. Food Prot.* **2015**, *78*, 1750–1755. https://doi.org/10.4315/0362-028X.JFP-15-115

113. Lanzl, M.I.; van Mastrigt, O.; Zwietering, M.H.; Abee, T.; den Besten, H.M.W. Role of substrate availability in the growth of *Campylobacter* co-cultured with extended spectrum beta-lactamase-producing *Escherichia coli* in Bolton broth. *Int. J. Food Microbiol.* **2022**, *363*, 109518. https://doi.org/10.1016/j.ijfoodmicro.2021.109518
114. Chon, J.-W.; Hyeon, J.-Y.; Yim, J.-H.; Kim, J.-H.; Song, K.-Y.; Seo, K.-H. Improvement of modified charcoal-cefoperazone-deoxycholate agar by supplementation with a high concentration of polymyxin B for detection of *Campylobacter jejuni* and *C. coli* in chicken carcass rinses. *Appl. Environ. Microbiol.* **2012**, *78*, 1624–1626. https://doi.org/10.1128%2FAEM.07180-11
115. Chon, J.-W.; Kim, H.; Kim, H.-S.; Seo, K.-H. Improvement of modified charcoal-cefoperazone-deoxycholate agar by addition of potassium clavulanate for detecting *Campylobacter* spp. in chicken carcass rinse. *Int. J. Food Microbiol.* **2013**, *165*, 7–10. http://dx.doi.org/10.1016/j.ijfoodmicro.2013.04.006
116. Chon, J.-W.; Kim, H.; Yim, J.-H.; Song, K.-Y.; Moon, J.-S.; Kim, Y.-J.; Seo, K.-H. Improvement of Karmali agar by addition of polymyxin B for the detection of *Campylobacter jejuni* and *C. coli* in whole-chicken carcass rinse. *J. Food Sci.* **2013**, *78*, 752–755. https://doi.org/10.1111/1750-3841.12096
117. Chon, J.-W.; Kim, H.-S.; Kim, D.-H.; Kim, H.; Choi, I.-S.; Oh, D.-H.; Seo, K.-H. Modification of Karmali agar by supplementation with potassium clavulanate for the isolation of *Campylobacter* from chicken carcass rinses. *J. Food Prot.* **2014**, *77*, 1207–1211. https://doi.org/10.4315/0362-028X.JFP-13-405
118. Chon, J.-W.; Kim, Y.-J.; Kim, H.-S.; Kim, D.-H.; Kim, H.; Song, K.-W.; Seo, K.-H. Supplementation of Bolton broth with triclosan improves detection of *Campylobacter jejuni* and *Campylobacter coli* in chicken carcass rinse. *Int. J. Food Microbiol.* **2014**, *181*, 37–39. http://dx.doi.org/10.1016/j.ijfoodmicro.2014.04.006
119. Chon, J.-W.; Kim, Y.-J.; Kim, Y.-J.; Jung, J.Y.; Bae, D.; Khan, S.; Seo, K.-H.; Sung, K. Addition of rifampicin to Bolton broth to inhibit extended-spectrum β-lactamase-producing *Escherichia coli* for the detection of *Campylobacter*. *J. Food Sci.* **2017**, *82*, 1688–1692. https://doi.org/10.1111/1750-3841.13761
120. Kim, Y.-J.; Whan, C.-J.; Kim, H.-S.; Kim, K.-Y.; Yim, J.-H.; Cho, S.-H.; Seo, K.-H. Improvement of Karmali agar by supplementation with tazobactam for detecting *Campylobacter* in raw poultry. *J. Food Prot.* **2016**, *79*, 1982–1985. https://doi.org/10.4315/0362-028X.JFP-16-105
121. Moran, L.; Kelly, C.; Cormican, M.; McGettrick, S.; Madden, R.H. Restoring the selectivity of Bolton broth during enrichment for *Campylobacter* spp. from raw chicken. *Lett. Appl. Microbiol.* **2011**, *52*, 614–618. https://doi.org/10.1111/j.1472-765X.2011.03046.x
122. Rautelin, H.; Jusufovic, J.; Hänninen, M.-L. Identification of hippurate-negative thermophilic campylobacters. *Diagn. Microbiol. Infect. Dis.* **1999**, *35*, 9–12. https://doi.org/10.1016/S0732-8893(99)00057-7
123. Totten, P.A.; Patton, C.M.; Tenover, F.C.; Barrett, T.J.; Stamm, W.E.; Steigerwalt, A.G.; Lin, J.Y.; Holmes, K.K.; Brenner, D.J. Prevalence and characterization of hippurate-negative *Campylobacter jejuni* in King County, Washington. *J. Clin. Microbiol.***1987**, *25*, 1747–1752. https://doi.org/10.1128%2Fjcm.25.9.1747-1752.1987
124. Bessède, E.; Asselineau, J.; Perez, P.; Valdenaire, G.; Richer, O.; Lehours, P.; Mégraud, F. Evaluation of the diagnostic accuracy of two immunochromatographic tests detecting campylobacter in stools and their role in campylobacter infection diagnosis. *J. Clin. Microbiol.* **2018**, *56*, e01567-17. https://doi.org/10.1128/JCM.01567-17
125. Franco, J.; Bénejat, L.; Ducournau, A.; Mégraud, F.; Lehours, P.; Bessède, E. Evaluation of CAMPYLOBACTER QUIK CHEK™ rapid membrane enzyme immunoassay to detect *Campylobacter* spp. antigen in stool samples. *Gut Pathog.* **2021**, *13*, 4. https://doi.org/10.1186/s13099-021-00400-0
126. Li, C.; Chen, X.; Wen, R.; Ma, P.; Gu, K.; Li, C.; Zhou, C.; Lei, C.; Tang, Y.; Wang, H. Immunocapture magnetic beads enhanced the LAMP-CRISP/Cas12a method for the sensitive, specific, and visual detection of *Campylobacter jejuni*. *Biosensors* **2022**, *12*, 154. https://doi.org/10.3390/bios12030154
127. Muralidharan, C.; Anwar, A.; Wilson, T.B.; Scott, P.C.; Moore, R.J.; Van, T.T.H. Development of an enzyme-linked immunosorbent assay for detecting *Campylobacter hepaticus* specific antibodies in chicken sera – a key tool in spotty liver disease screening and vaccine development. *Avian Pathol.* **2020**, *49*, 658–665. https://doi.org/10.1080/03079457.2020.1813252
128. Schnee, A.E.; Haque, R.; Taniuchi, M.; Uddin, J.; Petri, W.A., Jr. Evaluation of two new membrane-based and microtiter plate enzyme-linked immunosorbent assays for detection of *Campylobacter jejuni* in stools of Bangladeshi children. *J. Clin. Microbiol.* **2018**, *56*, e00702-18. https://doi.org/10.1128/JCM.00702-18
129. He, D.; Du, Z.; Wang, Y.; Xu, E.; Jin, Z.; Wu, Z. Quantitative detection of *Campylobacter jejuni* with a core-satellite assemblies-based dual-modular aptasensor. *Food Control* **2022**, *135*, 108828. https://doi.org/10.1016/j.foodcont.2022.108828
130. Quintela, I.A.; Vasse, T.; Lin, C.-S.; Wu, V.C.H. Advances, applications, and limitations of portable and rapid detection technologies for routinely encountered foodborne pathogens. *Front. Microbiol.* **2022**, *13*, 1054782. https://doi.org/10.3389/fmicb.2022.1054782
131. Babu, U.S.; Harrison, L.M.; Mammel, M.K.; Bigley III, E.C.; Hiett, K.L.; Balan, K.V. A loop-mediated isothermal amplification (LAMP) assay for the consensus detection of human pathogenic *Campylobacter* species. *J. Microbiol. Methods* **2020**, *176*, 106009. https://doi.org/10.1016/j.mimet.2020.106009

132. Phaneuf, C.R.; Mangadu, B.; Tran, H.M.; Light, Y.K.; Sinha, A.; Charbonier, F.W.; Eckles, T.P.; Singh, A.K.; Koh, C.-Y. Integrated LAMP and immunoassay platform for diarrheal disease detection. *Biosens. Bioelectron.* **2018**, *120*, 93–101. https://doi.org/10.1016/j.bios.2018.08.005
133. Asakura, H.; Yamamoto, S.; Kazuhiro, Y.; Kawase, J.; Nakamura, H.; Abe, K.; Sasaki, Y.; Ikeda, T.; Nomoto, R. Quantitative detection and genetic characterization of thermotolerant *Campylobacter* spp. in fresh chicken meats at retail in Japan. *Front. Microbiol.* **2022**, *13*, 1014212. https://doi.org/10.3389/fmicb.2022.1014212
134. Aydin, F.; Kayman, T.; Abay, S.; Hizlisoy, H.; Saticioğlu, I.B.; Karakaya, E.; Sahin, O. MLST genotypes and quinolone resistance profiles of *Campylobacter jejuni* isolates from various sources in Turkey. *Int. J. Food Microbiol.* **2023**, *391-393*, 110137. https://doi.org/10.1016/j.ijfoodmicro.2023.110137
135. Joseph, L.A.; Griswold, T.; Vidyaprakash, E.; Im, S.B.; Williams, G.M.; Pouseele, H.A.; Hise, K.B.; Carleton, H.A. Evaluation of core genome and whole genome multilocus sequence typing schemes for *Campylobacter jejuni* and *Campylobacter coli* outbreak detection in the USA. *Microb. Genom.* **2023**, *9*, 001012. https://doi.org/10.1099/mgen.0.001012
136. Bakhshi, B.; Kalantar, M.; Rastegar-Lari, A.; Fallah, F. PFGE genotyping and molecular characterization of *Campylobacter* spp. isolated from chicken meat. *Iran J. Vet. Res.* **2016**, *17*, 177–183.
137. Davedow, T.; Carleton, H.; Kubota, K.; Palm, D.; Schroeder, M.; Gerner-Smidt, P.; Al-Jardani, A.; Chinen, I.; Kam, K.M.; Smith, A.M.; Nadon, C. PulseNet international survey on the implementation of whole genome sequencing in low and middle-income countries for foodborne disease surveillance. *Foodborne Pathog. Dis.* **2022**, *19*, 332–340. https://doi.org/10.1089/fpd.2021.0110
138. Hodges, L.M.; Taboada, E.N.; Koziol, A.; Mutschall, S.; Blais, B.W.; Inglis, G.D.; Leclair, D.; Carrillo, C.D. Systematic evaluation of whole-genome sequencing based prediction of antimicrobial resistance in *Campylobacter jejuni* and *C. coli*. *Front. Microbiol.* **2021**, *12*, 776967. https://doi.org/10.3389/fmicb.2021.776967
139. Lakicevic, B.; Jankovic, V.; Pietzka, A.; Ruppitsch, W. Wholegenome sequencing as the gold standard approach for control of *Listeria monocytogenes* in the food chain. *J. Food Prot.* **2023**, *86*, 100003. https://doi.org/10.1016/j.jfp.2022.10.002
140. Natsos, G.; Mouttotou, N.K.; Ahmad, S.; Kamran, Z.; Ioannidis, A.; Koutoulis, K.C. The genus *Campylobacter*: detection and isolation methods, species identification & typing techniques. *J. Hellenic Vet. Med. Soc.* **2019**, *70*, 1327–1338. https://doi.org/10.12681/jhvms.20337
141. Al Amri, A.; Senok, A.C.; Ismaeel, A.Y.; Al-Mahmeed, A.E.; Botta, G.A. Multiplex PCR for direct identification of *Campylobacter* spp. in human and chicken stools. *J. Med. Microbiol.* **2007**, *56*, 1350–1355. https://doi.org/10.1099/jmm.0.47220-0
142. Linton, D.; Lawson, A.J.; Owen, R.J.; Stanley, J. PCR detection, identification to species level, and fingerprinting of *Campylobacter jejuni* and *Campylobacter coli* direct from diarrheic samples. *J. Clin. Microbiol.* **1997**, *35*, 2568–2572. http://jcm.asm.org/content/35/10/2568
143. Persson, S.; Olsen, K.E.P. Multiplex PCR for identification of *Campylobacter coli* and *Campylobacter jejuni* from pure cultures and directly on stool samples. *J. Med. Microbiol.* **2005**, *54*, 1043–1047. https://doi.org/10.1099/jmm.0.46203-0
144. Lanzl, M.I.; Zwietering, M.H.; Abee, T.; den Besten, H.M.W. Combining enrichment with multiplex real-time PCR leads to faster detection and identification of *Campylobacter* spp. in food compared to ISO 10272-1:2017. *Food Microbiol.* **2022**, *108*, 104117. https://doi.org/10.1016/j.fm.2022.104117
145. Hetman, B.M.; Mutschall, S.K.; Carrillo, C.D.; Thomas, J.E.; Gannon, V.P.J.; Inglis, G.D.; Taboada, E.N. "These aren't the strains you're looking for": Recovery bias of common *Campylobacter jejuni* subtypes in mixed cultures. *Front. Microbiol.* **2020**, *11*, 541. https://doi.org/10.3389/fmicb.2020.00541
146. Nayak, R.; Stewart, T.M.; Nawaz, M.S. PCR identification of *Campylobacter coli* and *Campylobacter jejuni* by partial sequencing of virulence genes. *Moll. Cell. Probes* **2005**, *19*, 187–193. https://doi.org/10.1016/j.mcp.2004.11.005
147. Commission Regulation (EU) 2017/1495. *Campylobacter* in broiler carcasses. Available online: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX%3A32017R1495 (accessed on 18 June 2023).
148. Dawson, P.; Buyukyavuz, A.; Ionita, C.; Northcutt, J. Effects of DNA extraction methods on the real time PCR quantification of *Campylobacter jejuni*, *Campylobacter coli*, and *Campylobacter lari* in chicken feces and ceca contents. *Poult. Sci.* **2023**, *102*, 102369. https://doi.org/10.1016/j.psj.2022.102369
149. Dubovitskaya, O.; Seinige, D.; Valero, A.; Reich, F.; Kehrenberg, C. Quantitative assessment of *Campylobacter* spp. levels with real-time PCR methods at different stages of the broiler food chain. *Food Microbiol.* **2023**, *110*, 104152. https://doi.org/10.1016/j.fm.2022.104152
150. Ito, S.; Kishimoto, M. Development of a sampling and real-time PCR method for the quantitative detection of *Campylobacter* spp. in retail chicken meat without DNA extraction. *J. Food Prot.* **2023**, *86*, 100028. https://doi.org/10.1016/j.jfp.2022.100028
151. Reese, K.R.; Elkins, K.M. Simultaneous detection of foodborne pathogens using real-time PCR triplex high-resolution melt assay. *Appl. Microbiol.* **2022**, *2*, 453–459. https://doi.org/10.3390/applmicrobiol2030034

152. Pacholewicz, E.; Buhler, C.; Wulsten, I.F.; Kraushaar, B.; Luu, H.Q.; Iwobi, A.N.; Huber, I.; Stingl, K. Internal sampling process control improves cultivation-independent quantification of thermotolerant *Campylobacter*. *Food Microbiol.* **2019**, *78*, 53–61. https://doi.org/10.1016/j.fm.2018.09.017
153. Stingl, K.; Heise, J.; Thieck, M.; Wulsten, I.F.; Pacholewicz, E.; Iwobi, A.N.; Govindaswamy, J.; Zeller-Pérronet, V.; Scheuring, S.; Luu, H.Q.; Fridriksdottir, V.; Gölz, G.; Priller, F.; Gruntar, I.; Jorgensen, F.; Koene, M.; Kovac, J.; Lick, S.; Répérant, E.; Rohlfing, A.; Zawilak-Pawlik, A.; Rossow, M.; Schlierf, A.; Frost, K.; Simon, K.; Uhlig, S.; Huber, I. Challenging the "gold standard" of colony-forming units – Validation of a multiplex real-time PCR for quantification of viable *Campylobacter* spp. in meat rinses. *Int. J. Food Microbiol.* **2021**, *359*, 109417. https://doi.org/10.1016/j.ijfoodmicro.2021.109417
154. Wulsten, I.F.; Galeev, A.; Stingl, K. Underestimated survival of *Campylobacter* in raw milk highlighted by viability real-time PCR and growth recovery. *Front. Microbiol.* **2020**, *11*, 1107. https://doi.org/10.3389/fmicb.2020.01107
155. Wulsten, I.F.; Thieck, M.; Göhler, A.; Schuh, E.; Stingl, K. Chicken skin decontamination of thermotolerant *Campylobacter* spp. and hygiene indicator *Escherichia coli* assessed by viability real-time PCR. *Pathogens* **2022**, *11*, 706. https://doi.org/10.3390/pathogens11060706
156. Ma, L.; Feng, J.; Zhang, J.; Lu, X. Campylobacter biofilms. *Microbiol. Res.* **2022**, *264*, 127149. https://doi.org/10.1016/j.micres.2022.127149
157. Kim, S.-H.; Park, C.; Lee, E.-J.; Bang, W.-S.; Kim, Y.-J.; Kim, J.-S. Biofilm formation of *Campylobacter* strains isolated from raw chickens and its reduction with DNase I treatment. *Food Control* **2017**, *71*, 94–100. http://dx.doi.org/10.1016/j.foodcont.2016.06.038
158. Laconi, A.; Tolosi, R.; Drigo, I.; Bano, L.; Piccirillo, A. Association between ability to form biofilm and virulence factors of poultry extra-intestinal *Campylobacter jejuni* and *Campylobacter coli*. *Vet Microbiol.* **2023**, *282*, 109770. https://doi.org/10.1016/j.vetmic.2023.109770
159. Gunther IV, N.W.; Chen, C.-Y. The biofilm forming potential of bacterial species in the genus *Campylobacter*. *Food Microbiol.* **2009**, *26*, 44–51. https://doi.org/10.1016/j.fm.2008.07.012
160. Kostoglou, D.; Mucka, E.; Andritsos, N.; Giaouris, E. A Combined Study on the Antibiotic Resistance and Biofilm-Forming Abilities of *Campylobacter jejuni* and *Campylobacter coli* Isolates from Retail Raw Chicken Samples. In Proceedings of the 4th International Conference on Biofilms (Asia-Pacific Biofilms 2022), Guangzhou, China, 18–23 October 2022.
161. Sulaeman, S.; Le Bihan, G.; Rossero, A.; Federighi, M.; Dé, E.; Tresse, O. Comparison between the biofilm initiation of *Campylobacter jejuni* and *Campylobacter coli* strains to an inert surface using BioFilm Ring Test. *J. Appl. Microbiol.* **2010**, *108*, 1303–1312. https://doi.org/10.1111/j.1365-2672.2009.04534.x
162. Karki, A.B.; Ballard, K.; Harper, C.; Sheaff, R.J.; Fakhr, M.K. *Staphylococcus aureus* enhances biofilm formation, aerotolerance, and survival of *Campylobacter* strains isolated from retail meats. *Sci. Rep.* **2021**, *11*, 13837. https://doi.org/10.1038/s41598-021-91743-w
163. Klančnik, A.; Gobin, I.; Jeršek, B.; Možina, S.S.; Vučkovic, D.; Žnidarič, M.T.; Abram, M. Adhesion of *Campylobacter jejuni* is increased in association with foodborne bacteria. *Microorganisms* **2020**, *8*, 201. https://doi.org/10.3390/microorganisms8020201
164. Ramić, D.; Klančnik, A.; Možina, S.S.; Dogsa, I. Elucidation of the AI-2 communication system in the food-borne pathogen *Campylobacter jejuni* by whole-cell-based biosensor quantification. *Biosens. Bioelectron.* **2022**, *212*, 114439. https://doi.org/10.1016/j.bios.2022.114439
165. The, K.H.; Flint, S.; French, N. Biofilm formation by *Campylobacter jejuni* in controlled mixed-microbial populations. *Int. J. Food Microbiol.* **2010**, *143*, 118–124. https://doi.org/10.1016/j.ijfoodmicro.2010.07.037
166. Ica, T.; Caner, V.; Istanbullu, O.; Nguyen, H.D.; Ahmed, B.; Call, D.R.; Beyenal, H. Characterization of mono- and mixed-culture *Campylobacter jejuni* biofilms. *Appl. Environ. Microbiol.* **2012**, *78*, 1033–1038. https://doi.org/10.1128/aem.07364-11
167. Sterniša, M.; Centa, U.G.; Drnovšek, A.; Remškar, M.; Možina, S.S. *Pseudomonas fragi* biofilm on stainless steel 9at low temperatures) affects the survival of *Campylobacter jejuni* and *Listeria monocytogenes* and their control by a polymer molybdenum oxide nanocomposite coating. *Int. J. Food Microbiol.* **2023**, *394*, 110159. https://doi.org/10.1016/j.ijfoodmicro.2023.110159