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Bacterial Bioremediation of Textile Azo Dyes – A Review

KEYWORDS: Azo dyes, Bioremediation, Consortium, Textile effluents

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ABSTRACT *Textile industries consume a considerable amount of water in their manufacturing processes. Considering both the volume and the effluent composition, the textile industry is rated as the most polluting among the industrial sectors. Important pollutants in textile effluents are mainly recalcitrant organics, dyes, toxicants, inhibitory compounds, surfactants, chlorinated compounds and salts. Improper textile effluent disposal into the aquatic systems affects the aesthetic merit, water transparency and gas solubility of the water bodies leading to the reduction in sunlight penetration which in turn, decreases the photosynthetic activity, reduces dissolved oxygen concentration, depicts toxic effect on aquatic flora and fauna. In addition, many synthetic azo dyes and their metabolites are toxic, carcinogenic and mutagenic leading to potential health hazards to the mankind. Therefore treatment of industrial effluent containing aromatic compounds becomes necessary prior to their final discharge into the environment. Physico-chemical methods have major limitations such as economically unfeasible, unable to remove the recalcitrant azo dyes and their metabolites, involves complicated procedures, more energy consumption and chemical usage. Whereas biodecolorization has been proposed as eco-friendly, generates less sludge and less expensive.*

Introduction

Textile industry is providing one of the most basic needs of the people and maintains sustained growth for improving quality of life. It has a unique position as a self reliant industry, from the production of raw materials to the delivery of finished products, with substantial value-addition at each stage of processing (Hemapriya *et al*., 2010). The textile industry has been condemned as being one of the world's worst offenders in terms of pollution because it requires a great amount of two components: (a) chemicals - as many as 2000 different chemicals are used in the textile industry from dyes to transfer agents; and (b) water - a finite source that is quickly becoming scarce and is used at each and every step of the process both to convey the chemicals used during that step and to wash them out before beginning the next step.

The textile industry is one of the greatest generators of liquid effluent pollutants, due to the high quantities of water used in the dyeing processes. It is estimated that 2,80,000 tones of textile dyes are discharged in such industrial effluents every year worldwide (Jin *et al*., 2007; Kalyani *et al*., 2009).The effluent from textile industries are complex, containing a wide variety of dyes and other products, such as dispersants, acids, bases, salts, detergents, hemectants, oxidants etc. (Kalyani *et al* ., 2009). Improper textile dye disposal in aqueous ecosystems leads to the reduction in sunlight penetration which in turn decreases photosynthetic activity, dissolved oxygen concentration, water quality and depicts acute toxic effects on aquatic flora and fauna, causing severe environmental problems worldwide (Vandevivere *et al*., 1998).

Dye removal techniques

Textile dyestuff and wastewater are recalcitrant to degradation. Several Physico-chemical and biological treatment techniques can be employed to remove color from the textile effluents. Several factors including dye type, effluent composition, operation costs, environmental fate and handling costs of the generated sludge determine the technical and economic feasibility of the treatment method. Several physico-chemical methods have been used in the treatment of textile effluents to achieve decolorization (Robinson *et al*., 2001). However, the implementation of physical/chemical methods have inherent drawbacks of being economically unfeasible (more energy consumption and chemical uses), unable to remove the recalcitrant azo dyes and/or their organic metabolites completely, generating a significant amount of sludge that may cause secondary pollution problems (Zhang *et al*., 2004).

Table 1: Various Physico-chemical Methods Employed for Wastewater Treatment (Robinson *et al*., 2001)

Sl.No	Physico-chemical methods	Advantages	Disadvantages
1	Fenton's reagent	Effective for both soluble and insoluble dyes.	Sludge generation poisonous
2	Ozonation	Applied in gaseous state	Short half-life (20 min)
3	Photochemical with H_2O_2	No sludge production	Formation of byproducts
4	Sodium Hypochlorite	Initiates and accelerates azo bond cleavage	Release of aromatic amines
5	Cucurbituril	Good sorption capacity for various dyes	High cost
6	Electrochemical destruct	Breakdown compounds are non-hazardous	High cost of electricity
7	Activated carbon	Good removal of wide variety of dyes	Very expensive
8	Silica gel	Effective for basic dye removal	Side reactions prevent
9	Membrane filtration	Removes all dye types	Concentrated sludge production
10	Ion exchange	Regeneration: no adsorbent loss	Not effective for all dyes
11	Irradiation	Effective oxidation at lab scale	Requires a lot of dissolved O_2
12	Electro kinetic coagulation	Economically feasible	High sludge formation

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Bioremediation of textile effluents by Bacterial strains

The microbial decolorization and degradation of azo dyes has been of considerable interest since it is inexpensive, eco-friendly and produces a less amount of sludge (Carvalho *et al*., 2008; Saratale *et al*., 2009). Microorganisms for dye decolorization may be obtained simply by isolation of existing dye degrading cultures from environmental samples (e.g., textile effluents), by adaptation of promising strains to conditions present in textile effluents or by construction of suitable organisms employing genetic engineering methods (Kandelbauer *et al*., 2004).

Isolation and Adaptation of Naturally Occurring Microorganisms

Although numerous microorganisms can decolorize dyes, only a few are able to mineralize these compounds into CO_2 and H_2O (Junghanns *et al*., 2008). The identification of efficient dye-decolorizing species requires a screening method. In general, enrichment of microorganisms with special effectiveness in dye degradation via natural adaptation occurs at any site where these xenobiotics are present in amounts above average (Zimmermann *et al*., 1984). Such sites may for example be natural ecosystems that are exposed to textile effluents for a long period or sewage treatment plants near textile mills. Isolation of dye-degrading bacterial strains is usually a tedious and time consuming task (Nigam *et al*., 1996). The enrichment of bacteria under chemostat conditions capable of growing on dye molecules as the only carbon source has been reported to take very long periods, from several months upto more than a year (Zimmermann *et al*., 1984). Since dye degradation is mainly accomplished via secondary metabolic routes, this nutritional restriction is not principally needed. Bacterial strains selected by adaptation from textile effluents have been shown to decolorize textile dyes (Saratale *et al*., 2009; Hemapriya *et al*., 2010; Phugare *et al*., 2011).

Decolorization of Synthetic Dyes by bacterial Consortium

The utilization of microbiotic consortiums offers considerable advantages over the use of pure cultures in the degradation of synthetic dyes (Forgacs *et al*., 2004; Hemapriya *et al*., 2013). The individual strains may attack the dye molecule at different positions or may use decomposition products produced by another strain for further decomposition. However, it should be stressed that the composition may change during the decomposition process, which interferes with the control of technologies using mixed cultures (Cetin and Donmez, 2006; Khadijah *et al*., 2009). Moreover, the efficacy of decomposition considerably depends on the chemical character of the synthetic dye and on the biodegradation capacity of the microbial consortium. Vijaya and Sandhya (2003) has reported the decolorization and complete degradation of synthetic azo dye, Methyl Red by a mixed culture isolated from textile effluents. Decolorization of various synthetic dyes by different bacterial consortium is shown in **Table.2.**

Table 4: Dye Decolorization by Genetically Engineered Bacterial Cells

Sl. No	Donor	Acceptor	Function	Reference
1	Caulobacter subvibrioides	Escherichia coli	Azoreductase	Govind *et al*. (1993)
2	Clostridium perfringens	Escherichia coli	Azoreductase	Rafii and Coleman (1999)
3	Pseudomonas luteola	Escherichia coli	Azoreductase	Chang *et al*. (2000).
4	Eschericia coli	Sphingomonas xenophaga	Flavinreductase	Russ *et al*. (2000).
5	*Bacillus* sp.	Escherichia coli	Azoreductase	Suzuki *et al*. (2001).
6	*Rhodococcus* sp.	Eschericia coli	Azoreductase	Chang and Lin (2001).
7	Rhodobacter sphaeroides	*Eschericia coli* JM109	Azoreductase	Jin *et al*. (2009).

Decolorization of Synthetic Dyes by Pure Cultures of Bacterial Strains

Several bacterial pure cultures were employed for the decolorization of azo dyes. Gram positive bacterial strains including *Clostridium perfringens*, *Bacillus cereus*, *Brevibacillus* sp. and *Paenibacillus azoreducens* were found to be efficiently decolorizing various structurally different textile azo dyes. Similarly gram negative bacterial strains including *Klebsiella pneumoniae*, *Proteus mirabilis*, *Pseudomonas putida*, *Citrobacter* sp. and *Escherchia coli* exhibited promising decolorizing efficacy on various dyes **(Table.3)**.

Table 3: Dye Decolorization by Pure Cultures of Bacterial Isolates

Sl. No	Bacteria	Dye	Reference
1	Klebsiella pneumoniae	Methyl Red	Wong and Yuen (1998)
2	*Kurthia* sp.	Brilliant Green,	Wong and Yuen (1998)
3	Bacillus gordonae	Tectilon Blue 4R-01	Walker and Weatherley (2000)
4	Escherichia coli	Reactive Red-22	Chang and Lin (2001)
5	Sphingomonas Xenophaga	Congo Red	Diniz *et al*. (2002)
6	Clostridium perfringens	Bromophenol Blue	Kim *et al*. (2002)
7	*Kocuria rosea* MTCC 1532	Malachite Green	Parshetti *et al*. (2006)
8	Pseudomonas desmolyticum	Direct Blue-6	Kalme *et al*. (2007)
9	Vibrio harveyi	Acid black-210	Ozdemir *et al*. (2008)
10	*Bacillus cereus* strain DCII	Anthraquinone dye	Deng *et al*. (2008)
11	*Pseudomonas* sp. SUK-1	Reactive Red-22	Kalyani *et al*. (2009)
12	Bacillus thuringiensis	Acid Red-119	Dave and Dave (2009)
13	*Klebsiella* sp.	Orange 3R	Ponraj *et al*. (2011)

Dye Decolorization by Genetically Engineered Organisms

The wide spread application of genetically engineered bacterial cells to enhance the efficacy of microbial decomposition of textile effluents can be expected in future (**Table 4**). The cloning and expression in *E.coli* of an 'azoreductase' gene from *Clostridium perfringens* (Rafii and Coleman, 1999), from a *Bacillus* sp. (Suzuki *et al*., 2001), from *Pseudomonas luteola* (Hu, 1994) have been reported. Furthermore, the feasibility of the use of a recombinant *E.coli* strain, harboring azo-dye-decolorizing genes from *Rhodococcus* sp. (Chang and Lin, 2001), and recombinant *Sphingomonas* sp. (Russ *et al*., 2000) for the decolorization of dye wastewater has been determined. Jin *et al*. (2009) has reported that *E. coli* JM109, the genetically engineered microorganism harboring the azoreductase gene of *Rhodobacter sphaeroides* AS1.1737 showed higher ability to decolorize Direct Blue-71. Mobilizing specific genes, encoding for non-specific multifunctional degradative sequences may decisively increase the degradative potential of natural synthropic community against synthetic dyes. Thus, the use of recombinants that harbor dye-decolorizing determinants from other species can essentially enhance the capacity of waste remediation technologies.

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Table 2: Decolorization of Synthetic Dyes by Bacterial Consortium

Sl. No	Consortium	Microbes Involved	Dye	Reference
1	JW-2	*Paenibacillus polymyxa*, *Micrococcus luteus* *Micrococcus* sp.	Reactive Violet 5R	Moosvi *et al*. (2007).
2	Unnamed	*Alcaligenes faecalis*, *Sphingomonas* sp. EBD *Bacillus subtilis*, *Bacillus thuringiensis* *Enterobacter cancerogenus*	Direct Blue-15	Kumar *et al*. (2007)
3	TJ-1	*Proteus mirabilis*, *Aeromonas caviae* *Rhodococcus globerulus*	Acid Orange-7	Joshi *et al*. (2008).
4	C-15	*Chryseobacterium* sp. *Flavobacterium* sp.	Procion Blue HERD	Khadijah *et al*. (2009)
5	GR	*Proteus vulgaris* *Micrococcus glutamicus*	Scarlet R	Saratale *et al*. (2009)
6	SDM	*Providencia* sp. SDS *Pseudomonas aeruginosa* BCH	Red HE3B	Phugare *et al*. (2010)

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