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ORIGINAL RESEARCH ARTICLE

Systematic Review on the Antibacterial Resistance of *Vibrio Cholerae*

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ABSTRACT

Background: *Vibrio cholerae* is the causative agent of cholera illness. Antibacterial resistance of *V. cholerae* is frequently experienced due to the environmental pressure from human and animal overuse and misuse of antibacterials. Among such antibacterials include Tetracycline, Chloramphenicol, Furazolidone, Ampicillin, and Trimethoprim-Cotrimoxazole as used against *V. cholerae* O1, O139 and non O1, O139 strains.

Objectives: This systematic review was aimed at providing an overview of Antibacterial resistant strains of *Vibrio cholerae* in terms of year, location and factors responsible for the resistance.

Material and Method: Systematic Electronic database search of PubMed (NCBI) by means of the key terms MeSH "Antimicrobial resistance of *Vibrio cholerae*" between the period of January 2000 to October 2018 was used.

Results: From the findings it showed that many factors are responsible for Antibacterial resistance of *Vibrio cholerae* which include genetic composition, mutation, enzymes. Also *V. cholerae*, both O1, O139, environmental and non O1/ non O139 such as *V. anginiloticus, paraheamolytcus* were incriminated in transferring resistance genes from one another. Antimimicrobial Susceptibility Testing phenotypic and Polymerase Chain Reaction (PCR) molecular procedure were employed in detecting the resistance and equally the use of Global Antimicrobial Surveillance System (GLASS) and Centre for Disease control (CDC) AR threat report 2019 was used successfully in the management of *Vibrio cholerae* epidemic.

Conclusions: Drug-resistant *Vibrio cholarae* is a problem that needs to be dealt with as soon as possible

ARTICLE HISTORY

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Vibrio cholerae, Antibacterial Resistance, Mutation, Systematic Review.

INTRODUCTION

Vibrio cholerae causes acute rice watery stool disease that affect human being which form biofilm on the surface water (Gupta *et al.*, 2018).Antibacterial resistance is the ability of bacteria to defeat the drugs designed to kill them and this is one of the greatest global public health difficulties of our period responsible for deaths, prolong hospitalization, and high expenses health-care for specific pathogen–drug treatment. Antimicrobial susceptibility pattern of humans and environmental isolates of *V. cholerae* is vital in monitoring antibiotic resistance within nations (Gupta *et al.*, 2018). Rise in Antibacterial resistance of *V. cholerae* has been recorded in numerous epidemics globally (Dengo-Baloi *et al.*, 2017). Integrons continue to be responsible in *Vibrio cholerae* Antimicrobial resistance (AMR) with capability to recognize AMR gene cassettes and direct them in their hosts (Sulca *et al.*, 2018). Genomic variation and antibacterial resistant *V. cholerae* have implications in the disease management (Campos *et al.*, 2004). *Vibrio cholerae* turn Antibacterial resistant by moving the agent through efflux pumps, chromosomal accident or developing genetic resistance via the exchange of conjugative plasmids, conjugative transposons, integrons or self-transmissible chromosomally by integrating SXT (Sulphamethozaxole Trimethoprim) elements (Kitaoka *et al.*, 2011).

MATERIALS AND METHODS

A systematized PubMed investigation was done by means of the key terms MeSH "Antimicrobial resistance of *Vibrio cholerae*" between January 2000 and October 2018. Given the extent of the issue, citations were selected for articles published in English. We found 249 papers (Figure 1), but only 77 were chosen and reviewed based on key terms 3 were duplications, 172 were antimicrobial resistance based on other organism and were removed from the review.

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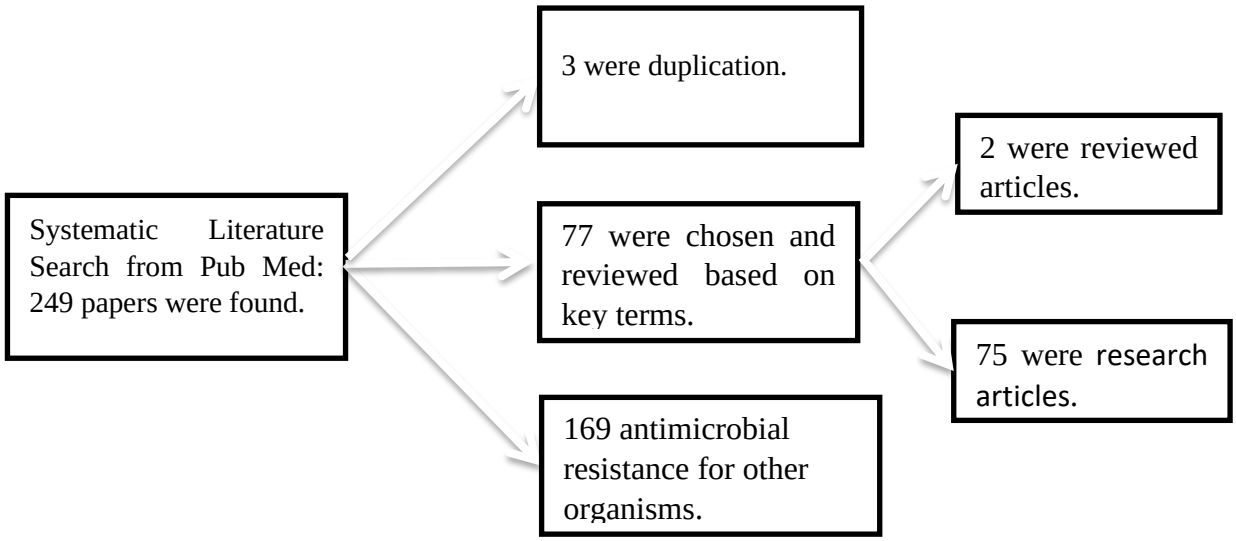

Figure 1: Systematic Literature Search

RESULT

Of the 77 manuscripts reviewed, there are two systematic reviews while the remaining 75 were studies conducted on *Vibrio cholarae* as mentioned in the Figure 2 below.

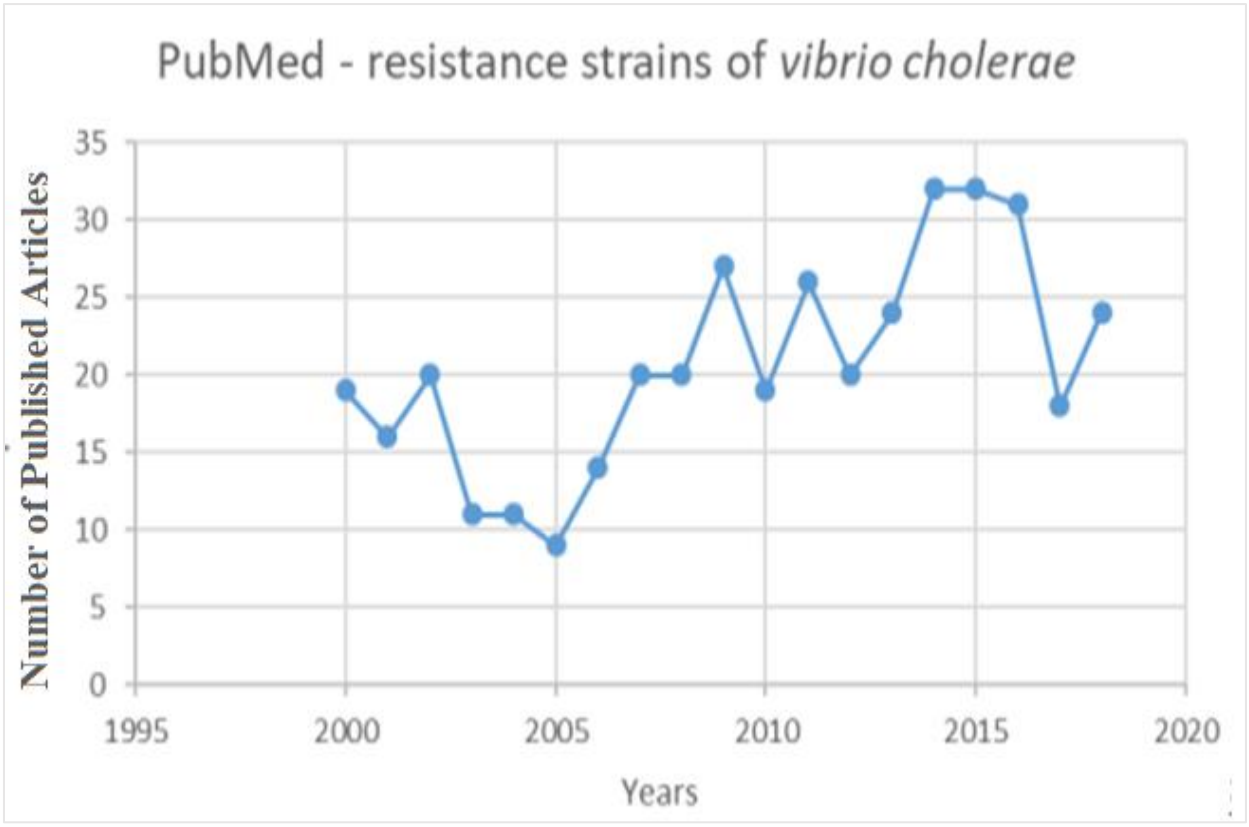

Figure 2: Distribution of articles published on resistance strains of *Vibrio cholerae* between January 2000 to October 2015

Antibacterial Resistance

The antibacterial resistance was discovered from both medical and ecological water origin to harbored the antimicrobial gene resistance of horizontal gene transfer (HGT) of the Sulfamethoxazole-trimethoprim elements (SXT) element (Mala *et al.*, 2016). The ecological water reported was found to be of significant origin for

antibacterial resistance genes in *V. cholerae* (Mala *et al.*, 2016).

Factors responsible for antibacterial resistance

1. **Spontaneous mutations**

Resistant to Antibacterial originated from spontaneous genetic accident in the bacterial chromosome, and spontaneous mutation being responsible for cell wall biosynthesis and DNA replication by alafosfalin and quinolones (Kitaoka *et al.*, 2011). Development of D87N in GyrA and D420N or P439S in ParE spontaneously promote resistant to fluoroquinolones in *V. cholerae* O139, and the increase of many changes in the quinolone-resistant determining regions (QRDRs) which is responsible for substantial resistance to fluoroquinolones in *V. cholerae* (Zhou *et al.*, 2013). Genetic variation in gyrA encodes sub-unit of DNA gyrase and followed mutation in parC which encodes DNA topoisomerase sub-unit (Kim *et al.*, 2010).

2. Sulfamethoxazole-trimethoprim elements (SXT)

This are mobile genetic element that encode for antibacterial resistant to *Vibrio cholerae* O1 strains Jain *et al.* (2008) reported Class 1 integrons and SXT elements conferring many Antibacterial resistance in the *V. cholerae* .Also studies show that *V. cholerae* belong to El Tor strain harboring ctxB gene of classical strain were 100% resistant to tetracycline (Kar *et al.*, 2015) equally *V. cholerae* isolated from patients and shallow water, belonging to serogroup O1, Ogawa serotype, biotype El Tor, all strains isolated were resistant to many antimicrobial such as Sulfamethoxazole-trimethoprim, Nalixidic Acid and Streptomycin (Dixit *et al.*, 2014) *V. cholerae* pathogens genes research has demonstrated high prevalence in spreading of toxS, toxaR and toxT genes among *V. alginolyticus* strains isolated demonstrated multidrug resistant (Mechri *et al.*, 2013) many drug resistant atypical El Tor species, with decreased susceptibility to ciprofloxacin and chloramphenicol, defined by the presence of the SXT element, and gyrA (Marin *et al.*, 2013).

3. Enzymes

Vibrio cholerae produce enzymes responsible for antibacterial resistant such as extended-spectrum-β-lactamase-(ESBL) (Ismail *et al.*, 2011), also Bier *et al.* (2015) reported TEM-63 ESBL gene from the strains were responsible for cholera outbreaks in South Africa, also found the quinolone resistance-determining regions of GyrA (Ser83-Ile), ParC (Ser85-Leu), Some of the *V.cholerae* strains were resistant to aminopenicillins and aminoglycosides and in addition, resistant toward carbapenems, quinolones, and folate pathway inhibitors were periodically studied (Zadnova *et al.*,2013).

4. Efflux Pump

Vibrio cholerae uses multidrug efflux pumps to export a broad range of Antibacterial, soaps and dyes that are chemically and structurally unrelated (Akoachere *et al.*, 2013). NorM, a putative efflux pump of *Vibrio cholerae*, is a member responsible for multidrug resistance and toxic compound extrusion family of transporters, Singh *et al.* (2006) demonstrated that NorM confers resistance to norfloxacin, ciprofloxacin, and ethidium bromide, deactivation of NorM gene rendered *V. cholerae* resistant towards these fluoroquinolones.

Table 1: Summary of some published articles that reported antibacterial resistance of *Vibrio cholerae*

SN	Year	Country	Strain	Antibiotic resistant	Mechanism	Laboratory methods	Reference
1	2018	Lima (Peru)	*Vibrio alginolyticus*	penicillin group	mutT gene	PCR	(Sulca *et al.*, 2018)
2	2014 - 2015	Ghana	classical *V. cholerae* 01 biotype El Tor, serotype Ogawa	Trimethoprim/sulfamethoxazole, ampicillin andceftriaxone	SXT, CtxAB and Tcp gene	ND	(Feglo and Sewurah, 2018)
3	2017	China	O1 and O139	Macrolides:Azithromycin	IncA/C plasmid, mphR-mrx-mph(K) and mel-mph2	minimum inhibitory concentration (MIC)	(Yu *et al.*, 2012)
4	2012 - 2015 .	Mozambique	El Tor *Vibrio cholerae* 01	Sulphamethoxazole-trimethropim, Trimethoprim Ampicillin, Nalidixic Acid,Chloramphenicol ,Nitrofurantoin ,Cotrimoxazole,Tetracycline,Doxycycline, Azithromycin	CTX genotype	Culture, standard biochemical tests, serotypes by antisera agglutination and PCR.	(Dengo-Baloi *et al.*, 2017)

Table 1: Continued

SN	Year	Country	Strain	Antibiotic resistant	Mechanism	Laboratory methods	Reference
5	2017	India	*Vibrio cholerae*	Amoxicillin, ampicillin,chloramphenicol, doxycycline, erythromycin, and tetracycline.	MurB protein	molecular docking	(Ragunathan, *et al.*, 2018)
6	2016	Mexico	*V. alginolyticus*	beta-lactams Antibacterial, cephalotin,amikacin, cephotaxime, and pefloxacin,	proA, wza, vopD, vopB, hcp, vasH and vgrG genes	PCR amplification	(Hernandez-Robles *et al.*, 2016)
7	2017	Thialand	*V. cholerae* O1 and non-O1/non-O139	ND	horizontal gene transfer (HGT) of the SXT element	ND	(Mala *et al.*, 2016)
8	2012 - 2013	Iran	*V. cholerae*	streptomycin, trimethoprim,co-trimoxazole, tetracycline and minocycline	Class 1 integron, SXT elementCarR confers polymyxin Bregulating expression of the almEFG genes,glycine and diglycine modification of lipid A.		(Rezaie, el al., 2017)
9	2015	German	*Vibrio vulnificus* and *Vibrio cholerae* non-O1/non-O139	aminopenicillins and aminoglycosides	Carbapenemases	Biochemical testing	(Bier *et al.*, 2015)
10	2008	Sauth Africa	*Vibrio cholerae* O1 serotype Ogawa	Quinolone	mutations in the quinolone resistance-determining regions of GyrA (Ser83-Ile), ParC (Ser85-Leu), and produced TEM-63 β-lactamase.	PCR	(Ismail *et al.*, 2011)
11	1970 - 1998	Russia	*Vibrio cholerae* El Tor	Tetracycline and Chloramphenicol	ND	ND	(Savel'ev *et al.*, 2010)
12	1998	Ethiopia	*V. cholerae* O1	Ampicillin, chloramphenicol,streptomycin, sulfamethoxazole and trimethoprim	IncC plasmid	Random Amplified Polymorphic DNA and Disk diffusion (KBDDT)	(Scrascia *et al.*, 2009)

Table 1: Continued

SN	Year	Country	Strain	Antibiotic resistant	Mechanism	Laboratory methods	Reference
13	2005	Cameroun	*V. cholerae* O1	Cotrimoxazole,Ampicillin	genes ctxA and ctxB	KBDDT,pulsed-field gel electrophoresis patterns.	(Ngandjio *et al.*, 2009)
14	2010	Nigeria	*Vibrio cholerae* O1 El Tor biotype	ciprofloxacin and chloramphenicol	SXT element, gyrA (Ser83Ile), parC (Ser85Leu) alleles CTX phage,TCP rstR(ElTor), ctxB-7 and tcpA(CIRS) alleles	standard culture methods by disk diffusion method and E-test. multilocus sequence analysis and pulsed-field gel electrophoresis.	(Marin *et al.*, 2013)

KEY ND= Not Determine CTX= cholera Toxin, SXT = Sulphamethozaxole Trimethoprim integaron Element

DISCUSSION

The review found that all the 77 articles reported resistance to one or more Antibacterial in *Vibrio cholerae* O1 El Tor Ogawa between January 2000 to October 2018 and most of the Antibacterial include Tetracycline, Trimethropim-sulphamethoxazole, Chloramphenicol and Nitrofurantoin. Antimicrobial resistance of *V. cholera* is reported in all regions of the world (Dengo-Baloi *et al.*, 2017), another important finding was that most of resistance strains are due to genetic composition of SXT element (Feglo and Sewurah, 2018) , In our review we found other factors such as efflux pump,Presence of Enzymes, spontaneous mutation, Also standard culture methods by disk diffusion method and E-test. PCR and pulsed-field gel electrophoresis are the most widely methods used in detection and this is agrees with the findins of Dengo-Baloi et al. 2017, isolation and Antimicrobial susceptibility testing (Marin *et al.*, 2013) More so virulence genes reported which include Cholera toxin *ctxA* and toxin-coregulated pilus, *tcpA*, contained by the majority of *V. cholerae* O1 strains, confirming the profile found in *V. cholerae* O1 El Tor variants B33 and CIRS 101 (Marin *et al.*, 2013).

Contribution to knowledge

To our knowledge, this review provides comprehensive information about burdens of antibacterials resistance of *Vibrio cholerae* some of the AR include Tetracycline, Chloramphenicol, Furazolidone, Ampicillin, and Trimethoprim-Cotrimoxazole are not recommended for the management of cholera disease.

CONCLUSION

To our knowledge, this study provides extensive information on burden of Antibacterial resistance of *Vibrio cholerae*, as well as an evaluation of the availability of data. AR is a major cause of mortality across the globe, finally Drug-resistant *Vibrio cholarae* is a problem that needs to be dealt with as soon as possible, and road-map tactics of the Centre for Disease Control (CDC) and Global Antimicrobial Surveillance System (GLASS) should be used to control it.

REFERENCES

Akoachere, J.-F. T. K., Masalla, T. N., & Njom, H. A. (2013). Multidrug resistant toxigenic Vibrio cholerae O1 is persistent in water sources in New Bell-Douala, Cameroon. BMC Infectious Diseases, 13, 366. https://doi.org/10.1186/1471-2334-13-366

Bier, N., Schwartz, K., Guerra, B., & Strauch, E. (2015). Survey on antimicrobial resistance patterns in Vibrio vulnificus and Vibrio cholerae non-O1/non-O139 in Germany reveals carbapenemase-producing Vibrio cholerae in coastal waters. Frontiers in Microbiology, 6, 1179. https://doi.org/10.3389/fmicb.2015.01179

Campos, L. C., Zahner, V., Avelar, K. E. S., Alves, R. M., Pereira, D. S. G., Vital, B. J. M. and Karaolis, D.

K. R. (2004). Genetic diversity and antibiotic resistance of clinical and environmental Vibrio cholerae suggests that many serogroups are reservoirs of resistance. Epidemiology and Infection, 132(5), 985-992. https://doi.org/10.1017/S0950268804002705

Dengo-Baloi, L. C., Sema-Baltazar, C. A., Manhique, L. V., Chitio, J. E., Inguane, D. L., & Langa, J. P. (2017). Antibiotics resistance in El Tor Vibrio cholerae 01 isolated during cholera outbreaks in Mozambique from 2012 to 2015. PloS One, 12(8), e0181496. https://doi.org/10.1371/journal.pone.0181496

Dixit, S. M., Johura, F.-T., Manandhar, S., Sadique, A., Rajbhandari, R. M., Mannan, S. B., … Alam, M. (2014). Cholera outbreaks (2012) in three districts of Nepal reveal clonal transmission of multi-drug resistant Vibrio cholerae O1. BMC Infectious Diseases, 14, 392. https://doi.org/10.1186/1471-2334-14-392

Gupta, P. K., Pant, N. D., Bhandari, R., & Shrestha, P. (2018). Cholera outbreak caused by drug resistant Vibrio cholerae serogroup O1 biotype ElTor serotype Ogawa in Nepal; a cross-sectional study. Antimicrobial Resistance and Infection Control, 5, 23. https://doi.org/10.1186/s13756-016-0122-7

Ismail, H., Smith, A. M., Sooka, A., & Keddy, K. H. (2011). Genetic characterization of multidrug-resistant, extended-spectrum- beta-lactamase-producing Vibrio cholerae O1 outbreak strains, Mpumalanga, South Africa, 2008. Journal of Clinical Microbiology, 49(8), 2976-2979. https://doi.org/10.1128/JCM.00293-11

Kar, S. K., Pal, B. B., Khuntia, H. K., Achary, K. G., & Khuntia, C. P. (2015). Emergence and spread of tetracycline resistant Vibrio cholerae O1 El Tor variant during 2010 cholera epidemic in the tribal areas of Odisha, India. International Journal of Infectious Diseases : IJID : Official Publication of the International Society for Infectious Diseases, 33, 45-49. https://doi.org/10.1016/j.ijid.2014.12.025

Kim, H. Bin, Wang, M., Ahmed, S., Park, C. H., LaRocque, R. C., Faruque, A. S. G., … Hooper, D. C. (2010). Transferable quinolone resistance in Vibrio cholerae. Antimicrobial Agents and Chemotherapy, 54(2), 799-803. https://doi.org/10.1128/AAC.01045-09

Kitaoka, M., Miyata, S. T., Unterweger, D., & Pukatzki, S. (2011). Antibiotic resistance mechanisms of Vibrio cholerae. Journal of Medical Microbiology, 60 (4), 397-407. https://doi.org/10.1099/jmm.0.023051-0

Mala, W., Kaewkes, W., Tattawasart, U., Wongwajana, S., Faksri, K., & Chomvarin, C. (2016). SXT ELEMENT, Class 1 Integron And Multidrug-Resistance Genes Of Vibrio cholerae Isolated From Clinical And Environmental Sources In Northeast Thailand. The Southeast Asian Journal of Tropical Medicine and Public Health, 47(5), 957-966.

Marin, M. A., Thompson, C. C., Freitas, F. S., Fonseca, E. L., Aboderin, A. O., Zailani, S. B., … Vicente, A. C. P. (2013). Cholera outbreaks in Nigeria are associated with multidrug resistant atypical El Tor and non-O1/non-O139 Vibrio cholerae. PLoS Neglected Tropical Diseases, 7 (2), e2049. https://doi.org/10.1371/journal.pntd.0002049

Mechri, B., Medhioub, A., Medhioub, M. N., & Aouni, M. (2013). Genotypic diversity, antimicrobial resistance and screening of Vibrio cholerae molecular virulence markers in Vibrio alginolyticus strains recovered from a Tunisian Ruditapes decussatus hatchery. Polish Journal of Microbiology, 62(3), 263-272. https://doi.org/10.33073/pjm-2013-034

Rezaie, N., Bakhshi, B., & Najar-Peerayeh, S. (2017). Distribution of resistance genetic determinants among Vibrio cholerae isolates of 2012 and 2013 outbreaks in IR Iran. Microbial Pathogenesis, 104, 12-16. https://doi.org/10.1016/j.micpath.2017.01.005

Savel'ev, V. N., Babenyshev, B. V, Savel'eva, I. V, Vasil'eva, O. V, Guseva, L. V, Grizhebovskii, G. M., … Antonenko, A. D. (2010). Antibacterial susceptibility/resistance of Vibrio cholerae el tor clinical strains isolated in the Caucasus during the seventh cholera pandemic. Antibiotics and chemotherapy science, 55(5-6), 8-13.

Scrascia, M., Pugliese, N., Maimone, F., Mohamud, K. A., Ali, I. A., Grimont, P. A. D., & Pazzani, C. (2009). Cholera in Ethiopia in the 1990 s: epidemiologic patterns, clonal analysis, and antimicrobial resistance. International Journal of Medical Microbiology : IJMM, 299(5), 367-372. https://doi.org/10.1016/j.ijmm.2008.10.004

Singh, A. K., Haldar, R., Mandal, D., & Kundu, M. (2006). Analysis of the topology of Vibrio cholerae NorM and identification of amino acid residues involved in norfloxacin resistance. Antimicrobial Agents and Chemotherapy, 50(11), 3717-3723. https://doi.org/10.1128/AAC.00460-06

Sulca, M. A., Orozco, R., & Alvarado, D. E. (2018). Antimicrobial resistance not related to 1,2,3 integrons and Superintegron in Vibrio spp. isolated from seawater sample of Lima (Peru). Marine Pollution Bulletin, 131(Pt A), 370-377. https://doi.org/10.1016/j.marpolbul.2018.04.050

Yu, L., Zhou, Y., Wang, R., Lou, J., Zhang, L., Li, J., … Kan, B. (2012). Multiple antibiotic resistance of Vibrio cholerae serogroup O139 in China from 1993 to 2009. PloS One, 7(6), e38633. https://doi.org/10.1371/journal.pone.0038633

Zadnova, S. P., & Smirnova, N. I. (2015). Isolation Of Antibiotics Resistance Genes In Vibrio Cholerae O1 And O139 Serogroup Strains. Zhurnal mikrobiologii, epidemiologii, i immunobiologii, (3), 3-10.

Zhou, Y., Yu, L., Li, J., Zhang, L., Tong, Y., & Kan, B. (2013). Accumulation of mutations in DNA gyrase and topoisomerase IV genes contributes to fluoroquinolone resistance in Vibrio cholerae O139 strains. International Journal of Antimicrobial Agents, 42(1), 72-75. https://doi.org/10.1016/j.ijantimicag.2013.03.004