

# Microbial Contamination Assessment of Ganga River, Rae Bareli, Uttar Pradesh, India

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## ABSTRACT

We are aware that the majority of germs pose a risk to both people and animals. There are other microorganisms in the Ganga River. Examining the kind and quantity of bacteria found in contaminated and uncontaminated environments is fascinating. The large quantity of these bacteria causes numerous ailments in people and animals, even in the face of substantial untreated and contaminated effluent drainage from the leather industry, pesticide industry, paper mills, metropolitan centers, and other sources. The many types of bacteria found in the Ganga River and their interactions with their animal hosts were discovered in a contaminated aquatic environment. For the study of the Ganga Raebareli UP, a total of three sampling sites were chosen. Samples were taken from Gengaso Ghat, Dalmau Ghat, Gokana, or Gokarna Ghat Raebareli.

**Keywords:** Microbial Contamination, Ganga River, Rae Bareli, Uttar Pradesh and bacteria.

## INTRODUCTION

Their microbiological study is significant since Raebareli is a neighboring district of Lucknow, Unnao, Pratapgarh, Barabanki, and Amethi. The holy Ganga originates in Kanpur and flows from Raebareli district to Pratapgarh and Prayagraj. The three most well-known ghats in the Raebareli district are Sankatha Mata Mandir, which is located on the bank of the Ganga River at Gengaso Ghat; Sankat Mochan Hanuman Mandir and Dalmau Fort, which are situated on the bank of the Ganga River at Dalmau Ghat; and Shiv Mandir, which is located on the bank of the Ganga River at Gokana, or Gokarna Ghat Raebareli, where all Ghats experience daily maximum crowds [1-3].

Nothing can replace water as the most vital natural resource that we utilize on a daily basis. Freshwater availability is becoming increasingly scarce due to the world's rapid population growth, which poses a serious problem for developing nations like India. An ecosystem that is out of balance is being caused by point and non-point sources of pollution. For water to be fit for human consumption, it must be free of contaminants. Contaminated water systems increase high dangers to human health. In addition to affecting the death rate, water-borne illnesses are also hurting the ecosystem as a whole, which makes their approach unsustainable and puts the environment at risk [4]. Evaluation of the temporal and geographical patterns of water quality and microbiological pollution is crucial because of the longitudinal variation in rivers. In general, a water quality analysis will determine how much contamination is present in the water and whether or not it is safe for human consumption from a certain source. If ingested, the presence of indicator microorganisms raises the possibility of harm to the human population [5-7]. Coliforms indicate that human activity has contaminated water sources with organic stuff. Coliform bacteria can cause serious health issues if left untreated. To assess the quality of the water, several additional aspects, including waterborne infections, need to be looked into.

## MATERIALS AND METHODS

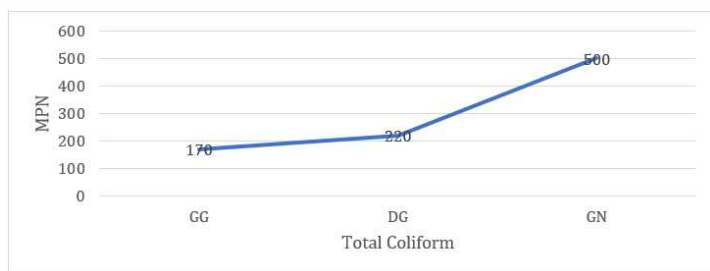
At Gengaso Ghat, Dalmau Ghat, and Gokana or Gokarna Ghat, water samples were collected. Then, they were aseptically transferred in sterile glass bottles to the Environmental Microbiology Departmental laboratory of Babasaheb Bhimrao Ambedkar University Lucknow. The summer was used to collect the samples. We estimated the water quality using the standard Most Probable Number (MPN) method. Coliforms were detected by inoculating the sample into a tube containing MacConkey broth and holding it there for 48 hours at 37°C. After being subcultured into Brilliant Green Bile Lactose Broth (BGBL), the positive tubes were incubated at 45°C. After 48 hours of incubation, the formation of gas shows the presence of faecal coli form. CFU/ml was computed using Nutrient Agar [8].

## RESULT AND DISCUSSION

Three Ganga River sampling sites (SS) from Raebareli district—Gengaso Ghat (GG), Dalmau Ghat (DG), and Gokana or Gokarna Ghat (GN)—have been assessed using a total coliform count study. At our first sampling sites, the total coliform count (TC) was 170 at GG, 220 at DG, and 500 at GN. According to the results, Gengaso Ghat had the lowest TC while Gokana or Gokarna Ghat had the most TC. It seems that new pathotypes arise from unique combinations of virulence genes [9]. Their genes are excellent candidates for molecular analysis of potential pathogenicity and pathotype typing because virulence factors directly influence the mechanism of pathogenicity. This is useful not only for medical diagnosis but also for processes like safety evaluations, food and water quality control, and other processes.

Because bacterial virulence genes have adapted to be host-specific, they may carry out various tasks throughout an infection. Because they may transmit not only between members of the same bacterial species but also between different bacterial species, they created a vast diversity of types

with varied pathogenicity within a species. Since plasmids and other mobile components include many E. Coli virulence genes, new pathotypes with unique combinations are constantly developing. It is also reasonable to anticipate a wide range of E. Coli strains with distinct virulence genes that, by themselves, do not produce any particularly hazardous phenotype. According to [10], these strains, which are mainly untyped or unanalyzed, can constitute a sizable ambient genetic reservoir for virulence features and might be crucial in the genesis of new illnesses. Studying the transfer of genes encoding virulence and antibiotic resistance within the bacterial flora is especially intriguing in this context [11-13].



**Figure 1. Total Coliform assessment of GG, DG and GN**

## CONCLUSION

In conclusion, the assessment of microbial contamination in the Ganga River at Rae Bareilly, Uttar Pradesh, India, highlights a significant environmental and public health concern. The presence of high levels of microbial contaminants, including potentially harmful bacteria and other microorganisms, indicates the urgent need for improved waste management and water treatment practices in the region. This situation not only poses a direct threat to the health of local communities relying on the river for various needs but also affects the ecological balance of the river ecosystem. Addressing this issue requires concerted efforts from government authorities, environmental organizations, and local communities to implement effective pollution control measures, enhance awareness about the impacts of contamination, and invest in sustainable solutions for water purification and waste management.

## REFERENCES

- Schubert, S., Rabin, A., Karch, H., Carniel, E. and Heesmann, J. (1998). Prevalence of the high pathogenicity island of *Yersinia* species among *Escherichia coli* strain that are pathogenic to humans. *Infect. Immun.* 66: 480-485.
- Kuhnert, P., Hacker, J., Muhldorfer, I., Burnens, A.P., Nicolet, J. and Frey, J. (1997). Detection system for *Escherichia coli* specific virulence genes: Absence of virulence determinants in B and C strains. *Appl. Environ. Microbiol.* 63: 703-709.
- Licht, T.R., Laugesen, D., Jensen, L.B. and Jacobsen, B.L. (2002). Transfer of the pheromone inducible plasmid pCF10 among *Enterococcus faecalis* Microorganism Colonizing the Intestine of Minipigs. *Appl. Environ. Microbiol.* 68(1): 187-193.
- Smallar, K., Hever, H., Gotz, A., Niemeyer, D., Krogemecklen post, E. and Tietz, E. (2000). Exogenous isolation of antibiotic resistance plasmids from piggery Manure Slurries Reveals a High Prevalence and Diversity of Inc. Q. Like Plasmids. *Appl. Environ. Microbiol.* 66: 48544862.
- Licht, T.R., Christensen, B.B., Krogfelt, K.A. and Molin, S. (1999). Plasmid transfer in the animal intestine and other dynamic bacterial population: the role of community structure and environment. 145: 2615-2622.
- Vinay S. Baghel, Krishna Gopal, Sanjay Dwivedi, Rudra D. Tripathi "Bacterial indicators of faecal contamination of the Gangetic River system right at its source". *Ecological Indicators* 5 (2005) 49-56.
- Dutta, V., Srivastava, R. K., Yunus, M., Pathak, S. A. V. V., Rai, A., & Prasad, N. (2011). Restoration plan of Gomti River with designated best use classification of surface water quality based on river expedition, monitoring and quality assessment. *Earth Science India*, 4.
- Parveen, S., Bharose, R., & Singh, D. (2017). Assessment of physico-chemical properties of tannery waste water and its impact on fresh water quality. *International Journal of Current Microbiology and Applied Sciences*, 6(4), 1879-1887.
- James, E., & Joyce, M. (2004). Assessment and management of watershed microbial contaminants. *Critical reviews in environmental science and technology*, 34(2), 109-139.
- Gutarowska, B., Skóra, J., Stępień, Ł., Szponar, B., Otlewska, A., & Pielech-Przybylska, K. (2015). Assessment of microbial contamination within working environments of different types of composting plants. *Journal of the Air & Waste Management Association*, 65(4), 466-478.
- Barbin, D. F., Elmasry, G., Sun, D. W., Allen, P., & Morsy, N. (2013). Non-destructive assessment of microbial contamination in porcine meat using NIR hyperspectral imaging. *Innovative Food Science & Emerging Technologies*, 17, 180-191.
- Kim, J. Y., Kim, S. R., Choi, J. G., Je, J. H., & Chung, D. H. (2006). Assessment of the level of microbial contamination in the processing company of sandwich products. *Journal of Environmental Health Sciences*, 32(4), 316-323.
- Hynds, P. D., Misstear, B. D., & Gill, L. W. (2012). Development of a microbial contamination susceptibility model for private domestic groundwater sources. *Water Resources Research*, 48(12).