http://www.pjbs.org

PJBS

ISSN 1028-8880

Pakistan Journal of Biological Sciences

ANSInet
Asian Network for Scientific Information
308 Lasani Town, Sargodha Road, Faisalabad - Pakistan

Pakistan Journal of Biological Sciences 14 (11): 610-618, 2011
ISSN 1028-8880 / DOI: 10.3923/pjbs.2011.610.618

Comparative Analysis of Bioremediation Potential of Adapted and Non-Adapted Fungi on Azo Dye Containing Textile Effluent

R. Rajendran, S. Karthik Sundaram, P. Prabhavathi, B.V. Sridevi and V. Gopi
PG and Research Department of Microbiology, PSG College of Arts and Science,
Coimbatore-641014, Tamil Nadu, India

Abstract: About 4 different predominant adapted fungal strains (screened from effluent sample) *Aspergillus* sp., *Penicillium* sp., *Fusarium* sp. and *Mucor* sp. and 4 predominant non-adapted strains (screened from soil, water and fungal fruiting bodies) *Aspergillus* sp., *Penicillium* sp., *Fusarium* sp. and *Rhizopus* sp., with potential dye decolorization ability on Reactive black 5, Amido black-10B, Red 5B, Reactive red 120 and Anthraquinone violet R were isolated. These organisms were used to develop a consortium which was used in analyzing the bioremediation efficiency on textile effluents containing a mixture of azo dyes. There was about 67% of reduction in color along with 34% of COD reduction by non-adapted fungal consortium while effective bioremediation efficiency was observed in adapted fungal consortium (Color 75% and COD 50%). The regression co-efficient for Langmuir and Freundlich adsorption isotherms were found to be higher for adapted fungal consortium ($R^2 = 0.97$ and $R^2 = 0.92$) than the non-adapted consortium ($R^2 = 0.97$ and $R^2 = 0.85$) proving that both monolayer and multilayer adsorption of dyes were observed on treating the samples with the adapted fungal consortium. On analyzing the results observed through chi-square test, the calculated value (28.712) was higher than the tabulated value (9.49) at a 4 degree freedom hence the hypothesis was rejected. So, there was an association between adapted fungal consortium and non-adapted fungal consortium and hence the adapted fungal consortium could be considered potentially useful for the bioremediation of textile effluent.

Key words: Adapted and non-adapted fungi, textile effluent treatment, physico-chemical analysis, adsorption kinetics, azo dye degradation

INTRODUCTION

Textiles industries in India hold a major source of income for the country through exports. The textile industries bring out wastes during the pre-processing stages like scouring, mercerizing etc and through the dyeing of processed materials. As a result organic load (from pre-processing) and dyes ends up in the effluent system (Tariq *et al*., 1996). Azo dyes are the commonly used dyes in India mainly because they are cheap and a wide spectral range of color that could be imparted to the textiles. These azo dyes have very poor exhaustion properties and as a result a large proportion of the used dyes end up as waste in the effluent (Omar, 2008). The major drawback about the usage of azo dyes is that they are recalcitrant in nature mainly because they are man-made (Cooper, 1995). These dyes when discharged into the natural water system create havoc in the system as they are toxic in nature and due to the color that they impart on the water system making it unsuitable for consumption (Igwe *et al*., 2007). On partial degradation these azo dyes gives rise to aromatic amines, which are mutagenic in nature. Hence, there should be a proper treatment technique in each of the textile industry to make sure that these effluents are treated properly before they are discharged (Olukanni *et al*., 2009).

Currently, the textile industries depend upon physical or chemical treatment of textile effluents like sedimentation, specific coagulation and filtration and subsequent chemical treatments such as flocculation, neutralization, use of activated carbon and electro-dialysis before disposal. These processes may not guarantee adequate treatment of the effluent. Moreover, they are often laborious and expensive (Maier *et al*., 2004). Whereas the biological treatment techniques are both could be deployed anywhere without any disadvantages and are cheaper (Tcjatcjiemg *et al*., 2009).

The use of bacterial system in the treatment of effluent is the order of any industries mainly because of its fast growing nature. But as far as the textile effluent treatment is concerned the bacterial system finds it tough to ensure the safe disposal of the waste as, the azo dyes should be treated under both anaerobic (break down of azo to intermediates (aromatic amines) and aerobic

Corresponding Author: S. Karthik Sundaram, PG and Research Department of Microbiology, PSG College of Arts and Science, Coimbatore-641014, Tamil Nadu, India

conditions (oxidation of aromatic amines) subsequently for the removal of the toxic dye products. Thus the process of employing bacteria in azo dye treatment becomes tedious and time consuming (Olukanni *et al*., 2009). On the other hand the use of eukaryotic fungi makes sure that the azo dyes are reduced under a different pattern of reducing ensuring that the aromatic amines are not formed on treatment. But the use of non-adapted or non-native fungi in the treatment could be of no use, as they could not tolerate the harsh environment of the textile effluent. But these non-native fungi are capable of reducing any dyes containing an aromatic ring under aerobic condition through their enzymes that are non-specific in nature (Khammuang and Sarnthima, 2009). On the other hand the adapted fungal strains could very well remediate the effluent at a faster rate as they have already acclimatized to the harsh environment of the textile effluent. These organisms could very well extract energy from both the organic load as well as from the dyes present in the system (Robinson *et al*., 2001). The objective of the research was to study the differences in the bioremediation potential of the adapted and non-adapted fungal consortia on textile effluents.

MATERIALS AND METHODS

Sample collection: Textile effluent sample was collected from a Karupanpalayam treatment plant (cETP) in Karur District, Tamil Nadu India. The effluent sample was used in the isolation of adapted fungal strains. Soil samples, water samples and fruiting bodies were collected from the different natural locations was used in the isolation of non-adapted fungal strains. The collected effluent sample was stored under 4°C for the treatment trials.

Isolation, screening and identification of fungi: Enumeration of potent decolorizers of fungal population of effluent and environmental samples were isolated by serially diluting the samples on Potato Dextrose Agar (PDA) containing 0.01% of synthetic dye (Structure, class in which the dye belongs to and absorption maxima of each dye used in the study are provided) (Table 1) (primary screening) which was then incubated at 27°C for 48 h. Those organisms that showed decolorization on the selected dyes were selected for further screening. Secondary screening was done using Potato Dextrose Broth (PDB) containing 0.01% of dye (used for primary screening) inoculating the selected fungal strains. These tubes were incubated at 27°C for 48 h. After incubation the tubes were centrifuged and the supernatant was analyzed for decolorization by measuring the sample in a UV-Visible Spectrophotometer according to the absorption maxima for the selected individual dye (Harley and Prescott, 1993). The efficient fungal strains screened were identified using lacto phenol cotton blue staining (Cappuccino and Sherman, 1999).

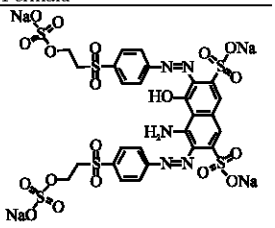
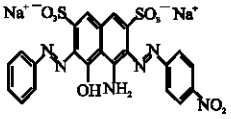
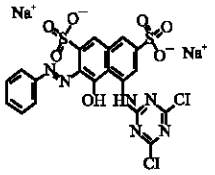
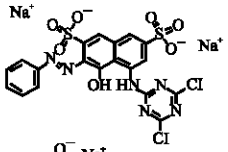
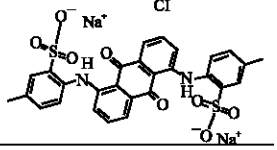
Compatibility analysis: The four selected adapted and non-adapted fungal strains were subjected for compatibility analysis before they were used for bioremediation purposes. Four PDA agar plates were taken and each plate was bored with three wells. The first plate was added with 10 μL of culture supernatants of the selected screened isolates 1, 2 and 3, respectively in the three wells and was swabbed with the isolate 4. This was to study the antagonistic effect of the first 3 adapted organisms on the growth of the swabbed organism. The test was repeated by changing the swabbed organism and the supernatants that were added to the bored wells to check the antagonistic effect of each organism screened. The plates were then kept for incubation at 27°C for 48 h. The culture was said to be compatible with each other if there was no zone of clearance around the bored well. The same procedure was repeated for analyzing the compatible characteristics of the selected non-adapted fungal strains also (Rajendran *et al*., 2011).

Physiochemical characterization of effluent: A number of physico-chemical parameters were analyzed to characterize both the untreated and treated textile effluent (Turbidity, pH, color, electrical conductivity, resistivity, alkalinity, Total Solid (TS) Total Dissolved Solids (TDS), Total Suspended Solids (TSS), Chemical Oxygen Demand (COD) and Hardness (Clesceri *et al*., 1989). Only based on the reduction in these physico-chemical parameters the efficiency of both the adapted and non-adapted fungal consortium were analyzed.

Comparison of treatment trails on bioremediation of azo dye containing textile effluent by both adapted and non adapted fungal isolate consortiums: From the selected adapted fungal strains about 5 mL of inoculum (each pure culture of fungi added in equal concentration to make up a volume of 5 mL) was added to 95 mL of textile effluent. Similarly, 5 mL of the selected non-adapted fungal strains were also added separately to 95 mL of textile effluent. These samples were incubated at 27°C in a metabolic shaker at 120 rpm for a period of 7 days. Sample without any inoculation served the control. The treated effluent samples were retrieved at the end of 7 days of incubation and were analyzed for the bioremediation efficiency of the selected non-adapted fungal consortium.

Comparison of treatment trails on bioremediation of azo dye containing textile effluent by both adapted and non adapted fungal consortium: Adsorption isotherms model was widely used to describe the adsorption progress and also investigated the mechanism of

Table 1: Characters of the synthetic dye used in the study

Name	Dye type	Absorption maxima	Formula
Reactive black 5	Azo	520	
Amido black-10B	Diazo	520	
Red 5B	Azo	535	
Reactive red 120	Azo	475	
Anthraquinone violet R	Anthraquinone	435	

adsorption viewed in energetic homogenous and heterogeneous system. This system was made use of in analyzing the bioremediation of both non adapted and adapted fungal consortium. These were analyzed according to the Langmuir and Freundlich isotherm models (Garg *et al*., 2003). The constant in the Langmuir isotherm can be determined by plotting Ce versus Ce/q_e and making use of Eq. 1:

$$(Ce/qe) = 1/Q^0b+Ce/Q^0 \quad (1)$$

where, Ce (mg L^{-1}): Equilibrium concentration of the solute, qe: Amount adsorbed at equilibrium (mg g^{-1}), Q^0 (mg g^{-1}) and b (l mg^{-1}): Langmuir constants.

Freundlich isotherm can be determined by plotting in Ce versus in q_e and making use of Eq. 2:

$$\text{Log } q_e = \text{Log } K_f+(1/n) \text{ log } Ce \quad (2)$$

where, Kf and 1/n = Freundlich constants.

Physico-chemical characterization of treated effluent-GCMS analysis: The raw effluent sample and the treated samples using both adapted and non-adapted fungal strains were characterized using GCMS. The effluent (treated and untreated) was mixed with equal volume of diethyl ether and allowed to evaporate. The remaining residue was collected and mixed with methanol. Sample was dissolved in methanol and GC-MS analysis of untreated and treated effluents was carried out using a THERMO GC-TRACE ULTRA VER: 5.0, THERMO MS DSQ II. The ionization voltage was 70 ev. Gas chromatography was conducted in temperature programming mode with a 100-250°C, RATE: 8 Min^{-1}, HOLDING TIME: 10 Min at 250°C. The initial column temperature was 40°C for 4 min, then increased linearly at 10°C per minute to 270°C and held at 4 min. The temperature of injection port was 275°C and GC/MS interface was maintained at 300°C. The helium was carrier gas; flow rate was 1.0 mL min^{-1} and 30 min run time. The compounds were identified on the basis of mass spectra and using the NIST library stored in the computer software (version 1.10 beta Shimadzu).

Statistical analysis: Chi-square distribution is a type of statistical tool deals with the association between adapted fungal consortium and non-adapted fungal consortium for the bioremediation of textile effluent. It is primarily used in testing the discrepancy between the expected and

observed frequency and the observed frequency was compared with the hypothesis (null or alternate hypothesis).

RESULTS

Isolation, screening and identification of fungi: On observing the incubated plates it was found that 7 adapted fungal isolates were able to reduce the chromophore of the synthetic azo dyes supplemented in the medium (Primary screening). Among the 7 fungal isolates, 4 fungi isolates were able to reduce the chromophores of the synthetic textile dyes by more than 50% (Table 2). Not all the organisms were able to exert a reduction on the dyes used in the study but only a few organisms were able to reduce the chromophore of dyes used in the study. Among the non-adapted fungal strains around 10 strains were able to reduce the chromophore of the synthetic dye and among the 10 isolated fungal strains 4 were able to reduce the 6 different synthetic dyes by more than 50% (Table 2). On comparison with that of adapted fungal strains the non-adapted fungal strains were slightly efficient in the reduction of the dyes as these studies were done in a congenial environment for providing all the necessary nutrients. The individual strains could not completely degrade textile wastewater (Coughlin *et al*., 1997) such as adapted and non adapted fungal consortium may be effective for the degradation of textile azo dye considering the results of a total color removal more than 50% obtained only 48 h of incubation compared with an yield of less than 50% of color removal obtained by microbial population used by Nigam *et al*. (1996).

The screened adapted fungal strains were identified as *Aspergillus* sp., *Penicillium* sp., *Fusarium* sp. and *Mucor* sp. and that of the non-adapted fungal strains were identified as *Aspergillus* sp., *Penicillium* sp., *Fusarium* sp. and *Rhizopus* sp. based on the microscopic appearance of fungi through lactophenol cotton blue staining. The *Aspergillus* sp., showed single-celled spore (conidia) in chains developing at the end of the sterigma arising from the terminal bulb of the conidiophores, the vesicles. Long conidiophores arise from a septate mycelium. The *Penicillium* sp. showed single-celled spore (conidia) in chains developing at the end of the sterigma arising from the metula of the conidiophores. Branching conidiophores arise from the septate mycelium. The *Fusarium* sp. showed multi-celled spores (conidia) are oval shaped and attached to conidiophores arises from a septate mycelium. The *Mucor* sp. showed spores are oval, non-septate mycelium gives rise to single sporangiophores with globular sporangium containing a columella. The *Rhizopus* sp. showed spores are oval, colorless, non-septate mycelium gives rise to straight sporangiophores that terminate with black sporangium containing a columella.

Compatibility analysis: The 4 adapted fungal strains were found to be compatible with each other in the artificial media. The adapted fungal strains did not exhibit any zone of inhibition around their colonies in all the plates incubated. The compatibility nature of the fungal strains isolated from the effluent system was because of the fact that in an effluent treatment system, the organism once inoculated would be recirculated again which serves as the inoculum for the next treatment cycle. Since the organisms co-existed in a common environment for a very long period of time they were found to be compatible with each other. From the 4 non-adapted fungal strains it was found that 3 were compatible with the other fungal strains

Table 2: Selection and screening of microbes based on decolorization

	% Decolorization				
Fungal isolates	Red M5B	Reactive red 120	Amido black-10B	Reactive black 5	Anthraquinone violet R
Adapted fungal isolates					
1	74.23	65.36	48.36	50.98	59.36
2	19.87	51.38	77.45	54.22	61.03
3	33.29	33.05	26.69	44.26	25.17
4	22.36	63.31	49.36	31.34	75.03
5	49.9	39.38	54.31	56.87	68.54
6	53.33	13.23	25.26	55.67	30.18
7	75.77	29.25	31.26	63.56	25.39
Non-adapted fungal isolates					
1	50.98	49.31	74.23	62.98	59.25
2	54.22	44.81	19.87	33.26	21.69
3	44.26	33.87	33.20	25.59	27.32
4	31.25	22.02	22.36	36.61	40.32
5	56.32	51.25	62.36	65.36	62.52
6	29.36	21.74	25.76	33.44	17.23
7	41.38	54.01	33.69	45.23	22.39
8	65.23	59.37	66.32	53.69	61.54
9	65.63	52.31	56.37	68.85	50.48
10	27.64	31.32	37.99	34.11	27.34

but one fungus was found to be incompatible with that of the other three fungi. A zone for clearance around the fungal colony (*Fusarium* sp.) indicated that biocidal products produced by the fungi, that restricted the growth of the other non-adapted fungi. On developing a consortium this fungus was excluded as it could deteriorate the effectiveness of bioremediation of the other fungi involved in the consortium. The fungal isolates showed efficient antagonistic activities against the two tested pathogenic bacteria and completely prevent their growth. Whereas, the fungal isolates could not counteract the pathogenic tested fungus *A. niger* although, its growth was inhibited by the filtrate of fungal isolates. This observation agrees with those studies of antagonistic activity like Berg *et al.* (1994). In our study deals the most of the fungal isolates were compatible with other fungal isolates, because they have already adapted this critical environmental condition for a longer period of time. Some of fungi produce enzymes, which catalyze the oxidation of a variety of aromatic compound including azo dyes.

Physiochemical analysis of untreated effluent: It was found that the values observed for the untreated effluent sample was found to be higher than the permissible limits of Central Pollution Control Board (CPCB) and Tamil Nadu Pollution Control Board (TNPCB) (Table 3). The high organic load of the effluent sample was evident from the high COD (1120 mg L^{-1}), TS (13600 mg L^{-1}), TSS (3330 mg L^{-1}) and TDS (10270 mg L^{-1}). The presence of color in the sample was also validated by measuring the sample in a UV-visible spectrophotometer. Such high organic load and color could not be discarded into the natural water system without prior treatment; else it would deteriorate the biota of the natural inhabitants of that particular environment by reducing the dissolved oxygen level due to the organic load and light penetration due to the presence of dye component (Ali *et al.*, 2009).

Comparison of treatment trails on Bioremediation of Azo dye containing textile effluent by both Adapted and non adapted fungal consortium: On analyzing the results observed for the effluent sample treated using both adapted and non-adapted fungal consortium, it was found out that sample treated with the adapted consortium has reduced the organic load and the dye present in the sample by a significant level. On the other hand though there was a considerable level of reduction in the organic load and the color by the non-adapted fungal consortium, it could not exceed the efficiency of the adapted fungal consortium. When comparing the adapted fungal consortium, the non-adapted fungal consortium was observed with less bioremediation efficiency (Colour 67%, TS 37%, TSS 55%, TDS 31.6%, COD 34.8%) (Table 4). The color removal and COD reduction was low at the end of 5th day incubation because of the drastic environmental conditions that the fungal strains were exhibited to, where as the adapted fungal strains can withstand such drastic environment and can make a living at such harsh environment leading to a more efficient reduction in the physico-chemical parameters (Colour 75%, TS 54%, TSS 33%, TDS 50%, COD 50%) (Table 4). This clearly indicates that the adapted fungi utilizes readily available carbon and dye as a source of energy for the biomass growth and starts degrading the compounds in Azo textile effluent.

Table 3: Physico-chemical analysis of untreated effluent and industrial permissible limits

Parameters	Untreated effluent	Permissible limits
Colour (435 nm)	0.8578	25HU
Turbidity (620 nm)	0.5713	Not objectionable
TS (mg L^{-1})	13600	2500
TSS (mg L^{-1})	3330	50
TDS (mg L^{-1})	10270	1500
COD (mg L^{-1})	1120	400
Conductivity (mS)	13.74	--
pH	5.58	6.5-9
Alkalinity (ppt)	7.958	--
Resistivity (Ω)	33.9	--
Hardness (mg L^{-1})	260	600

Non-adapted fungal strains could be efficient in bioremediation only when they were able to synthesize the enzymes that were non specific in nature. In the case of non-adapted fungal consortium, the main factor that keeps them lagging behind the adapted strains was that they were not acclimatized to that environment. These toxic azo dyes resist their activity of division and enzyme production. Also, the fact that the organic load in the effluent would not be enough in supporting the growth of these non-adapted organisms and that the azo dye would be reduced by some extracellular enzymes that have no substrate specificity hence they could not be used as a source of carbon. These were some of the limiting factors that split the efficiency of adapted and non-adapted fungal consortium. The adapted fungal consortium has already altered them towards the surrounding in which they act upon. These adapted strains not only utilize the organic load as a source of energy but would rather utilize the dyes present in the effluent too as a carbon source. That is the main reason why these acclimatized adapted organisms reacted well in the treatment rather than the non-adapted fungal consortium. The dyes present are

Table 4: Treatment of textile effluent by using both adapted and non adapted fungal consortium

		Adapted fungal consortium		Non adapted fungal consortium	
Parameters	Initial values	Values observed	% Reduction	Values observed	% Reduction
Colour (435 um)	0.8578	0.21	75.51	0.281	67.24
Turbidity (620 um)	0.5713	0.45	21.23	0.548	4.078
TS (mg L^{-1})	13600	6217	54.28	8517	37.30
TSS (mg L^{-1})	3330	2217	33.42	1497	55.04
TDS (mg L^{-1})	10270	5099	50.35	7020	31.64
COD (mg L^{-1})	1120	560	50.00	730	34.82
Conductivity (mS)	13.74	12.48	9.17	13.21	3.85
pH	5.58	5.28	5.37	5.11	8.42
Alkalinity (ppt)	7.958	6.98	12.28	7.552	5.10
Resistivity (Ω)	33.9	31.11	8.23	33.13	2.27
Hardness (mg L^{-1})	260	155	40.38	189	27.30

Table 5: Association between adapted and non-adapted fungal consortium (Chi-Square analysis)

Physico-chemical parameters	Adapted fungal consortium (% Reduction)	Non-adapted fungal consortium (% Reduction)	Total
Color	75.51	67.24	142.75
COD	50.00	34.82	84.82
TS	54.28	37.30	91.58
TSS	50.35	31.64	81.99
Hardness	40.38	27.30	67.68
Total	270.52	198.30	468.68

mineralized in the process as a result of the action of the adapted fungi thus getting rid of the toxic azo component from the effluent.

On analyzing the results observed using the chi-square test, it was found that calculated value of chi-square (28.712) was higher than the table value (9.49) at 4 degree of freedom in 0.05 levels and thus the null hypothesis was rejected (Table 5). Thus, it could be proved that there was an association between adapted fungal consortium and non-adapted fungal consortium since the bioremediation efficiency of both of them was analyzed using some common physico-chemical characters.

Mixed fungal cultures are better decolorizes than individual fungal cultures, suggesting a synergistic role of the fungal species of mixed cultures in dye decolorizaton (Knapp and Newby, 1995). Since the azo dyes were not easily biodegradable but rather the adapted fungal consortium secrete certain enzymes were relatively rare. Degradation of a dye involves aromatic ring cleavage, which was dependent on the identity of the ring substituent with the presence of phenolic, amino, acetamido, 2-methoxyphenol or other easily biodegradable functional groups resulting in a greater extent of degradation (Spadaro *et al*., 1992; Khammuang and Sarnthima, 2009).

Comparison of adsorption isotherms on bioremediation of azo dye containing textile effluent by both adapted and non adapted fungal consortiums: The adapted fungal consortium was found to fit in both the langmuir and freundlich isotherms with a high recreation constant that of the non-adapted fungal counterparts showing a high monolayer and multilayer adsorption of the dye present in the effluent. A plot of Ce/qe vs Ce (Langmuir) gave a straight line. The correlation coefficient values for both adapted (R^2 = 0.97) and non-adapted fungal consortium (R^2 = 0.98) were obtained from linear plots (Fig. 1a, 2a). These values were very close to unity and both are highly correlated with this adsorption isotherm model. In Freundlich isotherm, a plot of log C_e vs. log C_e/q_e made an energetic linear layer for both adapted and non-adapted fungal consortium. This isotherm does not fit well for the non-adapted fungal consortium (R^2 = 0.92, Fig. 2b) but rather adapted fungal consortium fits for this multilayer model (R^2 = 0.92, Fig. 1b) as the high recreation coefficient value preferred only the adapted fungal consortium than non-adapted fungal consortium (Garg *et al*., 2003).

Physico-chemical characterization of treated effluent-GCMS analysis: The untreated textile effluent showed a number of peaks in its chromatogram with a few peaks that were predominant and which were not found to be a contaminant of the column were studied. The compounds analyzed for these peaks were found to be Furan, 2-(methoxymethyl), n-cetyl thiocyanate and heptadecanoic acid-methyl ester which were the toxic product present in the untreated raw effluent sample (Fig. 3a).

The treated effluent using the adapted fungal consortium showed a major reduction in all the organic contents and the number of peaks that were observed was reduced to significant extent. About three peaks which were observed in the chromatogram for the treated effluent were analyzed and found to be 5-hexenal, iso-

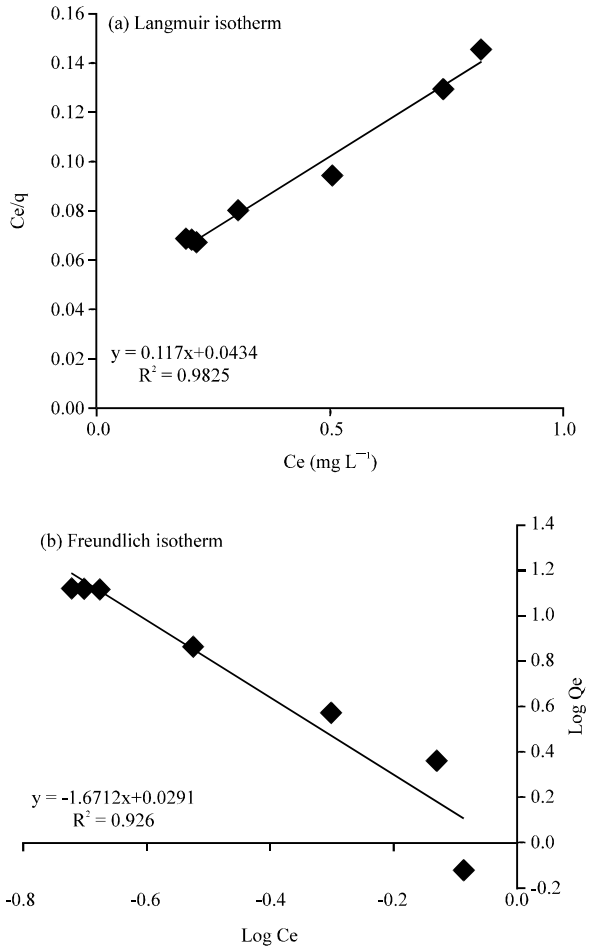


Fig. 1(a-b): (a) Langmuir and (b) Freundlich adsorption isotherms for bioremediation of Azo dye containing textile effluent by using Adapted fungal consortium

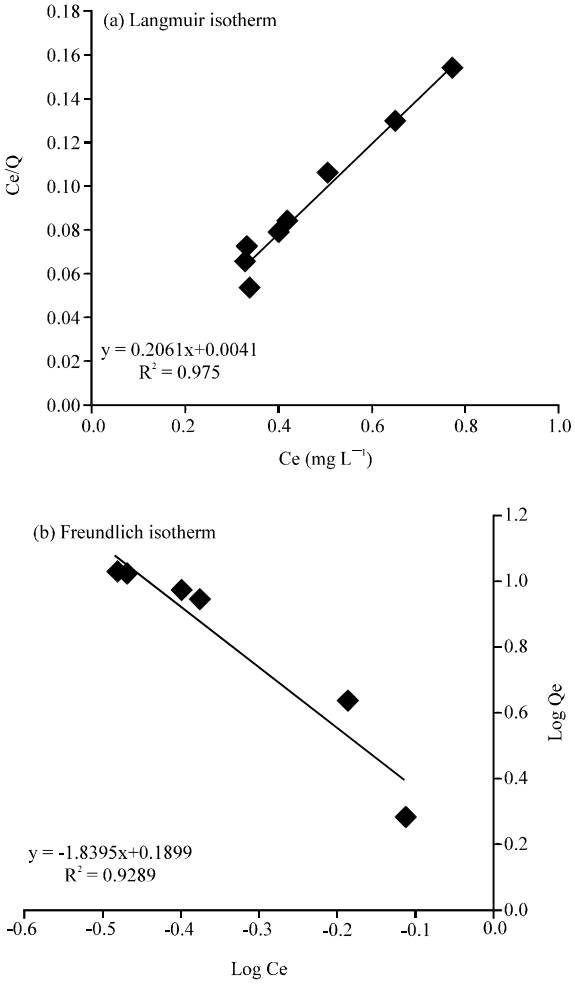


Fig. 2(a-b): (a) Langmuir and (b) Freundlich adsorption isotherms on bioremediation of Azo dye containing textile effluent by using non-Adapted fungal isolate consortium

tanshinone and hexanedioic acid bis (2-ethylhexyl ether) which were not found to be toxic. Apart from this the reduction in the number of peaks in the chromatograph also proves that the adapted fungal consortium is efficient in not only reducing the color and the organic content of the effluent but is also mineralizing it (Fig. 3b).

The effluent sample treated using the non-adapted fungal consortium was found to possess more peaks than the sample treated using the adapted fungal consortium. The peaks showed that the treated sample was said to contain compounds (with their retention time) like acetamide (6.823), metazachlor (9.8), benzodiazepine-2-one (11.7), tetradecamethyl (15.6), phenethylamine (21.78), borazine (29.73) and azonino (36.69) (Fig. 3c). Most of the compounds identified were found to be toxic in nature on contrary to the more efficient and non-toxic liberations by the sample treated by the adapted fungal consortium. The chromatograph shows that though there was a considerable reduction in the color of the effluent sample the partially degraded or broken down dye was found to produce toxic intermediates which were not mineralized further. This was the reason why there was no significant reduction in the physico-chemical parameters by the non-adapted fungal consortium on its comparison with the adapted fungal consortium. This shows that 4-nitroanisole production in the *Pleurotus ostreatus* has also been reported by other researches (Zhao *et al*., 2006). Compared with *Pleurotus ostreatus* and *Fusarium* sp. produces enzymes other than lignin degrading enzymes and these are the major exoenzymes responsible for the biodegradation of azo dyes.

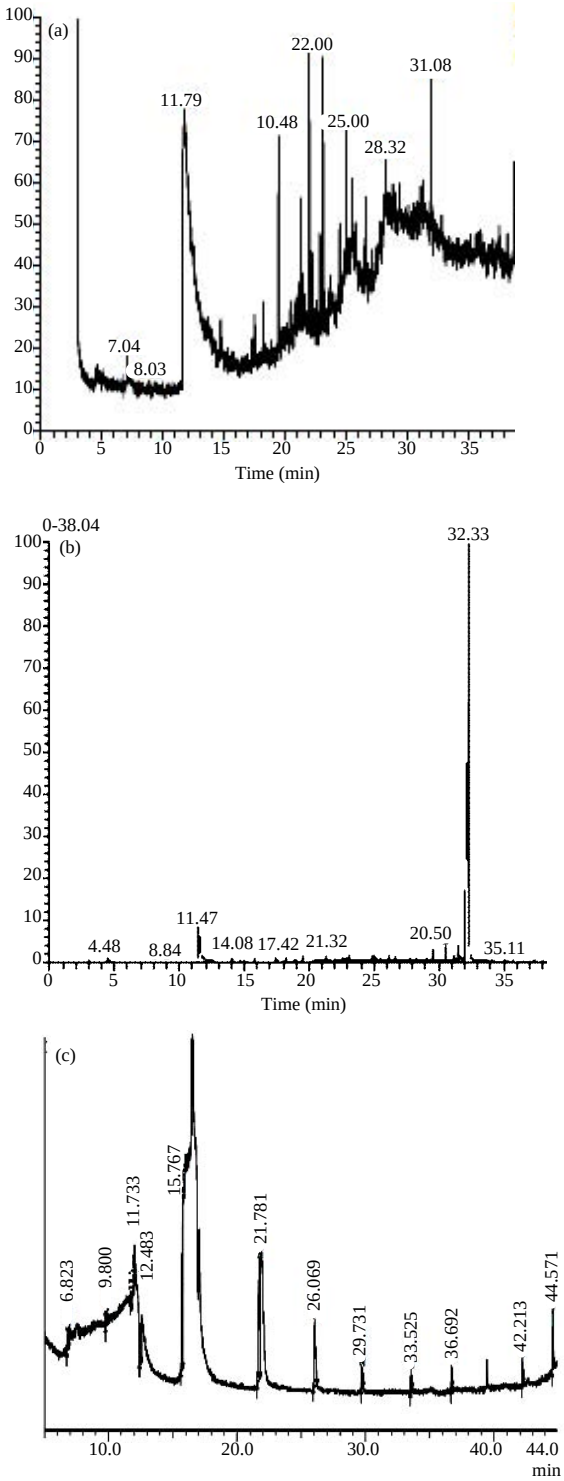


Fig. 3 (a-c): Physico-chemical characterization of untreated and treated effluent sample. (a) Untreated effluent sample, (b) Treated effluent sample (adapted fungal consortium) and (c) Treated effluent sample-Non-adapted fungal consortium

CONCLUSION

It could be concluded that an aerobic biological system can be in a continuous flow using a comparative study of both mixed adapted and non adapted fungal consortium for the Azo textile effluent bioremediation. Adapted fungal consortium presented a higher degradative capacity than non adapted fungal consortium. The synthetic azo dyes with typical chromophores were decolorized by the adapted fungal consortium which was able to produce a wide spectrum of enzymes thus helping in the reduction cleavage of the azo bond present in the dye. The adapted fungal consortium being capable of reducing more number of azo dyes could be employed in the treatment plants for an efficient color and organic content removal.

ACKNOWLEDGMENT

The authors thank the Department of Biotechnology, New Delhi for their financial support. They also thank the Secretary and the Principal of PSG College of Arts and Science, Coimbatore for their support.

REFERENCES

Ali, N., A. Hameed and S. Ahmed, 2009. Physicochemical characterization and Bioremediation perspective of textile effluent, dyes and metals by indigenous bacteria. J. Hazard. Mater., 164: 322-328.

Berg, G., Knaape, C., Ballin, G. and D. Seidel, 1994. Biological control of *Verticillium dahliae* Kleb. by natural occurring rhizosphere bacteria. Arch. Phytopathol. Pflanz., 29: 249-262.

Cappuccino, J.G. and N. Sherman, 1999. Microbiology Laboratory Manual. 4th Edn., Addison-Wilsey, California.

Clesceri, L.S., A.E. Greenberg and R.R. Trussel, 1989. Standard Methods for the Examination of Water and Wastewater. 17th Edn., APHA, AWWA, WPCF, Washington, DC.

Cooper, P., 1995. Colour in Dyehouse Effluent. Society of Dyers and Colourists, Bradford.

Coughlin, M.F., B.K. Kinkle, A. Tepper and P.L. Bishop, 1997. Characterization of aerobic azo dye-degrading bacteria and their activity in biofilms. Water Sci. Technol., 36: 215-220.

Garg, V.K., R. Gupta, A.B. Yadav and R. Kumar, 2003. Dye removal from aqueous solution by adsorption on treated sawdust. Bioresour. Technol., 89: 121-124.

Harley, J.P. and L.M. Prescott, 1993. Basic Laboratory and Culture Techniques. In: Laboratory Excercises in Microbiology, Harley, J.P. and L.M. Prescott (Eds.). 2nd Edn. W.C. Brown Publishers, Dubuque, pp: 14-46.

Igwe, J.C., O.F. Mbonu and A.A. Abia, 2007. Sorption kinetics, intraparticle diffusion and equilibrium partitioning of azo dyes on great millet (*Andropogon sorghum*) waste biomass. J. Applied Sci., 7: 2840-2847.

Khammuang, S. and R. Sarnthima, 2009. Mediator-assisted rhodamine B decolorization by *Tramates versicolor* laccase. Pak. J. Biol. Sci., 12: 616-623.

Knapp, J.S. and P.S. Newby, 1995. Decolorization of dyes by wood rotting basidiomycetes fungi. Water Res., 291: 1807-1809.

Maier, J., A. Kandelbauer, A. Erlacher, A. Cavaco-Paulo and G.M. Gubitz, 2004. A new alkali-thermostable azoreductase from *Bacillus* sp. Strain SF. Applied Environ. Microbial., 70: 837-844.

Nigam, P., I.M. Banat, D. Singh and R. Marchant, 1996. Microbial process for the decolorization of textile effluent containing azo, diazo and reactive dyes. Process Biochem., 31: 435-442.

Olukanni, O.D., A.A. Osuntoki and G.O. Gbenle, 2009. Decolorization of azo dyes by a strain of micrococcus isolated from a refuse dump soil. Biotechnology, 8: 442-448.

Omar, H.H., 2008. Algal decolorization and degradation of monoazo and diazo dyes. Pak. J. Biol. Sci., 11: 1310-1316.

Rajendran, R., S.K. Sundaram and K.U. Maheswari, 2011. Aerobic biodecolorization of mixture of azo dye containing textile effluent using adapted microbial strains. J. Environ. Sci. Technol., 4: 568-578.

Robinson, T., B. Chandran and P. Nigam, 2001. Studies on the production of enzymes by White-rot fungi for the decolorization of textile dyes. Enzyme Microb. Technol., 29: 575-579.

Spadaro, J.T., M.H. Gold and V. Renganathan, 1992. Degradation of azo dyes by the lignin degrading fungus *Phanerochaete chrysosporium*. Applied Environ. Microbiol., 58: 2397-2401.

Tariq, J., M. Ashraf, M. Jaffar and M. Afzal, 1996. Pollution status of Indus river Pakistan through heavy metal and micronutrient content of fish, sediment and water. Water Res., 30: 1337-1344.

Tcjatcjiemg, J.B., B.B. Loura, J. Atchana and R. Kamga, 2009. TiO_2 -MoO_3 as photocatalyst for azo and triphenylmethane dyes decoloration. J. Environ. Sci. Tech., 2: 31-39.

Zhao, X., I.R. Hardin and H.M. Hwang, 2006. Bioremediation of a model azo diperse dye by the white rot fungus *Pleurotus ostreatus*. Int. Biodeteroiat. Biodegradat., 57: 1-6.