Int.J.Curr.Res.Aca.Rev.2026; 14(1): 82-86

EXCELLENT PUBLISHERS

International Journal of Current Research and Academic Review

ISSN: 2347-3215 (Online) Volume 14 Number 1 (January-2026)

Journal homepage: http://www.ijcrar.com

doi: https://doi.org/10.20546/ijcrar.2026.1401.010

Biodegradation of Textile Dyes using Indigenous Bacterial Strains isolated from Contaminated Soil

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Abstract

Economical and eco-friendly approaches are essential for degrading dye-contaminated wastewater from various industries. In this study, we report the isolation and characterization of two bacterial strains, *Brevibacillus* sp. and *Pseudomonas* sp., capable of efficiently degrading Reactive Blue 19 (RB-19). Eight bacterial strains were initially isolated from textile dye-contaminated soil. Among them, the most efficient isolate was further tested on five other dyes, and it demonstrated the highest degradation efficiency for RB-19. Morphological, enzymatic, and molecular analyses, including 16S rRNA sequencing, confirmed the identity of these isolates. The degradation efficiency of RB-19 by these strains was characterized as a function of dye concentration, pH, temperature, and nutrient availability. Under optimal conditions, most of the RB-19 was degraded within 24 hours. The biodegradation data were analyzed statistically to validate the results.

Article Info

Received: 20 November 2025
Accepted: 31 December 2025
Available Online: 20 January 2026

Keywords

Textile dye, *Brevibacillus* sp., *Pseudomonas* sp., 16S rRNA analysis

Introduction

Rapid population growth and economic development in India have led to significant environmental degradation due to urbanization, industrialization, agricultural expansion, and deforestation. The textile industry is one of India's largest industrial sectors, contributing significantly to foreign exchange and employment. However, environmental concerns arise mainly from the discharge of wastewater during textile processing.

Textile industries extensively use reactive dyes due to their ease of synthesis and cost-effectiveness. Wet processing operations consume large volumes of water, generating substantial quantities of dye-containing wastewater, which is a major route for dyes entering the soil and water environment (Elliott, 1999). Reactive dyes are among the most common synthetic colorants, and their release causes serious pollution (Nigam et al., 1995).

Dyes are particularly difficult to remove by conventional treatment methods, which are often costly, energy-intensive, or produce hazardous by-products (Stolz, 2001). Biological treatment offers a sustainable alternative, relying on microorganisms capable of decolorizing and degrading reactive dyes of various chemical structures. Many bacteria and actinomycetes not only adsorb but also metabolize and mineralize dyes.

The objectives of this study were to isolate and characterize native bacterial strains capable of degrading

a broad spectrum of reactive dyes and to analyze dye decolorization under varying conditions of pH, temperature, and dye concentration.

Materials and Methods

Isolation and Identification of Bacteria

Soil samples were collected from a textile wastewater pond. Samples were serially diluted in sterile distilled water and plated on nutrient agar, followed by incubation at 30°C for 48 hours. Distinct colonies were initially grouped based on Gram staining and morphological characteristics. Morphologically unique strains were subjected to biochemical tests following Bergey's Manual of Determinative Bacteriology (9th edition) and phylogenetic analysis via 16S rRNA sequencing for species identification.

Dye Decolorization Study

The decolorization potential of bacterial strains was evaluated using RB-19. Four concentrations of the dye (25, 50, 75, and 100 mg/L) were prepared. For each concentration, bacterial-inoculated and control bottles were maintained. Decolorization was monitored using a UV-Visible spectrophotometer, and the percentage decolorization was calculated as follows (Sani and Banerjee, 1999):

$$\text{Decolonization (\%)} = \frac{\text{Initial absorbance-after decolorization absorbance}}{\text{Initial absorbance}} \text{ X } 100$$

Results and Discussion

Isolation and Identification of Dye-Degrading Bacteria

Using enrichment techniques, eight bacterial colonies capable of decolorizing reactive dyes were isolated, as indicated by clear zones around the colonies. Two isolates produced the largest decolorized zones on agar plates. 16S rRNA sequencing revealed 99% sequence similarity with *Brevibacillus* sp. and *Pseudomonas* sp. The 16S rRNA sequences (1517 bp for *Brevibacillus parabrevis* and 1526 bp for *Pseudomonas otitidis*) were submitted to GenBank under accession numbers D78463 and AY953147, respectively.

Dye Decolorization

Decolorization of RB-19 in 0.5% glucose medium was monitored at 592 nm over 10 days. At a lower dye concentration (25 mg/L), visual decolorization by both bacteria was observed within 24 hours. Maximum decolorization of RB-19 was 86% by *Brevibacillus parabrevis* and 78% by *Pseudomonas otitidis* on the 10th day. Higher dye concentrations reduced the decolorization rate.

The extent of color removal varied with pH, temperature, media composition, and dye type, consistent with previous reports (Cripps et al., 1990; Spadaro et al., 1992).

Figure.1 Effect of pH on percentage of decorization

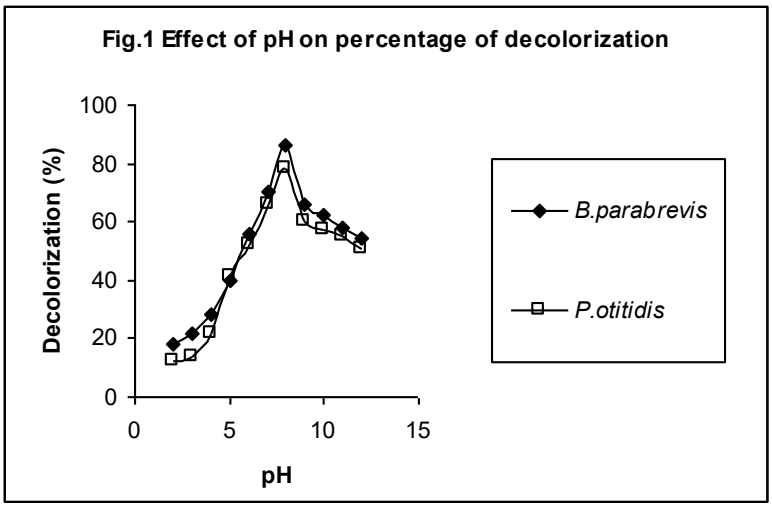


Figure.2 Effect of Temperature on percentage of decorization

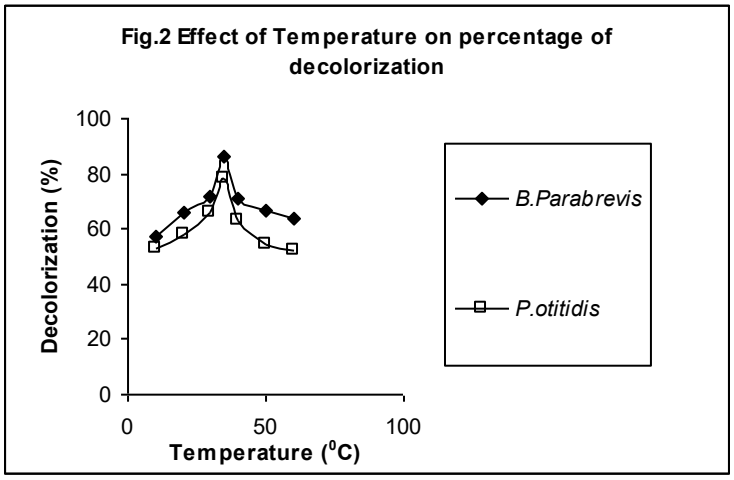


Figure.3 Effect of glucose concentration on percentage of decorization

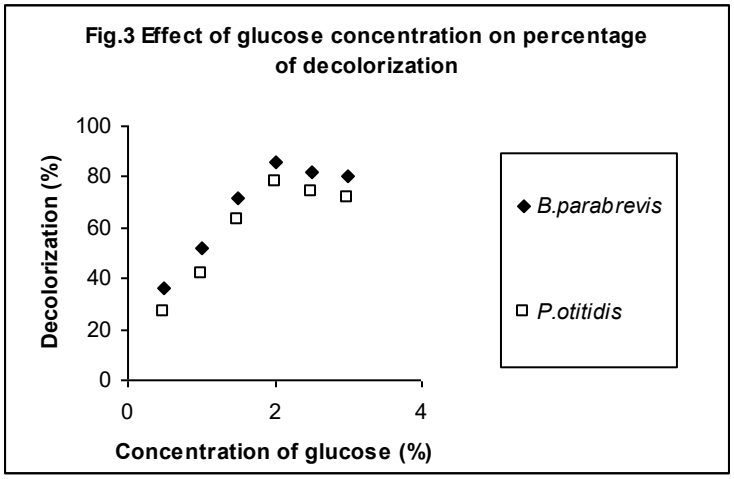


Figure.4 Effect of initial concentration of dye on percentage of decorization

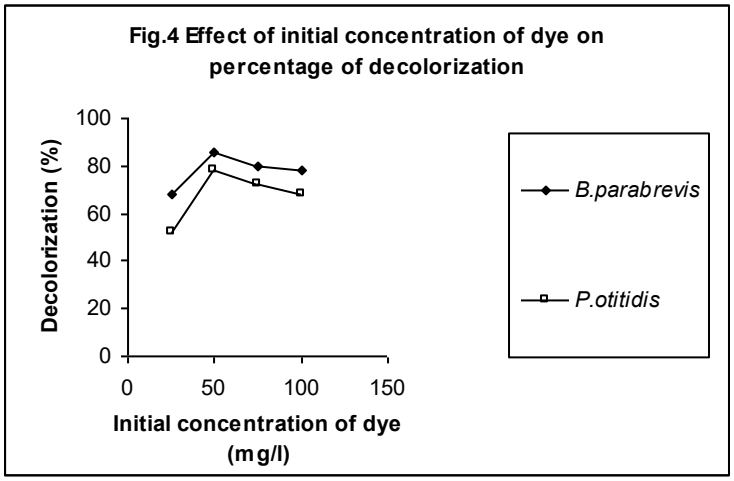
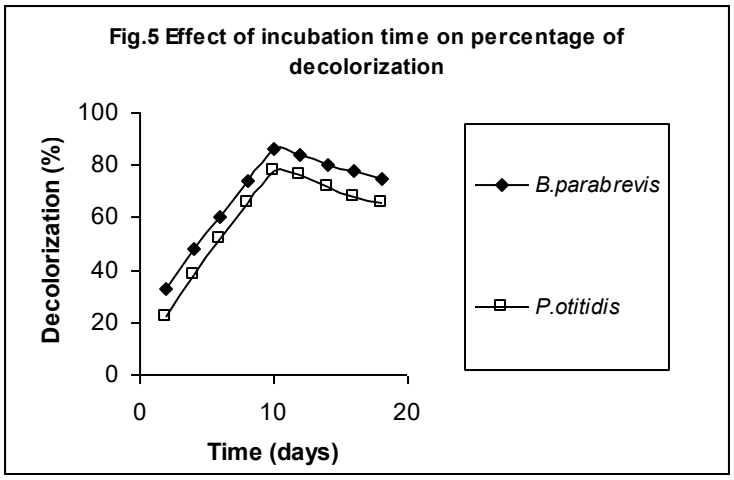


Figure.3 Effect of incubation time on percentage of decorization



Textile effluents typically contain 10–50 mg/L of dyes, though even 0.005 mg/L can be visually detected in water (Pandey et al., 2007). In this study, a simulated effluent containing 56 mg/L RB-19, supplemented with starch and yeast extract to enhance bacterial growth, was used (Padmavathy et al., 2003).

Conclusion

Eight bacterial strains capable of degrading reactive dyes were successfully isolated from textile-contaminated soil. Among these, *Brevibacillus parabrevis* and *Pseudomonas otitidis* showed the highest RB-19 decolorization potential, achieving 86% and 78% degradation, respectively. Decolorization efficiency decreased with increasing dye concentration, and was influenced by environmental and nutritional factors. These findings demonstrate the potential of native bacterial isolates for eco-friendly bioremediation of dye-contaminated wastewater.

Acknowledgement

The authors greatfully acknowledge the department members for continuous support.

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How to cite this article:

Nagulan, T. G., N. Sangeetha and R. Rasu. 2026. Biodegradation of Textile Dyes using Indigenous Bacterial Strains isolated from Contaminated Soil. *Int.J.Curr.Res.Aca.Rev.* 14(1), 82-86.
doi: https://doi.org/10.20546/ijcrar.2026.1401.010