

Effect of Bacterial Strains on Reduction of Physico Chemical Characteristics in Textile Industrial Effluent Treatment System

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Abstract

Textile is one of the major industrial sectors in the world, it requires huge amounts of consumables for different processes such as dyeing, washing, sizing, finishing and rinsing, which consists many types of chemical reagents includes polyurethane, polyamide, phosphates, softening agent, stiffening agents and chelating agents. During textile processing, a large quantity of textile wastewater has been produced. The wastewater generated from textile processing is highly concentrated and it includes huge amounts of ammonia, toxic elements, organic matter and non-biodegradable substances. These kinds of pollutants create serious effects on the environment through prolonged periods, hence appropriate treatment is essential to eliminate such kinds of highly toxic pollutants from textile wastewater to decrease the impacts of hazardous chemicals on the environment. The most common wastewater treatment systems used in India to treat this kind of effluents are activated sludge and aerated lagoons.

In the present investigation, Treatability studies in batch aerated reactors were made to define the best operating conditions that could treat efficiently a mixed effluent from several textile industries. Operating conditions evaluated were F/M relationship in a range of 0.2 – 0.7, kg COD/kg VSS*day⁻¹, volumetric organic load, HRT 2-4 days, kg COD ≥ 0.25 m³ day⁻¹. Polyurethane, polyamide, phosphates, softening agent, stiffening agents and chelating agents is highly toxic compounds are removed by aeration and the residual concentration degraded by the microbial biomass produced for each condition. Mixed liquor volatile suspended solids (MLVSS) were within the range of 2000 mg/L. During the experiment, microbial activity was followed. Selection of bacterial biomass was observed in the reactors. The main bacterial strains isolated were, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pantoea sp.*, *Chryseomonas luteola*, *Proteus penneri* and *Serratia sp.* These native microorganisms were acclimated to this kind of residues and are potentially suitable to biodegradation and bioremediate in the textile wastewater.

Key Words: Effluent treatment, bacterial isolation and textile industry.

Introduction

In developing countries like India, a major part of the textile sector is under the coverage area of unorganized sector, which lacks adequate treatment facility. Textile processing requires a broad range of dyes, surfactants and inorganic salts in several component processes. Equally ingenious salts such as Na₂SO₄ and NaCl and enormous cationic and anionic surfactants are consumed in textile processing. Even though reactive dyes lead the viable dyeing practice, several further water-soluble and uniformly insoluble organic dyes are still being used. The inorganic salts react together with organic complexes lead to compound water insoluble components. The organic compound himself eventually goes through chemical alteration at some stage in the dyeing process. The wastewater beside usually covers biomolecules created through

biofouling. Somewhere biological treatment has been utilized, supplementary bio foulants has too convinced. The treatment of such composite effluent schemes would substantially need various phases of effluent treatments. Many workers have tried their best to research on anaerobic granulation i.e. Barbeau, et. al., 1997; Baruah, et. al., 1993; Brown and Pico, 1979; Clerck, et. al., 2004; Das and Santra, 2010; Dereeper, et. al., 2008; Dibble and Bartha, 1979 and so on.

In recent years, tremendous improvement has been made in wastewater treatment technology and there is a need for additional changes in these techniques. The biological treatment of municipal or industrial effluents in wastewater treatment plants (WWTPs) is often accomplished by means of the application of conventional activated sludge processes, a one-century-old technology, which was firstly designed to oxidise organic matter and afterwards adapted for nutrient removal. Improper

disposal of dye sludge results in environmental pollution, particularly soil contamination and represents a significant threat to groundwater. Many of the constituents of dye sludge are carcinogenic and potent immunotoxicity (Marwaha, et. al., 2001; Munavalli, and. Saler, 2009; Palela, et. al., 2008; Priya, et. al., 2014; Sanjeet Mishra, et. al., 2001; Saranraj, and Stella, 2012). In these areas the wastewaters remain for large periods where they make possible the development Strategies of treatment of wastewater were either inattentive or else not satisfactory, which leads in the direction of total adverse effect on the river ecosystem. Insubstantial awareness of the environment as well as lack of proper legal guideline has leads to noticeable effects takes place on surface water, groundwater in addition to soil along through health problems of public. Hence, water is a limited resource and thus there is needs to encourage balanced utilization for controlling water anxiety adequately to the reinforcement of water supply for irrigation, industrial as well as domestic purposes. This study focusses on the treatment performances of an aerobic granular sludge continuous flow reactor treating textile wastewater and granules progression against time. Among the various techniques employed to decontaminate the affected sites, in place bioremediation using indigenous microorganisms is far and away the foremost widely used (Edgar, 2004; Eriksson, M., G. Dalhammar, et. al., 1999; Fantroussi and Agathos, 2005; Wate, et. al., 2014; Garcha, et. al., 2014a; Garcha, et. al., 2014b; Janda, and Sharon, 2007; Khojare, et. al., 2002; King, et. al., 1992). Some reports in the tropical regions of Maharashtra, India have shown the presence of biodegrading bacteria. This approach to reclaiming contaminated land reduces the threat to groundwater and enhances the speed of biodegradation. Many microbial strains, each capable of degrading a selected compound, are available commercially for bioremediation. However, indigenous bacteria within the soil can degrade an honest range of target constituents of the dye sludge, but their population and efficiency are affected when any toxic contaminant is present at high concentrations.

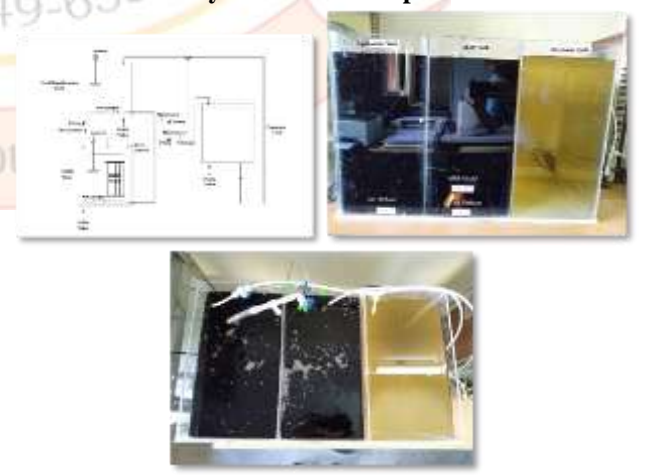
The present investigation was carried out to isolate the most frequently occurring and optimally

performing microorganisms from textile wastewater and sludge samples of unorganized sector and to test the bioremediation efficacy of the isolates by bio augmenting them in textile wastewater, we have selected toxic-resistant

Materials And Methods :

Five samples of textile wastewater and five samples of textile sludge were collected from unorganized textile industry located within the districts of Jalgaon, Maharashtra, the dry plastic bottles which were rinsed with water then with textile effluent. Physical properties like pH, temperature, odour, colour was recorded at the location of sample collection. The sample was transferred to the laboratory immediately and stored at 4°C to avoid any physical-chemical changes within the textile wastewater. Table 1: shows analysis of the wastewater and sludge samples parameters of textile waste samples which, includes temperature. BOD3 and MLSS were administered as per standing operating procedure, the BOD was analysed by titrimetric method. As shown in Fig: 1 Ten batch aerated reactors with fifteen litres, containing activated sludge, were displayed with wastewater of a textile wastewater monitored collecting three samples of every one among them, at different times and different percentual concentrations.

Figure 1: Experimental Set-Up of Reactors used for the bacterial isolation of wastewaters from a Textile industry frontside and upside view.



Bacterial isolation was administered by screening of microorganisms capable to biodegradation compounds derivate of wastewater treatment systems in textile processing was made by collecting 50 ml of every reactor system and

placing them in centrifuge tubes, then 30 ml were transfer to baffled flasks with 150 ml of mineral medium and 50 ml of wastewater. The flasks were incubated at 35°C for 24h. Triplicate plates were seeded in standard plate count agar with 5 ml of the mixed wastewater to conserve the selective pressure of the first conditions. altogether cases, the incubation temperature period was of three 5°C and a maximum of 3 days, respectively. the entire bacterial count was made using the expansion in plate using the serial dilution method. the choice of the dilution to use was made on a variety between 10⁻¹ and 10⁻⁶. Isolation and purification of bacteria was done by using Original samples which, were inoculated on Petri dish with standard plate count agar and incubated at 35°C for twenty-four to 48 h. from the expansion developed within the petri dishes, the first consortia in each condition were isolated by selective and propagation before the identification procedure. The organisms were taxonomically identified with the commercial system.

Results And Discussion

Microorganisms were isolate ready to "> which can be able to grow within the presence of wastewater of the textile industry of the mixed original reactor containing the various selective pressure. Six isolates producing colonies with a spread of colors where grown in petri dishes and selected for further characterization. These shows that, *Pseudomonas aeruginosa* might be isolated of the reactor mixed with 50% of wastewater, *Pseudomonas fluorescens* was isolated from the mixed reactor with 3, 20, 40 and 50% of textile wastewater.

The *Pantoea* sp was isolated from the mixed rector with 40% of wastewater, *Chryseomonas luteola* was found within the mixed reactor with 10 and 30% of wastewater. The strain of *Proteus peenneri* was isolated of the mixed reactor with 15% of wastewater and, finally, *Serratia* sp was found within the mixed reactors with 5 and 15% of wastewater. Similar result are noted by some researcher i.e. Talavera, and Castresana, 2007; Venosa, et. al., 1996; Vida, et. al., 2007).Six bacterial strains, two *Pseudomonas*, *Pantoea* sp, *Chryseomonas luteola*, *Proteus peenneri* and *Serratia*

sp, could grow within the presence of wastewater of textile industry. The *Proteus* and *Serratia* are classified as enteric, Gram-negative, facultative bacteria and may be utilized in the degradation of an excellent number of non-conventional organic molecules under aerobic conditions along side *E. Coli*, *Salmonella*, *Shigella* and *Enterobacter*. *Pseudomonas aeruginosa* may be a Gram negative, cosmopolitan bacterium, which will be found in soils, waters, vegetables and animals. it's an opportunistic pathogen that has been reported with degradation capacities of non-conventional organic compounds. *Chryseomonas luteola* is additionally a Gram-negative bacterium, recently was reclassified as *Pseudomonas luteola* and this bacterium has been reported as useful for the bioremediation of contaminated sites with heavy metals and phenols. Finally, *Pseudomonas fluorescens* and *Pseudomonas fluorescens pútida* are cosmopolitan bacteria, found in water and soil and recognized within the degradation of non-conventional compounds and useful in environmental bioremediation (Shivsharan and Kulkarni, 2013; Shruthi, et. al., 2012; Silambarasan, et. al., 2012; Sujatha, et. al., 2012). The bacterial isolates described here are potentially useful for removing contaminating compounds in effluents.

Table 1: Quality characteristics of influent and Operational parameters of Batch Aerated Reactor in textile industrial wastewater

Parameter	COD (mg/L)	BOD ₅ (mg/L)	Ntotal (mg/L)	NH ₄ p (mg/L)	PO ₄ 3 (mg/L)
Variation range	1,926–2,824	561–1,320	39.6–76.8	26–42	11.8–27
Average	1,598	876	54	34	18
Parameters	Reactors used for the bacterial isolation of wastewaters				
	HRT, h				
	08	06	04		
Days	1-30	31-60	61-90		
TMP (psi)	1.9-2.5	2.3-3.4		2.5-3.5	
Permeate flux (L/m ² h)	19.4-24.3	16.4-23.7		14-20.8	

F/M ratio (g BOD/g MLSS. d)	0.08- 0.14	0.08-0.17	0.08-0.15
MLSS (mg/L)	9412	10265	11039
OLR (kg BOD/m³.d)	0.31- 0.69	0.56-1.21	0.91-1.85
BOD influent (mg/L)	406- 471	402-452	401-441

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