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EVALUATION OF THE POTENTIAL APPLICATION OF LOW DENSITY POLYETHYLENE PLASTIC WASTE TREATMENT BY MARINE MICROORGANISMS IN THE COASTAL AREA OF BA RIA-VUNG TAU PROVINCE, VIETNAM

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ABSTRACT

Low density polyethylene (LDPE) plastic waste is a type of non-degradable solid waste that poses a significant threat to the environment globally. Among various degradation methods, biodegradation, which involves microorganisms, is the most efficient and sustainable solution. It stands out for its environmentally friendly process, lack of pollution, and cost-effectiveness. This study evaluates the potential application in the treatment of low density polyethylene plastic waste by marine microbiology isolated from the sea of Ba Ria - Vung Tau province, Vietnam. From 12 samples (09 marine sediment samples and 03 plastic waste samples), 27 microbial strains were selected through enrichment with 0.5% LDPE substrate. In which, marine sediment samples recorded a higher ratio of strains per sample than plastic waste samples. Based on the ability to produce laccase enzyme, 12 strains (with laccase enzyme activity from 750.0 ± 3.00 U/mL to 1430.0±3.66 U/mL) were selected for identification and study of antagonism between strains. There were 03 microbial formulas formed including: microbial formula 1 (MF1) including strains: S1.05, S3.01, S3.03, S4.01; microbial formula 2 (MF2) including strains: S2.02, S6.01, S6.03, S8.01; microbial formula 3 (MF3) includes strains: S9.04, S10.01, S11.01, S11.02. The three microbial formulas were cultured in mineral medium supplemented with 0.5 % LDPE substrate. MF3 is the microbial formula with the best ability to reduce substrate weight (reduced by 17.4% compared to the initial substrate amount after 90 days of culture). Microbial formula MF3 has the potential to be applied to create microbial preparations for treating plastic waste originating from LDPE. The results obtained from this study can be a reliable source of data for the research and development of a microbial preparation for treating plastic waste, contributing to solving the current plastic waste pollution situation.

Keywords: Microbial formula, biodegradation, LDPE, marine microorganisms, waste plastic.

1. INTRODUCTION

Plastic pollution has emerged as one of the most urgent and widespread environmental crises worldwide, with global plastic production reaching approximately 390.7 million tonnes in 2021, of which a significant portion ends up as waste in the environment [1]. Among various types of plastic, LDPE is particularly problematic due to its chemical stability and resistance to natural degradation processes. LDPE accounts for nearly 20% of global plastic production, primarily used in single-use items such as plastic bags, packaging films, and squeeze bottles [2]. Due to its non-biodegradable nature, LDPE can persist in the environment for hundreds of years, gradually breaking down into microplastics under physical, chemical, and biological weathering, which then infiltrate food chains and aquatic ecosystems [3]. Studies have shown that LDPE is one of the most commonly found polymers in marine debris, contributing significantly to the pollution of beaches and coastal areas. For example, surveys along Southeast Asian coastlines indicate that over 30% of collected plastic litter consists of polyethylene-based materials [4]. Vietnam generates approximately 3.27 million tons of plastic waste annually, with only about 10% being recycled. LDPE plastic waste poses a significant environmental challenge in Vietnam, particularly in coastal areas like Vung Tau. LDPE, commonly used in single-use plastic bags and packaging, is prevalent due to its low cost and widespread availability. However, its low recycling value means it is often discarded improperly, contributing to environmental pollution [5]. In Vung Tau, studies have identified microplastics in beach sediments, with chemical compositions primarily consisting of polystyrene (PS) at 40%, polyethylene (PE) at 38%, polypropylene (PP) at 19%, and polyvinyl chloride (PVC) at 3% [6]. These microplastics originate from the breakdown of larger plastic debris, including LDPE products. The presence of microplastics in marine environments poses risks to marine life and, by extension, human health through the food chain [7].

Traditional methods of plastic waste management such as landfilling and incineration have proven inadequate and often environmentally harmful. Landfilling requires large land areas and may lead to soil and groundwater contamination through leachates, while incineration releases toxic gases such as dioxins, furans, and greenhouse gases like CO_2, exacerbating climate change [8]. Furthermore, the economic cost of managing plastic waste through these methods is high, especially in developing countries where waste management infrastructure is limited. These challenges have prompted increased interest in biodegradation as a sustainable and eco-friendly alternative, particularly using microorganisms capable of breaking down persistent polymers like LDPE. Unlike traditional approaches, microbial degradation offers a low-cost, scalable, and environmentally benign solution that could be applied in natural settings or integrated into waste treatment systems [9].

Several bacterial species have been identified with the ability to degrade low-density polyethylene (LDPE), offering promising biological approaches to addressing plastic pollution. *Bacillus* spp., particularly *Bacillus subtilis* and *Bacillus cereus*, have shown significant LDPE-degrading potential due to their enzymatic activity and resilience in diverse environments [10]. In addition, *Pseudomonas* spp., including *Pseudomonas aeruginosa* and *Pseudomonas putida*, are well-documented for their capacity to colonize polyethylene surfaces and secrete oxidative enzymes such as laccases and monooxygenases that aid in polymer breakdown [11]. Other genera such as *Micrococcus*, *Streptomyces*, and *Rhodococcus* have also been reported to contribute to polyethylene biodegradation, often forming biofilms that enhance polymer surface degradation [12]. Recent studies have also highlighted the role of marine bacteria, including *Alcanivorax* and *Vibrio* species, which can degrade LDPE under saline conditions, suggesting their potential in coastal and marine bioremediation applications [13]. These findings underscore the diversity and adaptability of LDPE-degrading bacteria, providing a valuable foundation for the development of microbial consortia for plastic waste treatment.

Enzymes play a critical role in the microbial degradation of LDPE, primarily by initiating the breakdown of the long-chain hydrocarbon backbone into smaller, more accessible molecules. Among these, laccases—multi-copper oxidase enzymes—are of particular interest due to their ability to oxidize non-phenolic substrates and facilitate polymer oxidation, thereby enhancing the susceptibility of LDPE to microbial attack [14]. Several bacteria, including *Pseudomonas aeruginosa*, *Bacillus subtilis*, and *Streptomyces* spp., have been shown to secrete laccases during the biodegradation of polyethylene [15]. In addition to laccases, alkane hydroxylases and monooxygenases are also involved in the initial oxidation of polyethylene, converting hydrophobic surfaces into more hydrophilic compounds that can be further metabolized [16]. Another group of enzymes—esterases and lipases—has been reported to contribute to the degradation of oxidized polyethylene fragments, particularly under conditions where LDPE has undergone pre-oxidation via UV or thermal exposure [11]. The activity of these enzymes is often enhanced in bacterial consortia, where synergistic interactions promote more efficient degradation pathways. Understanding the enzymatic mechanisms involved provides valuable insight for optimizing microbial formulations and enhancing the biodegradation rate of LDPE in environmental and engineered settings.

This study initially evaluated the potential application of marine microbiology isolated from Vung Tau marine sediments in the treatment of LDPE plastic waste. The results of the study may open up a new, safe, environmentally friendly solution, exploiting indigenous microorganisms in the treatment of LDPE waste.

2. MATERIALS AND METHODS

2.1. Materials

12 samples collected in Vung Tau sea area were listed in Table 1.

Table 1. List of samples used for research.

№	Sample type	Location	Sample symbol	Total number of samples by location
1	Marine Sediments	Long Cung Beach	S1	04
2	Marine Sediments	Long Cung Beach	S2	
3	Marine Sediments	Long Cung Beach	S3	
4	Plastic Waste	Long Cung Beach	S4	
5	Marine Sediments	Thuy Van Beach	S5	04
6	Marine Sediments	Thuy Van Beach	S6	
7	Marine Sediments	Thuy Van Beach	S7	
8	Plastic Waste	Thuy Van Beach	S8	
9	Marine Sediments	Truoc Beach	S9	04
10	Marine Sediments	Truoc Beach	S10	
11	Marine Sediments	Truoc Beach	S11	
12	Plastic Waste	Truoc Beach	S12	
	Total			**12**

Chemical: LDPE (Sigma-Aldrich, code: 428043, form: pellets, melt index: 25 g/10 min (190 °C/2.16 kg), impact strength: 45.4 J/m (Izod, ASTM D 256, −50 °C, notched), density: 0.925 g/mL at 25 °C), Filter paper (Whatman Grade 43, 1443-090, intermediate particle

retention rating of 16 µm) mineral salt medium (MSM, 1.0 g NH_4NO_3, 0.2 g $MgSO_4.7H_2O$, 1.0 g K_2HPO_4, 0.1 g $CaCl_2.2H_2O$, 30.0 g NaCl and 0.15 g KCl per liter of distilled water) were used to study plastic degradation using a method described by Kanniahi et al. (2013) [17], nutrient agar (NA) according to Emenike et al. (2016) [18].

2.2. Methods

2.2.1. Sampling methods

Sediment samples: use a sterilized spoon to collect sediment samples at a depth of 5-10 cm from the sand surface and transfer them to a sample container [19].

Waste samples (PE bag, PE bottle): Use a sterile spoon or forceps to collect about 500g of waste and transfer them to a sample container [19].

2.2.2. Methods of microbiological research

Microbial enrichment method: Sediment samples were enriched in MSM medium supplemented with 0.5% LDPE plastic.

Microbial isolation method: dilute 10g of each sample in 90ml of artificial seawater, shake vigorously at 30 ºC for 30 minutes. Dilute the obtained solution in artificial seawater solution to the required dilution. Then spread 100 µL of each sample at different dilutions on a petri dish containing isolation medium. After spreading, the dish is incubated at 28-30 ºC until the colonies are observed and purified on a medium specific to each group of microorganisms [20].

16S rRNA gene sequencing: Use specific primer pairs to amplify the 16S rDNA gene bacteria (27F-5'AGAGTTTGATCMTGCCTCAG3', 1492R-5'TACGGTTACCTTGTTACGACTT3') with recommended components and reaction cycle. PCR products were checked on agarose gel, then purified and sent for sequencing.

2.2.3. Analytical methods

Reduced the weight of LDPE substrate: LDPE plastic pellets were cultured with bacteria in MSM medium. After 90 days, they were recovered by filtration. Next, they were washed with 70% ethanol and dried overnight at 50ºC. Finally, they were weighed to determine the mass [21]. The polymer weight loss rate was determined to evaluate the degradability of the bacterial strains through the following formula (the initial weight of plastic pellets was also determined in the same technique):

$$\text{Percentage weight loss} = \left(\frac{\text{Initial weight of polymer} - \text{Final weight of polymer}}{\text{Initial weight of polymer}}\right) \times 100.$$

Determining laccase enzyme activity: The enzyme reaction solution consisted of: 2.2 mL of 0.1M phosphate buffer pH 6.5; 0.3 mL of 0.216 mM syringaldazine solution in methanol, 0.5 mL of enzyme solution. Mix the reaction mixture well and measure the increase in absorbance at 530 nm of the reaction mixture compared with the control sample after each minute of reaction. The control reaction used deionized water instead of enzyme [22]. One unit of laccase activity is the amount of enzyme that in one minute at pH 6.5, 30 ºC converts 1 µmol of syringaldazine (ε = 65 mM^{-1} cm^{-1}). All experiments were performed at 30 ºC and repeated three times.

3. RESULTS AND DISCUSSION

3.1. Microbial isolation

The successful isolation of LDPE-degrading microbiology from both plastic waste and marine sediment samples collected along Vung Tau sea area underscores the microbial potential for bioremediation of plastic pollution in this region. The higher number of microbial isolates from sediment samples compared to plastic waste suggests that marine sediments may act as reservoirs for diverse microbial communities capable of degrading synthetic polymers. This aligns with previous findings that sediment environments support microbial enrichment due to the accumulation of organic matter and prolonged exposure to pollutants, including plastic debris [13].

Table 2. Results of microbial isolation from samples

№	Sample ID	Strain ID	Quantity	Total number of strains by location
1	S1	S1.01-S1.05	05	11
2	S2	S2.01, S2.02	02	
3	S3	S3.01 - S3.03	03	
4	S4	S4.01	01	
5	S5	S5.01,S5.02	02	07
6	S6	S6.01-S6.03	03	
7	S7	S7.01	01	
8	S8	S8.01	01	
9	S9	S9.01-S9.04	04	09
10	S10	S10.01	01	
11	S11	S11.01, S11.02	02	
12	S12	S12.01, S12.02	02	
Total				27

The notably high number of isolates from Long Cung Beach, particularly sample S1, indicates localized microbial adaptation to plastic-rich environments. This may be a consequence of sustained plastic contamination, promoting the selection of microorganisms with metabolic pathways suited for hydrocarbon degradation. The variation in isolate abundance among sites further reflects the influence of environmental factors such as nutrient availability, salinity, and plastic exposure history on microbial community structure and functional potential [23].

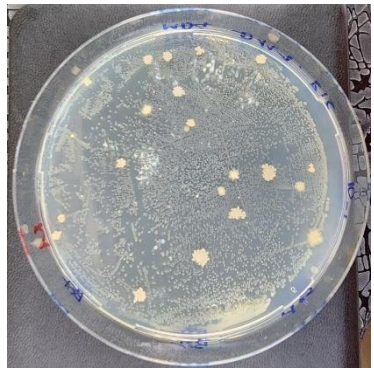

Figure 1. Isolation results of sample S1

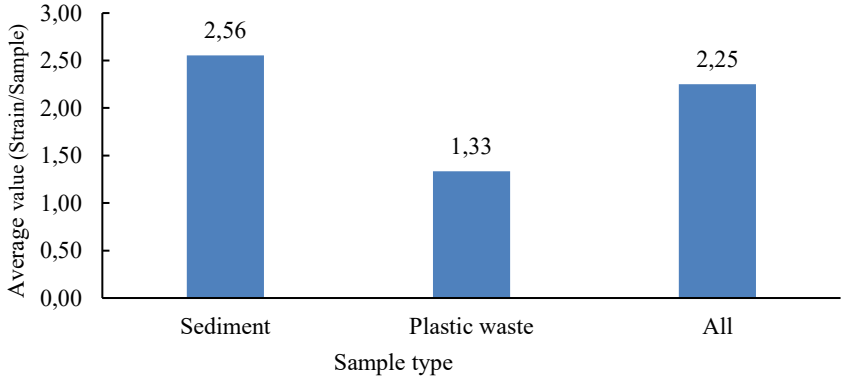

Figure 2. Average value of the number of strains by sample type

3.2. Determination of laccase enzyme activity

Among the 27 microbial strains analyzed, several demonstrated exceptionally high laccase enzyme activity, notably S1.05 (1430.0 ± 3.66 U/mL), S8.01 (1368.2 ± 3.64 U/mL), and S11.01 (1306.4 ± 3.62 U/mL). These strains are of particular interest for the biodegradation of LDPE, a persistent plastic polymer commonly found in packaging waste. Laccases are known for their ability to oxidize a wide range of recalcitrant compounds, including synthetic polymers such as LDPE, especially when assisted by mediators [23]. Research has shown that laccase-producing fungi and bacteria can enhance LDPE degradation through surface oxidation, which promotes fragmentation and microbial colonization [24].

The high laccase activities observed in these strains suggest strong oxidative capacity, making them potential candidates for LDPE treatment, either as free enzymes or whole-cell biocatalysts. In particular, S1.05, with the highest enzyme yield, could be optimized further through culture condition adjustment or co-cultivation strategies to maximize degradation efficiency. Previous studies have confirmed that laccase-producing microorganisms can reduce the molecular weight and surface hydrophobicity of LDPE films, thereby facilitating further microbial breakdown [25]. Moreover, integrating these strains into bioreactor systems or biofilm-based treatment models could offer sustainable alternatives to thermal or chemical LDPE disposal methods. Therefore, the identification of these potent laccase producers presents a promising foundation for developing environmentally friendly solutions to address plastic pollution in terrestrial and marine environments.

From 27 microbial strains, 12 strains with laccase activity from 750 U/mL were selected for further studies (Table 3).

Table 3. Laccase enzyme activity of microbial strains

№	Strain ID	Laccase enzyme activity (U/mL)	№	Strain ID	Laccase enzyme activity (U/mL)
1	S1.01	242.2 ± 1.22	15	S6.02	350.9 ± 1.29
2	S1.02	648.0 ± 1.37	16	**S6.03**	**997.3 ± 3.40**
3	S1.03	290.6 ± 1.84	17	S7.01	476.5 ± 1.29
4	S1.04	715.6 ± 0.82	18	**S8.01**	**1368.2 ± 3.64**
5	**S1.05**	**1430.0 ± 3.66**	19	S9.01	542.2 ± 1.22
6	S2.01	276.5 ± 1.29	20	S9.02	660.8 ± 0.67
7	**S2.02**	**874.0 ± 3.20**	21	S9.03	739.7 ± 0.78

№	Strain ID	Laccase enzyme activity (U/mL)	№	Strain ID	Laccase enzyme activity (U/mL)
8	**S3.01**	**750.0 ± 3.00**	22	**S9.04**	**1059.1 ± 3.45**
9	S3.02	460.8 ± 0.67	23	**S10.01**	**1182.7 ± 3.55**
10	**S3.03**	**935.5 ± 3.30**	24	**S11.01**	**1306.4 ± 3.62**
11	**S4.01**	**1120.9 ± 3.50**	25	**S11.02**	**850.0 ± 3.00**
12	S5.01	262.7 ± 1.57	26	S12.01	305.7 ± 1.07
13	S5.02	330.9 ± 1.45	27	S12.02	482.2 ± 1.30
14	**S6.01**	**1244.6 ± 3.60**			

3.3. Microbial identification

The identification of 12 marine microbial strains based on 16S rRNA gene sequence similarity revealed that several species with high potential for LDPE biodegradation were present. Notably, *Bacillus subtilis* (strains S1.05, S6.01 and S10.01) showed 99.7-100% similarity to reference strains, indicating a strong taxonomic match. *Bacillus subtilis* is well-known for its ability to secrete extracellular enzymes such as laccase and protease, which have been associated with polyethylene degradation [26]. Similarly, *Bacillus licheniformis* (S3.03 and S9.04) and *Bacillus cereus* (S2.02) have also been documented as efficient plastic-degrading bacteria, likely due to their robust enzymatic systems and biofilm-forming abilities [27].

The presence of *Pseudomonas* spp. (S4.01, S6.03, S11.01) including *P. aeruginosa*, further supports the potential for LDPE biodegradation, as members of this genus are widely recognized for their metabolic versatility and hydrocarbon degradation pathways [13]. *Pseudomonas aeruginosa*, in particular, has demonstrated efficient colonization of plastic surfaces and oxidative degradation capabilities.

Table 4. Microbial identification was based on 16S rRNA sequence similarity with reference strains in the NCBI database

№	Strain ID	Species name	16S rRNA gene sequence similarity (%)
1	S1.05	*Bacillus subtilis*	99.7
2	S2.02	*Bacillus cereus*	100
3	S3.01	*Streptomyces* sp.	100
4	S3.03	*Bacillus licheniformis*	98.5
5	S4.01	*Pseudomonas* sp.	100
6	S6.01	*Bacillus subtilis*	100
7	S6.03	*Pseudomonas aeruginosa*	100
8	S8.01	*Streptococcus sp.*	99.6
9	S9.04	*Bacillus licheniformis*	100
10	S10.01	*Bacillus subtilis*	100
11	S11.01	*Pseudomonas* sp.	100
12	S11.02	*Streptomyces* sp.	100

Additionally, strains affiliated with *Streptomyces* spp. (S3.01, S11.02) and *Streptococcus* sp. (S8.01) may contribute to LDPE degradation through secondary metabolite production and cooperative enzymatic activities. Streptomyces species are known producers of oxidative

enzymes such as peroxidases and monooxygenases, which are key to initiating polyethylene chain scission [28].

The high sequence similarity (≥98.5%) of all isolates to known species suggests accurate identification and indicates their strong taxonomic affiliation. The diversity of genera represented in the isolate collection - *Bacillus*, *Pseudomonas*, *Streptomyces*, and *Streptococcus* - reflects a broad enzymatic repertoire, making them promising candidates for bioaugmentation strategies targeting LDPE waste in marine environments.

3.4. Combination of microbial formulas

The integration of multiple bacterial strains into a synergistic formula has emerged as a promising strategy to enhance the biodegradation of LDPE. In this study, microbial isolates belonging to the genera *Bacillus*, *Pseudomonas*, *Streptomyces*, and *Streptococcus* exhibited high laccase enzyme activities and significant sequence similarity to known degraders. Each genus contributes uniquely to the degradation process: *Bacillus* species are prolific producers of oxidative enzymes and are efficient in biofilm formation; *Pseudomonas* species offer strong metabolic adaptability and hydrocarbon-degrading pathways; *Streptomyces* species provide secondary metabolites and powerful oxidases; while *Streptococcus* may assist through cooperative degradation mechanisms.

In addition, microorganisms with the same distribution location will have the ability to combine well with each other because they belong to the same natural community. Based on the isolation location and identification results, 03 microbial formulas were formed to evaluate the efficiency of LDPE degradation at the bacterial consortium level including: microbial formula 1 (MF1) including strains: S1.05, S3.01, S3.03, S4.01; microbial formula 2 (MF2) including strains: S2.02, S6.01, S6.03, S8.01; microbial formula 3 (MF3) includes strains: S9.04, S10.01, S11.01, S11.02.

This approach aligns with previous findings suggesting that microbial consortia are often more effective than single isolates in degrading recalcitrant polymers [29]. The formulation of a multi-strain biodegradation system offers a practical and environmentally friendly solution to LDPE pollution in marine and coastal ecosystems such as Vung Tau, Vietnam.

3.5. Evaluation of LDPE degradation ability of microbial formulations

In this study, three microbial formulas (MF1, MF2, and MF3) were cultured in a mineral medium containing 0.5% LDPE as the sole carbon source to assess their degradation efficiency. The graph illustrates the LDPE degradation performance of three bacterial formulas after 90 days of incubation in a mineral medium supplemented with 0.5% LDPE. The results clearly demonstrate significant differences in degradation efficiency among the formulas. MF1 showed the lowest LDPE weight reduction at 5.2%, indicating limited polymer degradation capability, likely due to weak enzymatic activity or suboptimal bacterial synergy. MF2 performed moderately better, achieving 11.8% reduction, which suggests the presence of more active strains or improved metabolic cooperation within the consortium.

The most promising result was obtained with MF3, which achieved the highest substrate weight loss at 17.4%, accompanied by a low standard error, demonstrating both effectiveness and stability. The superior performance of MF3 may be attributed to the synergistic interaction among its constituent microbial strains, which likely include high laccase-producing and biofilm-forming isolates such as *Bacillus subtilis*, *Pseudomonas aeruginosa*, and *Streptomyces* sp. These microorganisms, when combined, can enhance oxidative degradation through complementary enzymatic pathways, facilitating the initial oxidation and subsequent cleavage of LDPE chains. Furthermore, the biofilm matrix may support adhesion to the hydrophobic plastic surface and stabilize enzymatic microenvironments, thereby improving the overall

efficiency of degradation. This implies that MF3 contains a more potent combination of plastic-degrading microorganisms, potentially producing laccases, peroxidases, or alkane monooxygenases-enzymes known to contribute to polyethylene degradation [30, 31]. The ability of MF3 to significantly reduce LDPE substrate weight supports its candidacy for development into microbial formulations aimed at mitigating plastic pollution, especially in environments contaminated with LDPE.

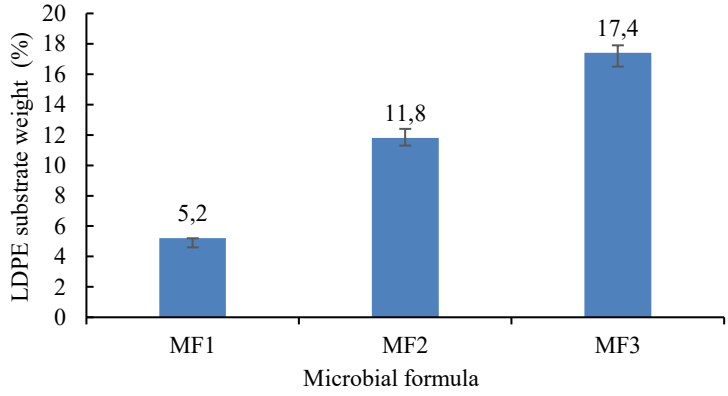

Figure 3. LDPE substrate reduction rate of microbial formulations

These findings are consistent with previous studies, which emphasize that microbial consortia often outperform single strains in polymer biodegradation due to metabolic diversity and synergistic enzyme production [21]. Future investigations should focus on optimizing MF3 composition, scaling up the process, and testing its effectiveness in real-world Given its proven capability to significantly reduce LDPE mass under laboratory conditions, MF3 holds strong potential for development into a microbial preparation for treating plastic waste, especially in marine-influenced environments such as coastal regions of Vietnam. Its application could be further optimized through scale-up in bioreactors, solid-state fermentation, or in-situ bioaugmentation approaches targeting plastic-polluted habitats.

4. CONCLUSION

This study demonstrated the potential of marine microorganisms, isolated from sediment and plastic waste samples collected in Ba Ria - Vung Tau province, Vietnam, to biodegrade LDPE plastic. A total of 27 microbial strains were obtained through enrichment culture with LDPE, and 12 strains exhibiting significant laccase enzyme activity (ranging from 750.0 ± 3.00 to 1430.0 ± 3.66 U/mL) were selected for further investigation. Molecular identification based on 16S rRNA gene sequencing revealed that these strains belong to the genera *Bacillus*, *Pseudomonas*, *Streptomyces*, and *Streptococcus* - all of which have been previously associated with plastic-degrading capabilities.

Three microbial formulas (MF1, MF2, MF3) were constructed from selected strains. Among them, MF3 (containing *Bacillus licheniformis*, *Bacillus subtilis*, *Pseudomonas* sp., and *Streptomyces* sp.) achieved the greatest LDPE degradation, reducing the substrate weight by 17.4% ± 0.9 after 90 days. These findings emphasize the potential of using marine-derived microbial consortia for the biodegradation of recalcitrant plastic waste, particularly LDPE. The results provide a valuable basis for the future development of microbial preparations aimed at addressing the persistent environmental issue of plastic pollution. Further research should explore large-scale application, long-term environmental impact, and the enzymatic mechanisms involved in LDPE degradation.

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TÓM TẮT

ĐÁNH GIÁ TIỀM NĂNG ỨNG DỤNG TRONG XỬ LÝ RÁC THẢI NHỰA LDPE CỦA VI SINH VẬT BIỂN PHÂN LẬP TẠI KHU VỰC BIỂN THUỘC TỈNH BÀ RỊA - VŨNG TÀU, VIỆT NAM

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Rác thải nhựa polyethylene mật độ thấp (LDPE) là loại chất thải không phân hủy gây ra mối đe dọa đáng kể cho môi trường trên toàn cầu. Trong các biện pháp phân hủy nhựa, phân hủy sinh học, sử dụng các chủng vi sinh vật, là biện pháp bền vững và hiệu quả nhất. Biện pháp phân hủy sinh học có ưu điểm thân thiện với môi trường, không gây ô nhiễm thứ cấp, chi phí thấp. Nghiên cứu này đánh giá khả năng ứng dụng trong xử lý rác thải nhựa polyethylene mật độ thấp bằng vi sinh vật biển phân lập từ vùng biển tỉnh Bà Rịa - Vũng Tàu, Việt Nam. Từ 12 mẫu (09 mẫu trầm tích biển và 03 mẫu rác thải nhựa), 27 chủng vi sinh vật đã được chọn lọc thông qua làm giàu với 0,5% cơ chất LDPE. Trong đó, các mẫu trầm tích biển ghi nhận tỷ lệ chủng trên một mẫu cao hơn so với các mẫu rác thải nhựa. Dựa trên khả năng sinh enzyme laccase, 12 chủng (có hoạt tính enzyme laccase từ 750,0 ± 3,00 U/mL đến 1430,0 ± 3,66 U/mL) đã được chọn để định danh và nghiên cứu tính đối kháng giữa các chủng. Có 03 tổ hợp vi sinh vật được hình thành bao gồm: tổ hợp vi sinh vật 1 (MF1) gồm các chủng: S1.05, S3.01, S3.03, S4.01; tổ hợp vi sinh vật 2 (MF2) gồm các chủng: S2.02, S6.01, S6.03, S8.01; tổ hợp vi sinh vật 3 (MF3) gồm các chủng: S9.04, S10.01, S11.01, S11.02. Ba tổ hợp vi sinh vật được nuôi cấy trong môi trường khoáng bổ sung 0,5% cơ chất LDPE. MF3 là tổ hợp vi sinh vật có khả năng giảm khối lượng cơ chất tốt nhất (giảm 17,4% so với khối lượng cơ chất ban đầu sau 90 ngày nuôi cấy). Tổ hợp vi sinh vật MF3 có tiềm năng ứng dụng để tạo ra chế phẩm vi sinh xử lý rác thải nhựa có nguồn gốc từ LDPE. Kết quả thu được từ nghiên cứu này có thể là nguồn dữ liệu đáng tin cậy cho việc nghiên cứu, phát triển chế phẩm vi sinh xử lý rác thải nhựa, góp phần giải quyết tình trạng ô nhiễm rác thải nhựa hiện nay.

Từ khóa: LDPE, phân hủy sinh học, rác thải nhựa, tổ hợp vi sinh vật, vi sinh vật biển.