

Unveiling the Bacteriophage Reservoir of the Ganga River: Ecological Roles, Environmental Drivers, and Biotechnological Potential



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ABSTRACT

Bacteriophages are key regulators of bacterial populations in aquatic ecosystems and are increasingly recognized for their ecological and applied significance. The Ganga River, one of the world's most important and culturally revered river systems, has long been associated with self-purifying properties that may partly reflect phage activity. However, rapid urbanisation, sewage discharge, industrial effluents, agricultural runoff, and religious practices have altered the river's microbial ecology and water quality, creating new challenges for understanding phage dynamics across the basin. This review synthesizes current knowledge on bacteriophage diversity, ecology, and functional roles in the Ganga River, with emphasis on their distribution across different stretches of the river and their association with host bacterial communities, physicochemical conditions, and pollution gradients. Available studies suggest the presence of diverse phage groups, including members of the families Myoviridae, Siphoviridae, Podoviridae, Microviridae, and other environmentally relevant viral taxa. Bacteriophages may contribute to microbial regulation, nutrient cycling, and ecological stability, while also offering potential applications in phage therapy, antimicrobial resistance control, wastewater treatment, bio-surveillance, and environmental bioremediation. The review also highlights major research gaps, including limited viromic data, insufficient genome-level characterization, and a lack of longitudinal studies spanning the full Ganga continuum. Understanding the phage reservoir of the Ganga River can inform river health assessment and the development of sustainable antimicrobial strategies in India.

Keywords: Ganga River, Phage Diversity, Health Risk, Ganga Pollution, Microbial Ecology

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1. Introduction

The River Ganga has long been venerated for its intrinsic self-cleansing and therapeutic properties, sustaining more than 450 million people who rely on its waters for diverse livelihood and cultural needs. The river originates from the melting of India's Himalayan permafrost. Several researchers have hypothesized that bacteriophages entrapped within Himalayan permafrost may be progressively liberated during thawing processes, thereby establishing a phage reservoir at Gaumukh- the source of the Ganga. Although this hypothesis remains empirically untested within the Ganga basin, it is grounded in established permafrost virology research conducted in Siberia and Antarctica. [1]. A distinct research team has identified a temperate bacteriophage from the Antarctic Dry Valley, which targets *Psychrobacter*, an extremophilic bacteria, and has analyzed its genetic attributes [2]. These findings together emphasize the need for further exploration of innovative opportunities for bacteriophages and their possible resurgence in the frozen Himalayan permafrost.

Water constitutes the most essential and invaluable resource for sustaining life on Earth [3]. India is abundantly endowed with water resources through its extensive network of rivers, which collectively fulfill the country's diverse water requirements [4].

The Ganga (Ganges) River is the world's third biggest river in terms of total water discharge. It originates in the western Himalayas from the Gaumukh ice cave (30°36'N; 79°04'E) in the Gangotri Glacier system, at an elevation of 4,100 m in Uttarkashi district, Uttarakhand. The river flows about 2,550 kilometres across the plains of Uttarakhand, Uttar Pradesh, Bihar, Jharkhand, and West Bengal, passing through several important towns such as Haridwar, Kanpur, Prayagraj (Allahabad), Patna, and Farakka before emptying into the Bay of Bengal [5] [6], [7], [8]. After passing through the Shivalik hills, the Ganga joins the plains near Haridwar and travels southward toward the plains of Uttar Pradesh. After leaving Uttar Pradesh, the river borders Bihar in the Rohtas district. It starts in Bihar and flows into Jharkhand's Sahibganj district before entering West Bengal and heading south. Approximately 40 kilometers downstream of Farakka, the river divides into two arms: the left arm flows eastward into Bangladesh, and the right branch, known as the Bhagirathi, flows southward through West Bengal. The Hooghly River is a part of the Bhagirathi that flows west and southwest of Kolkata. After entering Diamond Harbour, the river turns southward and divides into two streams before flowing into the Bay of Bengal [5], [9]. The Ganga River provides a key freshwater supply for almost 400 million people who live in its watershed and rely on it for their daily livelihoods.

The river has deep cultural and religious importance in India, and it is said to cleanse the soul. Additionally, it has been found to have antibacterial and therapeutic qualities [10], [11], [12].

For geographical, historical, sociological, and economic purposes, it is one of the most significant river for the Indian people [8], [13]. Ganga river water is frequently utilized for drinking and outdoor bathing by millions of people who become involved in ceremonial bathing rituals at least once annually along the whole length of the river, from Gangotri to Ganga Sagar, because of its profound socio-religious importance [5]. The Ganga encompasses a drainage basin of 861,404 km² within India, ranking 15th in Asia and 29th globally [4]. The Ganga River has the seventh greatest average annual water output on Earth, with 18,700 m³/s. The Ganga has significant flow variance within its catchment region, with a mean maximum flow of 468.7 × 10⁹ m³, accounting for 25.2% of India's total water resources [14]. The river system relies heavily on tributaries for freshwater flow, resulting in significant regional variation in water availability, ranging from 59,000 million m³ at Prayagraj (before confluence with the Yamuna) to 459,000 million m³ at Farakka in the lower reaches [4].

In recent decades, the Ganga River has faced escalating pollution driven by anthropogenic activities, rapid urbanization, open defecation, and the direct discharge of untreated wastewater through small drains into the river [15]. Despite anthropogenic pollution, the River Ganga supports extensive biodiversity owing to its intrinsic self-cleaning and regenerative properties. In 1896, British bacteriologist Ernest Hankin demonstrated the antimicrobial properties of Ganga water against *Vibrio cholerae*, the causative agent of cholera, observing that the pathogen was rapidly destroyed in Ganga water while thriving in tap water. Hankin proposed that a heat-labile, unknown substance capable of passing through fine porcelain filters was responsible for preventing cholera epidemics in downstream villages [16], [17]. To preserve the purity of the River Ganga, the Government of India launched the Ganga Action Plan (GAP) in 1986 with the objective of reducing pollution in the Ganga River [18]. The Ganga Action Plan was relaunched in 2009, with a rebuilt National Ganga River Basin Authority (NGRBA). The Ganga's water quality is decreasing due to excessive nutrient loading and eutrophication, which is causing the expansion of bacterial species that are detrimental to both aquatic ecosystems and human health [19]. River pollution is a critical and rising issue in most developing nations today. Rapid industrialization has led to a substantial increase in effluent discharge into natural water bodies. Industrial effluents and sewage that enter water bodies are significant causes of environmental toxicity, harming aquatic biota and decreasing water quality [5], [20]. Major contaminants found in water include volatile, biodegradable, and recalcitrant organic chemicals, poisonous metals, plant nutrients, suspended particles, microbial pathogens, and parasites [5].

Bacteriophages are associated with the distinctive properties of the River Ganga, and certain bacteriophages may remain stable under environmentally favorable conditions for extended periods [21], [22], [23]. Bacteriophages occupy all habitats worldwide where bacteria thrive. It has been estimated that for each bacterial cell, there exist ten bacteriophage particles. Viruses are considered obligate intracellular parasites that require a specific host cell for replication [23], [24].

In this review, we synthesize peer-reviewed studies through December 2025, prioritising research from the past decade, available data on PubMed, Web of Science, and Google Scholar by searching keywords such as "Ganga/Ganges bacteriophage," "Ganga metagenomic," and "river phage ecology," while also integrating seminal historical investigations of Ganga water and bacteriophages.

2. Microbial and Environmental Ecosystem of the Ganga River

2.1 Geographical, Hydrological and Physicochemical Features

Environmental pollution in the Ganga is caused by anthropogenic, agricultural, and industrial activities near aquatic environments. Given the crucial relevance of these ecosystems for varied water-based activities, aquatic systems are particularly susceptible, and such pollution has a negative impact on bacteriophage populations [25]. Compared to other examined riverine ecosystems, the Ganga River displays a significantly higher proportion of human population along its banks, leading to potentially larger pollution from industrial and human waste. Due to pollution, regular consumption of Ganga water or immersion in it today may cause serious illness in humans. We are approaching the solution to water pollution by microbial pathogens, including its impacts and implications, through the application of bacteriophage therapies [23]. Organization such as WHO, CPCB, BIS, ICMR, provide standards for the drinking water (Table 1) [26], [27]. According to standards established by WHO, CPCB, BIS, ICMR, ISI, and USEPA, water quality assessments revealed that approximately 70% of river water in India was contaminated, with some portions being too poor for human consumption [26], [27].

The principal reasons worsening the water quality of the River Ganga are the disposal of dead corpses, discharge of sewage and industrial waste, agricultural runoff, and the direct disposal of different veneration items into the river. To effectively maintain water quality through suitable management methods, continual monitoring of physicochemical parameters such as pH, temperature, turbidity, conductivity, total dissolved solids, dissolved oxygen, and biochemical oxygen demand is required. [28], pH is the most critical factor as it determines the alkalinity and acidity of river water. If the pH value falls below 6.5, it impairs the absorption of vitamins and minerals in aquatic organisms [28].

Table 1: Comparative water quality standards prescribed by ICMR, WHO, CPCB, BIS (IS 10500:2012), ISI, and USEPA

Parameter	ICMR	WHO	CPCB Surface Water Criteria	BIS IS 10500:2012 (Drinking Water)	ISI	USEPA
pH (units)	7.0–8.5	7.0–8.5	Class A: 6.5–8.5; Class B: 6.5–8.5; Class C: 6.5–9.0	Acceptable: 6.5–8.5; No relaxation	–	6.5–8.5*
Total Dissolved Solids (TDS, mg L ⁻¹)	500	500	–	Acceptable: 500; Permissible: 2000	–	500 (Secondary Standard)
Temperature (°C)	–	–	No significant deviation from natural conditions	–	–	–
Turbidity (NTU)	5	2.5	–	Acceptable: 1–5; Permissible: 10	–	≤ 1–5

Biochemical Oxygen Demand (BOD, mg L ⁻¹)	-	-	Class A: ≤2; Class B: ≤3; Class C: ≤3	Not specified	-	-
Dissolved Oxygen (DO, mg L ⁻¹)	-	-	Class A: ≥6; Class B: ≥5; Class C: ≥4	Not specified	-	-
Free CO ₂ (mg L ⁻¹)	-	10	-	10	-	-
Electrical Conductivity (μS cm ⁻¹)	-	-	-	750	-	-
Faecal Coliform (MPN 100 mL ⁻¹)	-	-	Class B (Bathing): ≤500 desirable; ≤2500 permissible	-	-	-
Faecal Streptococci (MPN 100 mL ⁻¹)	-	-	≤100 desirable; ≤500 permissible for bathing waters	-	-	-
E. coli / Thermotolerant Coliforms	-	Not detectable in 100 mL	-	Not detectable in 100 mL	-	Zero detectable organisms in drinking water
Total Coliforms	-	-	-	Not detectable in 100 mL	-	Total coliform rule applies

- **Abbreviations:** ICMR = Indian Council of Medical Research; WHO = World Health Organization; CPCB = Central Pollution Control Board; BIS = Bureau of Indian Standards; ISI = Indian Standards Institution; USEPA = United States Environmental Protection Agency; BOD = Biochemical Oxygen Demand; DO = Dissolved Oxygen; TDS = Total Dissolved Solids; NTU = Nephelometric Turbidity Unit
- **CPCB Surface Water Classification:** (Class A: Drinking water source without conventional treatment but after disinfection), (Class B: Outdoor bathing), (Class C: Drinking water source after conventional treatment and disinfection)

2.2 Microbial Diversity and Dynamics

Microorganisms in freshwater environments can be classified based on their feeding habits into two major groups: (1) autotrophs, which synthesize complex carbon compounds from environmental CO₂, this group includes microalgae and photosynthetic bacteria; and (2) heterotrophs, which include saprotrophs that acquire their food from non-living material either through direct uptake of dissolved molecules or indirect uptake via discharge of external enzymes followed by absorption of hydrolytic products. Biological analysis of the environment is instrumental in determining ecosystem health, as there exists a correlation between the chemical constituents (both organic and inorganic) and physical attributes of the water body with the microbial profile. One of the most effective approaches to determine this relationship is through the calculation of a diversity index, specifically the Shannon-Wiener diversity index, as it provides a mathematical framework to quantify species diversity within a particular ecosystem and further correlates this with the pollution level of the ecosystem.

Table 2: Classification of aquatic ecosystem health and pollution status based on Shannon diversity index (H'), Ref. [29]

Shannon Diversity Index (H')	Diversity Status	Indicative Pollution Level	Ecological Interpretation
> 4.0	Very High	Minimal or No Pollution	Highly diverse and stable microbial community; good ecological condition
3.0 – 4.0	High	Slight Pollution	Healthy ecosystem with minor environmental stress
2.0 – 3.0	Moderate	Light Pollution	Moderate diversity; signs of anthropogenic influence may be present
1.0 – 2.0	Low	Moderate Pollution	Reduced diversity indicating environmental disturbance and ecological stress
< 1.0	Very Low	Heavy Pollution	Severely impacted ecosystem dominated by a few tolerant taxa

This clear that the diversity level and pollution level is inversely proportional to each other i.e. when the diversity level is high then pollution level is less and when diversity level is low pollution level is high, the study conducted by Sood et al; 2010 [30] The diversity index of the lower Ganga River was identified as 1.5, and their study additionally demonstrated that the water quality of the river was correspondingly low. Hence, the microbial profile of the Ganga River reflects the pollution status of the river; therefore, the microbial profile of the Ganga has been determined several times, Mishra and Tripathi, 2008 [31], evaluated seasonal and temporal patterns in the bacteriological parameters of the River Ganga in Varanasi and revealed that the downstream stretch indicated a high bacterial concentrations, comprised of *Aerobacter aerogenes*, *A. cloacae*, *Micrococcus* sp., *Salmonella* sp., *Staphylococcus aureus*, *Bacillus* sp., and *Shigella* sp., indicating higher levels of fecal contamination in the water. Rai et al; 2010 [32] studied the microbial pollution if river Ganga at Varanasi during rainy and winter seasons. Kumar Singh *et al.* 2014 [33] studied the diversity of aquatic fungi in Ganga River at three banks of Varanasi in their study 23 microflora were identified to be dominant. Chauhan and Dhiman, 2015 [34] analysed the microbial diversity of river Ganga at Haridwar and

Rishikesh and reported the presence of *Staphylococcus aureus*, *Salmonella* sp., *Escherichia coli*, *Pseudomonas aeruginosa*, *Enterobacter aerogenes* and *Shigella* sp. Sinha and Paul, 2015 [35] analyzed the population of pollution indicator bacteria in river Ganga at Ichapore, West Bengal in their study all the bacterial population were abundant, Balagurunathan and Shanmugasundaram, 2015 [36] studied microbial diversity of major river basin of India and identified that Ganga has maximum microbial diversity followed by Cauvery, Krishna and Godavari basins. Basu et al., 2016 [37] they focused on the assessment of microbes (*Coliform* and *Enterobacteriaceae*) in and around Dakshineswar area of West Bengal. Niveshika et al., 2016 [38] isolate and characterized bacteria from Ganga River at Varanasi that have a capability to tolerate heavy metals. Vats, 2017 [39] analyzed microbiological characteristic of Ganga River from Kankhal to Bhogpur. Bisht et al., 2018 [40] studied bacterial diversity of Alaknanda River at Rudraprayag which give rise to river Ganga when unit with Bhagirathi at Devprayag and isolated bacterial species were identified as *Pseudomonas extremorientalis*, *Bacillus licheniformis*, *Paenibacillus glucanolyticus*, *Bacillus badius*, *Pseudomonas fulva*, *Pseudomonas azotoforman*, *Paenibacillus thiaminolyticus*. The latest comprehensive data is shown in the Table 3.

Table 3: Spatial and temporal distribution of dominant bacterial taxa and their ecological functions in the Ganga River (2020-2025)

Publication Year	Location	Dominant Bacterial Taxa	Major Ecological Functions	Ref.
2020	Farakka	<i>Streptomyces albogriseolus</i> , <i>S. aureus</i> , <i>S. bikiniensis</i> , <i>Rhodococcus erythropolis</i> , <i>R. qingshengii</i> , <i>Cupriavidus necator</i> , <i>C. taiwanensis</i> , <i>Paraburkholderia xenovorans</i>	OM, NC, PD	[41]
2020	Kanpur	<i>Pseudomonas citronellolis</i> , <i>Flavobacterium aquatile</i> , <i>Methylibium petroleiphilum</i> , <i>Pantoea agglomerans</i> , <i>Bordetella petrii</i> , <i>Flavobacterium aquatile</i> , <i>Methylibium petroleiphilum</i>	OM, NC, PD	[41]
2020	Gaumukh	<i>Bacillus circulans</i> , <i>Staphylococcus aureus</i> , <i>Serratia marcescens</i> , <i>Pseudomonas azatofixans</i> , <i>P. fluorescens</i>	OM, NC, PD	[42]
2022	Kanpur	<i>Fluviicoccus keumensis</i> , <i>Flavobacterium cheniae</i> , <i>Lacibacter cauensis</i> , <i>Flavobacterium sasangense</i> and <i>Flavobacterium cheonhonense</i>	OM, NC	[43]
2022	Mirzapur	<i>Arenimonas metalli</i> , <i>A. taoyuanensis</i> , <i>Sulfuricaulis limicola</i> , <i>Thiobacter sp.</i> , <i>Ahniella affigens</i>	SC, PD, NC	[43]
2022	Prayagraj	<i>Ahniella affigens</i> , <i>Thiobacter sp.</i> , <i>Caulobacter daechungensis</i> , <i>Gemmatimonas phototrophica</i> , <i>Caulobacter fusiformis</i>	SC, NC, OM	[43]
2022	Varanasi	<i>Candidatus Lloydbacteria</i> , <i>Candidatus Moranbacteria</i> , <i>Flavobacterium sasangense</i> , <i>Idiomarina sp.</i> , <i>Saccharofermentans acetigenes</i>	OM, NC	[43]
2022	Rishikesh	<i>Candidatus Lloydbacteria</i> , <i>Oleiharenicola alkalitolerans</i> , <i>Ohtaekwangia sp.</i> , <i>Solimonas sp.</i> , <i>Pseudoxanthomonas mexicana</i>	OM, NC, PD	[43]
2023	Barackpore	<i>Bacillus subtilis</i> , <i>Pseudomonas songnenensis</i>	OM, NC, PD	[44]
2023	Dakshineswar	<i>Bacillus subtilis</i> , <i>Pseudomonas songnenensis</i>		[44]
2023	Gangasagar	<i>Exiguobacterium aurantiacum</i>	OM, NC	[44]
2023	Kalyani-Kolkata Stretch	<i>Betaproteobacteria</i> , <i>Alphaproteobacteria</i> , <i>Gemmatimonadetes</i> , <i>Cytophagia</i> , <i>Planctomycetacia</i> , <i>Bacilli</i> , <i>Bacteroidia</i> , <i>Deltaproteobacteria</i> , <i>Flavobacteria</i> , <i>Actinobacteria</i> , <i>Gammaproteobacteria</i>	OM, NC, SC, PD	[45]
2023	Kanpur	<i>Streptomyces</i> , <i>Pseudomonas</i> , <i>Sphingomonas</i> , <i>Bradyrhizobium</i> , <i>Burkholderia</i> , <i>Azospirillum</i>	OM, NC, PD	[46]
2023	Farakka	<i>Pseudomonas</i> , <i>Streptomyces</i> , <i>Burkholderia</i> , <i>Sphingomonas</i> , <i>Bradyrhizobium</i>	OM, NC, PD	[46]
2024	Kanpur	<i>Acidovorax</i> , <i>Anaeromyxobacter</i> , <i>Bradyrhizobium</i> , <i>Burkholderia</i> , <i>Cupriavidus</i> , <i>Dechloromonas</i> , and <i>Ferribacterium</i> ,	NC, PD, IC	[47]
2024	Farakka	<i>Acidovorax</i> , <i>Anaeromyxobacter</i> , <i>Bradyrhizobium</i> , <i>Burkholderia</i> , <i>Cupriavidus</i> , <i>Dechloromonas</i> , <i>Ferribacterium</i>	OM, NC, PD	[47]
2024	Haridwar	<i>Sphingomonadaceae</i> , <i>Erythrobacteraceae</i> , <i>Moraxellaceae</i> , <i>Comamonadaceae</i> , <i>Caulobacteraceae</i> , <i>Rhodobacteraceae</i> , <i>Deinococcaceae</i> , <i>Burkholderiaceae</i> , <i>Xanthomonadaceae</i> , <i>Flavobacteriaceae</i> , <i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i> , <i>Rhizobiaceae</i> , <i>Planctomycetaceae</i>	OM, NC, PD	[48]
2025	Rishikesh	<i>Stutzerimonas stutzeri</i> , <i>Bacillus subtilis</i> , <i>B. cereus</i> , <i>Staphylococcus aureus</i> , <i>Pseudomonas sp.</i> , <i>B. pumilus</i>	OM, NC, PD	[49]
2025	Haridwar	<i>Bacillus altitudinis</i> , <i>Heyndrickxia sporothermodurans</i> , <i>Bacillus paralicheniformis</i> , <i>Pseudomonas songnenensis</i>	OM, NC, PD	[49]
2025	Kanpur	<i>Enterobacter hormaechei</i> subsp. <i>xiangfangensis</i> , <i>Pseudomonas aeruginosa</i> , <i>Bacillus sp. BSp-1</i>	OM, NC, PD	[49]
2025	Prayagraj	<i>Exiguobacterium mexicanum</i> , <i>E. acetylicum</i> , <i>Bacteroides caccae</i>	OM, NC	[49]
2025	Mirzapur	<i>Bacillus cereus</i> , <i>Staphylococcus hominis</i> , <i>Pseudomonas songnenensis</i>	OM, NC, PD	[49]
2025	Varanasi	<i>Pseudomonas sp. CE67</i> , <i>Bacillus subtilis</i> , <i>B. pumilus</i> , <i>Staphylococcus aureus</i>	OM, NC, PD	[49]
2025	Prayagraj	<i>Brachyobacterium</i> , <i>Dermabacteraceae</i> , <i>Geodermatophilaceae</i> , <i>Bacillus</i> , <i>Hyphomicrobiaceae</i> , <i>Thiobacillus</i> , <i>Anaeromyxobacter</i> , <i>Rheinheimera</i> , <i>Klebsiella</i> , <i>Methylomonas</i>	OM, NC, SC, IC	[50]
2025	Gaumukh-Rishikesh Stretch	<i>Thiobacillus</i> , <i>Sideroxydans</i> , <i>Burkholderia</i> , <i>Streptomyces</i> , <i>Gallionella</i> , <i>Pseudomonas</i> , <i>Acidovorax</i> , <i>Polaromonas</i> , <i>Methyllobacillus</i>	OM, NC, SC, IC, PD	[51]
2025	Haridwar	<i>Bacillus subtilis</i> , <i>B. cereus</i> , <i>Chromobacterium alkanivorans</i> , <i>Klebsiella pneumoniae</i> , <i>Delftia tsuruhatensis</i> , <i>Brevibacillus spp.</i> , <i>Lysinibacillus spp.</i> , <i>Sphingobacterium faecium</i>	OM, NC, PD	[52]

Abbreviations: OM = Organic Matter Degradation, NC = Nutrient Cycling, PD = Pollutant Degradation, SC = Sulphur Cycling, IC = Iron Cycling

2.3 Anthropogenic Influences and Faecal Pollution Load

The Ganga River serves a method of sustaining livelihood for approximately 400 million citizens who live around and along its banks and depend on the stream for their necessities. Meanwhile, driven by anthropogenic activities, habitual drinking of Ganga water or religious immersion in it may have significant deleterious health impacts [6]. The Ganga encompasses a drainage basin of 861,404 km² within India, ranking 15th in Asia and 29th globally. The river encompasses nearly one-quarter (26.2%) of India's geographic region. [4]. The Ganga River is predominantly polluted from three distinct sources: agriculture, industry, and city waste. Municipal sewage is the largest contribution, subsequent to industrial effluents and agricultural runoff. The river also hosts religious events, animal washing and watering, corpse disposal, and cremation procedures. Consequently, pollutants that originate in the Ganga may be generally classified into four categories: sewage pollution, industrial effluents, agricultural runoff, and religious activities.

Bacteriophage abundance exhibits a positive relationship with fecal pollution load across riverine sites. Elevated concentrations of fecal indicator bacteria in sewage-impacted stretches provide a larger host reservoir for phage replication, resulting in increased phage density. This finding supports the utility of bacteriophages as complementary indicators of fecal contamination and microbial dynamics in river ecosystems.

2.3.1 Sewage pollution

Sewage pollution is one of the primary factors influencing bacteriophage abundance and diversity in river ecosystems, as it introduces large numbers of bacteria into rivers, creating favorable conditions for bacteriophage proliferation. The emission of untreated wastewater sewage from urban settings is the primary source of Ganga water microbiological degradation. Effluent water contains organic materials, nutrients, inorganic matter, harmful compounds, and pathogens [53].

Several studies have demonstrated that water quality in the upper stretch of the Ganga (from Gaumukh to Haridwar), including at Rishikesh, does not meet criteria for safe consumption. Although water quality in Rishikesh is classified as "B category" (suitable for outdoor bathing) from 2019–2023, it exceeds permissible limits for drinking water due to elevated *E. coli* and total coliform levels [54]. In the upper Ganga, water quality deviations are minimal; however, in multiple locations along the middle and lower reaches, physicochemical and biological parameters exceed safe thresholds, rendering the water unsuitable for bathing and other livelihood-related uses [6]. About 75% of the pollutant load in the Ganga is derived from untreated or poorly treated municipal wastewater. Class I and II towns along the river contribute roughly 3,000 million liters per day (MLD) of sewage to the main stem, while installed sewage-treatment capacity falls far short of this input. Consequently, over three-quarters of the wastewater produced across India's northern plains is discharged into the Ganga without adequate treatment [55]. According to the Central Pollution Control Board (CPCB), in 1985 the 25 identified Class-I towns in Uttar Pradesh, Bihar, and West Bengal generated about 1,340 million liters per day (MLD) of municipal sewage. In response, the Ganga Action Plan (GAP) was launched in 1986; GAP Phase-I proposed construction of 35 sewage-treatment plants—3 in Uttarakhand, 10 in Uttar Pradesh, 7 in Bihar, and 15 in West Bengal—to reduce sewage pollution in the river [12]. GAP Phase-II, initiated in 1993, extended sewage-treatment interventions to several tributaries within the Ganga basin, resulting in the establishment of multiple STPs. Despite these investments, the programme did not meet its objectives for a range of technical, institutional, and operational reasons. The National Ganga River Basin Authority (NGRBA) was constituted in 2009 to coordinate basin-scale restoration and conservation efforts. Nonetheless, recent Central Pollution Control Board (CPCB) assessments indicate that the disparity between sewage generation and treatment capacity has widened substantially, with over half of the generated sewage still entering the Ganga—either directly or via tributaries—without adequate treatment, Table 4. According to Dwivedi et al; 2018 [6], the Ganga basin generates an estimated 8,250 MLD of municipal wastewater across 222 towns, while installed treatment capacity is approximately 3,500 MLD. Of the generated wastewater, about 2,538 MLD is discharged directly to the main stem of the Ganga, 4,491 MLD is delivered via tributaries, and the remainder is disposed of onto land or in low-lying areas. Among Class-I cities, West Bengal produces the largest proportion of sewage (~50%, ≈1,311 MLD), largely attributable to Kolkata (≈618 MLD), followed by Uttar Pradesh (~34%, ≈874 MLD), primarily from Kanpur (≈339 MLD) and Prayagraj (≈208 MLD). For Class-II towns, Uttar Pradesh contributes the greatest share (~52%, 63.5 MLD), followed by Bihar and Uttarakhand. Untreated sewage discharges are highest in West Bengal (≈548 MLD; 42% of its generated sewage) and Uttar Pradesh (≈461 MLD; 52% of its generated sewage) [6]. The Ganga basin produces roughly 12,000 MLD of municipal sewage, while installed treatment capacity is only about 4,000 MLD. Approximately 3,000 MLD of sewage enters the main stem from Class I and II towns situated along the river, but only about 1,000 MLD of treatment capacity has been established to handle this input. Industrial effluents account for roughly 20% of the pollutant load by volume; however, because they frequently contain toxic and non-biodegradable constituents, their ecological and public-health impacts are disproportionately large.

Key industrial pollution hotspots include the Ramganga and Kali catchments and the Kanpur industrial area, with tanneries in Kanpur and distilleries, paper mills, and sugar factories in the Kosi, Ramganga, and Kali basins identified as principal contributors [56]. According to Dwivedi et al. 2018 [6], Urban sewage generation across the five states of the Indo-Gangetic Plain (IGP) is estimated at 15,435 MLD, whereas installed treatment capacity amounts to only 3,458 MLD. Despite substantial financial investments, the volume of untreated sewage discharged into the Ganga in 2025 has increased by more than an order of magnitude relative to 1985, Table 4 [57].

Table 4: Temporal trend showing the widening disparity between sewage/wastewater generation and treatment capacity in the Ganga basin (values expressed in MLD)

Reference	[6]					[57]
	1985	2009	2012	2013	2015	2025
Sewage Generation	1340	2638	2723	8250	15,435	10,160
Treatment Capacity	-	1174	1208	3500	3458.43	7,820
Gap	-	1464	1515	4750	11,976.57	2,340

2.3.1.2 Temporal changes in microbial contamination of the Ganga River

The escalating discharge of untreated municipal wastewater into the Ganga has markedly elevated microbial loads throughout the river. Domestic sewage is the dominant source of these microbial contaminants, and progressive urbanization along the basin has driven pronounced declines in water quality. Faecal and total coliform counts (reported as MPN/100 ml) were highest in West Bengal and next highest in Uttar Pradesh in both pre- and post-NGRBA periods. Within Uttar Pradesh, Kanpur and Varanasi exhibited the greatest faecal coliform concentrations, reaching approximately 93,000 and 50,000 MPN/100 ml, respectively. In West Bengal, the most heavily impacted sites were Dakshineswar and Howrah, with peak faecal coliform levels of about 425,313 and 237,059 MPN/100 ml, respectively [6], [58]. Temporal trends indicate a modest decline in microbial contamination in Uttar Pradesh, Bihar, and West Bengal before the establishment of the NGRBA, whereas Uttarakhand exhibited a sustained upward trend. Measured microbial counts exceed regulatory thresholds by orders of magnitude relative to drinking-water (50 MPN/100 ml) and bathing-water (500 MPN/100 ml) standards. Spatially and temporally, the middle stretch (Uttar Pradesh) and lower stretch (West Bengal) consistently show the highest contamination levels, which correlate with the magnitude of wastewater inputs to those reaches. The pre-NGRBA reductions likely reflect STPs installed under the Ganga Action Plan; however, in recent years the divergence between sewage generation and treatment capacity has widened, driving renewed increases in microbial loads across states. Current analyses also show an expanded range (minimum to maximum) for most contaminants, indicating persistent hotspots with inadequate treatment infrastructure.

2.3.2. Industrial Effluent

Numerous industrial facilities discharge a variety of wastes into the Ganga basin; 956 of these units are concentrated in Uttar Pradesh alone. Reported industrial sectors include thermal power generation, electro-processing, textiles, wood and jute processing, sugar and distillery operations, pulp and paper production, synthetic rubber manufacturing, dairy processing, coal washeries (source of fly ash), pesticide production, dyeing operations, and tanneries [6]. Estimated industrial wastewater generation across the Ganga basin is approximately 2,500 MLD [59].

According to Dwivedi et al; 2018 [6], A total of 764 highly polluting industrial units—predominantly located in Uttar Pradesh—are reported to discharge effluents directly to the Ganga. The river stretch between Kannauj and Varanasi contributes the largest share of industrial wastewater inputs. Key industrial centres in Uttar Pradesh include Kanpur (tanneries), Prayagraj (engineering), and Varanasi (carpets and locomotive manufacturing), with the tannery sector accounting for the largest fraction ($\approx 58\%$) of grossly polluting industries. Two of India's three major tanning complexes are situated on the Ganga banks (Kanpur and Kolkata), and numerous small-scale tanneries across the basin further exacerbate contamination. In Kanpur, 151 tanneries are concentrated at Jajmou on the southern bank, discharging an estimated 5.8–8.8 MLD of wastewater; approximately 62 of these facilities use chrome-based tanning processes [60].

2.3.3 Agricultural Runoff

Agricultural runoff can significantly influence bacteriophage abundance, diversity, and distribution in river ecosystems. Runoff from croplands, livestock farms, and manure-amended fields transports bacteria, nutrients, organic matter, and associated bacteriophages into adjacent water bodies. The Indo-Gangetic Plain (IGP) is one of the world's largest fluvial plains. In India, it comprises approximately 13% of the national land area and includes the states of Uttarakhand, Uttar Pradesh, Bihar, Jharkhand, and West Bengal. These regions produce approximately 50% of India's total food grains, which feed 40% of the country's population [61]. In 2020, global agricultural pesticide use was approximately 3.39 million tonnes, of which India accounted for about 61,702 tonnes per year. India ranks fourth worldwide in pesticide production, after the United States, Japan, and China [62], [63]. Extensive pesticide application in agricultural areas of the river basin promotes environmental bioaccumulation via multiple pathways. These residues pose toxic risks to non-target biota, enable long-range transport, and degrade natural ecosystem conditions [64], [65], [66]. The total pesticide usage in the Ganga basin between 2012 and 2017 was 72,741 million tons, accounting for 27% of the country's total consumption [64]. In 2014, the pesticide consumption pattern was dominated by insecticides at 80%, followed by herbicides at 15% and fungicides at 2%. The most commonly used pesticides include phosphamidon, butachlor, mancozeb, quinalphos, monocrotophos, paraquat, endosulfan, and isoproturon [67]. Given the extensive pesticide application, the probability of pesticides entering aquatic systems via surface runoff, subsurface leaching, and flood events is elevated. Volatilized pesticides from soil and crops can be scavenged by precipitation, resulting in rainwater that, despite generally being regarded as safe, may carry pesticide residues and thus act as an additional pathway for contamination, as reported by Kumari et al. 2007 and Sakai 2002 [68], [69].

2.3.4 Pollution Due to Religious Activities

Religious activities along the Ganga River indirectly affect bacteriophage abundance and diversity by changing microbial loads, nutrient levels, and water quality. The Ganga is an integral part of Indian society, and its water is regarded as sacred, found in most Hindu households across the country, and strongly qualifies for inclusion in the Geographical Indication registry. Owing to its religious significance, Ganga water is incorporated into a wide range of yajña/homa and other ritual practices—such as Gangapūjā, Laghurudra, Maharudra, various Rudra and Chandi yagnas, Durgā and Gayatri rites, bhoomi pūjā,

śilānyāsa, murti pratishṭhā, vāstu and grah śānti ceremonies, śrādhā, nārāyanabali, śivliṅga abhiṣeka, and vivāha samskāra. For practicing Hindus, the river's water retains profound spiritual value throughout the life cycle; traditionally even a few drops administered at the time of death are believed to confer mokṣa (liberation) [70]. The Ganga basin includes numerous historic towns—Rishikesh, Haridwar, Garhmukteshwar, Kannauj, Prayagraj, Mirzapur, Varanasi, and Gangasagar—that function as major pilgrimage centres with continuous riverbank religious activities. Large-scale gatherings during festivals such as the Maha Kumbh and Makar Sankranti result in millions of participants undertaking ritual baths ("Ganga snāns"). Ritual offerings (e.g., sweets, milk, flowers, leaves, and lit earthen lamps), as well as the disposal of worn religious texts and idols, introduce organic and solid waste to the river. Furthermore, traditional funerary practices in some communities—including immersion of human remains and bone fragments—contribute additional biological and material inputs to the Ganga [6], [12]. The effects of various religious practices on Ganga water quality have been extensively investigated and are summarized below.

2.3.4.1 Religious Bathing

Daily bathing by millions occurs along the Ganga, with episodic peaks on particular auspicious dates when large congregations perform ritual immersions. The Kumbh Mela represents the largest such event; it is held sequentially at four pilgrimage sites—Haridwar (Har Ki Pauri), Prayagraj (Sangam), Nashik (Godavari Ghat), and Ujjain (Shipra Ghat)—with each location hosting the festival once every 12 years. Individual Kumbh celebrations extend for approximately six weeks [6]. During the Kumbh Mela, mass bathing occurs on designated river stretches and large numbers of devotees and ascetics camp along the Ganga throughout the event. Peak attendance on specific auspicious days—such as Makar Sankranti, Poush Purnima, Mauni Amavasya, Vasant Panchami, Magh Purnima, and Maha-Shivaratri—produces particularly dense bathing crowds. For example, the 2021 Haridwar Kumbh recorded an estimated 9.1 million bathers despite the concurrent COVID-19 pandemic [71]. At the 2025 Maha Kumbh in Prayagraj, an estimated 600 million ritual baths were recorded over a 45-day period. Peak attendance occurred on Mauni Amavasya, when approximately 50 million devotees undertook a holy dip in the Ganga [72]. Large-scale congregations substantially impair water quality through the introduction of surfactants (soaps, shampoos, detergents), solid wastes (plastic, fabric, general litter), and organic offerings (food items, flowers, milk, curd, ghee), all of which increase the pollutant load in the river. These ritual inputs therefore, represent a significant source of contamination to the Ganga. Environmental monitoring during the 2025 Maha Kumbh highlighted these impacts: Central Pollution Control Board (CPCB) data documented measurable deterioration in river-water quality, reflecting persistent systemic challenges in the management of India's water resources.

The CPCB conducted daily water-quality monitoring at five sites within Prayagraj and two upstream locations on the Ganga from 12 January to 4 February 2025. In a report to the National Green Tribunal, the agency documented markedly elevated faecal coliform concentrations during the Maha Kumbh, indicating the river was unsafe for bathing. Mean counts exceeded the regulatory limit by more than fourfold, reaching $\sim 11,000$ MPN/100 mL, and a peak measurement on 20 January attained $\sim 49,000$ MPN/100 mL—approximately 19 times the permissible threshold [73].

Another study by Mishra et al. 2025 [74] The study highlighted microbial contamination in the river water, showing a sharp increase in Total Coliforms, Faecal coliforms, *E. coli*, and *Enterococci* during the Kumbh—levels that far exceed CPCB and WHO limits. This rise indicates significant faecal contamination and poses public health risks linked to mass gatherings and ritual bathing. Although partial improvement was observed after the Kumbh, contamination levels remained above safe standards, (Table 5). The presence of faecal coliforms in Ganga water signals the presence of pathogenic microorganisms that can cause various waterborne diseases. Religious activities along the Ganga may indirectly affect bacteriophage abundance by increasing microbial and organic matter inputs into the aquatic environment. Mass bathing events, ritual offerings, and heightened human activity during pilgrimage seasons can raise bacterial host densities, which in turn promotes bacteriophage persistence and replication. As a result, river sites with intensive religious activity tend to show higher phage concentrations compared to less frequented stretches of the Ganga.

Table 5: Comparison of microbial contamination levels in river water during Maha Kumbh 2025 with WHO and CPCB guideline values [74]

Microbial Parameter	Permissible Limit (WHO/CPCB) (MPN 100 mL ⁻¹)	Observed Concentration (MPN 100 mL ⁻¹)	Exceedance Factor*	Water Quality Status
Total Coliforms	500	50,000	100×	Severely contaminated
Faecal Coliforms	2,500 (500 desirable)	1,400	Within maximum permissible limit; 2.8× above desirable limit	Moderately contaminated
Escherichia coli (E. coli)	200	5,800	29×	Severely contaminated
Enterococci	100	900	9×	Highly contaminated

- *Exceedance Factor = Observed concentration ÷ Permissible limit
- **Key Interpretation:** (Total coliforms exceeded the permissible limit by 100-fold, indicating substantial microbial contamination); (*E. coli* concentrations were approximately 29 times higher than recommended limits, suggesting significant faecal pollution); (Enterococci levels exceeded guideline values by 9-fold, indicating increased health risks associated with recreational water use); Although faecal coliforms remained below the CPCB maximum permissible limit for bathing waters (2,500 MPN 100 mL⁻¹), they substantially exceeded the desirable limit (500 MPN 100 mL⁻¹).

2.3.4.2. Pollution associated with ritual idol immersion

Idol immersion activities may indirectly affect bacteriophage communities in the Ganga River through increased inputs of organic matter, suspended solids, and anthropogenic contaminants. The resulting changes in bacterial abundance and community composition can influence phage replication dynamics, leading to localized variations in bacteriophage abundance and diversity following immersion events. In India, numerous religious activities occur throughout the year. Durga Pujā is a major festival in West Bengal, Bihar, and Uttar Pradesh, and over the past 15 years celebrations of Lakshmi Pujā and Ganesh Chaturthi have also increased in Uttar Pradesh and Bihar. Idols used in these rituals are typically constructed from plaster of Paris, clay, cloth, metal rods, and bamboo, and are finished with varnishes and water-based paints. Upon immersion, these materials can alter water quality: the pigments and coatings commonly contain heavy metals such as mercury (Hg), cadmium (Cd), arsenic (As), zinc (Zn), chromium (Cr), and lead (Pb). Certain colourants (red, blue, orange, green) often include Hg, ZnO, Cr, and Pb, which are associated with toxic and carcinogenic effects; lead and chromium are additionally introduced via sindoor (a traditional red cosmetic). As idols deteriorate in aquatic environments, released particulates and organic matter contribute to eutrophication, changes in pH, and elevated concentrations of heavy metals in the receiving water bodies, Table:6 (A and B) [75] [6], [76].

According to the Lal 2021 [76], An estimated 100,000 ritual idols are immersed annually in water bodies across India.

According to the recent reports of the State Pollution Control Board (SPCB) [76], A delayed monsoon has exacerbated pollution in the Ganga, with conditions projected to deteriorate further during winter. At Bithoor—where the river enters Kanpur—the water remains relatively clear (dissolved oxygen, DO = 7.6 mg L⁻¹), but DO declines downstream, reaching 6.3 mg L⁻¹ at the Jajmau stretch within the city, which is identified as the most contaminated segment. For context, the reported acceptable DO threshold for a drinking-water reservoir is 4 mg L⁻¹. The report also attributes part of the observed water-quality degradation to the mass immersion of idols during Ganesh Chaturthi. Another study by Das et al. 2025 [77], a delayed monsoon has intensified pollution in the Ganga, with conditions expected to deteriorate further during winter. At Bithoor, where the Ganga enters Kanpur, the water remains relatively clear, but pollution increases downstream. The most contaminated section is at Jajmau, within the city limits. Dissolved oxygen (DO) levels measure 7.6 mg per litre at Bithoor but decline to 6.3 mg per litre at Jajmau. The report notes that 4 mg per litre is the acceptable DO level for drinking water reservoirs. It also highlights that the immersion of numerous idols during Ganesh Chaturthi has already negatively impacted water quality.

Table 6 (A): Primary target organs/systems and associated health effects of selected heavy metals commonly detected in aquatic environments. [75]

Metal	Primary Target Organ/System	Major Health Hazards
Mercury (Hg)	Nervous system, kidneys, respiratory system, gastrointestinal tract	Neurotoxicity (tremors, confusion, insomnia, neurasthenia), nephrotoxicity, gingivostomatitis, hypersensitivity reactions (Pink disease), vomiting, diarrhoea, gastroenteritis, respiratory irritation, chest pain, dyspnoea, skin and eye irritation, weight loss.
Cadmium (Cd)	Lungs, kidneys, skeletal system	Pneumonitis, pulmonary oedema, proteinuria, nephrotoxicity, osteomalacia, osteoporosis, bone fragility, and increased risk of lung cancer.
Cobalt (Co)	Respiratory system, cardiovascular system, thyroid gland, liver, kidneys	Pulmonary fibrosis, asthma, irritation of the skin, eyes, nose and throat, cardiotoxicity, thyroid dysfunction, liver and kidney damage, reproductive toxicity, and potential carcinogenicity.
Zinc (Zn)	Gastrointestinal system, pancreas, hematopoietic system, skeletal system	Metal Fume Fever (MFF), nausea, vomiting, diarrhoea, abdominal pain, copper deficiency-induced anaemia, neurological degeneration, osteoporosis, pancreatic dysfunction, and reduced HDL cholesterol levels.
Chromium (Cr)	Respiratory system, kidneys, liver, skin	Gastrointestinal haemorrhage, haemolysis, acute renal failure, liver damage, pulmonary fibrosis, pulmonary oedema, respiratory tract irritation, nasal septum perforation, lung cancer, skin ulceration, allergic contact dermatitis, and tooth discoloration.
Lead (Pb)	Nervous system, kidneys, hematopoietic system, gastrointestinal system	Anaemia, abdominal pain, nephropathy, peripheral neuropathy (wrist-drop, foot-drop), encephalopathy, headaches, convulsions, ataxia, cognitive impairment, developmental delays, behavioural disorders, speech and hearing deficits, and irreversible neurological damage, particularly in children.

Abbreviations: MFF = Metal Fume Fever; HDL = High-Density Lipoprotein; Hg = Mercury; Cd = Cadmium; Co = Cobalt; Zn = Zinc; Cr = Chromium; Pb = Lead

Table 6 (B): Primary target organs/systems and associated health effects of selected non-metallic pollutants commonly detected in aquatic and industrial environments. [75]

Pollutant	Primary Target Organ/System	Major Health Hazards
Gypsum (CaSO ₄ ·2H ₂ O)	Respiratory system, auditory system, musculoskeletal system, nervous system	Respiratory irritation, breathing difficulties, chest discomfort, tinnitus, ear discharge, abnormal muscle tension, muscle numbness, joint pain, and neurological symptoms following prolonged exposure to dust.
Sulphur Compounds	Respiratory system, cardiovascular system	Asthma exacerbation, bronchitis, irritation of the nose, throat, and lungs, coughing, wheezing, excessive mucus production, choking sensation, reflex bronchoconstriction, and increased risk of cardiovascular disorders.
Phosphorus Compounds	Cardiovascular system, respiratory system, skin, eyes	Arterial calcification and hardening, increased risk of cardiovascular disease, coughing, wheezing, skin irritation, eye irritation, and potential ocular damage following excessive exposure.
Magnesium Compounds	Respiratory system, nervous system	Metal fume fever-like symptoms, coughing, chest tightness, headache, fever, chills, respiratory irritation, and metallic taste in the mouth.

Abbreviations: CaSO₄·2H₂O = Calcium sulfate dihydrate (Gypsum); MFF = Metal Fume Fever

2.3.4.3. Dead Body Cremation

Among anthropogenic activities, cremation practices represent a unique source of organic and nutrient inputs to the river ecosystem. Although their contribution is likely lower than that of municipal sewage, localized increases in microbial abundance near cremation ghats may create favourable conditions for bacteriophage persistence and replication. Therefore, cremation-related inputs should be considered as a potential factor influencing phage dynamics in culturally significant river stretches. Many Hindus believe that dying and being cremated on the banks of the Ganga—particularly in Varanasi—facilitates liberation from the cycle of rebirth. Consequently, thousands of cremations occur daily along the river. A study covering 2009–2011 reported that the two principal cremation grounds in Varanasi (Harishchandra Ghat and Manikarnika Ghat) averaged approximately 32,000 cremations per year [6], [75]. Study by Khwairakpam et al. 2018 [78] has shown an increase in the number of cremations, especially in Manikarnika ghat. The daily number of cremations rose from 410 in 2009 to 490 in 2012, indicating a clear upward trend. Following cremation, ashes and partially combusted remains are deposited in the Ganga, and family members often consign ashes from cremations performed elsewhere to the river for religious reasons. In addition, substantial numbers of uncremated human bodies (including women, children, ascetics, victims of envenomation, and persons with dermatological conditions) and numerous animal carcasses—predominantly cattle—are directly immersed.

These practices contribute both to deterioration of water quality and to the visual degradation of the riverine environment.

3. Diversity and Ecology of Bacteriophages in the Ganga

The Ganga has long been celebrated for purported self-purifying and therapeutic properties, a perception often attributed to its diverse assemblage of bacteriophages [79]. Bacteriophages are viruses that infect prokaryotes, including both eubacteria and archaea [80] that attacks on the bacteria at specific sites of their host organisms. They are abundantly present in Ganga water, where they thrive and demonstrate a strong capability to combat harmful bacteria [81], [82]. Their presence in the river has been documented historically, supporting the well-recorded self-cleansing and healing properties attributed to Ganga water. [83]. Under polluted conditions, the diverse bacteriophages in the Ganga interact with microbial hosts and can significantly influence bacterial populations [84]. Bacteriophages encapsulate their nucleic acid (DNA or RNA) within an icosahedral protein capsid and characteristically possess a tail structure composed of a helical contractile sheath surrounding a central core tube, terminating in a baseplate with tail fibers. Phage surface receptor proteins mediate specific recognition and attachment to complementary molecules on the bacterial host cell surface [85]. Bacteriophages are categorised according to the nature of their genomic nucleic acid into four principal groups: single-stranded DNA (ssDNA) phages, double-stranded DNA (dsDNA) phages, single-stranded RNA (ssRNA) phages, and double-stranded RNA (dsRNA) phages [85] (Figure 1).

Bacteriophages are acellular biological agents devoid of intrinsic metabolic machinery and therefore function as obligate intracellular parasites. They depend on bacterial host cells for replication, deploying their genomes to subvert host biochemical pathways and synthesise progeny virions [85]. Morphologically, bacteriophages exhibit a defined three-dimensional architecture: an icosahedral protein capsid enclosing the genome, a helical contractile tail surrounding a central core tube, and typically six tail fibers attached to a baseplate. The baseplate bears receptor-binding proteins that mediate specific recognition of bacterial surface molecules. These viruses are host-specific and can regulate bacterial populations in aquatic ecosystems, thereby contributing to microbial community balance and potentially lowering the risk of waterborne infections in humans exposed to the water [82], [86].

In 1896, Ernest Hanbury Hankin reported bacteriophages in Indian river waters that exhibited antibacterial activity against *Vibrio cholerae* [87]. After Felix d'Hérelle's work, he advocated using bacteriophages therapeutically and reported successful phage treatments for Shigella dysentery in France and for cholera control in India. Phage therapy has also been applied against Staphylococcus skin infections. These findings have motivated interest in the Ganga as a source for isolating phages and developing novel antimicrobials. Nevertheless, the diversity, abundance, and ecological functions of bacteriophages in aquatic environments remain largely uncharacterized. Recent research has therefore focused on characterizing phage diversity to evaluate their potential as biological control agents [18]. The phage population caused a rapid decline in the host bacterial population, after which phage abundances decreased—likely reflecting intraspecific competition among phages. Subsequent evolution of bacterial resistance permitted host populations to rebound, a process that was associated with an increase in phage diversity [88]. Subsequent work showed that parasite (phage) diversity exerts rapid effects on host-parasite population dynamics and evolutionary trajectories by selecting for diverse resistance mutations, thereby modulating the magnitude and tempo of bacterial suppression and recovery [88]. Since then, phage therapy has been regarded as a significant therapeutic tool and the sole treatment for bacterial infections [89].

In 1915 d'Hérelle advanced the lysis hypothesis—accounting for the observed plaque (halo) phenomenon—and proposed therapeutic applications for phage preparations. By 1917, he had reported successful use of bacteriophages in treating dysentery in France and in controlling cholera outbreaks in India [90]. Phage therapy subsequently developed as a clinical practice. The G. Eliava Institute of Bacteriophages in Tbilisi, Georgia—established in 1933 by George Eliava, a former collaborator of d'Hérelle—became and remains a principal centre for phage research. Initially regarded as a potent and, in some contexts, the sole treatment for bacterial infections, phage therapy was largely abandoned internationally after World War II following the widespread adoption of antibiotics. Nevertheless, geopolitical factors and constrained antibiotic access in some Eastern Bloc countries sustained phage therapy programs there, enabling the continued operation of institutions such as the Eliava Institute into the present day [89]. Commercial production of bacteriophage preparations active against *Staphylococcus* spp., *Streptococcus* spp., *Pseudomonas* spp., *Proteus* spp., and *Shigella* spp.

persisted until the mid-1950s at the G. Eliava Institute of Bacteriophages, Microbiology and Virology (EIBMV) and at Poland's Hirsfeld Institute of Immunology and Experimental Therapy (HIEET) [91]. The advent of antibiotics—with their broad-spectrum antibacterial efficacy—and apprehensions regarding the therapeutic use of bacteriophages precipitated a decline in phage therapy's widespread adoption. Nonetheless, phage-based treatments for human conditions (including skin infections, wound prophylaxis, burns, respiratory infections, and sepsis) have been employed intermittently for close to nine decades [92].

Multidrug-resistant pathogenic bacteria presently constitute a major scientific and public-health challenge, imposing substantial socio-economic burdens [89]. To address multidrug resistance, researchers are investigating alternative antimicrobial strategies. Promising approaches include the use of predatory bacteria (e.g., *Bdellovibrio bacteriovorus*, *Micavibrio aeruginosavorus*), antimicrobial peptides derived from amphibians and reptiles (such as frogs, alligators, and cobras), and metal-based agents (notably copper and silver) [93]. Among the emerging alternatives, bacteriophages—viruses that specifically infect and lyse bacteria—are especially promising. In natural ecosystems, most bacterial taxa are associated with specific predatory phages capable, in many instances, of causing host population collapse, which positions these viruses as potential biological control agents [94].

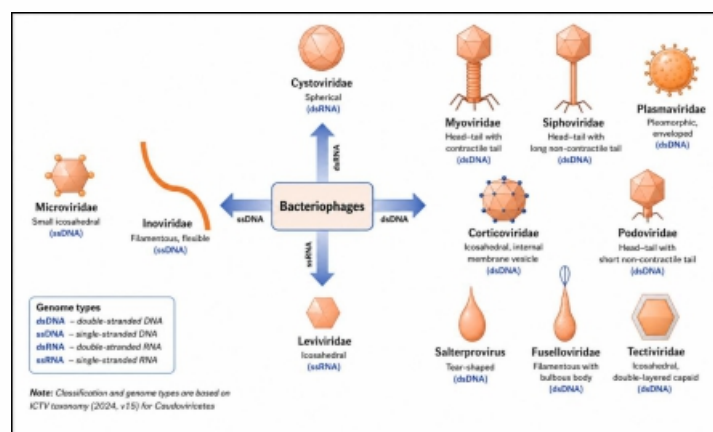


Figure 1: ICTV-Based Classification of Bacteriophages According to Morphology and Nucleic Acid Type

4. Phage-Host Interaction

Upon infection, bacteriophage-host interactions can result in host cell lysis or in non-lytic associations such as lysogeny or chronic infection. Lytic (virulent) phages introduce their genomes into the bacterial cytoplasm, replicate using host machinery, and subsequently lyse the cell to liberate progeny virions. Temperate (lysogenic) phages, after genome entry, may follow a lytic pathway or integrate their nucleic acid into the bacterial chromosome, replicating passively with the host without immediate production of virions [95]. An integrated phage genome is termed a prophage; in response to specific induction signals, the prophage can reactivate and enter the lytic cycle. In pseudo-lysogeny, phage nucleic acid persists as an episome rather than integrating into the host chromosome. When environmental conditions become favourable, the phage may proceed to either lytic replication or establish lysogeny. This flexibility is thought to support phage persistence and survival during adverse growth conditions in natural habitats [96], [97] (Figure 2).

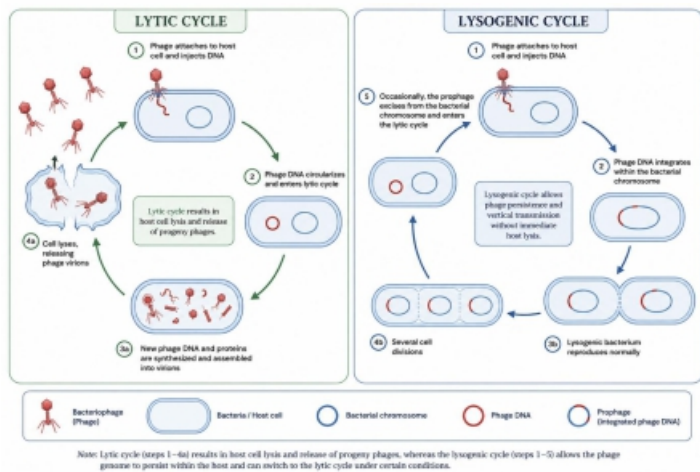


Figure 2: Schematic representation of the lytic and lysogenic life cycles of bacteriophages, illustrating host infection, genome replication, prophage integration, and phage progeny release [98]

5. Diversity of Bacteriophages in River Ganga

Surveys of the Ganga have revealed representation from multiple bacteriophage families. Over the past five decades, more than 5,100 phage isolates have been described, with over 90% being tailed phages that are taxonomically assigned to the Myoviridae, Siphoviridae, and Podoviridae groups [80], [99], [100], [101]. Over 2,200 complete bacteriophage genomes are deposited in the NCBI Genome database. Viral taxonomy is overseen by the International Committee on Taxonomy of Viruses (ICTV), with bacteriophage-specific guidance provided by its Bacterial and Archaeal Subcommittee. Phage classification integrates multiple attributes, including genome architecture, particle morphology, host range, sequence homology, and pathogenic potential (see Table 7). To date, the ICTV recognizes 19 families within the order Caudovirales; among these, Myoviridae, Podoviridae, Siphoviridae, Microviridae, and Inoviridae are the most extensively characterized, while Herelleviridae and Ackermannviridae have been more recently delineated [102]. According to Behera et al [18], In the Ganga River, two sampling sites were identified: a polluted site (Kanpur) and a non-polluted site (Farakka). At the polluted Kanpur site, higher numbers of bacteriophages belonging to Mimiviridae, Phycodnaviridae, Iridoviridae, Marseilleviridae, Papillomaviridae, Retroviridae, Myoviridae, and Podoviridae were abundantly present. In contrast, at the non-polluted Farakka site, bacteriophage diversity included Poxviridae, Baculoviridae, Caulimoviridae, Adenoviridae, and Tectiviridae.

Table 7: Major bacteriophage families classified according to ICTV, their genomic characteristics, morphology, and representative members current taxonomy (2024–2025) [107], [108]

Family	Genome Type	Virion Morphology	Distinguishing Characteristics	Representative Phage
Myoviridae	Linear dsDNA	Non-enveloped, icosahedral head with contractile tail	Long contractile tail facilitating DNA injection into host cells	T4 phage
Podoviridae	Linear dsDNA	Non-enveloped, icosahedral head with short tail	Short non-contractile tail	T7 phage
Siphoviridae	Linear dsDNA	Non-enveloped, icosahedral head with long flexible tail	Long non-contractile tail	Lambda (λ) phage
Herelleviridae	Linear dsDNA	Non-enveloped, tailed phages	Large virulent phages primarily infecting Gram-positive bacteria	Bacillus phage SPO1
Tectiviridae	Linear dsDNA	Non-enveloped, icosahedral	Internal lipid membrane beneath capsid	PRD1
Rudiviridae	Linear dsDNA	Non-enveloped, rod-shaped	Hyperthermophilic archaeal viruses with rigid rod morphology	SIRV1
Lipothrixviridae	Linear dsDNA	Enveloped, filamentous or rod-shaped	Flexible enveloped filaments infecting archaea	Thermoproteus virus TTV1
Corticoviridae	Circular dsDNA	Non-enveloped, icosahedral	Internal lipid membrane; infects Gram-negative bacteria	PM2

Besides these site-specific phages, some phages were commonly identified at both locations: Asfarviridae, Circoviridae, Herpesviridae, Nimaviridae, Geminiviridae, Ascoviridae, Hepadnaviridae, Bicaudaviridae, Alloherpesviridae, Polyomaviridae, Reoviridae, Inoviridae, and Anelloviridae. The Ganga River showed higher concentrations of Microviridae and ssDNA viruses in polluted areas near Kanpur, while non-polluted sites like Farakka exhibited more Myoviridae. Currently, scientists are using bacteriophages in several research areas. Similarly, research on the river Ganga for bacteriophages by Samson et al [103], conducted from Haridwar to Bhagalpur across two seasons explored nearly ten phage diversities in the Ganga River. Mimiviridae, Siphoviridae, Myoviridae, Podoviridae, Herpesviridae, Phycodnaviridae, Pithoviridae, Marseilleviridae, and Poxviridae were abundantly identified. The potential benefits of using bacteriophages isolated from Ganga water as an alternative to antibiotic treatment in phage therapy have increased, as antibiotic resistance in bacteria has risen due to the widespread use of antibiotics for treating bacterial infections [86], [104]. Additionally, 40 percent of the bacteria in the Ganga showed resistance to semisynthetic drugs such as ampicillin and amoxicillin. The river Ganga was also examined for the presence of multi-drug resistant (MDR) bacteria, Amp-C traits, and ESBL (extended-spectrum beta-lactamase) bacteria [86], [105]. The bacteriophage diversity in the Ganga River is markedly greater than in other Indian rivers. For example, while the Ganga harbors approximately 1,100 types of bacteriophages, rivers like the Yamuna and Narmada show significantly fewer varieties, with fewer than 200 types reported. This vast diversity is essential for maintaining the ecological balance and health of the river's microbial ecosystem. The predominance of bacteriophages in the Ganga suggests a natural mechanism for environmental regulation. These viruses help mitigate the impact of pathogenic bacteria, which is crucial for preserving the river's health, particularly in areas heavily affected by industrial pollution and urban waste [106]. Thus, the diverse bacteriophage community helps maintain ecosystem balance, supporting water quality and reducing health risks for communities that depend on the river [18]. The Ganga River hosts a diverse array of bacteriophages, including notable families such as Microviridae, Myoviridae, Mimiviridae, and Retroviridae. This diversity is shaped by environmental conditions, pollution levels, and the unique microbial communities in the river, especially at both polluted and non-polluted sites.

Plasmaviridae	Circular dsDNA	Enveloped, pleomorphic	Lack rigid capsid structure; infects mollicutes	Acholeplasma virus L2
Fuselloviridae	Circular dsDNA	Enveloped, spindle-shaped	Lemon- or spindle-shaped archaeal viruses	SSV1
Inoviridae	Circular ssDNA	Non-enveloped, filamentous	Chronic infection without host lysis	M13
Microviridae	Circular ssDNA	Non-enveloped, icosahedral	Small ssDNA phages infecting bacteria	ΦX174
Cystoviridae	Segmented dsRNA	Enveloped, spherical	Lipid-containing bacteriophages with segmented genome	φ6
Leviviridae	Linear ssRNA (+)	Non-enveloped, icosahedral	Small RNA phages infecting enteric bacteria	MS2

Abbreviations: dsDNA, double-stranded DNA; ssDNA, single-stranded DNA; dsRNA, double-stranded RNA; ssRNA, single-stranded RNA; ICTV, International Committee on Taxonomy of Viruses.

The Mimiviridae family is also present in the Ganga, recognized for its large size and complex structure. Mimiviruses possess unique characteristics that distinguish them from typical bacteriophages, and their presence in the Ganga contributes to the ecological complexity of the river's virome. Their ecological role includes interactions with various microbial hosts, which can shape community dynamics [18].

6. Bacteriophages as Indicators of Water Quality

Faecal indicator microorganisms are widely used to assess microbiological water quality because their occurrence signifies faecal pollution and the possible presence of enteric pathogens. Common faecal indicator bacteria (FIB) comprise total coliforms, faecal coliforms, *Escherichia coli*, *streptococci*, and *enterococci* [109]. Bacteriophages targeting enteric bacteria have been proposed as surrogate indicators of faecal and viral contamination. Relative to conventional bacterial indicators, these phages are often more abundant and more persistent in the environment, and they can better reflect risks associated with viral pathogens. Because they are excreted in faeces and generally do not replicate outside of metabolically active hosts, bacteriophages reliably signal recent faecal inputs. Moreover, phages that infect intestinal bacteria disperse and persist in the environment in ways analogous to human enteric viruses, so their occurrence and fate can serve as a proxy for viral contamination. Routine monitoring of every specific viral pathogen is neither practical nor cost-effective—especially in low-resource settings—so readily detectable bacteriophages have been adopted in many water-quality guidelines as operational indicators of faecal and viral pollution [110], [111], [112].

6.1 Families of Bacteriophages Used as Indicators of Faecal Pollution

Bacteriophages infecting enteric bacteria are typically categorised into three taxonomically distinct groups: somatic coliphages, F-specific (or male) coliphages, and phages that target *Bacteroides* spp. [110], [113]. Enterophages—phages that infect *Enterococcus* spp.—are less commonly used but represent promising indicator organisms because they are abundant in wastewater, exhibit survival characteristics comparable to enteric viruses, and display prevalence patterns that vary between human and animal gut microbiota [114], [115]. Somatic coliphages comprise a heterogeneous collection of phages that infect *Escherichia coli* and other coliforms by binding to receptors on the bacterial outer membrane and subsequently breaching the cell wall [116]. Under favorable physiological conditions, lysis typically follows ~30 minutes after adsorption, yielding on the order of 100 to 1,000 progeny virions per infected cell [117]. In contaminated wastewaters, four principal somatic coliphage families have been detected, with Myoviridae and Siphoviridae predominating, and

Podoviridae and Microviridae occurring at lower abundances [118].

F-specific bacteriophages constitute the second most prevalent group of indicator phages detected in environmental samples [119]. F-specific bacteriophages infect *Escherichia coli* and other coliforms by binding to sex pili, which are encoded by the F plasmid and may be transferred among enteric bacteria via conjugation [120]. This group comprises two families: Leviviridae, single-stranded RNA phages with isometric, tailless capsids of roughly 25 nm, and Inoviridae, single-stranded DNA phages characterized by flexible, filamentous capsids about 800 nm in length [121]. The third proposed indicator group targets *Bacteroides* spp.; their abundances in feces and fecally contaminated matrices are generally lower than those of coliphages. Most members of this morphologically uniform group are Siphoviridae and infect host cells by binding to cell-wall receptors [122], [123], [124].

7. Applications of Bacteriophages

7.1 Bacteriophages as Faecal Indicators in Water

Faecal indicator bacteria (FIB) are commonly employed to evaluate water microbiological quality, but they may not reliably predict the occurrence of enteric viruses. Enteric viruses typically exhibit greater resistance to wastewater and drinking-water treatment processes and persist longer in environmental waters than bacterial indicators [125], [126], [127], [128], [129]. Thus, exclusive reliance on bacterial indicators may lead to underestimation of microbial contamination and associated public-health risks. Incorporating at least one viral indicator yields a more representative appraisal of water quality and bolsters confidence in its safety. Coliphages originate primarily from human and animal feces and enter aquatic environments via untreated or treated wastewater discharges, septic-tank overflows, sewer leaks, and the application or runoff of wastes such as sewage sludge, slurry, manure, and feces from pets, livestock, and wildlife [119]. Guelin's 1948 study first highlighted coliphages as potential indicators of enteric contamination, reporting a strong correlation with coliform counts in both freshwater and marine environments. Since that work, numerous investigations have assessed bacteriophages as markers of faecal pollution across a variety of aquatic settings [109].

Wastewater treatment plants: Bacteriophages are useful indicators for assessing wastewater treatment performance because their removal by common treatment processes mirrors that of human enteric viruses, whereas conventional faecal indicator bacteria (FIB) are typically reduced to a much greater extent [111], [125], [130], [131], [132], [133]. Coliphage levels in wastewater do not exhibit clear seasonal variation and remain persistently high year-round worldwide, mirroring the patterns observed for bacterial indicators [133], [134].

Coliphage concentrations in wastewater are highly variable; however, the generally lower abundance of F-specific coliphages relative to somatic coliphages in both raw and treated effluents may constrain their applicability as wastewater indicators [135].

Drinking water: Detection of coliphages or phages infecting *Bacteroides* spp. in drinking-water sources is indicative of faecal contamination or insufficient treatment [136]. Bacterial indicators, human viruses, and bacteriophages are generally present at low concentrations in drinking-water sources and are infrequently detected after treatment. Limited studies that have evaluated phages for drinking-water monitoring indicate they may be superior to conventional faecal indicator bacteria (FIB), because phages tend to be less effectively removed by common drinking-water treatment processes [137], [138], [139], [140], [141].

Recreational water: The sanitary quality of recreational waters is assessed using faecal indicator bacteria (FIB) in accordance with EU Directive 2006/7/EC [142]; Alternative markers, including *Clostridium perfringens* and various bacteriophages, have likewise been suggested [143]. Somatic coliphages are detected in recreational water [143], and at beaches with unknown sources of faecal contamination, the

presence of coliphages correlates more frequently with disease occurrence than the presence of faecal indicator bacteria (FIB) [144], [145]. Epidemiological studies have found that the presence of coliphages in recreational waters is associated with an elevated risk of gastrointestinal illness among swimmers when faecal contamination is likely, but not when it is absent. Correlations with illness were comparable between enterococci and somatic coliphages, and were stronger for F-specific coliphages [146]. These findings indicate that coliphages may be suitable for application as indicators of bathing water quality.

Groundwater: Groundwater supplies a substantial fraction of water for domestic, municipal, agricultural, landscape-irrigation, and industrial uses. Surface-water contaminants can reach groundwater via pathways such as septic-system failures, leaking sewer lines, and transport through soils and fractures. One study demonstrated that combining a bacterial indicator with a phage indicator yields more informative assessments of groundwater microbiological quality than relying on two bacterial indicators alone [128]. However, as summarized in Table 8, only a single regulation (dating from 2006) currently lists bacteriophages as indicators of enteric viral contamination in groundwater, underscoring the need for further research in this domain.

Table 8: Adoption of bacteriophage-based monitoring guidelines and applications in water quality management across countries and organisations [109].

Country / Organization	Biosolids	Groundwater	Recreational Water	Drinking Water	Reclaimed Water	Membrane Integrity & UV Validation	Direct Potable Reuse
Australia	2012 (WA)	-	-	2011*	2005/2011 (QLD/WA)	-	-
Canada	-	-	-	2011 (QC)	-	-	-
Colombia	2014	-	-	-	-	-	-
European Union (EU)	-	-	-	2020	2020	-	-
India	-	-	-	2012	-	-	-
Singapore	-	-	-	2017* (WHO-based)	-	-	2017* (WHO-based)
South Africa	-	-	-	1996*	-	-	-
United States (USA)	-	2006	2015 (Proposed)	-	2011 (NC)	2015	-
World Health Organization (WHO)	-	-	-	2017*	2017 (I&AR)	-	2017*

- **Abbreviations:** WA = Western Australia; QLD = Queensland; QC = Quebec; NC = North Carolina; I&AR = Irrigation and Agricultural Reuse; UV = Ultraviolet Disinfection; - = No specific guideline or application reported
- **Footnote*** Indicates that bacteriophage monitoring recommendations were incorporated through risk-based water safety frameworks or referenced from WHO guidance rather than established as standalone regulatory standards.

7.2 Bacteriophages as Faecal Indicators in Solid Matrices

Solid and semisolid matrices are important reservoirs for pathogen persistence and dissemination within the water cycle; when contaminated with faecal material they can concentrate large numbers of pathogens, particularly viruses [112], [147]. To maximize the utility of bacteriophages as indicators in solid matrices, standardized procedures for extraction, detection, and enumeration are required. Available studies generally report that somatic coliphages occur in solids at higher concentrations than conventional faecal indicator bacteria and F-specific RNA coliphages, persist longer in soils and sediments, and are more resistant to treatments applied to sludge and manure. For a comprehensive review and additional data on solid matrices, consult the relevant literature [112].

8. Future Prospects

Future research on Ganga River bacteriophages should prioritize systematic, longitudinal mapping of phage diversity and abundance from Gaumukh to the Bay of Bengal across

seasons, integrating culture-dependent isolation with high-throughput metaviromics and parallel host community profiling. Particular emphasis is needed on phages infecting multidrug-resistant bacteria prevalent in the basin (for example ESBL-producing Enterobacteriaceae, *Pseudomonas* and *Acinetobacter*), including characterization of their genomes, host range, and potential for horizontal gene transfer of resistance and virulence factors. Another priority is to evaluate somatic and F-specific coliphages and *Bacteroides* phages as routine viral indicators within existing CPCB and NMCG monitoring frameworks, through coordinated pilot studies at major urban and pilgrimage centres such as Haridwar, Kanpur, Prayagraj, Varanasi and the Hooghly stretch. Finally, targeted exploration of glacier meltwater, permafrost and sediment at Himalayan source regions may reveal ancient or extremophile phage lineages, while experimental phage-based biocontrol and bioremediation trials in controlled mesocosms could clarify both the promise and ecological risks of using Ganga-derived phages for water quality management.

9. Conclusion

Bacteriophages constitute an integral yet underexplored component of the Ganga River ecosystem, tightly linked to the structure and dynamics of bacterial communities along its longitudinal and pollution gradients. Historical observations of the river's self-purifying properties and recent ecological and metagenomic studies together suggest that diverse phage assemblages contribute to microbial regulation, nutrient cycling and resilience under increasing anthropogenic stress. At the same time, intense inputs of sewage, industrial effluents, agricultural runoff and faecal contamination are reshaping both bacterial and phage populations, with important implications for the spread of antimicrobial resistance and water-borne disease risks. Harnessing Ganga-derived phages as tools for water-quality monitoring, faecal pollution assessment, AMR control and targeted bioremediation will require coordinated efforts that combine basic virology, environmental microbiology, and public-health surveillance. By integrating phage-centric approaches into existing river management programmes, the ecological and biotechnological potential of Ganga bacteriophages can be translated into more effective and sustainable strategies for safeguarding this culturally and economically vital river system.

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