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Bioremediation of Reactive Dyes using Bacterial Consortium: Application in Textile Wastewater Treatment

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ABSTRACT

Reactive dyes constitute the largest and most versatile class of synthetic dyes used in the textile industries. During processing unused dyes liberated in the industrial wastewater indirectly in natural water bodies. Such dyes containing wastewater is pose a threat to the environment. Application of microbial consortium to decolorize the textile dyes is efficient method and provides an eco-friendly option for remediation of dyes contaminants. Dye degrading bacteria were isolated from textile effluent. Out of 12, two isolates identified as *Citrobacter diversus* and *Acinetobacter lwoffii* exhibited more than 80% decolorization while their consortium showed 92.5% and 94.8% decolorization of Reactive Orange HE2R and Reactive Red HE7B dyes respectively. Consortium showed highest decolorization in presence of glucose as a carbon source and could tolerate the dyes concentration upto 0.06 g/L with pH 7.0 at 37 °C. FTIR analysis of decolorized medium confirms the degradation of dyes. Consortium was able to decolorize textile effluent efficiently and also resulted in significant reduction of BOD and COD values of effluent sample. These results suggest the use of consortium in *in situ* treatment of textile effluent.

1. Introduction

Textile dyeing industries use a large number of dyes and chemicals for dyeing processes. These dyes are very diverse in chemical composition, ranging from inorganic compounds to organic product and polymers. The artificial chemical structure of textile dyes is chemically and photolytically stable. Thus, the wastewater coming out from textile industry is a complex mixture of highly polluting substances. If such wastewater is discharged into the environment without proper treatment, it can cause serious threat to the receiving environment. It may lead to decreasing light absorption which may significantly affect photosynthetic activity of aquatic life and become toxic due to the presence of aromatics or heavy metals [1-3]. Kaushik and Sharma [4] studied the effect of direct dyes effluent used for irrigation of Maize and Sorghum plants. They observed that the unexhausted dyes and its concentration in the effluent leads to decrease in germination of the seeds, shoot length, root length, chlorophyll contents of the plants up to 44%, 55%, 45% and 48% respectively. Bhanu and Deepak [5] investigated the toxicity of textile mill effluent on economically important fish, *Labeo rohita*. They observed the decreased RBC and Heamoglobin (Hb) in blood of fish and the amount of WBC has been increased as an immunological defense to survive against the toxic substance in the effluent.

Several methods are used to treat such hazardous colored effluents. The physical and chemical treatments are available such as adsorption, photo-oxidation, coagulation; flocculation, photo degradation and chemical degradation. But these treatments are limited use and have high operational cost [6, 7]. On the other hand, the biological degradation process is highly promising, relatively inexpensive, ecofriendly and less sludge producing. It decolorizes complex chemical compounds into simple compounds in a much safer way [8, 9]. Many microorganisms belonging to different taxonomic group of bacteria, fungi, actinomycetes and algae have been reported for their ability to decolorize dyes. The study of Tripathi and Srivastava [10] confirms the ability of newly isolated bacterial culture *Bacillus megaterium* ITBHU01 to decolorize the textile dye Orange G (520 mg/L) with decolorization efficiency of 95%. However, *Bacillus subtilis, Bacillus megaterium, Erysipelothrix* and *Amphibacillus xylanus* were used to degrade seven different textile dyes such as Cibacron red FN-R, Novacron blue, Terasil green, Novacron navy, Novacron orange and Novacron yellow. Almost all dyes except Novacron red were decolorized up to 99% by each bacterial strain after three days of incubation [11].

Thus, the objective of the present work was to isolate textile dyes degrading bacteria from textile effluent and evaluate their application in textile effluent treatment.

2. Experimental Methods

2.1 Dyes and Chemicals

The textile reactive dyes including Reactive Orange HE2R and Reactive Red HE7B were collected from the textile dyeing industry. Nutrient agar media and all other chemicals of analytical grade were purchased from Himedia Laboratory, India.

2.2 Sample Collection

Total 5 effluent samples of different dyeing industries were collected from textile dyeing industries situated in Kalyan-Dombivali MIDC, Dist.: Thane, India. Samples were collected sterile plastic bottles and stored at 4 °C. The original color and pH of effluent samples noted during sample collection.

2.3 Enrichment of Samples

The samples were enriched to increase the number of dye decolorizing bacteria. 1 mL effluent sample was inoculated in 250 mL conical flask containing 100 mL sterilized nutrient broth medium supplemented with filter sterilized 100 mg/L dyes mixture. After 3 days of incubation (37 °C, 150 rpm), the enriched sample was used for isolation of dye decolorizing bacteria.

2.4 Isolation of Dye Decolorizing Bacteria

The isolation was carried out on sterile nutrient agar plates (pH 7.0) supplemented with 100 mg/L dye mixture. Serial dilutions of the enriched broth were made up to 10^{-6} dilutions. From each dilution, organisms were isolated by spread plate method. After incubation, morphologically distinct colonies were selected and purified through repeated streaking on sterile nutrient agar plates. The purified bacterial isolates were maintained on nutrient agar slants.

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2.5 Determination of Absorption Maxima of Dyes

Absorption maxima (λ_{max}) of each dye as well as dye mixture were determined through scanning the absorption of light within the visible range (400–700 nm) at an interval of 1 nm using Shimadzu UV spectrophotometer (UV-1800). The wavelength reflecting the highest optical density (O.D.) was regarded as their corresponding maximum wavelength (λ_{max}). The highest O.D. of Reactive Orange HE2R and Reactive Red HE7B dyes mixture were found to be as 530 nm and 580 nm respectively.

2.6 Dye Decolorization Analysis

Decolorization activity of isolated bacteria was determined using 100 mL nutrient broth containing 0.02 g/L dyes in 250 mL Erlenmeyer flask separately. The flasks were inoculated with 3 mL of 24 h old bacterial culture and incubated at 37 °C on a shaker (Make: Remi) with 150 rpm up to 7 days maximum. Uninoculated dye medium served as control. After every 24 h, the flasks were checked for decolorization. As the decolorization observed, percent decolorization study was performed by colorimetric analysis. The 10 mL decolorized medium and control medium was centrifuged at 5000 rpm for 15 min. The O.D. of supernatant of decolorized medium and control medium was determined at respective maximum wavelength of that particular dye [12]. Nutrient broth without dye was served as a blank. Percentage of decolorization was calculated by using the formula,

$$\% \text{ Decolorization} = \frac{Initial\ O.D. - Final\ O.D}{Initial O.D.} x\ 100$$

2.7 Identification of Most Potent Isolates

The most efficient isolates labelled as I-1 and I-2 were identified by Gram staining, morphological and biochemical tests using the taxonomic scheme of Bergey's manual of determinative Bacteriology.

2.8 Dyes Mixture Decolorization Assay by Consortium

A consortium of selected two isolates was developed and observed its dyes mixture decolorization ability. Both the organisms were grown overnight on nutrient agar. Equal volumes of saline suspension (0.6 O.D. 600 nm) of each isolate were added in sterile flask and mixed properly. The obtained suspension used as consortium. 3 mL of consortium suspension was used to inoculate 100 mL MSM medium containing 1 g/L yeast extract. Both the dyes were added in medium flask with 0.02 g/L concentration. Dyes decolorization activity was recorded.

2.9 Optimization of Dyes Decolorization Activity of Consortium

Decolorization activity of consortium was optimized by observing the effect of various carbon sources (glucose, sucrose, mannitol, maltose) and dye concentration (0.02 g/L to 0.1 g/L). Mineral salt medium (MSM) containing KH_2PO_4- 0.5 g, K_2HPO_4 - 0.5 g, $MgSO_4$ - 0.5 g, NH_4SO_4 - 1.0 g, NaCl- 0.5 g, carbon source - 0.5 g, $FeSO_4.2H_2O$- 0.02 g, Yeast extract – 1.0 g, D/W – 1000 mL was used for optimization studies. The final pH of the medium was adjusted to 7.0. A working volume of 100 mL MSM medium containing 0.02 g/L respective dye in 150 mL Erlen-Meyer flask was employed throughout the study.

Saline suspension of 24 h old culture of 0.6 O.D. at 600 nm was used for optimization experiment. The 100 mL medium was inoculated with 3 mL of suspension and incubated at R.T. (28 °C ± 2 °C) [13,14]. Uninoculated medium control flasks were kept to check abiotic decolorization of dyes. On incubation, the decolorization percentage was measured.

2.10 Analysis of Biodegradation of Dyes using FTIR

FTIR analysis was performed using JASCO FT/IR 4100. The FTIR was first calibrated for background signal- scanning without any sample (air blank- CO_2 curve). Clear supernatant of control medium containing dyes mixture and decolorized medium was used for the study.

1 µL of sample was taken and placed on the salt plate (KBr pellet). The salt plate was then fixed to the sample holder. The spectra were collected in scanning range of 400-4000 cm^{-1}. The IR solution software generates reports by subtracting the spectrum of the air blank (CO_2 curve) from the spectrum of the experimental samples.

2.11 Decolorization of Textile Effluent by Consortia

The Initial O.D., BOD, COD and pH of textile effluent was a measured to study the effect of microbial decolorization on respective parameters of effluent samples. 1500 mL sterile effluent sample was added in two flasks of 2000 mL. One flask was inoculated with 20 mL consortium culture (0.6 O.D. at 600 nm) and labeled as test flask while other flask was kept as it is for control analysis. Both the flasks were incubated at R.T. (28 °C ± 2 °C) in shaking condition (150 rpm) maximum for 5 days. Decolorization was observed after every 24 h. On decolorization, percentage decolorization was determined by taking O.D of decolorized and control effluent at 600 nm. 1 g/L yeast extract in 1500 mL D/W was used as a blank for colorimetric readings.

The decolorized effluent samples were first filtered through Whatmann filter paper No.1 and centrifuged for 10 min. The obtained clear supernatant used for pH, BOD and COD analysis of treated water.

3. Results and Discussion

3.1 Dye Decolorization Analysis of Isolates

The decolorization of enriched culture medium indicates the presence of dye decolorizing bacteria in collected effluent samples. Morphologically 12 different bacterial isolates were obtained from enriched effluent samples. The colony morphology was found to differ in color, shape, size, margin, surface texture, consistency and elevation. It shows bacterial adaptability towards dyes. The selected isolates were purified, labeled and stored on Nutrient agar slopes below 15 °C. Zone of dye decolorization on culture medium suggests that the isolated bacteria have ability to withstand against the dyes. Numerous scientists isolated efficient dye decolorizing bacteria from the textile dye effluent, activated sludge and soil contaminated with dye collected from the waste disposal sites. Kumar and Saravanan [15] isolated 13+ morphologically different dye degrading organisms with zone of clearance from textile effluent samples. Experiments by Bhimani et al. [16] to isolate different bacterial species from CEPT effluent resulted in isolation of 33 bacterial species. Similarly, Nanthakumar et al. [17] isolated 14 dye degrading bacteria from termite samples while 30 morphologically distinct bacterial colonies were isolated by Karim et al. [18].

3.2 Dye Decolorization Analysis

The selected 12 bacterial isolates were tested for decolorization of Reactive Orange HE2R and Reactive Red HE7B. 09 isolates were shown the decolorization of both the dyes while 03 isolates were able to decolorize only Reactive orange HE2R dye. 05 isolates showed more than 60% decolorization of medium. However, 02 isolates identified as *Citrobacter diversus* and *Acinetobacter lwoffii* showed 83.6% and 81.7% decolorization of Reactive Orange HE2R and 85% and 82.4% decolorization of Reactive Red HE7B respectively within 24 h (Fig. 1). Similarly, Rahi and Gupta [19] isolated indigenous bacterial strain *Mycobacterium oryzae* JC8 that showed 89.2% and 84.6% decolorization of reactive orange 3R and Reactive red HE7B respectively.

During investigation, decolorization was not observed in uninoculated control flasks. This confirms that the isolates decolorized the dyes and decolorizing efficiency was totally dependent on the growth of the isolate. The decolorization was only due to the metabolic activity of the organism and not due to any abiotic factors.

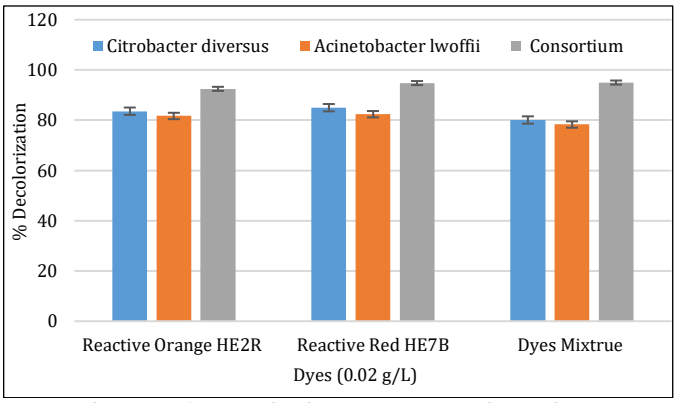

Fig. 1 Decolorization of Reactive dyes by most prominent Isolates and Consortium

3.3 Dyes Mixture Decolorization Assay by Consortium and Pure Culture

Citrobacter diversus and *Acinetobacter lwoffii* required 24 h to decolorize mixture of dyes while their consortium maximum decolorization within 18 h. 15% increase in decolorization extent as compared to both isolates by using consortium. 80.1% and 78.3% decolorization of dyes mixture was obtained through *Citrobacter diversus* and *Acinetobacter lwoffii* respectively. Mixture of both dyes found to be affecting on decolorization efficiency of each isolate. Fig. 1 illustrates the findings of dyes mixture decolorization assay.

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Microbial consortia of *Citrobacter diversus* and *Acinetobacter lwoffii* exhibited 92.5% and 94.8% decolorization of Reactive Orange HE2R and Reactive Red HE7B separately. Both organisms were found to be compatible with each other and their synergistic action resulted in 95.1% decolorization of dyes mixture consisting Reactive Orange HE2R and Reactive Red HE7B dyes within 18 h. The consortium of isolates was found to be more potent than pure isolates. The synergistic metabolic activity of organisms in consortium may lead to higher and rapid degradation of dyes mixture than individual cultures [20].

Similar to present findings, *Bacillus odyssey* SUK3, *Proteus* spp. SUK7 and *Morganella morganii* SUK5 showed 86%, 83% and 86% decolorization of Reactive Navy blue HE2R within 60 h, 50 h and 45 h respectively, while these bacteria in consortium showed 91% decolorization within 6 h. Consortium showed higher decolorization percentage within short period as compared to individual strains. It suggests the co-metabolic activity of consortium [21].

Azo bond (N=N) of reactive dye compounds is responsible dyes coloration. The degradation of azo bonds leads to decolorization of compound. Dyes adapted Bacteria may have ability to generate azo reductase enzyme which can break the azo bond more effectively. Azo bond degradation results in the production of colorless aromatic amines which may be toxic, mutagenic and carcinogenic to animals [22]. Thus, the degradation could be carried out by using of microbial consortium which results in higher degree of biodegradation and mineralization due to synergistic metabolic activities. Each strain of the consortium may attack the same dye molecule at different positions and may utilize metabolites produced by the other strains for further decomposition [23].

3.4 Identification of Most Potent Isolates

The bacterial isolate labelled as I-1 was found as rod-shaped Gram-negative bacteria producing late pink colonies on Mac-conkeys plate and found as non- heamolytic on SIBA plate. On result comparison with Bergey's manual, the first isolate was identified as *Citrobacter diversus.* The Gram staining of second isolates showed Gram negative rods, showed slight pink colonies on mac-conkeys agar and non-heamolytic colonies on SIBA plate. On the basis of these results, the isolate labelled as I-2 was identified as *Acinetobacter lwoffii* respectively. Table 1 shows the results of different biochemical characteristics of isolates.

Table 1 Biochemical characteristics of isolates

Isolate	GN	Glu.	Su.	La.	Ma.	Xy.	Man.	MR	VP	Ind,	Ct.
F CV 3	-	AG	D	A	D	A	A	+	-	+	+
P CV 3	-	-	-	-	-	-	-	-	-	-	-
Isolate	LDC	ODC	TSI	H_2S	Cat.	Oxi.	PPA	Ur.	Mot.	Nit.	
FCV 3	-	+	AG	-	+	-	-	D	+	+	
P CV 3	-	-	-	-	+	-	-	-	+	-	

In present study both dye decolorizing bacteria were found to be Gram Negative. Asthana et al. [24] suggested that the "Gram negative bacteria are more potent in dyes decolorization than Gram positive bacteria as they have a higher adsorption capacity than Gram positive bacteria due to their higher lipid contents in the cell wall".

Citrobacter genus of bacteria was well known for its xenobiotic compounds degrading ability and has been studied in the past specifically for its dyes degrading ability. Abdul-Wahab et al. [25] isolated *Citrobacter freundii* from sewage treatment plant. It able to decolorize azo dyes namely Acid Red 27, Direct Blue 15 and Reactive Black 5 in pure and mixed culture conditions.

Acinetobacter genus is a dominant dye decolorizing bacterial genus. Different species of Acinetobacter genus were obtained from textile effluent by researchers and their co-workers. Ghodake et al. [26] revealed that the *Acinetobacter calcoaceticus* NCIM 2890 has a potential to degrade textile dyes containing different chromophore groups. Ramya et al. [27] isolated and identified *Acinetobacter radioresistens* which exhibited 90% decolorization of Acid Red at neutral pH. Similar to above results, our investigation also reported presence of *Acinetobacter lwoffii* and *Citrobacter diversus* in textile effluent samples.

3.5 Optimization of Decolorization Activity for the Selected Isolate

The carbon sources were necessary substrates for the growth and product formation in microbial cultivation. The nature and characteristics of these substrates has a predominant role to play in the metabolism of microorganism. Both the parameters carbon sources and dye concentration showed significant effect on decolorization activity of *Citrobacter diversus* and *Acinetobacter lwoffii* consortium. The consortia required at least 1 g/L yeast extract in MSM medium with to achieve maximum decolorization of dyes. Results presented graphically in Fig. 2, indicate that, consortium showed highest decolorization (95.3%) in presence of glucose as carbon source.

However, increasing dyes concentration found to be affecting on dyes removal ability of isolates. Consortium showed 95.4% decolorization of dyes mixture with the dye's concentrations 0.02 g/L to 0.06 g/L within 18 h. It can be seen from graphical representation (Fig. 3), the decolorization rate was not affected up to the 0.06 g/L dye concentration. But at 0.08 g/L to 0.1 g/L dyes concentrations, the time of decolorization was found to be increases up to 24 h. Decolorization efficiency of consortium is not much affected as it showed 90.1% decolorization of 0.1 g/L dye concentration. Thus, the study suggests that microbial consortium of *Citrobacter diversus* and *Acinetobacter lwoffii* can withstand the dye concentration up to 0.1 g/L. In literature, Ranga et al. [28] reported that *Lysobacter* spp. P28 could decolorize azo dyes, Congo red and Yellow HEGR upto the 50 mg/L concentration resulting in approximately 80.4% and 80.1% decolorization in 72 h and could tolerate up to 200 mg/L of dye with 60.4% and 50.8% decolorization extent in 84 h. It indicates the dyes concentration is one of the major factors which effects on the biodegradation process.

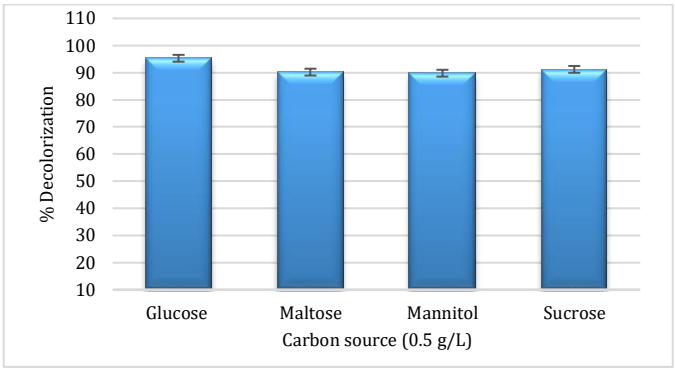

Fig. 2 Effect of carbon source on decolorization

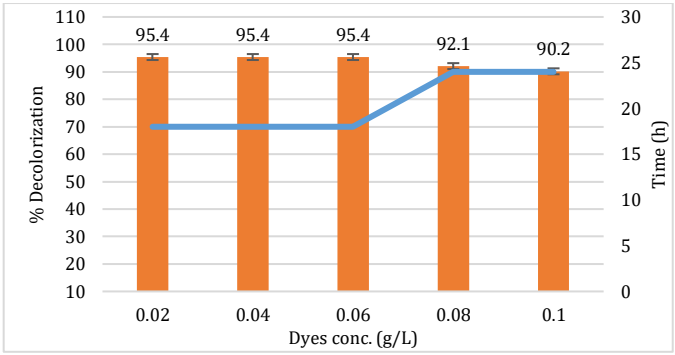

Fig. 3 Effect of Dyes concentration on decolorization

3.6 Analysis of Biodegradation of Dyes using FTIR

In present study, FTIR spectra (Fig. 4) obtained from the control dyes sample showed several peaks at 568 cm^{-1}, 720 cm^{-1}, 887 cm^{-1}, 964 cm^{-1}, 1335 cm^{-1}, 1595 cm^{-1} 1415 cm^{-1}, 2566 cm^{-1} and 3133 cm^{-1}. The peaks at 1595 cm^{-1} and 1415.49 cm^{-1} represent the azo bonds in control reactive dyes. The FTIR spectrum of decolorized sample showed new peaks at 472 cm^{-1}, 845 cm^{-1}, 1193 cm^{-1} and 3040 cm^{-1}. The cleavage of azo bond was confirmed by the absence of peak near 1400 cm^{-1} for N=N stretching vibrations in the FTIR spectrum of decolorized medium. This suggests that the consortium was able to degrade Reactive Orange HE2R and Reactive Red HE7B.

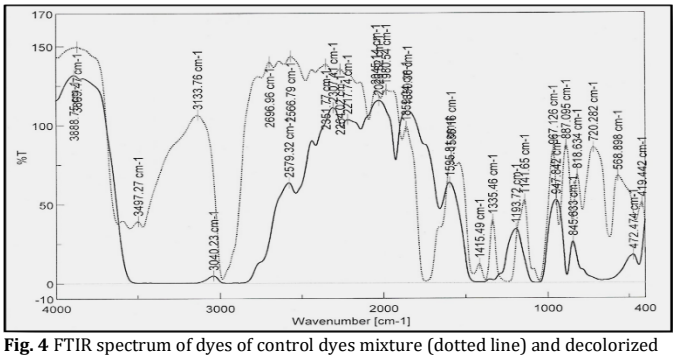

Fig. 4 FTIR spectrum of dyes of control dyes mixture (dotted line) and decolorized medium (continueos lines)

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3.7 Decolorization of Textile Effluent by Consortia

The consortium of present study could efficiently survive in textile effluent samples supplemented with yeast extract as a co-substrate. It resists the high level of toxic chemicals present in textile effluent and could decolorize it efficiently. The physiochemical characterization of Treated and Untreated effluent is presented in Table 2.

Table 2 Physiochemical parameters of treated and untreated effluent samples

S. No.	Parameter	Untreated	Treated
1.	pH	9.5	6.8
2.	Color	Black	Off white
3.	O.D. at 600 nm	0.46	0.05
4.	Decolorization (%)	-	87.00 % (48 h)
5.	Biological Oxygen Demand (mg/L)	990	138
6.	Chemical Oxygen Demand (mg/L)	1664	262

The present study reporting 87% decolorization of textile effluent by consortium consisting only two bacterial species including *Acinetobacter* spp. and *Citrobacter* spp., while Aruna et al. [29], utilized Bacterial consortium of four species including *Bacillus* spp.1, *Bacillus* spp.2, *Acinetobacter* spp. and *Citrobacter* spp. with 77.49% decolorization of textile effluent. It indicates that our consortium is more reliable and indigenous in textile effluent treatment.

Bacterial consortium not only degrades the dyes but also utilizes the organic and inorganic content of effluent which lowers BOD and COD values of effluent. The BOD and COD values of textile waste water is significantly reduced to 138 mg/L and 262 mg/L respectively that ranging within disposal standards limits. Similar to our results, Ajao [30] reported significant reduction in BOD and COD (>80%) values of textile effluent after *Pseudomonas aeruginosa* and *Bacillus subtilis* bacterial consortium treatment of textile effluent.

In earlier reports, Kochher and Jitendra [31] concluded that the textile effluent collected from Oswal Textile Industries, Ludhiana, is highly polluted according to obtained values of physicochemical parameters and also stated that, the isolated *Bacillus* strain from such toxic effluent efficiently degraded the Crystal violet dye (100 mg/L). Patel et al. [32] estimated 2840 mg/L and 1760 mg/L COD value of textile effluent. 1050 mg/L and 3050 mg/L COD value of textile effluent was determined by Singh et al. [33]. These results were very similar to results of present study, where COD values of untreated effluent sample was 1664 mg/L. Phugare et al. [12] reported significant reduction of COD by microbial consortium (*Providencia* spp. and *Pseudomonas aeruginosa* strain BCH) treatment. This indicates that the bacteria have the ability to degrade the dyes as well as can reduce the BOD and COD values of textile effluent.

4. Conclusion

The isolated *Citrobacter diversus* and *Acinetobacter lwoffii* decolorizes of Reactive Orange HE2R and Reactive Red HE7B efficiently in optimized conditions. FTIR analysis confirmed the degradation of Reactive dyes on microbial treatment. This will be the first report where the consortium of *Citrobacter diversus* and *Acinetobacter lwoffii* used for the treatment of textile effluent treatment. It is significantly affecting the on color as well as physiochemical parameters of textile effluent and made it dischargeable in natural waterbody resources. Thus, the study concludes that the studied microbial consortium can be ecofriendly promising approach for the cleanliness of environment. The future aspects of study recommend the identification and purification of dye degrading enzyme present in selected isolates.

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References

[1] I.M. Banat, P. Nigam, D. Singh, R. Marchant, Microbial decolorization of textile dye containing effluents, Bioresour. Technol. 58 (1996) 217-227.
[2] K. Jahnavi, R.K. Rao, P. Suvarna, Development of embedded systems to control toxic compounds in textile industries, Int. J. Sci. Res. 1(5) (2012) 46-50.
[3] N. Puvaneswari, J. Muthukrishnan, P. Gunasekaran, Toxicity assessment and microbial degradation of azo dyes, Indian J. Exp. Biol. 44 (2006) 618-626.
[4] C.P. Kaushik, J.K. Sharma, Effect of direct dyes effluent on germination/growth of Maize and Sorghum plants, J. Environ. Sci. Eng. 54(1) (2012) 50-54.
[5] A.P. Bhanu, M. Deepak, The influence of textile mill effluent on haematological changes of *Labeo rohita*, Int. J. Innov. Res. Sci. Eng. Technol. 2(12) (2013) 8001-8003.
[6] R.G. Saratale, G.D. Saratale, D.C. Kalyani, J.S. Chang, S.P. Govindwar, Enhanced decolorization and bio-degradation of textile azo dye scarlet R by using developed microbial consortium- GR, Bioresour. Technol. 100 (2009) 2493-2500.
[7] M. Rizwana, M. Darshan, D. Nilesh, Phytoremediation of textile waste water using potential wetland plant: Eco sustainable approach, Int. J. Interdiscip. Multidiscip. Stud. 1(4) (2014)130-138.
[8] D. Mazumder, Process evaluation and treatability study of wastewater in a textile dyeing industry, Int. J. Energy Environ. 2(6) (2011) 1053-1066.
[9] R. Siva, Status of natural dyes and dye-yielding plants in India, Curr. Sci. 92 (2007) 916-925.
[10] A. Tripathi, S.K. Srivastava, Ecofriendly treatment of azo dyes: Biodecolorization using bacterial strains, Int. J. Biosci. Biochem. Bioinform. 1(1) (2011) 37-40.
[11] K.R. Mahbub, A. Mohammad, M.M. Ahmed, S. Begum, Decolorization of synthetic dyes using bacteria isolated from textile industry effluent, Asian J. Biotechnol. 4(3) (2012) 129-136.
[12] S. Phugare, D. Kalyani, S. Surwase, J.P. Jadhav, Ecofriendly degradation, decolorization and detoxification of textile effluent by a developed bacterial consortium, Ecotoxicol. Environ. Saf. 74(5) (2011) 1288-1296.
[13] A. Alalewi, C. Jiang, Bacterial influence on textile wastewater decolorization, J. Environ. Prot. 3 (2012) 889-901.
[14] T. Kuberan, J. Anburaj, C. Sundaravadivelan, P. Kumar, Biodegradation of azo dye by *Listeria Spp.*, Int. J. Environ. Sci. 1(7) (2011) 1760-1769.
[15] N.M. Kumar, D. Saravanan, Isolation of dye degrading bacteria from textile effluent, J. Chem. Pharm. Res. 7(3) (2015) 2214-2218.
[16] H.D. Bhimani, D.V. Bhensdadia, C.M. Rawal, V.V. Kothari, R.K. Kothari, C.R. Kothari, G.C. Bhimani, Influence of some chemical parameters on decolorization of textile dyes by bacterial strains isolated from waste water treatment plant, Afr. J. Microbiol. Res. 8(11) (2014)1213-1220.
[17] K. Nanthakumar, K. Karthikeyan, S. Suriyanarayanan, P. Lakshmanaperumalsamy, Decolorization of structurally dissimilar dyes by a termite derived bacterial consortium BUTC17 in a cost-effective nutrient medium, Adv. Appl. Sci. Res. 4(2) (2013) 276-285.
[18] E. Karim, K. Dhar, T. Hossain, Decolorization of textile reactive dyes by bacterial monoculture and consortium screened from textile dyeing effluent, J. Genet. Eng. Biotechnol. 16 (2018) 375-380.
[19] R. Rahi, V. Gupta, Biodecolorization of reactive red HE7B and reactive orange 3R through indigenous bacterial isolate *Microbacterium oryzae* strain JC8 isolated from textile effluent, Ecol. Environ. Conserv. 26 (2020) 268-272.
[20] R. Rajendran, S. Karthik Sundaran, K. Uma Maheswari, Aerobic biodegradation of mixture of azo dye containing textile effluent using adapted microbial strains, J. Environ. Sci. Technol. 4(6) (2011) 568-578.
[21] P.S. Patil, Decolorization, degradation and kinetic study of textile dye Navy Blue HE2R using immobilized bacterial consortium PMB11, J. Environ. Sci. Pollut. Res. 2(3) (2016) 99-102.
[22] R.S. Gowri, R. Vijayaraghavan, P. Meenambigai, Microbial degradation of reactive dyes- A Review, Int. J. Curr. Microbiol. App. Sci. 3(3) (2014) 4-10.
[23] R. Saratale, G. Saratale, J. Chang, S. Govindwar, Decolorization and biodegradation of reactive dyes and dye wastewater by a developed bacterial consortium, Biodegradation 21(6) (2010) 999-1015.
[24] M. Asthana, A. Kumar, P. Vikrant, P. Gupta, Tannery effluents de colorization efficiency of bacterial isolates from River Yamuna and industrial effluents, Int. J. Curr. Microbiol. App. Sci. 3(5) (2014) 869-880.
[25] M.F. Abdul–Wahab, G.F. Chan, A.R.M. Yusuff, N.A.A. Rashid, Reduction of azo dyes by flavin reductase from *Citrobacter frundii* A1, J. Xenobiot. 3(2) (2013) 9-13.
[26] G. Ghodake, U. Jadhav, D. Tamboli, A. Kagalkar, S. Govindvar, Decolorization of textile dyes and degradation of mono-azo dye Amaranth by *Acinetobacter calcoaceticus* NCIM 2890, Ind. J. Microbiol. 51(4) (2011) 501-508.
[27] M. Ramya, S. Iyappan, A. Manju, J.S. Jiffe, Biodegradation and decolorization of acid red by *Acinetobacter radioresistens*, J. Bioremed. Biodegrad. 1(1) (2010) 1-6.
[28] P. Ranga, B.S. Saharan, S.A. Sharma, Bacterial degradation and decolorization of textile dyes by newly isolated *Lysobacter* spp., Afr. J. Microbiol. Res. 8(11) (2014) 1213-1220.
[29] B. Aruna, L.S. Rathna, E. Shivakumar, A. Srinu, P. Roja-rani, D. Vijaya Lakshmi, D.V. Prasad, Bacterial consortia for effective decolorization and bio degradation of anthraquinone dyes, Int. J. Adv. Res. Biol. Sci. 2(11) (2015) 14-21.
[30] A.T. Ajao, Bioremediation of textile industrial effluent using mixed culture of *Pseudomonas aeruginosa* and *Bacillus subtilis*, J. Microbiol. Biotechnol. 1(3) (2011) 50-56.
[31] S. Kochher, K. Jitender, Microbial decolorization of crystal violet by *Bacillus subtilis*, Biol. Forum Int. J. 3(1) (2011) 82-86.
[32] R. Patel, K. Tajddin, A. Patel, B. Patel, Physico chemical analysis of textile effluent, IJRSI 2(5) (2015) 2321-2705.
[33] D. Singh, V. Singh, A.K. Agnihotri, Study of textile effluent in and around Ludhiana District in Punjab, India, Int. J. Environ. Sci. 3(4) (2013) 1271-1278.

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