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Evaluating the ecophysiological response of marine fungi to textile dye degradation potential

S. Sathya*[1], G. Kanimozhi[1], A. Panneerselvam[2]

[1]*P. G. & Research Department of Microbiology, A. V. V. M. Sri Pushpam College (Autonomous), Poondi-613503, (Affiliated to Bharathidasan University, Trichy-24), Thanjavur, Tamil Nadu, India*

[2]*Indian Biotrack Research Institute, Thanjavur-613005, Tamil Nadu, India*

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ABSTRACT

This study investigated the diversity, distribution and dye decolorization potential of marine fungi isolated from soil and water samples collected at Andikkadu and Sarabendrajanpattinam. Fungal enumeration using serial dilution and Potato Dextrose Agar (PDA) revealed that Sarabendrajanpattinam exhibited higher fungal abundance and species richness than Andikkadu likely due to favorable environmental conditions. A total of 12 fungal species were identified, with *Aspergillus fumigatus*, *A. flavus*, *Penicillium brevicompactum*, and *Trichoderma viride* being common across all samples. Site-specific occurrences of species such as *Aspergillus citrisporum* and *Cladosporium* sp. highlighted localized environmental influences on fungal distribution. The decolorization potential of the fungal isolates was evaluated against increasing concentrations (25–100 µL) of textile dye. *T. viride*, *Cladosporium* sp., and *Curvularia lunata* showed strong tolerance and maintained high decolorization efficiency, whereas other species exhibited limited activity at higher dye levels. A one-way ANOVA revealed a significant effect of dye concentration on fungal growth ($F = 3.53$, $p = 0.0247$), indicating reduced viability at elevated effluent levels. Multivariate regression analysis showed that colour was removed positively correlated with fungal biomass (VSS; $\rho = 0.76$, $p = 0.049$), while growth was negatively impacted by nickel concentration ($\rho = 0.79$, $p = 0.048$). These findings suggest that marine fungi, particularly *T. viride*, possess potential for use in textile dye bioremediation under environmentally stressed conditions.

***Corresponding author:** S. Sathya ✉ sathyasuresh.ssb@gmail.com

INTRODUCTION

Environmental pollution, a pressing global challenge, significantly threatens the Earth's ecosystems and quality of life due to industrialization, population growth, and rapid development in both developed and developing nations. Major pollution sources include industrial discharges, improper use of fertilizers, insecticides, pesticides, mining operations, and sewage sludge, contributing to both biodegradable and non-biodegradable pollutants.

Non-biodegradable pollutants such as heavy metals, pesticides, polyaromatic hydrocarbons, and radionuclides, pose severe environmental risks due to their persistence (Peng *et al.*, 2008). While traditional physico-chemical treatment methods like sedimentation, filtration, and oxidation are effective, their high costs and complexity limit large-scale application, highlighting the urgent need for sustainable, cost-effective solutions. Microbial bioremediation particularly using fungi, has emerged as a promising approach, with fungi demonstrating remarkable potential in degrading high molecular weight compounds into less toxic substances (Akcil *et al.*, 2015; Deshmukh *et al.*, 2016).

Environmental pollution degrades the physical, chemical, and biological quality of ecosystems, with untreated industrial wastewater being a primary contributor (Mosley *et al.*, 2014; Ferguson *et al.*, 2020). In developing countries, industries often release untreated effluents due to the prohibitive costs of conventional treatments, exacerbating environmental damage. In Salem, Tamil Nadu, rapid industrialization and urbanization have severely impacted forest cover, agricultural lands, and water resources, particularly polluting the Cauvery River and groundwater in areas like Hasthampatti, Kondalampati, and Chinnaseeragapadi (Krishnaraj *et al.*, 2015). Similarly, in Tirupur, textile and dyeing industries have led to elevated levels of chlorides, sulfates, dissolved solids, oil, and grease in surface water, rendering it unfit for use (Jayanth *et al.*, 2011). Groundwater in Tirupur and nearby areas shows significant deviations in total alkalinity, hardness, calcium, magnesium, chloride, and salinity, largely due to urbanization and agricultural practices (Sathya *et al.*, 2025; Geetha *et al.*, 2008; Selvakumar *et al.*, 2017; Arulbalaji and Gurugnanam, 2017).

Conventional treatment methods, including neutralization, coagulation, flocculation, reverse osmosis, and phytoremediation, face challenges due to their environmental impact and the toxic, teratogenic, carcinogenic, and allergenic nature of pollutants, which also inhibit microbial, plant, and animal growth (Anjaneyulu *et al.*, 2005; Bansal and Goyal, 2005; Kaushik and Malik, 2009; Roy *et al.*, 2010).

Marine fungi, thriving in diverse oceanic niches as parasites, saprobes, or symbionts, offer significant bioremediation potential. Extracted from sediment, seawater, mangroves, and other marine sources, these fungi produce pharmacological metabolites, enzymes, and biosurfactants, with applications in antibacterial, antiviral, anticancer, and environmental remediation processes (Wang *et al.*, 2012; Imhoff, 2016; Bovio *et al.*, 2019). Their tolerance to heavy metals like copper and lead, along with their ability to degrade dyes and hydrocarbons, makes them ideal for bioremediation (Gazem and Nazareth, 2013; Bonugli-Santos *et al.*, 2015). Mycoremediation, the use of fungi for pollutant degradation, leverages their unique traits, such as resilience to extreme conditions, high surface area-to-volume ratio, mycelial growth, and production of extracellular ligninolytic enzymes like peroxidase and cytochrome P450, which facilitate detoxification (Khan *et al.*, 2019; Durairaj *et al.*, 2015; Divya *et al.*, 2014).

This study focuses on assessing the pollution load of textile industry effluents in Tirupur, Tamil Nadu, by analyzing their physicochemical parameters and exploring fungal bioremediation. Fungal strains isolated from effluents demonstrated effective dye decolorization, and their biomass was used to synthesize extracellular silver nanoparticles (AgNPs), characterized for antibacterial and dye degradation capabilities. Notably, this research pioneers the

repurposing of residual fungal biomass as a biosorbent for removing reactive dyes from synthetic wastewater, addressing a critical gap in the literature. Previous studies in Tirupur have provided only preliminary groundwater quality assessments, with limited focus on textile effluent impacts or fungal applications in dye degradation (Gola and Tyagi, 2021). By integrating AgNP synthesis, dye degradation, and biomass reuse, this study offers an innovative, eco-friendly approach to mitigate industrial pollution, reduce waste, and enhance contaminant uptake in wastewater treatment systems, paving the way for sustainable bioremediation strategies.

MATERIALS AND METHODS

Isolation of marine fungi

The soil and water samples were obtained from two locations, Andikkadu and Sarabendrarajanpattinam, in Tamil Nadu, India. These samples underwent dilution at 10 and 100 times with autoclaved filtered seawater (0.22 µm). From each marine soil and water sample, 200 ml aliquots were distributed onto PDA plates. Prevented bacterial growth, the antibiotics streptomycin was incorporated into each agar plate at final concentrations of 100 and 50 mg^{-1}, respectively. Each sample was represented by replicate agar plates. Following a two day incubated period at 27°C, the inoculated agar plates were inspected daily for the emergence of fungal hyphae, utilizing a dissecting microscope set at 20 × magnifications. Subsequently, distinct fungal colonies observed on the agar plates were transferred to new agar plates for isolation and purification (Xiong *et al.,* 2009).

Identification of the fungal isolates

Micromorphology was examined through the application of lacto phenol cotton blue staining. All isolates were classified at the genus level, relying on mycelial morphology (Lu *et al.,* 2012). The impact of salt concentration on the growth of the isolated fungi was assessed (Joshi *et al.,* 2008). The selected fungi were cultivated in PDA Broth with salt respectively. The incubated at 28°C for 4-5 days, the relative levels of fungal growth under specific conditions were evaluated.

Collection of textile effluent

Textile effluent was gathered from a textile processing industries situated in Karur. The effluent was stored in sterile plastic containers, transported to the laboratory, and maintained at 4°C until required. Before preparing the media, the effluent underwent filtration using Whatman No. 1 filter paper to eliminate particulate matter. The filtered effluent was then sterilized through autoclaving at 121°C for 15 minutes.

Preparation of potato dextrose agar (PDA) base medium

Potato infusion was created by boiling 200 g of peeled potatoes in 1 L of distilled water for 30 minutes, followed by filtration. To the resulting filtrate, 20 g of dextrose and 20 g of agar were incorporated. The medium was adjusted to a total volume of 1000 mL with distilled water and autoclaved at 121°C for 15 minutes (Juárez Hernández *et al.,* 2021).

Preparation of effluent-amended PDA plates

Following autoclaving and cooling the PDA medium to approximately 45–50°C, textile effluent was introduced in four distinct concentrations of 25 µL, 50 µL, 75 µL, and 100 µL into separate batches of PDA, along with a control batch that contained no effluent. Each mixture was gently swirled to ensure the even distribution of effluent and then poured into sterile Petri plates under aseptic conditions (Blánquez *et al.,* 2008).

Fungal inoculation

Fungal isolates were chosen based on previous identification and were cultured on fresh PDA plates. A 5 mm diameter mycelial disc was excised from the actively growing edge and positioned at the center of each experimental plate. Each treatment, was conducted in triplicate and control also maintained. All inoculated plates were incubated at 28 ± 2°C for duration of 5–7 days. The result were recorded every 24 hours and observed properly respectively.

Assessment of fungal growth and sustainability

Radial growth, measured as colony diameter, was assessed in two perpendicular directions. Morphological characteristics such as pigmentation,

surface texture, margin shape, and sporulation were documented. A comparison of fungal growth across various effluent concentrations was conducted to ascertain tolerance and sustainability (Modi *et al.,* 2025; Darwesh *et al.,* 2023).

Data analysis

The data were statistically analyzed using mean ± standard deviation. ANOVA was utilized to assess the significance of growth differences among the effluent concentrations. A graphical representation, such as a bar graph, was employed to illustrate the relationship between fungal growth and effluent concentration.

RESULTS

Marine samples were gathered from Andikadu and Sarabendrajanpattinam, with fungal isolates extracted from both soil and water utilizing the serial dilution method at dilution factors of 10^{-3}, 10^{-4}, and 10^{-5}. The enumeration of fungal colonies was conducted following incubation on Potato Dextrose Agar (PDA) plates. At Andikadu, the soil sample yielded 16, 6, and 3 colonies at the dilutions of 10^{-3}, 10^{-4}, and 10^{-5} respectively, culminating in a total colony count of 25. Conversely, the water sample from the same location demonstrated a slightly elevated fungal presence, with 18, 7, and 3 colonies across the identical dilutions, resulting in a total of 28 colonies. In contrast, Sarabendrajanpattinam displayed a markely higher fungal load. The soil sample generated 55, 19, and 8 colonies at the respective dilutions, leading to a total of 82 colonies. The water sample was similarly substantial, with 42, 18, and 8 colonies, aggregating to a total of 68 colonies. These findings suggest that Sarabendrajanpattinam supports a more abundant fungal population in both soil and water compared to Andikadu, likely attributable to environmental or nutrient factors present in that coastal region (Table 1).

Table 1. Isolation of fungi from marine samples

Name of the area	Soil				Water			
	Dilution factors							
	10^{-3}	10^{-4}	10^{-5}	Total no. of colonies	10^{-3}	10^{-4}	10^{-5}	Total no. of colonies
Andikadu	16	06	03	25	18	07	03	28
Sarabendrajanpattinam	55	19	08	82	42	18	08	68

Table 2. Identification of fungi from marine samples

SL	Name of the fungi	Different concentration of textile dye (µg/ml)				
		Control	25µl	50µl	75µl	100µl
1	*Aspergillus citrisporum*	07.15±0.00	05.35±0.00	04.47±0.00	04.34±0.03	02.31±0.00
2	*A. fischeri*	06.40±0.00	05.13±0.12	04.32±0.00	03.42±0.05	01.04±0.07
3	*A. flavus*	05.42±0.00	04.33±0.03	04.20±0.02	03.70±0.00	-
4	*A. fumigatus*	07.31±0.00	-	-	-	-
5	*Cladosporium herbarum*	06.48±0.00	04.36±0.42	03.62±0.20	03.04±0.00	-
6	*Cladosporium* sp	07.23±0.11	06.52±0.04	05.62±0.12	04.62±0.03	04.20±0.01
7	*Curvularia geniculata*	05.67±0.02	05.07±0.01	04.47±0.11	-	-
8	*C. lunata*	09.72±0.33	08.52±0.08	05.53±0.12	04.42±0.07	03.63±0.00
9	*Pencillium asperum*	05.35±0.02	04.50±0.04	03.23±0.04	03.06±0.12	-
10	*P. brevicompactum*	04.82±0.13	-	-	-	-
11	*P. janthinellum*	05.52±0.02	04.33±0.00	03.72±0.02	-	-
12	*T. viride*	09.76±0.04	09.42±0.11	09.02±0.14	08.45±0.02S	07.62±0.04

The values were expressed by Mean ± Standard deviation

Twelve species of fungi were isolated from marine soil and water samples obtained from Andikkadu and Sarabendrajanpattinam. In total, 25 colonies and 10 species were identified from the soil sample at Andikkadu, whereas 82 colonies and 12 species were isolated from the soil at Sarabendrajanpattinam. Regarding the water samples, 28 colonies (10 species) were recorded from Andikkadu, and 67 colonies (11 species) were recorded from Sarabendrajanpattinam.

A total of 12 fungal species were identified across the four sample categories. Among these, *Aspergillus fumigatus, A. flavus, Pencillium brevicompactum*, and *Trichoderma viride* were the most frequently encountered, being found in both soil and water samples at both sites. The species richness, defined as the number of distinct species, also varied by location: Andikkadu Soil: 10 species, Sarabendrajanpattinam Soil: 12 species, Andikkadu Water: 10 species and sarabendrajanpattinam Water: 11 species.

Table 3. Screening of marine fungi by different concentration of textile effluent

SL	Name of the fungi	Soil samples		Water samples	
		Andikkadu	Sarabendrarajanpattinam	Andikkadu	Sarabendrarajanpattinam
1	*Aspergillus citrisporum*	-	07	-	06
2	*A. fischeri*	05	02	03	02
3	*A. flavus*	04	04	03	08
4	*A. fumigatus*	05	10	05	11
5	*C. herbarum*	02	07	02	08
6	*Cladosporium* sp	-	06	-	05
7	*Curvularia geniculata*	03	10	01	04
8	*C. lunata*	02	05	02	-
9	*Pencillium asperum*	03	07	02	06
10	*P. brevicompactum*	05	09	05	05
11	*P. janthinellum*	03	06	01	05
12	*Trichoderma viride*	03	10	04	07
Total number of colonies		25	82	28	67
Total number of species		10	12	10	11

Cladosporium sp. was exclusively found in Sarabendrajanpattinam samples, whereas *C. lunata* was not detected in the Sarabendrajanpattinam water sample, suggesting site-specific distribution patterns that may be influenced by local environmental factors.

Aspergillus citrisporum was isolated solely from Sarabendrajanpattinam (7 colonies in soil and 6 in water), and was absent from Andikkadu. *A. fischeri* was present in all samples, but was more abundant in Andikkadu soil (5 colonies). *Trichoderma viride* exhibited a broad ecological tolerance, with colony counts ranging from 3 to 10 across all environments.

Cladosporium herbarum and *Curvularia geniculata* were more common in Sarabendrajanpattinam, with 7–10 colonies compared to only 1–3 in Andikkadu (Table 2).

The cumulative results clearly indicate that Sarabendrajanpattinam supports a richer and denser fungal community in both marine soil and water environments. This may be due to various factors such as sediment composition, organic pollution, salinity gradients, or microclimatic conditions that promote fungal survivability and proliferation.

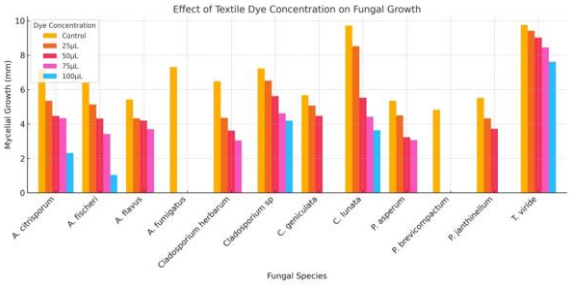

Fig. 1. Assessment of fungal growth and sustainability by textile effluent

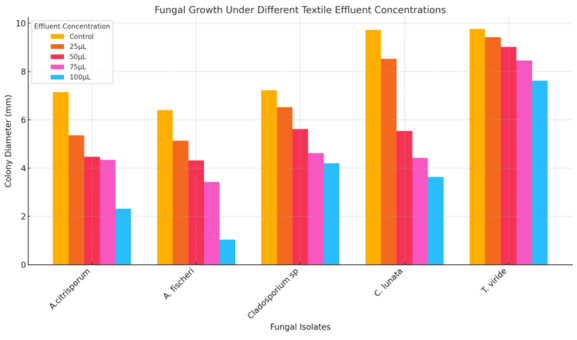

Fig. 2. Efficient fungi growth and sustainability against textile effluent

The decolorization efficiency of various marine fungal isolates was assessed against different concentrations (25–100 µl) of textile dye (Fig. 1). Among the tested fungi, *T. viride* showed the highest tolerance and

decolonization potential, maintaining activity across all concentrations, with a gradual decrease from 9.76 ± 0.04 (control) to 7.62 ± 0.04 at 100 µl. *Cladosporium* sp. and *Curvularia lunata* also exhibited strong dye tolerance, retaining notable decolorization at higher concentrations. In contrast, isolates such as *A. fumigatus*, *P. brevicompactum*, and *C. geniculata* showed limited or no activity at elevated dye levels.

Overall, the results suggest that *T. viride*, *C. lunata*, and *Cladosporium sp.* are promising candidates for textile dye bioremediation (Table 3; Fig. 2).

ANOVA

The impact of textile effluent on fungal viability, twelve fungal isolates were grown on Potato Dextrose Agar (PDA) amended with varying concentrations of textile dye effluent (25 µL, 50 µL, 75 µL, and 100 µL) were evaluvated. Colony diameters were measured after incubation and compared with control (unamended PDA). A one-way Analysis of Variance (ANOVA) was performed on the subset of fungi that showed complete growth data across all concentrations. The ANOVA revealed a statistically significant difference in fungal growth across the different effluent concentrations ($F = 3.53$, $p = 0.0247$), indicated that the textile effluent concentrations had a significant effect on fungal sustainability. These results suggested that while certain fungi (e.g., *Trichoderma viride*, *Cladosporium* sp.) maintained relatively better growth under higher effluent concentrations, the overall trend demonstrated a negative correlation between effluent concentration and fungal viability.

DISCUSSION

In the current investigation, twelve fungal isolates were obtained from Andikadu and Sarabendrajanpattinam, identified based on their morphological characteristics and slide view. *A. citrisporum* and *Cladosporium* sp. were exclusively found in Sarabendrajanpattinam, in both marine soil and marine water samples. Conversely, *C. lunata* was absent in the marine water sample from Sarabendrajanpattinam, although it was present in the soil sample. *A. fumigatus* and *T. viride* exhibited a higher number of colonies compared to the other isolates.

The fungal isolates belonged to the genera *Cladosporium* sp., *Curvularia* sp., *Penicillium* sp., and *Trichoderma* sp. Among the two locations, the soil sample from Sarabendrajanpattinam demonstrated the highest abundance of fungal populations. (Surajit *et al.,* 2009) reported a total of ninety fungal colonies isolated, numbered DSF225.1 to DSF225.84 (DSF - Deep Sea Fungi), and identified. *Aspergillus* was identified as the dominant genus, comprising 33%, followed by *Penicillium* at 13%, *Lulworthia* at 8%, others at 40%, and non-sporulating fungi at 6%. *Deuteromycotina* was the most prevalent group, contributing 72%, followed by *Ascomycotina* at 20% and *Basidiomycotina* at 2%. Our current study also corroborates that *Aspergillus* was the most abundant species in the Parangipettai area. (Parveen *et al.*, 2011) investigated the diversity of fungi in the Mahanadi River, located in India. A total of 31 fungal species were identified, with *Aspergillus niger* Tiegh. being the most notable. In a separate study conducted in 2016, 8 fungal genera were isolated from Masturah, Saudi Arabia, including *Aspergillus, Penicillium, Thielavia, Fusarium, Emericella, Cladosporium, Scytalidium* and *Alternaria* (Alwakeel, 2017).

The present investigation assessed the decolorization capabilities of various marine fungal isolates in response to increasing concentrations of textile dye, uncovering varying levels of tolerance and effectiveness among the strains examined. Significantly, *Trichoderma viride* was identified as the most resilient isolate, demonstrating substantial decolorization activity even at the maximum dye concentration (100 µl). The observed gradual reduction in activity from 9.76 ± 0.04 (control) to 7.62 ± 0.04 indicates that while the stress from the dye affected its performance, *T. viride* managed to preserve its enzymatic or metabolic functionality under challenging conditions.

This finding is consistent with previous studies that emphasize *T. viride's* enzymatic flexibility and robustness in contaminated environments. *Cladosporium* sp. and *Curvularia lunata* also exhibited significant dye tolerance, maintaining considerable decolorization potential at higher concentrations. Their ability to operate under such stress may be linked to their production of oxidative enzymes such as laccases and peroxidases, which are recognized for their role in degrading complex dye compounds. The efficacy of these fungi positions them as promising candidates for bioremediation efforts, especially in settings tainted by textile waste. Conversely, isolates like *Aspergillus fumigatus, Penicillium brevicompactum,* and *Chaetomium geniculata* showed minimal or no decolorization activity at elevated dye concentrations. This sensitivity may be attributed to toxicity induced by the dye, which could adversely affect fungal metabolism or enzyme synthesis. These findings highlight the necessity of selecting fungi not only based on their overall biodegradation potential but also their ability to withstand chemically challenging conditions commonly found in industrial wastewater.

Overall, the results indicated that specific marine-derived fungi, notably *T. viride, C. lunata,* and *Cladosporium* sp., exhibit promising characteristics for use in sustainable and efficient textile dye bioremediation. Future research should focus on elucidating the particular enzymatic mechanisms at play, optimizing growth conditions to achieve maximum dye degradation, and evaluating performance in actual effluent systems. Microbial cells extracted from industrial effluents have been investigated for potential biotechnological applications.

According to (Khokhar *et al.*, 2012), an isolate of the species *Trichoderma viride*, obtained from a textile effluent, demonstrated hydrolytic activity in culture media enriched with CMC, highlighting its cellulolytic capabilities. Imran *et al.*, 2018 characterized the production of a commercial cellulose derived from *Aspergillus niger* IMMIS1. In this study, the authors isolated twenty-three fungal species, including *Aspergillus, Trichoderma,* and *Penicillium*, sourced from various samples such as textile effluents and agricultural waste. The *A. niger* IMMIS1 strain was capable of producing between 400 and 500 U mL-1 when the authors optimized the pH and temperature conditions to 4.5 and 35°C, respectively.

The ANOVA analysis confirmed that textile effluent concentration significantly affects fungal growth ($F = 3.53$, $p = 0.0247$), indicating that increasing levels of effluent negatively impact fungal viability. While most isolates showed reduced growth with higher dye concentrations, *Trichoderma viride* and *Cladosporium* sp. displayed greater resilience, maintaining relatively consistent growth. This suggests their potential for application in bioremediation under stress conditions. However, the overall decline in colony diameter highlights the toxic effects of textile effluent on fungal physiology, emphasizing the need to select tolerant strains for effective treatment.

The study demonstrated that increasing concentrations of textile effluent significantly affected fungal growth, as confirmed by ANOVA ($F = 3.53$, $p = 0.0247$), indicating a general negative trend in viability. However, certain isolates like *Trichoderma viride* and *Cladosporium* sp. maintained better growth under stress, highlighting their bioremediation potential.

MLR analysis further supported these findings by showing that decolorization efficiency was primarily influenced by initial dye concentration and incubation time. A strong positive correlation was observed between colour removal and volatile suspended solids (VSS) ($\rho = 0.76$, $p = 0.049$), suggested that higher fungal biomass directly enhances dye degradation.

Conversely, biomass growth showed a significant negative correlation with nickel concentration ($\rho = 0.79$, $p = 0.048$), aligning with previous studies (Cao *et al.,* 2018), which reported that even micromolar levels of Ni can inhibit fungal growth such as in *Phanerochaete chrysosporium*.

CONCLUSION

The comparative analysis of fungal communities from marine environments in Andikkadu and Sarabendrajanpattinam revealed significant differences in both abundance and diversity. Sarabendrajanpattinam consistently exhibited higher fungal colony counts and greater species richness in both soil and water samples, suggesting that environmental conditions at this site are more conducive to fungal proliferation. Key fungal species such as *Aspergillus fumigatus*, *A. flavus, Penicillium brevicompactum*, and *T. viride* were common across all samples, whereas certain species like *Cladosporium* sp. and *Aspergillus citrisporum* showed site-specific distribution patterns.

Furthermore, the evaluation of fungal isolates for textile dye decolorization revealed that *T. viride*, *Cladosporium* sp., and *Curvularia lunata* possess significant bioremediation potential, particularly at higher dye concentrations. ANOVA results confirmed that textile effluent concentrations significantly affect fungal growth ($p = 0.0247$), with a general decline in viability at elevated effluent levels. However, some isolates demonstrated resilience, supporting their potential application in environmental remediation.

Overall, this study underscores the ecological richness of Sarabendrajanpattinam's marine environment and highlights specific fungal species with promising industrial applications in dye bioremediation.

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