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Prevalence of *Campylobacter* spp. among diarrhoeic HIV-patients in Kaduna, Nigeria

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ABSTRACT

***Campylobacter* diarrhoea is regarded as the most common type of bacterial diarrhoea worldwide but the disease burden among diarrhoeic HIV-patients in Kaduna State has not been characterised. A total of 230 faecal samples were collected and analysed for *Campylobacter* spp. using membrane filtration method and; the isolates were characterised based on the morphological appearance and biochemical testing using standard methods. Isolates were further analysed by API Campy kits®, to characterise the isolates' species level. Polymerase chain reaction (PCR) targeting the lpxA gene, 23S rDNA and napA gene was used to confirmed the isolates. Out of the 230 faecal samples that were collected and cultured for *Campylobacter*, 45 samples were culture positive giving a prevalence of 19.6%. All the isolates produce the expected bands (757, 746, 656 and 835 bp) during the PCR confirmation. The *Campylobacter* spp. identified were *Campylobacter jejuni, Campylobacter coli, Campylobacter fetus* and *Campylobacter hyointestinalis*. Age and sex distribution with campylobacteriosis was established. The prevalence was higher among female (14.3%) than male (5.2%) and the difference was statistically significant (p = 0.042). All the risk factors considered such as source of drinking water, consumption of raw milk, eating of under-cooked meat in the study were not found to be associated with the disease condition. The prevalence of this bacterium among the study population is relatively high. Studies are needed to reassess the effect of Zidovudine with this high prevalence since the risk factors were not statistically significant in this study.**

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INTRODUCTION

campylobacteriosis, an infectious disease caused by *Campylobacters* is regarded as the most common type of diarrhoea worldwide, exceeding cases of Salmonellosis, Shigellosis and *Escherichia coli* infection (Altekruse et al., 1999; Allos, 2001). It is usually self-limiting in immunocompetent and treatment may involve mere rehydration solution with antibiotics, but may become bacteremia in immunocompromised leading to life threatening condition (Tee and Mijch, 1998). This *Campylobacter* related diarrhoea has claimed over 33 million lives, and due to this alarming death rate, interests in the study of the potency of *Campylobacter* spp. in diarrhoea has increased in both developed and under developed countries (Coker et al., 2002). Most outbreaks of this disease are usually sporadic and are associated with eating or handling undercooked poultry, consumption of unpasteurized milk and drinking of contaminated water (Kaakoush et al., 2015). Among all *Campylobacter* spp., *Campylobacter jejuni* is reported to be responsible for over 90% of this diarrhoea (Adzitey et al., 2012), however, other *Campylobacter* spp. are also implicated in the diarrhoea. Diarrhoea, which is the passage of unformed or watery stool at least twice daily, often with enteric symptoms, is the leading cause of

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hospital visit among people with poor hygienic practice (Opintan et al., 2010). It has been identified as the most common health challenges in the management of HIV infections (Samie et al., 2011). Most screening for the causative agent of diarrhoea among HIV infected populace does not include *Campylobacter*; whereas, in the proper management of HIV- associated diarrhoea, a key agent such as *Campylobacter* cannot be ignored (Karikari et al., 2017). Since the outbreak of HIV/AIDS, it had become important to observe the distribution of gastrointestinal pathogens such as *Campylobacter* spp. among HIV seropositive individual (Samie et al., 2011). This is because, HIV/AIDS patients are at a higher risk of acquiring campylobacteriosis more than the general public, but it is unclear whether this risk increases during the course of the sickness (Angulo and David, 1995). Death due to campylobacteriosis among HIV/AIDS patients is usually due to the complications such as bacteremia, hepatitis, meningitis and arthritis, brain abscess, soft tissue infection, Guillain-Barr syndrome and Miller Fisher syndrome which are associated with the diarrhoea (Kaakoush et al., 2015). The implication of *Campylobacter* spp. in diarrhoeic HIV patients is not clear, despite the facts that these organisms connote a very important risk factor among HIV-infected patients (Adesiji and Oloke, 2015). However, it is believed that HIV/AIDS can increase the number of cases of campylobacteriosis in most countries. This observation further supports the need for improved understanding of the epidemiology of campylobacteriosis in these countries (Coker et al., 2002). Zidovudine, the ART-retroviral drugs administered to HIV/AIDS patients was observed to be efficient in *in vitro* on gram negative bacteria, mainly members of the family Enterobacteriaceae, including strains of *C. jejuni, E. coli, Salmonella typhimurium, Klebsiella pneumoniae, Shigella flexneri,* and *Enterobacter aerogenes* but after a 24 h exposure, these bacteria developed a stable high-level resistance (Sample et al., 1991). Demographic and occupational risk factors had been reported to be predisposing factors of campylobacteriosis, but these factors have not been studied intensively as a determinant of this disease among diarrhoeic HIV-patients (Chia-Ping et al., 2017). Cultural methods have been used commonly in most developing countries for the detection of this bacterium, but the major challenges are its limited sensitivity and lack of specificity (Samie et al., 2011). This is because, *Campylobacter* is bio-chemically inert and discrimination between two species may depend on one biochemical test. However, the advent of rapid test identification kits and molecular techniques which have acceptable level of specificity and sensitivity has made *Campylobacter* detection and characterization easier and efficient from faecal sample (Louwen et al., 2012). The aim of this study was to observe the distribution of this *Campylobacter*-related diarrhoea by isolating and identifying C*ampylobacter* spp. and evaluate some predisposing factors to this disease among diarrhoeic HIV/AIDS patients in Kaduna State, Nigeria.

MATERIALS AND METHODS

Study area and population

The study was carried out in Kaduna State, Nigeria. Kaduna State is located between latitude 10°20'N and 7°45'E and Longitude 10°33'N and 7°75'E. It has 23 local government areas (LGAs) in the three senatorial districts. The study was cross sectional, having a representative of the three senatorial districts but hospital based. The selected hospitals that were used for the study were General Hospital Kachia (GHK), Dr Gwamna Awan General Hospital, (DGAGH), General Hospital Sabon-Tasha (GHS), Hajia Gambo Sawaba General Hospital (HGSGH), National Tuberculosis and Leprosy Training Centre (NTBLTC). High attendances of patients are recorded among the selected hospitals due to the availability of expertise and diagnostic equipment.

Ethical approval (Reference Number: MOH/ADM/744/ VOL.1/524) was obtained from the State Ministry of Health prior to the study. The consent forms were given to eligible patients for approval before commencement of the study.

The study population were HIV infected patients who were diagnosed of diarrhoea in the selected Hospitals from August 2017 to December 2017. Two hundred and thirty (230) patients of age ≥ 10 years including both out-patients and in-patients were enrolled in this study. A well-structured questionnaire was administered to consenting patients to obtain relevant data on their age, sex, educational status, occupation, and risk factors such as source of drinking water, type of toilet, contacts with farm animals, and consumption of raw milk as well as use of medication that could affect the consistency of the stool. Selection of these predisposing factors was based on their understanding of conditions that exposes them to diarrhoea. The patients' hospital records were also reviewed for more clinical data.

Samples collection

Sterile stool sample containers were given to consenting patients whose questionnaires were satisfactorily filled to bring fresh stool sample. Fresh stool samples were defined as stool samples less than 2 h old. The samples

were transported in ice-pack container immediately to the Department of Microbiology Laboratory, Ahmadu Bello University, Zaria.

Samples processing, isolation and identification

Plating was done after diluting (1:10) the feacal sample using sterile 0.1% Buffered Peptone Water (BPW, CM0009, Oxoid). Ten (10) drops of the faecal suspension were inoculated into a 0.45 µm cellulose triacetate membrane filter of diameter 50 mm (Sartorius, Goettigen, Germany) centrally placed on a prepared *Campylobacter* sheep blood agar plate using a Pasteur pipette. It was allowed to stands for 30 mins, after which, the filter was removed aseptically using forceps and the plates kept in a 3.5 L anaerobic jar where Campy-Gen gas generating sachet (Campygen N25 Oxoid) was introduced to maintain the microaerophilic condition (6% O2 and 10% CO2 in 84% N2) and incubated at 37 ºC for 6 days (Lastovica, 2006). Presumptive isolates (colonies that were gray, flat, irregular and spreading) were plated onto modified Charcoal Cefoperazone Deoxycholate Agar (mCCDA, CM0739, with CCDA Selective Supplement SR0155E, Oxoid) using a sterile wire loop. The plates were transferred into a 3.5 L anaerobic jar where Campy-Gen gas generating sachet was introduced and incubated at 42°C for 2 days. Morphological characteristics such as colonial appearance and biochemical tests were used to characterise the isolates (Karikari et al., 2017). Small curved gram negative rods that were Catalase (+), Oxidase (+), Nitrate reduction (+) were further analysed using API Campy kits® (bioMèrieux, France) to identify the isolates to species level. The isolates were stored on a 5% glycerol plus Nutrient broth (CM0001, Oxoid) at -20°C.

Genetic characterization of *Campylobacter* spp.

The DNA of the bacterial isolates from the pure cultures was extracted using the Phenol-Chloroform method (Sample et al., 1991). Species-specific primers that have variability at the IpxA gene of the thermotolerant *Campylobacter* spp. were used to identify *C. jejuni* and *C. coli*. Because of the relatedness of these two thermotolerant *Campylobacter* spp., an additional primer, that target the *nap*A gene (specific for *C. jejuni*) was used in combination with the primer that detect IpxA of *C. jejuni* to maximized detection while species-specific primers which have variability at the 23S rDNA gene of the *Campylobacter* spp. were used for the identification of *C. fetus* and *C. hyointestinalis* (Table 1) (Bastyns et al., 1994; Klena et al., 2004; Miller et al., 2007). PCR amplification was performed on a Gene Amp® PCR system 2700 (Applied Biosystem). The PCR reaction mixture of 20 µl containing 10 mM of Tris-HCL (pH 8.3), 50 mM of KCL, 1.5 mM of $MgCL_2$, 100 µg/mL of bovine serum albumin, 1 µL of both primers, 200 µM of dNTPs, 1.25 U of Amplitaq DNA polymerase (Perkin-Elemer-Cetus), and 5 µL of extracted DNA were spun at high speed for 3 seconds. The samples were subjected to 35 amplification cycles, denaturation for 1 min at 95°C, annealing at 50°C for 1 minute (primers IpxACj/KK2 and IpxACc/KK2), at 53°C for 30 s (primer napAIF3/napAIR3), at 54°C for 1 min (primers HYO1/69ar and FET1/69ar), extension at 72ºC for 2 minutes and final extension at 72ºC for 8 minutes. The PCR products were separated by gel-electrophoresis on 1.2% agarose gel stained with 1 µg/ml Ethidium bromide at 90V for 1½ h. The size of the amplification products was estimated by using a 500+bp marker (Bioneer).

Statistical analysis

Prevalence was calculated and expressed as percentage (%). The results obtained were entered into Statistical Program SPSS version 20.0 and tested for significance using Chi-square. Significance was determined at $P<0.05$. Odds ratio was calculated to test for association between risk factors and infection.

RESULTS

Percentage of isolation of *Campylobacter* from diarrhoeic HIV-patients in Kaduna

The results in Table 2 show the Percentage Isolation of *Campylobacter* spp. among diarrhoeic HIV-patients. Forty five (45) out of the 230 diarrhoeic faecal samples collected and analysed were found to be positive for *Campylobacter* spp. giving a prevalence of 19.6%. This prevalence was based on the API Campy kits® (bioMèrieux, France) identification of the isolates.

Prevalence of *Campylobacter* spp. in diarrhoeic HIV-patients in Kaduna based on the study sites

Table 3 shows that out of the 65 samples collected from Hajia Gambo Sawaba General Hospital (HGSGH), Zaria city, 18 were positive for Campylobacter species giving a prevalence of 27.7%. Fifteen (15) out of the 60 samples collected from National Tuberculosis and Leprosy Training Centre (NTBLTC), Saye, were positive for Campylobacter species giving a prevalence of 25.0%.

Table 1. Primers sequence used for PCR amplification of *Campylobacter* spp. from HIV infected patients.

Species Gene	Primer	Sequence (5' - 3')	Size (bp)	Reference
*C. jejuni lpx*A	lpxACj lpxAR	(F)ACAACTTGGTGACGATGTTGTA (R)CAATCATGDGCDATATGASAATAHGCCAT	757	Klena et al. (2004)
*nap*A	napAF3 napAR3	(F)TAGAACAAATAATATCGATCCAAATGC (R)AAAAGTGTATCATCTTCGCTATAACCC	1454	Miller et al. (2007)
*C. coli lpx*A	lpxACc lpxAR	(F)AGACAAATAAGAGAGAATCAG (R)CAATCATGDGCDATATGASAATAHGCCAT	746	Klena et al. (2004)
C. fetus 23S rDNA	FET1 69ar	(F)CTCATAATTTAATTGCACTCATA (R)CTTAGGACCGTTATAGTTAC	835	Bastyns et al. (1994)
C. hyointestinalis 23S rDNA	HYO1 69ar	(F)ATCTAGGTGAGAATCCTAG (R)CTTAGGACCGTTATAGTTAC	656	Bastyns et al. (1994)

Table 2. Percentage isolation of *Campylobacter* spp. (%) from diarrhoeic HIV-patients in Kaduna (n=230).

***Campylobacter* spp.**	**No. Isolated**	**Percentage (%)**
C. jejuni	15	33.3
C. coli	20	44.4
C. fetus	7	15.6
C. hyointestinalis	3	6.7
Total	45	100

Table 3. Prevalence of *Campylobacter* spp. among diarrhoeic HIV-patients in Kaduna based on the study sites.

Study sites	Number examined	Number positive (%)	χ^2	P value
NTBLTC	60	15 (25.0)	8.340	0.080
HGSGH	65	18 (27.7)		
DGAGH	30	3 (10.0)		
GHS	40	5 (12.5)		
GHK	35	4 (11.4)		
Total	230	45 (19.6)		

P<0.05 is considered statistically significant. **NTBLTC,** National Tuberculosis and Leprosy Training Centre; **GHS,** General Hospital, Sabo-Tesha; **HGSGH,** Hajia Gambo Sawaba General Hospital; **GHK,** General Hospital, Kachia; **DGAGH,** Dr Gwamna Awan General Hospital.

Three (3) out of the 30 samples collected from Dr Gwamna Awan General Hospital (DGAGH), Kakuri, were positive for Campylobacter species with a prevalence of 10.0%. Five (5) out of the 40 samples collected from General Hospital (GH), Sabo, were positive for Campylobacter species with a prevalence of 12.5%. Four (4) out of the 35 samples collected from General Hospital (GH), Kachia, were positive for Campylobacter species giving a prevalence of 11.4%. However, the difference in prevalence rates in this study at the different hospitals was not statistically significant (P -value = 0.080; χ^2 = 8.340).

Genetic characterization of the isolates

Amplification of DNA from *Campylobacter* isolates yielded bands of 757 bp and (1454 bp), 626, 764 and 835 bp for *C. jejuni*, C. *hyointestinalis*, *C. coli* and *C. fetus* respectively. The result is as presented in Figure 1.

Age and Sex distribution of campylobacteriosis among diarrhoeic HIV-patients in Kaduna State

In this study, all age groups were affected by the

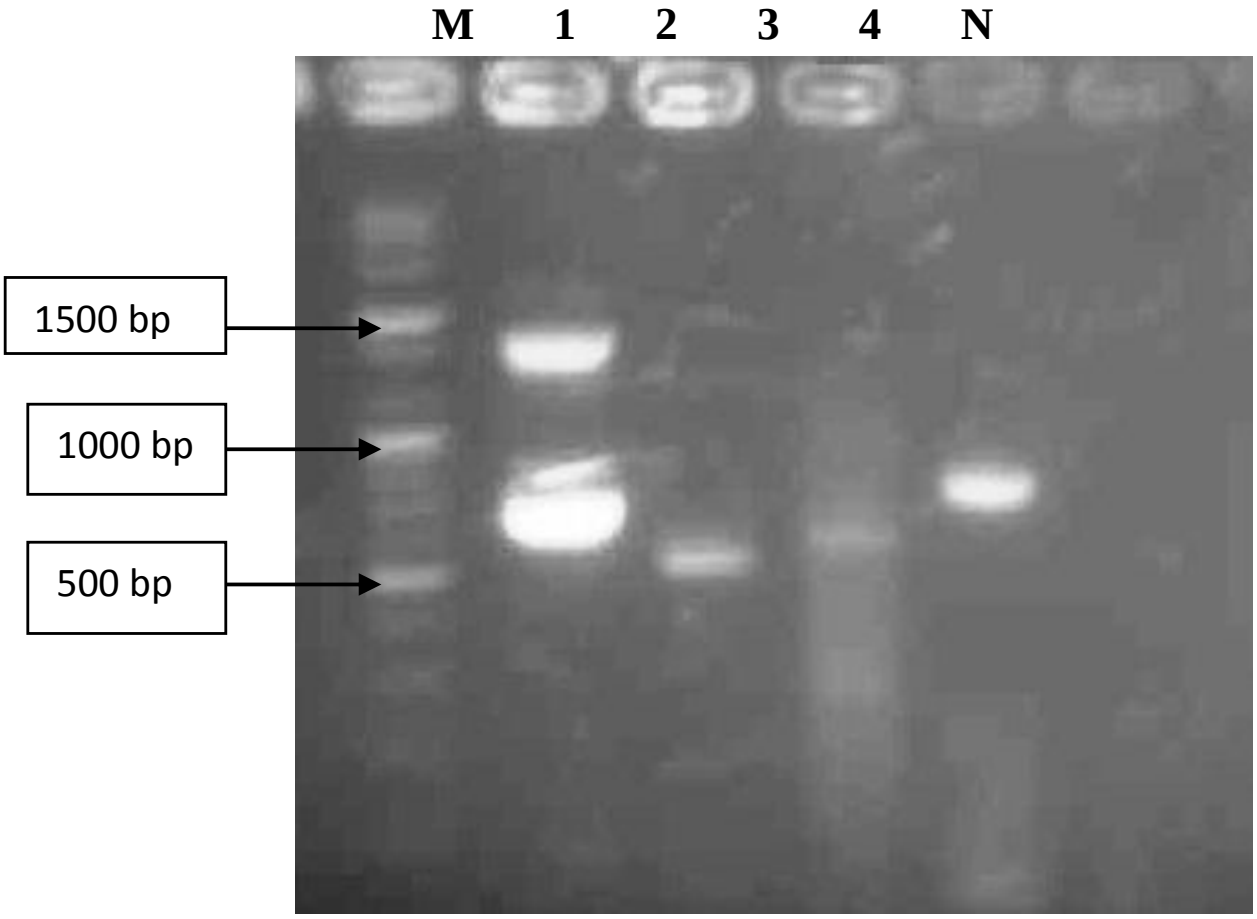

Figure 1: Agarose gel-electrophoresis of *Campylobacter* spp. from diarrhoeic HIV-patients in Kaduna.
Lane M, Molecular marker; **lane 1,** two amplicons at 1454 and 757bp detecting the *nap*A gene and the *lpx*A gene of *Campylobacter jejuni,* respectively; **Lane 2,** one amplicon at 656 bp detecting the 23S rDNA gene of *C. hyointestinalis*; **lane 3,** one amplicon at 746 bp detecting the *lpx*A gene of *C. coli*; **lane 4,** one amplicon at 835 bp detecting the 23S rDNA gene of *C. fetus*; **lane N,** Negative control.

Table 4. Age and Sex distribution of campylobacteriosis among diarrhoeic HIV-patients in Kaduna State.

Age (yrs)	No. examined	Male		Female		Total (%) Positive	x^2	p - value
		No. examined	No. (%) Positive	No. examined	No. (%) Positive			
10 - 19	8	4	0 (0.0)	4	1(25.0)	1(25.0)	**4.144**	**0.042***
20 - 29	45	18	3 (16.7)	27	7 (25.9)	10(42.6)		
30 - 39	78	33	6 (18.2)	45	14(31.1)	20(49.3)		
40 - 49	66	25	2 (8.0)	39	6 (15.4)	8 (23.4)		
≥ 50	33	12	1 (8.3)	23	5 (21.7)	6 (30.0)		
Total	230	92	12(13.0)	138	33(23.9)	45(19.6)		

*P-value significant at <0.05.

Table 5. Association of risk factors and campylobacteriosis among diarrhoeic HIV-patients in Kaduna.

Variable	Number examined	Positive (%)	P- value*	Odds Ratio	CI
Sewage disposal					
Pit latrine	136	31 (13.5)	0.138	1.687	0.842 – 3.380
Septic tank	94	14 (6.1)			
Water sources					
Tap	64	12 (5.2)	0.150		
River	23	8 (3.5)			
Well	101	15 (6.5)			
Others	42	10 (4.3)			
Contact with farm animal					
Yes	146	29 (12.6)	0.881	1.053	0.534 – 2.079
No	84	16 (7.0)			
Taking of Raw Milk					
Yes	209	43 (18.7)	0.383*	2.462	0.552 – 10.975
No	21	2 (0.9)			
Eating under-cooked meat					
Yes	128	25 (10.9)	0.988	0.995	0.517 – 1.917
No	102	20 (8.7)			

P<0.05 is considered statistically significant. **CI,** Confidence Interval; ***,** Fischer's exact test.

infections. However, patients in the age group 30-39 were mostly infected 20(49.3%) followed by the age group 20-29 (42.6%) while the least cases (25.0%) were observed in the age group 10-19. There was no significant association between campylobacteriosis and age. In this study, the infection was more common among female (23.9%) than male (13.0%). There was significant difference in the distribution of campylobacteriosis with sex in this study (p-value 0.04). The result is as presented in Table 4.

Prevalence of *Campylobacter* species in relation to risk factors among diarrhoeic HIV-patients in Kaduna State

The relationship of *Campylobacter* species with respect to risk factors of campylobacteriosis is presented in Table 5. Factors that were considered were; type of sewage disposal system, source of drinking water, contact with farm animals, taking of raw milk, eating of chicken, eating of undercooked meat and-or meat product. Under the sewage disposal system, pit latrine had the highest prevalence of 31 (22.7%) while septic tank had a lowest prevalence of 14 (14.8%). On the source of drinking water, participants that drank water from river had the highest prevalence of 8 (34.9%) while participants that drank water from well had the lowest prevalence of 15 (14.8%). Under contacts with farm animals, participants that have had contact with farm animals had a high prevalence of 29 (19.8%) while those that had no contact with farm animal had a low prevalence of 16 (19.0%). Under eating of chicken, participants that eat chicken had a high prevalence of 31 (20.8%) while those that did not eat chicken had a low prevalence of 14 (17.2%). Among those that consume raw milk, participants that take raw milk had a high prevalence of 43 (20.5%) while those that did not consume raw milk had a low prevalence of 2 (9.5%). Participants that ate under cooked meat and meat products had a high prevalence of 20 (19.6) while participants that did not eat under cooked meat and meat products had a low prevalence of 25 (19.5%). However, there were no significant association between *Campylobacter* isolates and the risk factors to campylobacteriosis at a p-value of 0.05.

DISCUSSION

The prevalence of *Campylobacter* was investigated in this research by isolating *Campylobacter* species from the stool of diarrhoeic HIV-patient and 19.6% was observed. This high prevalence in the study could be due to the resistance of *Campylobacter* to Zidovudine, making this bacterium to be persistent among the populace (Sample et al., 1991). This bacterium has several

extracellular and cell-mediated factors that may be important virulence determinants in its infection. Such a high prevalence agrees with the reports of previous studies of Campylobacter species among HIV-patients in Nigeria and other parts of the world such as Snijders et al., (1997) who reported 16% prevalence of *Campylobacter* species among HIV-patients in Netherland. This finding is similar to report of 18.5%, 21.8% and 20% prevalence of *Campylobacter* species among HIV-patients in Australia, Cape Town and Nigeria respectively (Grant and Tee 1998; Lastovica and Roux, 2000; Coker 2002). However, the study was at variance with the 7% prevalence of *Campylobacter* species among HIV-patients reported in Lagos (Smith et al., 2005). This discrepancy could be due to the media of *Campylobacter* isolation. In their study, Butzler virion medium was used to isolate *Campylobacter* species with primary isolation temperature at 42ºC. This *Campylobacter* media can only allow the growth of some thermotolerant *Campylobacter* species but never allowed the growth of emerging (other) *Campylobacter* species (Lastovica, 2006).

From the result, high prevalence of 27.7% and 25.0% were observed in HGSGH and NTBLTC respectively, both in Zaria metropolis. This high prevalence seen in Zaria could be due to the fact that most of the samples were collected from Zaria. Additionally, even though, the risk factors were not statistically associated with campylobacteriosis in this study, lack of adequate potable drinking water in Zaria metropolis which is a major risk factor for campylobacteriosis could as well be responsible for this high prevalence. This opinion is also shared by (Aboh et al., 2015).

The result of the molecular analysis confirms the isolates to be *C. jejuni*, *C. coli*, *C. fetus* and *C. hyointestinalis* by giving the expected bands. The genes that were detected are IpxA, napA and 23S rDNA. The primers used for the PCR confirmation is presented in Table 1.

Campylobacter is normally recovered from children less than 2 years in most developing countries (Samuel et al., 2006); this study rather had higher prevalence in the 30 - 39 age groups. This may be attributed to the design of this study which did not focus on children with acute diarrhoea and also a reflection of the infection sources which were mostly obtained from the outpatient department which is usually dominated by these age groups in the study hospitals. *Campylobacter* infections were more prevalent in female (23.9%) than in male (13.0%) patients. The results from this study doubtless consider the gender distribution of *Campylobacter* infections in patients attending the selected hospitals in Kaduna State. Despite the fact that there were more female participants in the study than male, no obvious reason has been reported on the impact of gender in *Campylobacter* acquisition. However, it is believed that infants and females had an increased risk of acquiring *Campylobacter* infection (Gillespie et al., 2006; Karikari et al., 2017). This finding was in line with the work of Gwimi et al., (2015) who reported a higher prevalence of 64.79% among the female than male (60.7%). It also agrees with Samie et al., (2011) who reported a prevalence of campylobacteriosis of 54% among the female than male (46%). A prevalence of 67.6% among female compared to a prevalence of 32.4% among men was reported by Karikari et al., (2017) in his study at Ghana.

Even though the risk factors considered in this study were not statistically associated with campylobacteriosis, these factors are still implicated in Campylobacter infection. Under the sewage disposal system, pit latrine users had a prevalence of 22.7%. This could be serving as a direct transmission of the bacteria to drinking water source as sewage is been washed to water source during raining period. A prevalence of 34.9% was found among participants that drank water from river. This could be as a result of pollution from untreated sewage disposed into the water bodies (rivers). Prevalence of 19.8% was recorded among the participants that have had contact with farm animals. This observation agrees with previous studies that contact with farm animal is a good source of contamination by *Campylobacter* species. For instance, Kaakoush et al. (2015) reported a high prevalence in Nigeria due to contact with animals; such as, 58% from contact with dogs, 33% from contact with Cattle, 85% from contact with pigs etc. This could be due to the fact that most people that had have contacts with farm animals are agricultural workers; viz; cultivation of crops, rearing and selling of animal products. Most farmers use animal faecal materials as manure without adhering to strict precautionary measures. These farmers may have cuts in their body while manuring their farms leading to contamination with this bacterium. Meat sellers with open wound or cut are at risk of infection with *Campylobacter*. This finding was in agreement with the work of Chia-ping et al., (2017) who reported a higher prevalence (17%) of campylobacteriosis among farmers in Maryland, Ohio and Virginia, 2014. A prevalence of 20.5% was also observed among participants that drank locally pasteurized milk product (nono). This could be due to direct transmission from contaminated personnel during milk processing, unhygienic milking, use of contaminated water and post-pasteurization contamination. This was in agreement with Longenberger et al., (2013) who reported a prevalence of 12.3% of *Campylobacter* species from raw milk. However, it disagrees with Lovett et al., (1983) who reported a lower prevalence of 1.5% in Ohio, USA. Eating of chicken has been implicated as a good source of campylobacteriosis. The study observed a prevalence

of 20.8% among participants that eat chicken. This high prevalence found in chicken could be due to direct contamination from unhygienic chicken handling during processing, cross contamination during evisceration, unhygienic rinsing of multiple carcasses in the same water and cross contamination of the meat slab by meat handlers with the organisms carried from different farms (Olatoye and Ogunsemoyin, 2016). This is because, the intestinal tract of chickens can harbour large amount of *Campylobacter* species; during processing, may leak or rupture and the contents transferred to the skin of the carcases (Silva et al., 2011). The bacteria will remain in films on the skin and become entrapped into the crevices and channels which provide a favourable environment for cross contamination (Silva et al., 2011). This was in agreement with Olatoye and Ogunsemoyin, (2016) who reported a higher prevalence of 96% from retail chicken sold in Oyo State. Salihu et al., (2009) also reported a prevalence of 81.9% in Sokoto.

Conclusion

A prevalence of 19.6% was recorded in the study population. Age and sex distribution of campylobacteriosis was established. The highest prevalence of 49.3% was found among age group 30- 39 years. The prevalence was more among female (23.9%) than male (13.0%). The association between *Campylobacter* species and risk factors to campylobacteriosis was not established in this study. There is a need to reassess the effect of Zidovudine on this bacterium. It is recommended that there should be vigorous public awareness campaign on campylobacteriosis considering the high prevalence recorded on this study.

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REFERENCES

Aboh E. A., Giwa F. J. & Giwa A. (2015). Microbiological assessment of well water in Samaru, Zaria, Kaduna, State, Nigeria. Annals of African Medicine, 14(1):32-38.

Adesiji Y.O. & Oloke J. K. (2015). Challenges of the control of opportunistic infections zoonotic origin in HIV/AIDS patients. Int. J. Immunol. 3 (2-1):1-7.

Adzitey, F., Rusul, G., Huda, N., Cogan, T. & CORRY, J. (2012). Prevalence, antibiotic, resistance and RAPD typing of *Campylobacter* species isolated from ducks, their rearing and processing environment in Penang, Malaysia. Int. J. Food Microbiol. 154:197-205.

Allos B. M. (2001). *Campylobacter jejuni* infections: update on emerging issues and trends. Clin. Infect. Dis. 32:1201-1206.

Altekruse S. F., Stern N. J., Fields P. I. & Swerdlow D. L. (1999). *Campylobacter jejuni* – an emerging foodborne pathogens. Emerg. Infect. Dis. 5(1):28-35.

Angulo F. J. & David L. S. (1995). Bacterial enteric infections in persons infected with human immunodeficiency virus. Clin. Infect. Dis. 21(1):S84-93.

Bastyns B., Chapelle S., Vandamme P., Goosens H. & De Wachter R. (1994). Species-specific detection of Campylobacters important in veterinary medicine by PCR amplification of 23S rDNA. Syst. Appl. Microbiol. 17:5563-85.

Chia-ping S., Marie A. D-P., Kathleen F., Meghan I.S., Elleb S., Seth L., Kareen G. & Sara E. L. (2017). Occupational distribution of Campylobacteriosis and Salmonellosis cases – Maryland, Ohio and Virginia, 2014. Morbidity and Mortality Weekly Report, 66(32):850-853.

Coker A. O., Isokpehi R. D., Thomas B. W., Amisu K. O. & Obi C.L. (2002). Human campylobacteriosis in developing countries. Emerg. Infect. Dis. 8:237-43.

Gillespie I. A., O'Brien S. J., Frost J. A., Tam C., Tompkins D., Neal K. R. (2006) The Campylobacter sentinel surveillance scheme collaborators: investigating vomiting and-or bloody diarrhea in *Campylobacter jejuni* infection. J. Med. Microbiol. 55:741-746.

Grant A. J. & Tee W. (1998). Prevalence of *Campylobacter upsaliensis*-associated diarrhoeic in HIV-infected patients. Clin. Infect. Dis. 27:816-21.

Kaakoush N. O., Castano-Rodriguez N., Mitchell H. M. & Man S. M. (2015). Global epidemiology of *Campylobacter* infection. Clin. Microbiol. Rev. 28 (3):687-720.

Karikari A. B., Danso K. O., Frimpong E. H. & Krogfelt K. A. (2017). Antibiotic resistance in *Campylobacter* species isolated from patients with gastroenteritis in a Teaching Hospital in Ghana. Open J. Med. Microbiol. 7:1-11.

Klena J. D., Parker C. T., Knibb K., Ibbitt C., Devane M. L. P., Horn S. T., Miller W. G. & Konkel M. (2004). Differentiation of *Campylobacter coli*, *Campylobacter jejuni*, *Campylobacter lari* and *Campylobacter upsaliensis* by a multiplex PCR developed from then nucleotide sequence of the lipid A gene IpxA. J. Clin. Microbiol. 42(12):5549-5557.

Lastovica A. (2006). Emerging *Campylobacter* species: The tip of the iceberg. Clin. Microbiol. Newslett. 28:49-55.

Lastovica A. J. & Roux L. E. (2000). Efficient isolation of *Campylobacter* from stools. J. Clin. Microbiol. 38:2798-802.

Longenberger A. H., Palumbo A. J., Chu A. K., Mou M. E., Wettman A. & Ostroff S. M. (2013). *Campylobacter jejuni* infection associated with pasteurized milk-multiple states, 2012. Clin. Infect. Dis. 57:263-266.

Louwen R., Van Baarlen P. Van Vliot A. H. M., Van Belkum A., Hays, J. P. & Endtz H. P. (2012). *Campylobacter bacteremia*: a rare and under-reported event? Eur. J. Microbiol. Immunol. 2 (1):76-87.

Man S. M. (2011).The clinical importance of emerging *Campylobacter* species. Natl. Rev. Gastroenterol. Hepatol. 8:665-685.

Miller W. G., Health S., Parker G. & Lastovica A. J. (2007). Identification of genomic differences between *Campylobacter jejuni* subsp *jejuni* and *Campylobacter jejuni* subsp *doylei* at the nap locus leads to the development of a *Campylobacter jejuni* sub-speciation multiplex PCR method. Biomed. Centre Microbiol. 7:11-18.

Opintan J. A., Newmann M. J., ayeh-kumi P. F., Affrim R., Gepi-Allee R., Sevilleja, J. E., Roche J. K., Nataro J. P., Warren C. A., & Guerrant R. L. (2010). Paediatric diarrhoea in Southern Ghana;

etiology and association with intestinal inflammation and malnutrition. Am. J. Trop. Med. Hyg. 83(4):936-43.
Samie A., Bessong P. O., Obi C. L., Dillingham R. & Guerrant R. L. (2011). Bacterial and parasitic agents of infectious diarrhoea in the era of HIV/AIDS- The cause of a semi-rural community in South Africa. microbes, viruses, and parasites in AIDS process; Prof. Vladin Ar Zajae (Ed). ISN: 978-938-307-601-0.
Sample D., Detrchis P., Leport C., Bouvet E., Karam D. & Mevohas M-C. (1991). Efficacy of Zidovudine in preventing relapses of *Salmonella bacteremia* in AIDS. J. Infect. Dis. 163:415-416.
Smith S., Otuoye N., Omonigbehin E., Ariyo F. & Nkoth N. (2005). Prevalence of *Campylobacter* species during HIV/AIDS patients in Nigeria. Retrovirology 2:76-8.
Snijders F., Kuijper E. J., De Wever B., van der Hoek L., Danner S. A. & Dankert J. (1997). Prevalence of campylobacter-associated diarrhoea among patients infected with human immunodeficiency virus. Clin. Infect. Dis. 24:1107-13.
Tee W. & Mijch A. (1998). *Campylobacter jejuni bacteremia* in HIV infected patients. Comparison of clinical features and review. Clin. Infect. Dis. 26:91-6.
Ugboma A. N., Salihu M. D., Magaji A. A. & Abubakar M. D. (2013). Prevalence of *Campylobacter* species in groundwater in Sokoto, Sokoto State, Nigeria. Veterinary World, 6 (6):285-7.