

Molecular diagnostics for *Vibrio cholera* based on *recA* gene isolated from human in Diwaniyah city

Syoof Khowman Alramahy

Biology Department, Collage of Science, University of Al-Qadisiyah, Iraq

Abstract

Vibrio cholerae is gram negative bacteria, motile, has a polar flagelum, curved bacillus, causes cholera in humans. *V. cholerae* attacks the intestinal cells through the production of toxins causing the loss of large amounts of salts and water causes severe diarrhea that can lead for death.

Twenty isolates of *V. cholerae* were obtained from Diwaniyah Teaching Hospital of diarrhea infections cultivate on differential cultures media, then genetic material DNA extracted and tested by using PCR technique based on *recA* gene primers, which were designed by using the Gene bank Site (NCBI) to obtain the *recA* gene sequence (Gene bank code (EF990328.1)), using the program design primers (primers plus) and then read the results through the ultraviolet radiation after the samples were carried by Electrical Relay.

The results showed that all *V. cholerae* isolates which were diagnosed by bacterial cultivates on culture media contain *recA* genes by using PCR technique is a fast, highly specialized and is of a great importance in confirming the specific diagnosis of clinical and bacteriological examination.

INTRODUCTION

Cholera is a serious and common disease worldwide, especially in developing countries (1). It is an epidemic disease, endemic and spread in nature caused by *Vibrio cholerae* (2).

These bacteria can be classified into more than 200 serotypes, however, only serotype 1 and O139 are responsible for epidemiological cholera (3). Cholera outbreaks is due to type O1 and *V. cholerae*, which occur regularly. Serotypes other than O1 and O139 are frequently isolated from seafood and aquatic sources, but do not result in any major outbreaks of the disease (4). Epidemiological cholera is acute, painful and often fatal. It had a serious impact on the world during the nineteenth century (5). It can lead to mortality in untreated patients due to dehydration within a few hours (6). The optimum conditions for the growth of *V. cholerae* are average saline (slightly alkaline) water with high nutrients and of tropical moderate temperature (7). In case of human infection, the pathogen is introduced to the host upon consuming contaminated water or food (8), or by direct contact with an infected person (9). Cholera pathology is a complex process involving a number of factors that assist the pathogen in colonizing intestinal epithelial cells and producing cholera intestinal toxins (CT) (10). These toxins lead to an unbalanced ion transport in the intestinal membrane and to a significant loss of salt and water in the form of diarrhea (9).

Bacterial species are categories of breeds that share morphological pattern and genotype (11). Many problems caused by cholera have been found due to the large variation in the biochemical characteristics, as well as its close genetic similarities with many other species (12). The preservative genes characterized by slow diversity and limited variation in the alkaline sequence are suitable for determining the genetic relationship among species (13). The *recA* gene has been suggested to be a potential marker for detecting genetic relationships among taxonomic classes such as families, classes, and divisions due to the bacterial preservative nature (14). *V. cholerae recA* has the advantage of resistance recovery against oxidation, UV ray factors and increasing re-

binding frequencies in the mutant *E. coli* bacteria (15). Therefore, the present study aims at diagnosing isolates of *V. cholera* by *recA* gene isolated from Diwaniyah hospitals. It is the first study in Iraq that uses this gene in the diagnosis of *V. cholerae* bacteria.

MATERIALS AND METHODS

Twenty *Vibrio cholerae* isolates were obtained from the laboratory of bacterial diagnosis at Diwaniyah Teaching Hospital, from diarrheal infection cases and diagnosed using bacterial culture in differential culture media and using Vitak test to confirm the types of the bacterial isolates.

Bacteria Isolates Culture

Vibrio cholerae isolates were cultured using BHI broth and incubated at 37 °C for 18hr. Then, bacterial growth was used in bacterial DNA extraction.

Bacterial DNA Extraction

Bacterial DNA was extracted from *Vibrio cholerae* isolates using Presto™ Mini gDNA Bacteria Kit, which was supplied by Genaid Company, USA. One ml of bacterial culture was taken for each isolate and put in sterilized 5.1 mL tubes. The tubes were put in the centrifuge at 10,000 RPM for one minute. The surfaced fluid was then removed and bacterial cells were used in the DNA extraction process according to the manufacturer's extraction instructions. Then, the DNA was examined for concentration and purity using the NANODROP spectroscopy device. Measuring was done with two wavelengths (260/280nm) in nanogram/microliter concentration unit. DNA samples were then kept at -20 °C in the refrigerator for the PCR sequence test.

PCR Chain Reaction Test

The PCR test was conducted to determine *recA* gene in the DNA in the *Vibrio cholerae* isolates (16) using specialized primers specially designed for this study using the NCBI-Genbank site to obtain the Nitrogen alkaloid sequence of *recA* gene (Genbank Code EF990328.1); and using the primer3 plus design program as the primers were supplied by Bioneer Korea Company (See the table below).

Table 1: Lengths of Nitrogen Alkaloid Primers in the PCR Test Results

Primers	Sequence (5'-3')		PCR Results
	Front	Rear	
<i>recA</i> gene	Front	TCGACCGGTTCTGTCTCT	516bp
	Rear	ACCGCCAGTGGTAGTTTCTG	

Table 2: PCR Mix Preparation

Volume	PCR master mix
5µL	DNA template
1.5µL	<i>recA</i> gene front primer (10pmol)
1.5µL	<i>recA</i> gene rear primer (10pmol)
12µL	PCR water
20µL	Total

Table 3: PCR Thermocycler conditions

PCR Step	Repeat cycle	Temperature	Time
Initial denaturation	1	95°C	5min
Denaturation	30	95°C	30sec.
Annealing		58°C	30sec
Extension		72°C	40sec
Final extension	1	72°C	5min
Hold	-	4°C	Forever

PCR Master Mix

PCR mix was prepared using the AccuPower® PCR Premix kit processed by Bioneer Korean Company and according to the manufacturer’s instructions as in Table 2. The components of the PCR mix were then put in 0.2 ml tubes of the PCP test kit (Accupower® PCR Premix) which contains other components of the PCR mix. All tubes were then put in the mixing centrifuge (Exispin) at 3000RPM for three minutes and then put in PCR Thermocycler. The PCR test was conducted by use of PCR Thermocycler as in Table 3.

PCR Test Results Analysis

Agarose gel electrophoresis was performed using 1% agarose gel and then the read of the result of PCR product analysis was taken by dissolving 1g of agarose gel in 100 mL of 1X TBE buffer solution and put in the microwave for 5 minutes. And then the gel was left to cool at 50°C and then 3mL of Ethidium bromide dye was added and mixed well with the gel. The agarose gel was then poured into the mold tray, which contained the comb to locate the PCR samples. Then the gel was left to harden at room temperature for 15 minutes and then the comb was removed carefully from the gel. Afterwards, 100bp DNA ladder was used and put in the first hole. After the completion of the loading process, the agarose was immersed in the 1X concentration protective solution and the cap was sealed. The device was then operated using 100V, 80Am for one hour. Finally, the gel containing the PCR product was tested by UV ray source to determine the results with the unit of measurement.

RESULTS AND DISCUSSION

The study included the collection of 20 isolates of *V. cholerae* from diarrhea cases in Diwanayah Teaching Hospital. The isolates were gender-categorized (13 isolates, 65% males and 35% females) (Figure 1). As for age groups, ages between 11 and 20 showed the highest rate of infection (40%) and the lowest was 13-40 age group (5%) as shown in Figure 2.

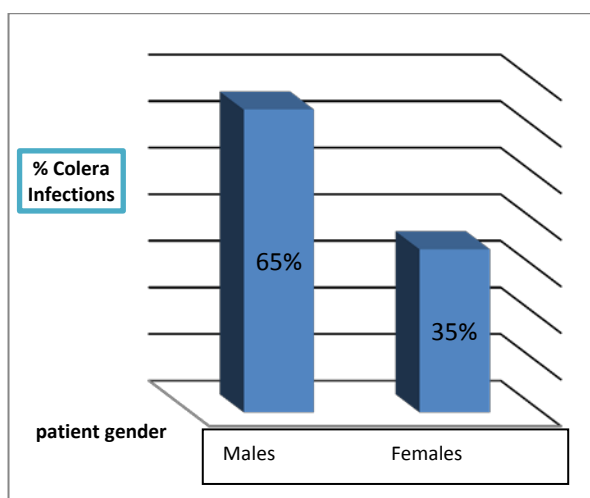


Figure 1: Gender-categorized Cholera Cases (%)

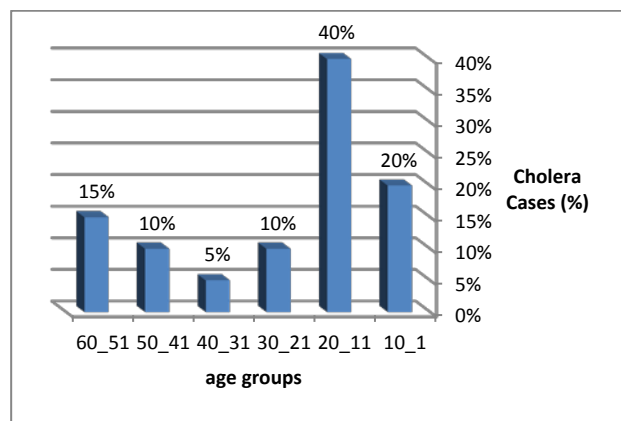


Figure 2: Cholera Infection Cases (%) According to Age Groups

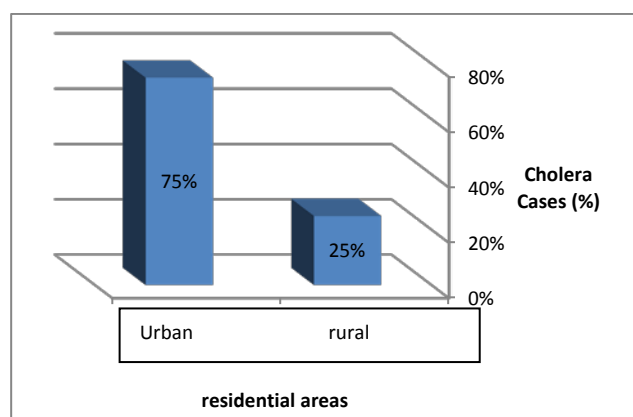


Figure 3: Cholera Infection Cases (%) According to the Residential Areas

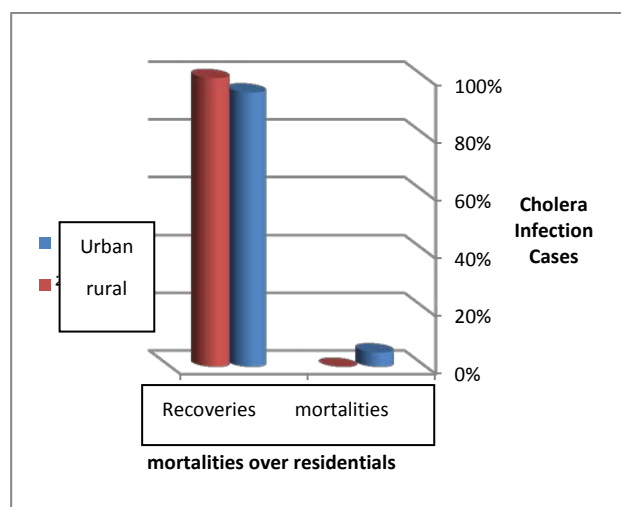


Figure 4: Mortalities Over Residential Areas



Figure 5: Electrical Relay for Agarose Gel with PCR Test Results of *recA* for Diagnosing 20 *V. cholerae* isolates Using PCR Technique on 100V, 80Am for One Hour

The bacterial isolates were geographically distributed into 5 isolates from urban population areas (25%) and 15 isolates from rural population areas (75%) (Figure 3). As for mortalities due to cholera infection, only one case found in a rural population (5%) (Figure 4).

Molecular results of the present study showed that all *V. cholerae* isolates contained *recA* gene with PCR technique because it is fast, accurate and sensitive in distinguishing bacterial species. The presence of a *recA* gene in all isolates confirms that these isolates are identified as *V. cholerae* isolates as shown in Figure 5

The *recA* gene is a multifunctional protein that contributes to identical re-binding, DNA repair and decomposition of DNA (18). The genetic diversity of this gene reflects the differences in the genome so it can be used as a predictor of the genomic relationships (19). The *recA* gene is highly susceptible to environmental stresses, resulting in point mutations, but they do not affect the general functions of the gene and its structure (20).

In addition, the sequence of alkaline in the *recA* gene is more distinct than the sequence of alkaline in 16SrDNA (21). This study recommends the use of *recA* gene to determine genetic relationships and differentiations among different species by analyzing the sequence of alkaline for this gene because it has diagnostic and molecular properties and characteristics.

REFERENCES

1- Taneja,N.;Mishra A.; Sangar,G.and Sharma,M. (2009). Outbreaks caused by variants of *Vibrio cholerae* O1 El Tor,India,Emerg in fact Dis.15(2)352-4 .
 2- Basak,S.;Bancricie,R.;Mukherjee,I.and Das.S.(2009). In domain architecture and codon usage pattern on the evolution of virulence factors of *Vibrio cholerae* . Biochem.Biophys.Res. Commun,379,803-805.
 3- Hunter,P.R.(1997). Waterborne Disease: Epidemiology and Ecology. England :John Wiley and Sons .
 4- Farugue,S.M.;Albert,M.J.and Mekalano,J.J.(1998). Epidemiology,genetics and ecology of toxigenic *vibrio cholerae* .Microbiol.Mol.Biol.Re V.62,1301-1314.
 5- Speck,R.S.(1993) Cholerae .In:Kiple KF,ed.The Cambridge world history of human disease. Cambridge University Press,642-649.

6- Tognotti,E.(2011). The dawn of medical microbiology : germ hunters and the discovery of the cause of cholerae . J.Med Microbioli 60:555-558
 7- Akanda,AS.;Jutla,AS.and Gute,D.(2013). Population vulnerability to biannual cholerae outbreaks and associated macro-scale drivers in Bengl Delta . Am J Trop Med Hyg;89:950-9 .
 8- Rippey,SR.(1994). In factious disease associated with mollscan shellfish consumption.Clin. Microbiol Rev;7:419-25 .
 9- Kaper,JB.;Morris,JG.and Levine,MM.(1995). Cholera.Clin Microbiol Rev;8:48-86
 10- ShahAli,M.;Mutreja,A.;Thomson,N.;Baker,S.;Parkhill,J.;Dougan,G (2014) Genomic Epidemiology of *Vibrio cholerae* O1 Associated with Foods,Pakistan ,2010. Emerging infectious Diseases.20(1) :13-20 .
 11- Gevers,D.,Cohan,F.M.;Lawrence,J.G.;Spratt,B.G.;Coenye,T.;Feil,E.J.; Stackbrandt,E.;Van De Peer,Y.;Vandamme,P.(2005). Opinion : re-evaluating prokaryotic species .Nat Rev Microbiol . 733-739 .
 12- Thompson,F.L. & Swings,J.(2006). Taxonomy of the vibrios .In the Biology of Vibrios,PP.29-43,Edited by F.L.Thompson,B.Austin & J.Swings.Washington :American Society for Microbiology .
 13- DaninPoleg,Y.;Cohen,L.A.;Gancz,H.;Broza,Y.Y.;Goldshmidt,H.;Malul,E.;Val insky,L.and Lerner,L.(2007).*Vibrio cholerae* strain typping and phylogeny study based on simple sequence repeats.J Clin Microbiol 45,736-746 .
 14- Zeigler,D.R.(2003). Gene sequence useful for predicting relatedness of whole genomes in bacteria . Int Syst Evol Microbiol.53,1893-1400 .
 15- Goldbery,I, and Mekalanos,j.j.(1986). Cloning of the vibrio cholerae rec A mutant and contraction of a *vibrio choleare recA* mutant,j.Bacterial 185:715-722.
 16- Nei M. and Kumar S. Molecular Evolution and Phylogenetics. Oxford University Press, New York.(2000).
 17- Van Belkum,A.;Struelens,M.;De Visser,A.;Verbrugh,H. and Tibaayrenc,M.(2001).Role of genomic typing in taxonomy ,evolutionary genetics , and microbial epidemiology . Clin microbial Rev 14,547-560 .
 18- Cox,M.M.(2003). The bacterial *recA* protein as a motor protein Annu Rev Microbiol 57,551-577 .
 19- Zeigler,D.R.(2003) . Gene sequences useful for predicting relatedness of whole genomes in bacteria. Int J Syst Evol Microbiol 53,1893-1900 .
 20- Dashtban-Roozbehani,A.;Bakhshi,B.;Katouli,M. and Pourshafie,M.R.(2011).Comparative sequence analysis of *recA* gene among *vibrio cholerae* isolates from Iran with globally reported sequences. Letters in Applied Microbiology 53,313-323 .
 21- Thompson,C.C.;Thompson,F.;Vandemeulebroecke,K.;Hoste,B.;Dawyndt,P. and Swings,J.(2004).Use of *recA* as an alternative phylogenetic marker in the family vibriionaceae. Int J Syst Evol Microbiol 54,919-924.