Review Article

Campylobacter species: New insight, clinical diagnosis and laboratory approach

ABSTRACT

Campylobacter, a prevalent cause of global gastroenteritis, has exhibited an escalating impact worldwide, affecting both industrialized and developing nations. Even though Campylobacter jejuni and C. coli are the main causes of infection, new pathogens make it imperative to comprehend the disease mechanisms, dynamics of transmission, and evolution of less-studied species. Accessible whole-genome sequences obtained through high-throughput sequencing have made it easier to conduct in-depth pathogenomic studies, particularly on species such as C. fetus and C. concisus. These studies have shown novel applications in clinical microbiology by revealing genomic traits associated with pathogenicity and offering insights into the evolutionary mechanisms shaping their genomes. Effective pathogen management urgently requires deeper understanding of the evolution of pathogenicity in emerging Campylobacter species are urgently required for effective pathogen management. This comprehensive review synthesizes existing knowledge and outlines future research directions in this crucial field. The Gram-negative, non-spore-forming, curved or spiral rods known as campylobacters include a "thermophilic group" that is important to the water industry and includes C. jejuni, C. coli, and C. upsaliensis. Acute diarrhea is the usual symptom of a human Campylobacter infection, and key virulence factors have been identified as antibiotic resistance genes and flagellar DNA. Many campylobacters are frequently found in sewage and treated sewage effluents, whereas surface waters are less contaminated. Testing for Campylobacter prevalence through epidemiological methods requires a careful balance between phenotypic and genotypic data. Campylobacters are sensitive to oxygen, but they have strong survival strategies that may involve the formation of biofilms. Methods of inactivation that work well for coliforms are thought to be appropriate for Campylobacter. In addition to providing a synthesis of current knowledge and identifying future research directions to advance strategies for the effective management and mitigation of Campylobacter-related infections, this thorough review highlights the urgent need for additional research to deepen our understanding of these pathogens. The investigation of genetic features linked to pathogenicity, dynamics of transmission, and survival strategies highlights the complex character of Campylobacter infections. The dynamic nature of Campylobacter as a primary cause of gastroenteritis necessitates continued research endeavors to guide focused interventions and lessen the worldwide impact of this grave public health issue.

Keywords: *Campylobacteriosis, Whole-genome Sequencing, Pathogenicity Evolution, Campylobacter Species*

1.1 INTRODUCTION

“The most prevalent bacterial species, campylobacter, is responsible for food-borne gastroenteritis in people worldwide. The Centers for Disease Control and Prevention (CDC) released data in 2011 that indicated there were approximately 845,000 cases annually in the

United States.Even while these conditions rarely result in death, they can do so if an immunocompromised person contracts them. The two types of bacteria most frequently linked to human campylobacteriosis are Campylobacter jejuni and *C. col*i. In addition, a number of additional Campylobacter species have been linked to illness. In Ireland and throughout Europe, campylobacter species is the most frequent bacterial cause of gastroenteritis. The Campylobacter species are microaerophilic, Gram-negative, spiral-shaped cells that move like corkscrews. They are the most common cause of bacterial gastroenteritis in many countries, including Ireland, and they are typically transmitted by food. Along with Campylobacter coli and Campylobacter lari, Campylobacter jejuni is the species most frequently associated with human illness"[4].

Foods with an animal origin usually include isolated Campylobacter species. One of the most prominent sources of Campylobacter spp. is considered to be poultry, which also plays a key role in the pathogen's transmission to people. Campylobacter infections are among the most common bacterial diseases that affect people. They cause both systemic and diarrhoeal diseases. Enteric Campylobacter infections cause an inflammatory, occasionally bloody diarrhea or dysentery condition in industrialized areas[5]. The most frequent cause of community-acquired inflammatory enteritis is typically Campylobacter jejuni. In underdeveloped areas, diarrhea could be watery.

"Since the early 20th century, campylobacter species have been thoroughly characterized in veterinary medicine. The significance of Campylobacter species as gastrointestinal infections in humans, however, wasn't widely acknowledged until the 1970s. In the 1970s and 1980s, as laboratory testing and capacity increased, Campylobacter species was swiftly identified as one of the major causes of bacterial enteritis in humans globally"[5]. "There was indications that the data were reflecting an actual upward trend above and above the apparent increase that would be anticipated to occur with enhanced detection and surveillance methods as reported incidence rates grew throughout the later decades of the twentieth century". [5]

"In many industrialized countries today, Campylobacter infections are the most often reported cause of bacterial gastroenteritis. In poor countries, Campylobacter infections are a significant cause of bacterial gastroenteritis in young children. The true incidence almost certainly exceeds the number of reported cases by a significant margin"[4]. "Although some nations have recently seen a decrease in the incidence of Campylobacter disease, there is concern that the human immunodeficiency virus (HIV) epidemic may significantly increase the disease burden of Campylobacter in developing nations. Concurrent HIV infection is known to increase the incidence risk and severity of Campylobacter gastroenteritis"[3].

There are other public health issues associated with these organisms in addition to the significant disease burden of Campylobacter gastroenteritis. Recent studies have emphasized the crucial part that Campylobacter infection plays in the pathogenesis of reactive arthritis and other post-infectious disorders including Guillain-Barré syndrome (GBS), a devastating neurological condition.

"Given the pervasive contamination of the food supply chain by Campylobacter and the numerous ways that humans can become infected through food and water, campylobacter infection is particularly relevant to the food production industry"[6].

"In a subsequent section of this text, a number of methods for disease prevention and management are discussed, however it is obvious that managing Campylobacter infection is a

difficult undertaking. The condition known as campylobacteriosis is brought on by a campylobacter infection. After bacterial infection, illness symptoms often appear 2 to 5 days later, but they can also appear up to 10 days later. Campylobacter infections commonly manifest as diarrhea (often bloody), abdominal pain, fever, headaches, nausea, and/or vomiting. The symptoms usually go away in three to six days. A rare cause of mortality, campylobacteriosis usually strikes very young children, elderly patients, or those suffering from another life-threatening illness such as AIDS. Many side effects have been reported, such as hepatitis, pancreatitis (infections of the liver and pancreas, respectively), bacteremia (the presence of germs in the blood), and miscarriage. Post-infection complications include painful joint inflammations such as reactive arthritis and neurological conditions such as Guillain-Barré syndrome, which mimics polio-like paralysis and can, in a small number of cases, result in severe neurological and respiratory dysfunction".[1].

"The first Campylobacter infection was identified in 1913 when McFaydean and Stockman discovered a curved-shaped bacterium that caused abortion in sheep and cattle. The same bacteria were identified as Vibrio fetus by Smith and Taylor in 1919 after they isolated it from a cow's fetal secretions. Then, in 1973, the genus Campylobacter was established by Véron and Chatelain, who reclassified V. fetal as Campylobacter fetus. Apart from its extensive history and well-established significance as a veterinary pathogen that dates back to the turn of the 20th century, C. fetus was also found to be the main cause of bloodstream infections in humans. However, the significant significance of campylobacters as a primary cause of human disease was not identified until the early 1980s, with the development and widespread application of selective media for the isolation of Campylobacter from stool samples. The most significant species in the genus at the moment is C. jejuni, a major cause of bacterial gastroenteritis in humans that is even more common globally than highly recognized pathogens that cause acute gastrointestinal infections like Salmonella, Shigella, or Escherichia coli. As a close relative of C. jejuni, C. coli causes one to twenty-five percent of diarrheal illnesses associated with Campylobacter. Although the remaining species in the genus have gotten far less attention, a growing number of Campylobacter species that are different from C. jejuni and C. coli have been described and identified as relevant pathogens for humans and other animals. This is due to routinely applied molecular techniques, improved culture media, and improved growth conditions"[8].

"Many of these emerging Campylobacter species were identified clinically around the same time that high-throughput sequencing became a popular tool for studying the microbial world. This led to an increased interest in using whole-genome sequencing and comparative genomics to learn how emerging campylobacters cause illness, spread, and evolve. Many thousands of C. jejuni and C. species are now accessible through public databases, nearly two decades after the first C. jejuni whole genome sequence was published.genomes of Coli. Because there are an increasing number of whole-genome sequences available, comparative genomics studies that previously only included a small number of genomes can now include hundreds or even thousands of them. The slow and fragmented pace of genomic data availability for new Campylobacter species is impeding our understanding of the biology of nonclassical Campylobacter infections. In this review, we provide an overview of the latest findings on emerging campylobacters through the lens of comparative genomics. We also talk about how basic Campylobacter pathobiology and its applications in clinical microbiology are being clarified by these data. Lastly, we highlight some of the field's upcoming challenges, like the

need for more work to lessen sequencing bias favoring well-known species. In order to integrate recent data and address open questions in the study of developing Campylobacter pathogens, this review provides a comprehensive resource for researchers looking at Campylobacter genomes and emerging pathogens".[6].

"Depending on the species, gram-negative bacteria in the Campylobacter genus can have morphologies that vary from spiral to rod to curved. Some species are aflagellate, while others have bipolar or a single polar flagellum. The genus Campylobacter contains 25 species, two provisional species, and eight subspecies. Apart from their presence in humans, Campylobacter species are widely distributed across various ecosystems and can be found in domesticated or wild animals such as cattle, birds, reptiles, and shellfish. C. jejuni is the most frequent cause of gastroenteritis in the world. It is known that certain Campylobacter species, including C. coli and C. fetal, are dangerous to humans and animals alike. A number of other species, such as C. concisus, C. ureolyticus, and C. lari, are referred to as "emerging Campylobacter species" because of their increasing importance in human and animal infections. This chapter covers the Campylobacter genus's epidemiology, genetic characteristics, attachment and invasion mechanisms, production of toxins, glycosylation, capsular polysaccharide synthesis, biofilm formation, and profile of antibiotic resistance. We also give a summary of how host immune responses and animal models are used to study the pathophysiology of these species".[9].

"Members of the Campylobacteriaceae family include campylobacters. These bacteria can have a spiral, S, or curved shape and are Gram-negative bacilli. The majority move in a distinctive corkscrew pattern, which is controlled by polar flagella. At either end of the cell, a cell may have a single polar flagellum or two"[10].

"Campylobacter species need a microaerobic environment with 3 to 5% oxygen and 5 to 10% carbon dioxide for growth. The ideal temperature for most species, which are thermophilic, is 420C"[12].

"One major worry is the possibility of Campylobacter developing antibiotic resistance. People with weakened immune systems, such as those with HIV/AIDS or receiving immunosuppressive medication, may get infections that are more serious, which increases the need for antibiotics. Due to their immature or compromised immune systems, children and the elderly are more prone to serious infections, which could lead to a rise in the number of antibiotic prescriptions written. The overuse or misuse of antibiotics in clinical and agricultural settings puts the general public at risk and aids in the emergence and spread of antibiotic resistance"[10].

In order to increase the selective pressure for antibiotic resistance, doctors may be more likely to prescribe antibiotics more frequently to populations that are considered vulnerable. Antibiotic-resistant strains are also present in food sources due to the overuse of antibiotics in agriculture, particularly in poultry farming. Traveling abroad makes antibiotic-resistant Campylobacter strains more widespread worldwide[11].

"It is imperative to encourage prudent antibiotic use in clinical settings, impose stringent laws on antibiotic use in agriculture, and improve surveillance of antibiotic-resistant Campylobacter strains in humans and animals in order to reduce the risk of antibiotic resistance. Campaigns for

public health awareness are crucial in educating the public and medical professionals about the appropriate use of antibiotics and the possible risks associated with antibiotic resistance"[12].

The many facets of Campylobacter, a major global cause of gastroenteritis, are covered in this review. Although most cases are caused by Campylobacter jejuni and C. coli, which have been studied in great detail, new species like C. fetus and C. concisus need to be given more attention because of their increasing pathogenicity. By utilizing high-throughput sequencing, we have been able to uncover genetic characteristics associated with pathogenicity and gain understanding of the evolutionary processes influencing the genomes of different Campylobacter species. These discoveries pave the way for novel applications in clinical microbiology. In order to develop effective strategies for combating these evolving pathogens, the review emphasizes the critical need for deeper insights into genome dynamics and the evolution of pathogenicity in emerging Campylobacter species.

The Gram-negative, non-spore-forming, curved or spiral rod characteristics of Campylobacters—particularly those belonging to the "thermophilic group" that are pertinent to the water industry—are also clarified by this review. Surface waters are vulnerable to the presence of C. jejuni, C. coli, and C. upsaliensis, which are frequently found in sewage and treated sewage effluents. A combination of phenotypic and genotypic tests is required for effective epidemiological investigations into Campylobacter prevalence, as these bacteria have robust survival mechanisms despite their sensitivity to oxygen. Moreover, the formation of biofilms might contribute to their persistence. Techniques for inactivation that work well for coliforms are also thought to work well for Campylobacter. This thorough review emphasizes the need for more investigation into these pathogens' survival, inactivation, and transmission mechanisms.

2.1 PREVALENCE OF CAMPYLOBACTER IN DIFFERENT PARTS OF THE WORLD

Campylobacter species, are common and have an impact on public health around the world. Research carried out in Iran and Nigeria illuminated the prevalence of Campylobacter in various sources, highlighting the necessity of all-encompassing approaches to reduce the risk of infection.

A review study conducted in Iran from 2004 to 2017 found that the pooled prevalence of 10.2% for Campylobacter species was found in a variety of sources, including food products, animals, and human clinical specimens. The study demonstrated how widespread Campylobacter is and how crucial it is to comprehend how common it is across a variety of reservoirs. The study also revealed chicken as a major reservoir, highlighting the need for preventive measures to be taken at every stage of chicken production in order to limit the spread of Campylobacter to humans[18].

Ansarifar *et al*. (2021) conducted a systematic review and meta-analysis in Iran, which examined 119 articles and yielded a more detailed analysis. According to the study, "white meat—mostly chicken—had the highest pooled prevalence of Campylobacter species, at 43.9%. The next two most common foods were eggs and red meat, at 5.5% and 7.9%, respectively. Furthermore, 14.9% of environmental samples and 8.4% of human samples had the same prevalence. The

importance of comprehending species-specific dynamics was further highlighted by the prevalence of C. jejuni over C. coli in the majority of samples. This thorough analysis highlighted the importance of chicken as Iran's main source of Campylobacter, highlighting the need for a variety of preventive measures"[16].

Audu *et al*. (2022) examined "the genetic diversity and antimicrobial resistance profile of Campylobacter in cattle and humans, with a focus on Nigeria. The study revealed an intriguing finding: the prevalence of Campylobacter in livestock was higher than in humans, highlighting the possibility of zoonotic transmission. This regional variation in prevalence raises the possibility that environmental factors, hygiene standards, and farming practices may have an impact on Campylobacter epidemiology"[17].

These studies demonstrate the variability in rates across different regions and emphasize the global significance of Campylobacter prevalence. The need for region-specific control measures is highlighted by the thorough understanding of reservoirs and prevalence rates in Iran and Nigeria. This emphasizes the significance of ongoing surveillance and preventive strategies to protect public health.

This is a thorough narrative review that covers a number of Campylobacter topics, such as pathogenicity, transmission dynamics, genomic diversity, and prevalence. This narrative review, which incorporates insights from several studies and research findings, offers a comprehensive overview of the current understanding of Campylobacter.

This thorough narrative review's search approach comprised a methodical and thorough examination of pertinent literature in scientific databases. Databases including PubMed, Scopus, and Web of Science were searched. In addition to "Campylobacter," other terms that were used were "Campylobacteriosis," "Campylobacter prevalence," "Campylobacter genomics," and "Campylobacter transmission." In order to properly combine keywords, Boolean operators (AND, OR) were used. The search was not limited by publication date in order to include a wide range of studies.

To guarantee the inclusion of significant and pertinent research, manual searches were carried out in addition to database searches by carefully going through the reference lists of articles that were identified. Studies pertaining to Campylobacter pathogenicity, genomics, transmission dynamics, and prevalence were all included in the inclusion criteria. The selection of studies was based on their significance to the main theme and their ability to shed light on various aspects of Campylobacter.

2.2 ANTIMICROBIAL RESISTANCE OF CAMPYLOBACTER

Global public health is seriously threatened by antimicrobial resistance (AMR) in Campylobacter species, which impacts both human and animal populations. Antimicrobial resistance patterns are revealed by two studies from Iran and Nigeria, highlighting the critical need for surveillance and control measures.

Campylobacter isolates in the Iranian study by Moradi *et al*. (2019) showed an alarming trend of antibiotic resistance. The resistance rates to trimethoprim-sulfamethoxazole, gentamicin, and cephalothin were 33.3%, 67.2%, and 67.2%, respectively. This suggests that treating Campylobacter infections with commonly prescribed antibiotics presents a significant challenge, requiring a reevaluation of therapeutic approaches[18].

The genomic diversity and antimicrobial resistance of Campylobacter in humans and livestock were studied in Nigeria by Audu *et al*. in 2022. According to the research, Campylobacter isolates from livestock had higher rates of resistance to fluoroquinolones and beta-lactam antibiotics than those from humans. This highlights the connection between human and animal health and highlights the possible role of the livestock reservoir in the spread of resistant strains[17].

All of these studies' results point to the growing concern over Campylobacter antibiotic resistance around the world. Antibiotic usage in animal husbandry, especially in chicken farming, may have a role in the emergence and spread of resistant strains. Beyond isolated infections, AMR in Campylobacter has far-reaching consequences that make clinical case management difficult and require a comprehensive approach to antibiotic use in the human and animal sectors.

The aforementioned studies highlight the significance of continuous monitoring and management strategies to counteract the appearance and dissemination of Campylobacter strains that are resistant to antibiotics. The interdependence of animal and human health as well as regional differences highlight the need for a coordinated, multidisciplinary response to this threat to public health.

2.3 CURRENT CAMPYLOBACTER TAXONOMY

There are officially 32 species having 9 subspecies of the genus campylobacter, which are, *C. avium, C. blaseri, C. canadensis, C. coli, C. concisus, C. corcagiensis, C. cuniculorum, C. curvus, C. fetus subsp. fetus, C. fetus subsp. venerealis, C. fetus subsp. testudinum, C. geochelonis, C. gracilis, C. helveticus, C. hepaticus, C. hominis, C. hyointestinalis subsp. hyointestinalis, C. hyointestinalis subsp. lawsonii, C. iguaniorum, C. insulaenigrae, C. jejuni subsp. jejuni, C. jejuni subsp. doylei, C. lanienae, C. lari subsp. lari, C. lari subsp. concheus, C. mucosalis, C. ornithocola, C. peloridis, C. pinnipediorum subsp. pinnipediorum, C. pinnipediorum subsp. caledonicus, C. rectus, C. showae, C. sputorum , C. subantarcticus, C. troglodytis, C. upsaliensis, C. ureolyticus, and C. volucris.*The five distinct phylogenetic groups that these species belong to all contain pathogenic microorganisms, underscoring the genus's clinical significance. While this scenario demonstrates the taxonomic diversity and the ubiquity of pathogenic lineages within the genus Campylobacter, certain species, such as C. canadensis, C. troglodytis, and C. mucosalis, lack a single genome. Furthermore, only one representative genome per species is available for a large number of other species, such as 31% of the genus's members, *C. volucris, C. peloridis, C. rectus, C. insulaenigrae, C. hominis, C. helveticus, C.*

cuniculorum, C. corcagiensis, C. ornithocola, and C. avium.It's important to note that, after ruling out C. jejuni and C. coli, 13 of the 30 species that remain have been reported to cause infections in humans and/or other animals at least occasionally. Many of these species are also frequently linked to a variety of clinical presentations, including invasive blood infections, periodontal infections, abscesses, meningitis, diarrhea, and gastroenteritis. The investigation of intraspecific genetic variability and patterns of genomic evolution is hampered by the inadequate genomic data on the agents causing these infections. As a result, pertinent data regarding the mechanisms by which numerous newly discovered Campylobacter species spread among hosts and cause illness is presently lacking. Nonetheless, a number of groups have worked hard to produce whole-genome sequences for a few newly discovered campylobacters, whose importance to public health is usually overstated. These sequences have revealed genomic characteristics that are crucial for comprehending the biology of disease and the epidemiology of these microbes. These cases are therefore examined for each distinct species that has merited study in the field of comparative genomics.[15].

Phylogenetic connections among identified species of Campylobacter. A phylogenetic tree of Campylobacter species is displayed, which breaks the genus up into five different groups: C. ureolyticus, C. jejuni, C. lari, C. concisus, and C. fetus. Within each group, names were assigned based on which species was the most clinically relevant.[11].

The genus *Campylobacter* was created in 1963, but it required the development and refinement of isolation techniques in the decades that followed for members of the genus to be readily obtained in pure culture. In addition, the lack of biochemical activity shown by species of *Campylobacter*, which had hindered their classification, was overcome by the rapid development of analytical techniques, many **DNA** based, late in the twentieth century. In 1984, *Bergey's Manual of Determinative Bacteriology* listed only five species of *Campylobacter*. In 1991, a major taxonomic reorganization of campylobacters and related organisms was undertaken, based in part on DNA hybridization studies. This led to the genus *Campylobacter* being assigned to the newly created order *Campylobacterales*, in the class *Epsilonproteobacteria*. *Campylobacterales* also included the genera *Arcobacter* and *Sulfurospirillum*. In 1996, a probability matrix for the identification of campylobacters (and related organisms) was published that listed 13 species of *Campylobacter* with several subspecies also being described. Over the following years, the number of recognized species has more than doubled. However, none of the new species appeared to affect humans as significantly as those described in 1984.

Because of the perceived difficulty in culturing campylobacters, noncultural detection methods, based on DNA extraction and analysis, were applied to sample matrices suspected of harboring undetected species. Human feces from asymptomatic adults yielded positive results for *Campylobacter* DNA and led to proposals that as-yet-undiscovered campylobacters could be present in humans as commensal organisms, as was known to happen in birds. However, it was later established that some *Campylobacter* spp., such as *Campylobacter rectus*, could colonize the human buccal cavity, and that these organisms could therefore be present in the lower gastrointestinal (GI) tract as itinerants, and give rise to the positive results for these members of the genus[4].

As genetic analyses became mainstream tools to identify organisms, and the physiological requirements of campylobacters were better understood, new species were identified and the

relationships between species were better defined. The main causes of human illness associated with foods are *C. jejuni* and *C. coli*, but when stool samples are analyzed, medical laboratories normally identify isolates only to the level of genus. Differentiating these two species was based on the hippurate hydrolysis test because *C. jejuni* can perform this reaction whereas *C. coli* cannot. To avoid false-negative reactions, this test must be conducted with care, but it can be replaced by polymerase chain reaction (PCR)–based testing targeting the hippuricase gene[9].

Fig 1 : A specie of Campylobacter (Olsen, et al., 2001)

Fig 2 : Another specie of Campylobacterfig 3 : Different specie of Campylobacter(Olsen, *et al.*, 2001)

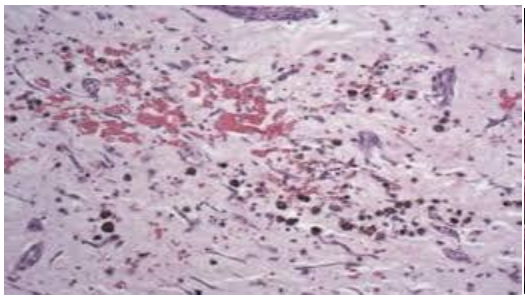

Fig 4 :Specie of Campylobacter **fig 5 : Specie of Campylobacter (Olsen, *et al*., 2001)**

Fig 6: Different Specie of Campylobacter **fig 7 : Specie of Campylobacter (Olsen, *et al*., 2001)**

2.4 EPIDEMIOLOGY

Campylobacter is known to be distributed throughout the world. While it rarely affects older children and adults in developing countries, *Campylobacter* is a major bacterial cause of diarrhea in children under the age of two. When infection does happen in people older than two years old, it usually has no symptoms. Patients in these nations most likely contract Campylobacter infections early in life and subsequently become immune, which increases the likelihood of asymptomatic infections in older children and adults[5].

The majority of *Campylobacter* infections in the industrialized world result in symptoms. It is now known that these nations have a high prevalence of Campylobacter infections; in fact, some research indicates that this organism is the most common cause of bacterial diarrhea. Young adults and infants in their first year of life are the two age groups that are most commonly infected by Campylobacter. With an estimated 2 million infections per year, Campylobacter spp. is the most frequent cause of bacterial enteric infections in the US[11].

Campylobacter can spread through contaminated food and water sources as well as direct contact. It has been suggested that undercooked eggs, meat, and milk can cause outbreaks. These sources might be tainted by excrement from humans, or the organisms might be housed in farm animals that show no symptoms. In daycare centers, campylobacter is commonly spread among the child population. Eating fruits and vegetables cooked at home, visiting or living on a farm,

traveling outside of the US, riding in a shopping cart near meat or poultry, and drinking well-water were all found to be risk factors for campylobacteriosis in a population-based case-control study. It was less common for infants with campylobacteriosis to be breastfed or to live in a home where hamburgers were cooked[13].

Once more, *Campylobacter* infection is an international anthropozoonosis, with C. jejuni most likely the most significant bacterial cause of human infectious diarrhea. Commensals, such as chickens, dairy cows, and household pets, are home to a variety of wild and domestic birds and mammals, including C. jejuni and C. coli. Therefore, animals and animal products—especially raw milk and poultry meat—as well as untreated water—which is frequently contaminated by birds or farm animals—are sources of *Campylobacter* infection in humans. Poultry, milk, and water have also been linked to outbreaks in communities. Milk contains 500 organisms per infectious dose. One significant contributor to traveler's diarrhea is C. jejuni.[8].

2.5 METABOLISM AND PHYSIOLOGY

With the exception of *C. jejuni* subspecies doylei, the majority of *Campylobacter* species produce catalase and convert nitrate to nitrite. The only species that can hydrolyze sodium hippurate is *Campylobacter jejuni.* Rather than using sugars or generating indole, campylobacter get their energy from amino acids or intermediaries in the tricarboxylic acid cycle. All *Campylobacter* species are oxidase positive, with the exception of *Campylobacter gracilis* (formerly *Bacteroides gracilis*). When specific electron acceptors like fumarate, aspartate, or nitrate are present, certain species of *Campylobacter* can grow anaerobically. While *Campylobacter sputorum, Campylobacter concisus, Campylobacter mucosalis, Campylobacter curvus, Campylobacter rectus, and Campylobacter hyointestinalis* require hydrogen for primary growth, *Campylobacter sputorum* has been described as an aerotolerant anaerobe.[10].

2.6 SOURCES AND ROUTES OF TRANSMISSION OF CAMPYLOBACTER SPECIES TO HUMANS.

Among domesticated and wild birds and mammals, the alimentary tract serves as the main reservoir for Campylobacter spp. While most Campylobacter species are commensal, on rare occasions they can act as enteric pathogens in the young of certain species, such as calves, lambs, and puppies. Additionally, they have been kept apart from estuaries, rivers, streams, and seas that have been contaminated by feces[4].

Humans can contract campylobacter species through direct or indirect contact. Contact with contaminated water, infected carcasses, or infected animals can result in direct transmission of the infection. Consuming tainted food or water can result in indirect transmission[1].

Many species of campylobacter can be found in most warm-blooded animals. They are common in pets like cats and dogs as well as in food animals like pigs, cattle, ostriches, sheep, and poultry. Seafood has also been discovered to contain the bacteria[3].

It is generally accepted that raw or contaminated milk, as well as undercooked meat and meat products, are the primary foodborne routes of transmission. An additional source of infection is tainted ice or water. A percentage of cases happen after recreational activities involving contact with contaminated water[3].

A zoonosis, or disease contracted by humans from animals or animal products, is campylobacteriosis. Most frequently, during slaughtering, *Campylobacter* from feces contaminates carcasses or meat. *Campylobacter* rarely causes illness in animals[2].

It is unclear how much each of the aforementioned sources contributes in relation to the overall disease burden, but eating undercooked, contaminated poultry is thought to be a significant factor. Since a relatively small percentage of cases are caused by common-source outbreaks, the great majority of reports discuss isolated cases with no clear pattern[1].

Because of this, determining the relative importance of all available sources is very challenging. Moreover, the widespread presence of *Campylobacter* impedes the creation of management plans at every stage of the food chain. However, a comparable decline in human cases is seen in nations where particular measures have been implemented to lower the prevalence of *Campylobacter* in live poultry[5].

Diarrheal sickness and gastrointestinal infections are brought on by Campylobacter. A zoonotic pathogen, campylobacter can contaminate foods from animals like pigs, sheep, cattle, and chickens. Organisms appear as seagull-shaped, Gram-negative rods on the Gram stain. A temperature of 42°C and additional CO2 concentrations are needed for colonies to grow on *Campylobacter* selective media, such as Campy-CVA (cefoperazone, vancomycin, and amphotericin), or Skirrow media. Some species of *Campylobacter* are oxidase positive. Hippurate hydrolysis can be used to distinguish *Campylobacterjejuni* from Campylobacter coli. Erythromycin and azithromycin can be used to treat infections[1].

2.7 CAMPYLOBACTER SPECIES AND FOOD

Foods originating from animals are often the source of isolated *Campylobacterspecies*. One of the main reservoirs for these species is poultry, which is also a major means of human transmission. An EU-wide baseline study found that the prevalence of *Campylobacter* spp. in Ireland was 83.1% in broiler batches and 98.3% on carcasses at the end of the slaughtering process. Other important modes of transmission include cross-contamination of ready-to-eat foods, direct hand-to-mouth transfer during food preparation, and, to a lesser extent, consumption of undercooked poultry meat.It is estimated that 20% to 30% of human cases of campylobacteriosis in European Member States may be related to the handling, preparation, and consumption of broiler meat. Fresh produce, raw drinking milk (which can get contaminated from feces or mastitic infections), contaminated drinking water, and bivalve molluscs are other foods linked to *Campylobacterspp*[14].

The majority of *Campylobacter* species are zoonotic, meaning that they are carried by many food animals asymptomatically. The primary human pathogen that causes *Campylobacter* infections is poultry and poultry products. The pathogen may also be present in other foods like red meat, unpasteurized raw milk, fresh produce, and tainted water[13].
Foods do not support the growth and multiplication of Campylobacter species because of their particular requirements for temperature and atmosphere. But only a small number of these cells—roughly 500–1000—are needed to cause illness due to their high pathogenicity and low infectious dose[7].

According to microbiological standards, a 25g sample of foods that are ready to eat should not contain any *Campylobacter*.

2.8 RISK FACTORSASSOCIATED WITH CAMPYLOBACTER

Previous research has indicated that one of the main risk factors for contracting a Campylobacter infection is the consumption of tainted food and water (10). The two most frequently linked food-borne outbreaks were cross-contamination incidents in the kitchen from raw poultry and consumption of unpasteurized milk[6].
Many species of campylobacter can be found in most warm-blooded animals.
They are common in pets like cats and dogs as well as in food animals like pigs, cattle, ostriches, sheep, and poultry. Shellfish have also been reported to contain the bacteria.
Because of the low infective dose (less than 500) of campylobacter, even a small amount of the bacteria can be harmful. Patients with Campylobacter infections may feel sick from mild to severe. Bloody diarrhea, nausea, headaches, fever, and abdominal pain are possible symptoms. The illness usually lasts between two and five days, but it can last up to ten. Serious complications may arise from an infection[10]The most prevalent ones, which cause gastroenteritis in people, are *C. jejuni and C. coli*.
Gastritis and periodontitis have been linked to other emerging species, including *C. consicus, C. upsaliensis, C. ureolyticus, C. hyointestinalis, and C. sputorum*. These bacteria can sometimes cause infections of the gastrointestinal tract, which can lead to potentially fatal extra-gastrointestinal illnesses[4].
Additionally, *C. jejuni* is thought to be one of the most frequent risk factors for Guillain-Barré syndrome (GBS), a rare autoimmune disorder in which nerve damage from the body's own immune system results in muscle weakness, paralysis, and occasionally even death.
GBS is caused by Campylobacter infections in about 1 in 1,000 cases that are reported. The illness's symptoms can linger for a few weeks to several years. Infection with Campylobacter is the cause of up to 40% of GBS cases in the US[4].
Because of the sporadic nature of the infection and the significant role that cross-contamination plays, it is frequently challenging to identify the sources of exposure to Campylobacter. The prevention of campylobacteriosis remains a challenge, and the global trend in infection epidemiology is still quite high[9].

2.9 CAUSES OF CAMPYLOBACTERIOSIS

The bacterium known as *Campylobacter* is the source of the infection known as campylobacteriosis. Healthy birds' intestines are home to these bacteria, and raw poultry meat frequently contains *Campylobacter*[15].

The most frequently reported bacterial enteric pathogen in Minnesota is *Campylobacter*, which is also one of the most frequent bacterial causes of diarrheal illness in the US. In Minnesota, reports of *Campylobacter* cases range from 800 to 1200 per year. Almost all cases happen as random, isolated incidents rather than as a component of significant outbreaks[13].

Most cases of Campylobacter infections are most likely caused by eating undercooked or raw poultry or anything that came into contact with it. In addition, contact with animals, ingestion of untreated water, and other foods like seafood, meat, and produce can all spread campylobacter[11].

2.10 SYMPTOMS OF CAMPYLOBACTERIOSIS

Among the symptoms are:

1. Diarrhea
2. Abdominal pain and cramps
3. Fever
4. Vomiting.

As a result, symptoms typically appear two to five days after exposure to the organism [12].

2.11 CLINICAL MANIFESTATIONS

Several clinical manifestations have been linked to Campylobacter species as a risk factor. Acute polyneuropathy is the result of C. jejuni infection-related chronic sequelae known as Guillain-Barré syndrome (GBS) and Miller-Fisher syndrome. These autoimmune disorders are brought on by the production of antibodies to C. jejuni lipooligosaccharide (LOS), which react with peripheral neural tissues.According to a meta-analysis by Sejvar and colleagues, the incidence of GBS increased by 20% for every ten years of age increase in North America and Europe, with cases ranging from 0.81 to 1.89 (median, 1.11) per 100 000 person-years. Contrary to findings from Western countries, the incidence of GBS in populations other than those in Western countries has been reported to be 0.66 per 100 000 person-years in Harbin, China, with the highest incidence occurring in the youngest age group[4].

According to research by Clark and colleagues, patients who developed acute gastroenteritis after consuming drinking water tainted with E. coli O157:H7 or Campylobacter were more likely to develop hypertension, renal impairment, and self-reported cardiovascular disease. Additionally, cases of bacteremia, colorectal cancer, Barrett oesophagus, lung infections, brain abscess, meningitis, and reactive arthritis have been linked to Campylobacter species.A survey of the literature revealed that at least ten different *Campylobacter* species have been reported in patients with bacteraemia, with the most commonly reported being *C. jejuni* and *C. fetus*. The elderly or those who are immunocompromised are the most susceptible to *Campylobacter* bacteraemia. Bacteraemia and systemic organ and tissue infections associated with *Campylobacter* species are considered uncommon. However, it has been argued that these species are often under-reported[5]

There is increasing evidence to suggest that *Campylobacter* species play a role in gastrointestinal conditions other than gastroenteritis and IBD. For example, Wu and colleagues performed pyrosequencing on faecal samples of 19 patients with colorectal cancer and 20 healthy controls and found that members of the *Campylobacter* genus were one of 16 genera that were significantly increased in number in patients as compared with controls. However, in their study the specific species that correlated with the increase was not determined. In another study, Macfarlane and colleagues found 57% (4/7) of patients with Barrett oesophagus to be colonized with *C. concisus* and *C. rectus* (with *C. concisus* being recovered in high numbers), but not in any of the seven healthy controls. Further in a study based on a larger cohort of subjects, Blackett and colleagues, using real-time PCR, detected members of the *Campylobacter* genus in

oesophageal biopsies of 51.4% (19/37) of patients with gastro-oesophageal reflux disease and 42.2% (19/45) of patients with Barrett oesophagus, which was shown to be higher than that in patients with oesophageal adenocarcinoma (8.8%; 3/34) or controls with no endoscopic evidence of oesophageal, gastric or duodenal disease (12.8%; 5/39). Interestingly, sequencing analyses revealed all positive *Campylobacter* species to be *C. concisus*. Given that an increasing number of studies have identified *C. concisus* in the upper gastrointestinal tract, it is plausible that *C. concisus* may play a role in diseases at these sites. Consistent with this hypothesis, von Rosenvinge and colleagues found that *C. concisus* made up more than 90% of the *Campylobacter* species detected in the stomach of patients with a range of clinical manifestations, including erythematous gastropathy, gastric ulcers and Barrett oesophagus. In addition, their study showed the levels of *Campylobacter* RNA to be increased by 444% when compared to *Campylobacter* DNA, indicating that these species were transcriptionally active in the stomach fluid. These results may suggest that *Campylobacter* species, particularly *C. concisus*, are natural colonizers of gastric tissues and could well be opportunistic pathogens in the stomach. Of particular relevance to this hypothesis is that children with CD infected with *C. concisus* generally have L4 involvement (upper gastrointestinal tract (GIT): oesophagus and stomach) [61]. Furthermore, it has been reported that children with CD and UC have an increased prevalence of *Helicobacter pylori*-negative chronic active gastritis and duodenitis than children without IBD. Given the findings from these recent studies, further studies investigating the role of *Campylobacter* species in upper gastrointestinal conditions are warranted[7].

The first secreted factor discovered in Campylobacter is called Campylobacter Invasion Antigen B (CiaB), and it has a weak homology with T3SS effectors found in other pathogens. Since the CiaB protein translocates into the host cell's cytoplasm, it may be a real effector molecule that aids in invasion. A whole family of other secreted Cia proteins that are stimulated in the presence of FCS require CiaB expression to be secreted. Nevertheless, in the model strain 81-176, there is no discernible decrease in invasion by a ciaB mutant, indicating that additional research is necessary to validate the function of this protein during infection.[6].

Infection with *Campylobacter* remains a serious public health concern. Despite the fact that *Campylobacterjejuni* and *Campylobactercoli* are common foodborne pathogens that cause an estimated 1.3 million illnesses annually in the US, diagnosing them can be difficult due to the organism's difficult to isolate, grow, and identify characteristics. There are currently no best-practice clinical or public health laboratory guidelines for laboratory diagnosis of *Campylobacter* infections, despite recent reports detailing clinical laboratory practices for Campylobacter diagnostics in Pennsylvania and the Foodborne Diseases Active Surveillance Network (FoodNet) sites highlighting the variety of testing practices in use. As the "gold standard" for diagnosis, direct plating onto a Campylobacter selective medium and 72 hours of microaerobic incubation at 42°C have long been known[3].

Campylobacter testing on stool samples is becoming more common with the use of culture-independent diagnostic tests (CIDTs), which could have significant effects on patient care and public health surveillance programs. Stool antigen tests are quick and provide results the same day for the direct detection of Campylobacter in fecal samples; however, issues with positive predictive value (PPV) and specificity have been brought up. As of right now, there are no rules governing the interpretation and reporting of inconsistent stool antigen test and culture results. Furthermore, culture confirmation is required according to the current national case definition for

a confirmed case of Campylobacter, Individuals who only have positive CIDT results are considered probable cases. Even though CIDT results are monitored, the Campylobacter incidence and trend reports available through Food Net currently only include cases that have been confirmed by culture. Evaluation of the efficacy of culture-independent assays is obviously necessary, as is improved education for microbiologists and physicians regarding the application of these tests in patient management. Additionally, data from public health surveillance programs and real-world sources must be verified in order to make well-informed decisions about whether and how to alter Campylobacter case definitions. We carried out a prospective, multicenter study to assess the efficacy of stool antigen tests in comparison to culture and PCR for Campylobacter detection instool[1].

2.12 CLINICAL DIAGNOSIS/LABORATORY APPROACH IN NIGERIA

Methods for Identification and Detection of *Campylobacter:*

When Campylobacter bacteria are found in bodily fluids, tissue, or stool (poop), a laboratory test is used to diagnose Campylobacter infection. A quick diagnostic test that finds the bacteria's genetic material could be used, or a culture that isolates the bacteria could be used[7].

Stool Antigen Tests.

As directed by the manufacturer, all stool specimens at each study site can be subjected to the following four stool antigen tests. Two are formatted as lateral flow devices, ImmunoCard Stat! Campy (ICS; Meridian Bioscience Inc., Cincinnati, OH) and Xpect Campy (Remel Inc., Lenexa, KS), and two are formatted as microplate assays, ProSpecT Campylobacter (Remel Inc., Lenexa, KS) and Premier Campy (Meridian Bioscience Inc., Cincinnati, OH).

Polymerase Chain Reaction (PCR).

Following the manufacturer's instructions, genomic DNA can be isolated for molecular diagnosis using the automated QIAcube system (Qiagen, Valencia, CA) or the QIAamp DNA stool minikit. Following the manufacturer's instructions, study sites tested every stool specimen using the Seeplex diarrhea-bacterial panel 1ACE detection PCR kit (Seegene Inc., Seoul, South Korea). Study site 4 (GA) conducted PCR testing for the remaining four study sites (CA, CT, IA, and MD), while the remaining four study sites (CO, GA, MN, and PA) tested their own specimens.After all other testing was finished, stool specimens were sent frozen on dry ice to study site 4 for this PCR testing. Based on dual priming oligonucleotide technology (DPO), this multiplex PCR kit can identify the following: *Salmonella spp. (Salmonella bongori and Salmonella enterica), Shigella spp. (Shigella flexneri, Shigella boydii, Shigella sonnei, and Shigella dysenteriae), Vibrio spp. (Vibrio cholerae, Vibrio parahaemolyticus, and Vibrio vulnificus), and Clostridium difficile* toxin B. When it comes to detecting Campylobacter in stool, this previously validated PCR assay is said to be more sensitive than culture.[3].

Culture-Based Methods

The International Standards Organization provides guidelines for the isolation and detection of Campylobacter from food using culture-based techniques. The procedures for enumeration are specified by ISO/TS 10272-2:20064, while the procedures for detection are defined by ISO 10272-1:20063[4].

The pathogen is isolated by culturing it on specific media and then incubating it under microaerobic conditions for 44 hours at 41.5oC. To aid in the recovery of damaged cells, food and environmental samples require an extra pre-enrichment step. A selective enrichment broth medium is used for enrichment, and it is then incubated for five hours at 37 °C. It is possible to cultivate clinical samples directly onto specific media[14].

After being isolated, Campylobacter is identified using their growth, biochemical, and morphological traits. Gram staining and biochemical tests like catalase, oxidase, hippurate hydrolysis, and nitrate/nitrite reduction are the most often used identification schemes[13].

There are several commercially available selective agars that are intended to separate Campylobacter colonies.Numerous selective agents, the majority of which are antibiotics that inhibit the growth of additional enteric bacteria, are present in these media. Pre-enrichment media include components that shield cells from the harmful effects of oxygen derivatives that are toxic to them. These consist of blood that has been lysed or defibrinated, charcoal, and a mixture of sodium pyruvate, ferrous sulfate, and sodium metabisulfite (FBP)[5].

You can get selective and enrichment media as ready-to-use formulations or as base powders. In addition, the precise microaerobic environment required for Campylobacter recovery and enumeration can be produced using commercially available atmosphere generation systems[7].

These culture-based techniques have a few drawbacks despite being comparatively inexpensive and requiring little specialized equipment. The length of time needed to receive the final results and Campylobacter's restricted reaction to biochemical testing are the two biggest disadvantages. In addition, these methods require a lot of labor and are less sensitive than molecular and serological approaches. Additionally, under unfavorable circumstances, Campylobacter cells may enter the viable but not culturable (VBNC) state, producing false negative results.

There are several ways to prepare cultures in order to expedite the enrichment process. Filtration and centrifugation are two of these techniques for cell separation and concentration.

Fig 8 :A culture method (Jeanette *et al*., 2006 fig 9 : A culture method (Jeanette *et al*., 2006)

Fig 10 : **A culture method (Jeanette *et al*., 2006)**

fig 11 : A culture method (Jeanette *et al*., 2006)

Rapid detection methods

There are numerous commercially available immunological and molecular techniques for Campylobacter detection and identification. When compared to traditional methods, these techniques yield results that are more sensitive, accurate, and fast. These techniques also have

the benefit of being able to identify Campylobacter cells in the VBNC state. Nevertheless, some of these techniques call for specialized personnel and more sophisticated equipment. They are also unable to discriminate between living and dead cells[8].

Commercially available immunoassay systems based on antibody/antigen interactions include Latex agglutination and the enzyme-linked immunosorbent assay (ELISA).

Commercial kits for nucleic acid-based techniques like real-time PCR and polymerase chain reaction (PCR) are also widely accessible. Additional molecular methods for identifying and detecting the organism include Random Amplified Polymorphic DNA (RAPD) and Pulsed Field gel Electrophoresis (PFGE)[9].

Moreover, a blend of conventional and contemporary methods can be employed to augment the dependability and velocity of the outcome. [14].

2.13 TREATMENT

With the exception of electrolyte replacement and rehydration, treatment is typically not necessary. In invasive cases—when bacteria infiltrate intestinal mucosa cells and cause tissue damage—or to eradicate the carrier state—the state in which individuals harbor Campylobacter in their bodies and continuously excrete the bacteria while exhibiting no symptoms—antimicrobial treatment is advised[6].

The majority of people with Campylobacter infections recover without the need for antibiotics. For as long as the diarrhea persists, patients should consume more fluids.

Some patients with severe illnesses or those who are at risk for them may require antibiotic therapy. These individuals include those who are 65 years of age or older, those who are pregnant, and those with compromised immune systems, such as those undergoing chemotherapy, those with blood disorders, or those with AIDS[12].

Certain Campylobacter species may not respond well to a particular class of antibiotic. Healthcare professionals can use laboratory testing to help determine which type of antibiotics are likely to be effective when they are needed[15].

When prescribed antibiotics are taken, patients should follow all instructions and notify their doctor if their symptoms do not improve [11].

2.14 PREVENTION

There are several tactics that can be employed to stop Campylobacter infections:

Control measures at every point of the food chain, from farm-based agricultural production to the processing, manufacturing, and preparation of foods for both domestic and commercial use, are the foundation of prevention[10].

It might be necessary to disinfect excrement and items contaminated with it before discarding them in nations without sufficient sewage disposal systems.

Enhanced biosecurity is one strategy to lower the prevalence of Campylobacter in poultry by preventing the bacteria from entering the farm's flock of birds from the surrounding area. This method of control is only practical in situations where birds are housed in enclosed spaces[1].

Although clean slaughtering procedures lessen the chance of feces contaminating carcasses, they cannot ensure that meat and meat products are free of Campylobacter. To reduce contamination to a minimum, abattoir staff and producers of raw meat must receive training in hygienic food handling[2].

The prevention techniques used for other foodborne bacterial diseases are also applicable to domestic kitchen infections.

The only treatment that effectively removes Campylobacter from contaminated food is bactericidal treatment, such as cooking, pasteurization, or radiation[3].

2.15 WORLD HEALTH ORGANIZATION (WHO) RESPONSE

Working with other relevant parties, WHO is adamantly promoting food safety as a crucial component of guaranteeing that people have access to healthy, safe diets. WHO uses a variety of sector-specific expertise to provide policies and recommendations that address the whole food chain, from production to consumption[7].

WHO strives to make food safety systems stronger in a world that is becoming more interconnected. Among the most important interventions in the prevention of foodborne illnesses are the establishment of international food safety standards, the improvement of disease surveillance, consumer education, and training for food handlers in safe food handling practices[9].

The World Health Organization is enhancing the capabilities of national and regional laboratories to monitor foodborne pathogens, including Salmonella and *Campylobacter*.

The World Health Organization is also pushing for integrated surveillance of antibiotic resistance in food chain pathogens, which involves gathering samples from people, food, and animals and analyzing data from various sectors[13].

By coordinating global efforts for early detection and response to foodborne disease outbreaks through the network of national authorities in Member States, WHO and FAO are helping Member States[5].

In order to prevent foodborne illnesses, the FAO/WHO Codex Alimentarius Commission develops international food standards, guidelines, and recommendations based on scientific assessments that WHO also provides [1].

2.18 RECOMMENDATIONS FOR THE PUBLIC AND TRAVELLERS

The following advice will assist people in traveling safely:

Make sure the food is served hot and properly prepared.

Steer clear of raw milk and products manufactured with it. Only consume boiled or pasteurized milk.

If ice isn't made with safe water, steer clear of it.

If there is any doubt about the safety of the drinking water, boil it or, in the event that boiling is not an option, disinfect it with a dependable, slow-acting disinfectant (often found in pharmacies).

Hands should be thoroughly and often cleaned with soap, especially after using the restroom or coming into contact with farm animals or pets.

Produce should be thoroughly cleaned, especially if it will be consumed raw. Fruits and vegetables should ideally be peeled.

2.19 RECOMMENDATIONS FOR FOOD HANDLERS

The WHO offers the following advice to those who handle food:

Food handlers, whether in a professional or domestic setting, should follow hygienic guidelines and exercise caution when preparing food.

If a professional food handler experiences vomiting, diarrhea, fever, or visible infected skin lesions, they should notify their employer right away.

Programs to educate consumers and train food handlers are built around the WHO Five Keys to Safer Food. Their significance lies in their ability to avert food poisoning.

The Five keys are:

1. Keep clean
2. Separate raw and cooked
3. Cook thoroughly
4. Keep food at safe temperatures
5. Use safe water and raw materials.

CONCLUSION

One of the most prevalent bacterial species causing diarrheal sickness globally is Campylobacter. The ingestion of raw milk, undercooked poultry, and tainted water are linked to this infection. Patients usually arrive with a 5–7 day self-limited diarrheal illness.

Even though campylobacteriosis is the most common bacterial foodborne illness in the developed world, efforts to prevent it have not been very successful. Here, we draw attention to an aspect of this infection that has received little attention up to this point: how it exploits other microbes.

REFERENCES

1. Courouble, G., D. Dufillot, A. Sans, E. Malpote, C. Berchel, and M. Nicolas (2000). Acute childhood gastroenteritis study at Central University Hospital of Pointe-a-Pitre/Abymes, Guadeloupe, from November 1997 to March 1998. Bull. Soc. Pathol. Exot. 93**:**58-61. (In French.)

2. De Boer, P., B. Duim, A. Rigter, J. van Der Plas, W. F. Jacobs-Reitsma, and J. A. Wagenaar (2000). Computer-assisted analysis and epidemiological value of genotyping methods for *Campylobacter jejuni* and *Campylobacter coli*. ***J. Clin. Microbiol***. 38**:**1940-1946.
3. Endtz, H. P., C. W. Ang, N. van Den Braak, B. Duim, A. Rigter, L. J. Price, D. L. Woodward, F. G. Rodgers, W. M. Johnson, J. A. Wagenaar, B. C. Jacobs, H. A. Verbrugh, and A. van Belkum (2000). Molecular characterization of *Campylobacter jejuni* from patients with Guillain-Barré and Miller Fisher syndromes. ***J. Clin. Microbiol***. 38**:**2297-2301.
4. Fitzgerald, C., L. O. Helsel, M. A. Nicholson, S. J. Olsen, D. L. Swerdlow, R. Flahart, J. Sexton, and P. I. Fields (2001). Evaluation of methods for subtyping *Campylobacter jejuni* during an outbreak involving a food handler. ***J. Clin. Microbiol.*** 39**:**2386-2390.
5. Friedman, C. R., J. Neimann, H. C. Wegener, and R. V. Tauxe (2000). Epidemiology of *Campylobacter jejuni* infections in the United States and other industrialized nations, p. 121-138. *In* I. Nachamkin and M. J. Blaser (ed.), *Campylobacter*, 2nd ed. American Society for Microbiology, Washington, D.C
6. Jeanette, K. M, Jilian, M. T, and Blackall, P. J.(2006) AntibioticResistance in Campylobacter jejuni and Campylobacter coli isolated from Poultry in the South- East Queensland region. ***Journal of Antimicrobial Chemotherapy*** ;59, 775-778
7. Melby, K. K., J. G. Svendby, T. Eggebo, L. A. Holmen, B. M. Andersen, L. Lind, E, Sjogren, and B. Kaijser**.** 2000. Outbreak of *Campylobacter* infection in a subarctic community. ***Eur. J. Clin. Microbiol. Infect. Dis***. 19**:**542-544.
8. Oberhelman, R. A., and D. N. Taylor (2000). *Campylobacter* infections in developing countries, p. 139-153. *In* I. Nachamkin and M. J. Blaser (ed.), *Campylobacter*, 2nd ed. American Society for Microbiology, Washington, D.C.
9. Olsen, S. J., G. R. Hansen, L. Bartlett, C. Fitzgerald, A. Sonder, R. Manjrekar, T. Riggs, J. Kim, R. Flahart, G. Pezzino, and D. L. Swerdlow (2001). An outbreak of *Campylobacter jejuni* infections associated with food handler contamination: the use of pulsed-field gel electrophoresis. ***J. Infect. Dis***. 183:164-167.
10. Paredes, P., S. Campbell-Forrester, J. J. Mathewson, D. Ashley, S. Thompson, R. Steffen, Z. D. Jiang, A. M. Svennerholm, and H. L. DuPont (2000). ***Etiology of travelers' diarrhea on a Caribbean island. J. Travel Med***. **7:**15-18.
11. Ribot, E. M., C. Fitzgerald, K. Kubota, B. Swaminathan, and T. J. Barrett. (2001). Rapid pulsed-field gel electrophoresis protocol for subtyping of *Campylobacter jejuni*. ***J. Clin. Microbiol***. 39**:**1889-1894.
12. Rosef, O., G. Rettedal, and L. Lageide**.** (2001). Thermophilic campylobacters in surface water: a potential risk of campylobacteriosis. ***Int. J. Environ. Health Res***. 11**:**321-327.
13. Salihu. M. D, Junaidu, A. U, and Abubakar, A. A. (2009), Magaji A, Mohammed LG. Isolation and Characterization of Campylobacter jejuni From Cannel (Cannelus dramedarius) in Sokoto State, Northern Nigeria ***Internal J Animal and Vet Adv***.,1(1):25–29.
14. Tenkate, T. D., and R. J. Stafford**.** 2001. Risk factors for campylobacter infection in infants and young children: a matched case-control study. Epidemiol. B Infect. 127**:**399-404.

15. Van Belkum, A., N. van Den Braak, P. Godschalk, W. Ang, B. Jacobs, M. Gilbert, W. Wakarchuk, H. Verbrugh, and H. Endtz. 2001. A *Campylobacter jejuni* gene associated with immune-mediated neuropathy. Nat. Med. **7:**752-753.
16. Ansarifar, E., Riahi, S. M., Tasara, T., Sadighara, P., & Zeinali, T. (2021). Campylobacter prevalence from food, animals, human and environmental samples in Iran: a systematic review and meta-analysis. **BMC Microbiology**, 21(1), 1-14.
17. Audu, B. J., Norval, S., Lopes, B., Ramjee, M., Macrae, M., & Forbes, K. J. (2022). Genomic diversity and antimicrobial resistance of Campylobacter spp. from humans and livestock in Nigeria. **J Biomedical Science**, 29(1), 1-14.
18. Moradi, F., Akbari, M., Zandi, H., & Rouhi Jahromi, R. (2019). Prevalence and antimicrobial resistance of Campylobacter coli and Campylobacter jejuni in the animals, food products, and human clinical specimens in Iran during 2004-2017: A review study. **J Food Safety**, 39(6).