



Molecular Identification and Antibigram of *Vibrio Cholerae* from Some Sources of Water in Tudun Wada and Malali Areas of Kaduna State

¹*Bilikis Abdulateef, ¹Abdullahi Isyaku Alhaji and ²Gabriel Adeboyega Ajibade

¹Department of Biotechnology, Nigerian Defense Academy, Kaduna, Nigeria

²Department of Medicinal Plant, Nigerian Defense Academy, Kaduna, Nigeria

*Corresponding author: - Email: bilikis.abdulateef2020@nda.edu.ng, Tel: 07030875748

Abstract

Vibrio cholerae, a Gram-negative bacterium, is the causative agent of cholera, a severe diarrheal disease associated with contaminated water and poor sanitation. This study aimed to isolate, identify, and determine the antibiotic susceptibility of *V. cholerae* from water sources in Tudun Wada and Malali areas of Kaduna State, Nigeria. A total of 18 water samples were collected from wells, taps, and rivers, with physicochemical analysis revealing pH values ranging from 5.8 to 7.4, indicating potential contamination, particularly in river sources. Presumptive *V. cholerae* isolates were identified using Thiosulphate Citrate Bile Salt (TCBS) agar and biochemical tests, followed by molecular confirmation via PCR targeting the *ompW* gene. Only one isolate from tap water in Tudun Wada was confirmed as *V. cholerae*, highlighting discrepancies between biochemical and molecular methods. Antibiotic susceptibility testing revealed multidrug-resistant (MDR) strains, with high resistance to ampicillin, nalidixic acid, and sulfamethoxazole/trimethoprim, while ciprofloxacin remained effective. The Multi-Antibiotic Resistance Index (MARI) indicated high-risk contamination in some isolates ($MARI \geq 0.2$). These findings underscore the presence of *V. cholerae* in local water sources and the growing threat of antimicrobial resistance, emphasizing the need for improved water quality monitoring, sanitation infrastructure, and updated treatment protocols to mitigate public health risks.

Keywords: Cholera, *Vibrio cholerae*, *ompW* gene, Antibiotic susceptibility, water quality

Introduction

Water is fundamental to life, covering approximately 70% of Earth Surface. Access to clean, safe water is critical for public health. However, in many developing countries, water contamination and poor sanitation remain significant challenges, contributing to the spread of waterborne diseases such as cholera, diarrhoea, typhoid and hepatitis A (WHO, 2022). Cholera, caused by the gram-negative bacterium *Vibrio cholerae*, continues to pose a global health threat, especially in regions with inadequate water treatment and hygiene infrastructure. *V.*

cholerae is typically found in aquatic environments and can cause severe diarrhoeal disease upon ingestion of contaminated food or water. While over 200 serovars have been identified, only O1 and O139 are linked to epidemic cholera (Islam *et al.*, 2023). Cholera outbreaks often correlate with environmental factors such as water quality, temperature and rainfall patterns. Outbreaks are often linked to contamination in water or food sources, especially during seasons that favour bacterial proliferation (Faruque *et al.*, 2018).

Figure 1: Map of Kaduna State showing Tudun Wada, Malali areas

Source: Department of Geography GIS unit KASU, 2023.

2.2 Sample Collection

A total of eighteen 1L water samples were collected aseptically from wells, tap and rivers using a convenience sampling method. The sample were gathered in sterile plastic bottles, transported in icebox, and processed immediately at the Biotechnology Laboratory, Kaduna State University.

2.3 Physiochemical Testing

The quality of the water was assessed based on the qualities that can be easily assessed by the consumer, these include; colour, turbidity, taste, odour, suspended solids (impurities), also pH test was carried out and observations were recorded.

2.4 Isolation of *Vibrio cholerae*

The culture media used was Thiosulphate Citrate Bile Salt (TCBS) agar. The media was prepared according to the manufacturer's instruction.

Membrane filtration was employed; were 100ml of each water sample was filtered through a standard membrane MF-Millipore filter. (47 mm, 0.45 µm pore size) using sterile forceps the membrane filter was placed aseptically in 100ml of alkaline peptone water (APW) pH 8.6 and enriched for 6-8 hours at 35-37°C (Alkaline peptone water has been described as enrichment media that is effective for culturing *V. cholerae* due to the fact that the alkaline nature does not allow the growth of other bacteria (Huq *et al.*, 2013)). Two loopfuls of broth was streaked on already prepared sterile Thiosulphate citrate bile salt sucrose (TCBS) agar. The inoculated TCBS agar was incubated at 35- 37°C for 18- 24 hours to determine the presumptive microbial load. After incubation, a distinct yellow and green colony observed on the plates was counted as presumptive *Vibrio* isolates.

2.5 Biochemical Characterization

Isolates were characterized using standard biochemical tests such as Indole, Methyl red, Citrate, Kligler Iron Agar and Oxidase test (Chesbrough, 2006; Sylvia, 2013).

2.6 Antimicrobial Susceptibility Test

The Kirby–Bauer disc diffusion assay was used to determine the antimicrobial resistance patterns of isolates in accordance with the guidelines of the Clinical Laboratory Standards Institute (2021). Isolate were screened against Ampicillin (AMP, 30µg), Ciprofloxacin (CPX, 10µg), Nalidixic acid (NA, 30µg), Sulfamethoxazole/Trimethoprim (SXT, 30µg), Streptomycin (S, 30µg), 30 µg), Ofloxacin (OFX, 30µg), Pefloxacin(PEF, 30µg), Amoxicillin/Clavulanate (AU, 30µg), Cephalexin (CEP, 30µg), and Gentamicin (CN, 10µg). The zones were interpreted as susceptible, intermediate or resistant using Clinical and Laboratory Standards Institute guidelines (CLSI, 2021).

2.7 DNA Extraction and Polymerase chain reaction (PCR) confirmation

DNA was extracted using phenol-chloroform method and amplified via PCR targeting the *ompW* gene (588 bp). PCR products were analysed via 1% agarose gel electrophoresis stained with ethidium bromide and visualized under UV light.

Targeted specific primer *ompW* gene:

Forward primer:
CACCAAGAAGGTGACTTTATTGTG

Reverse primer:
GAACTTATAACCACCCGCG (Nandi *et al.*, 2000).

STASTICAL ANALYSIS

Data obtained was subjected to one-way ANOVA test using a probability level of *P*

>0.05 as the threshold for statistical significance.

3. Results

3.1 Physicochemical Characteristics of Water Samples

Table 1 represents the physicochemical characteristics (colour, turbidity, impurities, pH) of 18 water samples collected from tap, well and river sources in Tudun-wada and Malali areas.

Table 1: Physicochemical Properties of Water Samples From the Study Areas

Sample	Location	Source	Turbidity	impurity	Colour	pH
T1	Tudun-wada	Tap	Clear	None	Colourless	7.3
T2	Tudun-wada	Tap	Clear	None	Colourless	7.4
T3	Tudun-wada	Tap	Clear	None	Colourless	7.3
T4	Tudun-wada	Tap	Clear	None	Colourless	7.2
W1	Tudun-wada	Well	Mildly turbid	Small debris	Brownish	6.3
W2	Tudun-wada	Well	Mildly turbid	Small debris	Mildly clear	6.8
W3	Tudun-wada	Well	clear	Clear	Colourless	6.8
W4	Tudun-wada	Well	Mildly turbid	Small debris	Brownish	6.9
R1	Tudun-wada	River	Turbid	Suspended particles	Brownish	7.4
T1	Malali	Tap	Clear	None	Colourless	6.2
T2	Malali	Tap	Clear	None	Colourless	6.9
T3	Malali	Tap	Clear	None	Colourless	6.7
T4	Malali	Tap	Clear	None	Colourless	6.8
R1	Malali	River	Turbid	Suspended particles	Brownish	6.1
R2	Malali	River	Turbid	Suspended particles	Brownish	5.8
W1	Malali	Well	Mildly turbid	Small debris	Mildly clear	6.1
W2	Malali	Well	Clear	Small debris	Colourless	6.8
W3	Malali	Well	Clear	Small debris	Colourless	6.0

Key; w= Well, T= Tap, R= River

From the above Table (1) river water had the lowest pH values, particularly in Malali having as low as 5.8 suggesting possible contamination with suspended particles

which could be as a result of industrial waste, heavy metal contaminations like aluminum and cadmium or acid producing bacteria could lead to a decrease in the pH

of the river water . Out of 18 samples obtained, 16 samples yielded smooth yellow circular and slightly flattened colonies on TCBS agar which showed that they are presumptive *Vibrio cholerae*.

3.2 Biochemical Characterization of Presumptive *V. cholerae* Isolates

The biochemical profiles of suspected *V. cholerae* isolates from Tudun-wada and

Malali water sources are presented in Tables 2a and 2b, respectively. Five biochemical tests were performed: oxidase, indole, citrate utilization, Triple Sugar Iron (TSI), and methyl-red tests. Isolates demonstrating oxidase positivity, indole production, and citrate utilization, while testing negative for methyl red, were considered presumptive *V. cholerae*.

Table 2a: Biochemical test of suspected *V. cholerae* isolated from some water sources from Tudun wada

Isolate ID	Oxidase	Indole	Citrate	Methyl red	Gas	H ₂ S	TSI Test		
							G	L	S
W1	-	-	-	+	-	-	+	-	+
W2	-	-	-	+	-	-	+	-	+
W3	-	-	-	+	-	-	+	-	+
R1	+	-	+	-	-	-	+	-	+
T1	-	-	-	+	-	-	+	-	+
T2	-	-	-	+	-	-	+	-	+
T3	+	+	-	-	-	-	+	-	+
T4	-	+	+	-	-	-	+	-	+

Key: W= Well, T= Tap, R= River, TSI= Triple Sugar Iron, G=glucose, L=lactose, S=sucrose, H₂S=Hydrogen Sulphide, (+) = positive result, (-) = negative result

Table 2b: Biochemical test of suspected *V. cholerae* Isolated from Some Sources of Water from Malali

Isolate ID	Oxidase	Indole	Citrate	Methyl red	Gas	H ₂ S	TSI Test		
							G	L	S
W1	+	-	+	-	-	-	+	-	+
W2	-	-	-	-	-	-	+	-	+
W1	-	-	-	+	-	-	+	-	+
R1	+	+	+	-	-	-	+	-	+
R2	+	+	+	-	-	-	+	-	+
T1	-	-	-	+	-	-	+	-	+
T2	-	-	-	+	-	-	+	-	+
T3	+	-	+	-	-	-	+	-	+

Key: W= Well, T= Tap, R= River, TSI= Triple Sugar Iron, G=glucose, L=lactose, S=sucrose, H₂S=Hydrogen Sulphide, (+) = positive result, (-) = negative result

3.3 Antibiotic Susceptibility Patterns

The antibiotic susceptibility profiles of presumptive *Vibrio cholerae* isolates from Tudun-wada and Malali are presented in Tables 3a and 3b.

Table 3a. Antibiotic Susceptibility of *V. cholerae* Isolates from Tudun-wada Water Sources

Isolate ID	OFX 10mcg	PEF 10mcg	CPX 10mcg	AU 30mcg	CN 10mcg	S 10mcg	CEP 10mcg	NA 30mcg	SXT 30mcg	PN 30mcg
W1	I	R	I	R	S	R	I	I	R	R
W2	S	S	S	S	S	S	S	S	S	S
W3	S	S	S	S	S	S	S	S	S	I
R1	S	I	S	I	S	I	R	R	I	R
T1	I	S	S	S	S	S	I	S	S	R
T2	S	S	S	I	S	S	I	S	S	R
T3	S	S	S	S	S	S	S	S	S	R
T4	S	S	S	S	S	S	I	S	S	R

Key: W= Well, T= Tap, R= River, S= susceptible, I= intermediate, R= Resistance OFX= Ofloxacin, PEF= Pefloxacin, CPX= Ciprofloxacin, AU= Amoxicillin/Clavulanate, CN= Gentamicin, S= Streptomycin, CEP= Cephalexin, NA= Nalidixic Acid, SXT=Sulfamethoxazole/Trimethoprim, PN= Ampicillin

Table 3b. Antibiotic Susceptibility of *V. Cholerae* Isolates from Malali Water Sources

Isolate ID	OFX 10mcg	PEF 10mcg	CPX 10mcg	AU 30mcg	CN 10mcg	S 10mcg	CEP 10mcg	NA 30mcg	SXT 30mcg	PN 30mcg
R1	S	S	I	R	I	S	I	I	I	I
R2	S	S	I	I	S	S	I	S	S	S
W1	S	S	S	S	S	S	I	I	R	S
W2	S	S	S	S	S	S	S	S	S	S
W3	I	I	I	R	R	R	I	R	I	R
T1	I	I	S	I	I	I	R	I	I	I
T2	S	S	S	I	S	S	S	I	S	I
T3	I	I	I	I	R	R	I	R	I	R

Key: S= susceptible, I= intermediate, R= Resistance OFX= Ofloxacin, PEF= Pefloxacin, CPX= Ciprofloxacin, AU= Amoxicillin/Clavulanate, CN= Gentamicin, S= Streptomycin, CEP= Cephalexin, NA= Nalidixic Acid, SXT=Sulfamethoxazole/Trimethoprim, PN= Ampicillin

The antibiotic susceptibility testing revealed distinct patterns between the two study areas: in Tudun-wada, isolate W2 showed complete susceptibility to all antibiotics while ampicillin (PN)

demonstrated universal resistance in other isolates, gentamicin (CN) maintained full effectiveness, while cephalexin (CEP) showed the lowest susceptibility; similarly in Malali, well isolate W2 was fully

susceptible to all the classes of Antibiotics used. Figure (2) represents the comparative antibiotic susceptibility patterns between Tudun-wada (2a) and Malali (2b) isolates, displaying mean susceptibility percentages with standard error bars. The analysis revealed that fluoroquinolones (OFX, PEF,

CPX) maintained consistently high efficacy in both regions, with susceptibility rates exceeding 75%. In contrast, β -lactam antibiotics, particularly ampicillin (PN), showed the most pronounced resistance patterns.

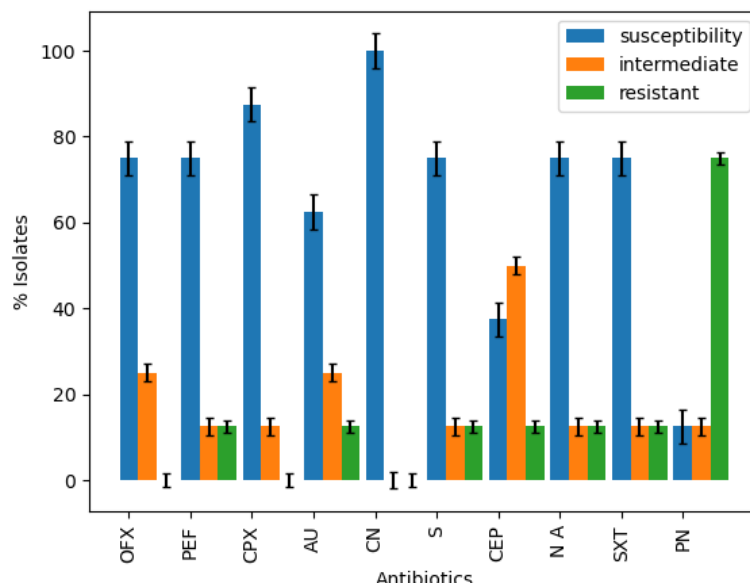


Figure 2a: Antibiotic susceptibility profile of *V. cholerae* isolates from Tudun-wada.

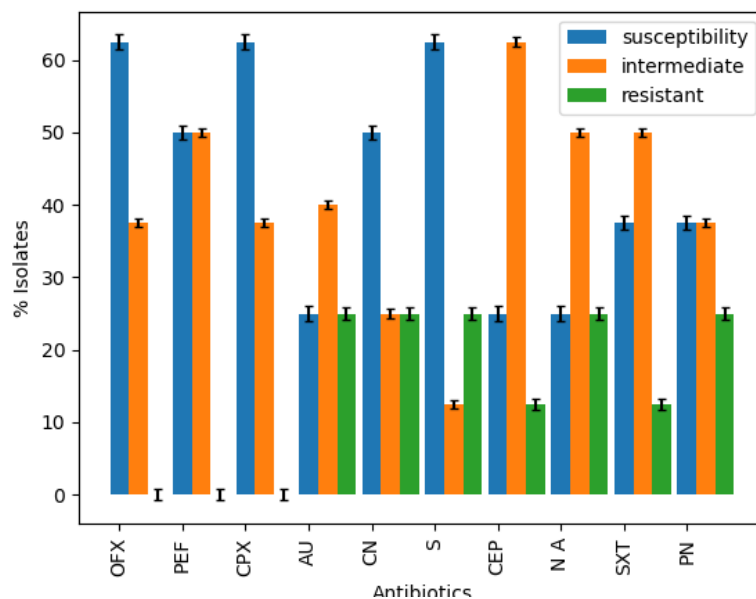


Figure 2b: Antibiotic susceptibility profile of *V. cholerae* isolates from Malali

3.4 Multi-Antibiotic Resistance Index (MARI)

The MARI analysis revealed concerning resistance patterns among the *V. cholerae* isolates (Table 4). Values ranged from 0-0.5, with several isolates exceeding the 0.2 threshold that indicate high-risk

contamination. In Tudun-wada, well water isolate W1 showed the highest resistance (MARI=0.5), followed by river isolate R1 (MARI=0.3). Similarly, Malali isolates demonstrated elevated resistance in well W3 (MARI=0.5) and tap T3 (MARI=0.4).

Table 4: Multi Antibiotics Resistant Index of suspected *V. cholerae* from some sources of water from Tudun-wada and Malali area.

Isolate ID	Location	a	b	MARI
W1	Tudun-wada	5	10	0.5
W2	Tudun-wada	0	10	0
W3	Tudun-wada	0	10	0
R1	Tudun-wada	3	10	0.3
T1	Tudun-wada	1	10	0.1
T2	Tudun-wada	1	10	0.1
T3	Tudun-wada	1	10	0.1
T4	Tudun-wada	1	10	0.1
R1	Malali	1	10	0.1
R2	Malali	0	10	0
W1	Malali	1	10	0.1
W2	Malali	0	10	0
W3	Malali	5	10	0.5
T1	Malali	1	10	0.1
T2	Malali	0	10	0
T3	Malali	4	10	0.4

Key: a= number of antibiotic resisted, b= number of antibiotic used, MARI = multi antibiotic resistant index, R = river source, W= well source, T = taps source.

3.5 Molecular Confirmation of *V. cholerae*

PCR analysis targeting the species-specific *ompW* gene was performed on four biochemically presumptive *V. cholerae* isolates (R1 and T3 from Tudun-wada; W1 and R1 from Malali). As demonstrated in Figure 3, only isolate T3 - obtained from tap

water in Tudun-wada - showed amplification of the expected 588bp fragment, confirming its identity as *V. cholerae*. The remaining three isolates failed to produce this diagnostic band, suggesting they may represent other *Vibrio* species or strains lacking the targeted *ompW* sequence.

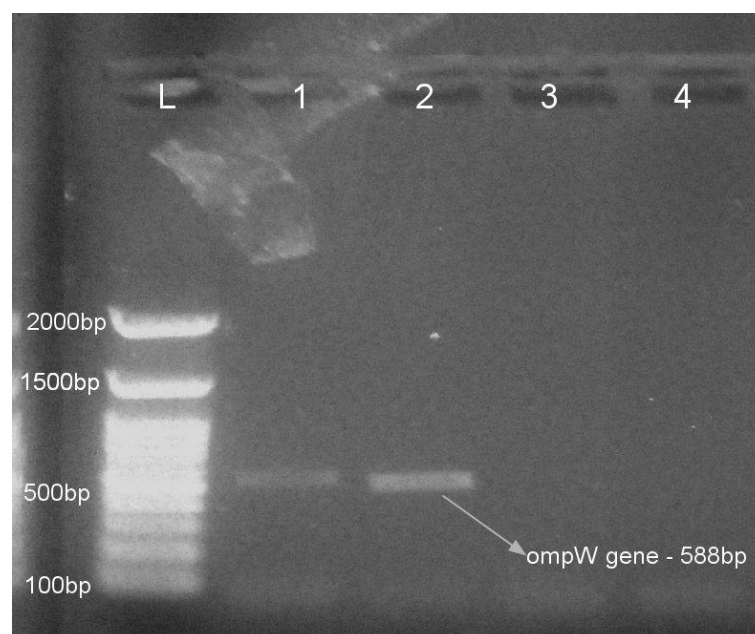


Figure 3: Agarose Gel Electrophoresis of PCR product showing *ompW* gene of *V. cholerae*

Key:

Lane L: represent Molecular ladder,
Lane 1 represents W1 (well source) from Malali Area location
Lane 2 represents T3 (tap source) from Tudun-wada Area
Lane 3 represents R1 (river source) from Tudun-wada Area
Lane 4 represents R1 (river source) from Malali Area.

4. Discussion

Safe drinking water access remains crucial for preventing waterborne diseases like cholera. Our study recorded pH values ranging from 5.8 to 7.4 across water sources, with river samples showing the

most acidic conditions (pH 5.8), likely due to suspended particulate matter affecting water quality (Godfrey et al., 2020). While tap and well water maintained near-neutral pH levels meeting WHO standards (WHO, 2022), the detection of *Vibrio cholerae* in

these sources raises public health concerns. Previous studies confirm *V. cholerae*'s optimal growth between pH 6.0-9.0, with reduced survival in highly acidic environments (Adeolu et al., 2021; Tonye et al., 2022).

Among 18 water samples, 16 produced presumptive *V. cholerae* colonies on TCBS agar, yet only one isolate (T3 from Tudun Wada tap water) was confirmed through ompW gene PCR amplification (Shrestha et al., 2022). This aligns with Bulus et al. (2015), who similarly reported molecular confirmation of waterborne *V. cholerae*. Biochemical testing revealed inconsistencies, including oxidase-negative results contradicting typical *V. cholerae* profiles (Parimal et al., 2017; Bulus et al., 2015), underscoring the necessity of molecular confirmation over biochemical methods alone (Ahmed et al., 2019).

Antibiotic resistance patterns showed concerning trends, with high resistance to ampicillin, nalidixic acid, and sulfamethoxazole/trimethoprim, while ciprofloxacin remained effective. The antibiotic susceptibility test results revealed varying resistance patterns amongst isolates however statistical analysis using one-way ANOVA test showed no significant difference among the antibiotic resistance levels ($p > 0.05$). These findings mirror global reports of increasing antimicrobial resistance in environmental *V. cholerae*

strains (Parvin et al., 2020). Multidrug resistance (MARI 0.3-0.5) suggests contamination from high-risk sources (Tahoun et al., 2021), consistent with previous characterizations of *V. cholerae* using biochemical and molecular markers (Rahman et al., 2019; Gupta et al., 2021). These results highlight the organism's persistence in aquatic environments, particularly where sanitation infrastructure is inadequate.

5. Conclusion

This study confirms the presence of *Vibrio cholerae* in water sources from Tudunwada and Malali, with molecular identification verifying its occurrence in tap water—a concerning finding given this source's presumed safety. The organism's detection, coupled with observed multidrug resistance patterns, highlights significant public health risks, particularly in communities relying on untreated or poorly maintained water systems. While ciprofloxacin remains effective against local strains, widespread resistance to ampicillin and other first-line antibiotics underscores the growing threat of antimicrobial resistance in waterborne pathogens. These findings emphasize the urgent need for strengthened water quality monitoring, improved sanitation infrastructure, and evidence-based updates to cholera treatment protocols. The persistence of *V. cholerae* in these

environments calls for integrated interventions combining enhanced water treatment, community education, and antimicrobial stewardship to mitigate outbreak risks and combat the emergence of resistant strains. Continued surveillance using both culture-based and molecular methods will be essential for tracking epidemiological trends and guiding preventive measures in vulnerable regions.

Acknowledgments:

The authors gratefully acknowledge the institutional support provided for this research. We extend our appreciation to the Department of Biotechnology at the host

institution for academic resources and guidance. Technical assistance from affiliated research laboratories is duly recognized. Finally, we thank colleagues and family members for their encouragement throughout this work.

Funding:

This research did not receive external funding.

Conflicts of Interest:

The authors declare no competing interests.

Ethical Approval:

Not applicable.

Data Availability:

Data are available upon reasonable request.

References

- Adeolu, M. A., Adebayo, A. A., Yusuf, K. O. (2021). Waterborne pathogens and public health: A case study of *Vibrio cholerae* in Nigeria. *Journal of Public Health Research*, 10(3), 105-118.
- Ahmed, H. A. Bello, A., Musa, A (2018) Molecular characterization, antibiotic resistance pattern and biofilm formation of *Vibrio parahaemolyticus* and *V. cholerae* isolated from crustaceans and humans. *International Journal of Food Microbiology* 274, 31–37
- Ahmed, H., Bello, A., Musa, A. (2019). *Molecular characterization of Vibrio cholerae in environmental waters*. *African Journal of Microbiology Research*, 13(5), 220-229.
- Bulus, G. H., Ado, S. A., Yakubu, S. E. and Ella, E. E., (2015) Isolation and Characterization of *Vibrio cholerae* from Water Sources in Zaria, Nigeria. *Annals of Experimental Biology* . 3 (3):8-13.
- CLSI (2021). Title Method for antifungal disk diffusion susceptibility testing of non-dermatophyte filamentous fungi; Approved Guideline, CLSI document M51-A. Wayne, PA: Clinical and Laboratory Standards Institute.
- Daboul J., Weghorst L., DeAngelis C., Plecha S.C., et al., (2020) Characterization of *vibrio cholerae* isolates from fresh water sources in northwest Ohio.
- Faruque, S.M., Islam, M.J., Hossain, M.A. (2018). Environmental isolates of *V. cholerae*: Reservoirs and antibiotic resistance. *Journal of Infectious Diseases*, 217(5), 827–834.

- Godfrey, Bwire, David, A., Tonny Obala, (2020). The quality of drinking and domestic water from the surface water source (lakes, rivers, irrigation canals and ponds) and spring in cholera prone communities of Uganda: an analysis of vital physicochemical parameter. Jul 17;20(1):1128. doi:10.1186/s12889-020-09186-3
- Gupta, R., Sharma, P., Singh, A. (2021). *Vibrio cholerae* identification using biochemical and molecular techniques. *Infectious Disease Journal*, 37(4), 412-425. <https://doi.org/10.1186/s12889-020-09186-3>
- Islam, M.T., Ahmed, T., Rahman, M. (2023). Molecular detection and antibiotic resistance pattern of *Vibrio cholerae* in water sources in Bangladesh. *Frontiers in Public Health*, 11, 112345. <https://doi.org/10.3389/fpubh.2023.112345>.
- Parimal, Dua, Amit, Karmakar, Kunal, Dutta (2017) A Simple Procedure For Isolation, Identification And Characterization Of *Vibrio Cholerae* From Clinical Samples *International Journal of Pharmacy Biological Science* 2017 October; 8(4): (B) 57-64
- Parvin I, Shahunja KM, Khan SH, Alam T, Shahrin L, Mahmuda Ackhter M, (2020) Changing susceptibility pattern of *Vibrio cholerae* o1 isolates to commonly used antibiotics in the largest diarrheal disease hospital in Bangladesh during 2000–2018. *America Journal of Tropical Medical Hygiene*.103(2):652–8
- Rahman, M. M., Hasan, M. N., Islam, M. T. (2019). Characterization of *Vibrio cholerae* in aquatic environments: Biochemical and molecular approaches. *Journal of Microbiology Research*, 45(3), 205-215. <https://doi.org/10.1186/s12889-020-09186-3>
- Shakya, G., Pant, N.D., Paudel, A. (2022). Prevalence of multidrug-resistant *Vibrio cholerae* in water samples from Kathmandu, Nepal. *BMC Microbiology*, 22(1), 112.
- Shrestha, B., Giri, B., Thapa, S. (2022). *Comparative study of biochemical and molecular identification of Vibrio cholerae in water sources*. *Environmental Health Perspectives*, 130(9), 985-992.
- Sylvia, M. (2013). Methyl Red and Vogues-Proskauer test protocol. *American Society for Microbiology*. ASM Microbe library.
- Tahoun, A. B. M. B., Rasha, M.M., Samah, S., Ibrahim Elsohaby, Hend, S. (2021) Genotypic characterization and antimicrobial resistance of *Vibrio cholerae* and *Vibrio parahaemolyticus* isolated from milk, dairy products, and humans with respect to inhibitory activity of a probiotic *Lactobacillus rhamenosus*. *LWT* 150, 111930
- WHO drinking water factsheet. (2022). Available from: <https://www.who.int/news-room/fact-sheets/detail/drinking-water>.
- Zhou, X., Li, J., Wang, Y. (2021). Rapid detection of *Vibrio cholerae* using PCR targeting ompW gene. *International Journal of Environmental Research and Public Health*, 18(14), 7562.