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Bioremediation Of Textile Dye Effluents Using Bacterial Consortium

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***Abstract**: The inappropriate and unselective discharge of textile effluent in natural water and land is posturing serious difficulties and it has also adverse effects on different crops. Based on the aim of this paper, the sample of the bacterial consortium was screen for its activities and inoculated according to standard microbiological procedure. And the bioremediation potential of bacterial consortia in treating textile dye effluents was evaluated. Data from Table 4.2 and 4.3 indicates a significant reduction in dye concentration due to microbial activity. The study revealed an average dye reduction of 49.6% for Blue, 53.3% for Malachite green, and 59.6% for Congo red within 120 hours. Primary screening of 14 bacterial isolates identified six with notable dye-reducing properties. Morphological and biochemical analyses revealed the presence of Staphylococcus xylosus, Bacillus korlensis, Pseudomonas fluorescens, Pseudomonas cichorii, Brevundimonas diminuta, and Enterococcus columbae. The isolates demonstrated diverse staining and spore-forming characteristics, crucial for bioremediation processes. The study underscores the potential of these bacterial species in mitigating dye pollution, highlighting their application in sustainable effluent treatment strategies.*

Keywords: Bioremediation, Bacterial consortium, textile dye effluents

INTRODUCTION

The inappropriate and unselective discharge of textile effluent in natural water and land is posturing serious difficulties and it has also adverse effects on different crops (Rathode and Pathk, 2014). Textile waste reduces seed growth and germination growth of all vegetable and this effect is more distinct at the high amount of textile effluent (Rehman *et al.*, 2011). The incidence of even very low concentration of dyes in effluent is extremely visible and objectionable (Nigam *et al.*, 2010). Thus, the decolourization of textile wastewater has been a foremost environment apprehension since a long time. Diverse methods are used for the decolourization of textile wastewater; mechanical, chemical, physico-chemical and biological or in combination and for this, this research h is hereby focusing only on the use of endogenous bacterial in decolorizing the dye effluents using the remediation techniques.

Textile companies have been grouped in the class of the utmost polluting manufacturing units by various government agencies. India has a huge system of textile trades of variable size that are scattered throughout the country. The increasing population and advanced adoption of an industrial-based life style has certainly led to an enlarged anthropogenic impact on the atmosphere. In textile processing, chances exist for the release into the ecosystem of possibly hazardous substances at different stages of the operation and these pollutants impact undesirably on the environment (Dwivedi and Tomar, 2018). The inappropriate and unselective discharge of textile effluent in natural water and land is posturing serious difficulties and it has also adverse effects on different crops (Rathode and Pathk, 2014). Textile waste reduces seed growth and germination growth of all vegetable and this effect is more distinct at the high amount of textile effluent (Rehman *et al.*, 2011). The incidence of even very low concentration of dyes in effluent is extremely visible and objectionable (Nigam *et al.*, 2010). Thus, the decolourization of textile wastewater has been a foremost environment apprehension since a long time. Diverse methods are used for the decolourization of textile wastewater; mechanical, chemical, physico-chemical and biological or in combination (Schulze-Rettmer, 1998; ParacOsterman *et al.*, 2017; Vikrant *et al*., 2018).

Bioremediation is attractive significant approach, as of its efficacy and environment responsive nature (Robinson *et al.*, 2011). Many microorganisms can decolourize the azo dyes under laboratory and field conditions (Sani and Banerjee, 1999; Moosvi *et al.*, 2005) and fungi (Balanand, 2011; Verma and Madamwar, 2005). Environmental microbiology trusts upon the pollutants degrading potential if naturally occurring microorganisms in which bacteria play central role. Bioremediation in alkaline environment (due to high pH of effluent) certainly needs the claim of microorganisms, which can grow under exacting conditions. Subsequently augmented bacteria may have some toxic effects on the atmosphere, applying or stimulating the indigenous micro-flora is chosen if possible. Moreover, the bacterial consortia are more operative than individual cultures in bioremediation because of their broad enzymatic potential (Moosvi *et al.*, 2017; Mahmood *et al*., 2015). So, the current study was focused on the developing effective microbial consortia from aerobic textile bacteria isolated from textile waste contaminated soil of an industrial estate. The effect of the non-treated and bio-treated effluent was investigated on the germination of *Vigna radiata*. The aim of this study is to test the ability of bacterial consortium in bioremediation of textile effluents (Azo dye).

MATERIALS AND METHODS

3.1 Sample collection

Textile effluent was obtained from Kasarau, Zai and Sabuwar Kasuwa of Dutse metropolis, Dutse local Government, Jigawa State. The site is where effluent of the textile dye is usually discharge on soil, so the soil were serve as the sample to obtain the organisms of interest. The samples was obtained in pre-sterilized plastic bottles. The color of the soil waste were dark reddish brown due to contamination, hence, different soil samples (affected) was obtained aseptically from many sites of the study area especially the dumping site.

3.2 Isolation and screening of textile effluent decolorizing bacteria

All the chemicals and media composition was procured from Microbiology Laboratory of Federal University Dutse, Jigawa State. The textile Azo dyes: Golden Yellow 3RL (G.Y. 3RL), Red HE7B (R. HE7B), and Triphenylmethane dye - Malachite Green (MG) was purchase from the dye sellers' of Dutse Ultra-modern market and then taken to the laboratory for analysis.

The isolation of textile dye degrading microbe from soil samples was performed by serial dilution using nutrient medium (Nutrient broth) containing different dyes (G.Y 3RL, R. HE7B, and MG) at concentration of 10 mgL^{-1}. The incubation was done at 37 °C for 5 days. Pure colonies of bacteria based on their morphology was subculture and maintained at 27 °C. The bacterial isolates was further screened for the de-colorization of textile effluent using modified mineral broth containing various concentration of textile effluent ranging (25%, 50%, 75% and 100% (v/v)) and incubated at 37 °C for 5 days (120hrs). The decolourization was studied at regular interval of 12 h. The amount of decolourization was recorded spectrophotometrically (*i.e.* G.Y 3RL at 400 nm, R. HE7B – 550 nm, MG – 620 nm and Textile effluent – 555 nm). Decolourization efficacy was stated in terms of % decolourization (Sani and Banerjee, 1999).

$$\text{Decolourization (\%)} = \frac{\text{Initial absorbance - Final absorbance} \times 100}{\text{Initial absorbance}}$$

3.3 Identification and characterization of isolates

The isolates was identified after obtaining the morphological characteristic using plate morphology and gram staining. The biochemical test like indole, urease, oxidase, and vogues pasture test are used for identification of the bacterial consortium. The results were displayed inform of tables for easy determination.

4.0 RESULTS AND DISCUSSION

4.1 RESULTS

The results obtained from isolation and identification of bacterial consortium capable of degrading textile dye effluent in some selected dye shops in Dutse metropolis was summarized in the table 4.1 below of which most of the organisms are circular form, with 3 sample irregular, creamy, off-white and brownish in color respectively with all smooth surface. Similarly, the biochemical results of the isolates was summarized in table 4.2 of this chapter. The identified bacteria were cultured in nutrient agar medium comprising different concentrations of textile dye (Congo red, Blue and Green ($10gL^{-1}$) at 100, 75, 50 and 25% respectively. The results of the absorbance were read before inoculation and after 120hr to determine the ability of the organisms in remediating the dye.

Table 4.1: Colony morphology of the bacterial isolates using nutrient agar as the medium.

Samples	**Colony characteristic**				
	Color	Elevation	Margin	Surface	Form
A1	Off-white	Raised	Entire	Smooth	Circular
A2	Cream	Raised	Entire	Smooth	Circular
A3	Off-white	Raised	Entire	Smooth	Circular
A4	Off-white	Raised	Undulate	Smooth	Irregular
A5	Cream	Raised	Undulate	Smooth	Irregular
A6	Cream	Raised	Undulate	Smooth	Circular
A7	Off-white	Raised	Entire	Smooth	Circular
A8	Brownish	Convex	Entire	Smooth	Circular
A9	Cream	Flat	Undulate	Smooth	Irregular

Table 4.2 Morphological, cultural, physiological, and biochemical characteristics of isolates.

Parameters			**Observations**			
	A1	**A2**	**A3**	**A4**	**A5**	**A6**
Vegetative cell	short rod	short rod	shot rod	short rod	Coccobacillary	Coccobacillary
Cell arrangement	single	single	single	single	single	single

Gram staining	+	+	–	–	–	+
Catalase test	+	+	+	+	+	+
Citrate utilization	–	+	–	+	+	+
Voges-Proskauer test	–	–	–	+	–	–
Methyl red test	–	–	–	–	–	–
Indole test	+	–	–	–	–	–
Urease test	–	–	–	–	–	–
Oxidase test	–	–	+	–	+	+
Provisionally identified organism	*Staphylococcus xylosus*	*Bacillus korlensis*	*Pseudomonas fluorescens*	*Pseudomonas cichorii*	*Brevundimonus diminuta*	*Enterococcus columbae*

Note: +: means positive, -: Negative

Table 4.3: Result of discoloration of textile dye by the bacterial consortium

Concentration (%)	**Absorbance**		**Dye**	
		Blue	**Green**	**Congo red**
100%				
Before		2.551	2.451	2.458
After		1.389 (54.4%)	1.399 (57.1%)	1.400 (56.9%)
75%				
Before		2.324	2.331	2.324
After		1.121 (48.2%)	1.151 (49.4%)	1.211 (52.1%)
50%				
Before		2.186	0.866	0.573
After		1.001 (45.8%)	0.711 (82.1%)	0.441 (76.9%)
25%				
Before		1.006	0.467	0.189
After		0.501 (49.8%)	0.114 (24.4%)	0.099 (52.4%)

4.2 DISCUSSION

Primary screening of the 14 bacterial isolates collected from the study samples, and the bacteria positively grew in the culture medium containing metal salts. Six isolates with significant textile dye-reducing properties were further studied. Based on the morphological and biochemical characterization, we identified indigenous and intrinsic bacteria at the species level as *Staphylococcus xylosus* (A1), *Bacillus korlensis* (A2), *Pseudomonas fluorescens* (A3), *Pseudomonas cichorii* (A4), *Brevundimonus diminuta* (A5), and *Enterococcus columbae* (A6). Based on the gram and spore staining, isolates A1, A2, A5 were gram-negative and non-spore forming, A3 and A4 were gram-positive and non-spore forming, whereas isolate A6 was gram-positive and spore forming. Noorjahan (2012) identified *Staphylococcus* sp., along with other bacterial genera, from tannery effluent in India and Bangladesh. Notably, bacterial isolate A6 was short, rod shaped, single, motile, aerobic, indicated positive results in catalase and citrate tests and identified as *Bacillus korlensis* (Table 4.2).

The potential of *Bacillus* as a textile dye-degrading genus has been identified and described by several authors (Marzan et al., 2017). Both A1 and A5 isolates were from the genus *Pseudomonas* and identified as *P. fluorescens* and *P. cichorii*, respectively. Khan et al., (2023) and Sriram and Reetha (2016) isolated and characterized *Pseudomonas fluorescens* bacterium from textile dye effluents. Senan and Abraham (Khan et al., 2023) also identified and reported bioremediation of textile azo dyes by aerobic *Pseudomonas* sp. Both A1 and A4 isolates, named *B. diminuta* and *B. Enterococcus columbae*, respectively indicating coccobacilary and single vegetative cell formation, and were motile and aerobic (Table 4.2). Other researchers also reported *Brevundimonus* and *Enterococcus* genera from waste effluents. Tsiamis et al. (2011) isolated *B. diminuta* from olive mill wastewater.

Data obtained from table 4.3 shows that there is significance decrement of the dye due to the utilization of the dye by the organisms introduced in the study. Although the study was done only for 120hrs, however, the study shows the influence of the organisms on remediation capability. This research was also in agreement on the research of another scientist conducted in Congo (Hooda, 2007).

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CONCLUSION

Industrial wet processing activities generated and discharged a considerable volume of effluents containing dyes and other chemicals. This study was performed to isolate and identify potential metal- degrading bacteria, which are indigenous and efficient in degrading dyes in effluents. The target isolates were provisionally identified as *Staphylococcus xylosus*, *Bacillus korlensis*, *Pseudomonas fluorescens*, *Pseudomonas cichorii*, *Brevundimonus diminuta*, and *Enterococcus columbae*. Almost all the isolates were able to reduce heavy metals that makeup the dyes in the medium, and six isolates exhibited the potential to reduce most of the dyes including the one used in the study. Although the results of this study provide insights into efficient biological remediation of PTEs in industrial wastewater, further studies with a higher number of bacterial isolates, composition of reduced effluent, and speciation of dyes are recommended.

RECOMMENDATIONS

This research is hereby recommending the following;

i. The significance of using indigenous consortium of bacteria in bioremediation cannot be over emphasized, hence it need to be encouraged.
ii. Genetically modification of these organisms should be done to stimulate the remediation process.
iii. More research should be done to understand the mechanisms as well as the utilization process of bacteria on waste water in general.

REFERENCES

Balanand, D. S. and Monteiro, R. T. (2011). Decolorization of textile indigo dye by ligninolytic fungi. *Journal of Biotechnology*. 89(2-3): 141-145.

Dwivedi P. and Tomar R. S. (2017). Microbial Degradation and Decolorization of Azo and Anthraquinone Textile Dyes. *International Journal of Pharma and Bio Sciences*. 8(2): (B): 989-998

Dwivedi, P. and Tomar, R. S. (2018). Bioremediation of textile effluent for degradation and decolourization of synthetic dyes: A review. *International Journal of Current Research in Life Sciences*. 7(04): 1948-1951.

Gupta, J. Joia, A. Sood, R. Sood, C. Sidhu, G. Kaur, A. (2016) Microbes as potential tool for remediation of heavy metals: a review, J. Microb. Biochem. Technol. 8, 364–372.

Hooda, V. (2007) Phytoremediation of toxic metals from soil and waste water, J. Environ. Biol. 28, 367–376.

Khan, H.A. Aziz, N.A. Khan, S. Ahmed, M.S. Mehtab, S. Vambol, V. Vambol, F. Changani, S. Islam, A.H. (2023) Pharmaceuticals of emerging concern in hospital wastewater: removal of Ibuprofen and Ofloxacin drugs using MBBR method, Int. J. Environ. Anal. Chem. 103, 140–154.

Mahmood, R., Sharif, F., Ali, S. and Hayyat, M. U. (2015). Enhancing the decolorizing and degradation ability of bacterial consortium isolated from textile effluent affected area and its application on seed germination. *The Scientific World Journal*.

Marzan, M. Hossain, S.A. Mina, Y. Akter, A.M. Chowdhury, L.W. (2017) Isolation and biochemical characterization of heavy-metal resistant bacteria from tannery effluent in Chittagong city, Bangladesh: bioremediation viewpoint, Egypt J. Aquat. Res. 43, 65–74.

Moosvi, S., Keharia, H. and Madamwar, D. (2005). Decolourization of textile dye Reactive Violet 5 by a newly isolated bacterial consortium RVM 11.1. *World Journal of Microbiology and Biotechnology*. 21(5): 667-672.

Moosvi, S., Kher, X. and Madamwar, D. (2017). Isolation, characterization and decolorization of textile dyes by a mixed bacterial consortium JW-2. *Dyes and Pigments*. 74(3): 723-729.

Nigam S.V., Rao N.C., Srinivas S., Prasad K.K., and Karthikeyan J. (2012). Treatment of simulated Reactive Yellow 22 (azo) dye effluents using *Spirogyra species*. *Waste Manag* 22: 575-82.

Rathod, T. E. (2014). Bioremediation of textile azo dyes by aerobic bacterial consortium aerobic degradation of selected azo dyes by bacterial consortium. *Biodegradation*. 15(4): 275-280.

Rehman, P., Saharan, B. S. and Sharma, D. (2015). Bacterial degradation and decolorization of textile dyes by newly isolated *Lysobacter* sp. *African Journal of Microbiology Research*. 9(14): 979-987.

Sani, R. C. and Banejee Rathod, M. G. and Pathak, A. P. (2014). Wealth from waste: Optimized alkaline protease production from agroindustrial residues by *Bacillus alcalophilus* LW8 and its biotechnological applications. *Journal of Taibah University for Science*. 8(4): 307-314.

Schulze-Rettmer, R. and Zuckut, S. W. (1998). Treatment of Textile Dyeing Wastewater by Adsorption/BioOxida

Tsiamis, P. and Cameotra S. S. (2010). Decolorization of toxic dyes in wastewater. *In Trends in Bioremediation and Phytoremediation*, ISBN 978-81-308-0424-8, Ed.Grazyna Plaza, Poland, 173-187.