



# Impact of Textile Effluent on Bacterial Biodiversity In Noyyal River Bed Soil, Tirupur.

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**Abstract:** Bacteria are the most important living organisms and abundant organisms in the soil which perform various biological activities. Tirupur is a textile city located on the banks of noyyal river. Most of the textile based dyeing houses are located on the banks of the noyyal river in tirupur which contribute to the abundant release of dye effluent and sludges into the river. The present experiment is designed to evaluate the extent to which bacterial biodiversity has been affected in the noyyal river bed soil in comparison with wasteland soil and cultivable soil. The plate counting method is used to evaluate the bacterial growth and basic composition of bacterial species in different soil samples. The bacterial growth and basic composition of bacterial species increased in the order of noyyal river bed soil, wasteland soil and cultivable soil. The recording of decreased bacterial growth and bacterial species in noyyal river bed soil is due to the contamination of dye effluent in the river. From the experimental results, it is clearly understood that the sufficient effluent treatment plants are to be installed very close to the Noyyal river in order to save both soil microorganisms and the environment.

**Keywords:** Abundant, Effluent, Biodiversity, Contamination and Environment.

## Introduction

Bacteria are the most important living organisms and abundant organisms in the soil in view of the fact that the decomposition of organic matter, decontamination of toxic substance, fix up nitrogen, potassium, phosphorus, and other subordinate trace minerals, and provide the ability to transform into suitable habitats for plants and soil-based organisms (Jacoby et., 2017). The diversity of bacteria in soil depends on their chemical composition, moisture, pH, and structure. Human activity has a necessary influence on the emergence of ecosystems ( Furtak K and Gajda AM, 2018). The pollutants affecting the environment formed from various steps committed in the textile industries fabricate different ecological difficulties due to the propagation of a large amount of wastewater encompassing pollutants (Hossain et al., 2018).Textile industry wastewater is composed of a variety of endurance coloring pollutants and synthetic dyes, phenols, formaldehyde, phthalates, surfactants, chlorophenol and aromatic compounds and heavy metals such as lead (Pb), cadmium (Cd), arsenic (As), chromium (Cr), zinc (Zn), and nickel (Ni), chlorides, and sulfates (Kishor et al., 2021). The primary cause for damaging the soil environment is due to the addition of synthetic chemicals, pigments, and dyes that creates complexity in wastewater effluents and sludge (Chen et al., 2021; Manickam and Vijay, 2021; Methneni et al., 2021). Dye effluent discharged from textile industries is a major cause of soil and soil bacterial infestation in cities with high levels causing major changes in the growth of soil-based bacteria and diversity of bacteria (Krishnamoorthy et al., 2020). Microbes play a crucial role in decontaminating polluted sites and degrading the pollution load of textile effluent sedimented in soil (Prabha et al, 2016). Tirupur is a textile city in Tamilnadu with a large number of textile industries. There are several hundreds of dye units around the city

of Tirupur mostly along the banks of the noyyal river. The textile industry here produces more than average cotton garments, less terry cotton garments and very less polyester fabrics. Alkaline dyes are widely used in dye factories to apply dye to fabrics. The water is frequently used in various processes of dyeing. The wastewater must be thoroughly treated for the removal of sludge and effluent before leaving the dyeing unit that may not pollute and contaminate the water and soil. But the wastewater is released directly into the noyyal river or adjoining water channel that leads into the noyyal river without undergoing any wastewater treatment. Even though various research studies have been carried out on the impact of effluent on various ecological factors of the surrounding environment and microbial distribution in effluent discharged wastewater and effluent contaminated soil. The effect of untreated effluent water and sludges that contaminate soil may have adverse effects on the soil biodiversity and their growth yet to be found out. Hence the present work is designed to evaluate the extent to which bacterial biodiversity has been affected in the noyyal river bed soil in comparison with wasteland soil and cultivable soil.

## **Materials and Methods**

### **Study area**

For the present study, three different soil samples were collected from each area of agricultural land, wasteland and dyeing sites. The first soil samples were taken from cultivable land or agricultural land found in periya negamam area nearly 40 kilometres away from the dyeing sites of tirupur. The second soil samples were taken from the wasteland area of Chinnur via Palladam, 20 kilometres away from tirupur. The third soil samples collected from dyeing sites of vanjipalayam area found along the banks of noyyal river.

### **Plate count method**

The quantitative determination of bacterial populations was carried out by the plate count method. The soil samples were collected in sterile glass bottles and they were taken to the laboratory for counting.

### **Counting of bacterial population**

There are various steps to the technique and all must be carried out precisely in order to procure unerring results.

1ml of sample is added to 9ml of a sterile buffer as diluent. The sample and sterile buffer are mixed together. This new sample has a concentration 1/10th that of the original sample. Again 1ml of new sample is added to another 9ml of sterile buffer. Now it is 1/100th that of the original sample. This process is repeated until we have a series of dilutions

To find out how many viable bacterial species are in each of our dilutions we need to put some of the sample onto an agar plate. 0.1ml of sample is pipetted onto the agar surface and spread around using a sterile glass rod. This is repeated so that we have 2 or 3 replicate plates for our original sample and for each of our dilutions. Once all of the plates have been prepared they are left to dry and then moved to an incubator at a suitable growth temperature for the microorganism being studied. The plates were kept at 37°C for 48–72 hours.

The incubation time depends on the organism and the growth medium but during the incubation, each viable cell that was spread to a discrete position on the agar surface will grow and divide many times to form a visible colony of microorganisms. After the incubation period we can count the colonies to determine how many microorganisms were present in the original sample.

The plates will have different numbers of colonies depending on the dilution of the sample. If there are too many colonies it can be impossible or very difficult to count them. If there is only a small number of colonies it is easy to count them but the results are prone to error. The petri dishes, which contained 30–300 bacterial colonies, were selected

for enumeration of bacterial colonies and the bacterial populations were expressed as the number of colony forming units per gram or ml (CFU/gm or ml) of the sample analysed.

### **Basic components of bacterial species**

The remote bacterial strains with different surface structural growth characteristics were selected and restriped in air-dried nutrient agar plates to inspect the clarity or pureness of bacterial strains. The pure culture was then restriped in nutrient agar slants and kept at 4°C for supplementary studies. The bacterial strains segregated were picked up to non-specific levels following the scheme of Simudu and Aiso and Gilmour et al. The Bergey's manual of determinative bacteriology (1984–1989) was also referred in the identification process.

### **Result and Discussion**

The aggregate of heterotrophic microbial population distribution obtained from three different soils is given in Table 2. Among the three different soil source, the sum feasible computation was identified and it was found to be elevated in cultivable soil ( $89 \times 10^7$ ) followed by wasteland soil ( $74 \times 10^6$ ) and noyyal river bed soil ( $37 \times 10^4$ )

This extravagant inequality could be due to the unfavorable conditions that continued for the production of microorganisms in the noyyal river bed area. The increase in the number of bacterial colonies from noyyal river bed site to cultivable land site could be due to countless rationality. Tirupur is a city with countless numbers of small and big textile industries. Most of the dye houses are located near the banks of the Noyyal River. Dyes used for dyeing cotton and other fabrics are basically highly reactive alkaline. Most researchers have studied the dyeing of cotton with highly reactive alkaline dyes (Khatrī et al., 2015). They noticed that alkaline dyes are doing better exhaustion and fixation with cotton fibres. (Das et al., 2014). The effluent that is discharged after the dyeing work for the fabrics is completed and should be disposed of after the waste debris has been removed. Conversely, effluent and sludges discharged without effluent treatment is likely to increase alkalinity in the soil zone as it mixes with the river. Generally, if the soil alkalinity is 6.5 to 7.0, it does not affect the growth of soil based bacteria. Excess alkalinity can inhibit the growth of bacteria. Most bacteria are neutrophils, meaning they grow optimally at a pH within one or two pH units of the neutral pH of 7 (Fernández-Calviño D and Bååth E, 2010). Therefore, the growth of bacteria in soil samples taken during the course of the present experiment was examined and the bacterial species growth in noyyal river site was found to be less than the growth of bacteria in other soil samples taken from wasteland and cultivable areas. Comparatively bacterial growth was found to be higher in cultivable soil that may be due to the regular ploughing of cultivable soil that provides aeration, temperature, moisture and salt for better bacterial strains growth. The growth of bacteria in the soil of wasteland was known to be between the two. The same result was observed by Dhasarathan et al (2010) and they found that the total viable count was found to be high in cultivable soils followed by wasteland city area and fireworks sites.

**Table-1 showing the basic composition of bacterial species identified in soil collected from cultivable area, wasteland area and noyyal river bed soil, tirupur**

SL.NO.	Bacterial species	Percentage of basic composition of bacterial strains in cultivable soil	Percentage of basic composition of bacterial strains in wasteland soil	Percentage of basic composition of bacterial strains in noyyal river soil
1	Bacillus species	23%	19%	14%
2	Achromobacter species	58%	52%	12%
3	Pseudomonas species	-	-	23%
4	Corynebacterium species	56%	22%	-

5	Micrococcus species	62%	18%	-
6	Escherichia coli species	-	-	21%
7	Clostridium species	72%	32%	
8	Klebsiella species	-	6%	12%
9	Flavobacterium species	68 %	38%	-
10	Proteus Species	-	-	16%
11	Alcaligenes species	65%	37%	12%
12	Aeromonas species	-	-	17%
13	Salmonella species	-	-	21%
14	Shigella species	32%	22%	-
15	Mycobacterium species	37%	19%	08%
16	Arthrobacter species	35%	17%	10%
17	Xanthomonas species	51%	23%	-
18	Streptococcus species	-	-	13%
19	Giardia species	-	-	11%

**Table-2 showing the comparison of bacterial density obtained in cultivable soil, wasteland soil and noyyal river bed soil**

SL.NO.	Soil types	Bacterial density (cfu/gm)
1	Cultivable soil	89 x 10 <sup>7</sup>
2	Wasteland soil	74 x 10 <sup>6</sup>
3	Noyyal river bed soil	37 x 10 <sup>4</sup>

**Basic composition of bacterial species in cultivable soil, wasteland soil and noyyal river bed soil**

The aim of the present study was to isolate potential dye degrading bacteria from textile effluent contaminated soil and compared with bacterial strains of other soil samples. So that the soil sample was collected from the noyyal river bed. The present study result in table-1 conveyed that the noyyal river bed soil had the basic composition of bacterial species of Bacillus (14%), Achromobacter (12%), Pseudomonas (23%), Escherichia (21%), Klebsiella (12%), Proteus (16%), Alcaligenes (12%), Aeromonas (17%), Salmonella (21%), Mycobacterium (08%), Arthrobacter (10%), Streptococcus (13%), and Giardia(11%). This study was aimed to isolate potential dye degrading bacteria from textile effluent contaminated soil and compare with bacterial strains of other soil samples. So that the soil sample was collected from the noyyal river bed. Effluents from textile and dyeing industries cause serious pollution of soil, water and environment. Bacteria have potential ability to decolorize synthetic commercial dyes used for textile dyeing ( Mahbub et al., 2012). Further, it was noticed that the growth of bacterial species in noyyal river bed soil was found to be very poor when compared with growth of bacterial strains in wasteland soil and cultivable soil. The present study results were firmly supported by Lee et al (2020). They found that improper anthropogenic management can create soil disturbances that determine bacterial community structures, specific bacterial taxa, and their relationships with soil chemical parameters like aeration, temperature, pH, salt concentration, electrolyte balance etc.

The present result showed that the wasteland soil was composed of bacterial species of Bacillus (19%), Achromobacter (52%), Corynebacterium (22%), Micrococcus (18%), Clostridium (32%), Flavobacterium (38%), Alcaligenes (37%), Shigella (22%), Mycobacterium 19%), Arthrobacter (17%), and Xanthomonas (23%). The cultivable soil was composed of bacterial species of Bacillus (23%), Achromobacter (58%), Corynebacterium (56%), Micrococcus (62%), Clostridium (72%), Flavobacterium (68%), Alcaligenes (65%), Shigella (32%), Mycobacterium (37%), Arthrobacter (35%), and Xanthomonas (51%). The bacterial composition of wasteland soil was somewhat lesser in growth compared to the growth of bacterial strains found in cultivable soil. The reason may be the regular maintenance of soil parameters by farmers to obtain better agricultural turnover in the cultivable soil whereas the moderate growth of bacterial strains in wasteland soil is due to the absence of soil maintenance.

### Conclusion

The ideal conservation and livable expansion strategies endeavor to concede this as being constitutive to any perspective to keep alive biodiversity. The preservation of soil biodiversity is indispensable to both the environment and to agricultural industries. Soil biodiversity reflects the mix of living organisms in the soil. These organisms interact with one another forming a web of biological activities. Declining biodiversity of bacteria is due to various anthropogenic activities. In the present investigation, it is clearly pointed out that the decline in the bacterial species growth and the basic composition of bacterial strains in noyyal river bed soil that is due to the development of textile industries along the banks of river side which causes the contamination of soil profile through sludges and untreated effluent. On the other hand, It is clearly indicated that the regular maintenance of soil for cultivation which restore the better growth and basic composition of bacterial species than the other two soil samples. It is inevitable to install textile industries in cities like tirupur but the effluent from textile industries must be treated until not to contaminate the soil and disturb the soil based microorganisms especially bacterial species which perform various biological activities of soil. This is the time to install effluent treatment plants along the banks of the Noyyal river in order to save both soil microorganisms and the environment.

### Reference

- 1.Chen X, Ning X, Lai X, Wang Y, Zhang Y and He Y. (2021). Chlorophenols in Textile Dyeing Sludge: Pollution Characteristics and Environ. Risk Control. J. Hazard. Mater.416,125721.doi:10.1016/j.jhazmat.2021.125721.
- 2.Das D, Bakshi S and Bhattacharya, P. 2014. "Dyeing of Sericin-Modified Cotton with Reactive Dyes." The Journal of The Textile Institute 105 (3): 314-20.
- 3.Fernández-Calviño D and Bååth E (2010). Growth response of the bacterial community to pH in soils differing in pH. FEMS Microbiology Ecology, Volume 73, Issue 1, July 2010, Pages 149–156, <https://doi.org/10.1111/j.1574-6941.2010.00873.x>
- 4.Furtak K and Gajda AM (2018). Activity and Variety of Soil Microorganisms Depending on the Diversity of the Soil Tillage System. Sustainability of Agroecosystems, Alexandre Bosco de Oliveira, IntechOpen, DOI: 10.5772/intechopen.72966.
- 5.Hossain L, Sarker SK and Khan MS (2018). Evaluation of Present and Future Wastewater Impacts of Textile Dyeing Industries in Bangladesh. Environ. Dev. 26, 23–33. doi:10.1016/j.envdev.2018.03.005.
- 6.Jacoby R, Peukert M, Succurro A, Koprivova A and Kopriva S (2017). The Role of Soil Microorganisms in Plant Mineral Nutrition. Front. Plant Sci., 19: Front. Plant Sci., 19.doi.org/10.3389/fpls.2017.01617.
- 7.Khatri A, Peerzada, MH, Mohsin M and White M (2015). "A Review on Developments in Dyeing Cotton Fabrics with Reactive Dyes for Reducing Effluent Pollution." Journal of Cleaner Production 87: 50-7.
- 8.Kishor R, Purchase D, Saratale GD, Saratale RG, Ferreira LFR and Bilal M (2021). Ecotoxicological and Health Concerns of Persistent Coloring Pollutants of Textile Industry Wastewater and Treatment Approaches for Environmental Safety. J. Environ. Chem. Eng. 9, 105012. doi:10.1016/j.jece.2020.105012
- 9.Krishnamoorthy R, Roy Choudhury A, Arul Jose P, Suganya K, Senthilkumar M, Prabhakaran J, Gopal NO, Choi J, Kim K and Anandham R (2020). Long-Term Exposure to Azo Dyes from Textile Wastewater Causes the Abundance of Saccharibacteria Population. Appl. Sci.11, 379. <https://doi.org/10.3390/app11010379>
- 10.Lee SA, Kim JM and Wean M (2020). Different types of agricultural land use drive distinct soil bacteria. Scientific Reports,10: Article number: 17418.

11. Mahbub KR, Mohammad A, Ahmad, MM and Begum S (2012). Decolorization of Synthetic Dyes Using Bacteria Isolated from Textile Industry Effluent. *Asian Journal of Biotech.* Volume 4 (3): 129-136.
12. Manickam P and Vijay D (2021). "Chemical Hazards in Textiles," in *Chemical Management in Textiles and Fashion* (Elsevier), 19–52. doi:10.1016/b978-0-12-820494-8.00002-2
13. Methneni N, Morales-González, JA, Jaziri A, Mansour HB, and Fernandez-Serrano M (2021). Persistent Organic and Inorganic Pollutants in the Effluents from the Textile Dyeing Industries: Ecotoxicology Appraisal via a Battery of Biotests. *Environ. Res.* 196, 110956. doi:10.1016/j.envres.2021.110956
14. Prabha S, Gogoi A, Mazumder, P, Ramanathan AL and Kumar, M (2016). Assessment of the impact of textile effluents on microbial diversity in Tirupur district, Tamil Nadu. *Shashi. Applied Water Science* 7(5), DOI: 10.1007 / s13201-016-0394-3
15. Simidu V and Aiso K (1962) Occurrence and distribution of heterotrophic bacteria in sea water from the Kanagawa Bay. *Bull Jap Sci fish* 28:1137

