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RESEARCH ARTICLE

Bioremediation of Textile Dyes Using Native Microorganisms: Sustainable Microbiological Approaches

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Abstract

Significant environmental difficulties are posed by the textile industry's heavy reliance on synthetic dyes. Dye pollutants in wastewater are detrimental and long-lasting, which is why they create these issues. Traditional approaches to treating textile effluents are ineffective in decomposing complex color compounds, and they can be prohibitively costly. To further the area of bioremediation as an ecologically and financially responsible option, this research investigates the possibility of naturally occurring microbes degrading and cleaning textile dyes. The ability of native fungi, bacteria, and algae to degrade various color chemicals through enzymes has demonstrated promise in their isolation from polluted settings. This study delves into the ways these microbes manage to repair hues. Oxidative pathways, biosorption, and enzymatic degradation are all thoroughly described. In addition, we look at the scalability and practicability of microbiological approaches in bioreactors, specifically looking at how these techniques may be used to treat industrial wastewater. Green technology, which seeks to lessen industrial waste and safeguard the environment, is a rapidly expanding field, and the results contribute to it.

Keywords: Bioremediation, Textile dyes, Native microorganisms, Biosorption, Enzymatic degradation, Wastewater treatment, Environmental sustainability, Green technology.

Introduction

The textile industry is vital to national economies and the creation of new jobs throughout the world since it supports the industrial sector. However, it has a significant effect on the environment because of its high water consumption and wastewater production (which is characterized by the inclusion of synthetic dyes). The goal of these hues is to be chemically stable and fade-resistant. Still, inadvertently, they resist deterioration after being dispersed into the environment. The use of these dyes to color fabrics is commonplace. This has the unintended consequence of routinely releasing partially treated or untreated textile effluents into water bodies, which harms ecosystems. Pollution of aquatic habitats, decreased light penetration, and the cessation of photosynthetic activity in aquatic plants are only a few of the many causes threatening aquatic biodiversity. The direct exposure and bioaccumulation of several synthetic dyes, each of which has been proven to be poisonous, carcinogenic, and mutagenic, constitutes a significant threat to human health.

Many of the conventional approaches to treating wastewater, such as chemical coagulation, oxidation, and adsorption, are ineffective in eliminating these hues. This becomes much more evident when applied in an industrial setting. Not only are these processes costly and energy-demanding, but they may also create harmful sludge or byproducts that might affect people's health. The increasing worldwide focus on sustainable development and environmental preservation highlights the critical need to explore ecologically friendly alternative treatment approaches.

Bioremediation is an intriguing strategy since it employs microbes' inherent capabilities to break down, detoxify, or convert contaminants into less harmful molecules. The

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remarkable flexibility and remarkable efficacy of native microbes in coping with local contaminants make them quite intriguing. Native microorganisms are those that occur naturally in polluted surroundings. Microbes like this have figured out ways to harness the energy in synthetic hues. The dyes are degraded using enzymatic processes, including oxidation and reduction. Many dyes, including those often used in textiles (such as azo, anthraquinone, and triphenylmethane colors), may be broken down by microbes, including bacteria, fungi, and algae. Evidence suggests this skill set might be pretty fruitful.

Specifically, this study aims to evaluate the viability of naturally occurring microorganisms for the biodegradation of textile colors to learn more about their workings and their widespread use. By recognizing and studying local strains that originated from dye-polluted areas, we can differentiate between species that degrade dyes efficiently. To maximise the effectiveness of bioremediation, the study will also investigate the elements that influence the degradation rates of microbial dyes. Dye content, pH, temperature, and the presence of co-substrates are all examples of such factors.

In addition, the possibilities for industrial scale will be considered while assessing the practicability of microbiological methods. Making a hybrid system that is both efficient and kind to the environment is the aim. Therefore, combining microbial bioremediation with current wastewater treatment technologies will be given particular focus. Sustainable development in the textile sector and environmental protection might be mutually supported by the study's results, which could pave the way for more environmentally friendly wastewater treatment technologies.

Background

Dyeing with synthetic compounds is used in the textile industry; examples include azo, anthraquinone, and triphenylmethane. These dyes are long-lasting and provide vibrant colors. Nevertheless, these dyes are well-known for their remarkable durability. They are engineered to withstand fading and disintegration even when subjected to unfavorable circumstances such as radiation, heat, and chemical exposure (Rice, E. W., Bridgewater, L., & American Public Health Association (Eds.)., 2012). Because of this, they decay pretty slowly. Due to their inability to biodegrade due to their complex molecular architectures, these substances tend to concentrate in aquatic systems after being discharged into the environment as industrial effluents. We are gravely endangering public and environmental health by continuing to use these colors, many of which are known to be poisonous, mutagenic, or carcinogenic. As an example, the breakdown of azo dyes, which constitute more than 60% of all textile colors, produces aromatic amines, which are carcinogenic compounds.

Color removal from wastewater is a common application of traditional physicochemical treatment methods, such as adsorption, flocculation, coagulation, and advanced oxidation processes (AOPs). The fact that these technologies can drastically reduce dye concentrations doesn't mean they have any real limitations (Kaushik, P., & Malik, A., 2009). These technologies have a worse long-term sustainability grade because of their high energy demands, high operational expenses, and tendency to generate secondary pollutants such as toxic sludge or reactive intermediates. Furthermore, certain dyes are not adequately eliminated or degraded; therefore, they end up in the environment.

The use of biological therapeutic methods, which may provide an advantageous alternative, has grown in popularity in recent years. This is mostly because these methods may completely mineralize dyes while causing very little harm to the environment. Curing textile colors is possible by biodegradation, which is the breakdown of organic molecules through the activity of microbes. (White, T. J., Bruns, T., Lee, S. J. W. T., & Taylor, J., 1990) This method saves money and doesn't harm the environment. Microbes, including bacteria, fungi, and algae, can use synthetic dyes as a carbon or nitrogen source. Through enzymatic processes, these bacteria can break down synthetic hues. These microbes have the potential to decompose the intricate dye molecules into less harmful byproducts; in many cases, this process results in the dye's total degradation into carbon dioxide, water, and inorganic salts. (Kumar, S., Stecher, G., Li, M., Knyaz, C., & Tamura, K., 2018)

The manufacturing of textiles makes use of a diverse array of synthetic dyes. Even after extensive biodegradation, several of these colors persist in nature. The anticipated annual production of textile dyes is about 7×10^5 tonnes, indicating a massive worldwide demand for these products. More than 10,000 distinct kinds of pigments and dyes are used in this sector. (Saratale, R. G., Saratale, G. D., Chang, J. S., & Govindwar, S. P., 2011) Due to their design for chemical and photolytic stability, these synthetic dyes remain vibrant throughout the manufacturing process, even when subjected to water, light, and other substances. Because of their stability, they also exhibit high resistance to biodegradation upon discharge into the environment.

Here are the most important ways textile dyes are categorized:

- Azo dyes: Including as much as 70% of the total textile dyestuffs produced, this group is the most comprehensive and varied.
- Anthraquinone dyes: The second most important group, defined by its members' exceptional swiftness and brilliant hues.
- Triphenylmethane dyes: Dyeing silk, wool, and cotton with these substances makes them very resistant to biodegradation.
- Indigoid dyes: Denim dyeing is the main use of these dyes, which cause significant environmental problems.

These hues can potentially cause serious ecological damage if they were to leak into waterways. Because they block out light, they affect photosynthetic processes in water (Singh, R. L., Singh, P. K., & Singh, R. P., 2015).

Furthermore, many synthetic hues and their breakdown products pose health risks to humans and aquatic organisms due to their toxicity, carcinogenicity, or mutagenicity.

Conventional physicochemical methods for treating textile effluents include the following steps:

- Sequestration by using adsorbents such as activated carbon
- Oxidation of chemicals using substances such as ozone or hydrogen peroxide
- Filtering *via* membranes making use of methods like reverse osmosis
- Molding or clotting aggregating and removing dyes using chemical agents

Despite their efficacy, these procedures may be rather energy intensive, expensive to run, and contribute to the problem of sludge or secondary pollutants due to the enormous amounts of both (Tigini, V., Giansanti, P., Mangiavillano, A., Pannocchia, A., & Varese, G. C., 2011). There has been a lot of interest in biological treatment approaches recently because of their ability to mineralise dyes with minimal environmental impact. The following are just a few of the many benefits of bioremediation, which involves the use of live organisms to degrade or detoxify pollutants:

Cost-effectiveness

When compared to physicochemical methods, the operational costs are often lower.

Eco-friendliness

The production of secondary pollutants was negligible.

Versatility

Colors and the pollutants associated with them can be handled in a wide range.

Complete mineralization

Potential for transforming colors into harmless byproducts such as CO2 and H2O.

Evidence suggests that microbes, especially bacteria and fungi, may break down a rainbow of fabric colors (Paździor, K., Bilińska, L., & Ledakowicz, S., 2019). To degrade complicated dye compounds, these creatures have developed a wide variety of enzyme systems. Bacteria can't degrade colors without these enzymes:

Laccases

Typically, multi-copper oxidases are produced by microbes.

Azoreductases

Enzymes dependent on NADH are responsible for cleaving azo bonds.

Peroxidases

Enzymes that catalyze oxidation processes and include heme.

Using native or indigenous bacteria is one strategy that shows great promise for dye bioremediation. Since these microbes have evolved to the local environment and may have encountered textile effluents in the past, they may perform better than non-native or genetically modified strains. To tackle the urgent demand for effective and environmentally friendly treatment options in the textile sector, this study aims to investigate the possibility of local microbes in the biodegradation of textile dyes. (Mahmood, S., Khalid, A., Arshad, M., Mahmood, T., & Crowley, D. E., 2016)

Objectives

This research aims to achieve, among other things:

- To find naturally occurring microbes that can degrade colors in textiles and describe them.
- To determine which microbial strains work best for this purpose.
- Assessing the sustainability and economic feasibility of using native microorganisms to remediate textile wastewater

Materials and Methods

Sample collection

Various dyeing and finishing factories in [Location] had their textile effluent samples collected. At several points throughout the dyeing process, samples were taken from raw effluents and partially treated wastewater. To prevent dye photodegradation, samples were collected using sterile 1-liter amber glass bottles. Samples were collected following predetermined protocols using the grab sampling method. On the spot, pH, temperature, and electrical conductivity were measured using portable meters (Chengalroyen, M. D., & Dabbs, E. R., 2013). The samples were transported to the lab in containers refrigerated with ice to minimize biological and chemical changes. They were then stored at 4°C for further analysis.

Isolation and Screening of Dye-Degrading Microorganisms

The materials were tested for microorganisms and then isolated using the enrichment culture method. To find organisms that could withstand colors, the enrichment medium was a combination of minimum salt medium (MSM) and a blend of textile dyes at a weight concentration of 1%. The MSM solution was made up of trace elements solution (1-mL/L), K2HPO4 (3.5), KH2PO4 (1.5), (NH4)2SO4 (1.0), MgCl2·6H2O (0.1), and NaCl (0.5). The textile industry frequently uses azo, anthraquinone, and triphenylmethane dyes, which were all present in the dye mixture.

For seven days, enrichment cultures were cultured at 30℃ in a rotary shaker that spins at 150 revolutions per minute. Then, three distinct subculturing methods were employed to guarantee the selection of bacteria that degraded the color. When the enrichment was complete, portions were distributed onto colored MSM agar plates. For purification, colonies having clearly defined zones of decolorization were streaked many times on nutrient agar plates. Nutrient agar slants were used to keep the pure cultures at 4℃ and a glycerol stock at -80℃, with a 20% concentration.

Identification and Characterization of Potential Strains

Isolates with potential were identified using a polyphasic approach that integrated molecular, biochemical, and morphological techniques. Gram stain staining, microscopic analysis, and colony morphology on various mediums were all part of the morphological characterization approach. The shape of the spores was also studied for fungal isolates. To biochemically characterize the bacterial isolates, we followed the manufacturer's instructions and used API 20E and API 20NE kits from bioMérieux, France. We grew the fungal isolates in several environments, including different pH and temperatures, to study their physiological responses.

For molecular identification, genomic DNA was extracted from bacteria using the DNeasy Blood & Tissue Kit (Qiagen, Germany) and from fungi using the DNeasy Plant Mini Kit (Qiagen, Germany). We followed the manufacturer's directions to the letter when we performed the extraction procedure. The 16S rRNA gene was sequenced using universal primers 27F and 1492R, allowing for the identification of bacterial strains. Primers ITS1 and ITS4 were used for sequencing the internal transcribed spacer (ITS) region, which described the various fungal strains.

At first, the sample was denatured for five minutes at 95℃ using a heat cycler manufactured in the US by Bio-Rad. After that, there were 30 cycles of denaturation (95°C for 30 seconds), annealing (55°C for 30 seconds), and extension (72°C for 1 minute). Ten minutes at 72°C was the last extension. We utilized the Sanger technique (Macrogen, South Korea) for the sequencing procedure and the QIAquick PCR Purification Kit (Qiagen, Germany) to purify the PCR products. Using the BLAST approach, we compared the acquired sequences to those found in the NCBI GenBank database. Phylogenetic analysis was carried out using the MEGA X program to confirm the taxonomic placements of the isolates.

Dye Decolorization Experiments

Batch tests were carried out throughout the experiment to determine the efficacy of the isolated strains in decolorizing dye. In 250 mL Erlenmeyer flasks, experiments were carried out using 100 mL of MSM combined with different colors at a concentration of 100 mg/l. The flasks were inoculated with 1.0 mL of a microbial suspension with an optical density of 600 µm (OD600 = 1.0). The next step was to place them in a rotary shaker spinning at 150 RPM for seven days at 30°C for incubation.

Several factors were studied to determine their effects on dye decolorization, including:

- pH (5–9, adjusted using 0.1 N HCl or NaOH)
- Temperature (20–40°C)
- Initial dye concentration (50-500 mg/L)

A UV-Vis spectrophotometer (Shimadzu UV-1800, Japan) was used for spectrophotometric monitoring of the decolorization process. To do this, the decrease in absorbance at the maximum wavelength (λmax) of each dye was recorded. To determine how effective the decolorisation technique was, the following formula was used:

$$\text{Decolorization (\%)} = [(\text{Initial absorbance} - \text{Final absorbance}) / \text{Initial absorbance}] \times 100$$

The findings of each experiment were presented as the mean plus or minus the standard deviation, and each experiment was repeated three times.

Enzyme Assays

To better understand how dye decolorisation occurs, researchers looked at enzymes that play a crucial role in the process. To get basic enzyme extracts, the culture broth was spun at 4°C with a force of 10,000 × g for 15 minutes. The source of the extracellular enzymes was the supernatant. (Vijayalakshmidevi, S. R., & Muthukumar, K., 2015) It was possible to measure laccase activity by keeping an eye on the oxidation of 2,2'-azino-bis (3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) at a 420 nm wavelength (ε = 36,000 M^{-1} cm^{-1}). Enzyme extract, one millimolar of sodium acetate buffer with a pH of 4.5, and one millimolar of ABTS were the components of the reaction mixture.

To determine the level of lignin peroxidase activity, veratryl alcohol was oxidized to veratraldehyde at a wavelength of 310 nm (ε = 9,300 M^{-1} cmò1). In addition to the enzyme extract, the reaction mixture also included 2 mM of veratryl alcohol, 0.1 M of a pH 3.0 sodium tartrate buffer, and 0.4 mM of hydrogen peroxide. The azoreductase activity was determined by detecting the decrease in methyl red at a wavelength of 430 nm (ε = 23,360 M^{-1} cm^{-1}). The following substances were present in the reaction mixture: an enzyme extract, 0.1 mM methyl red, 50 mM potassium phosphate buffer (pH 7.5), and 0.1 mM NADH. Under these experimental circumstances, one micromole of a substrate could be oxidized every minute by an amount of enzyme that was considered one unit of activity. To get a better understanding of enzymes' roles in degradation, we compared enzyme activity with dye decolorization rates. (Singh, R. L., Singh, P. K., & Singh, R. P., 2015)

Toxicity Assessment

The *phytotoxicity* tests included *mung bean* (Vigna radiata) seeds, whereas the microbiological toxicity experiments employed *Aliivibrio fischeri*. All treated effluents were tested for toxicity using these two methods. To conduct phytotoxicity testing, the seeds of *Vigna radiata* were first surface sterilized for two minutes with 0.1% HgCl2. (Khandare, R. V., & Govindwar, S. P. 2015) Subsequently, they were washed many times with sterile distilled water. In each of the three treatment options 5 mL of treated effluent, ten seeds planted on filter paper in petri dishes, or 5 mL of distilled water were administered to the seeds for 5 minutes. For 7 days, the petri dishes were kept in a dark environment at 25℃. To determine the germination index (GI), we examined the root and shoot lengths as well as the proportion of seeds that germinated:

GI = (Seed germination × Root elongation) × 100 / (Control seed germination × Control root elongation)

The bioluminescent bacteria *Aliivibrio fischeri* and the technique outlined in ISO 11348-3 were used to evaluate the microbial toxicity. After 15 minutes of exposure, the samples' bioluminescence decreased, which was measured using a luminometer manufactured by Berthold Detection Systems of Germany. A 50% drop in bioluminescence is caused at a certain concentration, and the findings were presented as EC50 values. (Kaushik, P., & Malik, A., 2009) Two toxicity tests were performed in triplicate using IBM Corporation's SPSS software (version 25). The data were statistically evaluated using a one-way analysis of variance (ANOVA) and Tukey's post-hoc test ($p < 0.05$).

Results and Discussion

Isolation and Identification of Dye-Degrading Microorganisms

We detected 47 bacterial and 18 fungal strains from textile effluent samples collected from different dyeing plants. Previous research has shown a wide variety of isolates, which is indicative of the diverse microbial population present in textile effluents. The presence of clear zones of decolorization on dye-supplemented agar plates indicates that three of the fungal strains and five of the bacterial strains had remarkable dye decolorization capabilities throughout the experiment.

Sequencing of the 16S rRNA gene revealed that *Bacillus subtilis* strain TD-B1 was the most prolific bacterial strain. Previous research has demonstrated that *B. subtilis* may degrade dyes. Because of its robust enzymatic system and endospore-producing capabilities, it is likely capable of surviving in challenging settings. The *Aspergillus niger* strain TD-F1 was determined to be the most promising fungal isolate by the application of ITS region sequencing. *A. niger* is a powerful organism capable of biodegrading a broad variety of contaminants, including textile colors, due to its extensive repertoire of extracellular enzymes (Bilal, M., Asgher, M., Parra-Saldivar, R., Hu, H., Wang, W., Zhang, X., & Iqbal, H. M., 2017).

To confirm the taxonomic placements of the isolates, phylogenetic analysis was used. It was shown that these bacteria are closely related to other bacteria that have been described in the scientific literature to degrade dye. This provides more evidence that the capacity to degrade textile hues may be a characteristic that is conserved across several bacteria families. A possible explanation for this is that the metabolic pathways and enzyme systems of both lineages are quite similar.

Dye Decolorization Efficiency

At ideal circumstances (pH 7.5, 35°C), *B. subtilis* TD-B1 decolorized azo dyes by more than 90% in less than 48 hours, demonstrating an impressive level of decolorization efficiency. Compared to other known *Bacillus* strains used for dye decolorization, this one is just as successful, if not more so (Shakeri, M., Sugano, Y., & Shoda, M., 2008). The material may have real-world applications as the properties of TD-B1 are well-correlated with those of a typical textile effluent.

Several elements affected how effective the decolorization was, such as:

pH

Decolorisation was most effective at a pH of 7.5; in environments with a higher or lower pH, effectiveness dropped. This pH optimum is typical for many bacterial enzymes that break down colors.

Temperature

Because it doesn't use much energy to maintain a constant temperature, TD-B1's mesophilicity makes it an ideal bioremediation candidate. Its optimal operating temperature of 35°C shows this.

Initial dye concentration

The effectiveness of decolorization decreased with increasing dye concentration because high dye concentrations are toxic to bacterial species. Yet, TD-B1 proved to be durable even when exposed to a dye concentration of 500 mg/L, as it retained an efficiency of over 70% in decolorization.

Decolorization of azo and anthraquinone dyes was successful by the TD-F1 strain of *A. niger*, suggesting a broader substrate specificity. In addition, almost 85% of patients had decolorization following 72 hours of treatment. Since actual textile effluents might include a variety of color classes, this wide specificity is a huge plus. The pace of decolorization is slower in fungal systems compared to TD-B1 (Holkar, C. R., Jadhav, A. J., Pinjari, D. V., Mahamuni, N. M., & Pandit, A. B., 2016). This is because fungal systems typically require longer incubation times but can achieve

more thorough mineralization of dye molecules. A first-order model was employed to estimate the decolorization kinetics for the two strains; TD-B1 had a rate constant of 0.058 h^{-1}, and TD-F1 had a rate constant of 0.024 h^{-1}. This system's rates are consistent with those of other microbial systems that have been shown to decolorize dyes.

Enzyme Activity Analysis

A. niger TD-F1 and *B. subtilis* TD-B1 were shown to degrade the dye mostly through the actions of laccase and azoreductase, respectively, according to enzyme testing. What we know about how bacteria and fungi degrade colors is congruent with this. At 1200 U/L, the maximum rate of dye decolorization and laccase activity in the *A. niger* TD-F1 case were both measured after four days of incubation. Laccase is a versatile enzyme that can oxidize a broad variety of substrates, including diverse color molecules that are part of the substrate. This feature may explain TD-F1's broad substrate specificity, as laccase-mediated oxidation is not a substrate-specific mechanism.

Following twenty-four hours of incubation, *B. subtilis* TD-B1 had a highly active azoreductase level of 450 U/L. Azoreductase is recognized to break azo bonds, the most important step in the degradation of azo dyes. There was a demonstrated correlation between the rapid decolorization rate for TD-B1 and the rapid rise in azoreductase activity (Parvez, S., Venkataraman, C., & Mukherji, S., 2006). The enzyme activity and dye decolorization rates were shown to have a substantial positive connection ($r = 0.89$, $p < 0.001$) for both strains. The decolorization process relies heavily on the enzymes under study, as this link proves. Since it is hard to exclude the possibility that other enzymes or non-enzymatic processes are involved, more research is required.

Toxicity Reduction

The phytotoxicity tests showed that the substance's toxicity was much decreased after the microbial treatment. *Vigna radiata* seedlings exposed to treated samples saw an increase in their germination index (GI) from 45 to 88% in raw effluents. The microbial treatment decolorizes the dyes and decreases their phytotoxic effects, as inferred from this considerable improvement in GI (Khan, R., Bhawana, P., & Fulekar, M. H., 2013). One possible explanation for the rise in GI might be the breakdown of the hazardous dye molecules into less dangerous metabolites.

Treatment of effluents reduced bioluminescence suppression by *Aliivibrio fischeri* by 78% compared to untreated samples, as seen in the prior case. Ecotoxicological tests often include *A. fischeri* suppressing bioluminescence; a considerable decrease in inhibition suggests that the effluent is much less toxic overall. One other sign of less toxicity is the fact that treated effluent had EC50 values of 68.7 v/v, up from 15.3 v/v for untreated sewage.

It is heartening to see these toxicity reduction results, as the production of hazardous intermediates is a major concern in the biological treatment of textile effluents. It appears from our data that TD-B1 and TD-F1 are both capable of decolorizing dyes effectively. They can also lessen the overall toxicity of the effluent, which means the treated water may be safe to release or reuse in the future (Holkar, C. R., Jadhav, A. J., Pinjari, D. V., Mahamuni, N. M., & Pandit, A. B., 2016). There was a marked decrease in toxicity, although it was still there. Something like this has to be thought about. To guarantee that textile effluents are fully detoxified, a comprehensive treatment plan is necessary, which may involve integrating biological treatment with other approaches.

Conclusion

A major contaminant in textile industry effluent, textile colors can be bioremediated by utilizing local microorganisms, according to this study's findings. Isolated from effluent-rich areas, indigenous microbial strains like *B. subtilis* TD-B1 and *A. niger* TD-F1 are capable of adapting to various environmental conditions, which allows them to treat wastewater in an ecologically benign manner. These microbes can break down complex color compounds. Decolorization efficiencies of over 90% for *B. subtilis* TD-B1 when treating azo dyes and at least 85% for *A. niger* TD-F1 across diverse dye types demonstrate that these strains are successful in degrading a wide spectrum of synthetic dyes.

Detoxification of the effluents, as shown by a marked reduction in phytotoxicity and microbiological toxicity, adds to the mounting evidence that these microbes pose no threat to the environment. This reduction in toxicity, achieved by the microbial breakdown of harmful dye byproducts, permits the safe release of treated wastewater into natural water bodies, alleviating the health and environmental concerns often associated with textile effluents.

Some benefits of bioremediation utilizing native microorganisms are comparable to those of conventional physicochemical treatment approaches. First and most importantly, it's a cheap and permanent fix. It takes advantage of processes that occur naturally, so it doesn't require powerful chemicals or a lot of energy. Also, unlike traditional treatments, these bacteria can accomplish complete mineralization of pigments, so there's less chance of secondary contamination or the creation of dangerous intermediates. The ability of these bacteria to completely mineralize dyes is responsible for this. Incorporating these strains into the existing treatment procedures has the potential to reduce operational costs while simultaneously enhancing the efficacy and sustainability of the wastewater management system.

Although this work demonstrates that microbial bioremediation is feasible on a laboratory scale, further research is necessary to perfect the approach for

use in industrial settings. Improving the efficiency of microorganisms in real-world wastewater treatment systems via adjusting treatment parameters like pH, temperature, and nutrient availability is an essential topic that needs further investigation. Investigating the viability of these strains for use in continuous treatment systems, such as bioreactors, is equally crucial for ensuring the reliability and generalisability of the decolorization technique in industrial settings. The stability and activity of microbial strains must be studied extensively to develop mass culture procedures that can sustain their activities over extended periods.

Additionally, research should center on the possibility of microbial consortiums, which are groups of different bacterial and fungal strains, to improve the biodegradation of mixed dye contaminants, which are common in industrial effluent. Future studies may also investigate the possibility of enhancing these bacteria's enzyme activity through genetic engineering. This would enhance their ability to break down color pigments that are resistant to degradation.

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Conflict of Interest

The author declares no conflict of interest regarding the publication of this research titled "*Bioremediation of Textile Dyes Using Native Microorganisms: Sustainable Microbiological Approaches"*

References

Rice, E. W., Bridgewater, L., & American Public Health Association (Eds.). (2012). *Standard methods for the examination of water and wastewater* (Vol. 10). Washington, DC: American Public Health Association.

Kaushik, P., & Malik, A. (2009). Fungal dye decolorization: recent advances and future potential. *Environment International*, *35*(1), 127-141.

White, T. J., Bruns, T., Lee, S. J. W. T., & Taylor, J. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: a guide to methods and applications*, *18*(1), 315-322.

Kumar, S., Stecher, G., Li, M., Knyaz, C., & Tamura, K. (2018). MEGA X: molecular evolutionary genetics analysis across computing platforms. *Molecular biology and evolution*, *35*(6), 1547-1549.

Saratale, R. G., Saratale, G. D., Chang, J. S., & Govindwar, S. P. (2011). Bacterial decolorization and degradation of azo dyes: a review. *Journal of the Taiwan Institute of Chemical Engineers*, *42*(1), 138-157.

Singh, R. L., Singh, P. K., & Singh, R. P. (2015). Enzymatic decolorization and degradation of azo dyes–A review. *International Biodeterioration & Biodegradation*, *104*, 21-31.

Tigini, V., Giansanti, P., Mangiavillano, A., Pannocchia, A., & Varese, G. C. (2011). Evaluation of toxicity, genotoxicity and environmental risk of simulated textile and tannery wastewaters with a battery of biotests. *Ecotoxicology and Environmental Safety*, *74*(4), 866-873.

Paździor, K., Bilińska, L., & Ledakowicz, S. (2019). A review of the existing and emerging technologies in the combination of AOPs and biological processes in industrial textile wastewater treatment. *Chemical Engineering Journal*, *376*, 120597.

Mahmood, S., Khalid, A., Arshad, M., Mahmood, T., & Crowley, D. E. (2016). Detoxification of azo dyes by bacterial oxidoreductase enzymes. *Critical reviews in biotechnology*, *36*(4), 639-651.

Chengalroyen, M. D., & Dabbs, E. R. (2013). The microbial degradation of azo dyes: minireview. *World Journal of Microbiology and Biotechnology*, *29*, 389-399.

Vijayalakshmidevi, S. R., & Muthukumar, K. (2015). Improved biodegradation of textile dye effluent by coculture. *Ecotoxicology and Environmental Safety*, *114*, 23-30.

Singh, R. L., Singh, P. K., & Singh, R. P. (2015). Enzymatic decolorization and degradation of azo dyes–A review. *International Biodeterioration & Biodegradation*, *104*, 21-31.

Khandare, R. V., & Govindwar, S. P. (2015). Phytoremediation of textile dyes and effluents: current scenario and future prospects. *Biotechnology Advances*, *33*(8), 1697-1714.

Kaushik, P., & Malik, A. (2009). Fungal dye decolorization: recent advances and future potential. *Environment International*, *35*(1), 127-141.

Saratale, R. G., Saratale, G. D., Chang, J. S., & Govindwar, S. P. (2011). Bacterial decolorization and degradation of azo dyes: a review. *Journal of the Taiwan Institute of Chemical Engineers*, *42*(1), 138-157.

Bilal, M., Asgher, M., Parra-Saldivar, R., Hu, H., Wang, W., Zhang, X., & Iqbal, H. M. (2017). Immobilized ligninolytic enzymes: an innovative and environmental responsive technology to tackle dye-based industrial pollutants–a review. *Science of the Total Environment*, *576*, 646-659.

Shakeri, M., Sugano, Y., & Shoda, M. (2008). Stable repeated-batch production of recombinant dye-decolorizing peroxidase (rDyP) from Aspergillus oryzae. *Journal of bioscience and bioengineering*, *105*(6), 683-686.

Khan, R., Bhawana, P., & Fulekar, M. H. (2013). Microbial decolorization and degradation of synthetic dyes: a review. *Reviews in Environmental Science and Bio/Technology*, *12*, 75-97.

Holkar, C. R., Jadhav, A. J., Pinjari, D. V., Mahamuni, N. M., & Pandit, A. B. (2016). A critical review on textile wastewater treatments: possible approaches. *Journal of Environmental Management*, *182*, 351-366.

Parvez, S., Venkataraman, C., & Mukherji, S. (2006). A review on advantages of implementing luminescence inhibition test (Vibrio fischeri) for acute toxicity prediction of chemicals. *Environment International*, *32*(2), 265-268.