



Microbiological Study of Solid Waste from CETP Naroda

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Article info

Received: 29/11/2025

Revised: 22/12/2025

Accepted: 10/01/2026

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Abstract

In this study, solid waste samples were collected from the Common Effluent Treatment Plant Naroda Enviro Projects Limited (NEPL-CETP) located at Naroda. Ahmedabad GIDC and microbial studies were conducted to determine the presence of bacterial and fungal communities. This is a wastewater plant where solid waste is separated into primary and secondary by biological methods. The samples were analysed. Solid waste is managed safely and scientifically as per the norms of Gujarat Pollution Control Board.

Key-words: Wastewater; Solid waste; Microorganisms; NEPL

Introduction

Water is treated to reduce pollutants. When solid waste is separated and removed, it contains many types of impurities, including organic and inorganic substances, as well as microorganisms. Wherever there is the presence of decaying organic matter, microorganisms are present. Wastewater from domestic and industrial sources contains various pollutants, including organic matter, nutrients, toxic chemicals and microorganisms, which can harm the environment if left untreated. Effluent Treatment Plants (ETPs) use physical, chemical and biological processes to reduce these pollutants, in which biological treatment plays a major role due to its efficiency and environmentally friendly nature. Microorganisms present in wastewater and sludge are responsible for the degradation of organic matter (The Role of Microorganisms in Wastewater-2024). The composition and activity of these microbial communities directly influence the treatment performance and quality of the effluent. Since the amount of microorganisms in

sludge is high, it is necessary to study its microbiology to assess the treatment efficiency and prevent environmental and public health hazards. In the present study, microbiological analysis of solid waste (sludge) from CETP, Naroda was carried out using culture-based techniques. Selective and differential media were used to isolate and identify different groups of bacteria based on their growth characteristics and biochemical properties (Forbes, Sahm, & Weissfeld, 2007).

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In addition, nutrient agar supplemented with sodium chloride (NaCl) was used to isolate bacteria capable of growing under high-TDS conditions (Madigan *et al.*, 2018). This approach enables the identification of halotolerant and alkali-resistant bacteria present in CETP sludge. The findings of this study contribute to a better understanding of the microbial population in CETP sludge and provide insight into microbes that can survive and function in high salinity environments, which may have potential applications in bioremediation and wastewater treatment processes. And it is useful for biological treatment of polluted water by helping to decompose organic matter.

Methodology

Sludge samples were collected from different treatment stages (as given in fig.1). Chemical effluent sludge was collected from primary, secondary, and tertiary treatment units, while sludge from sewage, food, and textile effluents was collected from primary and secondary treatment units. For microbial analysis, a general dilution technique was followed by weighing 1gm of sludge sample and diluting it in 9 mL of sterile distilled water or saline to obtain a 10^{-1} dilution. The sample was vortexed thoroughly, and serial dilutions were prepared up to 10^{-6} using sterile test tubes. Bacterial enumeration was carried out (Rakesh J. Patel & Kiran R. Patel, 2015) isolating microorganisms on nutrient agar (NA) medium. Plates were labelled as 10^{-5} and 10^{-6} for each sample, and 0.1 mL from the respective dilutions was aseptically plated and spread using a sterile glass spreader. All plates were incubated at 37°C for 24–48 hours for bacterial growth. Isolation on selective and differential media was performed by plating 0.2 mL from the 10^{-1} dilution onto sterile potato dextrose agar (PDA) and spreading aseptically (Deacon, 2005).

Additionally, loopful of the sample were streaked on MacConkey's and XLD agar plates. MacConkey's and XLD plates were incubated at 37°C for 24–48 hours, whereas PDA plates were incubated at 25°C for 5–7 days. For the isolation of anaerobic microorganisms, screw-cap tubes containing Robertson's Cooked Meat Medium were labelled for 10^{-5} and 10^{-6} dilutions. Loopful of the respective samples were inoculated into the

medium, sealed with parafilm where required, and incubated at 37°C for 40–48 hour (APHA,2023).

Results and Discussion



Fig. 1 Different type of Sample Collections

PST: Primary settling tank (Decanter)

T-2: Tubesettler-2

T-1: Tubesettler-1

S-1: Secondary Clarifier-1

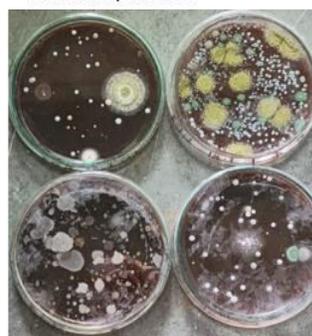


Fig. 2 Potato Dextrose Agar (PDA)



Fig.3 Robertson's Cooked Meat Medium

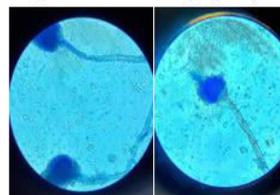


Fig.4&5 Microscopic examination of Fungi (*Aspergillus sp.*)

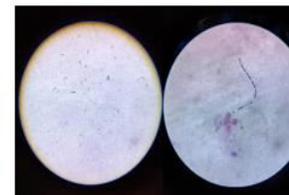


Fig. 6&7 Gram positive rods (Bacilli)



Fig. 8&9 N-Agar Plates.



Fig. 10&11 N-Agar with NaCl

presence of filamentous fungi like *Aspergillus* or

Fungi (<i>Aspergillus</i> <i>sp.</i>)	SAMPLE	PURPOSE	SHAPE	SIZE	COLOUR	TEXTURE	ELEVATION	OBSERVATION
MEDIA N-Agar	1.PST 2.T-2 3.T-1 4.S-1	Total viable counts	Circular	Small to medium	White/creamy; bluish green	Mucoid/Sticky	Flat; convex	Maybe the presence of <i>Bacillus spp.</i> or <i>Pseudomonas spp.</i>
Mac-Conkey's Agar	1.PST 2.T-2 3.T-1 4.S-1	Detection of coliforms	Circular	Small	Pale yellow	Smooth	Convex	Non-lactose fermenting colonies were observed; maybe the presence of <i>Pseudomonas spp.</i> or <i>Salmonella spp.</i>
XLD	1.PST 2.T-2 3.T-1 4.S-1	Detection of salmonella sp.	Circular	Small	Black centred; pink/red colonies	Smooth and mucoid	Slightly raised	Black centred; red pigmented colonies of <i>Salmonella spp.</i> were observed.
PDA	1.PST 2.T-2 3.T-1 4.S-1	Detection of fungi	Irregular	Large	Green, black, white and brown	Dry; powdery growth	Irregular; fuzzy	Likely the presence of <i>Aspergillus spp.</i> or <i>Penicillium spp.</i>
N-Agar with NaCl High TDS	1.PST 2.T-2 3.T-1 4.S-1	Detection of halophiles	Circular; lawn growth	Small	White	Dry; mucoid	Flat	Halophiles were grown; likely to be <i>Bacillus spp.</i>

The microbial analysis of sludge samples revealed a diverse population of bacteria and fungi. Growth on Nutrient Agar indicated a high total viable bacterial count, with probable presence of *Bacillus spp.* and *Pseudomonas spp.*(fig.8 & 9). Non-lactose fermenting colonies observed on MacConkey's agar, along with black-centred colonies on XLD agar, suggest the possible presence of pathogenic bacteria such as *Salmonella spp.* (Forbes, Sahn, & Weissfeld, 2007). Growth of anaerobic microorganisms was observed in Robertson's Cooked Meat Medium (fig.3). Fungal growth on PDA, characterized by dry, powdery, pigmented colonies, indicates the

Penicillium spp. (fig. 2). Additionally, growth on high-salinity Nutrient Agar reflects the occurrence of halotolerant microorganisms(fig.10 & 11). These findings highlight the complex microbial nature of sludge and the need for proper treatment before disposal.

Conclusion

The observed results indicate that the existing treatment processes at the CETP are effective in reducing pollutant loads and supporting controlled biological activity. The microbial diversity detected, including both heterotrophic and specialized microorganisms, reflects an efficiently functioning treatment system operating under

appropriate environmental conditions. Overall, the performance of NEPL CETP is largely in accordance with applicable CPCB and environmental guidelines, highlighting the importance of continued monitoring and optimized sludge management to maintain compliance and ensure sustainable environmental protection.

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Cite this article as:

Verma A., Mayekar H., Yadav N., Khan B. and Patel S. S. (2026). Microbiological Study of Solid Waste from CETP Naroda *Int. J. of Pharm. & Life Sci.*, 17(1):19-22.

Source of Support: Nil

Conflict of Interest: Not declared

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