

SCIENCE | ENGINEERING | TECHNOLOGY

e-ISSN: 2319-8753 | p-ISSN: 2347-6710

EDIA

INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN SCIENCE | ENGINEERING | TECHNOLOGY

Volume 10, Issue 8, August 2021

INTERNATIONAL STANDARD SERIAL NUMBER INDIA

Impact Factor: 7.569

9940 572 462

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|| Volume 10, Issue 8, August 2021 ||

| DOI:10.15680/IJIRSET.2021.1008105 |

Bioremediation of Textile Dye Wastewater of Sanganer in Jaipur

Dr. Abhishek Lunayach

Assistant Professor, Social Sciences, Engineering College, Bharatpur (An Autonomous Institute of Govt. of

Rajasthan), India

ABSTRACT: Synthetic dyes are extensively used by textile industries leading to the generation of enormous volumes of coloured effluents post dyeing and printing process. People are using synthetic colors and textile dye industries are producing huge volumes of wastewater, creating aquatic pollution all over the globe. Dyes in wastewater often lead to calamities viz. the incidence of bladder tumors has been reported to be particularly higher in dye industry workers than in the general population. These anthraquinone dyes and their metabolites released in the effluents are both carcinogenic and mutagenic to life forms. The study area selected was textile cluster units of Sanganer, Jaipur region. These clusters units at Sanganer, Jaipur use lot of water during dye processing and then the untreated waste water from these units is directly discharged into drains, ponds, lakes and rivers. Bioremediation is a process used to treat contaminated media, including water, soil and subsurface material, by altering environmental conditions to stimulate growth of microorganisms and degrade the target pollutants. Cases where bioremediation is commonly seen is oil spills, soils contaminated with acidic mining drainage, underground pipe leaks, and crime scene cleanups. These toxic compounds are metabolized by enzymes present in microorganisms. Bioremediation can be carried out by microbes that are naturally present in the environment or adding nutrients, this process is called biostimulation. Researchers are currently investigating ways to augment contaminated sites with nonnative microbes—including genetically suited to degrading the contaminants of concern at particular sites.

KEYWORDS: textile, dye, sanganer, bioremediation, microbes, wastewater

I. INTRODUCTION

Sanganer textile industry in Jaipur is one of the largest handloom manufacturing zone from western India covers more than 154 block printing units. It is because of the toxic nature of effluents generated by textile cluster, it has gained much attention. However, existing physio-chemical technologies to clean up polluted water or soil are expensive and cause secondary problems in terms of disposal. Moreover azo dyes have been linked to human bladder cancer, splenic sarcomas, hepatocarcinomas and nuclear anomalies in experimental animals and chromosomal aberrations in mammalian cells. Some azo dyes induce liver nodules in experimental animals and there are a higher numbers of bladder cancers in dyeing industries workers. Nevertheless, studies have shown that certain group of microorganisms produce enzymes to degrade dyes, decolorize and metabolize them. Microbial bioremediation of textile wastewaters is sought after as an eco-friendly and sustainable alternative to the conventional treatment methods. Given the adaptive nature of microorganisms to xenobiotic pollutants, a large number of microorganisms, including bacteria, fungi, yeasts, algae or microbial consortia and microbial communities have been tested for the biodecolourization, biodegradation and mineralization of various types of textile dyes and wastewaters in recent years.[1]



|| Volume 10, Issue 8, August 2021 ||

| DOI:10.15680/IJIRSET.2021.1008105 |



Sanganer handblock printing

The isolation of aerobic bacterial strains capable of degrading different dyes has been carried out for more than two decades. Biodegradation of the dye by certain groups of fungi during dye removal has been extensively demonstrated. Ligninolytic enzymes secreted by white rot fungi bind non-specifically to the substrate and therefore can degrade a wide variety of recalcitrant compounds and even complex mixtures of pollutants including dyes.[2]

II. OBSERVATIONS

Different algal sp. (*Chlorella* sp. Oscillatoria sp. etc) have also been investigated to check the efficiency of their azoreductase enzymes for disintegration of textile based azo dyes. According to some studies, the algal azo reductases have been shown to produce aromatic amines by breaking down azo bond of azo dye compounds. In relation to this, there are some algae that can carry out the direct degradation of azo dyes instead of converting them into aromatic compounds first. Bacterial azo dye degradation involves an electron donor and sequence of enzymatic steps aided by azoreductase that catalyze the cleavage of azo linkages. Lignin-degrading system (LDS) of fungi has been reported for effective degradation of variety of industrial dye wastewaters. Fungi can be classified on the bases of its degradation efficacy [3] under following terms:

- Ligninolytic fungal degradation
- Fungal biosorption
- Mycorrhizal fungal degradation



|| Volume 10, Issue 8, August 2021 || | DOI:10.15680/IJIRSET.2021.1008105 |



Textile Industry dye wastewater

In general, the diseases provided by textile dyes comprise from dermatitis to disorders of the central nervous system or may be related to the substitution of enzymatic cofactors that result in the inactivation of the enzymatic activities themselves. The acute toxicity to textile dyes is caused by oral ingestion and inhalation, especially by exposure to dust triggering irritations to the skin and eyes .The workers who produce or handle reactive dyes may have contact dermatitis, allergic conjunctivitis, rhinitis, occupational asthma or other allergic reactions .The latter are the result of the formation of a conjugate between human serum albumin and the reactive dye, which acts as an antigen producing immunoglobulin E (IgE) antibodies, which combine with histamine . Some dyes reveal mutagenic potentiality. The textile dyes may offer carcinogenicity, especially those of the azo and nitro type, and its effects manifest themselves over time. In humans, dyes are capable of generating chemical cystitis, irritation of the skin and digestive tract, respiratory and renal failure, among others.[4]



Allergic conjunctivitis



|| Volume 10, Issue 8, August 2021 || | DOI:10.15680/LJIRSET.2021.1008105 |

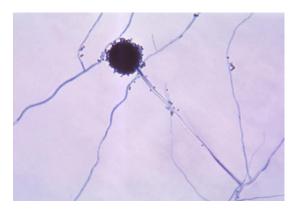


Tumour induced by dye wastewater

Textile wastewater constitutes a large number of chemicals like acids, bases, salts, dispersants, etc. and most importantly dyes that altogether are responsible for high biological oxygen demand (BOD), chemical oxygen demand (COD) and total organic carbon (TOC). Dyes therefore are one of the most important constituents of the textile industry and are major polluters of water reservoirs.[5]

IV. DISCUSSION

Fungi can survive in a variety of habitats with complex soil matrix serving as the major location for fungal colonization along with freshwater as well as marine habitats which also show stable colonization of fungi. Fungi can largely thrive in the soils of different climatic conditions including the extreme ones and propagate through the dispersal of spores in the air and also help in maintaining the balance of ecosystem. They have also been reported to survive in effluent treatment plants (ETPs) treating various waste waters. The diversity of habitats and ability for secreting multitude of enzymes makes fungi potential candidates for bioremediation at various sites.Examples of fungi *are Aspergillus, Phanerochaete, Mucor, Rhizopus, Agaricus* etc.This is called Mycoremediation.[6]



Aspergillus niger

Algae like Chlorella, Spirulina etc are commonly used in bioremediation technology. This is called Phycoremediation.



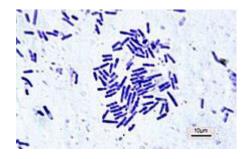
|| Volume 10, Issue 8, August 2021 ||

| DOI:10.15680/IJIRSET.2021.1008105 |



Chlorella species

Another strategy, bioaugmentation or bioaddition, is the addition of microbial populations to indigenous, alien or genetically modified organisms (GMO), in places where there is an insufficiency of indigenous microorganisms with ecophysiological characteristics compatible with the habitat conditions that are conducive to the promotion of bioremediation.Examples of bacteria in this regard are *Pseudomonas*, *Bacillus*, *Streptococcus* etc.[7]



Bacillus species

Currently, there is wide variety of microorganisms (bacteria, fungi, yeasts, algae) that are being studied for use in bioremediation processes. Even plants have the capability of absorbing dyes and heavy metals through roots and stem cellulose thus making their contribution in bioremediation technology. This is called phytoremediation. *Phragmitis* species is a common example here.



Phragmitis species

International Journal of Innovative Research in Science, Engineering and Technology (IJIRSET)

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| e-ISSN: 2319-8753, p-ISSN: 2347-6710| <u>www.ijirset.com</u> | Impact Factor: 7.569|

|| Volume 10, Issue 8, August 2021 ||

| DOI:10.15680/IJIRSET.2021.1008105 |

IV. RESULTS

Pseudomonas sp., *Citrobacter* sp., *Escherichia coli*, and *Micrococcus* sp. showed that plasmid was present in all isolates. *Micrococcus* sp. was reported to work well in an adapted environment, while *E. coli* showed the same decolorization potential in adapted and non-adapted environments. *Pseudomonas putida* and *Portulaca grandiflora* and reported complete degradation of a sulfonated diazo dye. Enzymes involved were reported as 2,6-dichlorophenol indophenol reductase, riboflavin reductase, lignin peroxidase, and tyrosinase in *P. grandiflora* and veratryl alcohol oxidase, laccase, and 2,6-dichlorophenol indophenol reductase in *P. putida*.[8]

	Table1: Degradation of Various Dyes using Bacteria						
#	Dye	Bacteria	Mechanism	Reference			
1	Synazol Red 6HBN	Alcaligenes aquatilis	Mineral salt medium, 4 days, 37 °C, pH 7, static with yeast extract, and saw dust	Aja <i>z et al.</i> 2019			
2	Novacron Super Black G	Bacillus cereus AZ27, Alcaligenes faecalis AZ26, and Bacillus sp. AZ28	Nutrient broth medium, 4 days, 37 °C, pH 8, and at static condition	Hossen e <i>t al.</i> 2019			
3	Congo Red, Phenol Red, Direct Yellow, Direct Red, Acid Orange, Direct Violet, Direct Blue, Direct Pink	Staphylococcus sp., Bacillus sp., Pseudomonas sp., Enterobacter sp., Micrococcus sp., and Klebsiella sp.	Nutrient broth medium, 3 days	Islam e <i>t al.</i> 2017			
4	Methyl Orange and Congo Red	Sphingomonas paucimobilis, Rhizobium radiobacter, and Bacillus subtilis (Consortia)	Nutrient broth medium, 4 days, 37 °C, pH 7.5, shaken at 120 rpm (free cell <i>vs</i> . immobilized consortia)	Allam 2017			
5	Red and Green dye	Bacillus sp., Pseudomonas sp., and Aspergillus sp.	Nutrient broth 1 day for bacteria and Sabouraud's Dextrose broth 3 days for fungi, 37 °C, occasional shaking	Fatima and Alamgir 2015			
6	Reactive Blue 172	<i>Providencia rettgeri</i> strain HSL1	Wheat bran medium,20 h, 30±0.2°C, pH 7, shaken at 120 rpm, under microaerophilic conditions (correlated with NADH- DCIP reductase and azoreductase activity)	Lade <i>et al.</i> 2015			
7	Textile effluent	Enterobacter asburiae and Enterobacter cloacae (consortium)	Nutrient broth, 10 min, 32 °C, pH 1.67, under aerobic conditions	Singh <i>et al.</i> 2017			
8	Reactive Black 5	Arthrobacter soli BS5	Nutrient broth, 5 days, 37 °C, pH 5 to 9, static	Khan and Malik 2018			
9	Direct Red 2B	Klebsiella sp. and Staphylococcus sp.	Bushnell Hass minimal salt medium,5 days, 37°C, pH 7, rotary shaker at 100 rpm, supplementation 1% glucose	Desai 2017			
10	Direct Blue 151 and Direct Red 31	Bacillus flexus strain NBN2, Bacillus cereus strain AGP-03, Bacillus cytotoxicus NVH 391-98, and Bacillus sp.L10	Mineral salt medium, 5 days, 36 °C, pH 9.5, on shaker, supplementation of sucrose and yeast extract	Lalnunhlimi and Krishnaswamy 2016			



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| DOI:10.15680/LJIRSET.2021.1008105 |

A. flavus, A. niger, Fusarium oxysporium, and Penicillium notatum and used them for the decolorization of azo textile dyes. The studies have reported that A. niger decolorized basic fuchsin (81.85%)>Nigrosin (77.47%)>Malachite green (72.77%) >dye mixture (33.08%), while Phanerochaete chrysosporium decolorized Nigrosin (90.15%)> basic fuchsin (89.8%)>Malachite green (83.25%)>mixture (78.4%) under shaking condition

#	Dye	Microbe	Mechanism	Reference
1	Reactive Black 5, Reactive Red 120, Reactive Blue 19, Acid Scarlet GR, and Azure B	Sterigmatomyces halophilus	Minimal Salt (MS) medium, 24 hours, 115 °C, pH 5, 50 mgL ⁻¹ dye concentration, supplemented with carbon and energy sources, including glucose, ammonium sulfate, and yeast extract	Al-Tohamy et al. 2020
2	Congo Red	Aspergillus niger	Synthetic nutrient broth medium, 6 days, 28 °C, pH 5, shaken at 120 to 150 rpm (correlated with manganese peroxidase and lignin peroxidase)	Asses et al. 2018
3	Biebrich Scarlet, Direct Blue 71, Orange G, and Ponceau 2R	Coriolopsis sp. Strain arf5	Kirk's basal medium,7 to 12 days, room temperature to 35 °C, pH 4.5 to 6, static under nitrogen-limiting conditions and an additional carbon source (glucose)	Cheng et al. 2016
4	Acid Blue 40, Acid Blue 193, Acid Blue 62, Acid Blue 113, Acid Red 73 Reactive Red 11, Reactive Blue 74	Myrothecium verrucaria, Colletotrichum dematium, Corynespora cassiicola, Dictyosporium zhejiangensis, Plectosporium tabacinum, Fusarium thapsinum, Alternaria alternate, Acrogenospora sphaerocephala, and Ceriporia lacerate	Malt agar medium, 7 days, 25 °C	Yang e <i>t al.</i> 2016
5	Procion Red MX-5B	Aspergillus terreus and Aspergillus niger	Aqueous solution, 3 h (biosorption), 1 day to 14 days (biodegradation),30±1 °C, and pH 4	Almeida and Corso 2014
6	Reactive (Navy Blue M3R, Red M8B, Green HE4B, Orange M2R, RedM5B), Direct (Orange RS, Black BT, Blue GLL, Sky Blue FF)	Aspergillus flavus, Aspergillus niger, Fusarium oxysporium, and Penicillium notatum	Potato dextrose broth, 3 to 7 days, 30 °C, pH 5, in rotary shaker at 120 rpm, biotransformation enzymes (lignin peroxidase>laccase>manganese peroxidase>tyrosinase)	Laxmi and Nikam 2015
7	Malachite Green, Nigrosin Disodium, and Basic Fuchsin	Aspergillus niger, and Phanerochaete chrysosporium	Potato dextrose broth, 10 days, 25 °C, pH 7, rotary shaker at 100 rpm	Rani et al. 2014

Table 2: Degradation of Various Dyes using Fungi

Elkatothrix viridis, Chlorella vulgaris, Nostoc linckia, Lyngbya lagerlerimi, Oscillatoria rubescens, and *Volvox aureus* using methyl red, orange II, basic cationic, G-Red (FN-3G), and basic fuchsin and concluded that decolorizing using *C. vulgaris* or *N. Linckia* with G-Red or methyl red, respectively, induced the algal azo dye reductase enzyme by 72 and 71%.



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| DOI:10.15680/LJIRSET.2021.1008105 |

Table 3: Degradation of Various Dyes using Algae

#	Dye	Microbe	Mechanism	Reference
1	Disperse Red 3B	<i>Chlorella sorokiniana</i> XJK and <i>Aspergillus</i> sp. XJ-2 (consortia)	BG 11 and Czapek's medium, respectively, 4 days, 30 °C, pH 7, and shaken at 170 rpm (due to lignin peroxidase and manganese peroxidase enzyme activities)	Tang e <i>t al.</i> 2019
2	Congo red	Chlorella vulgaris	Bold's basal mineral medium, 25±3 °C, 3 days	Hernandez- Zamora e <i>t al.</i> 2015
3	Malachite green	Xanthophyta alga, Vaucheria sp.	Dye solution, pH 1.5 – 8.5, temperature 5-45 °C and initial dye concentration 2.5 – 17.5 mg L ⁻¹	Khataee et al. 2010
4	Methyl red, orange II, basic cationic, G-Red (FN-3G) and basic fuchsin	Elkatothrix viridis, Chlorella vulgaris, Nostoc linckia, Lyngbya lagerlerimi, Oscillatoria rubescens, and Volvox aureus	Bold's basal mineral medium, pH 7, 25±1 °C, continuous light intensity 5000 to 3000 lux on rotary shaker	El-Sheekh et al. 2009
5	Reactive Black 5, Direct Blue 71 and Disperse Red 1.	Chlorella vulgaris	Mineral salt media, 100 mg L ⁻¹ dye, 12 days, 30 °C, dye concentration 100- 500 mg L ⁻¹ in static conditions	lshchi and Sibi 2020

Nanoparticles, however, have gained attention due to their small size range (1 nm to 100 nm), large surface area, high adsorption properties, less resistance to diffusion and the fact that they show faster rates of equilibrium and increased chemical reactivity.Gold nanoparticles (AuNPs) synthesized using cell-free extract of *Bacillus marisflavi* showed outstanding catalytic activity in the decolorization of CR and methylene blue. Synthesis of AgNPs using *Bacillus pumilus* was verified that nano-based remediation was more efficient as compared to microbial remediation.[9]

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| e-ISSN: 2319-8753, p-ISSN: 2347-6710| <u>www.ijirset.com</u> | Impact Factor: 7.569|

|| Volume 10, Issue 8, August 2021 ||

| DOI:10.15680/LJIRSET.2021.1008105 |

Table 4: Degradation of Azo Dyes Using Microbe Nanoparticle Approach

C N					Defense
S.No.	Nanoparticles	Dye	Microbes	Remarks	References
1.	Cobalt	Remazol	-	CoNPs removed the	Cruz et al.
	nanoparticles	golden yellow		RGY with high	2019
	(CoNPs)	RNL; textile		efficiency, reaching	
		effluent		almost 100%	
				removal in 30min;	
				textile effluent	
				resulted in 88%	
				degradation of dyes	
				and 32% reduction	
				in CO	
2.	Bimetallic	Orange G		High efficacy at	Foster et al.
۷.	nanoparticles	Orange O	-	1000 mg/L	2019
				1000 mg/L	2015
	comprising of iron				
	(Fe) and nickel				
	(Ni)				
3.	Silver	Methylene	Strain AN-1	Promising agents for	Amabye and
	nanoparticles	blue		treatment of	Hagos 2017
				synthetic dyes	
4.	Silver	Congo Red,	Pestalotiopsis	Good azo dye-	Rajput et al.
	nanoparticles	Rhodamine B,	versicolor	degrading potential	2017
		and Orange G		- grang parental	
5.	Silver	Methyl Orange	Leuconostoc	Exopolysaccharide-	Saravanan et
J.	nanoparticles	and Congo	lactis	stabilized (EPS)	al. 2017
	nanoparticles	Red	10000	AgNPs efficient in	ai. 2011
		Rea			
				degradation	
				process of industrial	
				textile dyes; the	
				electron transfer	
				takes place from	
				reducing agent to	
				dye	
				molecule via	
				nanoparticles,	
				resulting in the	
				destruction of the	
				dye chromophore	
6	Oliver	Mathed Ocean	Ota a ku ta a	structure	Domeliacom
6.	Silver	Methyl Orange	Staphylococcus	62% of MO	Ramalingam
	nanoparticles		aureus	(2000µg/mL)	et al. 2017
				degraded with	
				200µg/mL of AgNPs	
				in 1 day	
7.	Gold	Congo Red	Bacillus	Outstanding	Nadaf and
	nanoparticles	and Methylene	marisflavi	catalytic activity;	Kanase 2016
		blue		pseudo-first-order	
				kinetics and reaction	
				rate constant of	
				0.2192 and 0.2484	
-	01	0	0 '''	min ⁻¹ , respectively	Mark (
8.	Silver	Congo Red	Bacillus	Nano-based	Modi <i>et al.</i>
	nanoparticles		pumillus	bioremediation was	2015
				found 13% more	
				efficient than the	
-		•	•	•	

International Journal of Innovative Research in Science, Engineering and Technology (IJIRSET)

L IJIRSET | e-ISSN: 2319-8753, p-ISSN: 2347-6710| <u>www.ijirset.com</u> | Impact Factor: 7.569|

|| Volume 10, Issue 8, August 2021 ||

| DOI:10.15680/LJIRSET.2021.1008105 |

V. CONCLUSION

Bioremediation using nanoparticles represent a promising new technology for environmental clean-up technology, not only because of their high treatment efficiency, but also for their cost-effectiveness, as they have the flexibility for *in situ* and *ex situ* applications. Nanoparticles work by increasing the surface area of a heterogeneous catalyst (its active component), enhancing the contact between the catalytic site and its substrate moiety. Efficacy of microbe-associated nanoparticle in bioremediation and its translational effects are unexploited. Thus, recovery of environmentally relevant microorganisms in combination with the 'omics' concept would facilitate an improved understanding of the physiology of microorganisms together with their nanoparticle synthesis catalyzing environmental processes. This increased understanding will further help to design and operate relevant bioremediation strategies.

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Impact Factor: 7.569





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