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Assessment of Indigenous Bacterial Communities for Bioremediation of Pulp and Paper Mill Wastewater

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Abstract: *The pulp and paper industry contributes significantly to environmental pollution due to the generation of chemically complex wastewater rich in recalcitrant organic compounds. Conventional physicochemical treatments have mainly been proven inadequate in completely remediating these effluents. This study investigates the biodegradation capacity of indigenous bacterial communities remoted from wastewater generated by KR Pulp and Papers Ltd., Uttar Pradesh, India. Through physicochemical profiling, microbial isolation, enzymatic assays, and pollutant evaluation, the research highlights the function of bacterial consortia in degrading continual pollutants like lignin and chlorinated organics. The findings emphasize the feasibility of bacterial treatment as a sustainable and scalable alternative to traditional methods, with implications for environmental protection and business sustainability*

Keywords: pulp and paper industry

I. INTRODUCTION

1.1 Background

The pulp and paper industry, a huge cornerstone of modern industrialization, is very much known for its high resource consumption as well as environmental footprint (Sharma *et al.*). Wastewater discharged from pulping and bleaching operations is a first-rate concern because of its darkish color, high Chemical Oxygen Demand (COD), Biological Oxygen Demand (BOD), and poisonous parts, including lignin derivatives, chlorinated organics, tannins, and heavy metals.

1.2 Problem Statement

Conventional wastewater treatments—comprising coagulation, sedimentation, and oxidation—fail to remove recalcitrant pollutants adequately, especially under variable industrial conditions. Moreover, the lack of perception of microbial metabolic pathways limits the optimization of organic tactics (Tripathi *et al.,* 2021). This study addresses these gaps by exploring the potential of native bacterial lines for pollutant degradation.

II. LITERATURE REVIEW

According to a study by Sharma (2021), the profiling of microbial communities in pulp and paper industry wastewater reveals a very significant potential for bacterial adaptation and detoxification in metal-polluted environments. The studies highlight the usage of metagenomic evaluation, especially targeting the 16S rRNA V3-V4 vicinity, as an effective approach to understanding the variety and purposeful roles of microbial populations in such complex waste streams. The observer recognized dominant bacterial phyla, including Proteobacteria, Bacteroidetes, Firmicutes, and others, showcasing the resilience and adaptability of microbial communities in the presence of heavy metals and excessive natural hundreds. These microbes have been discovered to play a vital role in breaking down pollution and facilitating natural remediation processes (Sharma *et al.,* 2021). The findings recommend that in spite of the variation in

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microbial distribution, lots of those bacteria possess the enzymatic functionality to oxidize and detoxify industrial contaminants, supporting their utility in sustainable wastewater treatment strategies. By demonstrating how those bacterial communities respond to environmental stressors, they have a look at contributing to the design of more powerful bioremediation technologies and emphasize the value of indigenous microbes in restoring ecological balance in polluted water bodies.

According to a study byGholami (2021), the profiling of microbial communities in pulp and paper industry wastewater reveals a significant potential for bacterial adaptation and detoxification in metal-polluted environments. The research highlights the use of metagenomic evaluation, especially targeting the 16S rRNA V3-V4 vicinity, as a powerful technique to determine the variety and functional roles of microbial populations in such complex waste streams. The examination identified dominant bacterial phyla such as Proteobacteria, Bacteroidetes, Firmicutes, and others, showcasing the resilience and flexibility of microbial communities within the presence of heavy metals and high natural masses(Gholami *et al.,* 2021). These microbes have been located to play a vital position in breaking down pollution and facilitating natural remediation approaches. The findings propose that despite the version in microbial distribution, many of these bacteria own the enzymatic functionality to oxidize and detoxify commercial contaminants, helping their software in sustainable wastewater remedy strategies. By demonstrating how these bacterial communities respond to environmental stressors, the look contributes to the layout of more effective bioremediation technology and emphasizes the cost of indigenous microbes in restoring ecological stability in polluted water bodies.

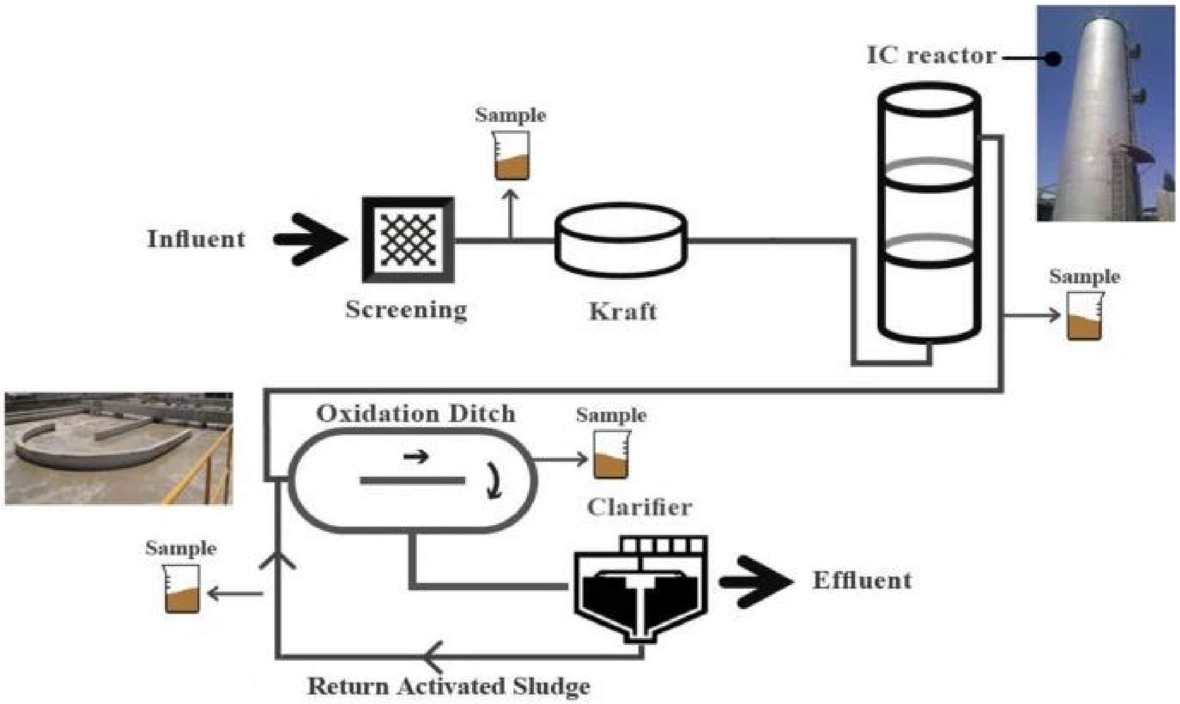

Figure 1: Indigenous Bacterial Communities for Bioremediation of Pulp and Paper Mill Wastewater
(Source: Gholami *et al.,* 2021)

In the opinion of Tyagi (2021), the study discusses the bacterial diversity present within the wastewater treatment systems of Indian paper industries, highlighting its actual relationship with water quality as well as pollution levels. The research employed gene amplicon sequencing of the 16S rRNA location to pick out the structure and network profile of bacterial populations inside the effluent. The evaluation discovered a numerous range of bacterial phyla, consisting of Bacteroidetes, Proteobacteria, Patescibacteria, Firmicutes, and Actinobacteria, with numerous genera such as Cloacibacterium, Aerococcus, Chryseobacterium, and Acinetobacter contributing to key metabolic features. These functions concerned the breakdown and transformation of complicated compounds through methods like carbohydrate metabolism and fatty acid degradation. The findings indicated that the microbial community composition became intently linked to the physicochemical parameters of the wastewater, which include chemical oxygen call for, biochemical oxygen call for, and overall suspended solids, which have been discovered to be above advocated environmental limits. This correlation suggests that microbial variety can serve as a bioindicator of water fine and pollution intensity in commercial wastewater(Tyagi *et al.,* 2021). The study emphasized the importance of knowledge of microbial community dynamics to enhance treatment efficiency and broaden centered bioremediation strategies. By characterizing the purposeful roles of precise bacteria, the studies contribute to the optimization of biological procedures in wastewater control and support the implementation of sustainable practices inside the paper enterprise. The integration of microbial and chemical records gives valuable perception into how indigenous microbial populations reply to commercial pollution and may be harnessed for more powerful environmental interventions.

III. OBJECTIVES

- To characterize pollutants in pulp and paper mill wastewater.
- To isolate and identify native bacterial strains.
- To evaluate enzymatic activity (laccase, LiP, MnP) for pollutant degradation.
- To assess growth conditions and microbial synergy in bioremediation.
- To propose a scalable bacterial treatment strategy for industrial use.

IV. METHODOLOGY

This study adopted an actual integrated experimental approach to mainly investigate the biodegradation potential of the indigenous bacterial strains present within the wastewater of KR Pulp and Papers Ltd., located in Uttar Pradesh, India. The method protected systematic pattern collection, physicochemical evaluation of the effluent, bacterial isolation and characterization, and enzymatic screening to assess the bioremediation ability of the native microbial communities.

4.1 Sampling and Physicochemical Analysis

Effluent samples were collected from multiple discharge points within the wastewater treatment facility of KR Pulp and Papers Ltd. Sterilized glass bottles were used to save contamination. The series was changed to be executed at distinct instances of the day and across several days to account for fluctuations in wastewater composition because of operational adjustments. The samples have been immediately stored in cool, insulated packing containers and transported to the laboratory for further analysis.

Once in the laboratory, the samples underwent particular physicochemical characterization following the usual techniques prescribed by the American Public Health Association (APHA). The parameters analyzed covered pH, Chemical Oxygen Demand (COD), Biological Oxygen Demand (BOD), Total Suspended Solids (TSS), and Total Dissolved Solids (TDS). The pH is measured by the usage of a calibrated digital pH meter, presenting insights into the acidity or alkalinity of the effluent, which directly impacts microbial survival and enzymatic features(Saxena *et al.,* 2021). COD and BOD have been decided through dichromate oxidation and respirometric strategies, respectively, which mirror the levels of organic pollution and biodegradability. TSS and TDS were assessed via gravimetric strategies after filtration and drying.

To pick out the specific natural pollutants present inside the wastewater, Gas Chromatography-Mass Spectrometry (GC-MS) was hired. Prior to analysis, organic compounds had been extracted using a liquid-liquid extraction method with ethyl acetate because of the solvent. The extracted samples were then focused and analyzed via GC-MS, enabling the identity of poisonous materials, which include lignin derivatives, chlorinated phenols, and resin acids. This analysis helped decide the types of pollution that the bacterial isolates would be tested towards throughout the biodegradation trials.

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4.2 Bacterial Isolation and Identification

Bacterial isolation was performed using the serial dilution technique, which was particularly followed by plating on that for selective nutrient agar media. Effluent samples have been serially diluted in sterile saline answers and plated to inspire the increase of awesome colonies. Different subculture media, which include nutrient agar, tryptic soy agar, and lignin-supplemented media, were used to target numerous bacterial companies.

Once grown, colonies were selected based totally on versions in morphology, including coloration, form, texture, and elevation. Each selected colony changed into further purification through sub-culturing(Sharma *et al.,* 2021). Morphological identification changed and was complemented by biochemical characterization and the use of trendy microbiological assessments. These blanketed Gram staining, catalase, and oxidase exams, nitrate reduction, and carbohydrate fermentation profiling. The consequences have been move-referenced with Bergey's Manual of Systematic Bacteriology to achieve genus-stage or species-level identification of the isolates.

4.3 Enzymatic Activity Screening

Qualitative enzymatic screening was effectively conducted to assess the biodegradation potential of the bacterial isolates. The consciousness was on identifying ligninolytic enzyme activity, which is critical for breaking down recalcitrant natural compounds together with lignin. The tests blanketed guaiacol and Azure B agar plate assays(Kumar *et al.,* 2021). In the guaiacol assay, the oxidation of guaiacol through laccase or peroxidase enzymes resulted in a reddish-brown halo-round bacterial colonies, indicating enzyme pastime. In the Azure B assay, decolorization around colonies suggested lignin peroxidase hobby. Manganese peroxidase activity was additionally examined through the usage of media supplemented with manganese salts and suitable indicators. Bacterial isolates that confirmed sturdy enzymatic hobbies have been shortlisted for similarly in-intensity biodegradation experiments.

V. RESULTS AND DISCUSSION

5.1 Physicochemical Profile of Effluent

The wastewater samples collected from KR Pulp and Papers Ltd. displayed severe environmental contamination, confirmed by an actual range of the physicochemical parameters. The effluent confirmed a dark brown color, a feature of high lignin and tannin content, which also contributes to decreased light penetration in aquatic ecosystems. Laboratory analyses discovered elevated ranges of Chemical Oxygen Demand (COD), Biological Oxygen Demand (BOD), Total Dissolved Solids (TDS), and Total Suspended Solids (TSS), far exceeding standard permissible limits(Verma*et al.,* 2021). The excessive COD and BOD values mediated the presence of huge quantities of oxidizable and biodegradable natural fabric, indicative of a massive natural load that would significantly expand dissolved oxygen in natural water bodies, affecting aquatic life. Total dissolved and suspended solids pointed to an extra of non-degradable substances, fibers, and chemical substances ultimate in the effluent submit-processing.

Further profiling using Gas Chromatography-Mass Spectrometry (GC-MS) showed the presence of toxic and chronic natural pollution, which includes chlorinated phenols, furans, and lignin derivatives. These compounds are known to be resistant to conventional treatment strategies, and many are categorized as bioaccumulative and doubtlessly carcinogenic. Their presence underscores the want for more superior and targeted remediation tactics.

5.2 Bacterial Diversity

The microbial isolation and identification process revealed a rich and huge diversity of indigenous bacterial strains naturally present in the wastewater environment. Among the most distinguished genera identified were Pseudomonas spp., Bacillus spp., Streptomyces spp., and Cellulomonas spp. These microorganisms are normally related to environments infected by complex natural pollution and had been formerly identified for their metabolic versatility and enzymatic abilities.

Pseudomonas spp. They are widely studied for their capacity to degrade aromatic hydrocarbons and chlorinated compounds. Bacillus spp. They are regarded for their resilience under harsh conditions and their potential to provide a number of extracellular enzymes. Streptomyces spp., generally related to soil ecosystems, are also effective degraders

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of lignin and phenolic compounds(Ayalew *et al.,* 2021). Cellulomonas spp. Play an important position in cellulose and hemicellulose breakdown, contributing to the overall nutrient recycling method in wastewater.

5.3 Enzymatic Activity and Biodegradation Potential

Enzymatic screening confirmed the production of ligninolytic as well as cellulolytic enzymes across several bacterial isolates. Pseudomonas spp. Confirmed good-sized laccase activity that is instrumental within the oxidative breakdown of lignin and different fragrant pollution. These enzymes act on phenolic substrates, contributing to the discount of shade and toxicity inside the effluent.

Bacillus spp. Produced a combination of lignin peroxidase, cellulase, and hemicellulase enzymes, enabling them to degrade each lignin shape and plant-derived polysaccharides. Streptomyces spp. Have been located to secrete robust oxidative enzymes such as laccases and peroxidases(Yeber *et al.,* 2021). These strains also demonstrated the ability to shape biofilms, improving their stability and useful sturdiness in fluctuating wastewater conditions. Cellulomonas spp. It often contributes to cellulose degradation, complementing the lignin-degrading interest of different lines and helping in nutrient cycling.

The enzymatic motion of these bacteria together led to the breakdown of complicated aromatic compounds, facilitating detoxing, color discount, and a measurable decrease in COD and BOD values.

5.4 Synergistic Interactions in Bacterial Consortia

One of the most significant findings was the enhanced degradation efficiency, which was observed when multiple forms of bacterial strains were combined into the consortia. Unlike person isolates, the consortia exhibited cooperative behavior through complementary metabolic pathways and enzymatic activities. This synergy allowed for the entire breakdown of pollutant mixtures that character lines alone couldn't absolutely degrade.

The formation of microbial biofilms, in addition, stabilized bacterial interest, allowing the consortia to function correctly under various pH ranges, temperature fluctuations, and pollutant concentrations normal to commercial effluents(Haq *et al.,* 2021). This resilience makes bacterial consortia an ideal candidate for actual-world bioremediation programs. Their ability to resist environmental strain while retaining enzymatic capability helps the use of blended bacterial cultures in sustainable wastewater remedy technology.

VI. INDUSTRIAL AND ENVIRONMENTAL IMPLICATIONS

6.1 Scalability and Economic Feasibility

Biological treatment is cost-effective due to reduced chemical input as well as lower sludge generation. Indigenous bacteria eliminate the main need for foreign microbial introduction, minimizing biosafety concerns.

6.2 Sustainability and Compliance

The integration of bacterial systems helps industry compliance with international environmental standards (e.g., Stockholm Convention) and contributes to the UN Sustainable Development Goals (SDGs), especially SDG 6 (Clean Water and Sanitation).

VII. CONCLUSION

This study establishes the ability of indigenous bacterial groups to remediate pulp and paper mill wastewater efficiently. The diagnosed strains exhibit full-size enzymatic pastime, capable of degrading continual pollutants underneath industrially relevant conditions. Biological treatment offers a sustainable, reasonable, and scalable alternative to conventional strategies. Further research must be conducted on optimizing microbial consortia dynamics, applying omics technology, and pilot-scale implementation to allow enterprise-wide adoption.

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