

Epidemic and PCR-based identification of vibrio cholera through OmpW gene from diarrhoeal patients admitted at different hospitals of Baluchistan

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Abstract

Objective: To study the different epidemiological and polymerase chain reaction-based identification of vibrio cholera.

Method: The cross-sectional study was conducted at the Center for Advanced Studies in Vaccinology and Biotechnology, University of Balochistan, Quetta, Pakistan, from January 5 to December 6, 2019, and comprised faecal / rectal swab samples from patients with a history of untreated severe diarrhoea of <12-hour duration. The samples were collected from suspected cholera patients at different hospitals of the province. The isolates were examined and identified on the basis of colony characters on thiosulfate-citrate-bile salts-sucrose agar. Suspected colonies were subjected to gram staining, biochemical tests and polymerase chain reaction-based identification. Data was analysed using SPSS 19.

Results: Of the 444 samples, 33(7.43%) were positive for vibrio cholera and 411(92.56%) were negative. The incidence was higher in individuals aged 1-20 years 12(2.7%); males 18(4.05%); Balochs 18(4.05%); lower socioeconomic class 18(4.05%); and illiterates 26(5.85%). The incidence was more in summer 19(4.27%) and spring 8(1.80%) seasons. Polymerase chain reaction was highly effective diagnostic approach, with findings showing clear bands of 588bp of ompW gene.

Conclusion: Surveillance for diarrhoeal disorders is necessary to control future outbreaks of cholera in the region.

Keywords: Cholerae, Infection, Biochemical, PCR, ompW. (JPMA 71: 1189; 2021)

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Introduction

Vibrio cholerae comprises gram-negative, facultative, short-rods and filamentous bacillus of genus vibrio.¹ The vibrio belongs to phylum proteobacteria, class gammaproteobacteria, order vibrionales, and is a member of the vibriaceae family.² The species V. cholerae is classified on the basis of its O antigens. There are more than 200 serotypes of V. cholerae.³ V. cholerae is a known aetiological agent of cholera, which causes severe outbreaks of diarrhoea.⁴ V. cholerae is mainly transmitted through the oro-faecal route or after ingestion of contaminated water or food. V. cholerae is transmitted to humans, invades and colonises the small intestine, producing toxins and resulting in massive secretory diarrhoea.⁵ There are natural barriers against infectious agents that secrete strongest mucosal immunoglobulin A (IgA) that help in limiting the infection.⁶

Diagnosis of V. cholerae is based on biochemical characterization of bacteria strain isolated from human stool. V. cholerae can also be isolated from vomiting, water source and contaminated food. Around the world, 3-5 million annual cases of cholera have been reported, with about 100,000-120,000 deaths.⁷

Cholera in Bangladesh, India and various parts of the developing world occur as endemic.⁸ It is one of the most important endemic diseases in Pakistan. In August 2010, massive cholera cases were reported in Pakistan⁹ and all the cases were found in the flood-affected provinces of Khyber Pakhtunkhwa (KP), Punjab and Sindh.

Balochistan province lacks sewage system and experiences dry weather, drought and water shortage. People and animal drink water from the same pool that has contaminated water. Cholera is found rather consistently in the province that also has serious lack of healthcare infrastructure. The current study was planned to assess the different epidemiological and polymerase chain reaction (PCR)-based identification of V. cholera in Balochistan.

Materials and Methods

The cross-sectional study was conducted at the Center for Advanced Studies in Vaccinology and Biotechnology

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(CASVAB), University of Balochistan, Quetta, Pakistan, from January 5 to December 6, 2019. After approval from the institutional ethics review committee, the sample size was calculated with 5% significance level, 95% confidence level and 80% power of test. Faecal samples or rectal swabs were taken from patients regardless of age or gender with a history of untreated severe (rice water) diarrhoea of less than 12-hour duration and with evidence of significant dehydration. Patients who had taken antibiotics were excluded. The samples were immediately transported to CASVAB and were processed for microbiological analysis. The working area was regularly disinfected with 70% ethanol, and gloves, microscope slides, masks and all the cultures were autoclaved before disposal. For isolation of *V. cholerae* from stool samples or rectal swabs were incubated in alkaline peptone water (APW)-enriched medium. After 6-8 hrs of incubation, a loop from the enrichment medium was streaked on thiosulfate citrate bile salts (TCBS) agar plates and the samples were incubated at 37°C for 24 hrs.¹⁰

The isolates were examined and identified on the basis of colony characters observed with the naked eye on TCBS agar. Suspected colonies were subjected to gram staining and various biochemical reaction tests.¹¹

Entire genomic deoxyribonucleic acid (DNA) was extracted from samples using Genomic DNA purification kit (Promega, USA), and it was then stored at -20°C for additional use. PCR was used for colonies identified as *V. cholerae*. Primers used were F1 (CACCAAGAAGGTGACTTTATTGTG) R1 (GAACTTATAACCACCCGCG). The reaction mixture was subjected to an amplification of 30 cycles, each of which consisted of three steps: denaturation of template DNA at 94°C for 30s, annealing of the template DNA at 64°C for 30s, and extension of the primers at 72°C for 30s. Before the initiation of the first cycle, the reaction mixture was heated at 94°C for 5 min to allow complete denaturation of the template.¹²

Blood samples for serum electrolyte were drawn using standard venepuncture technique and collected in a sterile plain tube at the time of collecting faecal samples and rectal swabs. The blood samples were centrifuged for 5 min at 10,000 rpm. The supernatant serum was collected from the blood samples and were further processed for electrolytes, such as sodium, potassium, and chloride, using EasyLight plus ion selective electrode automated analyser.

The isolates were checked for antibiotic sensitivity using an agar disk diffusion method on Mueller-Hinton agar. The antibiogram was done according the criteria set by the Clinical and Laboratory Standards Institute (CLSI),

formerly known as the National Committee for Clinical Laboratory Standard, to determine susceptibility patterns to commonly used antibiotics.¹³

Data was analysed using SPSS 19.

Results

Of the 444 samples, 33(7.43%) were positive for *V. cholerae* and 411(92.56%) were negative (Figure-1). The infection was found in 12(2.70) cases aged 1-20 years, 6(1.35%) aged 21-40 years, 6(1.35%) aged 41-60 years and 9(2.02%)

Table-1: *Vibrio cholerae* epidemiological incidence in different parameter of Balochistan population.

Vibrio Cholerae incidence in Balochistan population			
Sex wise %	Female	3.37% (n=15)	7.43% (n=33)
	Male	4.05% (n=18)	
Race wise %	Panjabi	0.45% (n=2)	7.43%(n=33)
	Hazara	0.9% (n=4)	
	Pushtoon	2.02% (n=9)	
	Baloch	4.05% (n=18)	
Class wise %	Higher	1.12% (n=5)	7.43%(n=33)
	Middle	2.25% (n=10)	
	Lower	4.05% (n=18)	
Season wise %	Winter	0.45% (n=2)	7.43%(n=33)
	Autumn	0.90% (n=4)	
	Summer	4.27% (n=19)	
	Spring	1.80%(n=8)	
Literacy wise %	Illiterate	5.85%(n=26)	7.43%(n=33)
	Literate	1.57%(n=7)	

Table-2: Serum electrolytes result of *Vibrio cholerae* positive patients.

Positive Patients	Sodium	Chloride	Potassium
7	115-120mEq/L	75-80mEq/L	2.95-3.2mEq/L
10	121-130 mEq/L	83-89 mEq/L	3.2-3.8mEq/L
16	132-136 mEq/L	90-97 mEq/L	4.0-4.7 mEq/L
Normal range	136 -156 mEq/L	91-129 mEq/L	3.4-6.9mEq/L

Table-3: Biochemical tests and sugar fermentation tests for isolation of *V. cholerae*.

Selective Media (TCBS Agar)	Flat, yellow color colonies, 2-3mm in size	
Gram Staining	Curved rods with 2-4 um in diameter	
Biochemical Tests	Indole	Positive
	Methyl red	Positive
	Voges- prokauras	Variable
	Oxidase	Positive
	Citrate	Positive
	Catalase	Positive
	Sugar Fermentation Tests	Glucose
Lactose		Negative
Manitol		Positive
Sorbitol		Negative
Sucrose		Positive

Table-4: Antibiotic trail against V.cholerae isolated from suspected cholera samples.

Classes	Antibiotics	Abbreviation and Potency	Zones (mm)	CLSI Slanderd (Sensitivity)	Remarks
Penicillin	Amoxicillin	AML 10	21mm	>=18	Sensitive
Trimethoprim/sulphamethoxazole	Trimethoprim/sulphamethoxazole	1.25 + 23.75	14mm	>=16	Resistant
Phenicols	Chloramphenicol	Cap 30	13mm	>=18	Resistant
Quinolones	Ciprofloxacin	CIP 5	22mm	>=21	Sensitive
	Nalaxic acid	NA 30	11mm	>=19	Resistant
Ceftriaxone	Ceftriaxone	CRO 30	12mm	>=21	Resistant
Macrolides	Erythromycin	E 15	20mm	>=18	Sensitive
Aminoglycoside	Gentamycin	CN 10	16mm	>=15	Sensitive
	Amikacin	AK 30	18mm	>=17	Sensitive
Imipenum	Imipenum	IMP 10	19mm	>=16	Sensitive
Fluoroquinolone	Levofloxacin	LEV 5	21mm	>=17	Sensitive
Tetracyclin	Tetracyclin	TE 30	19mm	>=15	Sensitive
Vancocin	Vancomycine	VA 30	17mm	>=16	Sensitive

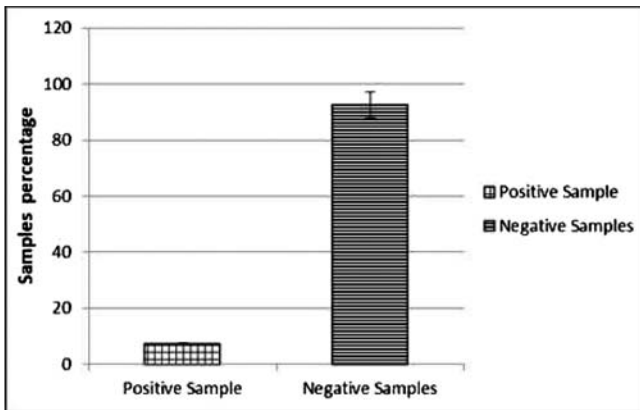


Figure-1: The incidence of cholera infection in suspected diarrhoeal patients of Balochistan.

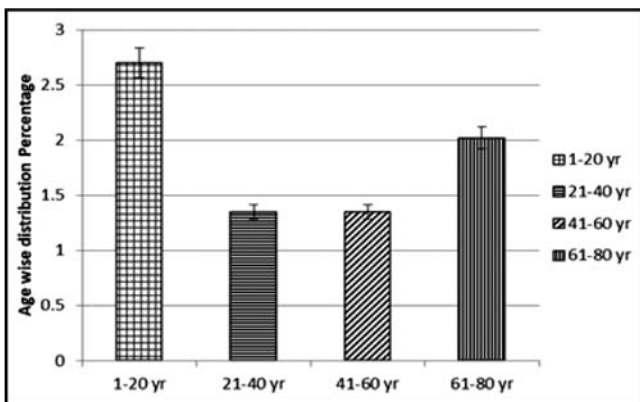
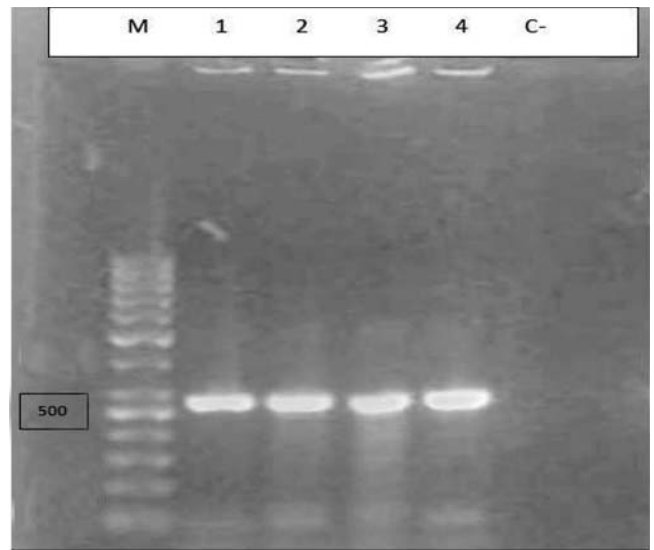


Figure-2: Age wise rate of infection in patients admitted a different Hospital of Quetta.

aged 61-80 years (Figure-2).

Cholera infection was found high 18(4.05%) male patients and 15(3.37%) female patients. The infection was detected in 18(4.05%) patients of Baloch ethnicity,



PCR: Polymerase chain reaction.

Figure-3: Direct PCR for Vibrio cholera detection. Lane M : 100 bp plus DNA ladder; Lane 1 to 4: isolates; Lane 5 :Negative control.

9(2.02%) Pushtun, 2(0.45%) Punjabi and 4(0.90%) having Hazara ethnicities. the infection was found in 18(4.05%) cases belonging to the lower socioeconomic class, 10(2.25%) middle class and 5(1.75%) upper class. Among those infected 26(5.85%) were illiterate patients, while 7(1.57%) were literates. The incidence of cholerae infection was more in summer 19(4.27%) and spring 8(1.80%) seasons.

All the isolates produced the predicted size of 588 base pair amplicons of ompW gene (Figure-3).

At the time of admission, children <5 years were comatose and drowsy, while adults were fully conscious but with missing radial pulse and low systolic blood

pressure (SBP). Sodium, potassium and chloride levels were low in all 33(100%) cholera patients.

V. cholerae isolates were sensitive to amoxicillin, ciprofloxacin, tetracycline, vancomycin, amikacin, gentamycin, levofloxacin, imipenem and erythromycin. They were resistant to ceftriaxone, chloramphenicol, sulfonamides, trimethoprim and nalidixic acid.

Discussion

The age-related findings of the current study were similar to those reported earlier,¹⁴ and the same was the case with gender-related findings.¹⁵ Likewise, findings related to the socioeconomic status and literacy were in line with literature.^{16,17} The seasonal variation noted in the current study is also supported by literature.¹⁵ The confirmation of *V. cholerae* through gram staining, biochemical tests and different sugar fermentation tests was also in agreement with literature.¹⁸ The study demonstrated that PCR method was a highly effective diagnostic approach for rapid and trustworthy diagnosis of cholera infection. The finding matched earlier studies.¹² The antibiotic sensitivity and resistance results also matched the findings of earlier studies.^{19,20}

Conclusion

There were more males affected by cholera than females and the frequency was the highest in those aged 1-20 years. The most relevant antibiotics were tetracycline, vancomycin, amikacin, gentamycin, levofloxacin, imipenem, erythromycin, ciprofloxacin and amoxicillin.

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Conflict of Interest: None.

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References

1. Matz C, McDougald D, Moreno AM, Yung PY, Yildiz FH, Kjelleberg S. Biofilm formation and phenotypic variation enhance predation-driven persistence of *Vibrio cholerae*. *Proc Natl Acad Sci U S A*. 2005; 102:16819-24.
2. Dikow RB, Smith WL. Genome-level homology and phylogeny of Vibrionaceae (Gammaproteobacteria: Vibrionales) with three new complete genome sequences. *BMC Microbiol*. 2013; 13:80.
3. Chatterjee SN, Chaudhuri K. Lipopolysaccharides of *Vibrio cholerae*: I. Physical and chemical characterization. *Biochim Biophys Acta*. 2003; 1639:65-79.
4. Wachsmuth IK, Evins GM, Fields PI, Olsvik Ø, Popovic T, Bopp CA, et al. The molecular epidemiology of cholera in Latin America. *J Infect Dis*. 1993;167:621-26.
5. Holmgren J. Actions of cholera toxin and the prevention and treatment of cholera. *Nature*. 1981; 292:413-17.
6. Jertborn M, Svennerholm AM, Holmgren J. Saliva, breast milk, and serum antibody responses as indirect measures of intestinal immunity after oral cholera vaccination or natural disease. *J Clin Microbiol*. 1986; 24:203-9.
7. Eibach D, Leon HS, Gil H, Hogan B, Ehlkes L, Adjabeng M, et al. Molecular epidemiology and antibiotic susceptibility of *Vibrio cholerae* associated with a large cholera outbreak in Ghana in 2014. *PLoS Negl Trop Dis*. 2016; 10:e0004751.
8. Nizami SQ, Farooqui BJ. Cholera in children in Karachi from 1990 through 1995: a study of cases admitted to a tertiary care hospital. *J Pak Med Assoc*. 1998; 48:171-3.
9. Shah MA, Mutreja A, Thomson N, Baker S, Parkhill J, Dougan G, et al. Genomic epidemiology of *Vibrio cholerae* O1 associated with floods, Pakistan, 2010. *Emerg Infect Dis*. 2014; 20:13-20.
10. Citil BE, Derin S, Sankur F, Sahan M, Citil MU, *Vibrio alginolyticus* associated chronic myringitis acquired in Mediterranean waters of Turkey. *Case Rep Infect Dis*. 2015; 2015:187212.
11. Rahman M, Islam MN, Islam MN, Hossain MS. Isolation and identification of oral bacteria and characterization for bacteriocin production and antimicrobial sensitivity. *Dhaka Uni J Phar Sci*. 2015; 14:103-9.
12. Nandi B, Nandy RK, Mukhopadhyay S, Nair GB, Shimada T, Ghose AC. Rapid method for species-specific identification of *Vibrio cholerae* using primers targeted to the gene of outer membrane protein OmpW. *J Clin Microbiol*. 2000; 38: 4145-51.
13. Performance standards for antimicrobial susceptibility testing. 15th informational supplement. Wayne, Pennsylvania: Clinical and Laboratory Standards Institute, 2005.
14. Gupta PK, Pant ND, Bhandari R. Cholera outbreak caused by drug resistant *Vibrio cholerae* serogroup O1 biotype El Tor serotype Ogawa in Nepal; a cross-sectional study. *Antimicrob Resist Infect Control*. 2016; 5:23.
15. Rahim Shah, Ghazala Parveen, Maria Shoukat, Sofia Khalid, Abdul Hameed. Isolation, identification, characterization and antibiotic susceptibility of *Vibrio cholera* during 1998-99. *Int J Biosci*. 2017; 11:135-47.
16. Root ED, Rodd J, Yunus M, Emch M. The role of socioeconomic status in longitudinal trends of cholera in Matlab, Bangladesh, 1993-2007. *PLoS Negl Trop Dis*. 2013; 7:e1997.
17. Schwartz BS, Harris JB, Khan AI, Larocque RC, Sack DA, Malek MA, et al. Diarrheal epidemics in Dhaka, Bangladesh, during three consecutive floods: 1988, 1998, and 2004. *American J Trop Med Hyg*. 2006; 74:1067-73.
18. Kaper JH, Lockman H, Colwell RR, Joseph SW. Ecology, serology, and enterotoxin production of *Vibrio cholerae* in Chesapeake Bay. *Appl Environ Microbiol*. 1979; 37:91-103.
19. Shrestha SD, Malla S, Adhikari R. Antibiotic susceptibility patterns of *Vibrio cholerae* isolates. *JNMA J Nepal Med Assoc*. 2010; 49:232-6.
20. Dalsgaard A, Forslund A, Bodhidatta L, Serichantalergs O, Pitarangsi C, Pang L, et al. A high proportion of *Vibrio cholerae* strains isolated from children with diarrhoea in Bangkok, Thailand are multiple antibiotic resistant and belong to heterogeneous non-O1, non-O139 O-serotypes. *Epidemiol Infect*. 1999; 122:217-26.