

# International Journal of Innovative Research in Science, Engineering and Technology

(A High Impact Factor, Monthly, Peer Reviewed Journal)

Website: [www.ijirset.com](http://www.ijirset.com)

Vol. 3, Issue 12, December 2014

## Microbial Biodegradation of Textile Dye Wastewater of Sanganer, Jaipur

Dr. Gagan B Khanna

BBD Govt. College, Chimanpura, Shahpura, Jaipur, Rajasthan, India

**ABSTRACT:** In recent years, India has emerged as a promising industrial hub. It has a cluster of textile, dyeing, and printing industries. The adjoining rivers/water bodies receive mostly untreated discharge from these industries especially in Sanganer, Jaipur. Textile industrial effluent contains various contaminants (dyes, heavy metals, toxicants, and other organic/inorganic dissolved solids) that alter the physico-chemical properties of adjoining land and waterbodies in which it is discharged, thereby degrading the water quality and subsequently affecting the landscapes in the vicinity. This ultimately affects the flora and fauna of the locale and has adverse effects on human health. Out of the total dyes (approximately 10,000 dyes) exploited in the textile dyeing and printing units, azo dyes possess a complex structure and are synthetic in origin. They contribute nearly 70% to the total effluent discharge. Biological processes are based on the ability of inhabiting indigenous microorganisms in these contaminated environments to tolerate, resist, decolorize/degrade, and mitigate the recalcitrant compounds. Exploring microbes with higher efficacy of azo dye degradation can reduce the amount of chemical discharged from the process. The present review explores the potential of microbial diversity for the development of an effective bioremediation approach.

**KEYWORDS:** microbes, biodegradation, biosorption, algae, fungi, bacteria, yeasts, textile, Sanganer, azo dyes, wastewater

### I.INTRODUCTION

Microbial biodegradation is the use of bioremediation and biotransformation methods to harness the naturally occurring ability of microbial xenobiotic metabolism to degrade, transform or accumulate environmental pollutants, including hydrocarbons (e.g. oil), polychlorinated biphenyls (PCBs), polyaromatic hydrocarbons (PAHs), heterocyclic compounds (such as pyridine or quinoline), pharmaceutical substances, radionuclides and metals. Interest in the microbial biodegradation of textile dyes of Sanganer, Jaipur, has intensified in recent years,<sup>[1][2]</sup> and recent major methodological breakthroughs have enabled detailed genomic, metagenomic, proteomic, bioinformatic[1] and other high-throughput analyses of environmentally relevant microorganisms, providing new insights into biodegradative pathways and the ability of organisms to adapt to changing environmental conditions. Biological processes play a major role in the removal of contaminants and take advantage of the catabolic versatility of microorganisms to degrade or convert such compounds.[2] In environmental microbiology, genome-based global studies are increasing the understanding of metabolic and regulatory networks, as well as providing new information on the evolution of degradation pathways and molecular adaptation strategies to changing environmental conditions. The increasing amount of bacterial genomic data provides new opportunities for understanding the genetic and molecular bases of the degradation of organic pollutants. Aromatic compounds are among the most persistent of these pollutants and lessons can be learned from the recent genomic studies of *Burkholderia xenovorans* LB400 and *Rhodococcus* sp. strain RHA1,[3] two of the largest bacterial genomes completely sequenced to date. These studies have helped expand our understanding of bacterial catabolism, non-catabolic physiological adaptation to organic compounds, and the evolution of large bacterial genomes.[4] First, the metabolic pathways from phylogenetically diverse isolates are very similar with respect to overall organization. Thus, as originally noted in pseudomonads, a large number of "peripheral aromatic" pathways funnel a range of natural and xenobiotic compounds into a restricted number of "central aromatic" pathways. Nevertheless, these pathways are genetically organized in genus-specific fashions, as exemplified by the b-

## International Journal of Innovative Research in Science, Engineering and Technology

(A High Impact Factor, Monthly, Peer Reviewed Journal)

Website: [www.ijirset.com](http://www.ijirset.com)

Vol. 3, Issue 12, December 2014

keto adipate and Paa pathways. Comparative genomic studies further reveal that some pathways are more widespread than initially thought. Thus, the Box and Paa pathways illustrate[5] the prevalence of non-oxygenolytic ring-cleavage strategies in aerobic aromatic degradation processes. Functional genomic studies have been useful in establishing that even organisms harboring high numbers of homologous enzymes seem to contain few examples of true redundancy. For example, the multiplicity of ring-cleaving dioxygenases in certain rhodococcal isolates may be attributed to the cryptic aromatic catabolism of different terpenoids and steroids[6]. Finally, analyses have indicated that recent genetic flux appears to have played a more significant role in the evolution of some large genomes, such as LB400's, than others. However, the emerging trend is that the large gene repertoires of potent pollutant degraders such as LB400 and RHA1 have evolved principally through more ancient processes. That this is true in such phylogenetically diverse species is remarkable and further suggests the ancient origin of this catabolic capacity[7].

Anaerobic microbial mineralization of recalcitrant textile dyes of Sangner, Jaipur is of great environmental significance and involves intriguing novel biochemical reactions[8]. In particular, hydrocarbons and halogenated compounds have long been doubted to be degradable in the absence of oxygen, but the isolation of hitherto unknown anaerobic hydrocarbon-degrading and reductively dehalogenating bacteria during the last decades provided ultimate proof for these processes in nature. While such research involved mostly chlorinated compounds initially, recent studies have revealed reductive dehalogenation of bromine and iodine moieties in aromatic pesticides[9]. Other reactions, such as biologically induced abiotic reduction by soil minerals[10] has been shown to deactivate relatively persistent aniline-based herbicides far more rapidly than observed in aerobic environments. Many novel biochemical reactions were discovered enabling the respective metabolic pathways, but progress in the molecular understanding of these bacteria was rather slow, since genetic systems are not readily applicable for most of them. However, with the increasing application of genomics in the field of environmental microbiology,[11] a new and promising perspective is now at hand to obtain molecular insights into these new metabolic properties. Several complete genome sequences were determined during the last few years from bacteria capable of anaerobic organic pollutant degradation. The ~4.7 Mb genome of the facultative denitrifying *Aromatoleum aromaticum* strain EbN1 was the first to be determined for an anaerobic hydrocarbon degrader (using toluene or ethylbenzene as substrates). The genome sequence revealed about two dozen gene clusters (including several paralogs) coding for a complex catabolic network for anaerobic and aerobic degradation of aromatic compounds. The genome sequence forms the basis for current detailed studies on regulation of pathways and enzyme structures.[12] Further genomes of anaerobic hydrocarbon degrading bacteria were recently completed for the iron-reducing species *Geobacter metallireducens* (accession nr. NC\_007517) and the perchlorate-reducing *Dechloromonas aromatica* (accession nr. NC\_007298), but these are not yet evaluated in formal publications. Complete genomes were also determined for bacteria capable of anaerobic degradation of halogenated hydrocarbons by halo-respiration: the ~1.4 Mb genomes of *Dehalococcoides ethenogenes* strain 195 and *Dehalococcoides* sp. strain CBDB1 and the ~5.7 Mb genome of *Desulfotobacterium hafniense* strain Y51. Characteristic for all these bacteria is the presence of multiple paralogous genes for reductive dehalogenases, implicating a wider dehalogenating spectrum of the organisms than previously known. Moreover, genome sequences provided unprecedented insights into the evolution of reductive dehalogenation and differing strategies for niche adaptation[13]

Recently, it has become apparent that some organisms, including *Desulfotobacterium chlororespirans*, originally evaluated for halo-respiration on chlorophenols, can also use certain brominated compounds, such as the herbicide bromoxynil and its major metabolite as electron acceptors for growth. Iodinated compounds may be dehalogenated as well, though the process may not satisfy the need for an electron acceptor[14]

Bioavailability, or the amount of a substance that is physiochemically accessible to microorganisms is a key factor in the efficient biodegradation of textile dye wastewater of Sangner, Jaipur. It has been showed that, with the exception of kaolinite clay, most soil clays and cation exchange resins attenuated biodegradation of 2-picoline by *Arthrobacter* sp. strain R1, as a result of adsorption of the substrate to the clays. Chemotaxis, or the directed movement of motile organisms towards or away from chemicals in the environment is an important physiological response that may contribute to effective catabolism of molecules in the environment. In addition, mechanisms for the intracellular accumulation of aromatic molecules via various transport mechanisms are also important[15] Sustainable

# International Journal of Innovative Research in Science, Engineering and Technology

(A High Impact Factor, Monthly, Peer Reviewed Journal)

Website: [www.ijirset.com](http://www.ijirset.com)

Vol. 3, Issue 12, December 2014

development requires the promotion of environmental management and a constant search for new technologies to treat vast quantities of wastes generated by increasing anthropogenic activities. Biotreatment, the processing of wastes using living organisms, is an environmentally friendly, relatively simple and cost-effective alternative to physico-chemical clean-up options. Confined environments, such as bioreactors, have been engineered to overcome the physical, chemical and biological limiting factors of biotreatment processes in highly controlled systems. The great versatility in the design of confined environments allows the treatment of a wide range of wastes under optimized conditions. To perform a correct assessment, it is necessary to consider various microorganisms having a variety of genomes and expressed transcripts and proteins. A great number of analyses are often required. Using traditional genomic techniques, such assessments are limited and time-consuming. However, several high-throughput techniques originally developed for medical studies can be applied to assess biotreatment in confined environments[16]

In the textile wastewater environ Sanganer, different substrates are attacked at different rates by consortia of organisms from different kingdoms. *Aspergillus* and other moulds play an important role in these consortia because they are adept at recycling starches, hemicelluloses, celluloses, pectins and other sugar polymers also alongwith dyes. Some aspergilli are capable of degrading more refractory compounds such as fats, oils, chitin, and keratin. Maximum decomposition occurs when there is sufficient nitrogen, phosphorus and other essential inorganic nutrients. Fungi also provide food for many soil organisms[17]

For *Aspergillus* the process of degradation is the means of obtaining nutrients. When these moulds degrade human-made substrates, the process usually is called biodeterioration. Both paper and textiles (cotton, jute, and linen) are particularly vulnerable to *Aspergillus* degradation. Our artistic heritage is also subject to *Aspergillus* assault. Many fungi have been known to degrade textile azo dyes used in Sanganer viz. white rot fungi or wood rotting fungi eg. *Phanerochaete chrysosporium*. [18]

## II.DISCUSSION

Textile dyes were classified as azo, diazo, cationic, basic, anthraquinone and metal complex based, depending on the nature of their chemical structure [2]. There are more than 100,000 commercially available dyes with over  $7 \times 10^5$  tons of dyestuff produced annually [3,4]. Around 8000 chemical products associated with the dyeing process are listed in the Colour Index (Society of Dyers and Colourists 1976). Chemical structure of the dyes was resistant to fading on exposure to light, water and many chemicals [5]. Dyeing industry effluent textile dye wastewater, Sanganer, Jaipur, alters the color and quality of the water bodies has been proved to be hazardous to aquatic ecosystem and it reduces the sunlight penetration which is essential for photosynthesis, it leads to toxicity of fish and mammals. They also inhibit the activity and growth of microorganisms [9,10, 2]. Dyes having higher stability under sunlight and resistance to microbial attack and temperature were identified [11]. The presence of dyes or their degraded products in water will also cause human health disorders such as nausea, hemorrhage, ulceration of skin and mucous membranes. The presence of such toxic compounds also resulted into severe damage to kidney, reproductive system, liver, brain and central nervous system. The environmental and health concern of these potentially carcinogenic pollutants present in textile waste waters has drawn the notice of many workers.[19] Many dyes were known as carcinogens, such as benzidine and other aromatic components all of which might be reformed as a result of microbial metabolism. It has been already well documented that azo and nitro-compounds were reduced in the sediment and intestinal environment, resulting in the regeneration of the parent toxic amines this compound was not readily removed by typical microbial based waste treatment processes. The highest rates of toxicity were observed for basic, diazo and direct dyes [12]. Some algae and higher plants exposed to effluent rich in disperse dyes at higher concentration have a tendency to bioaccumulate the heavy metal ions from textile effluents.[20] They contaminate not only the environment but also transform the toxicity through the entire food chain, leading to biomagnification. Dye waste water discharged from textile and dye stuff industries containing wide range of chemicals . Government legislation was becoming more stringent in most developed countries regarding the removal of dyes from industrial effluents, which in turn is becoming an increasing problem for the textile industries. Most textile industries were developing onsite or implant facilities to treat their own effluent before discharge was fast forthcoming reality [6]. Various techniques have been

# International Journal of Innovative Research in Science, Engineering and Technology

(A High Impact Factor, Monthly, Peer Reviewed Journal)

Website: [www.ijirset.com](http://www.ijirset.com)

Vol. 3, Issue 12, December 2014

employed for the treatment of dye metal bearing industrial effluents, which usually come under two broad divisions: abiotic and biotic methods.[21]

Bacterial biodegradation of textile dyes is an attractive and inexpensive method. Isolation of new strains or adaptation of existing strain for decomposition of dyes will increase the efficiency of bioremediation. Mechanism involved in color removal by bacteria was absorption or adsorption. Effectiveness of biological treatment system was greatly influenced by the operational parameters such as pH, temperature, dye concentration and nutrients.[22] The influence of each parameter on the color removal process must be optimized to increase dye reduction. *Citrobacter* sp. decolorizes several recalcitrant triphenylmethane and azo dyes by adsorption mechanism [19]. Reactive orange 16 was effectively degraded by *Enterococcus faecalis* YZ 66 was evaluated by [15]. Biodegradation of acid orange 7 are facilitated by the presence of organism in the surfaces that have convenient pores to permit microbial growth [20]. The majority research focused on studying the biodegradation/decolorization potential of bacteria. An effluent adapted bacterium was found to be more capable in decolorizing the effluent containing reactive black B dye than the effluent non adapted bacteria [21]. Two bacterial strains *Bacillus cereus* (KEB-7) and *Bacillus pumilus* (KEB-10) decolorize indigo dye were reported by [22]. Decolorization and degradation of orange II containing textile effluent with biodigester sludge from a local municipality waste treatment plant using sulphate reducing bacteria was a cheaper alternative way [23]. Decolourization of textile azo dyes by *Staphylococcus arlettae* strain VN -11 by sequential microaerophilic / aerobic process was shown to be very effective in azo dye decolourization .[24]. Since the bacteria were widely used in different food and pharmaceutical industries they were generated as waste, which can be attained free or at low cost from these industries. Due to the cell wall constituents of bacteria such as peptidoglycan and the role of functional groups, such as carboxyl, amine and phosphonate, many bacteria have been found to bind with variety of dye classes. The binding mechanisms as well as the parameters influencing the passive uptake of dyes from textile effluents were pH, temperature and dye concentrations [23].

Fungus was capable for oxidizing different chemical compounds and degrading several dyes, including azo dyes and mineralizing persistent aromatic pollutants. The ability of fungus to degrade diverse group of compounds depends upon the nonspecific ligninolytic enzymatic system containing lignin peroxidase, manganese peroxidase and laccase[24]. The degradation and mineralization of dyes by white rot fungi was widely studied. The fungus *Geotrichum* sp. CCM1 1019 has ability to decolorize large amounts of dyes like reactive black 5, reactive red 158 and reactive yellow 27 [25]. In the case of *Phanaerochaete chrysosporium* a ligninolytic fungus preadapted to the medium and degrade the azo benzene constitute of azo dye for aromatic ring cleavage [40]. Textile industry waste water has been decolorized by production of manganese dependent peroxidase (MnP), lignin peroxidase (Lip) and laccase which are the enzymes of white rot fungus *Irpex lacteus* in stationary cultures without adding any chemicals [21]. Fungal biosorption was identified by binding of solute to the biomass by processes which do not involve metabolic energy or transport, although such processes may occur simultaneously where live biomasses were used. Therefore, it can occur in either living or dead biomass [26]. Dead cells remove dyes through the mechanism of biosorption which involve physico-chemical interactions such as adsorption, deposition and ion exchange. In case of *Aspergillus niger* different functional groups in the fungal biomass play different roles in biosorption of different dyes [27]. Consortium containing *Aspergillus flavus*, *Aspergillus wentii*, Basidiomycetes and *Acremonium kiliense* act as biosorbent and effectively decolorize wide range of dyes was reported by [21] Use of certain low cost adsorbents for dye removal has been extensively reviewed [19]. Waste fungal biomass which was a byproduct of industrial fermentation can be used as a cheap source of biosorbent [11]. Amino, carboxyl, thiol and phosphate groups present in the fungal cell wall were responsible for binding of dye molecules [3]. Dye molecule biosorption onto cell surface appears to be a quick process and often completes in a matter of hours [26].

## III.RESULTS

Starting from the 1970s, *Bacillus cereus*, *Bacillus subtilis*, and *Aeromonas hydrophila* were marked as potential remediators on the basis of various studies [10]. Textile effluents contain a pool of structurally complex synthetic dyes and other chemicals, which when released into water bodies, reduced dissolved oxygen concentrations, creating anoxic



# International Journal of Innovative Research in Science, Engineering and Technology

(A High Impact Factor, Monthly, Peer Reviewed Journal)

Website: [www.ijirset.com](http://www.ijirset.com)

Vol. 3, Issue 12, December 2014

conditions that are toxic for most organisms. Recent research studies on cultures of *Proteus mirabilis*, *Pseudomonas luteola*, and *Pseudomonas* sp. have shown promising results for azo dye degradation under anoxic conditions. Isolation of pure cultures from textile wastewater can be time-consuming and laborious.[17] In addition, it is difficult to obtain complete decolorization by a pure bacterial culture. Mixed bacterial cultures, due to their cooperation for an enhanced effect, provide better results in decolorization and mineralization. They can efficiently degrade toxic aromatic amines. Nonetheless, the fact that these results are not readily reproduced and that mixed cultures do not provide the exact view of the dye metabolism makes the process and the results hard to interpret.[18] Textile dye wastewater, Sanganeer, Jaipur, requires appropriate treatment prior to their release into the environment. Residual dyes have complex structural compositions which are toxic for the organisms in soil and water of the affected area. The industries need a cost-efficient and feasible method to treat their effluents, so that when released into the water bodies, it will have little impact on the environment. Microbial and enzymatic decomposition of the wastewater is a viable option, as they do not produce large amounts of sludge, have no adverse effect on the environment, and are inexpensive.[19] On the basis of available literature studies, several lab-based study findings have been explored in this review. Nevertheless, relative data of the performance of isolated microorganisms at an industrial level requires to be generated. It is crucial to optimize all the parameters in order to achieve maximum decolorization by isolated bacterial strains. There is scope for studies on scaling-up of the successful laboratory experiments with newly identified bacteria for future implementation in industries. Experiments should be conducted to measure the toxicity levels in treated effluent, alongside the decolorization rate.[25] Based on the successful laboratory results, efforts should then be made to scale up and apply bacterial decolorization techniques in real industrial effluents. In addition, with the latest advances in genomics and proteomics, there is a possibility to enhance the performance of bacterial or enzymatic treatments of textile wastewater. With all the positive research findings and ongoing developments, microbiological treatment is hoped to be predominant in the elimination of dyes and toxic chemicals in textile dye wastewater, Sanganeer, Jaipur [22]

## IV. CONCLUSIONS

Textile dyeing processes utilize enormous volumes of potable water and auxiliary chemicals along with toxic dye compounds. Textile dye wastewater, Sanganeer, Jaipur are hazardous mixtures of unused textile dyes, partially degraded dye intermediates (aromatic amines) and several other xenobiotic compounds which resist biodegradation. If these wastewaters are released untreated into the aquatic ecosystems, textile dyes can enter into the food webs, bioaccumulate, disrupt photosynthesis and exhibit a potential to induce ecotoxic, mutagenic and carcinogenic effects [24]. The xenobiotic and recalcitrant nature of constituent pollutants in the textile dye wastewaters makes their treatment extremely challenging. Therefore, it is imperative to devise eco-sustainable technologies for the remediation of textile dye wastewaters. Recently, various biological and physico-chemical technologies have been applied for the treatment of textile dye wastewater with varying efficacies [26]. Recent research has demonstrated that microbiotechnology approaches, such as biodegradation of textile dyes using yeast, fungal, algal and bacterial processes are effective in the eco-friendly treatment of textile dye wastewaters. Similarly, enzymatic biodegradation of textile dyes by bacterial, fungal, and algal enzymes such as oxidoreductases, azo reductases, laccases, lignin peroxidases is also considered as a feasible alternative approach [25]. Recent approaches utilizing bacterial communities, bacterial-biofilm reactors and hybrid bioelectrochemical processes such as constructed wetland microbial fuel cells (CW-MFC) system or bacteria augmented CW-MFCs have also shown promising results in the biological treatment of textile dye wastewaters.[27]

## REFERENCES

1. Pandey AK, Sarada DV, Kumar A. Microbial Decolorization and Degradation of Reactive Red 198. *Proceedings of the National Academy of Sciences, India*; 2011. p. 805–15. [Google Scholar]
2. Hassaan MA, Nemr AE. Health and Environmental Impacts of Dyes: Mini Review. *American J Environ Sci Eng*. 2011;64–7. [Google Scholar]
3. Doble M, Kumar A. Biotreatment of Industrial Effluents. *Resour Conserv Recycl*. 2007;507–8. [Google Scholar]

# International Journal of Innovative Research in Science, Engineering and Technology

(A High Impact Factor, Monthly, Peer Reviewed Journal)

Website: [www.ijirset.com](http://www.ijirset.com)

Vol. 3, Issue 12, December 2014

4. Sala M, Gutiérrez-Bouzán MC. Electrochemical Techniques in Textile Processes and Wastewater Treatment. *Int J Photoenergy*. 2012. [Google Scholar]
5. Khan R, Bhawana P, Fulekar MH. Microbial decolorization and degradation of synthetic dyes: A review. *Rev Environ Sci Bio/Technol*. 2013;75–97. [Google Scholar]
6. Singh L, Singh VP. Textile Dyes Degradation: A Microbial Approach for Biodegradation of Pollutants. In *Microbial Degradation of Synthetic dyes in Waste waters, Environmental Science and Engineering*. Springer International Publishing; Switzerland; 2013. [Google Scholar]
7. Saratale RG, Saratale GD, Chang JS, Govindwar SP. Bacterial decolorization and degradation of azo dyes: A review. *J Taiwan Inst Chem Eng*. 2011;138–57. [Google Scholar]
8. Jafaria N, Soudib MR, Kasra-Kermanshahi R. Biodegradation Perspectives of Azo Dyes by Yeasts. *Microbiology*. 2013;484–97. [Google Scholar]
9. Vijayaraghavan K, Yun Y. A Study on Biosorption Potential of *Aspergillus* sp. of Tannery Effluent. *Adv Biosci Biotechnol*. 2013;266–91. [Google Scholar]
10. Wuhrmann K, Mechsner K, Kappeler T. Investigations on rate determining factors in the microbial reduction of Azo Dyes. *Eur J Appl Microbiol Biotechnol*. 1980;9:325–38. [Google Scholar]
11. Chang JS, Chou C, Lin Y, Ho J, Hu TL. Kinetic Characteristics of Bacterial Azo Dye Decolorization by *Pseudomonas luteola*. *Water Res*. 2001b;35:2041. [PubMed] [Google Scholar]
12. Chen KC, Huang WT, Wu JY, Houg JY. Microbial Decolorization of Azo Dye by *Proteus mirabilis*. *J Ind Microbiol Biotechnol*. 1999;23:686. [PubMed] [Google Scholar]
13. Kalyani DC, Telke AA, Dhanve RS, Jadhav JP. Ecofriendly Biodegradation and Detoxification of Reactive Red 2 Textile Dye by Newly Isolated *Pseudomonas* sp. *SUKI. J Hazard Mater*, 2008;163:735. [PubMed] [Google Scholar]
14. Sarayu K, Sandhya S. Aerobic biodegradation pathway for Remazol Orange by *Pseudomonas aeruginosa*. *Appl Biochem Biotechnol*, 2010;1241–53. [PubMed] [Google Scholar]
15. Lin J, Zhang X, Li Z, Lei L. Biodegradation of Reactive Blue 13 in a Two-Stage anaerobic/aerobic fluidized beds system with a *Pseudomonas* sp. isolate. *Bioresour Technol*. 2010;34–40. [PubMed] [Google Scholar]
16. Khandare RV, Govindwar SP. Microbial Degradation Mechanism of Textile Dye and Its Metabolic Pathway for Environmental Safety. Chandra R, editor. *Environmental Waste Management*. CRC Press; 2013. [Google Scholar]
17. Vimala G, Jeyakumar P, Devi C, Singh A, Iyer P. Azo Dye Degrading Bacteria from Textile Effluent. *Int J Curr Microbiol Appl Sci*. 2013;199–210. [Google Scholar]
18. Karim ME, Dhar K, Hossain MT. Decolorization of Textile Reactive Dyes by Bacterial Monoculture and Consortium Screened from Textile Dyeing Effluent. *J Genet Eng Biotechnol*. 2011;375–80. [PMC free article] [PubMed] [Google Scholar]
19. Khehra MS, Saini HS, Sharma DK, Chadha BS, Chimni SS. Decolorization of various azo dyes by bacterial consortium. *Dyes Pigments*. 2005;55–61. [Google Scholar]
20. Khalid T, Fatima A, Shafiq A, Javed S, Nadeem SG. Microbial Decolorization of Textile Effluent. *RADS J Biol Res Appl Sci*. 2011;28–34. [Google Scholar]
21. Moosvi S, Kher X, Madamwar D. Isolation, characterization and decolorization of textile dyes by a mixed bacterial consortium JW-2. *Dyes Pigments*. 2007;723–729. [Google Scholar]
22. Kumar NM, Saravanan D. Isolation of dye degrading bacteria from textile effluent. *J Chem Pharm Res*, 2013;2214–18. [Google Scholar]
23. Jadhav SU, Jadhav MU, Kagalkar AN, Govindwar SP. Decolorization of Brilliant Blue G Dye Mediated by Degradation of the Microbial Consortium of *Galactomyces geotrichum* and *Bacillus* sp. *J Chin Inst Chem Engrs*, 2008;39:563 [Google Scholar]
24. Sani RK, Banerjee UC. *Decolorization of Triphenylmethane Dyes and Textile and Dyestuff Effluent by Kurthia sp*, *Enzyme Microb Technol*. 1999;24:433. [Google Scholar]
25. Saratale RG, Saratale GD, Chang JS, Govindwar SP. Ecofriendly Decolorization and Degradation of Reactive Green 19A Using *Micrococcus glutamicus* NCIM-2168. *Bioresour Technol*. 2009c;110:3897 [PubMed] [Google Scholar]
26. Tony BD, Goyal D, Khanna S. Decolorization of Textile Azo Dyes by Aerobic Bacterial Consortium. *Int Biodeter Biodegr*. 2009a;63:462. [Google Scholar]
27. Tony BD, Goyal D, Khanna S. Decolorization of Direct Red 28 by Mixed Bacterial Culture in an Up-Flow Immobilized Bioreactor. *J Ind Microbiol Biotechnol*. 2009b;36:955. [PubMed] [Google Scholar]