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Review Article

A REVIEW ON DECOLOURIZATION OF AZO DYE BY MICRO - ORGANISMS

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Abstract

Microorganisms have developed enzyme system for the decolourization and mineralization of azo dyes under certain environmental conditions. Since the bacterial isolates were originated from the dye contaminated textile wastewater of local industry, so they can easily adapt to the prevailing local environment. Therefore, such bacteria can be used to develop an effective biological treatment system for the wastewaters contaminated with azo dyes.

Keywords: Microorganism, azo dyes, decolourization.

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Introduction

One of the major problems that humans are facing is the restoration of the contaminated environment. Textile dyes contribute as the most important environment-polluting agents. Several classes of such contaminants have been synthesized, and still new products are being synthesized now and then. The textile industry is a large water consumer and produces large volumes of contaminated water. The textile industry generally has difficulty in meeting waste water discharge limits, particularly with regard to dissolved solids, ionic salt, pH, COD, color and heavy metal. Treatment of dye contaminated waste water discharged from the textile and other dye stuff industries is necessary to prevent of soil, surface and ground water. Synthetic dyes and colourants are being increasingly used these days by paper, textile, food, cosmetics, and pharmaceutical industries. Among these, textile industries are the largest consumer of dyes and pigments, accounting for 80 % of total production (Jyoti Kumar Thakur *et al.*, 2014).

Bacterial biodegradation

The ability of bacteria to metabolize azo dyes has been investigated by a number or research groups .Under aerobic conditions, azo dyes are not readily metabolized, although the ability of bacteria with specialized reducing enzymes to aerobically degrade certain azo dyes was reported. In contrast, under anaerobic conditions many bacteria reduce azo dyes by the activity of unspecific, soluble, cytoplasmatic reductase, known as azo reductases. The anaerobic reduction degrades the azo dyes that are converted into aromatic amines, which may be toxic, mutagenic, and possibly carcinogenic to mammalians. Therefore, to achieve complete degradation of azo dyes, another stage that involves aerobic biodegradation of the produced aromatic amines is necessary.

Bacterial biodegradation of non-azo dyes has only recently been studied. It has been observed that several bacteria can degrade anthraquinone dyes. Aerobic decolorization of triphenylmethane dyes has also been demonstrated. In phtalocyanine dyes, reversible reduction and decolorization under anaerobic conditions have been observed.

Fungal biodegradation

The most widely researched fungi in regard to dye degradation are the ligninolytic fungi. White-rot fungi in particular produced enzymes as lignin peroxidase, manganese peroxidase and laccase that degrade many aromatic compounds due to their non-specific activity. Large literature exists regarding the potential of these fungi to oxidize phenolic, non-phenolic, soluble and non-soluble dyes. In particular laccase from *Pleurotus ostreatus, Schizophyllum commune, Sclerotium rolfsii* and *Neurospora crassa,* seemed to increase up to 25% the degree of decolorization of individual commercial triarylmethane, anthraquinonic, and indigoid textile dyes using enzyme preparations. Fungal degradation of aromatic structures is a secondary metabolic event that starts when nutrients (C, N and S) become limiting. The influence of the substitution pattern on the dye mineralization rates and between dye structure and fungal dye biodegradability is a matter of controversy. However, these difficulties are even greater if one considers that complex mixed effluents are extremely variable in composition even from the same factory, as is often the case of the textile industry.

Review of Literature

Water-pollution control is presently one of the major areas of scientific activity. While coloured organic" compounds generally impart only a minor fraction of the organic load to wastewater, their colour renders them aesthetically unacceptable. Effluent discharge from textile and dyestuff industries to neighbouring water bodies and wastewater treatment systems is currently causing significant health concerns to environmental regulatory agencies. Colour removal, in particular, has recently become of major scientific interest, as indicated by the multitude of related research reports. During the past two decades, several physico-chemical decolorization techniques have been reported, few, however, have been accepted by the textile industries. Their lack of implementation has been largely due to high cost, low efficiency and inapplicability to a wide variety of dyes. The ability of microorganisms to carry out dye decolorization has received much attention. Microbial decolorization and degradation of dyes is seen as a cost-effective method for removing these pollutants from the environment. Recent fundamental work has revealed the existence of a wide variety of microorganisms capable of decolorizing an equally wide range of dyes. In this review we have examined biological decolorization of dyes used in textile industries and report on progress and limitations (Ibrahim M. Banat *et al*.,1996).

A microbial consortium, PDW, was isolated capable of the rapid decolourisation of

commercially important textile dyes under anaerobic conditions. Decolourisation was dependent upon the presence of a carbon and energy source in addition to the textile dyes. PDW was capable of dye decolourisation when utilising cheap and readily available carbon sources such lactose, starch and distillery waste. PDW removed 76% of colour from textile plant effluent after 3 days(Poonam Nigam *et al.,*1996).

Three bacterial strains, which degraded azo dyes, were isolated from soil and sewage samples. The strains were identified as Bacillus sp. OY1-2, Xanthomonas sp. NR25-2 and Pseudomonas sp. PR41-1. The bacteria produced azo-dyes-degrading enzymes. That catalyzed the reduction of methyl red and produced dimethyl p-phenylenediamine and o-aminobenzoic acid. The enzymes could thus be applied to white discharge printing of azo-dyed fabric by owing to there(Sugiura W *et al*., 1999).

Aeromonas sp. B-5, which has the ability to decolorize azo dyes, was isolated from soil. Aeromonas sp. B-5 completely decolorized 100 mg/l of Bordeaux S by reductive cleavage of azo bonds under static conditions in 24 h. Though the decolorization of Bordeaux S by Aeromonas sp. B-5 was suppressed under shaking, rapid decolorization was observed when the culture was changed to static conditions after cultivation with shaking. The indigoid dye, Acid blue 74, was decolorized by Aeromonas sp. B-5 under shaking conditions, in contrast to the decolorization of azo dyes(Hayase N *et al*., 2000).

Colour removal of textile dyes from effluent was evaluated using a laboratory upflow anaerobic sludge blanket reactor. Several commercial dyes were selected to study the effect of dye structure on colour removal. The anaerobic reactor was fed with glucose, an easily biodegradable organic matter and selected individual dyes. Results show that some of the dyes are readily reduced under anaerobic conditions even at high concentration of 700 mg/l. The average removal efficiency for acid dyes using this method was between 80 and 90% and that observed for the direct used was 81%. Laboratory experiments using the anaerobic reactor with disperse dyes, such as an anthraquinone based dye, were unsuccessful even at low concentrations of 35 mg/l. Additional experiments were conducted to evaluate the toxicity of a selected disperse dye to an anaerobic environment. Results indicate that the purified dye is more toxic to the biomass than the commercial one (Gonçalves,I.C *et al.,*2000).

The delivery of colour in the form of dyes onto textile fibres is not an efficient process. The degree of efficiency varies, depending on the method of delivery. As a result, most of the wastewater produced by the textile industry is coloured. It is likely that coloured wastewater was a feature of the first practices of textile dyeing. However, treatment to remove this colour was not considered until the early natural dyestuffs were replaced by synthetic dyes, and the persistence of such synthetic dyes in the environment .Colour pollution in aquatic environments is an escalating problem, despite the fact that there has been substantial research into the modification of the dyeing process to improve the level of affinity/fixation of the dyestuffs onto the substrate. The recalcitrant nature of modern synthetic dyes has led to the imposition of strict environmental regulations. The need for a cost-effective process to remove the colour from wastewater produced by the textile industry has been recognized. The biotechnology approach to colour removal from textile effluent. Several strategies have been investigated. However, the review presented here concerns the use of whole bacterial cells for the reduction of water-soluble dyes present in textile dyeing wastewater (Pearce C.I *et al.,* 2003).

Six bacterial strains with the capability of degrading textile dyes were isolated from sludge samples and mud lakes. *Aeromonas hydrophila* was selected and identified because it exhibited the greatest color removal from various dyes.

Although *A. hydrophil*a displayed good growth in aerobic or agitation culture (AGI culture), color removal was the best in anoxic or anaerobic culture (ANA culture). For color removal, the most suitable pH and temperature were pH 5.5-10.0 and 20-35 degrees C under anoxic culture (ANO culture). More than 90% of RED RBN was reduced in color within 8 days at a dye concentration of 3,000 mg l(-1). This strain could also decolorize the media containing a mixture of dyes within 2 days of incubation. Nitrogen sources such as yeast extract or peptone could enhance strongly the decolorization efficiency. In contrast to a nitrogen source, glucose inhibited decolorization activity because the consumed glucose was converted to organic acids that might decrease the pH of the culture medium, thus inhibiting the cell growth and decolorization activity. Decolorization appeared to proceed primarily by biological degradation (Chen KC *et al*.,2003).

The operation of an anaerobic/aerobic process used to degrade the colorants present in textile wastewater is presented. The objective is to produce water that can be reused. Two particular cases were studied: the degradation of a synthetic wastewater containing the colorant disperse blue 79 (DB79) as a model compound and a real textile effluent containing reactive azo dyes. The biodegradation was achieved using a single tank operated as sequencing batch reactor. It was observed that the DB79 was biotransformed to amines in the anaerobic stage decolorizing the wastewater. The amines formed were subsequently mineralized in the aerobic phase. An increase of toxicity was observed in the anaerobic stage due to the amines formation, but the wastewater was detoxified after the aerobic treatment. Removal efficiencies of DB79 around 92% were observed after the treatment. Around 96% of the initial color of the real wastewater was effectively removed. It was observed that the biomass pre-acclimatized to the degradation of DB79 was more effective for the color removal than a freshly inoculum used (Melgoza R. Ma *et a*l.,2004)

Bacteria were inoculated on different solid media to attain biodegradability of an azo dye (Acid Orange 7). Kaolin, bentonite and powdered activated carbon (PAC) were selected to be used with cultures of *Enterobacter, Pseudomonas* and *Morganella* sp., as bacteria would be able to degrade several textile dyes. For the solid, to be employed as media, special characteristics are needed with regards to adsorption capacity for concentrating substrate within the cell environment and an adequate particle size and surface texture for assuring bacterial colonization. Only PAC with 0.490 mm particle size shows these characteristics among the solids used and it was colonized by a high number of cells from the three cultures. Dye was degraded following a second-order kinetics. A mechanism for dye degradation is proposed in which anaerobic and aerobic microniches in the PAC particle perform cleavage of the azo bond and oxidation of the amines formed in the same biocatalytic particle (Blanca E. Barragan *et al.*, 2007).

The isolated Actinomycete, *Streptomyces krainskii*, SUK -5 was found to decolorize and degrade textile dye Reactive blue–59.This azo dye was decolorized and degraded completely by *Streptomyces krainskii* SUK–5 at 24 h in shaking condition in the nutrient medium at pH 8. Induction in the activity of Lignin Peroxidase,and NADH-DCIP Reductase and MR reductase represents their role in degradation .The biodegradation was monitored by TLC, UV vis spectroscopy, FTIR. and GCMS analysis. Microbial and phytotoxicity studies of the product were carried out(Mane, U. V *et al.,* 2008).

A stab-culture method was adapted to screen for azo dyes-decolorizing bacteria from soil and water samples. Decolorized azo dye in the lower portion of the solid media indicates the presence of anaerobic azo dyes-decolorizing bacteria, while aerobic decolorizing bacteria decolorizes the

surface portion of the solid media. Of twenty soil samples tested, one soil sample shows positive results for the decolourisation of two azo dyes; Biebrich scarlet (BS) and Direct blue 71 (DB) under anaerobic conditions. A gram negative and oxidase negative bacterial isolate was found to be the principal azo dyes degrader. The isolate was identified by using the BiologTM identification system as *Serratia marcescens* (Syed, M.A *et al*., 2009).

Four different azo dyes were decolourized and biodegraded in a sequential microaerophilic–aerobic treatment by a facultative Klebsiella sp. strain VN-31, a bacterium isolated from activated sludge process of the textile industry. Dye decolourization was performed under microaerophilic conditions until no colour was observed (decolourization percentage >94%). The medium was then aerated to promote the biodegradation of the amines produced. The presence of aromatic amine in the microaerophilic stage and its absence in the aerobic stage demonstrate azo bond reduction and an oxidative biodegradation process, respectively. Total Organic Carbon (TOC) reduction for the growth medium plus dyes was _50% in the microaerophilic stage and _80% in the aerobic stage. The degradation products were also characterized by FT-IR and UV–VIS techniques and their toxicity measured using Daphnia magna. The reults provide evidence that the successive microaerophilic/aerobic stages, using a single Klebsiella sp. strain VN-31 in the same bioreactor, were able to form aromatic amines by the reductive break down of the azo bond and to oxidize them into non-toxic metabolites(Elisangela Franciscon *et al*.,2009).

Bacillus species isolated from soil contaminated with untreated textile mill effluent utilized an Azo dye (Golden Yellow HER) as sole source of carbon & nitrogen. Highest decolourization (100%) was obtained by isolated *Bacillus* species for Golden Yellow dye. The Azo-nitrogen of the dye substrates provides nitrogen requirement of the organism in cultures in absence of nitrogen. Decolourization of dyes is a reduction process which requires redox equivalents (electron donors) that transfer electrons to the chromographic group dyes. Nitrate (NO_3^-) has higher oxidation character compared to the chromophoric group dyes. The result obtained was attributed to competition between (NO_3^-) and the chromophoric group for the redox equivalents, which result in preferential reduction of (NO_3^-) relative to the chromophoric group. Decolourization was accompanied by increase in total viable count. Ring opening of the aromatic moiety of the dyes produce the carbon source for the organism. The results have shown the potential of the isolated *Bacillus* species under nitrate-starvation condition for the treatment of dye wastewater (Akhilesh Dubey *et al.,* 2010).

A bacterial consortium (consortium GR) consisting of Proteus vulgaris NCIM-2027 and Micrococcus glutamicus NCIM-2168 could rapidly decolorize and degrade commonly-used sulfonated reactive dye Green HE4BD and many other reactive dyes. Consortium GR shows markedly higher decolorization activity than that of the individual strains. The preferable physicochemical parameters were identified to achieve higher dye degradation and decolorization efficiency. The supplementation of cheap co-substrates (e.g., extracts of agricultural wastes) could enhance the decolorization performance of consortium GR. Extent of mineralization was determined with TOC and COD measurements, showing nearly complete mineralization of Green HE4BD by consortium GR (up to 90% TOC and COD reduction) within 24 h. Oxidoreductive enzymes seemed to be involved in fast decolorization/degradation process with the evidence of enzymes induction in the bacterial consortium. Phytotoxicity and microbial toxicity studies confirm that the biodegraded products of Green HE4BD by consortium GR are non-toxic. Consortium GR also shows significant biodegradation and decolorization activities for mixture of reactive dyes as well as the effluent

from actual dye manufacturing industry. This confers the possibility of applying consortium GR for the treatment of industrial wastewaters containing dye pollutants (Saratale, R.G *et al*., 2010).

Azo dyes, which are widely used in textile industries when left in water bodies without any treatment cause environmental pollution and in turn are toxic, carcinogenic and mutagenic. The efficient treatment of the sludge from the industries is not economical and a challenging task. Biodegradation of an Azo dye Reactive Yellow was carried out by microorganisms isolated from the activated sludge by enrichment culture techniques. The isolates were maintained on PDA slants with 0.005% (5mg/100ml) of the dye. The isolated organisms were acclimatized to different concentrations of dye in VMM initially from 0.005-0.200% (mg/100ml). Based on the cultural and morphological characteristics the isolates were identified as actinomycetes. The consortium was developed by mixing five actinomycetes and the degradation pattern for 0.01% (mg/100ml) of dye for actinomycetes A, B and Consortium was found to be 97.44%, 97.45% and 94% respectively in 15 days. The results obtained from the experiments revealed that the degradation of dye depends on the concentration of dye as well as the growth of the actinomycetes. The media containing 0.02% (mg/100ml) dye was degraded in 3 days, 0.05% (mg/100ml) in 8 days and 0.1% (mg/100ml) in 15 days by Actinomycete B, with adsorption process taking place simultaneously. The growth pattern of the actinomycetes was studied and the concentration of dye adsorbed by the actinomycetes A, B and Consortium was found to be 85mg, 80mg and 44mg in 100ml respectively. The enzymes responsible for degradation such as lignin peroxidase, laccase and tyrosinase showed steady activities during the 8 days of incubation. Biosorption of Reactive Yellow dye was carried out using dead biomass for different concentration of dye and 90% of dye was adsorbed in 1 hour effectively (Zabin K. Bagewadi *et al.*,2011).

Azo dyes are released into wastewater streams without any pretreatment and pollute water and soil environments. To prevent contamination of our vulnerable resources, removal of these dye pollutants is of great importance. For this purpose, wastewater samples were collected from dye-contaminated sites of Faisalabad. About 200 bacterial isolates were isolated through enrichment and then tested for their potential to remove Remazol Black-B azo dye in liquid medium. Five bacterial isolates capable of degrading Remazol Black-B azo dye efficiently were screened through experimentation on modified mineral salt medium. Isolate SS1 (collected from wastewater of Supreme Textile Industry) was able to completely remove the Remazol Black-B dye from the liquid medium in 18 h. Further, the isolate showed the best performance at the dye concentration of 100 mg L-1 medium (pH 7) and at temperature 35oC. Similarly, yeast extract proved to be the best carbon source for decolorization purpose. The results imply that the isolate SS1 could be used for the removal of the reactive dyes from textile effluents (Shahid Mahmood *et al.*,2011).

An attempt was made to examine the potential of different bacterial strains for decolorization of Acid Orange 10, (azo dye) in batch reactors. The effect of media condition, pH, temperature and initial concentration of dye was studied with an aim to determine the optimal conditions required for maximum decolorization and degradation. The bacterial strains used in the study were Pseudomonas putida, Bacillus cereus, Pseudomonas fluorescens, Bacillus subtilis, *Alcaligens* sp. and *Staphylococcus aureus*. Out of these *Pseudomonas putida* emerged out to be most potent decolorizer, being selected for further studies. The selected bacterium shows higher decolourization in static condition as compared to shaking condition. The optimum pH for decolourization of Acid Orange 10 by Pseudomonas putida was 7.0. It shows good decolourization efficiency even in alkaline region. The optimum temperature was 37°C. The strain

could decolorize Acid Orange 10 (250 mg/l) by 90% within 24 h under the optimum conditions of static condition, pH 7.0, temperature of 37°C and initial dye concentration of 250 mg/l. The result shows that the selected culture has good potential in removal of Azo dyes from waste water under static conditions(Tripathi,A and Srivastava,S.K, 2011)

Azo dyes constitute the largest and most versatile class of synthetic dyes used in the textile, pharmaceutical, food and cosmetics industries and represent major components in wastewater from these industrial dying processes. Biological decolorization of azo dyes occurs efficiently under low oxygen to anaerobic conditions. However, this process results in the formation of toxic and carcinogenic amines that are resistant to further detoxification under low oxygen conditions. Moreover, the ability to detoxify these amines under aerobic conditions is not a wide spread metabolic activity. In this study we describe the use of Brevibacterium sp. strain VN-15, isolated from an activated sludge process of a textile company, for the sequential decolorization and detoxification of the azo dyes Reactive Yellow 107 (RY107), Reactive Black 5 (RB5), Reactive Red 198 (RR198) and Direct Blue 71 (DB71). Tyrosinase activity was observed during the biotreatment process suggesting the role of this enzyme in the decolorization and degradation process, but no-activity was observed for laccase and peroxidase. Toxicity, measured using *Daphnia magna*, was completely eliminated (Elisangela Franciscon *et al*., 2011).

The present research was carried out to explore potential dye decolorizing bacterial trains from the textile industry waste located in Erode and Tripur districts. Total heterophilic bacterial populations were confirmed and they were ranged from 2 x 104 to 62 x 106 CFU/gm. There was 96 morphologically distinct bacterial isolates were isolated from 12 different sludge, textile effluent and dye contaminated soil samples. Generic composition of the 96 isolates comprised of *Bacillus* sp., *Enterobacteriaceae, Pseudomonas sp., Micrococcus sp., Alcaligenes sp., Aeromonas sp., Staphylococcus sp.,* and *Lactobacillus sp*. These bacterial strains were freshly screened by plate method on solid media containing Remazol golden yellow (RNL), Red (RGB) and Blue (RGB) for the detection of preliminary decolorization. Among 96 strains tested, 20 exhibited significant decolorization. Liquid culture method was adopted for secondary screening decolorization confirmed that 6 efficient strains decolorize the dye concentration within 24 hours under static condition. The strains utilized Remazol golden yellow dye as a carbon sources for their growth. RNL dye decolorization by 6 strains was attained and maximum of 84% decolorization was recorded at 48 hours in microaerophilic condition. Furthermore the mixed cultures of the potential strains were attributed to effectively decolorize the dye contaminated effluent along with RNL dye in the stimulated time period of 24-48 hours. These strains have the capability to withstand and tolerate the sodium chloride concentration up to 30g/l. This study clearly resulted selected potential dye decolorizing bacterial strains could be used for decolorization of textile effluent(Palani Velan, R *et al*.,2011).

Dye decolourization using spent mushroom substrate (SMS) is influenced by the category of SMS, type of dye, initial dye concentration, form of mushroom mycelia, pH, temperature and the growing media. Among SMS of different mushrooms, the SMS from *P. sajor-caju* exhibited highest population along with variability of both fungi and bacteria. Five fungi viz., *Aspergillus fumigatus*, *Paecilomyces variotii*, *Pichia guilliermondii*, *Schizophyllum commune* and *Pezizomycotina* sp. with potential dye decolourization potential have been recorded to thrive on SMS of different mushrooms by using 5.8S rRNA gene sequencing and BLASTn techniques. Out of these *Schizophyllum commune* from *P. sajor-caju* SMS has been recorded to exhibit highest decolourization potential (95%)

within 10 days against Chicago sky blue. This fungus also exhibited dye decolourization potential of 100, 92.50, 81.60, 73.40 and 67.80% against other dyes like Starch Azure, Reactive blue, Rhodamine B, Orange II sodium salt and Methyl blue, respectively. Similarly, by using 16S rRNA gene sequencing and BLASTn, six potential bacteria viz., *Bacillus subtilis*, *B. pumilus*, *B. licheniformis*, *Pseudomonas fluorescens*, *Sphingobacterium multivorum* and *Rummelibacillus stabekissi* have also been identified, out of which *B. licheniformis* isolated from *P. sajor-caju* SMS, exhibited highest decolourization potential of 66.10% against Orange II sodium salt, followed by *Bacillus pumilus* (57.7%). Temperature and pH optima of 25ºC and 6.0 respectively, have been recorded for achieving highest level of decolourization through *B. licheniformis*. The study highlights the utility of SMS for unconventional activities like dye decolourization, which indirectly supports its use in bioremediation activities (Om Parkash Ahlawat and Rajender Singh,2011).

The degradation and detoxification of three textile azo dyes (Reactive Red 198, Reactive Red 141 and Reactive Blue 214) by mixed fungal cultures from semi-arid region of Brazilian Northeast. Sediment samples of twenty water reservoirs in the surroundings of Serra da Capivara National Park, area of environmental preservation in the caatinga in the State of Piauí, with semi-arid climate, were evaluated in order to select the consortia of fungi capable to degrade and detoxify these dyes. The mixed fungal culture from Caldeirao Escurido (CE) reservoir was the most efficient in the degradation and detoxification of the dyes tested (Carlos Nascimento *et al.*,2011).

A bacterial culture was isolated from soil in the vicinity of textile industry and was identified as *Bacillus subtilis* SPR42. It was found to be the most active azo dye degrader using submerged fermentation technology. *B. subtilis* SPR42 was able to decolourize azo dyes: Vaxent Red HE7B(Reactive Red 141) and Vaxent Yellow HEGR at a concentration of 100 mgL^{-1} upto 73% and 92%, respectively within 24 hr at 37 °C (pH 8.5) during static conditions(Baljeet Singh Saharan and Poonam Ranga, 2011).

Bioflocculant-producing bacteria were isolated from activated sludge of a wastewater treatment plant located in Durban, South Africa, and identified using standard biochemical tests as well as the analysis of their 16S rRNA gene sequences. The bioflocculants produced by these organisms were ethanol precipitated, purified using 2% (w/v) cetylpyridinium chloride solution and evaluated for removal of wastewater dyes under different pH, temperature and nutritional conditions. Bioflocculants from these indigenous bacteria were very effective for decolourizing the different dyes tested in this study, with a removal rate of up to 97.04%. The decolourization efficiency was largely influenced by the type of dye, pH, temperature, and flocculant concentration. A pH of 7 was found to be optimum for the removal of both whale and mediblue dyes, while the optimum pH for fawn and mixed dye removal was found to be between 9 and 10. Optimum temperature for whale and mediblue dye removal was 35 °C, and that for fawn and mixed dye varied between 40–45 °C and 35–40 °C, respectively. These bacterial bioflocculants may provide an economical and cleaner alternative to replace or supplement present treatment processes for the removal of dyes from wastewater effluents, since they are biodegradable and easily sustainable(Simphiwe P. Buthelezi *et al*.,2012).

Textile dyes have been used since the Bronze Age. They also constitute a prototype 21st-century speciality chemicals market. Effluent and soil samples were collected from textile industry at Surat. The pH, temperature, BOD, COD, Nitrate and Nitrite values were compared with the values given by the Bureau of Indian Standards. The culture medium was designed and standardized in the laboratory for the isolation and degradation of the dyes. Pure cultures were screened on the basis of colony morphology.

Three different types of unique cultures were selected and named as isolates S1, S2 & S3. Out of 12 dyes used, isolate S1 showed degradation on the maximum number of dyes (five) in comparison to other isolates (isolates S2 and S3). Thus, isolate S1 was used for the further studies. The isolate S1 was used for the study of the amount of dye to be degraded. For this study Red BB dye was chosen. Because, isolate S1 showed maximum degradation on Red BB dye within less time of incubation in comparison with other dyes. Almost all isolates showed the positive results in some of the biochemical tests. Thus most of the isolates can have the capacity to produce the enzyme tryptophanase, indole production, citrate permease (citrate as carbon and energy source), catalase enzyme, degradation of glucose oxidatively as well as fermentatively, urease, gelatinase, production of acid and gas (allow to ferment lactose and/or sucrose) and fermentation of sugar, lactose, sucrose, mannitol and glucose. Total cellular fatty acids profiling has been considered to be one of the important and ideal tool for identification of microorganisms. On the basis of fatty acid profiling of isolate S1 the similarity index indicated as *Bacillus cereus* GC subgroup A (similarity index 0.825), *B. thuringiensis* sub sp. *israelensis* (similarity index 0.552) and for *B. thuringiensis* sub sp. *Kurstakii* (similarity index 0.511). The isolate S1 was assumed to be *B. cereus* GC subgroup A. Thus this isolates can be used to degrade harmful azo dyes utilized by the dye, textile, paper, ink industries etc(Mukund Chandra Thakur *et al*., 2012).

A study was conducted to standardize the dyeing variables of hot reactive dye for tie and dye technique. The optimum wave length was 520 nm, out of a set of wave length ranging from 400-700 nm on the basis of highest optical density. Eight dye concentrations (1, 2, 3, 4, 5, 6, 7, and 8 %) were tried and two dye concentrations were selected on the basis of dye absorption and colour fastness properties. 4 percent dye concentration gave maximum percent dye absorption and 2 percent dye concentration showed excellent fastness to wash and light. Five different dyeing temperatures (60, 70, 80, 90 and 100ºC) were tried and 80ºC was found best for 2 and 4 percent dye concentration respectively. Five different dyeing times (80, 90, 100, 110, 120 minutes) were tried and 90 minutes was found to be the best for both 2 and 4 percent dye concentration. Dyeing was carried out at seven different pH values (9, 9.5, 10, 10.5, 11.0, 11.5 and 12.0), the maximum dye absorption was observed at 10.5 percent for both the dye concentration. 60g/l sodium sulphate was found best for 2% dye concentration and 70g/l was found best for 4% dye concentration. Similarly 15g/l of sodium carbonate was found best for 2% dye concentration and 20g/l was found best for 4% dye concentration in two instalments of both the auxiliaries(Jyoti Singla *et al.*,2012).

The release of azo dyes into the environment is a concern due to coloration of natural waters and due to the toxicity, mutagenicity of dyes and their biotransformation products. Economical and bio-friendly approaches are needed to remediate dye contaminated waste water from various industries. In this study, a novel bacterial consortium SpNb1 capable of decolorizing RR M8B dye was isolated from the waste water treatment plant in Naroda G.I.D.C. Bacterial consortium SpNb1 was shown to decolorize different reactive, direct, disperse dyes within 7 – 24 hrs with colour removal range from 24.90 ±0.03 to 96.75 ± 0.04 %. The optimum condition for decolorization of RR M8B by SpNb1 was observed in static condition; dye concentration, 300 mgL-1; pH, 7.5; inoculums size, 3% vv-1; temperature, 37°C. Biodegradaded products of the dye were monitored by UV-visible, and HPTLC, FTIR spectroscopy. Decolorization study of simulated waste water containing reactive dye RR M8B has been studied by Down Flow Fixed Film Reactor with bacterial consortium SpNb1. The performance of the bioreactor was evaluated by monitoring pH, ORP, Chemical Oxygen Demand (COD), % of decolorization. The COD reduction and colour

removal in the range of 72.07 to 82.22 % and 91.20 ± 0.05 to 97.82 ± 0.06 % respectively(Bhatt Nikhil *et al.*,2012).

Dyes and pigments are widely used, mostly in the textile, paper, plastics, leathers, food and cosmetics industry to color products. Textile industry consumes large volume of water and produce large amount of wastewater during all phases of textile production and finishing. The release of colored effluents represents a serious green pollution and a human health concern particularly in developing countries like Ethiopia (East Africa). Color removal, especially from textile effluents, has gargantuan challenge over the last decades, and up to now there is no single and cost-effectively attractive treatment that can effectively decolourise as well as treat the dyes effluents. The objective of this review article is to discuss a variety of textile wastewater treatment techniques (physical,chemical and biological techniques) from the environmental point of view(Bizuneh Adinew, 2012).

Textile industries effluent contain a variety of polluting substances among dyes are major. Environmental legislation is being imposed to control the release of dyes, in particular azo-based compounds into the environment. For the last few years, intensive research has been carried on decolonization of dye and textile wastewater by various microorganisms. The ability of microorganisms to decolorize and metabolize dyes has long been known, and the use of bioremediation based technologies for treating textile effluent has attracted interest. In this review, we have pointed out the microbial decolorizing treatment technologies along with the mechanism by which diverse categories of microorganisms bring about the degradation of dyestuffs (Abu Mohammad Azmal Morshed *et al.,* 2012)

Twenty one bacterial isolates were obtained from textile affected soil, sludge and textile effluent. All the isolates were screened at 50, 100, 150 and 200ppm of red, green, yellow and black textile dyes. The Isolates 1, 3, 5, 7, 9, and 20 were screened on the basis of ability to degrade the dyes efficiently more than 60%, within 24h at 50, 100, 150 and 200ppm of red, green, yellow and black dyes. Four consortia were developed using combinations of these bacterial isolates. Among them consortium BMP1/SDSC-01 had maximum decolorization ability. It was 84% for green and red textile dyes while 85% for black and yellow. This study will help to establish low cost treatment of textile effluents in Pakistan by applying bioremediation (Rashid Mahmood *et al*., 2012).

Assessing the ability of *Pseudomonas spp.* to decolourize and degrade methyl orange dye. *Pseudomonas spp.* could tolerate methyl orange dye for up to 500 mg–1. A bacterium identified as *Pseudomonas spp.* was isolated from dye-contaminated soil. This strain rapidly decolourized a methyl orange azo dye solution. Features of the decolourizing process related to biodegradation and biosorption were also studied. The dye was remarkable colour-removal capability over a wide range of dye concentrations (50–200 mg/l), pH (6–10) and temperatures (30–40°C). The *Pseudomonas spp.* decolourized the repeated addition of methyl orange dye for up to four cycles with variable decolourization rates (10–94%). The strain can tolerate and decolourize azo dyes at high concentrations, making it an advantage for treatment of textile industry wastewaters. However, the strain needs to be tested on the treatment of real dye-bearing wastewaters using appropriate bioreactors (Shah *MP et al*.,2013).

The isolation, identification and screening of bacterial species capable to decolorize variety of dyes. Decolorization of dyes and growth of the bacterial species are investigated. The strain ETL-1942 decolorized all the selected dyes except Remazol Brilliant Blue R, Reactive Blue H5G, Remazol Turquoise Blue G and Fast Green. In our

study, we identified three groups of dyes on the basis of the pattern of dye decolorization by strain ETL-1942. The results indicate that decolorization rate is faster for the dyes of the third group than the second group. The strain can grow with all the six dyes tested, but decolorization rates are different for each dye. These results demonstrate that the strain ETL-1942 have ability to decolorize wide range of dyes and therefore further investigation for physico-chemical parameter were carried out(Maulin P Shah *et al.,* 2013).

The textile industry is one of the industries that generate a high volume of waste water. Strong colour of the textile waste water is the most serious problem of the textile waste effluent. The disposal of these wastes into receiving water causes damage to the environment. Dyes may significantly affect photosynthetic activity in aquatic habitat because of reduced light penetration and may also be toxic to some aquatic life due to the presence of aromatics, metals, chlorides and other toxic compounds. The present study was carried out to degrade the textile Reactive azo dyes by using bacteria isolated from dye contaminated soil. Three different bacterial isolate such as, *Bacillus* sp., *Escherichia coli* and *Pseudomonas fluorescens* were isolated from textile dye effluent contaminated soil sample and used for the degradation study. It was noticed that there was a decrease in the OD in all the three species of all the five dyes as the incubation period increased. *Pseudomonas fluorescens* was more effective followed by *Bacillus* and *Escherichia coli.* It was found that all the isolated bacteria were efficient decolourizers of Reactive textile azo dyes (Sriram, N *et al.,* 2013).

Turquoise blue dye (Remazol Blue BB) is a reactive dye which is used by almost all textile industries. The sample was collected from dye industries near VATVA G.I.D.C. (Gujarat) and adjourning surrounding area. On the basis of colony morphology and certain biochemical tests the strain was identified as *Bacillus megaterium* species and gave maximum decolourization of turquoise blue dye within 48 hours at pH 7.00 and 37°C in the medium followed by blue M2R, Safranin, Congo red, Malachite green Orange ME2RL and Yellow M8G dyes. This organism can decolourize turquoise blue dye up to a concentration of 5mg/ml but showed maximum dye degradation at 1mg/ml concentration. Glucose (1g%) was found to be the best Carbon source while NH4Cl (1g%) was found as the best Nitrogen source for maximum biodegradation process. The isolated strain is even able to degrade wide range of dyes. Further, there is a need to test this organism at large scale degradation of this dye (Bhoomi Joshi *et al.,* 2013).

In Karur, the textile factories discharge millions of litres of untreated effluents into the drains that eventually empty into river, Amaravathy. The release of coloured compound into water bodies is undesirable not only because of their impact on photosynthesis of aquatic plants but also due to the carcinogenic nature of these dyes and their breakdown products. In this work, bacteria capable of decolourising Textile effluents mixed with sewage (TES) were isolated. Based on the results of these various biochemical tests, the isolates were identified. The identification was confirmed by 16s rRNA sequencing. They were identified as *Bacillus cereus* AK1968 and *Pseudomonas* sp. AKDYE14. The sequences were deposited in GENBANK. The accession numbers were JN689235 and JN674167 respectively (Karthikeyan,A and N. Anbusaravanan, 2013).

The enriched aerobic cultures of indigenous microbes can be used successfully for decolorizing dye effluents. Physico-chemical analysis of dye effluent revealed high load of pollution indicators. Textile dye effluent and contaminated soils were collected and analyzed for selection of suitable bacteria for dye degradation. The residual bacterial load was found to be in the range of 108 cfu/mL. Six

bacterial strains *viz.,* two species of *Bacillus,* two species of *Klebsiella,,* one species each of *Planococcus* and *Micrococcus luteus* were isolated. The best two dye degraders namely species of *Planococcus* and *Bacillus* were further optimized for the effect of carbon and nitrogen source, pH, temperature and percentage of inoculum. The optimized conditions for both the isolates of *Planococcus* sp. and *Bacillus* sp. were used in bio-decolorization studies of textile effluent. More than 50% of decolorization was achieved within 4 d of incubation. After 6 d of incubation, decolorization was achieved above 80%. The isolates *Planococcus* sp. and *Bacillus* sp. exhibited maximum decolorization ability at pH between 5-8 and temperature 37°C. Moreover, 10% (v/v) inoculums, glucose and peptone as carbon and nitrogen sources were found to be the optimum for decolorization. Both the isolates showed highest decolorization percentage of Coractive Blue 3º dye effectively during optimization and more interestingly showed consistent decolorization of textile dye throughout the study(Mohan,V *et al.*, 2013).

Chemically treated textile waste-water released by manufacturers pose a detrimental effect to the environment. This study is to identify microorganism that can degrade dyes present in the waste-water as this technique is more eco-friendly. The dye decolourizer were isolated and identified using 16s RDNA sequencing methods and analyzed using Dot Plot programme and sequences obtained were compared with data from GeneBank in BLAST programme. The bacteria isolated have 99% similarities to *Bacillus sp., Bacillus cereus* and *Bacillus thuringiensis* (Iwana I. Zainudin and Azrimi N. Umor, 2013).

Effluent from textile industries often contains toxic dyes and other chemicals, which make it become difficult to reuse such wastewaters. The present study was aimed at decolourizing wastewater collected from a textile dyeing industry using the white rot fungus *Phanerochaete chrysosporium* in batch shake flasks. The wastewater was initially characterized for the parameters chemical oxygen demand (COD), color index, total suspended solids, pH, heavy metals and alkalinity. Wastewater decolourization using P. chrysosporium was then investigated under different conditions such as, dilution with water and with the fungal growth media at 1:1 and 1:3 proportions. During the wastewater decolourization, high enzyme activities of lignin peroxidase and manganese peroxidase produced by the fungus were observed at 84 and 96 h, respectively, particularly in the experimental flasks containing the wastewater and the fungal growth media. Laccase activity by the fungus was, however, absent in the experiments. This study clearly demonstrated the role of lignolytic enzymes in decolourization of the wastewater (Kannan Pakshirajan and P. Radhika,2013).

Water pollution caused by industrial effluent discharges has become an alarming trend worldwide, while textile industries are considered as the most polluting among all others. In recent years, bio-treatment took attraction in removing the unwanted colour and toxicity of textile effluents than other conventional treatment processes. The present study concentrates in the isolation and identification of indigenous bacteria from textile dye effluent and evaluation of their ability to decolourize dyes. The decolourizing activity was measured spectrophotometrically after incubation of the isolates for 3, 5 and 7 days in mineral salt medium modified with 0.05% of respective Novacron dye, viz orange W3R, red FNR, yellow FN2R, blue FNR or navy WB. Three bacterial isolates exhibiting strong decolourizing activity were identified up to species as *Micrococcus luteus, Listeria denitrificans* and *Nocardia atlantica*. All the bacteria exhibited maximum decolourizing activity after 7 days of incubation with little deviation. The bacterium *Micrococcus luteus* caused 60% decolourization of yellow FN2R and navy WB, and 85-90% of orange W3R, red FNR

and blue FNR. Likewise, *Listeria denitrificans* decolourized 70-80% of Blue FNR, Orange W3R, Red FNR and Navy WB. In contrast, the bacterium caused no significant decolourization of yellow FN2R. Notably, *Nocardia atlantica* caused almost complete decolourization of Blue FNR and Red FNR, while at least 80% of other dyes tested. This study thus reveals that some bacteria inhabit in textile effluent whereby utilize the dyes as their source of energy and nutrition, and imply their importance in treatment of industrial effluents (Hassan M.M *et al*.,2013).

Novel azo dye-degrading bacterium T312D9 strain has been isolated from Abou Quir Gulf, Alexandria, Egypt. The identification of the isolate by 16S rRNA gene sequencing revealed to be *Lysobacter* sp. This marine ecofriendly isolate was exploited for its ability to degrade two synthetic azo dyes considered as detrimental pollutants from industrial effluents: congo red and methyl red. Using different dye concentrations showed the highest metabolic activity for complete degradation obtained from 100 to 500 mg/L within 30 h under static condition, also, sustaining higher dye loading of 1g/L was carried out. The significant induction of enzymes NADH - 2,6-dichloroindophenol (NADH-DCIP) reductase and tyrosinase indicated their prominent role in dye degradation. The biodegradation of two azo dyes were analyzed by gas chromatographic mass spectrum analysis (GC-MS) and Fourier transforms infrared spectroscopy (FTIR) before and after treatment. Toxicity study revealed the much less toxic nature of the metabolites produced after complete decolorization. *Lysobacter* sp T312D9 represent an inexpensive and promising marine bacteria for removal of both methyl and congo red. High sustainable metabolic activity for biodegradation under static condition. NADHDCIP reductase and tyrosinase were significantly induced during biodegradation of dyes. The obtained metabolites revealed to be less toxic in nature which offers a practical biological treatment (Khouloud M. I. Barakat, 2013).

Forty five bacterial strains were isolated from contaminated textile wastewater and soil, and then isolates were screened for their ability to decolorize textile dyes from aqueous solution. Initially twenty four bacterial isolates were screened based on their ability to decolorize a wide spectrum of dyes efficiently such as Black WNN, Blue FNR, Red FN2BL, Blue RC, TURQ Blue and Diresul RDT Black dye, by a rapid microtiter plate screening method. Among all isolates, NF-23 was found to decolorize maximum number of dyes followed by NF-22 and NF-21. NF-23 decolorized Black WNN (95%), Blue FNR (50%), Diresul RDT black (90%) and Red FN2BL (80%) after 72 h of incubation at pH-9 and temperature 35°C under anoxic condition. These results signify that bacterial isolates could effectively be used in development of alternative and eco-friendly method for decolorization and biodegradation of textile dyes from industrial effluent(Anamika Pokharia *et al.*,2013)

Azo dyes are widely used by different industries including the textile industry. A substantial amount of these colorants exist in the water discharged from the textile outlets which contaminate the surrounding water bodies and soil. These colorants could be degraded by bacteria. For this purpose, thirty bacterial strains capable of degrading azo dyes were isolated from textile effluents. Strain IFN4 identified as *Shewanella* sp. was most efficient in decolorizing RB-5 (200 mg L-1) in mineral salt medium and color was removed >90% in just four h. Decolorization efficiency of this stain was also examined using mixture of AR-81, DR-88 and RB-5 dyes and conditions were optimized for their faster degradation. Bacterium degraded the dyes mixture at all pH (5-10) and temperature (20-50°C) values, but with different efficiency. Maximum decolorization of the dyes mixture was recorded at pH 8.5 and at 35°C. Bacterium showed very fast decolorization under static incubation while negligible decolorization occurred under shaking incubation. However, bacterial growth was more under shaking than

static culture. Furthermore, 10% (v/v) inoculum concentration was found to be the optimum for decolorization. The decolorization rate of *Shewanella* sp. strain IFN4 was very high under optimal conditions, which increased its applicability in the treatment of the wastewater(Muhammad Imran *et al*., 2013).

This paper deals with the intensive review of reactive azo dye, Reactive Black 5. Various physicochemical methods namely photo catalysis, electrochemical, adsorption, hydrolysis and biological methods like microbial degradation, biosorption and bioaccumulation have been analyzed thoroughly along with the merits and demerits of each method. Among these various methods, biological treatment methods are found to be the best for decolorization of Reactive Black 5. With respect to dye biosorption, microbial biomass (bacteria, fungi, microalgae, etc), and outperformed macroscopic materials (seaweeds, crab shell, etc.) are used for decolorization process. The use of living organisms may not be an option for the continuous treatment of highly toxic organic/inorganic contaminants. Once the toxicant concentration becomes too high or the process operated for a long time, the amount of toxicant accumulated will reach saturation. Beyond this point, an organism's metabolism may be interrupted, resulting in death of the organism. This scenario is not existed in the case of dead biomass, which is flexible to environmental conditions and toxicant concentrations. Thus, owing to its favorable characteristics, biosorption has received much attention in recent years (Jagadeesan Vijayaraghavan *et al.,* 2013).

Studies were carried out on the decolorization of azo dyes by *Bacillus* species from effluent of textile industries. About 10 bacterial strains were isolated from the effluent of textile industries, Bacillus sp. showed remarkable ability in decolorizing the widely utilized azo dyes. Phenotypic characterization and phylogenetic analysis based on 16S rDNA sequence comparisons indicate that these strains belonged to the genus Bacillus subtilis. It showed nearly 90% decolorization ability within 3 days of incubation. Textile wastewater having diverse characteristics could be decolorized effectively using *Bacillus subtilis*. The *Bacillus subtilis* could decolorize azo dyes in a wide range of salt concentration (up to 20% w/v), temperature (25–40oC), and pH (5–11) after 4 days of incubation in static culture. Bacillus subtilis readily grew in and decolorized the high concentrations of dye (5000 ppm). UV–Vis analyses before and after decolorization and the colorless bacterial biomass after decolorization suggested that decolorization was due to biodegradation, rather than surface adsorption (Sathish. S and Joshua Amarnath.D, 2014).

Textile industry is one of the major industries in the world that provide employment with no required special skills and play a major role in the economy of many countries. There are three different types of fibres used in the manufacture of various textile products: cellulose fibres, protein fibres and synthetic fibres. Each type of fibre is dyed with different types of dyes. Cellulose fibres are dyed using reactive dyes, direct dyes, napthol dyes and indigo dyes. Protein fibres are dyed using acid dyes and lanaset dyes. Synthetic fibres are dyed using disperse dyes, basic dyes and direct dyes. The textile industry utilizes various chemicals and large amount of water during the production process. About 200 L of water are used to produce 1 kg of textile. The water is mainly used for application of chemicals onto the fibres and rinsing of the final products. The waste water produced during this process contains large amount of dyes and chemicals containing trace metals such as Cr, As, Cu and Zn which are capable of harming the environment and human health. The textile waste water can cause haemorrhage, ulceration of skin, nausea, skin irritation and dermatitis. The chemicals present in the water block the sunlight and increase the biological oxygen demand thereby inhibiting photosynthesis and reoxygenation process. The effluent water discharged from the

textile industries undergoes various physio-chemical processes such as flocculation, coagulation and ozonation followed by biological treatments for the removal of nitrogen, organics, phosphorous and metal. The whole treatment process involves three steps: primary treatment, secondary treatment and tertiary treatment. The primary treatment involves removal of suspended solids, most of the oil and grease and gritty materials. The secondary treatment is carried out using microorganisms under aerobic or anaerobic conditions and involves the reduction of BOD, phenol and remaining oil in the water and control of color. The tertiary treatment involves the use of electrodialysis, reverse osmosis and ion exchange to remove the final contaminants in the wastewater. The major disadvantages of using the biological process are that the presence of toxic metals in the effluent prevents efficient growth of microorganisms and the process requires a long retention time. The advanced oxidation processes is gaining attention in the recent days due to the ability to treat almost all the solid components in the textile effluents. The photo oxidation of the effluents is carried out using H2O2, combination of H2O2 and UV and Combination of TiO2 and UV. Advanced oxidation process generates low waste and uses hydroxyl radicals (OH●) as their main oxidative power. The hydroxyl radicals (OH●) are produced by chemical, electrical, mechanical or radiation energy and therefore advanced oxidation processes are classified under chemical, photochemical, catalytic, photocatalytic, mechanical and electrical processes. The effluents treated with advanced oxidation process were found to reduce 70-80% COD when compared to 30-45% reduction in biological treatment(Ghaly, A.E, *et al*.,2014)

Studies were carried on the decolorization of the textile dye reactive blue 19 (RB 19) by a novel isolate of *Coprinus plicatilis* (*C. plicatilis*) fungi. We describe an in vitro optimization process for decolorization and its behavior under different conditions of carbon and nitrogen sources, pH, temperature and substrate concentration. The optimal conditions for decolorization were obtained in media containing intermediate concentrations of ammonium oxalate and glucose (10 g/L) as nitrogen and carbon sources, respectively, at 26°C and pH = 5.5. Maximum decolorization efficiency against RB 19 achieved in this study was around 99%. Ultra-violet and visible (UV-vis) spectrophotometric analyses, before and after decolorization, suggest that decolorization was due to biodegradation. This effect was associated with laccase enzyme displaying good tolerance to a wide range of pH values, salt concentrations and temperatures, suggesting a potential role for this organism in the remediation of real dye containing effluents. In conclusion, laccase activity in *C. plicatilis* was firstly described in this study (Hatice A Akdogan *et al.*,2014).

The textile industry, which is one of the largest consumers of water in the world, produces wastewater comprising various recalcitrant agents such as dyes, sizing agents and dying aids Strong colour of the textile waste water is the most serious problem of the textile waste effluent. The disposal of these wastes and their Dyes may significantly affect photosynthetic activity in aquatic habitat and damage to the environment. It is retards biological activity by reducing the light penetration and also causes metal toxicity to both aquatic and terrestrial life. It also leads to toxicity of fish and mammals and Major problem is that Dyes having higher stability under sunlight and resistance to microbial attack. Therefore,care should be taken when releasing these types of wastewater into the environment. For solving these now a Days novel approach based on bioremediation using bacteria is widely used. In which natural biota and the microbial consortia have been used and found that it is more effective. Bioremediation is the cost effective process and their end products are also non-hazardous. For these purpose mostly, bacterial culture was used widely(Patel Feni and Marjadi Darshan,2014).

Bacteria capable of degrading the sulfonated azo dye Red HE7B were isolated from textile mill effluent contaminated soil. The most efficient isolate was identified as Bacillus sp. Azo1 and the isolate could successfully decolorize up to 89 % of the dye. The decolorized cultural extract analyzed by HPLC confirmed degradation. Enzymatic ana ysis showed twofold and fourfold increase in the activity of azoreductase and laccase enzymes, respectively, indicating involvement of both reductive and oxidative enzymes in biodegradation of Red HE7B. Degraded products which were identified by GC/MS analysis included various metabolites like 8-nitroso 1-naphthol, 2-diazonium naphthalene. Mono azo dye intermediate was initially generated from the parent molecule. This mono azo dye was further degraded by the organism, into additional products, depending on the site of cleavage of R–N=N–º molecule. Based on the degradation products identified three different pathways have been proposed. The mechanism of degradation in two of these pathways is different from that of the previously reported pathway for azo dye degradation. This is the first report of a microbial isolate following multiple pathways for azo dye degradation. Azo dye Red HE7B was observed to be phytotoxic, leading to decrease in root development, shoot length and seedling fresh weight. However, after biotreatment the resulting degradation products were non-phytotoxic(Jyoti Kumar Thakur *et al., 2014).*

In the present study absorption maxima (λmax) and absorption spectrum of six textile reactive azo dyes were studied. The absorption maxima (visible range) for the various dyes obtained were: - Red-5B (512 nm) Orange-3R (492 nm), Yellow-GR (415 nm), Black-B (597 nm), Turquoise Blue-G (661 nm) and Blue-3R (666nm). During the absorption spectrum study multiple peaks were obtained, in UV as well as Visible range. All the dyes were showing multiple peaks in UV range and single peak in the visible range except Turquoise Blue-G and Blue-3R. This study provides some information regarding structure of the relatively less studied dyes and could be utilized to follow the course of dye degradation by the microbial cultures. (Poonam Gupta *et a*l., 2014).

Conclusion

In conclusions, the textile, dyeing and finishing industry use wide variety of dyestuffs due to the rapid changes in the customer's demands. Thus by the use of the above isolates sustainable biodegradation of the harmful azo dyes utilized by the dye, textile, paper ink etc. industries can be possible. These methods are not only eco-friendly but also commercially viable even for the small scale industries. A thorough investigation, taking into consideration of certain parameters such as optimization of the dye concentration for the isolates as well as for the dye to be degraded, effect of physicochemical parameters on degradation etc. at large scale is necessary to provide unequivocal evidence for the usefulness of these isolates in sustaining dye degradation capability. Further molecular study on their enzymatic property and degradation process could reveal them as an important textile dye degrader.

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