**List of ten best papers highlighting the important discoveries/contributions**

1. **Pal BB\*, Nayak AK, Nayak SR. Emergence and spread of different *ctx*B alleles of *Vibrio cholerae* O1 in Odisha, India. International Journal of Infectious Diseases. 2021;105:730-2.**

This study reported variants of the *ctx*B allele of *Vibrio cholerae* O1 isolated between 1995 and 2019 in Odisha, India. *ctx*B1 genotypes dominated from 1995 to 2016. The Haitian variant and El Tor *ctx*B3 genotypes of *V. cholerae* O1 emerged in 1999, and were most common in 2018-2019 and 2005-2011, respectively. The *ctx*B7 genotype of the Haitian variant of *V. cholerae* O1 was quiescent from 2000 to 2006, but further spread was noted from 2007 to 2019.

1. **Nayak AK, Nayak SR, Behera DR, Pal BB\*. Dissemination of *Vibrio cholerae* O1 isolated from Odisha, India. Environmental Microbiology Reports. 2021;13(3):355-63.**

This article reported the antimicrobial susceptibility trends, virulence genes, and drug resistance genes of *Vibrio cholerae* O1 strains isolated from outbreaks and epidemics over two and half decades (1995–2019) from Odisha, India. Antimicrobial susceptibility testing was performed by disc diffusion method. Virulence and drug resistance genes were detected by multiplex PCR assays. All *V. cholerae* O1 strains were sensitive to gentamicin, chloramphenicol, norfloxacin and ciprofloxacin while resistant to one or more antibiotics used. About 90% of the isolates of *V. cholerae* O1 carried antibiotic drug resistant genes (*SulII*, *dfrA1* and *strB*) and SXT elements and the results correlated with the phenotypic antibiotic data obtained through disc diffusion assay. The *tcpA* Haitian variant *V. cholerae* O1 first appeared in 1999, gradually showing its increasing number upto 2019. TcpA El Tor strains only prevailed from 1995 to 2006; whereas the *tcpA* classical strains of *V.cholerae*O1 were found in less number from 1995 to 2016. Two multiplex PCR assays confirmed the presence of various toxigenic and virulence genes (*toxR*, *ompU*, *ace*, *rtxC*, *ctxA*, *tcpA*, *rfbO1* and *ompW*) in all isolate of *V. cholerae* O1 strains. The present findings demonstrated the origin and spread of Haitian variants *tcpA* in *V. cholerae* O1 strains over two and half decades.

1. **Pal BB\*, Nayak SR, Biswal B, Das BK. Environmental reservoirs of *Vibrio cholerae* serogroups in the flowing freshwater environs from the tribal areas of Odisha, Eastern India. Environmental Microbiology Reports. 2021:13(2):119-125.**

The environmental reservoirs of different serogroups of *Vibrio cholerae* causing cholera in the flowing freshwater bodies of the tribal areas of Odisha are not known. So this study was conducted from June 2017 to March 2020 to find out the environmental reservoirs of *V. cholerae* serogroups in the water and plankton samples collected from the river, nala, stream and chua from Rayagada district. Similarly, rectal swabs were collected from diarrhoea patients and correlation was established among the *V. cholerae* strains isolated from diarrhoea patients and environmental *V. cholerae* isolates through routine culture, different multiplex PCR assays and pulse field gel electrophoresis (PFGE) analysis using standard techniques. The multiplex PCR assays on biotypes and different toxic genes exhibited similar correlation between the clinical and water isolates, which was further strengthened by PFGE analysis. The planktonic DNA was positive for *ctx*A gene which established that the environmental water bodies were the reservoirs for virulence genes of *V. cholerae* serogroups. The detection of environmental reservoirs of *V. cholerae* serogroups in temporarily stagnant condition of water; partially encircled by stones, and near the bank of the river, nala and stream were the reservoirs which is a rare report from Odisha, India and Globe.

1. **Pal BB\*, Mohanty A, Biswal B, Nayak SR. New variant of *Vibrio cholerae* O139 in Odisha, India. Journal of clinical microbiology. 2019;57(5):e01877-18.**

Three interesting findings emerged from this investigation, namely (i) the reemergence of V. cholerae O139 in Odisha after a hiatus of 10 years; (ii) the reemerged O139 strains carried a novel ctxB genotype, and this is the first report of such strains of O139 causing outbreaks of cholera; and (iii) a new variant of V. cholerae O139 has again emerged from the Bay of Bengal region. By sequencing and comparing hundreds of bacterial genomes, recent studies have shown that all of the explosive epidemics of cholera in Africa and the Americas in the past half-century arose after the arrival of new strains that had evolved in Asia. Although the O139 serotype of V. cholerae has not spread to the African or American continents, the likelihood of this new variant spreading to other parts of the world should not be underestimated.

1. **Pal BB\*, Khuntia HK, Nayak SR, Mohanty A, Biswal B. *Vibrio cholerae* O1 Ogawa Strains Carrying the *ctx*B7 Allele Caused a Large Cholera Outbreak during 2014 in the Tribal Areas of Odisha, India. Japanese journal of infectious diseases*.* 2017;70(5):549-553.**

This study reported *ctx*B genotypes of *Vibrio [cholerae](https://www.sciencedirect.com/topics/medicine-and-dentistry/cholera" \o "Learn more about cholerae from ScienceDirect's AI-generated Topic Pages)* O1 isolated between 1995 and 2019 in Odisha, India. The predominance of *ctx*B1 genotypes was noted from 1995 to 2016. The Haitian variant and El Tor *ctx*B genotypes of *V. cholerae* O1 emerged in 1999, and were most common between 2018 and 2019 and between 2005 and 2011, respectively. Further spread of the Haitian variant of *V. cholerae* O1 was noted from 2007 to 2019.

1. **Kar SK, Pal BB\*, Khuntia HK, Samal SK, Khuntia CP, Achary KG. Emergence and spread of Tetracycline resistant *V. cholerae* O1 El Tor variant during 2010 cholera epidemic in the tribal areas of Orissa, India. International Journal of Infectious Disease. 2015;33:e45-e49.**

The epidemics of cholera were reported in the Kashipur, K.singhpur, B cuttack blocks of Rayagada district and Mohana block of Gajapati district of Odisha during 2010. This study was carried out to isolate the bacterial pathogen, its drug sensitivity pattern and to describe the spread of the disease in those areas. A total of 68 rectal swabs collected from patients with severe diarrhea, admitted to different health centers and diarrhea affected villages were bacteriologically analyzed. Similarly 22 water samples collected from different villages from nala, chua, etc were tested for the presence of *V. cholerae*. Out of 68 rectal swabs tested 35 (51.5%) were *V. cholerae* O1 Ogawa and 14(20.6%) were *E coli*; which might be commensals. All water samples were negative for *V. cholerae*. The *V. cholerae* strains were sensitive to gentamicin, norfloxacin, ciprofloxacin, azithromycin and ofloxacin; but were resistant to ampicillin, tetracycline, nalidixic acid, furazolidone, streptomycin, erythromycin, co-trimoxazole, neomycin and chloramphenicol. All *V. cholerae* strains were 100% resistant to tetracycline and they were El Tor variants harboring *ctx*B gene of classical strain. The present study indicated the emergence and spread of tetracycline resistant *V. cholerae* O1 El Tor variant in the tribal areas which needs close monitoring.

1. **Pal BB\*, Khuntia HK, Samal SK, Kar SK, Pattnaik B. Epidemics of severe cholera caused by El Tor Vibrio cholerae O1 Ogawa possessing the ctxB gene of the classical biotype in Orissa, India. International Journal of Infectious Disease. 2010;14:384-389.**

This study represents an investigation of epidemic of [cholera](https://www.sciencedirect.com/topics/medicine-and-dentistry/cholera) that occurred in Kashipur and Dasmantpur blocks of Orissa, reported during July–September 2007. Sixty-two rectal swabs and 28 water samples collected from diarrhea patients at different hospitals and villages were bacteriologically analyzed for the identification, [antibiogram](https://www.sciencedirect.com/topics/medicine-and-dentistry/antibiogram), and detection of toxic genes of [*Vibrio cholerae*](https://www.sciencedirect.com/topics/medicine-and-dentistry/vibrio-cholerae). The cholera outbreaks were caused by V. cholerae O1 Ogawa [biotype](https://www.sciencedirect.com/topics/immunology-and-microbiology/biovar) El Tor in both Kashipur and Dasmantpur blocks. All the V. cholerae isolates from the clinical and environmental samples were sensitive to [tetracycline](https://www.sciencedirect.com/topics/medicine-and-dentistry/tetracycline), [gentamicin](https://www.sciencedirect.com/topics/medicine-and-dentistry/gentamicin), [azithromycin](https://www.sciencedirect.com/topics/medicine-and-dentistry/azithromycin), and [chloramphenicol](https://www.sciencedirect.com/topics/medicine-and-dentistry/chloramphenicol), but were resistant to [ampicillin](https://www.sciencedirect.com/topics/medicine-and-dentistry/ampicillin), [ciprofloxacin](https://www.sciencedirect.com/topics/medicine-and-dentistry/ciprofloxacin), [norfloxacin](https://www.sciencedirect.com/topics/medicine-and-dentistry/norfloxacin" \o "Learn more about Norfloxacin from ScienceDirect's AI-generated Topic Pages), [co-trimoxazole](https://www.sciencedirect.com/topics/medicine-and-dentistry/trimethoprim-sulfamethoxazole), nalidixic acid, [neomycin](https://www.sciencedirect.com/topics/medicine-and-dentistry/neomycin), and [furazolidone](https://www.sciencedirect.com/topics/medicine-and-dentistry/furazolidone" \o "Learn more about Furazolidone from ScienceDirect's AI-generated Topic Pages), except the water isolates, which were sensitive to ciprofloxacin and norfloxacin. The [multiplex PCR assay](https://www.sciencedirect.com/topics/medicine-and-dentistry/multiplex-polymerase-chain-reaction) revealed that all the clinical and environmental V. cholerae isolates were positive for the ctxA and tcpA genes, showing biotype El Tor. Interestingly, 88% of the clinical and environmental isolates of V. cholerae were El Tor biotype with mutation at the ctxB gene of the classical strain, as confirmed by mismatch amplification of mutation (MAMA)-PCR assay. This is the first report of the El Tor variant of V. cholerae O1 Ogawa having the ctxB gene of the classical strain with altered antibiogram causing epidemics of cholera in Orissa, India.

1. **Khuntia HK, Pal BB and Chhotray GP. Quadriplex PCR assay simultaneous for detection of biotype, serotype, toxigenic potential and central regulating factor of *V. cholerae*. Journal of clinical Microbiology. 2008;46:2399-2401.**

A quadruplex PCR was developed for the simultaneous detection of genes specific for Vibrio cholerae O1 and/or O139 serogroup (wbe and/or wbf), cholera toxin A subunit (ctxA), toxin-coregulated pilus (tcpA), and central regulating protein ToxR (toxR) in a single tube reaction. This is a simple, rapid, and accurate approach for the detection of toxigenic V. cholerae O1 and/or O139 and can prevent the rapid spread of the disease by early detection.

1. **Chhotray GP, Pal BB, Khuntia HK, Chowdhury NR, Chakraborty S, Yamasaki S, Ramamurthy T, Takeda Y, Bhattacharya SK, Nair GB. Incidence and molecular analysis of *Vibrio cholerae* associated with cholera outbreak subsequent to the super cyclone in Orissa, India.  Epidemiol Infect*.* 2002;128:131- 138.**

An epidemiological study was carried out to find out the etiological agent for diarrheal disorders in the cyclone and flood affected areas of Orissa, India. Rectal swabs collected from 107 hospitalized diarrhea patients were bacteriologically analyzed to isolate and identify the various enteropathogens. Detection of toxic genes among *E. coli* and *V. cholerae* was carried out by polymerase chain reaction (PCR) assay. Of the 107 rectal swabs analyzed, 72.3% were positive for *V. cholerae* O1 Ogawa, 7.2% for *V. cholerae* O139, 1.2% for *E. coli* (EAggEC) and 1.2% for *Shigella flexneri* type 6. Using multiplex PCR assay it was found that all *V. cholerae* isolates were *ctx*A positive and El Tor biotype. Strains of *V. cholerae* O1 were observed to be resistant to nalidixic acid, furazolidone, streptomycin, co-trimoxazole and ampicillin. Except for nalidixic acid, the resistance pattern for O139 was identical to that of O1 strains. Representative strains of *V. cholerae* were further characterized by randomly amplified polymorphic DNA (RAPD) analysis and ribotyping. Both O1 and O139 *V. cholerae* strains exhibited the R3 pattern of ribotype and belonged to a similar pattern of RAPD compared with that of Calcutta strains. Early bacteriological and epidemiological investigations have revealed the dominance of *V. cholerae* O1 among the hospitalized patients in cyclone affected areas of Orissa. Drinking water scarcity and poor sanitation were thought to be responsible for these diarrheal outbreaks. Timely reporting and implementation of appropriate control measures could contain a vital epidemic in this area.

1. **Pal BB\*, Mohanty A, Biswal B, Nayak SR, Das BK, Lenka PP. Haitian variant *Vibrio cholerae* O1 Ogawa caused cholera outbreaks in Odisha. Indian Journal of Medical Microbiology. 2021 Mar 31.**

Diarrheal disorders particularly cholera cause a significant threat resulting in high morbidity and mortality in the coastal and tribal areas of Odisha. Two sequential diarrheal outbreaks reported in 2016 from Balasore and Rayagada districts of Odisha were investigated to find out the causative organisms, antibiogram profile and molecular analysis of the isolated pathogens. Bacteriological analysis and antibiogram profiles of the pathogens were carried out as per the standard procedure followed. The double mismatch amplification mutation (DMAMA) PCR for *ctx*B gene, sequencing and pulse-field gel electrophoresis (PFGE) were carried out on *Vibrio cholerae* O1 strains. The rectal swabs and water samples from these districts were positive for *V. cholerae* O1 Ogawa biotype El Tor. The *V. cholerae* O1 strains isolated from Balasore district were multidrug resistant to many antibiotics which differed from the isolates of Rayagada district. The DMAMA PCR assay on all clinical and water isolates from these areas and some strains from other districts exhibited *ctx*B7 allele of *V. cholerae* O1 which correlates with the sequencing results having different pulsotypes. The Haitian variant of *V. cholerae* O1 strains which were compared with the *V. cholerae* O1 strains of 1999 and 2000 exhibited different pulsotypes. This study reports cholera outbreaks due to multidrug resistant *ctx*B7 allele of *V. cholerae* O1 from both coastal (Balasore) and tribal (Rayagada) areas of Odisha.