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Potential of Indigenous Bacteria from Textile Industry Treatment Plants for COD and BOD Reduction in Wastewater

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Abstract: The textile industry generates approximately 20% of global industrial wastewater, characterized by high organic loads that result in elevated Chemical Oxygen Demand (COD) and Biochemical Oxygen Demand (BOD). This study investigates indigenous bacterial isolates from textile wastewater treatment plants and evaluates their potential to reduce COD and BOD levels. Twenty-three bacterial isolates were obtained from sediment and effluent samples, of which seven demonstrated strong biodegradation potential. Under optimized conditions, the bacterial consortium reduced COD by 57.11% and BOD by 99% after 72 hours of treatment. The isolates were characterised using morphological, Gram staining, and biochemical analyses, which identified *Bacillus*, *Pseudomonas*, and *Chryseomonas* as potential bioremediation agents. These findings highlight the promise of indigenous bacterial consortia as an eco-friendly alternative for improving the efficiency of textile wastewater treatment.

Keywords: biochemical oxygen demand; chemical oxygen demand, indigenous bacteria; textile; waste; bioremediation.

1. Introduction

The textile industry is a vital component of the global economy, but also a major source of environmental pollution due to the discharge of large volumes of wastewater containing complex mixtures of organic and inorganic contaminants [1–4]. Effluents from textile processing, especially those released after physico-chemical treatment, are typically rich in dyes, surfactants, heavy metals, and other chemical additives [5,6]. These pollutants contribute to elevated Chemical Oxygen Demand (COD) and Biochemical Oxygen Demand (BOD), key indicators of organic load and wastewater biodegradability [7]. If not properly treated, such

effluents can deplete dissolved oxygen, disrupt aquatic ecosystems, and pose health risks to humans and other organisms [8–10]. Conventional treatment methods, such as coagulation, flocculation, and chemical oxidation, can partially remove these contaminants but are often expensive and energy-intensive, and they generate large volumes of sludge [11-17]. In contrast, biological treatment using microorganisms offers a more sustainable and eco-friendly alternative due to its lower operational cost, reduced sludge production, and ability to mineralise organic pollutants into harmless end products [18,19].

Recent research has shown that bacteria isolated from highly contaminated environments, particularly textile wastewater treatment plants, can adapt to harsh chemical conditions and possess enzymatic systems capable of degrading complex organic molecules [20–25]. Some indigenous bacteria can even utilise dyes as carbon and nitrogen sources through the activity of enzymes such as azo-reductases, contributing to significant reductions in COD and BOD levels [26-27]. Despite these advances, limited information remains on the composition and biodegradation potential of indigenous microbial consortia from textile wastewater treatment plants, particularly regarding their synergistic performance in reducing COD and BOD. Addressing this gap is crucial for developing effective bioaugmentation strategies for industrial wastewater remediation.

Therefore, this study aims to isolate and characterise indigenous bacterial strains from the physicochemical wastewater treatment plant of PT Sari Warna Asli Unit 1, Karanganyar, Indonesia, and to evaluate their capacity to reduce COD and BOD in textile wastewater. We hypothesize that indigenous bacterial consortia adapted to textile effluents can significantly enhance organic matter degradation and contribute to more efficient and sustainable wastewater treatment processes.

2. Materials and Methods

2.1. Isolation of indigenous bacteria.

Indigenous bacterial isolates were obtained using the spread plate method. Sediment and wastewater samples collected from the textile industry physico-chemical wastewater treatment plant were serially diluted (10^{-1}–10^{-5}) using sterile distilled water following standard microbiological protocols [28]. One millilitre of each dilution was plated in duplicate onto Nutrient Agar (NA) medium, evenly spread using a sterile glass spreader, and incubated at 37°C for 24 h in an inverted position. Distinct colonies were purified by streaking on slanted NA in test tubes, incubated for 24 h at 37°C, and subsequently stored at 4 C for further characterisation.

2.2. Characterisation of bacterial isolates.

Each isolate was characterised based on colony morphology (shape, margin, elevation, texture, and colour) and microscopic appearance after Gram staining, following the procedures of Cockerill [28]. Morphological characteristics were recorded to support preliminary identification.

2.3. Screening of potential isolates.

Screening was conducted on a minimal agar medium containing different carbon sources (glucose, fructose, sucrose, mannitol, and maltose). Isolates were streaked on the

solidified medium and incubated at 37°C for 72 h. Isolates showing visible growth on all five carbon sources were selected as potential degraders for subsequent biochemical testing and COD/BOD evaluation.

2.4. Biochemical tests.

Potential isolates were subjected to a series of biochemical assays to determine their probable genus. The tests included endospore staining, catalase, motility, Simmons' citrate, triple sugar iron agar (TSIA), indole, urease, methyl red–Voges-Proskauer (MR–VP), nitrate/nitrite reductase, phosphate reductase, and ammonia production assays, following standard microbiological protocols (Bergey's Manual of Determinative Bacteriology, 2009).

2.5. Sample preparation for COD and BOD tests.

Liquid cultures of potential isolates were incubated for 24 h until reaching an optical density (OD_{600}) of 0.6. Sterile wastewater samples were prepared by autoclaving, cooled to room temperature, and diluted 1:1 with sterile distilled water to obtain 50% wastewater concentration (450 mL). Bacterial consortia were added at 10% (v/v; 50 mL) of the total volume. The mixture was incubated at ambient temperature for 72 h. COD was measured using the reactor digestion method, and BOD using the standard dilution method, both performed at the Semarang City Health Laboratory. Analytical instruments were calibrated with standard potassium hydrogen phthalate and glucose–glutamic acid solutions before measurement.

2.6. Control experiments for abiotic degradation and sterilisation effects.

To distinguish biological activity from non-biological (abiotic) effects, appropriate control treatments were included. An abiotic control was prepared using sterile distilled water in place of the bacterial inoculum to evaluate dye or pollutant degradation due solely to photolysis, adsorption, or chemical instability under the same incubation conditions (temperature, agitation, and illumination). Additionally, a sterilised control containing autoclaved bacterial biomass was used to assess any potential adsorption or catalytic degradation unrelated to active metabolism. All controls were incubated in parallel with the experimental samples, and measurements of colour removal, COD, and BOD were recorded at the same time intervals. No significant changes observed in these controls were subtracted from the corresponding experimental data to ensure that the reported reductions reflected true biological degradation.

2.7. Statistical analysis.

All measurements were conducted in triplicate. Results are expressed as mean ± standard deviation (SD). Statistical significance among treatments was assessed using a one-way analysis of variance (ANOVA) with a 95% confidence interval ($p < 0.05$).

3. Results and Discussion

3.1. Bacterial isolation and characterisation.

The isolation of water and waste sediment from the textile industry's physico-chemical WWTP yielded 13 isolates (F1-F13), and the isolation of industrial wastewater bacteria yielded

10 isolates (AF1-AF10) with different colony colours, shapes, margins, elevations, and textures (Table 1 and Table 2). After that, Gram staining is carried out to group bacteria.

Table 1. Characteristics of sedimentary isolates of WWTP waste physico-chemical textile industry.

Isolates	Colony form	Margin	Elevation	Texture	Color	Shape	Grams
F1	Regular	Regular	Flat	Moist	Chocolate	Ovoid coccus	+
F2	Irregular	Irregular	Flat	Moist	White	bacilli	+
F3	Irregular	Irregular	Raised, spreading edge	Dry	White	bacilli	+
F4	Irregular	Irregular	Flat	Dry	White	Streptobacilli	+
F5	Irregular	Irregular	Flat	Moist	Transparent	Ovoid coccus	-
F6	Irregular	Irregular	Flat	Dry	Opaque white	bacilli	+
F7	Regular	Regular	Convex	Moist	Milky white	Coccus	+
F8	Irregular	Irregular	Flat	Moist	White	Streptobacilli	-
F9	Irregular	Irregular	Flat	Dry	White	bacilli	+
F10	Irregular	Irregular	Umbonate	Moist	Transparent	bacilli	+
F11	Regular	Regular	Convex	Moist	Yellow	bacilli	-
F12	Irregular	Lobate	Flat	Moist	Transparent	bacilli	-
F13	Irregular	Lobate	Flat	Dry	Transparent	bacilli	-

Macroscopic morphological characterisation is carried out by visually comparing 23 isolated colonies. The characteristics of the colonies recorded include colour, shape, edges, elevation, and texture (Tables 1 and 2). The results of the data obtained on the isolates from the sediment are 2 isolates with a circular colony shape and smooth edges, convex elevation, moist colony texture, have a milky white and darkyellow color, eleven other isolates have an irregular colony shape that is dominated with white and yellowish-white colors, various elevations exist in the form of flat, umbonate, and raised spread edges, moist and dry colony textures. In these 11 isolates, bacterial colonies have lobate margins.

Microscopic morphologicalcharacterisation is performed after colony morphology is assessed by preparing Gram-stained preparations from pure isolates [29]. The bacteria are isolated and analysed for morphological characteristics, and then Gram staining is performed. The results of Gram staining showed that 8 isolates from sediments, including 5 Gram-positive and 3 Gram-negative bacteria, were obtained.

Table 2. Characteristics of wastewater isolates of WWTP physico-chemical textile industry.

Isolates	Colony form	Margin	Elevation	Texture	Color	Shape	Grams
AF1	Irregular	Irregular	Raised, spreading edge	Moist	Chocolate	Streptobacilli	+
AF2	Irregular	Irregular	Raised, spreading edge	Dry	Brownish pink	Streptobacilli	-
AF3	Irregular	Irregular	Raised, spreading edge	Dry	Milky white	bacilli	+
AF4	Irregular	Irregular	Raised, spreading edge	Dry	Milky white	bacilli	-
AF5	Irregular	Irregular	Convex	Moist	Milky white	Streptobacilli	-
AF6	Irregular	Irregular	Raised, spreading edge	Moist	Crimson	Streptobacilli	-
AF7	Regular	Regular	Convex	Moist	Milky white	Coccus	+
AF8	Irregular	Irregular	Raised, spreading edge	Dry	Milky white	Streptobacilli	+
AF9	Regular	Regular	Convex	Moist	White yellow	bacilli	-
AF10	Irregular	Irregular	Convex	Moist	Yellow	Streptobacilli	+

The morphology of the isolate colony fromwastewater is characterised by 7 bacterial isolates with irregular colony forms, raised edges, dry and moist colony textures, and white to brownish-white colony colours. Three other isolates have a regular colony shape with convex elevation, moist colony texture, andwhite to yellow colour. From water, 5 Gram-positive and 5 Gram-negative bacterial isolates were obtained.

3.2. Screening for potential isolates.

Results from 23 sediment and water isolates showed that 7 isolates grew well on all 5 minimum media with different carbonsources. The isolates are F3, F8, F12, F13, AF1, AF4, and AF8 (Figure 1). This shows that the seven isolates can survive by using glucose, fructose, sucrose, mannitol, andmaltose as carbon sources to obtain energy. It is reported that bacterial screening using a minimum amount of agar with different sugar sources can demonstrate the ability of bacteria to use various carbon sources as energy sources [30]. After it was discovered that 7 isolates could use various carbon sources, they were tested biochemically to determine the genus of each bacterium.

3.3. Biochemical assays and identification of potential bacteria.

A biochemical test is an important qualitative test for identifying microbes. Each microbe has a biochemical fingerprint, the set of biochemical characteristics that define it. Biochemical fingerprints are used to assess similarities and differences among isolates. Biochemical tests are intended to characterise the seven isolates that grow well in the minimum medium, thereby determining their morphological and physiological characteristics. The biochemical tests carried out are staining endospores, catalase, motility, Simmons' citrate, TSIA, indole, urease, MR-VP, nitrate reductase, phosphate reductase, and ammonia (Table 3).

Table 3. Characteristics of wastewater isolates of WWTP physico-chemical textile industry.

No	Test	Isolates						
		F3	**F8**	**F12**	**F13**	**AF1**	**AF4**	**AF8**
1.	Grams	+	-	-	-	+	+	+
2.	Endospores	+	-	-	-	+	+	+
3.	Catalase	+	+	+	+	+	+	+
4.	Motility	+	+	+	+	+	+	+
5.	Simmon's Citrate	-	+	+	+	-	-	-
6.	TSIA	m/k	-	-	-	m/k g	m/k	m/k g
7.	Indole	-	-	-	-	-	-	-
8.	Urease	-	+	-	-	-	-	-
9.	MR	+	-	-	+	++	+	+
10.	VP	-	-	-	-	-	-	-
11.	Nitrate	+	+	+	+	+	+	-
12.	Phosphate	+	+	+	+	+	+	+
13.	Nitrogen ammonia	+	+	+	+	+	+	+
Genus of suspects		*Bacillus*	*Pseudomonas*	*Chryseomonas*			*Bacillus*	

The biochemical test results showed that 4 suspected genera had the potential to reduce the COD and BOD values of textile waste.

3.3.1. Genus *Bacillus*.

Isolates F3, AF1, AF4, and AF8 are based on the morphological features of the colony, namely the shape of a round colony with choppy colony edges, convex colony elevations, raised spreading edges, and white to yellowish-white or beige colony colours belonging to the genus *Bacillus* (Figure 1). Biochemical test results showed that the four isolates were Gram-positive, endospore-forming, motile, catalase-positive, methyl red-positive, Voges-Proskauer-negative, indole-negative, urease-negative, and nitrate reductase-positive.

This is in accordance with the study of [31], which reported that *Bacillus* has a convex colony elevation and a yellow or cream colony colour. Catalase-positive, indole-negative, MR test-positive, and citrate test-negative. According to [32], *Bacillus* sp. is a bacterium from the gram-positive group, having a locomotor in the form of a peritrichous flagellum, so that it is motile. In a nutrient-deficient state, they form oval-shaped endospores, sometimes round or

cylindrical, and are resistant to unfavourable conditions. *Bacillus* colonies have a milky white to yellowish colour and choppy margins. Included in the class of aerobic bacteria based on oxygen demand. Biochemical test results show that bacteria of the genus Bacillus can ferment glucose, sucrose, and lactose, produce the enzyme catalase, and do not produce indole gas. According to [33], the genus *Bacillus* is widely distributed in a variety of habitats and includes a few pathogenic species. The optimum growing temperature is 28ºC-35ºC.

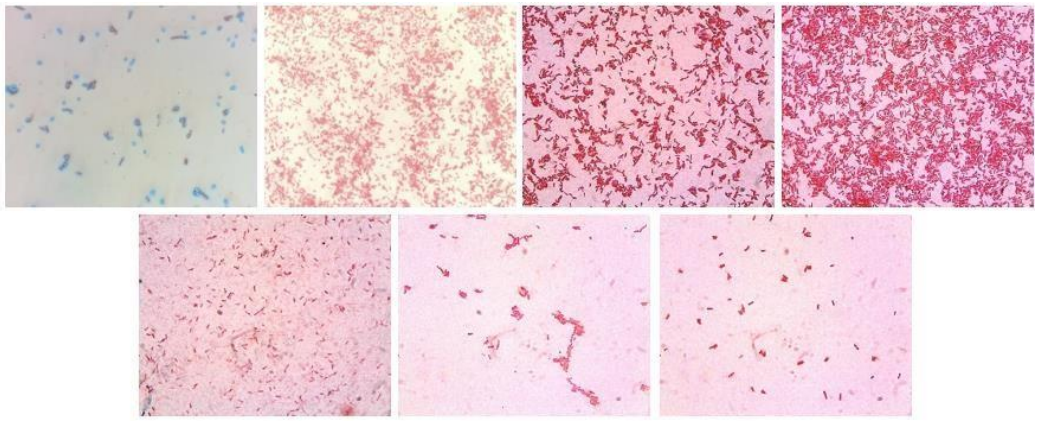

Figure 1. Potential isolate endospore staining under UV light microscope with 1000x magnification (F3, F8, F12, F13, AF1, AF4, and AF8).

3.3.2. Genus *Pseudomonas.*

Based on the colony's morphological features — white, moist, and wavy in elevation — the F8 isolate belongs to the genus *Pseudomonas*. Has biochemical properties that do not form endospores, positive catalases, motile due to the presence of flagella, positive citrate, negative TSIA, negative indole, positive urease, MR-VP negative, nitrate positive reductase, positive phosphate, and positive ammonia. According to [34], who isolated bacteria from textile waste effluents, potential isolates from the Genus *Pseudomonas* were obtained, which have rod-shaped characteristics, are Gram-negative bacteria, motile, unable to ferment sugar, do not produce indole, MR-VP negative, able to use citrate as a carbon source, positive catalase, positive oxidase, and unable to produce H2S.

3.3.3. Genus *chryseomonas.*

Based on their morphological features, isolates F12 and F13 are similar to bacteria of the genus *Chryseomonas.* This is consistent with [32], which reported that Chryseomonas is a Gram-negative bacillus that can move due to flagella. It grows on a dense medium with a transparent yellow colour. Colonies are usually circular and convex, and some produce wrinkles.

3.4. COD and BOD test sample preparation.

Samples in the form of wastewater from PT Sari Warna Asli Unit 1, as a control, and sterile wastewater are then diluted by 50%, and an additional 10% bacterial consortium is incubated for 3 days (Table 4). The bacterial consortium was created by incubating bacteria in nutrient broth (NB) for 24 hours until each bacterium reached an OD of 0.6 at 600 nm. Then, a consortium of bacteria, equivalent to 50 ml at 10%, is mixed with 450 ml of wastewater to a final volume of 500 ml. According to [35], an absorbance of 0.6 corresponds to MacFarland

standard no. 6, which has a bacterial density of 1.8×10^8/mL. Then, every 24 hours, COD and BOD levels are checked.

Table 4. Table of measurement of COD and BOD values in 50% waste.

IncubationDay to-	COD (mg/L)		BOD (mg/L)	
	Control (mg/L)	Treatment (mg/L)	Control (mg/L)	Treatment (mg/L)
1 (24 hours)	562	530	7,03	3,25
2 (48 hours)	558	423	6,32	0,17
3 (72 hours)	546	241	6,11	0,05

(a) **(b)**

Figure 2. 50% Waste **(a)** COD; **(b)** BOD value measurement chart for 72 hours.

Based on these results, the COD measurements for 3 days in the control were 562 mg/L, 558 mg/L, and 546 mg/L, while in the samples with the treatment were 530 mg/L, 423 mg/L, and 241 mg/L. The percentage decrease in waste treatment samples over three days was 5.69%, 24.73%, and 57.11% (Figure 2A). The greatest decrease in COD levels occurred on the third day, at 57.11%. In waste that has been mixed with bacterial consortia, there is a faster decrease in COD than in the control without bacterial inoculation. This shows that bacterial consortia can degrade organic compounds in textile waste. The highest submersion occurred at 72 hours of incubation, with a decrease of 182 mg/L in wastewater incubated for 48 hours. After an incubation period of 72 hours, the COD content in wastewater is 241 mg/L, which is still above the wastewater quality standard set by the Central Java Regional Regulation [36], which states that the COD level of waste discharged into waters should not exceed 150 mg/L. Furthermore, [37] also stated that the decrease in COD of woven waste with endophytic bacteria at 3-day incubation was 51.2%.

BOD measurements over 3 days in the control showed successive results of 7.03 mg/L, 6.32 mg/L, and 6.11 mg/L, while in the treatment, as low as 3.25 mg/L, 0.17 mg/L, and 0.05 mg/L. Decreases in BOD percentage compared to controls over 3 days were 53%, 97.31%, and 99% (Figure 2B). The BOD value in the control is higher than in the waste inoculated with bacteria. This shows that, in waste control, the levels of organic substances, oil, and TSS remain high. The absence of bacterial inoculation results in a gradual decrease in BOD. In waste with inoculation, BOD levels decrease, indicating lower levels of organic substances, oil, and TSS due to bacterial activity that converts these materials into energy and gas. This is consistent with [38], which reported that using a bacterial consortium in an aerobic-anaerobic system for 6 days reduced BOD levels by 94%. The BOD level at the start of the measurement was within the quality standards set by the Central Java Regional Regulation [36], i.e., below 60 mg/L. The smaller the BOD value, the lower the organic content and dissolved oxygen in the water.

The results obtained in this study demonstrate the significant potential of bacterial isolates from textile industry physicochemical processing plants to reduce the COD and BOD levels of textile wastewater. The observed reductions indicate active microbial degradation of

organic pollutants, validating the role of these bacteria as viable agents for biological treatment processes. The reduction in COD values suggests that the bacterial isolates can degrade a wide range of complex organic compounds commonly present in textile effluents, including dyes, surfactants, and residual chemicals from fabric treatment processes. The concurrent decrease in BOD further supports the hypothesis that these bacteria not only degrade non-biodegradable components but also convert them into simpler, more biodegradable forms that are easily assimilated by other microbial communities.

Compared to traditional physicochemical treatment methods, using indigenous bacteria offers several advantages. Firstly, these organisms are already acclimatized to the specific conditions of textile wastewater, including high salinity, pH variation, and chemical toxicity, giving them a survival and performance advantage. Secondly, biological treatment is more sustainable, producing less sludge and requiring lower operational costs. Interestingly, some bacterial strains demonstrated greater efficiency in COD and BOD reduction than others, highlighting the importance of strain selection for optimising treatment performance. The enzymatic activity, metabolic versatility, and synergistic interactions among microbial communities are likely crucial to their effectiveness. Further studies on microbial consortia, genetic profiling, and enzyme characterization could provide deeper insights into the mechanisms of pollutant degradation.

Moreover, this study's findings align with previous research highlighting the potential of bioaugmentation and bioremediation for industrial wastewater treatment. The practical implications include the potential integration of these bacterial strains into existing wastewater treatment plants, either as a standalone biological treatment step or in combination with conventional methods to enhance overall efficiency. However, factors such as operational stability, scalability, and regulatory compliance must be carefully considered for large-scale applications. Pilot-scale trials and long-term monitoring would be essential to evaluate the real-world performance and feasibility of these microbial solutions in diverse textile industry settings.

3.5. Mechanistic on bacterial degradation pathways and enzyme systems.

The present study demonstrates that indigenous bacterial consortia isolated from textile physicochemical treatment plants possess substantial potential to reduce Chemical Oxygen Demand (COD) and Biochemical Oxygen Demand (BOD) in textile wastewater [17,18]. Unlike laboratory-adapted or genetically modified strains commonly reported in literature, these indigenous isolates have evolved under continuous exposure to high loads of dyes, surfactants, and heavy metals. This long-term adaptation confers unique enzymatic tolerance and metabolic flexibility, enabling efficient degradation of complex organic mixtures under real effluent conditions [19,20]. The degradation of complex organic pollutants and dyes in textile wastewater by indigenous bacterial consortia proceeds through a combination of oxidative, reductive, and hydrolytic reactions mediated by extracellular and intracellular enzymes [21]. The metabolic versatility of genera such as *Bacillus, Pseudomonas*, and *Chryseomonas* enables the sequential breakdown of high-molecular-weight compounds into simpler intermediates that can enter central metabolic pathways such as the tricarboxylic acid (TCA) cycle [22,24].

The novel aspect of this work lies in harnessing native microbial communities already acclimatised to industrial stressors. These bacterial populations represent a naturally optimised biocatalytic system, capable of performing under fluctuating pH, temperature, and chemical

loads typical of textile wastewater. By leveraging consortia derived from the treatment plant environment itself, this study bypasses the limitations of exogenous strains that often lose activity or viability when transferred to high-strength effluents. The approach thus offers a sustainable, site-specific bioremediation strategy compatible with existing physicochemical treatment frameworks [23,25].

Azo dyes and other recalcitrant chromophores are initially reduced under microaerophilic or anoxic conditions by azoreductases (EC 1.7.1.6), which cleave the –N=N– bond using NADH or NADPH as electron donors [16,26]. This reaction converts the parent dye into colourless aromatic amines. In facultative anaerobes such as *Pseudomonas*, azoreductases are often plasmid-encoded and inducible by dye molecules, indicating adaptive enzymatic expression [17,29]. Under microaerophilic zones of the treatment matrix, *Pseudomonas* and *Bacillus* spp. initiate the degradation process via azoreductases (EC 1.7.1.6) that cleave azo linkages using NADH/NADPH. This reductive attack breaks chromophoric –N=N– bonds, converting dyes into colourless aromatic amines, markedly lowering chromaticity and partial COD [18,30].

Following reduction, aromatic amines undergo oxidative degradation via laccases, peroxidases, and monooxygenases, which catalyse ring hydroxylation and cleavage. Laccases (EC 1.10.3.2) and manganese peroxidases (MnP, EC 1.11.1.13) initiate electron transfer reactions that generate reactive radicals, leading to the breakdown of phenolic and non-phenolic compounds [19,31]. Catechol 1,2-dioxygenase (EC 1.13.11.1) and catechol 2,3-dioxygenase (EC 1.13.11.2) catalyse intradiol and extradiol cleavage, respectively, converting catecholic intermediates into cis,cis-muconate or 2-hydroxymuconic semialdehyde, which subsequently enter the β-ketoadipate pathway [33]. Catechol 1,2- and 2,3-dioxygenases further metabolise catecholic intermediates into cis,cis-muconate or 2-hydroxymuconic semialdehyde, which then funnel into the β-ketoadipate pathway, ultimately forming TCA cycle intermediates [34].

Bacillus spp. are known to produce esterases, amidases, and deaminases that hydrolyse and deaminate the side chains of aliphatic or aromatic intermediates, facilitating further oxidation. These reactions contribute to the overall reduction in Chemical Oxygen Demand (COD) by converting complex organic matter into smaller, more readily oxidizable molecules. Deamination and oxidation convert these products into CO_2 and H_2O, achieving measurable reductions in both COD and BOD [16,36]. The final degradation products—primarily short-chain fatty acids, organic acids, and CO_2—enter the TCA cycle through acetyl-CoA or succinate intermediates. This mineralisation step is critical for reducing Biochemical Oxygen Demand (BOD), as it reflects the complete biodegradation of utilizable organics [18,37].

In mixed consortia, synergistic interactions enhance degradation efficiency. *Pseudomonas* initiates dye reduction under low-oxygen conditions, producing aromatic amines that are subsequently oxidised by *Bacillus* laccases or *Chryseomonas* peroxidases under aerobic conditions [24,25]. Such sequential redox cycling allows efficient degradation across variable physicochemical conditions typical of textile effluents. The indigenous consortia exhibit complementary enzymatic functions [17,26]. *Pseudomonas* provides reductive initiation, while *Bacillus* and *Chryseomonas* contribute oxidative and hydrolytic steps, maintaining degradation continuity under alternating aerobic–anaerobic microenvironments. This metabolic division of labour exemplifies adaptive cooperation unique to naturally selected consortia (Table 5) [18,37].

Table 5. Key enzymes implicated in COD/BOD reduction.

Enzyme	Function	Key genera	Reaction type
Azoreductase	Reductive cleavage of azo bonds	*Pseudomonas*, *Bacillus*	Reduction
Laccase	Oxidation of phenolics and aromatic amines	*Bacillus*, *Chryseomonas*	Oxidation
Peroxidase (LiP/MnP)	Breakdown of chromophores and lignin-like structures	*Bacillus*, *Chryseomonas*	Oxidation
Monooxygenase/Dioxygenase	Aromatic ring hydroxylation and cleavage	*Pseudomonas*	Oxygenation
Esterase/Amidase	Hydrolysis of side chains and amides	*Bacillus*	Hydrolysis

The mechanistic insights suggest that these indigenous consortia not only detoxify but also mineralise organic pollutants, making them strong candidates for integration into hybrid bioreactor systems downstream of physicochemical units [17,18]. Their resilience to fluctuating redox conditions allows stable performance in secondary or tertiary treatment steps, reducing overall operational costs and environmental impact. This study establishes that indigenous bacterial consortia from textile industry physicochemical plants can achieve significant reductions in COD and BOD through synergistic enzymatic degradation pathways [29,30]. Their adaptive metabolic networks, developed through prolonged environmental selection, enable them to serve as self-sustaining biocatalysts for eco-compatible wastewater remediation. This represents a novel, application-oriented approach to enhancing biodegradative efficiency within existing industrial treatment infrastructures.

4. Conclusions

This study demonstrates the promising potential of indigenous bacterial isolates obtained from textile industry physico-chemical wastewater treatment plants to reduce Chemical Oxygen Demand (COD) and Biochemical Oxygen Demand (BOD) levels in textile effluent. A total of 23 isolates were recovered—13 from sediment samples (F1–F13) and 10 from wastewater samples (AF1–AF10). Among these, a consortium comprising isolates F3, F8, F12, F13, AF1, AF4, and AF8 achieved the highest reduction in COD and BOD after 72 hours of incubation. COD decreased from 562 mg/L to 241 mg/L (a 57.11% reduction), while BOD declined by 99%, from 6.11 mg/L to 0.05 mg/L. Based on biochemical assays, the dominant bacterial genera were identified as Bacillus (F3, AF1, AF4, AF8), Pseudomonas (F8), and Chryseomonas (F12, F13). These results indicate that bacteria adapted to complex industrial effluents possess the metabolic capacity to degrade a wide spectrum of organic pollutants, thereby offering a potential biotechnological approach to improve wastewater treatment. However, while the observed COD and BOD reductions are substantial, claims regarding industrial-scale applicability should be considered preliminary, as the experiments were conducted under controlled laboratory conditions. This study was limited by a relatively short incubation period (72 hours) and the absence of molecular identification (e.g., 16S rRNA sequencing) to confirm taxonomic placement. Future investigations should incorporate genomic and enzymatic profiling to elucidate degradation pathways, quantify specific enzyme activities, and validate the performance of these bacterial consortia in pilot-scale bioreactor

systems. Such studies will provide a stronger foundation for integrating indigenous bacterial strains into large-scale, sustainable textile wastewater treatment processes.

Author Contributions

Conceptualization, A.B. and D.W.; formal analysis, H.T.R.; investigation, A.A.K.P.; writing—original draft preparation, A.B., D.W., R.H.B.S., and M.P. All authors have read and agreed to the published version of the manuscript.

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Not Applicable.

Data Availability Statement

Data supporting the findings of this study are available upon reasonable request from the corresponding author.

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Conflicts of Interest

The authors declare no conflict of interest.

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