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Analysis on Presence of Pathogenic Bacteria from Drinking Water

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ABSTRACT

Aim of this study is bacterial isolation (pathogenic) from beverage and makes some awareness about waterborne disease. Infectious diseases caused by pathogenic bacteria, viruses and parasites are the foremost common and widespread health risk related to beverage. Water contamination not only affects the developing countries but is additionally a serious problem in developed countries. Thus, contamination of water resources with pathogenic bacteria resulting in illness may be a major concern throughout the planet.

Keywords: antibiotics, bacteriostatic, Water contamination, waterborne disease.

INTRODUCTION

India has been gifted with many rivers and Himalayas to satisfy majority of water requirements of the country. Water resources mainly accomplish the deeds like drinking, domestic in conjunction with agriculture, aquaculture and in power generation. Therefore, water plays an important role within the lives of citizenry. Out of the various water resources, the resource that's used for drinking and domestic purpose should be taken into consideration seriously thanks to contamination problem. Hence, Physico-chemical and microbiological quality of beverage has become a crucial tool to ascertain before its use. Water acts as a medium for various microorganisms and thus plays a key role in spreading transferable diseases[1].

Infectious diseases caused by pathogenic bacteria, viruses and parasites are the foremost common and widespread health risk associated with beverage[2]. Water quality is affected by faecal matter, domestic and industrial sewage and agricultural, additionally to a scarcity of aware-ness and education among the users [3]. The detection of bacterial indicators in beverage suggests the presence of pathogenic organisms that are sources of waterborne disease [4]. Indicator microorganisms survive better and longer than pathogens, with uniform and stable properties, and will be easily detected using standard laboratory techniques [5]. ground water may be a crucial source of drinking and household water in both rural and concrete areas. Studies [3], [6] assessing the microbiological quality of beverage have found varying rates of contamination with coliforms and other heterotrophic bacteria. The pathogenic bacteria that sometimes appear in water contamination include *Bacillus sp., botulinus*, *Escherichia coli, Pseudomonas aeruginosa, Shigella sp., Salmonella sp., Staphylococcus aureus and Vibrio cholera*. Recent reports have shown the presence of pathogenic bacteria in beverage which are responsible to water borne diseases. Contaminating pathogenic bacteria will cause several diseases like diarrhoea and gastric disorders. Mostly the kids get affected with these pathogens. As per WHO, nearly 3.4 million people die once a year because of the diseases related to water contamination[7]. As per UNICEF, approximately 4000 children die each day because of water contamination [8]. Improving water quality is that the main parameter to reduce the water related diseases[4]. Most of the people of such areas use water directly from available sources, with none treatment and thus are exposed to a selection of water- related diseases.

REVIEW OF LITERATURE

Infectious diseases caused by pathogenic bacteria, viruses, protozoa and other parasites are the foremost common and widespread health risk related to beverage. Experimental studies of infectivity provide relative information, but it's doubtful whether the infective doses obtained are relevant to natural infections. Many people depend on surface and ground- water sources for their daily water needs. Water from ground water sources is used directly by communities and the water sources are contaminated by pathogens and devoid of treatment. Among the pathogens disseminated in water sources. Enteric pathogens such as E. coli, S. typhimurium are usually transmitted to humans by the ingestion of contaminated water and foods. The impact of waterborne diseases (such as diarrhoea) is significant in South Africa. Studies have shown that diarrhoea is the detection of specific pathogenic microorganisms capable of causing infections and diseases in such communities.

In order to control these bacteria, from contaminating water and further causing illness, extensive knowledge is required regarding

their origin, biology, physiology, ecology, survival, growth and prevalence in seafood and related products, along with the epidemiology and symptomatology of the diseases with which they are associated[9]

Clostridium botulinum:

Clostridium botulinum is an anaerobic, Gram-positive, peritrichous, rod-shaped, spore and gas forming bacterium ubiquitous in soils and aquatic sediments. The organism is assessed into types consistent with serological specificity. Each type secretes a special toxin, mentioned as A, B, C, D, E, F and G. According to [10] spores of the E type can germinate at temperatures below 3° C and are often found in association with cold-stored seafood.Botulinum toxin is an active exotoxin with neurotropic action. It is the sole toxin which may be fatal upon ingestion and should be considered a biological poison. It is lethal at very small doses; unlike the spores of the toxin is thermo liable and is destroyed if exposed to 65-80 °C for 30 minutes or to 100 ° C for five minutes.

Cholera:

Characterization of the Disease

- Personal immunity: Both previous infections and by vaccines;
- Inoculum: the disease only occurs after ingestion of a minimum amount of cells [11];
- The gastric barrier: Patients consuming anti-acidic medications are more susceptible to infection than healthy people;
- Blood group: some unknown reasons, people with O-group blood are more susceptible than others

Shigellosis or Bacillary Dysentery:

Shigella are Gram-negative, non-sporeforming, non-motile, straight rod-like members of the *Enterobacteriaceae*. Cells ferment sugars without gas production. Salicin, adonitol and myo-inositol aren't fermented. Cells don't utilize citrate, malonate and acetate as sole carbon source and don't produce H2S. Lysine isn't decarboxylated. Cells are oxidase-negative and catalase-positive. Members of the genus have a posh antigenic pattern, and taxonomy is predicated on their somatic O antigens [13].

Characterization of the Disease

The disease usually begins with fever, anorexia, fatigue and malaise. Twelve to 36 hours later, diarrhoea progresses to dysentery, blood, mucus and pus appearing in faces that decreases in volume [14], [15].

Mode of infection

Although, the initial step in pathogenesis is penetration of the colonic mucosa. Degeneration of the epithelium and by an acute inflammatory colitis within the lamina propria. Under these conditions the absorption of water by the colon is inhibited and therefore the volume of stool depends upon the ileocecal flow[16], [17]. so as for Shigella to enter an somatic cell, the bacterium must first adhere to its target cell. Generally, the bacterium is internalized via an endosome, which it subsequently lyses to realize access to the cytoplasm where multiplication occurs [16][17].

Escherichia coli Strains

E. coli strains main groups are differentiated under the subsequent basis:

- ➢ epidemiological evidence,
- phenotypic traits,
- clinical features of the disease and
- specific virulence factors.

From these, enterotoxigenic (ETEC, namely O148), enterohemorrhagic (EHEC, namely O157) and enteroinvasive serotypes (EIEC, namely O124) are of outstanding importance and may be transmitted through contaminated water

EnterotoxigenicE. coli (ETEC) Strains

Enterotoxigenic *E. coli* (ETEC) serotypes can cause infantile gastroenteritis. the amount of reports of their occurrence in developed countries is relatively small, but it's a particularly important explanation for diarrhea within the developing world, where there's no adequate clean water and poor sanitation. In developing countries, these strains are the foremost commonly isolated bacterial enteropathogen in children below 5 years aged, and account for several hundred million cases of diarrhea and a number of other ten of thousand deaths each year[10]. Disease caused by ETEC follows ingestion of contaminated food or water and is characterized by profuse watery diarrhea lasting for several days that always results in dehydration and malnutrition in young children [18]. ETEC are also the foremost common explanation for travelers' diarrhea that affects individuals from industrialized countries travelling to developing regions of the planet [18].

EnterohemorrhagicE. coli (EHEC)

Strains Reported outbreaks had been associated mainly with the consumption of contaminated foods, like raw or undercooked ground meat products and milk . the first reservoir of this bacterium has been found to be healthy cattle. E. coli serotype O157:H7 causes abdominal pain, bloody diarrhea, and hemolytic uremic syndrome. This bacterium produces Shiga-like toxins. The time period is 3–4 days, and therefore the symptoms occur for 7–10 days. it's estimated that 2–7% of E. coli O157:H7 infections end in acute kidney failure [19]. Although E. coli O157:H7 isn't usually a priority in treated beverage , outbreaks involving consumption of beverage contaminated with human sewage or cattle faeces are documented. An increasing number of outbreaks are related to the consumption of fruits and vegetables contaminated with faeces from domestic or wild animals at some stage during cultivation or handling. EHEC has also been isolated from bodies of water, wells and water troughs, and has been found to survive for months in manure and water-trough sediments. Person-to-person contact is a crucial mode of transmission through the oral-faecal route, where individuals show no clinical signs of disease but are capable of infecting others. American Type Culture Collection, Rockville, MD bacterial strains of Escherichia coli ATCC 25922, Salmonella typhimurium ATCC 14028 and National Collection of Type Cultures, London, UK obtained culture of Vibrio cholerae NCTC 5941 were confirmed by morphological and biochemical tests and used for further reference [20].

The water sources are:

- Lenge Dam, the Tyume River, the Sityi River and therefore the Mnikina River (surface water).
- boreholes within the villages of Ngqele, Njwaxa, Dyamala and Ngwenya, South Africa (ground water).

Although all the boreholes are covered, they're surrounded by animal excreta and every one of them are located on the brink of pit latrines (with the exception of the Dyamala borehole). Groundwater is surrounded by sandstones and shale and dolerite intrusions. Water samples obtained time is November 2001, January- March 2002. The river and dams waters were sterilely collected using 2 litre glass bottles. The samples were then placed in ice bags and transported to the laboratory at the University of Fort Hare for analyses within 2hours of collection. An analysis of the water samples obtained from the various beverage sources resulted within the isolation of presumptive *E. coli and V. cholerae*by culturing methods. Biochemical identification results indicated the presence of *E. coli*, from the Ngqele, Dyamala and Lenge sources, whereas Vibrio spp. was identified from the Njwaxa, Nqele and Tyume sources. However, Salmonella spp. was identified only from the Lenge source. Subsequent PCR analysis of the isolates indicated the presence of *E. coli* in Tyume, Ngqele, Dyamala, and Ngwenya and toxigenic *V. cholerae* strains in Tyume and Ngqele. While the PCR analysis of the isolates showed that 75% and 25% of groundwater samples tested positive for *E. coli* and toxigenic *V. cholerae* respectively, only 25% of the surface water samples tested positive for either bacterial strain. Several factors may have contributed to the apparently high E. coli and *V. cholerae* frequency using culturing methods and their low frequency or absence using the PCR method.

In South Africa, diarrhoea is responsible for about 20% of all deaths of one- to five-year-olds and an annual estimated 43,000 deaths and 3 million incidences of the illness, with an associated treatment cost of some 3.4 billion. *Escherichia coli* are capable of causing urinary tract infection, neonatal meningitis and intestinal disease caused by ETEC, EIEC, EPEC, EAggEC and EHEC. Therefore, the presence of this organism in drinking water sources may pose a serious health risk to the communities. Some communities receive drinking water directly from uncovered or covered boreholes and wells whereas for others the water is drawn from the boreholes to a reservoir, and from the reservoir the water is delivered to the people through standpipes. In both cases groundwater is distributed to the community without any purification. The quality of the water may be improved by cleaning of the groundwater distribution system from the reservoir to the standpipes, the removal of organic and sediment organics from the water, the addition of a disinfectant or the boiling of drinking water before use. It has long been known that cholera is a waterborne disease that is transmitted via water, with mostly surface water being implicated.

E. coli can best fulfil conditions possible to act as a perfect indicator of faecal pollution. These organisms survive longer in water than most pathogens, and thus can detect recent also as earlier pollution. In terms of public health significance, *E. coli* has frequently been reported to be the causative agent of traveller's diarrhoea, tract infection, haemorrhagic colitis, and haemolytic uraemia syndrome. Moreover, *Klebsiella pneumonia* is related to pneumonia and upper tract infection. However, *Enterobacter* and *Citrobacter* species have also been previously reported as causes of cystitis, enteritis, pneumonia, diarrhoea, and gastrointestinal disorder. *Proteus vulgaris* in association with other bacteria has been reported to be the causative agent of cystitis and pyelitis[6].

The water samples were processed using the multiple fermentation tube method to work out the presumptive coliform count MPN of coliforms supported standard methods. Suspensions from positive tubes were subcultured on MacConkey agar and incubated at 37 °C for 24-48 hours. The antimicrobial testing of the isolates against commonly used antibiotics was performed consistent with CLSI guidelines and therefore the detection of ESBL production was performed with a phenotypic method employing a double disc synergy test[4].

The quality of house hold water from 80 samples collected at the source in rural and urban communities. The contamination rate:

- E. coli or Enterococcus spp., 22 samples: urban- 12 and rural- 10.
- > Total *coliforms* 74 in household water sources urban-39; rural-35.
- A total of 44 well water sources showed the absence of *E. coli* and *Enterococcus* spp. and the presence of ≥ 10 coliforms per 100 ml.
- ▶ Nine samples without *E. coli* or *Enterococcus* spp. had lower *coliform* counts (<10 coliforms/ml).
- The absence of *E. coli*, *streptococci* and total *coliforms* was found in only 5 samples.
- A total of 48 samples: urban- 21 and rural- 27 samples showed a high MPN of >180.
- ▶ A total of 170 bacterial isolates were obtained and included coliforms (119):
- \blacktriangleright Enterococcus spp. -3,
- ➢ Saprophytic bacteria − 48,
- ▶ The *coliforms* isolated included *Klebsiellaspp.* 48,
- Enterobacter spp. 30,
- Escherichia coli 19,
- ➢ Proteus spp. −14,
- ➤ Citrobacter spp. 8,
- ➢ Pseudomonas aeruginosa − 36,
- ➤ Acinetobacterspp. 8.

Although the majority of the 119 coliform strains were susceptible to commonly used antibacterial agents, a significant resistance was observed among the isolates to beta lactam antibiotics. In total, 91 strains were resistant to:

- All of the coliform strains were susceptible to amikacin. Multi-drug resistance was observed in a significant number of the isolates.
- Twenty-five coliform strains and two *Enterococcus* spp. were resistant to more than two classes of ampicillin antibiotics. Significantly, among the coliform bacteria, ESBL production was detected in 11 isolates.
- Six E. coli, 3 Klebsiella spp. and 2 Enterobacter spp. from 9 water samples produce ESBL.
- P. aeruginosa was sensitive to commonly used antimicrobials, whereas three isolates of Acinetobacter spp. were resistant to more than two different classes of antimicrobial agents.

SUMMARY AND CONCLUSION

A clean and treated water system to every house could also be the norm in Europe and North America, but in developing countries, two and a half billion people haven't any access to improved sanitation, and quite 1.5 million children die annually from diarrheal disease. According to the WHO, the mortality of water associated diseases exceeds 5 million people per annum. In general terms, the best microbial risks are related to ingestion of water that's contaminated with human or animal faeces. Wastewater discharges in fresh waters and costal seawaters are the main source of faecal microorganisms, including pathogens. Acute microbial diarrheal diseases are a serious public ill health in developing countries. This review going to examined the pathogenic bacteria which was isolated from the drinking water. The water samples were collected from Puducherry areas, and the sample was kept in 4°c for further use. The sample was diluted viz., serial dilution technique, and the plates (both pour and spread) were serially sub cultured and maintained for study purpose. The isolated sample were identified morphologically, especially Gram's staining. The samples were standardized under the condition of EUBAC and 16S RNA gene. finally the samples were test against the standard antibiotics.

ABBREVIATION

UNICEF	United Nations Children's Fund
PCR	Polymerase Chain Reaction
EPEC	Entero pathogenic
ETEC	Enterotoxin-Forming
EIEC	Entero-Invasive
EHEC	Enterohemorrhagic E. Coli
EAggEC	Enteroaggregative E. Coli
CLSI	Clinical Laboratory Standards Institute guidelines
ESBL	Extended-Spectrum Beta-Lactamase Production
MPN	Most Probable Number

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