River/Canal Bank Water in Terms of Transmitting the Hazardous Microorganism in Human Population

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The aim of present study is to determine the load of pathogenic microorganism and possible disease potentials of the water sources to prevent possible disease outbreak for the inhabitants. A total number of 50 water samples were collected from different river/canal bank sources and were subjected to standard microbiological analysis. The result of total heterotrophic bacterial count (cfu/ml) ranged between $21x10^5$ to $16.6x10^6$. Different bacterial isolates were microscopically and biochemically characterized as: ***Escherichia coli****,* ***Staphylococcus spp.****,* ***Klebsiella spp.****,* ***Streptococcus spp.****, and* ***Proteus spp.*** *In 50 water samples, 40(80.0%) samples were positive for* ***Escherichia coli****, 35(70.0%) for* ***Staphylococcus spp.****, 25(50.0%) for* ***Klebsiella spp.****, 25(50.0%) for* ***Streptococcus spp.****, and 15(30.0%) for* ***Proteus spp.****, respectively. This showed that* ***Escherichia coli*** *and* ***Staphylococcus spp.*** *occurred highest (80% and 70%) in water samples followed by* ***Klebsiella*** *and* ***Streptococcus spp.*** *(50.0%) while the lowest occurrence was recorded by Proteus spp. (30.0%), respectively. The results show that river/canal bank water sources are not free from enteric pathogens and expose users to diseases like dysentery, diarrhoea, skin, soft tissue, respiratory, urinary or respiratory tract infections, endovascular to wound infections etc.*

Keywords: Pathogenic microorganism, *Escherichia coli*, *Staphylococcus* spp., *Klebsiella* spp., *Streptococcus* spp. and *Proteus* spp..

1. INTRODUCTION

Water has been recognized as a potential carrier of disease causing agent for a long time. A wide range of bacterial, viral, and protozoan diseases results from the pollution of water with human faecal wastes. Although many of these pathogens can be detected directly, indicator organisms are generally used as an index of possible water pollution by human pathogens [1]. Many important human pathogens can survive in water and infect humans. The lack of water sanitation that is easily accessible, adequate in quantity, free from contamination, safe and readily available throughout the year, is the primary reason why diarrheal diseases are so common in developing countries [2,3]. Two and a half billion people have no access to improved sanitation, and more than 1.5 million children die each year from diarrhea diseases [4]. When waters are used for recreation or as a source of food that is consumed uncooked, the possibility for disease transmission certainly exists [1]. Faecal bacteria originate from the faeces of humans and warm-blooded animals. Their presence and quantity is used to measure faecal pollution in water.

The presence of enteric pathogens in drinking and recreational waters is of great concern. As a result of the danger to public health due to the presence of pathogens, it is extremely important to determine the microbiological safety of these waters. This practice is not perfect and there is considerable variety in the ways that different indicator microorganisms are applied in various geographical areas and situations, however, public health concerns are generally well served [5]. *Escherichia coli*, *Staphylococcus* spp., *Klebsiella* spp., *Streptococcus* spp., and *Proteus* spp used as indicator species in this study.

According to the WHO, the mortality of water associated diseases exceeds 5 million people per year; from these more than 50% are microbial intestinal infections [6]. Freedom from contamination with fecal matter is the most important parameter of water quality because human fecal matter is generally considered to be a greater risk to human health as it is more likely to contain human enteric pathogens that are agents of diarrhea [7].

The decision of WHO's 29th session (May, 1976) emphasized that the water delivered to the consumer should meet the high requirements of modern hygiene and should at least be free from pathogenic organisms and toxic substances [8,9].

2. MATERIALS AND METHODOLOGY

A total of 50 river/canal bank water samples were collected in sterilized plastic containers (Tarson) from the area of Western U.P. and Uttarakhand (India), one of them is shown in Figure 1. At each sampling site, composite samples were collected and pooled together as one sample.

Fig. 1: One of sampling sites.

Thermacol boxes containing ice packs were used to carry the samples to the laboratory for analysis. As soon as possible to prevent over growth of contaminating microorganisms and death of potential pathogens, thoroughly mixed water samples were streaked on different culture media using triple streaking method and for quantitative

estimation of bacteria, water samples were serially diluted (tenfold) in sterilized physiological saline in sterile screw capped tubes to get dilution 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}, 10^{-5}, 10^{-6} and 10^{-7}. Each of these dilutions (200µl each) was poured and spread on the surface of nutrient agar and blood agar media and incubated at 37^0C for 24 hrs. for the growth of microorganisms. After incubation period colonies were counted on the plates. The isolates were sub cultured on different media for the identification of pure culture. The number of colonies per ml of water was calculated by applying the formula:-

Bacteria ml of water = No. of colonies/Amount plated X Dilution factor

Then isolated strains were identified on the basis of colony characteristics, microscopic examination and biochemical characterization (catalase, oxidase and IMViC test).

3. RESULTS AND DISCUSSION

Most bacterial organisms have been implicated as causative agent of diseases [10]. The isolated and identified microorganisms in the present study become important when their impact is considered in terms of human health. As a result of the present scenario, all of 50 river/canal bank water samples yielded two or more than two species of bacteria. The result of total heterotrophic bacterial count (cfu/ml) is ranged between $21x10^5$ to $16.6x10^6$ as shown in Figure 2. But previous study showed that river water samples include total heterotrophic bacterial count ranged between $1.8x10^4$ to $2.0x10^5$ cfu/ml [11]. The number of microorganisms in water depends on the contamination and the ability of the organisms to survive and multiply [12]. The resulting difference in prevalence of isolated and identified microorganisms at different points of sampling could be due to flood carrying waste materials that enter the river and other forms of pollution from human activities. The significant increase of microbial load in rivers could lead to higher risk of infectious diseases [13].

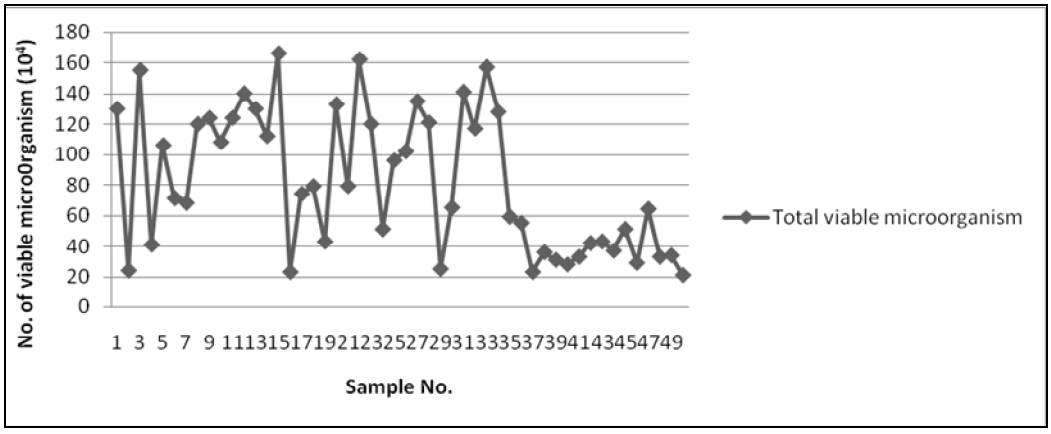

Fig. 2: Result shows total heterotrophic bacterial count (cfu/ml).

From all these samples 5 different bacterial genera were isolated, which includes *Escherichia coli* (80.0%), *Staphylococcus* spp. (70.0%), *Klebsiella* spp. (50.0%), *Streptococcus* spp. (50.0%), and *Proteus* spp. (30.0%). The data reveals that

Escherichia coli and *Staphylococcus* spp. occurred highest (80% and 70%) in water samples followed by *Klebsiella and Streptococcus spp.* (50.0%) while the lowest occurrence was recorded by *Proteus* spp. (30.0%), respectively, as shown in Figure 3.

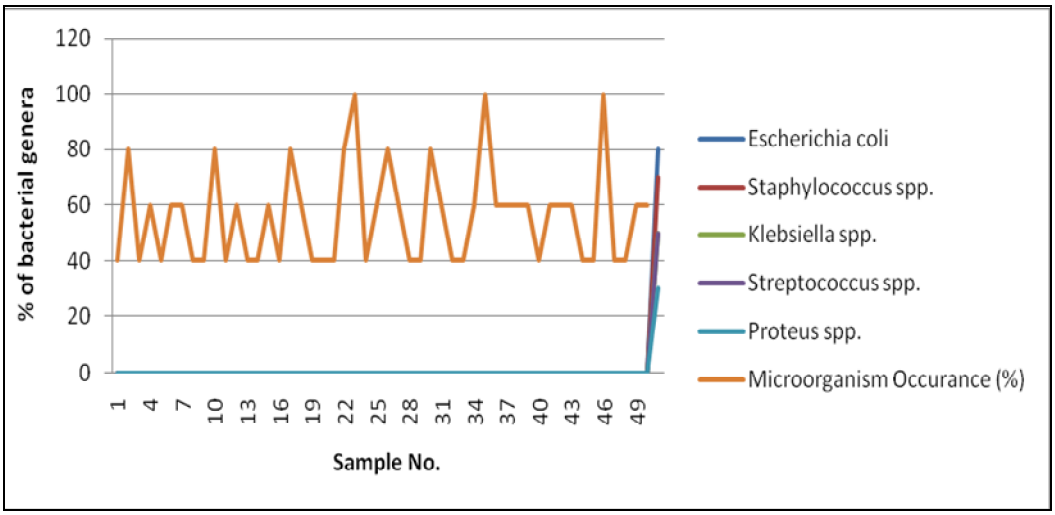

Fig. 3: Result shows % of isolated different bacterial genera per sample.

E. coli (50%) was isolated from stream water samples only; it indicated recent fecal contamination of the different sources [11]. This result is also supported by the other works [6,14,15]. While most strains of *E. coli* are non-pathogenic, some causes serious diarrheal infection in humans [14]. The higher bacterial concentrations also strongly linked to total coliform and faecal coliform [16]. Incidence of waterborne diseases such as dysentery, diarrhoea, typhoid and cholera, *etc.*, has been reported to cause millions of death in developing nations [17,18]. *Staphylococcus aureus* can survive for hours to weeks, or even months, on dry environmental surfaces, depending on strain [19]. Its incidence is from skin, soft tissue, respiratory, bone, joint, endovascular to wound infections. The frequency of detecting *Staphylococcus* sp. in recreational waters as well as illnesses of bathing people depending on the number of these bacteria suggests the necessity of monitoring these pathogens in surface waters used for recreational purposes [20]. *Klebsiella* spp. (80.0%) is ubiquitous in the environment and associated with contaminants like wastewaters, plant products, fresh vegetables, food with a high content of sugars and acids, frozen orange juice concentrate, sugarcane waste and living trees [6]. *Klebsiella* spp. can cause human disease, ranging from asymptomatic colonization of the intestinal, urinary or respiratory tract infections, wound infections to significant septicemia [21]. *Streptococcus* spp. (50%) isolated in some of the water sources might be due to fecal contamination of water sources [22]. This was supported that *Streptococcus* spp. is responsible for gastrointestinal illness among humans [23]. *Proteus* spp. (30.0%) is an enteric pathogen associated with the feces of animals including humans [15]. Its low percent occurrence might be due to the fact that it exists in minority of contaminating human feces [24]. *Enterobacter* spp. (50.0%) might be an implication of fecal contamination of the water sources [25]. Apart from fecal contamination, *Enterobacter* spp. might have been introduced from other sources like

soil, polluted water, and plants [15]. *Proteus species are* the causative agents of wound infections, septicaemia [26] and typhoid fever, dysentery, urinary tract infection, respectively [27].

4. CONCLUSION

The present study has revealed the microbial load of different river/canal bank sites of the area of Western U.P. and Uttarakhand (India). The present work is also shows that river/canal bank water is not free from enteric and other significant pathogens and might expose users to diseases ranges from dysentery, diarrhoea, skin, soft tissue, respiratory, urinary or respiratory tract infections, endovascular to wound infections and other significant diseases.

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