https://doi.org/ 10.33472/AFJBS.6.5.2024. 6409-6444

African Journal of Biological Sciences

Microbiological Quality Investigation and AntibioticSensitivityTest of Sai River, Raebareli, U.P., India

Prashant Singh, Vishvas Hare,Vinay Singh Baghel*

Department of Environmental Microbiology

Babasaheb Bhimrao Ambedkar University, Lucknow(226025)

*Corresponding Author

Email: baghelbbau@gmail.com

Article History
Volume 6, Issue 5, 2024
Received: 09 May 2024
Accepted: 17 May 2024
doi: *10.33472/AFJBS.6.5.2024. 6409-6444*

Abstract

In the Indian state of Uttar Pradesh, the Gomti River receives tributaries from the Sai River (Sai Setu), also known as the Aadi Ganga. The river Sai originates in the hamlet of Bijgwan, close to Pihani in the district of Hardoi. It flows for around 600 kilometres, forming the district border between Lucknow and Unnao. It then travels through the districts of Jaunpur, Raebareli, and Hardoi until joining the Gomati River in Rajepur (25°39'8.63"N 82°48'5.00"E) in Jaunpur district of Uttar Pradesh, India. The overall water quality index of the samples was ascertained by microbiological tests of twelve water samples collected from the Raebareli area: Rajghat Raebareli, Shaheed Smarak Raebareli, Behta Bridge Raebareli, and Bhanvareshvar Temple Raebareli. Here, the important and observational method is called MPN (Most Probable Number). The present study will center on the quantity of Total Coliform (TC), Faecal Coliform (FC), and Faecal Streptococci found in the Holy Water Sai. Additionally, a thorough discussion of water quality, antibiotic resistance, and sensitivity will be included. Since water is essential to all living things, including people, it must be pure and of high quality for human health, particularly in light of microbial contamination.

Introduction

The majority of prehistoric societies developed alongside riverbanks. Millions of people rely on rivers for their life and still live along their banks now all over the world. The Raebareli River spans around 100 kilometres during its whole course. The Gomti River is 940 kilometres long and drains 30,437 square kilometres. The Ganga watershed borders the Sai catchment on the south, and the Ghaghara catchment on the north. Sai River flows over alluvial terrain during its route, carrying silt from the Himalayan region. The rivers Bhainsta,

Loni, Sakarni, and Bakulahi provide water to the river over its extensive course (Kumari and Chaurasia et al., 2015).

It is well recognized that one of the most significant natural resourceswatersis the sole thing that allows life on Earth to exist (Gupta and Orbán, 2018). For many human activities, including transportation, manufacturing, and agriculture, water is a vital natural resource. It comprises 50–97% of the weight of plants, animals, and around 70% of the human body. It is necessary for all life forms. According to WHO estimates, over 20% of the world's population lacks access to clean drinking water, and over 40% of people do not have proper sanitation. Unhealthy water is a major issue in many regions of the world. In more severe situations, it may even endanger humans and other living things. It frequently restricts the usage of essential resources. According to Ogwo and Ogu (2014), solid particles and insoluble liquid droplets that become suspended in water can also contaminate it. Despite the fact that these water sources are untreated, the great majority of people who live near water bodies in Nigeria still get their drinking water from rivers, streams, and other bodies of water. Numerous microbial species, many of which have not even been described or grown, can be found in these natural waterways.It is widely acknowledged that surface waters contaminated by sewage have a higher concentration of bacteria than uncontaminated waters due to the significant differences in the number of organisms present between the various types of water (WHO 2013).A wide range of harmful microorganisms, such as bacteria, viruses, and protozoa, can be found in contaminated surface waters (Servais P et al., 2007). These pathogens, which are frequently faecal in nature, may originate from non-point sources like domestic and wild animal defecation, malfunctioning sewage and septic systems, storm water drainage, and urban runoff, or from point sources like municipal wastewater treatment plants (Okoh et al., 2007; Igbinosa et al.,2009; Lata et al.,2009; Chigor et al., 2010; Odjadjare et al.,2010); drainage from areas where livestock are handled (Williams et al., 2012). One of the main causes of waterborne illnesses is acknowledged worldwide to be faecal contamination of water. It is commonly known that drinking water has the capacity to spread microbial infections to large populations, leading to subsequent sickness in nations with varying economic development levels. A notable example is the 1993 cryptosporidiosis outbreak that occurred in Milwaukee, Wisconsin, in the United States. An estimated 400,000 people experienced gastrointestinal symptoms, with a significant percentage of those cases being attributed to Cryptosporidium (MacKenzie et al., 1994). Nevertheless, further studies indicate that this could be a marked exaggeration (Hunter et al., 2001). More recent Escherichia coli O157:H7 outbreaks have resulted in over 2,300 illnesses and six fatalities; the most severe of

these outbreaks happened in Walkerton, Ontario, Canada in the spring of 2000. The sheer number of outbreaks that have been documented worldwide indicates that drinking waterborne pathogen transmission is still a major source of disease. The World Health Organization states that safe drinking water must be good for human life and free of any harmful impacts on health.Deforestation and land degradation are predicted to further fall in two-thirds of nations by 2025 as a result of the growing global population, which eventually has a significant influence on the scarce water resources (Kamble et al., 2020; Mohsin et al., 2013; World Health Organization, 2017).

Sampling Sites and Sample Collection

Total three sampling sites were identified for the assessment of Sai River flows from Raebareli district of Uttar Pradesh state. Samples was collected in every season like in winter season, summer season as well as monsoon season. First sampling site was Bhanvareshvar Temple (BT) which is an ancient and famous Hindu temple situated at the bank of Sai River Raebareli district, here total three samples named as BT1, BT2 and BT3 were collected. Second sampling site was Rajghat (RG) where Sai River enters the city Raebareli and here total three samples were collected named as RG1, RG2 and RG3. Another one sampling site was Shaheed Smarak (SS) where Bharat Mata temple is established, from here three samples was received and name was mentioned as SS1, SS2 and SS3. Last sampling site was Behta Bridge(BB) and here also three samples was collected and name was BB1,BB2 and BB3.

Materials and Methods

Water samples were taken in sterile glass bottles from three distinct locations from the Sai River in Raebareli, India. They were then sent to the lab on ice and processed there over the course of six to seven hours. The three samples that make up the collection came from three distinct locations. Three divisions were made in the research area. The conventional most probable number (MPN) approach was used to evaluate the quality of the water. In order to identify total coliforms, fecal streptococci, and fecal coliforms, samples were to be inoculated into MacConkey broth tubes and incubated for 48 hours at 37 ±1ºC. The positive tubes were incubated at 44.5±1ºC while being subculture in Brilliant gGeen Bile Broth (BGBB). After 48 hours of incubation, gas generation in BGBB at 44.5±1ºC revealed the presence of fecal coliform. Water samples were inoculated into Azide Dextrose broth and incubated at 37.5±1ºC for 24 to 48 hours in order to identify fecal streptococci (Baghel et al., 2005).

Result and Discussion

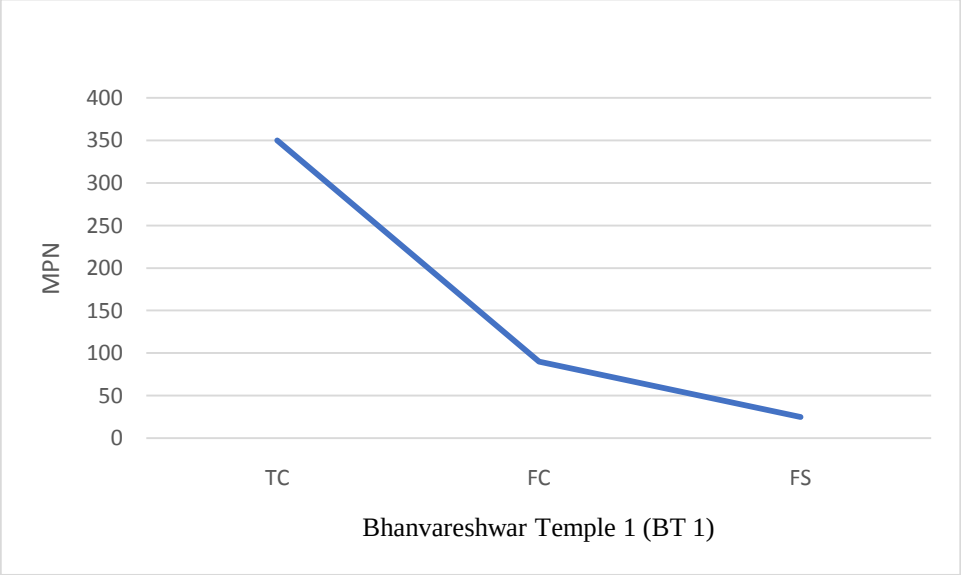
1. Winter Season

Total 12 samples were analyzed during winter season of Sai River. First three samples were taken from BT sampling site and samples were labelled as BT1, BT2 and BT3. Results suggested thatTC was 350, FC was 90 and FS was 25 of BT1 sample (Fig 1.1).TC was 220, FC was 50 and FS was 35 of BT2 sample(Fig 1.2)and BT3 results were TC 220, FC 70 and FS 25 (Fig 1.3).

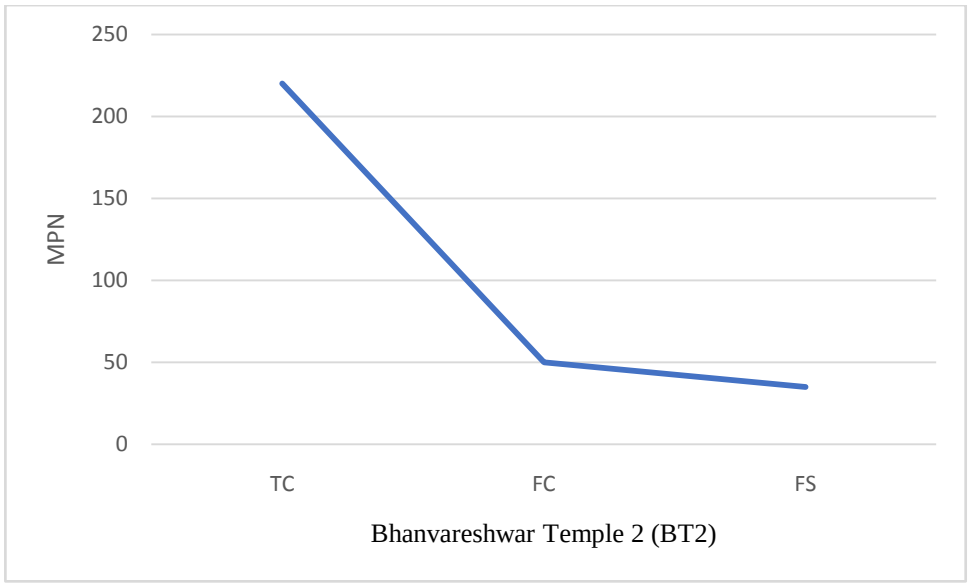
Total three samples were analyzedfrom RG sampling Site, where RG1suggested that TC 220, FC 70 and FS 35(Fig 1.4). RG2 result was TC 280, FC 90 and FS 35(Fig 1.5). RG3 result was TC 350, FC 70 and FS 35(Fig 1.6).

Three Samples were analyzed from SS sampling site and result of SS1wasTC 280, FC 70 and FS 35(Fig 1.7). Result ofSS2 sample was TC110, FC 40 and FS 35(Fig 1.8). SS3 assessment's result was TC 110, FC 40 and FS 25(Fig 1.9).

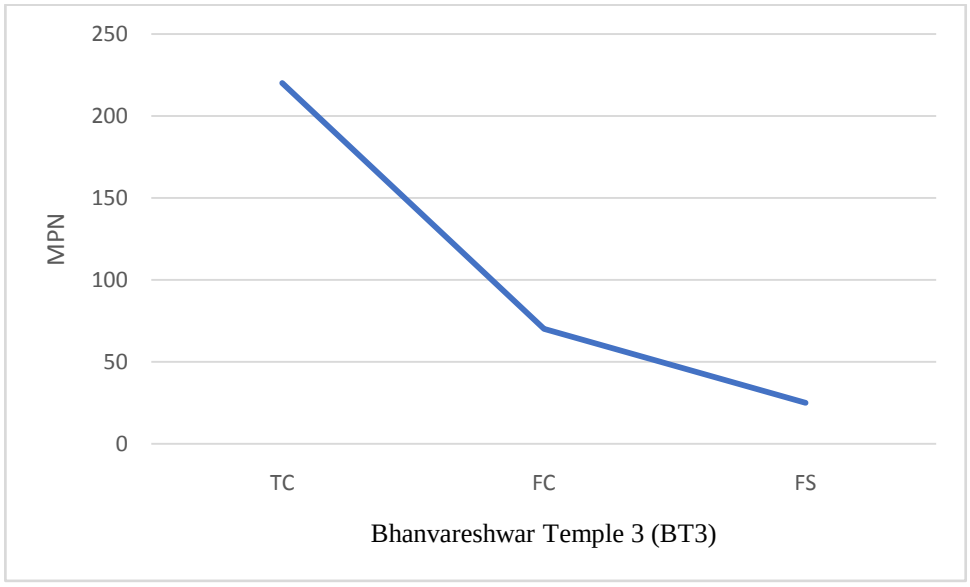
BB sampling site assessment of BB1 was TC 350, FC 90 and FS 35(Fig 1.10). BB2 result was TC 280, FC 70 and FS 35(Fig 1.11). BB3 result was TC 280, FC 50 and FS 35(Fig 1.12).



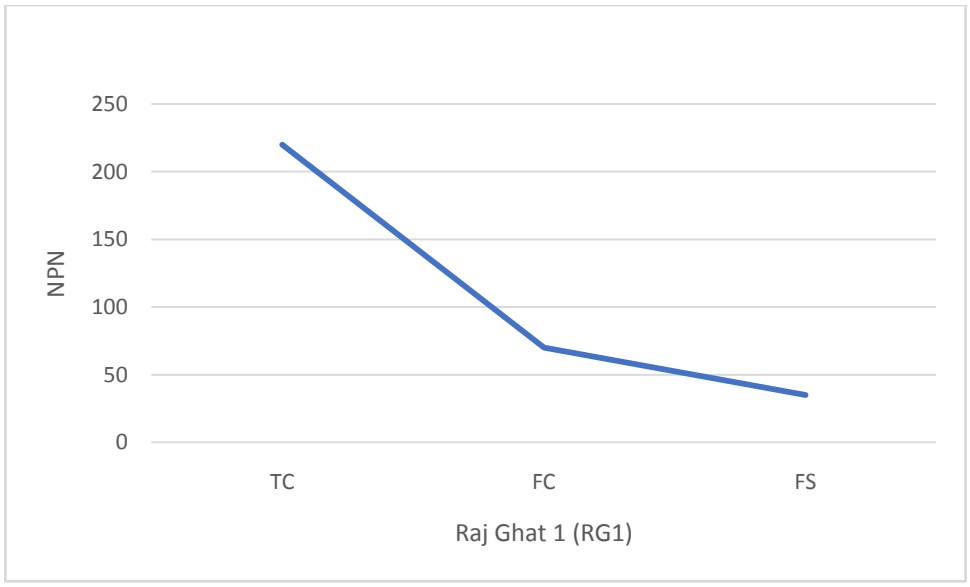
(Fig 1.1 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



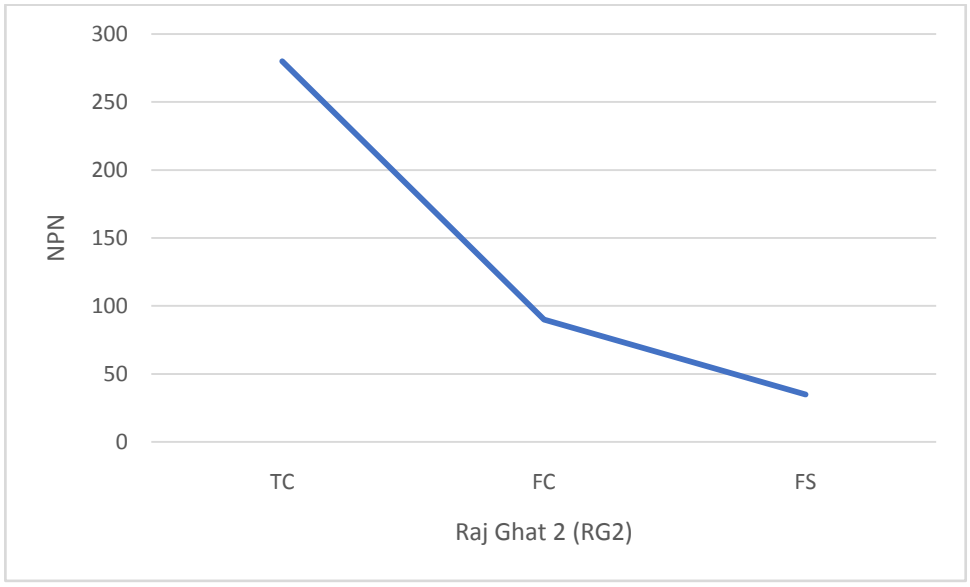
(Fig 1.2 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



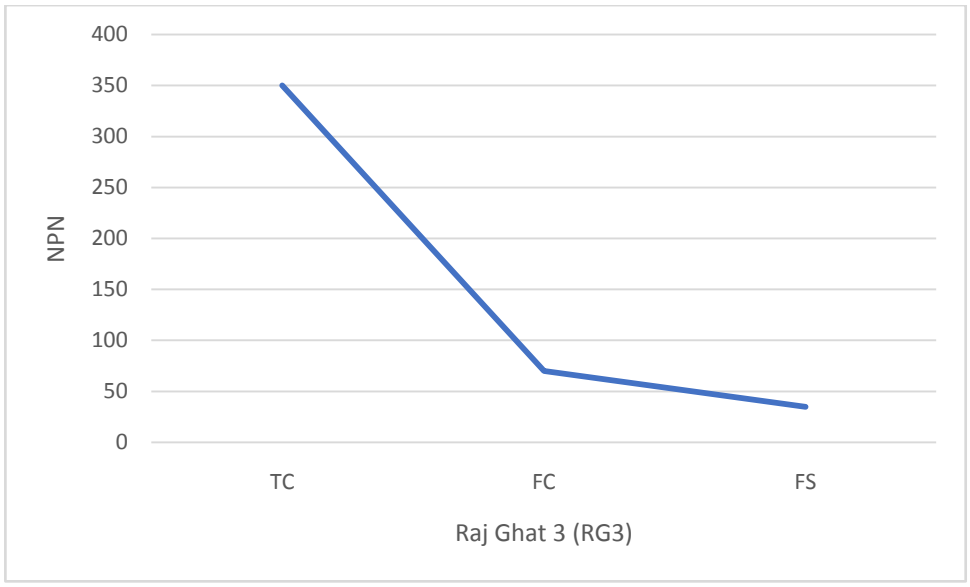
(Fig 1.3 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



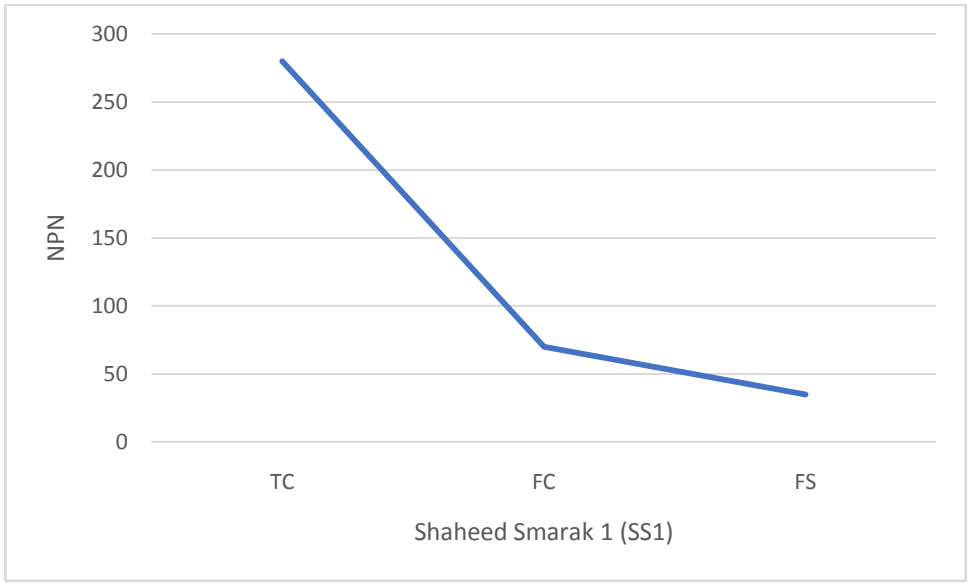
(Fig 1.4 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



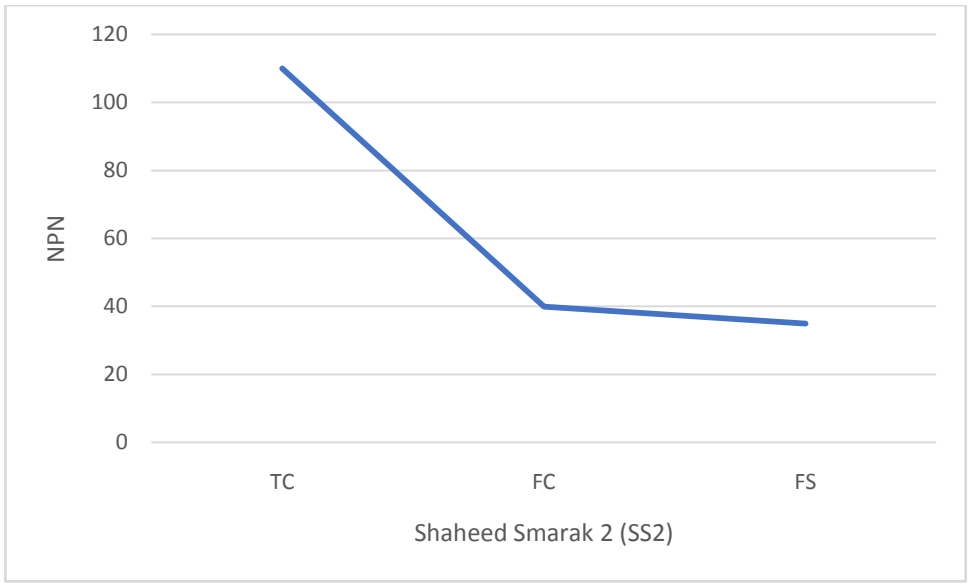
(Fig 1.5 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



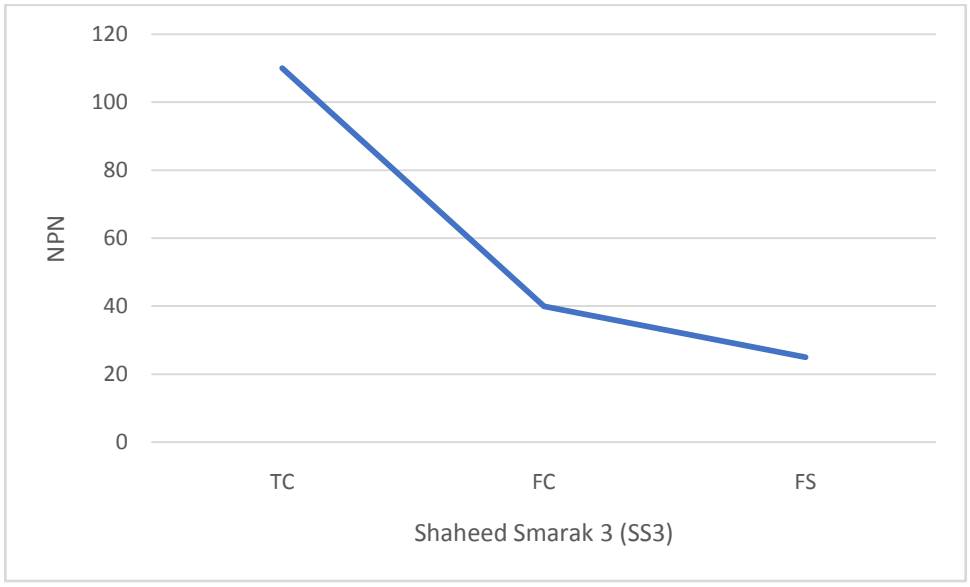
(Fig 1.6 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



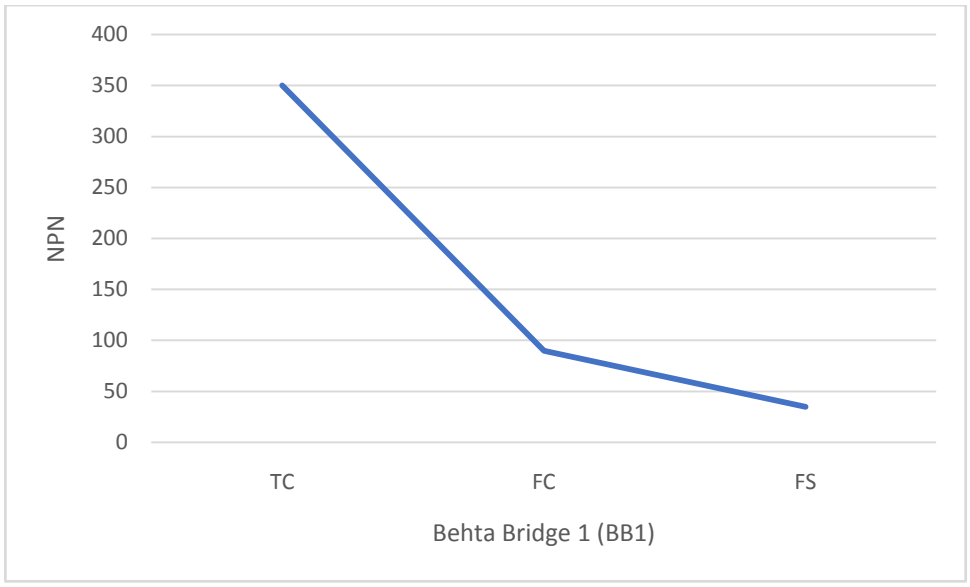
(Fig 1.7 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



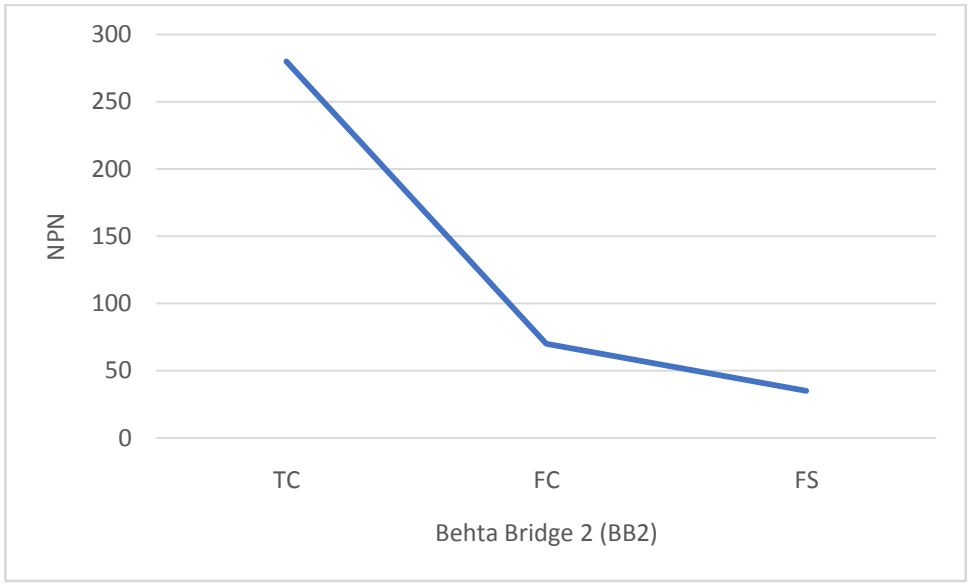
(Fig 1.8 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



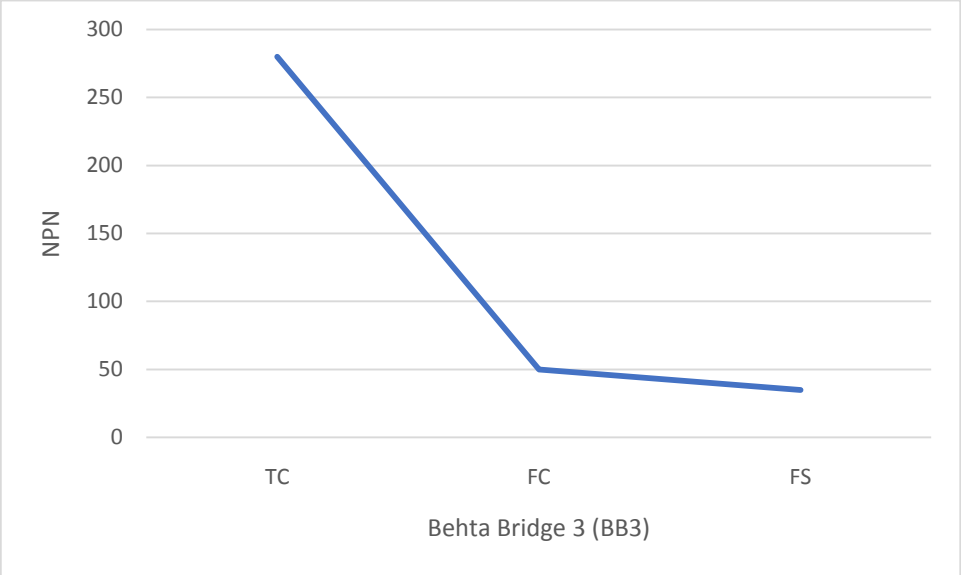
(Fig 1.9 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 1.10 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 1.11 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 1.12 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)

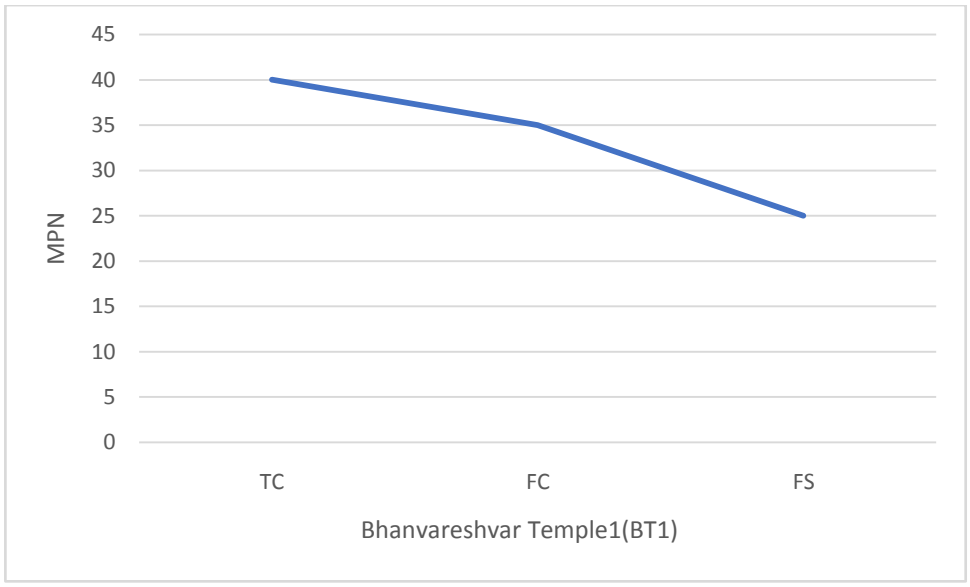
2. Summer Season

Total 12 samples were analyzed during summer season of Sai River. First three samples were taken from BT sampling siteand samples were labelled as BT1, BT2 and BT3. Results suggested that TC was 40, FC was 35 and FS was 25 of BT1 sample (Fig 2.1). TC was 55, FC was 25 and FS was 20 of BT2 sample (Fig 2.2) and BT3 results were TC 35, FC 35 and FS 20 (Fig 2.3).

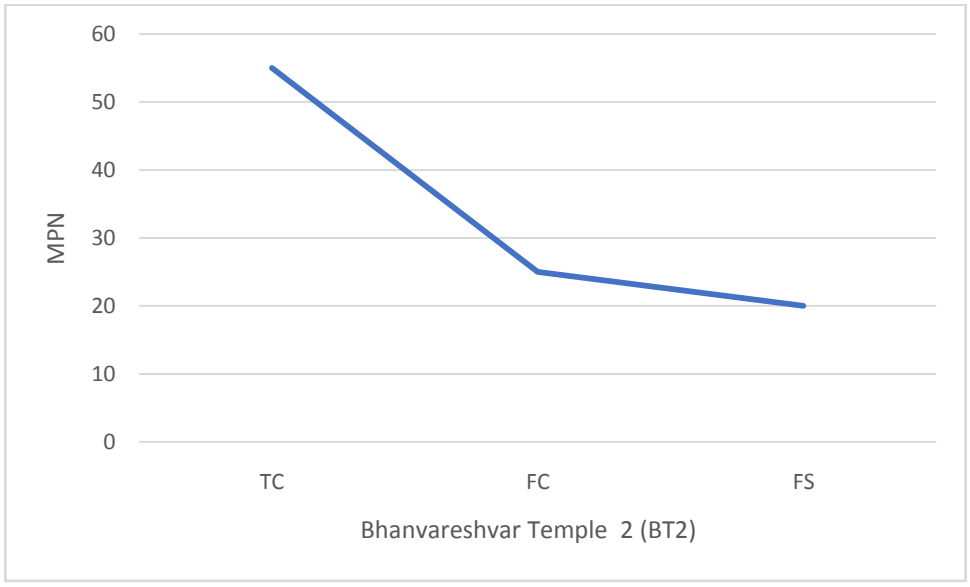
Total three samples were analyzed from RG sampling Site, where RG1 suggested that TC 63, FC 55 and FS 25(Fig 2.4). RG2 result was TC 55, FC 46 and FS 20 (Fig 2.5). RG3 result was TC 35, FC 35 and FS 20(Fig 2.6).

Three Samples were analyzed from SS sampling site and result of SS1 was TC 80, FC 65 and FS 35 (Fig 2.7). Result of SS2 sample was TC 77, FC 67 and FS 25(Fig 2.8). SS3 assessment's result was TC 56, FC 46 and FS 25 (Fig 2.9).

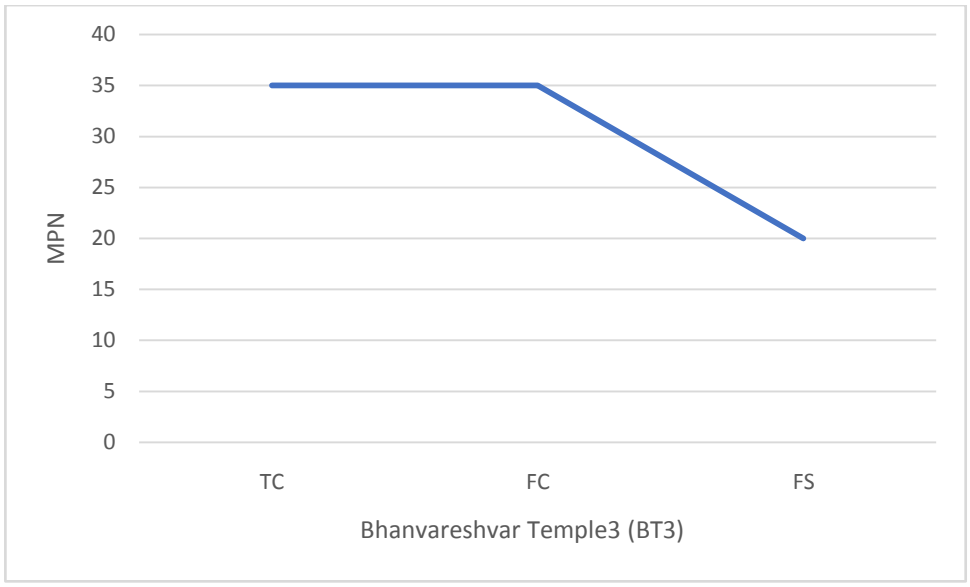
BB sampling site assessment of BB1 was TC 63, FC 55 and FS 25 (Fig 2.10). BB2 result was TC 55, FC 25 and FS 20 (Fig 2.11). BB3 result was TC 40, FC 35 and FS 20(Fig 2.12).



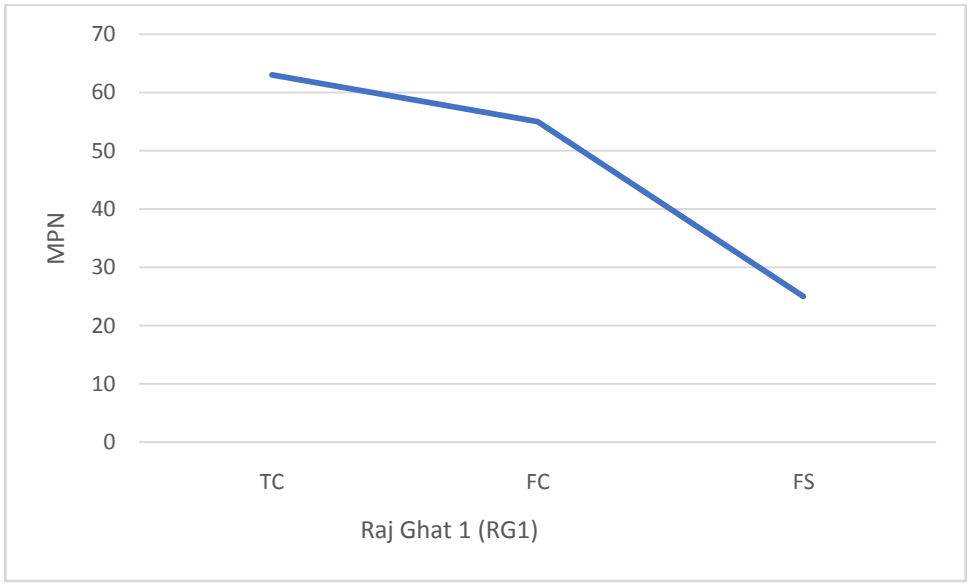
(Fig 2.1 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



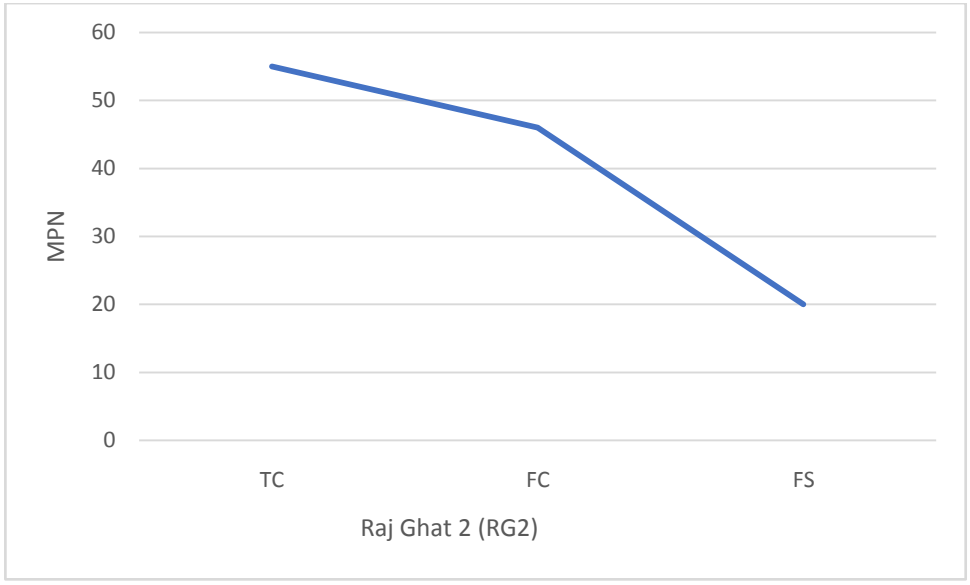
(Fig 2.2 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



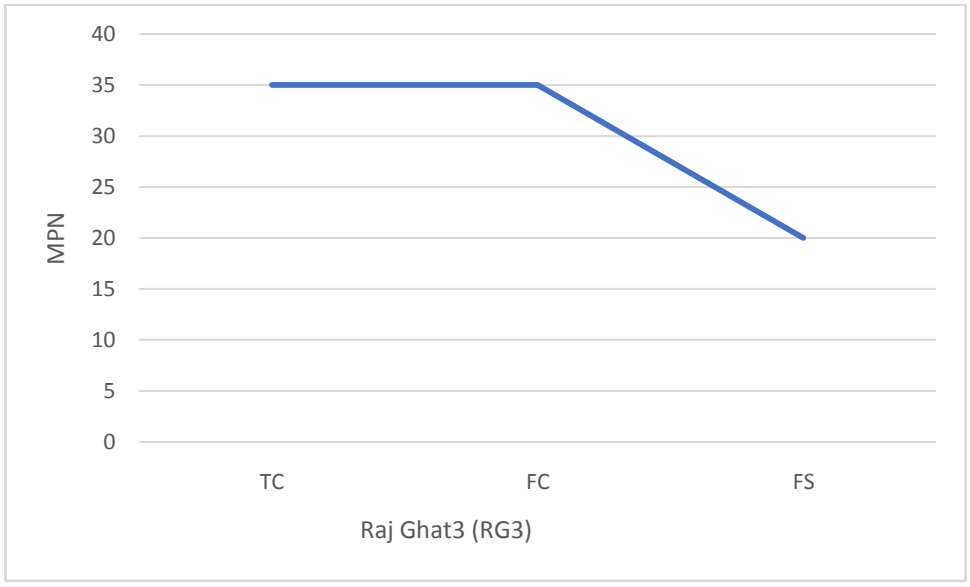
(Fig 2.3 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



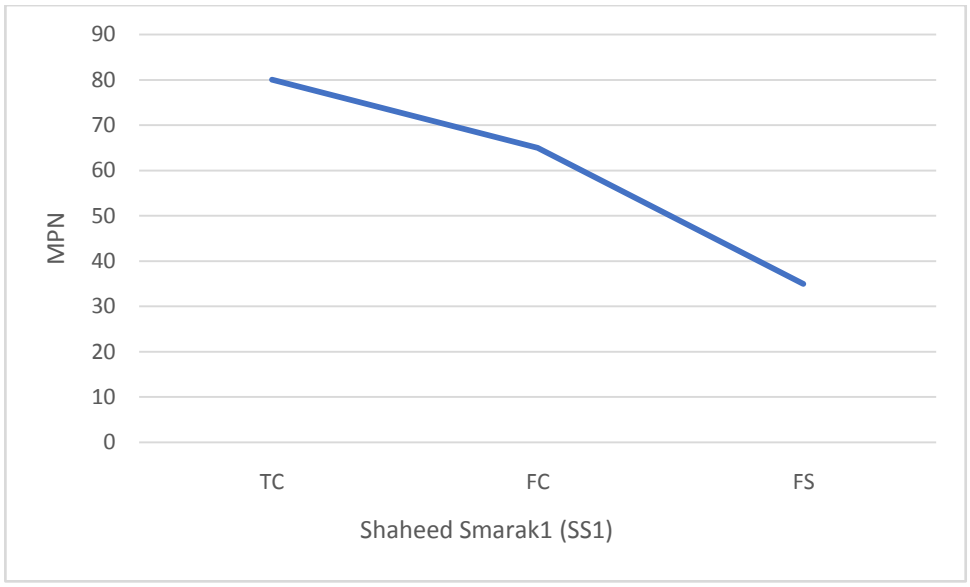
(Fig 2.4 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



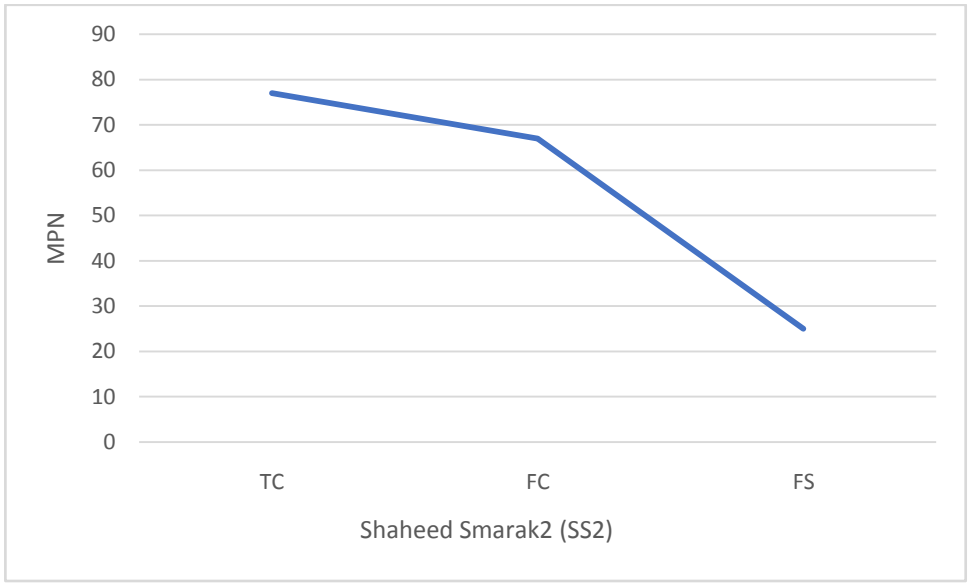
(Fig 2.5 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



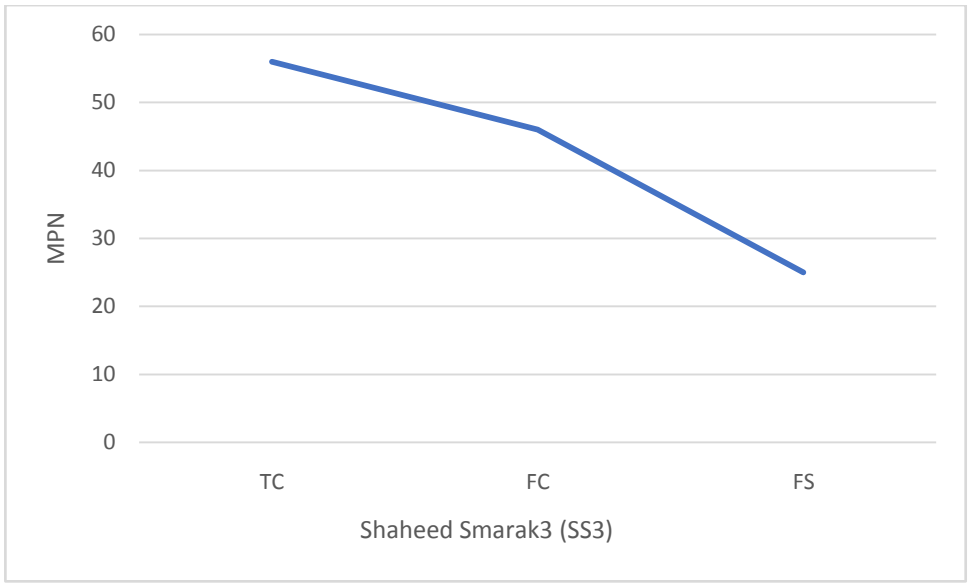
(Fig 2.6 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



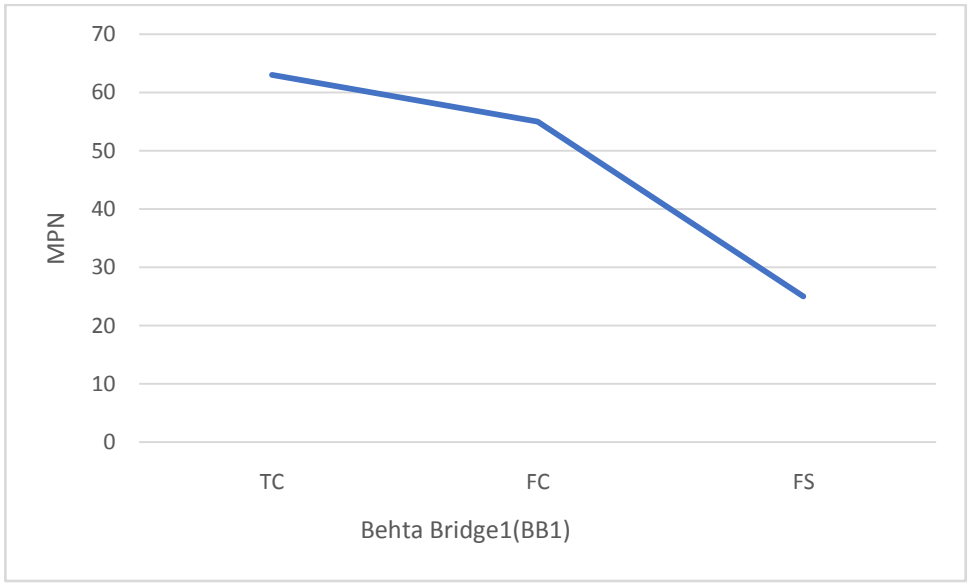
(Fig 2.7 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



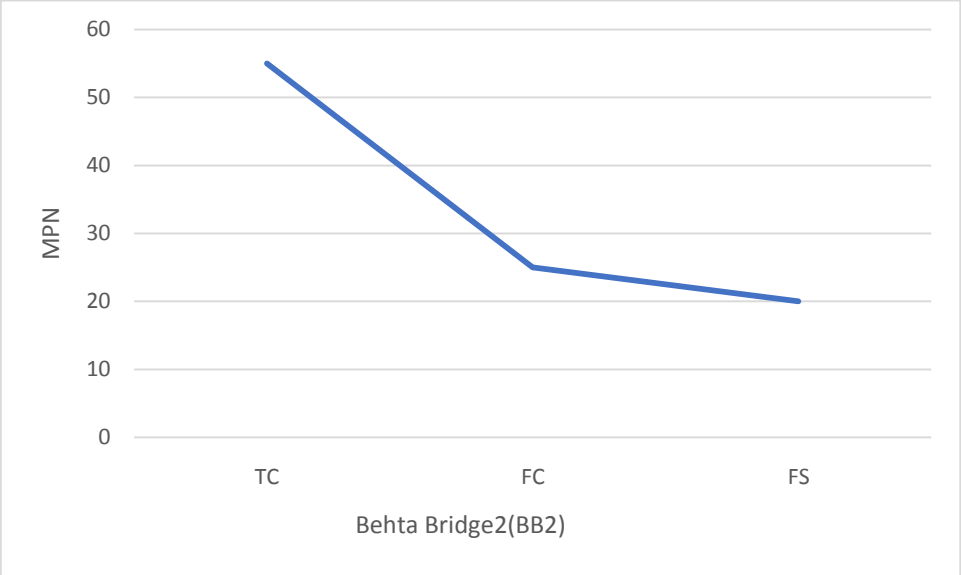
(Fig 2.8 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



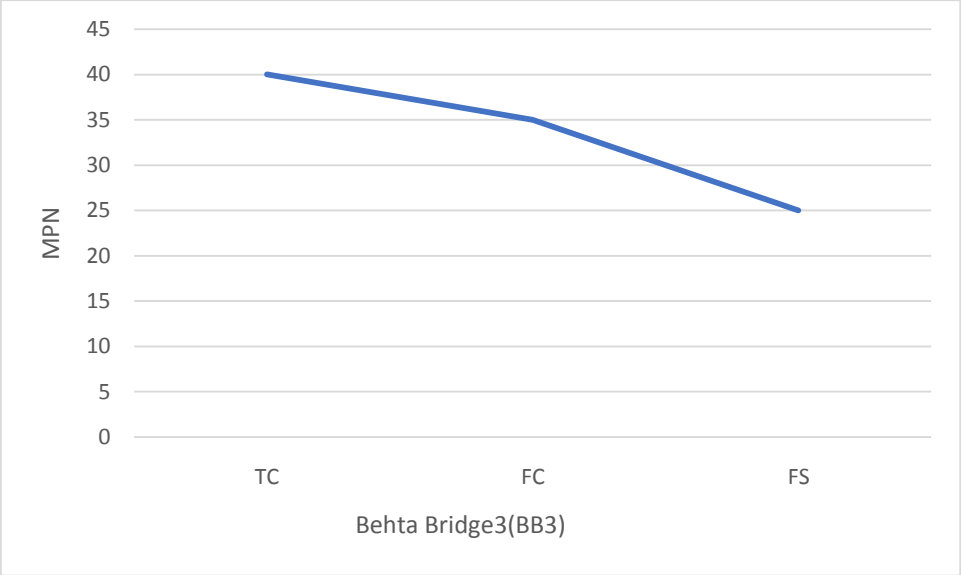
(Fig 2.9 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 2.10 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 2.11 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 2.12 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)

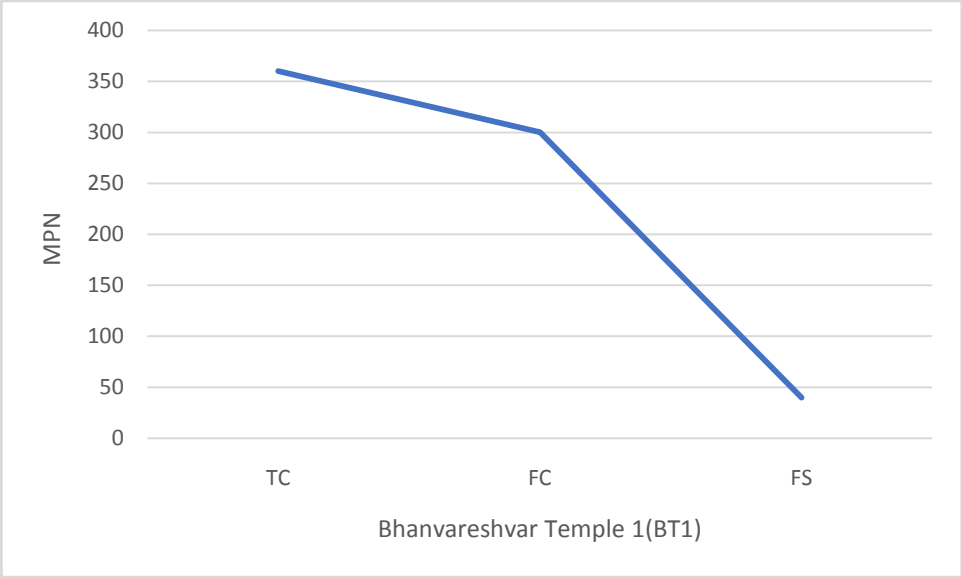
3. Monsoon Season

Total 12 samples were analyzed during monsoon season of Sai River. First three samples were taken from BT sampling siteand samples were labelled as BT1, BT2 and BT3. Results suggested that TC was 360, FC was 300 and FS was 40 of BT1 sample (Fig 3.1). TC was 250, FC was 250 and FS was 35 of BT2 sample (Fig 3.2) and BT3 results were TC 580, FC 300 and FS 40 (Fig 3.3).

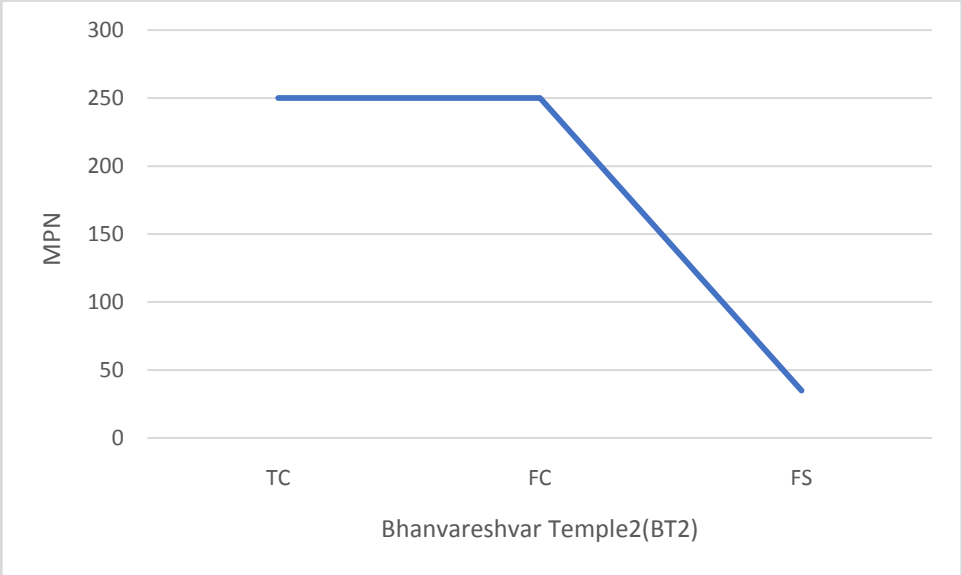
Total three samples were analyzed from RG sampling Site, where RG1 suggested that TC 180, FC 150 and FS 25(Fig 3.4). RG2 result was TC 150, FC 120 and FS 35(Fig 3.5). RG3 result was TC 140, FC 110 and FS 35(Fig 3.6).

Three Samples were analyzed from SS sampling site and result of SS1 was TC 480, FC 390 and FS 70 (Fig 3.7). Result of SS2 sample was TC 690, FC 580 and FS 100 (Fig 3.8). SS3 assessment's result was TC 410, FC 390 and FS 50 (Fig 3.9).

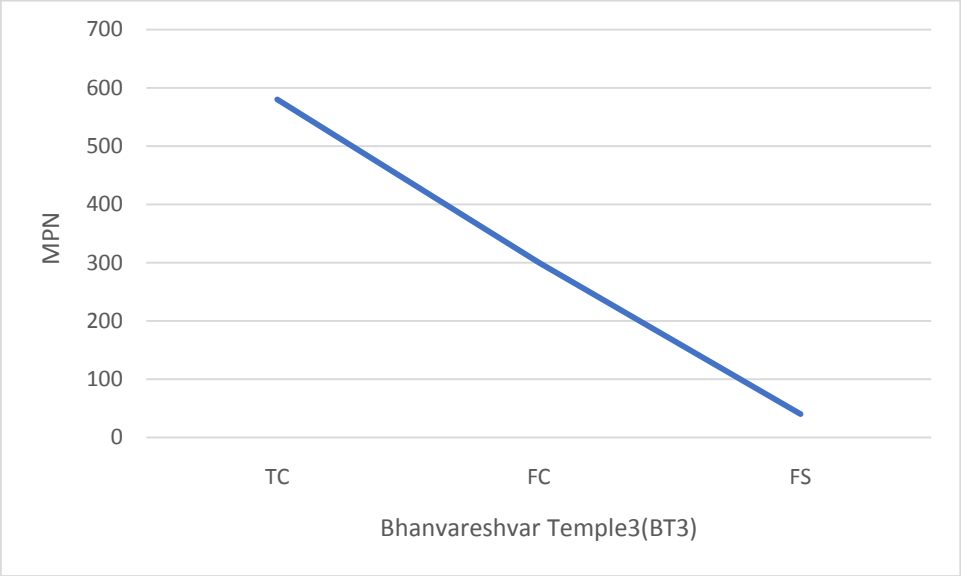
BB sampling site assessment of BB1 was TC 980, FC 820 and FS 160 (Fig 3.10). BB2 result was TC 1300, FC 940 and FS 100 (Fig 3.11). BB3 result was TC 820, FC 690 and FS 120 (Fig 3.12).



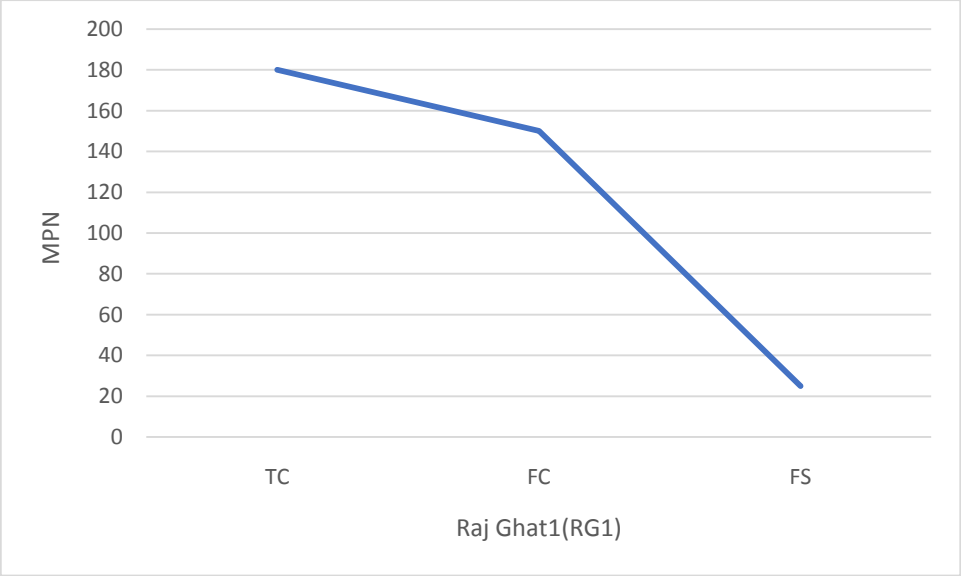
(Fig 3.1 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



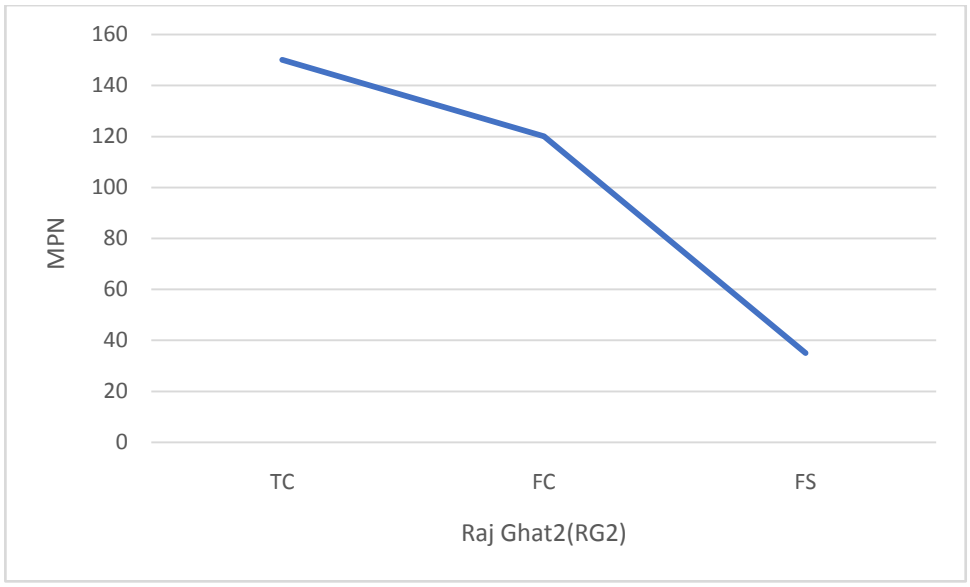
(Fig 3.2 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



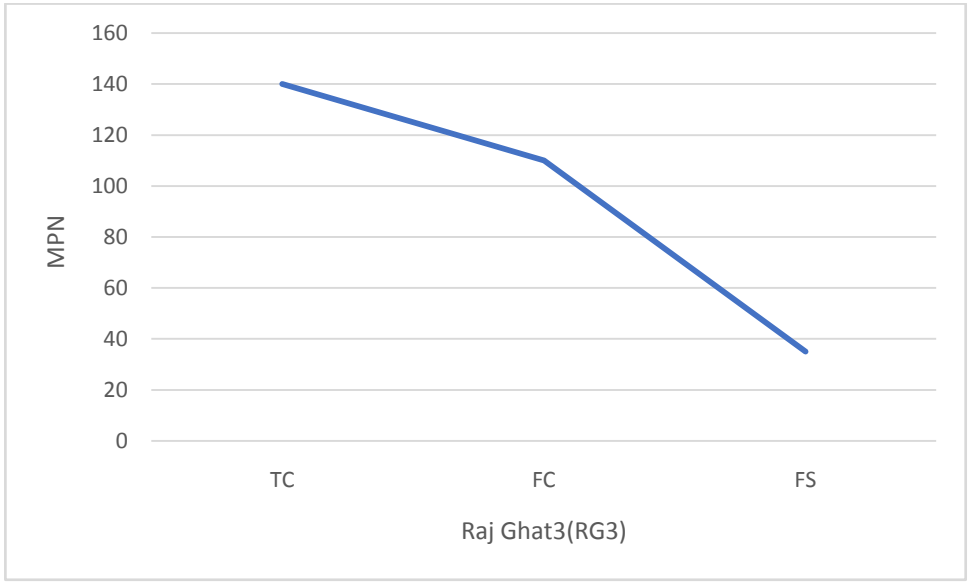
(Fig 3.3 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



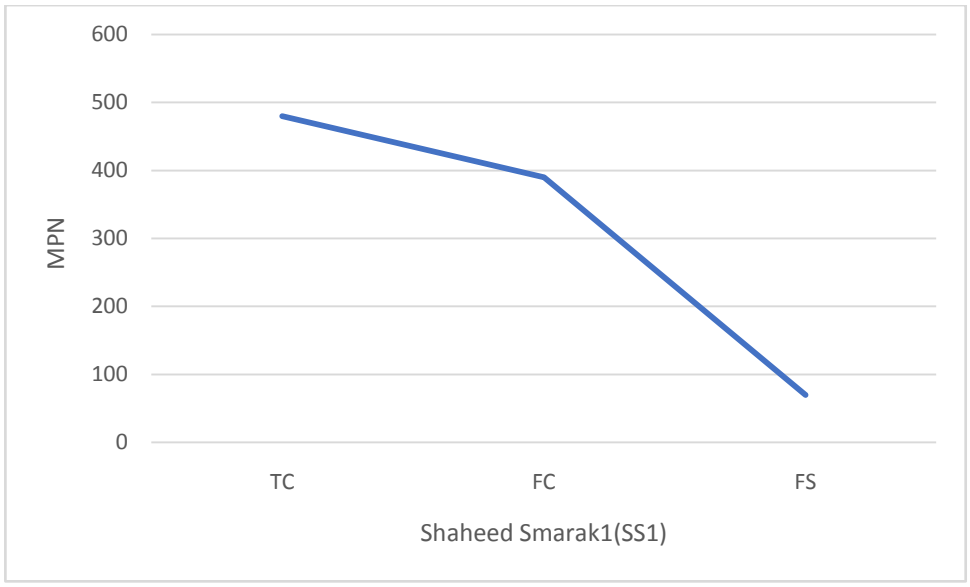
(Fig 3.4 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



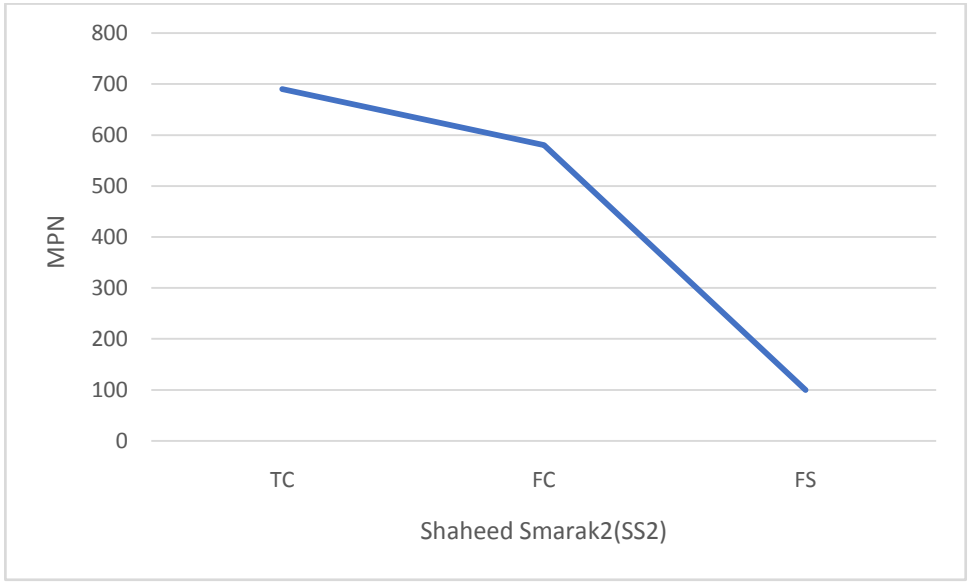
(Fig 3.5 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



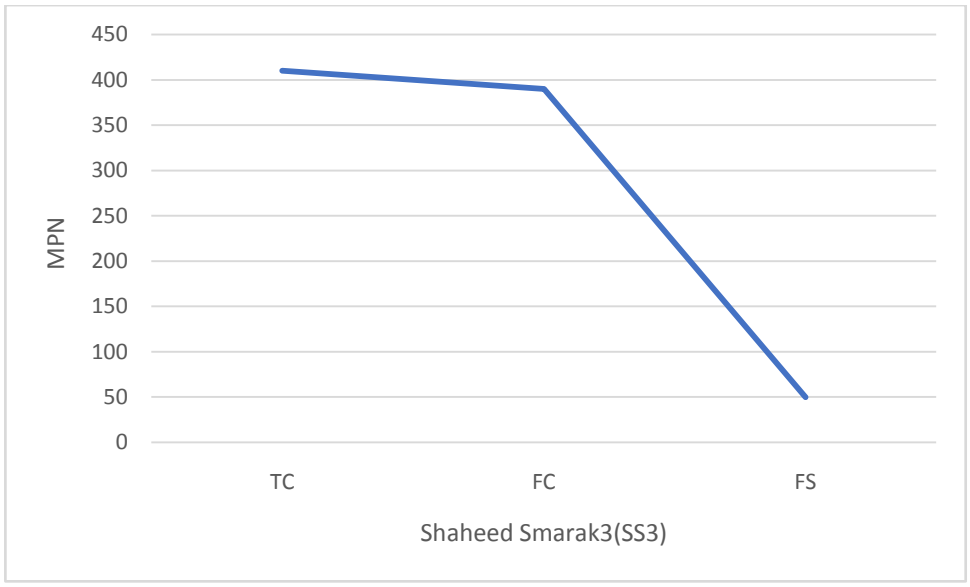
(Fig 3.6 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



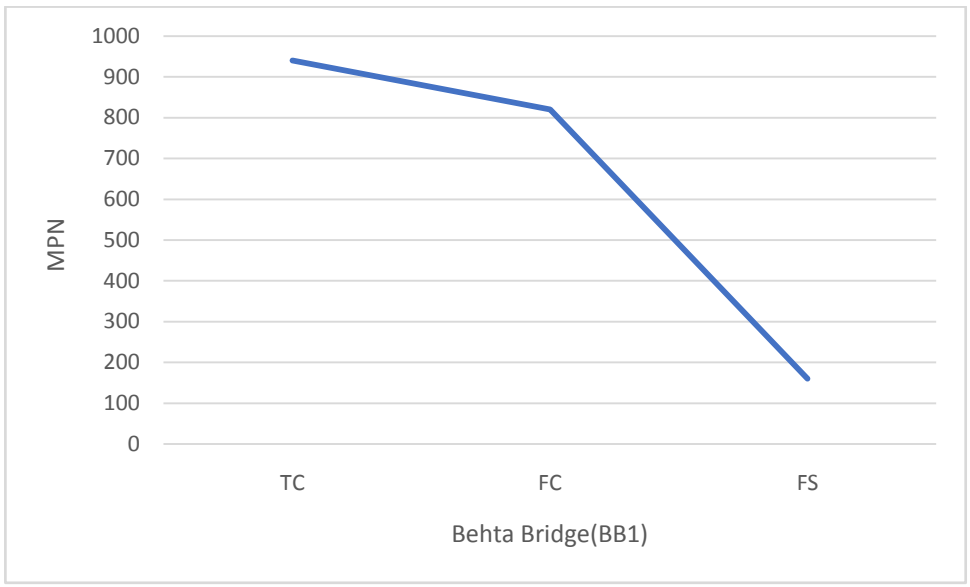
(Fig 3.7 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



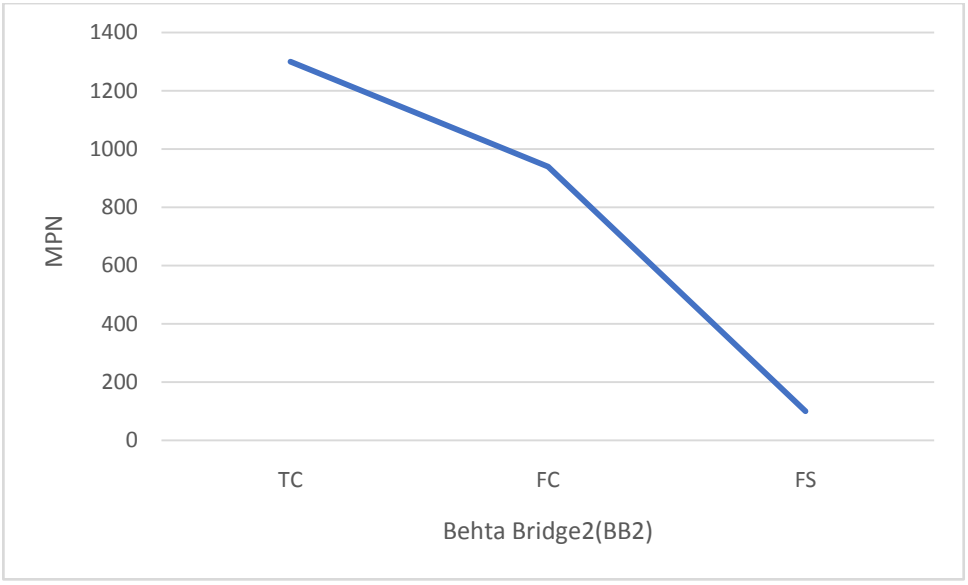
(Fig 3.8 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



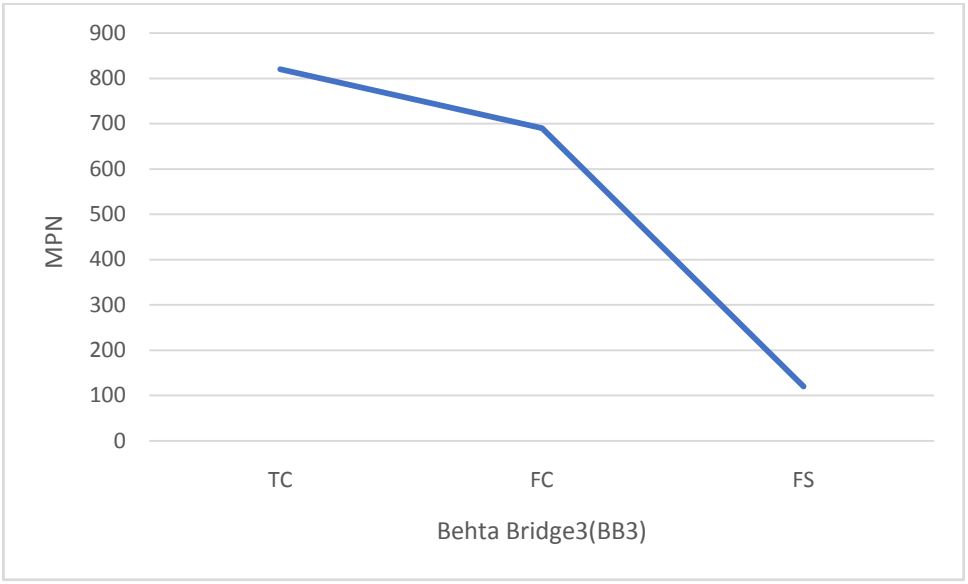
(Fig 3.9 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 3.10 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 3.11 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)



(Fig 3.12 Total Coliform, Fecal Coliform and Fecal Streptococci count of study area)

TABLE NO. 1 Winter Season

SAMPLING SITE	SAMPLE	ISOLATES	ANTIBIOTIC RESISTANCE		
			AMPICILINE	TETRACYCLINE	CEFIXIME
		TC1	S	R	R
		TC2	S	R	R
		TC3	S	R	S

BHANVARESHVAR TEMPLE	BT1	FC1	S	R	R
		FC2	R	S	S
		FC3	S	R	S
		FS1	R	R	S
		FS2	S	R	R
		FS3	S	R	S
	BT2	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	R
		FC1	R	R	S
		FC2	S	S	S
		FC3	S	S	S
		FS1	S	R	S
		FS2	S	R	R
		FS3	S	R	S
	BT3	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	S	S
		FC2	S	S	R
		FC3	S	R	S
		FS1	S	R	S
		FS2	R	R	S
		FS3	S	R	S
RAJ	RG1	TC1	S	R	R
		TC2	R	R	S
		TC3	S	R	S
		FC1	S	R	S
		FC2	S	R	R
		FC3	R	R	S
		FS1	S	R	S
		FS2	S	R	R

G		FS3	S	R	R
H	RG2	TC1	S	R	S
A		TC2	S	R	S
T		TC3	S	R	S
		FC1	S	R	S
		FC2	S	R	S
		FC3	S	R	S
		FS1	R	R	S
		FS2	S	R	S
		FS3	S	R	S
	RG3	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	R
		FC2	S	R	R
		FC3	S	S	R
		FS1	R	R	S
		FS2	R	R	S
		FS3	S	R	S
	SS1	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	R
		FC1	S	R	S
		FC2	S	R	S
S		FC3	S	R	R
S		FS1	S	R	S
H		FS2	R	S	S
A		FS3	S	R	S
H	SS2	TC1	S	R	S
E		TC2	S	R	S
E		TC3	S	R	R
D		FC1	S	S	S

S M A R A K		FC2	S	R	S
		FC3	S	R	S
		FS1	R	R	S
		FS2	S	R	S
		FS3	S	R	R
	SS3	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	R
		FC2	R	R	R
		FC3	S	S	R
		FS1	S	R	S
		FS2	S	S	S
		FS3	S	S	S
B E H T A B R I D G E	BB1	TC1	S	R	S
		TC2	S	R	R
		TC3	S	R	R
		FC1	R	R	R
		FC2	S	R	S
		FC3	S	S	S
		FS1	S	R	R
		FS2	S	R	S
		FS3	S	R	S
	BB2	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	R
		FC2	R	R	S
		FC3	S	R	R
		FS1	S	R	R
		FS2	S	R	S
		FS3	S	R	S

	BB3	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	S
		FC2	S	R	R
		FC3	S	R	R
		FS1	S	R	S
		FS2	R	R	S
		FS3	S	R	S

TABLE NO. 2 Summer Season

SAMPLING SITE	SAMPLE	ISOLATES	ANTIBIOTIC RESISTANCE		
			AMPICILINE	TETRACYCLINE	CEFIXIME
BHANVARESHVARTE	BT1	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	S
		FC2	R	R	R
		FC3	S	S	S
		FS1	S	R	R
		FS2	S	R	R
		FS3	R	R	R
	BT2	TC1	S	R	S
		TC2	S	S	S
		TC3	S	R	R
		FC1	S	R	R
		FC2	R	R	R
		FC3	S	R	S
		FS1	R	R	S
		FS2	S	R	R
		FS3	S	R	S
	B	TC1	S	R	S

M P L E	T 3	TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	R
		FC2	S	R	R
		FC3	S	R	S
		FS1	R	S	R
		FS2	S	S	S
		FS3	S	R	S
R A J G H A T	R G 1	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	R
		FC2	S	R	S
		FC3	S	R	S
		FS1	S	R	R
		FS2	R	S	S
		FS3	S	R	S
	R G 2	TC1	S	R	R
		TC2	S	R	S
		TC3	S	R	R
		FC1	R	R	R
		FC2	S	R	R
		FC3	S	R	S
		FS1	R	R	S
		FS2	S	R	S
		FS3	S	S	S
	R G 3	TC1	S	S	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	R
		FC2	R	R	S
		FC3	R	R	S

		FS1	S	R	R
		FS2	S	R	S
		FS3	S	R	S
S H A H E E D S M A R A K	S S 1	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	R
		FC2	S	R	R
		FC3	R	R	R
		FS1	S	R	S
		FS2	S	R	S
		FS3	S	R	S
	S S 2	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	S
		FC2	S	R	R
		FC3	S	R	R
		FS1	S	S	R
		FS2	S	S	S
		FS3	S	S	S
	S S 3	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	S
		FC2	S	R	R
		FC3	S	R	R
		FS1	R	R	R
		FS2	S	R	R
		FS3	S	R	R
	B B	TC1	S	R	S
		TC2	S	R	S

BEHTABRIDGE	1	TC3	S	R	S
		FC1	R	R	S
		FC2	R	R	S
		FC3	S	R	S
		FS1	S	S	S
		FS2	S	R	R
		FS3	S	R	S
	BB2	TC1	S	R	S
		TC2	S	R	S
		TC3	S	S	S
		FC1	S	R	S
		FC2	S	R	S
		FC3	S	R	R
		FS1	R	R	S
		FS2	S	R	R
		FS3	S	R	S
	BB3	TC1	S	R	R
		TC2	S	R	S
		TC3	S	R	R
		FC1	R	R	R
		FC2	R	S	S
		FC3	S	S	S
		FS1	S	R	R
		FS2	S	R	S
		FS3	S	R	S

TABLE NO. 3Monsoon Season

SAMPLING SITE	SAMPLE	ISOLATES	ANTIBIOTIC RESISTANCE		
			AMPICILINE	TETRACYCLINE	CEFIXIME
	BT1	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	R

BHANVARESHVARTEMPLE		FC1	S	R	S
		FC2	R	R	R
		FC3	S	R	S
		FS1	S	R	S
		FS2	S	R	R
		FS3	S	R	R
	BT2	TC1	S	R	R
		TC2	S	R	R
		TC3	S	R	R
		FC1	S	R	S
		FC2	S	R	S
		FC3	S	S	R
		FS1	S	R	S
		FS2	R	R	R
		FS3	S	R	S
	BT3	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	R
		FC1	S	R	R
		FC2	S	S	R
		FC3	S	R	S
		FS1	S	R	S
		FS2	S	R	S
		FS3	S	R	R
RAJG	RG1	TC1	S	S	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	R
		FC2	S	R	R
		FC3	R	R	S
		FS1	R	S	S
		FS2	S	R	S

H A T		FS3	S	S	R
	R G 2	TC1	S	S	R
		TC2	S	R	R
		TC3	S	R	R
		FC1	S	R	S
		FC2	S	R	S
		FC3	S	R	R
		FS1	S	R	R
		FS2	S	R	S
		FS3	S	R	S
	R G 3	TC1	S	R	R
		TC2	S	R	S
		TC3	S	R	R
		FC1	S	SR	S
		FC2	S	R	S
		FC3	S	R	S
		FS1	S	R	R
		FS2	S	R	S
		FS3	S	R	S
S	S S 1	TC1	S	R	R
		TC2	S	R	S
		TC3	S	R	R
		FC1	S	R	R
		FC2	S	S	R
		FC3	S	R	S
		FS1	S	R	S
		FS2	R	R	S
		FS3	S	R	S
		TC1	S	R	R
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	S

H A H E E D S M A R A K	S S 2	FC2	S	R	R
		FC3	S	R	R
		FS1	S	R	R
		FS2	S	S	S
		FS3	S	R	S
	S S 3	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	S
		FC1	S	R	S
		FC2	S	R	R
		FC3	S	R	S
		FS1	S	R	R
		FS2	S	S	S
		FS3	S	R	R
B E H T A B R I D G E	B B 1	TC1	S	R	R
		TC2	S	R	R
		TC3	S	R	R
		FC1	S	R	S
		FC2	S	R	S
		FC3	S	R	R
		FS1	S	R	R
		FS2	S	S	R
		FS3	S	S	S
	B B 2	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	R
		FC1	R	R	S
		FC2	R	R	R
		FC3	S	R	S
		FS1	S	R	R
		FS2	S	R	R
		FS3	R	R	S

	B B 3	TC1	S	R	S
		TC2	S	R	S
		TC3	S	R	R
		FC1	S	R	R
		FC2	S	R	S
		FC3	S	R	S
		FS1	S	R	R
		FS2	S	R	R
		FS3	S	R	S

Important diseases caused by microbe contamination include Salmonella spp., enteropathogenic E. coli, and Vibrio spp. The genus Salmonella has over 2400 serotypes, most of which are considered endemic public health issues worldwide (Baker et al, 1983; Baggesen et al, 2000; Soto et al, 2006). Enteric-coated salmonella servers Typhimurium has been connected to water-borne infections in humans and animals (Davies, 2001; Kariuki et al, 1999; Martinez-Urtaza et al, 2004). It is a prevalent cause of gastrointestinal disease in many countries (Soto et al, 2006). Antimicrobial resistance, integron and plasmid profiles, and random amplified polymorphic DNA typing are used in its diagnosis. Microorganisms may be found in a variety of natural habitats, and their diversity and abundance can be used as indicators of the appropriateness of the water, according to Okpokwasili and Akajobi (1996). A reduction in water quality and the negligent use of heavy metal-containing fertilizers and pesticides in agriculture have led to major environmental issues that endanger aquatic biodiversity and human health. These operations include mining, the final disposal of waste effluents, both treated and untreated, that include hazardous metals, and the extraction of metal chelates from a variety of businesses, including thermal power plants, tanneries, steel mills, and battery manufacturers.

One of the main concerns in clinical medicine today is the widespread emergence of antibiotic resistance, especially multidrug resistance, among bacterial diseases. Environments tainted with antibiotics promote selection and aid in the development of resistant microbes. Due to the potential health risk, a great deal of study has focused on antibiotic-resistant bacteria from a variety of ecosystems. One of the main concerns in clinical medicine today is the widespread emergence of antibiotic resistance, especially multidrug resistance, among bacterial diseases. Antibiotic-contaminated settings promote the establishment of resistant

bacteria and drive selection.Due to the potential health risk, a great deal of study has focused on antibiotic-resistant bacteria from a variety of ecosystems.

Conclusion

Different isolates were analysed for Antibiotic test at different season (Table No. 1,2and 3).Result of Antibiotic tests were suggested that tetracycline was more resistance to various isolates and cefixime antibiotic showed less resistant than tetracycline and ampicillin was more sensitive for various isolates. This research is telling that river was more contaminated in Monsoon season.Increasing MPN count of the river samples is alarming and threat to environmentin view of human health.Increasing antibiotic resistanceamong environmental isolates is also a serious concern and needs more attention.

References

1. Baggesen D L, Sandvang D and Aarestrup F M (2000) Characterization of *Salmonella enterica* serovar *Typhimurium* DT104 isolated from Denmark and comparison with isolates from Europe and the United States. *J. Clin. Microbiol.* **38**, 1581–1586.
2. Baker D A, Smitherman R O and McCaskey T A (1983) Longevity of *Salmonella typhimurium* in *Tilapia aurea* and water from pools fertilized with swine waste. *Appl. Environ. Microbiol.* **45**, 1548– 1554.
3. Chigor VN, Umoh VJ, Okuofu CA, Ameh JB, Igbinosa EO, Okoh AI. Water quality assessment: Surface water sources used for drinking and irrigation in Zaria, Nigeria are a public health hazard. Environ Monit Assess. 2012; 184:3389–3400.
4. Chigor VN, Umoh VJ, Smith SI. Occurrence of Escherichia coli O157 in a river used for fresh produce irrigation in Nigeria. Afr J Biotechnol. 2010;9: 178–82.
5. Davies R H (2001) *Salmonella typhimurium* DT104: has it had its day? *In Pract.* **23**, 342–351.
6. Gupta, G.S. and Orbán, A., 2018. Water is life, life is water:(Un) sustainable use and management of water in the 21st century. Corvinus Journal of Sociology and Social Policy, 9(1), pp.81-100.
7. Hunter PR, Syed Q. Community surveys of self-reported diarrhea can dramatically overestimate the size of outbreaks of waterborne cryptosporidiosis. Water Science and Technology. 2001;43(12): 27-30.
8. Igbinosa EO, Okoh AI. Impact of discharge wastewater effluents on the physicochemical qualities of a receiving watershed in a typical rural community. Int J Environ Sci Technol. 2009;6:175–82.

9. Kamble, B. S., Saxena, P. R., Kurakalva, R. M., Shankar, K. (2020). Evaluation of seasonal and temporal variations of groundwater quality around Jawaharnagar municipal solid waste dumpsite of Hyderabad city, India. SN Applied Sciences., 2(3), 1-22.

10. Kariuki S, Gilks C, Kimari J, Muyodi J, Waiyaki P and Hart C A (1999) Analysis of *Salmonella enterica* serotype *Typhimurium* by phage typing, antimicrobial susceptibility and pulsed-field gel electrophoresis. *J. Med. Microbiol.* **48**, 1037–1042.

11. Kistemann T, Classen T, Koch C, Dagendorf F, Fischeder R, Gebel J, Vacata V, Exner M. Microbial load of drinking water reservoir tributaries during extreme rainfall and runoff. Appl Environ Microb. 2002; 68:2188–97.

12. Lata P, Ram S, Agrawal M, Shanker R. Enterococci in river Ganga surface waters: propensity of species distribution, dissemination of antimicrobial-resistance and virulence-markers among species along landscape. BMC Microbiol. 2009; 9:140

13. MacKenzie, WR, Hoxie NJ, Proctor ME, Gradus MS, Blair, KA, Peterson DE, Kazmierczak JJ, Addiss DG, Fox KR, Rose JB, Davis JP. A massive outbreak in Milwaukee of Cryptosporidium infection transmitted through the public water supply. New England Journal of Medicine. 1994; 331:161-7.

14. Martinez-Urtaza J, Liebana E, Garcia-Migura L, Perez-Pin˜eiro P and Saco M (2004) Characterization of *Salmonella enterica* serovar *Typhimurium* from marine environments in coastal waters of Galicia (Spain). *Appl Environ Microbiol.* **70**, 4030–4034.

15. Mohsin, M., Safdar, S., Asghar, F., Jamal, F. (2013). Assessment of drinking water quality and its impact on residents' health in Bahawalpur city. Int. J. of Humanities and Social Sci., 3(15), 114-128.

16. Odjadjare EEO, Obi LC, Okoh AI. Municipal wastewater effluents as a source of listerial pathogens in the aquatic milieu of the Eastern Cape Province of South Africa: A concern of public health importance. International Journal of Environmental Research and Public Health. 2010; 7:2376–94

17. OGWO, P.A., and OGU, O.G., 2014 "Impact of Industrial Effluents Discharge on the Quality of Nwiyi River Enugu South Eastern Nigeria", IOSR Journal of Environmental Science, Toxicology and Food Technology, vol.8, no.11, pp. 22-27.

18. Okoh AI, Odjadjare EE, Igbinosa EO, Osode AN. Wastewater treatment plants as a source of microbial pathogens in the receiving watershed. Africa Journal of Biotechnology. 2007; 6:2932–44.

19. Okpokwasili G C and Akujobi T C (1996) Bacteriological indicators of tropical water quality. *Environ. Toxicol. Water Qual.***11**(2), 7 7 - 8 1.

20. Servais P, Billen G, Goncalves A, Garcia-Armisen T. Modelling microbiological water quality in the Seine River drainage network: past, present and future situations. Hydrology and Earth System Science 2007; 11:1581–92.

21. Soto S M, Rodrý´guez I, Rodicio M R, Vila J and Mendoza M C (2006) Detection of virulence determinants in clinical strains of *Salmonella enterica* serovar *Enteritidis* and mapping on macro restriction profiles. *J. Med. Microbial.* **55**, 365–373.

22. Vinay S. Baghel, Krishna Gopal, Sanjay Dwivedi, Rudra D. Tripathi (2005) "Bacterial indicators of faecal contamination of the Gangetic River system right at its source". Ecological Indicators 5 49–56

23. Vineeta Kumari, Girdhari Lal Chaurasia (2015) "Study of Water Quality Status of Sai River in Uttar-Pradesh with Reference to Water Quality Index Assessment" International Journal of Innovative Research in Science, Engineering and Technology Vol. 4, Issue 1.

24. Williams AP, Quilliam RS, Thorn CE, Cooper D, Reynolds B, Jones DL. Influence of land use and nutrient flux on Nwabor et al.; IJTDH, 12(4): 1-14, 2016; Article no. IJTDH.21895 11 metabolic activity of E. coli O157 in river water. Water Air Soil Pollute. 2012;223: 3077–83

25. World Health Organization (WHO). Heterotrophic Plate Counts and Drinking water safety. Edited by J. Bartram; 2003.

26. World Health Organization. (2017). Guidelines for Drinking water Quality. https://www.who.int/ tea ms/environment-climate-change-and-health/watersanitation-and-health/water-safety-and-quality/drinking-water-quality-guidelines.