



Article Biodeterioration of Microplastics by Bacteria Isolated from Mangrove Sediment

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Abstract: As a kind of ubiquitous emerging pollutant, microplastics (MPs) are persistent in the environment and have a large impact on the ecosystem. Fortunately, some microorganisms in the natural environment can degrade these persistent MPs without creating secondary pollution. In this study, 11 different MPs were selected as carbon sources to screen the microorganisms for degradable MPs and explore the possible mechanism of degradation. After repeated domestication, a relatively stable microbial community was obtained after approximately 30 days later. At this time, the biomass of the medium ranged from 88 to 699 mg/L. The growth of bacteria with different MPs ranged from 0.030 to 0.090 optical density (OD) 600 of the first generation to 0.009–0.081 OD 600 of the third generation. The weight loss method was used to determine the biodegradation ratios of different MPs. The mass losses of polyhydroxybutyrate (PHB), polyethylene (PE), and polyhydroxyalkanoate (PHA) were relatively large, at 13.4%, 13.0%, and 12.7%, respectively; these figures for polyvinyl chloride (PVC) and polystyrene (PS) were relatively slight, 8.90% and 9.10%, respectively. The degradation half-life $(t_{1/2})$ of 11 kinds of MPs ranges from 67 to 116 days. Among the mixed strains, Pseudomonas sp., Pandoraea sp., and Dyella sp. grew well. The possible degradation mechanism is that such microbial aggregates can adhere to the surface of MPs and form complex biofilms, secrete extracellular and intracellular enzymes, etc., break the hydrolyzable chemical bonds or ends of molecular chains by attacking the plastic molecular chains, and produce monomers, dimers, and other oligomers, leading to the reduction of the molecular weight of the plastic itself.

Keywords: MPs; domestication; mechanism of biodegradation; 16S rDNA; mangrove sediment

1. Introduction

As one of the most common synthetic materials [1], global output of plastics has soared from 150 tons in 1950 to 391 million tons in 2021 [2]. Consequently, a huge volume of plastic waste infiltrates the environment each year. However, only 28% of plastics are recycled or incinerated [3]. Plastics can break into small pieces in the environment, ultimately forming stable small particles with a diameter of less than 5 mm that are known as microplastics (MPs) [4,5]. Generally, MPs include plastic fragments, particles, and textile fibers [6].

MPs are ubiquitous and are detected in the atmosphere, water, soil, and other environmental media [7–10]. The accumulation of MPs in the environment has adverse effects on organisms, soil, and water. In particular, widespread MP infiltration is a global concern for the aquatic environment, posing a threat to existing life forms. For example, MPs in aquatic ecosystems can lead to false satiety, pathological stress, reduced growth rates, and reproductive complications [11–13]. In addition, MPs easily bind to other toxic chemicals or metals, acting as vectors for such toxic substances [14] and causing synergetic pollution effects [15,16]. To control the ecological risk of MPs, the decontamination of MPs in the environment is crucial.

Microbial degradation is a promising ecofriendly method for the removal of MPs with no harm to the environment [17]. Therefore, screening and identifying microorganisms that can degrade different types of MPs is conducive to the natural bioremediation



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Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). process and the cleaning of the natural ecosystems. Most microorganisms are opportunistic and have inherent adaptability. They can adapt to every environment they find and have the potential to transform a variety of compounds, including plastic polymers [18]. During polymer degradation, microorganisms first adhere to the polymer surface, subjecting it to microbial colonization. Then, the microorganisms will secrete extracellular enzymes that bind to the polymer and cause hydrolysis and cleavage [19]. After that, the polymer is degraded into a low-weight polymer and mineralized into carbon dioxide and water for microorganisms to use as energy [20]. It has been found that certain microorganisms can degrade certain plastic particles. For example, polypropylene (PP) can be degraded by *Rhizopus arrhizus* [21] and *Vibrio* and *Pseudomonas* sp. [22]; *Bacillus* sp. can degrade polyethylene (PE) [18] and *Klebsiella*, *Citrobacter*, and other bacteria can degrade polystyrene (PS) [23].

The high temperature, high salinity, pH value, organic matter level, and low ventilation and humidity of mangrove sediment improve the substrate conditions to be conducive to the growth of a variety of microorganisms [24,25]. Additionally, mangroves can also improve the availability of a wide range of microorganisms with multiple types of potential. To the best of our knowledge, microbial degradation of different kinds of MPs has rarely been observed simultaneously. On that basis, this study was aimed at demonstrating the growth and biodegradation ability of bacterial isolates from mangrove sediment in the degradation of 11 kinds of MPs. The degradation degree of MPs in the sample can be examined according to the change in mass and the change in optical density (OD) value. 16S rDNA technology was used to identify microorganisms that can degrade different kinds of MPs. This study attempts to identify a remedial option for the accumulation of MPs in the marine environment and has certain significance for ecological restoration.

2. Materials and Methods

2.1. Chemicals

A total of 11 kinds of MPs—polyamide (PA), poly(butylene succinate) (PBS), polycaprolactone (PCL), polyethylene (PE), polyhydroxyalkanoates (PHA), polyhydroxybutyrate (PHB), polylactic acid (PLA), polypropylene (PP), polystyrene (PS), polyvinyl alcohol (PVA), and polyvinyl chloride (PVC)—were selected as carbon sources to screen microorganisms (Zhejiang Shangyu Yixin Ball Industry, Shaoxing, China). The particle size of the abovementioned MPs was determined by a 1000 mesh (13 μ m). Additionally, disodium phosphate (Na₂HPO₄), sodium dihydrogen phosphate (NaH₂PO₄) and ammonium dihydrogen phosphate (NH₄H₂PO₄) were added to cultivate microorganisms.

2.2. Sample Collection and Screening of MP-Degrading Bacteria

Sediment samples were collected in the mangrove area of Shenzhen, China ($114^{\circ}03'$ E, 22°32′ N). A sterile shovel was used to collect samples from a sediment depth of 1 to 5 cm. Different MP beads, NH₄H₂PO₄, and O₂ were used as the sole sources of carbon, nitrogen, and oxygen for culturing microorganisms. A liquid mixture of NH₄H₂PO₄ (5.00 g/L), sediment (67.0 g/L), and different MPs (1.00 g/L) was used to cultivate and domesticate microorganisms in mangrove sediment (pH 6.50–7.50, regulated by Na₂HPO₄ and NaH₂PO₄). Additionally, a blank cross reference was set. For the first generation of culture, 50.0 mL of liquid mixture was domesticated in the incubator shaker at ~29 °C at a vibration speed of 150 rpm [18].

Then, the cells were transferred to another fresh MPs–inorganic salt medium. An inoculation of 10% was conducted every 10 days. The weight of the medium and its OD 600 (0.05 < OD 600 < 0.90) were measured. For the blank control, the uninoculated medium without MPs was kept under similar conditions. This process was repeated until the microbial culture was adapted to the specific environment. After subculture was conducted three times, the relative abundance of operational taxonomic units (OTUs) of some strains in the growth medium increased significantly, while the concentration of MPs decreased. The main degrading microorganisms come from the third generation of bacterial suspensions.

2.3. Microbial Degradation of MPs

The mass change of the culture medium can reflect the degradation of the MPs to a certain extent. A four decimal balance (AL204-IC, Mettler Toledo, Shanghai, China) was used to weigh the mass change [26]. The turbidity method uses the OD (0.05 < OD 600 < 0.90) value to characterize the growth curve of microorganisms [27]. The OD 600 value mirrors the growth trend of microorganisms measured by ultraviolet spectrophotometry. The biomass (mg/L) was recorded as b, and the absorption coefficient was recorded as x. Then, the biomass of the microorganisms in the bacterial suspension was estimated by Equation (1) according to the OD value [28]:

$$\ln b = -1.05 \ln x + 4.26 \tag{1}$$

The weight loss of the MPs as a percentage was determined using Equation (2):

v

veight loss (%) =
$$\frac{(W_0 - W)}{W_0}$$
 (2)

where the initial weight and current weight were designated as W_0 and W, respectively. The data were further processed to determine the rate constant of MP reduction by using a first-order kinetic model (Equation (3)) based on initial and final weights at a specific time interval (10 days) [29]:

$$\mathbf{k} = -\frac{1}{t} \left(\ln \frac{\mathbf{W}}{\mathbf{W}_0} \right) \tag{3}$$

2.4. 16S rDNA

The total genomic DNA in the samples was extracted using a Soil DNA Kit. DNA (20.0–30.0 ng) was used to produce amplicons and the concentration was monitored with a Qubit 3.0 Fluorometer. The V3 and V4 hypervariable regions of prokaryotic 16S rDNA were selected to generate amplicons and perform classification analysis. Additionally, the index adapter was added to the end of the 16S rDNA amplicon to generate index libraries and prepare for the upstream and downstream next-generation Illumina sequencing. During the sequencing process, Illumina's built-in software was used to determine whether to retain or discard each sequencing fragment, i.e., read, based on the quantity of the first 25 bases. The original sequencing data (pass filter data) were obtained, and the results were stored in FASTQ file format, which includes sequencing information and the corresponding sequencing quantity information. Then, 1.00 μ L of each primer, 2.00 μ L dNTPs, 2.50 μ L TransStart Buffer, and 20.0 ng template DNA were used to carry out a chain reaction in a mixture of 25.0 μ L. These polymerase chain reactions were performed in triplicate.

Double-end sequencing was conducted and the positive and negative reads of the first of the two sequences were connected together to carry out filtering, with the results contained in the N sequence being joined together to retain the sequence lengths larger than 200 bp. The chimeric sequence was filtered and purified, and the obtained OTU cluster sequence was subjected to clustering with VSEARCH clustered (1.9.6) (sequence similarity was set to 97%). Moreover, the 16S rDNA reference database used was Silva 132. Additionally, the representative sequences were analyzed using the ribosomal database program classifier Bayesian algorithm for OTU species classification, and the community composition of each sample was determined on the basis of the statistics of different species classification levels.

3. Results and Discussion

3.1. Bacterial Screening and Identification

Compared with other degradable materials, plastics are not susceptible to microbial attack [30]. However, MPs provide a new niche for microorganisms, support the colonization and growth of microorganisms, and serve as a carbon source. To explore the degradation behavior of MPs, different kinds of MP-degrading microorganisms were screened from mangrove sediment.

Optical density, reflecting the growth of strains, is widely used to estimate the concentration of cells in liquid cultures [18]. Figure 1 shows the growth curve of microorganisms cultured with different kinds of MPs as the sole carbon source.



Figure 1. Change in OD values of culture liquid with various MPs as carbon sources. The line colors from light to dark represent the first generation to the third generation of domestication. Subfigures (**a**–**k**) represents the changes in 11 types of MPs.

In the first three days, the growth of microorganisms usually has a lag time for the microbial OD value, during which the OD value basically decreases rather than increases. The reason for this phenomenon is that cell proliferation is required to synthesize various

substances and undergo a process of adjustment and adaptation [28]. Within 4–5 days of culture, the microorganisms showed signs of growth around the polymer particles and began to attach to the polymer particles. After 10 days, the OD of the bacterial suspension fluctuated, and the microorganisms extended around the particles within 10–15 days, when the microbial growth rate was the highest. At this stage (the growth regulation period), the enzyme system was active, and metabolism was vigorous. No growth was observed on the control sample. After repeated domestication, the ability to degrade MPs was stronger, the degrading strains were continuously enriched, and a relatively stable microbial community was formed approximately 30 days later. At this time, the biomass range was 88 mg/L (PP)–699 mg/L (PE). Specifically, the growth of bacteria with different MPs ranged from 0.30 to 0.90 in the first generation to 0.09–0.81 in the third generation indicating that mixed strains of microorganisms adapted to the culture conditions and used MPs as the corresponding carbon source for growth.

In general, the time trends for the OD values of different MPs were the same (Figure 1). Taking PP as an example, obvious growth was observed from Day 0 (0.60) to Day 10 (0.80) (Figure 1c). Our results were comparable to those of other studies [27]. The effect of a single strain on the degradation of PP was studied, and it was found that its OD value ranged from Day 0 (0.251) to Day 10 (0.903) [27]. However, the increase in the growth rate on Day 10 does not indicate a strong reaction and performance of microorganisms when exposed to MPs. The increase shows that this period was conducive to the interaction between the bacterial cell membrane and MPs, thus allowing rapid metabolism. From Day 20 to Day 30 after exposure to PP, it was observed that the growth of microorganisms decreased from 0.80 to 0.64. The decline in the OD value may have been caused by dilution of the culture medium, cell lysis, nutrient depletion, etc. [31]. Different types of MPs can be used as the sole carbon source to screen microorganisms in the mixed bacterial suspension with different MPs as the sole carbon source was different. For example, the original structure of the microbial populations in mangrove sediment may be responsible for this.

3.2. Reduction Rate of MPs

The weight loss of MPs after inoculation of mangrove mixed strains caused by microbial action was examined (Figure 2). With the increasing of culture time, the quantity of MPs decreased. However, there were obvious differences between different MPs. After 30 days of degradation, the gravimetric weight losses of PHB, PE, PHA, PVC, and PS were 13.4%, 13.0%, 12.7%, 8.90%, and 9.10%, respectively.

Our results (Table S1) were comparable with those of previous studies that obtained the gravimetric weight loss of PS (12.4%) and PE (7.50%) after 42 days and 56 days of degradation, respectively [32] (Figure 3). According to the present study, after 30 days of culture, the gravimetric weight loss of PS and PE reached 9.10% and 13.0%, respectively. These results were lower than that of PS degraded for 140 days (52.4%). A possible explanation may be that four strains that were most suitable for PE degradation were used in their study, and their degradation time was also much longer than ours [33]. In a previous study [27], two single strains were used to degrade PP, and the weight loss of PP was 6.40% and 4.00% after 40 days of culture. Our result (13.1%) was higher than these figures. This underscored that a mixed culture performs better than a single microbial culture in the environment [34]. PLA is a biodegradable plastic and its gravimetric weight loss reached 12.2%. A previous study [35] found that after incubation with *Stenotrophomonas maltophilia LB 2-3*, the molecular weight and tensile properties of PLA decreased rapidly.



Figure 2. The mass reduction ratios of 11 kinds of MPs over time. The blue and green dots refer to the weight change after 3 days and 30 days of culture.



Figure 3. Comparison of this study with other studies. The boxes and dots display the degradation ratios of microplastics in the previous studies and in this study.

Via dynamic simulation based on the experimental data, the biodegradation kinetic curves (Figure 4), kinetic equations, and corresponding coefficients of different MPs and the biodegradation half-life ($t_{1/2}$) of different MPs were obtained (Table 1). In general,

the fitted linear graph shows that the degradation data conform to the first-order kinetic equation, with an R^2 of 0.70–0.90. According to mathematical statistical analysis, when the correlation coefficient R^2 of the model is between 0.5 and 1, it is considered to indicate a strong correlation [36]. The K value of the 11 MPs was 0.006–0.010 (Table 1). Regarding the relative order of biodegradation difficulty, PA was the most difficult to degrade, followed by PS, and PHB was the easiest to degrade. For all 11 kinds of MPs involved in this study, the main difference lies in their carbon chain structure. For example, the main chain of polyolefin plastics (e.g., PS) is composed of a carbon skeleton with stable chemical properties and a low degradation rate [37]. However, polyester (e.g., PLA) contains ester bonds that are easy to hydrolyze and are easily biodegradable [38]. For example, the t_{1/2} of PLA was 85.76 days and that of PS was 114.1 days.



Figure 4. Degradation kinetics of 11 MPs in response to bacteria isolated from mangrove sediment. The different colored lines represent the degradation kinetics curves of 11 types of MPs.

Table 1. Eleven MP deg	radation kinetic	equations and	coefficients.
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Types	OD	R ²	K	Degradation Kinetics	t _{1/2} (Day)
PVC	0.13	0.89	0.0074	$W = W_0 \times 10^{-0.007t}$	93.34
PS	0.21	0.89	0.0061	$W = W_0 \times 10^{-0.006t}$	114.1
PVA	0.47	0.89	0.0102	$W = W_0 \times 10^{-0.01t}$	68.17
PA	0.68	0.80	0.0060	$W = W_0 \times 10^{-0.006t}$	115.6
PHB	0.35	0.73	0.0102	$W = W_0 \times 10^{-0.01t}$	67.98
PCL	0.24	0.90	0.0061	$W = W_0 \times 10^{-0.006t}$	113.3
PBS	0.40	0.66	0.0069	$W = W_0 \times 10^{-0.007t}$	100.6
PLA	0.26	0.88	0.0081	$W = W_0 \times 10^{-0.008t}$	85.76
PP	0.82	0.76	0.0082	$W = W_0 \times 10^{-0.008t}$	84.84
PE	0.12	0.80	0.0085	$W = W_0 \times 10^{-0.008t}$	81.83
PHA	0.81	0.71	0.0067	$W = W_0 \times 10^{-0.007t}$	103.6

3.3. MP-Degrading Bacteria

16S rDNA detection of the microbial culture medium after 30 days of degradation provided species information on the MP-degrading bacteria (Figure 5). The results indicated that *Pseudomonas* sp., *Pandoraea* sp., and *Dyella* sp. could grow well in the mixed strains with the progress of domestication. These bacteria can make good use of a variety of organic and inorganic compounds, which enables them to live flexibly on the surface of MPs [39–41].



Figure 5. MP-relative abundance of degrading bacteria. The first column in the grid is the blank control and the next three columns correspond to the third generation of microorganisms.

Overall, different MP-degrading bacteria isolated from different environmental media are usually different with different degradation abilities. Specifically, the PS mass decreased by 9.20% within 30 days under the effect of *Hyphomicrobium* sp. and *Pandoraea* sp. Other studies showed that PS weight could be reduced by 12.4–40.2% under the action of *Pseudozyma japonica* Y7-09 [26,42]. Apparently, different bacteria that play a main role are responsible for this.

The main screened MP-degrading bacteria for PHB, PCL, and PVA in this study were *Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium* sp., *Pandoraea* sp., and *Pseudomonas* sp. Under their influence, the weight of the two kinds of MPs decreased by 13.4% and 9.70% within 30 days, respectively. Previous studies found that PHB (*Pseudomonas mendocina DS04-T*) [43], PCL (*Micorbispora rosea* subsp. *Taiwanensis HS* 45-1) [44], and PVA (*Penicillium* sp. *WAH02-21*) [45] can reach 100% degradation in approximately 10 days under the action of some specific bacteria. Obviously, the degradation effect of mangrove sediment mixed flora on PHB is relatively poor. This could be attributed to different

sources of bacteria. Our flora came from mangrove sediment, while *Micorbispora rosea* subsp. *Taiwanensis HS* 45-1 and other bacteria were isolated from soil.

Previous studies found that PBS (14 days) and PE (60 days) can degrade more than 87% under the action of fungi (*Bacillus pumilus 1-A*) [46] and soil bacteria (*Bacillus cereus VASB1/TS*) [47]. The bacteria we screened were different. For PBS, 11.8% of particles were degraded in 30 days, and *Pandoraea* and *Dyella* played a major role. The bacteria for PE degradation were *Acidovorax*, *Bdellovibrio*, and *Acinetobacter*.

Under the action of *Burkholderia-Caballeronia-Paraburkholderia*, the weight of PVC and PP decreased by 8.90% and 13.1%, respectively, within 30 days. Existing studies on the degradation of PVC have found that under the action of *Chaetomium globosum*, PVC can be degraded by ~9% after 28 days [48]. The main MP-degrading bacteria for PP is *Stenotrophomonas panacihumi PA3-2*, which can degrade PP by 18.4% in 40 days [49]. Our results show that the main degrading bacteria for PA, PLA, and PHA are *Novosphingobium*, *Dyella*, and *Burkholderia-Caballeronia-Paraburkholderia*, which degrade approximately 12.0%. The *Bacillus* sp. mentioned above can achieve 7% and 40% degradation rates for PA and PLA, respectively.

3.4. Degradation Mechanism

In the culture medium, first, some microbial aggregates composed of cells and extracellular polymers can adhere to each other or adhere to the surface of MPs to form complex biofilms [50–52] (Figure 6a). The biofilm includes one or more bacteria, which is a biological community with diversity in phylogeny and function [53]. Microbes in biofilms usually have the potential to metabolize a variety of substances, so the formation of biofilms plays a very important role in the microbial degradation of plastics. For example, using *Bacillus* sp. *JY36* to degrade PHB, PBS, PCL, and PBAT, the growth area of *Bacillus* sp. *JY36* was obvious after 7 days [54]; bacteria such as *Alcanivorax* sp., *Marinobacter* sp., and *Arenibacter* sp. were detected in biofilms formed on the surface of marine plastic fragments, and a large number of oxygen-containing functional groups were formed on the plastic surface, proving the potential of biofilms to degrade plastics [55].

Taking PE as an example, microorganisms with the ability to degrade MPs in the biofilms secrete extracellular and intracellular enzymes (Figure 6b), which break the end of the hydrolyzable chemical bond or molecular chain by attacking the plastic molecular chain, producing monomers, dimers, and other oligomers, leading to a reduction in the molecular weight of the MPs themselves [56,57]; meanwhile, PE is further oxidized under the action of oxygen to form hydroxyl-, carbonyl-, carboxyl- and other oxygen-containing functional groups (Figure 6c) [58]. The broken molecular chains and oligomers formed will be released into the surrounding environment, and some water-soluble short-chain intermediates in these depolymerized products will be recognized by the receptor and transported to the microbial body across the membrane as a carbon source for microbial metabolism and growth [59,60]. It is worth noting that some bacteria not only have the ability to degrade the polymer itself, but also have a strong ability to degrade the monomers, dimers, and other oligomers that make up the polymer [61].

The oligomer entering the microorganism will gradually remove the carbon atom on the plastic polymer molecular chain and degrade under the effect of the metabolic mechanism (mainly β -oxidation mechanism) in vivo [62] (Figure 6d). The β -oxidation mechanism starts from the combination of fatty acids produced after oligomer oxidation with coenzyme A (HSCoA) to produce fatty acetyl coenzyme A. Then, it goes through dehydrogenation, water addition, dehydrogenation, and sulfur hydrolysis. In the fatty acid, the connection of carbon atoms $\alpha 0$ and $\beta 0$ is broken to produce acetyl coenzyme A and fatty acetyl coenzyme A with two carbon atoms removed. The cyclic reaction between coenzyme A and fatty acetyl coenzyme A with two carbon atoms removed completely oxidizes the fatty acid.



Figure 6. This represents the mechanism by which the microbial culture medium degrades microplastics. Subfigures (**a**) represents the microorganisms attach on the MPs surface to form biofilm. Subfigures (**b**) represents the microorganisms with plastic degrading ability secrete enzymes and other substances to attack the MP surface. Subfigures (**c**) represents some long chain polymers break to form oligomers and oxidize under the influence of oxygen to form carbonyl. Subfigures (**d**) represents some oligomers are ingested and assimilated by in vivo metabolism mechanism by microorganisms.

Acetyl coenzyme A enters the tricarboxylic acid cycle (TCA cycle) (Figure 6d). The TCA cycle is one of the important ways for microorganisms to metabolize organic substances and obtain energy for growth and development [63]. In the TCA cycle, acetyl coenzyme A generated from oligomers through a β -oxidation mechanism acts as a key intermediate to oxidize organic substances and produce adenine triphosphate (ATP) to provide energy for cells.

Finally, after a series of metabolism processes in vivo, the oligomers undergo mineralization (Figure 6d). The type of mineralization products of mineralization depends on the availability of oxygen: after mineralization in an aerobic environment, organisms mainly release CO_2 and H_2O , while under anoxic or anaerobic conditions, they produce CH_4 , NH_3 or H_2S [64].

3.5. Limitations

In this study, mangrove sediment was used to domesticate and degrade different MPs. By measuring the weight loss of different MPs before and after microbial degradation and comparing the weights with that of the control, the degradation effect of microorganisms on MPs can be judged intuitively by percentage, which is conducive to comparing the degradation ability of different strains horizontally. The weight loss method is currently a widely used method. However, there are some limitations; for example, the degradation phenomenon cannot be displayed directly and the decomposition rate is generally slow.

Appropriate improvements can also be made in the methods for screening MPdegrading bacteria, such as through directional acclimation of the in situ environment, stable isotope probe technology combined with laboratory culture, and construction of highly efficient MP-degrading bacteria based on synthetic microbiome, which can improve the efficiency of isolation of MP-degrading bacteria from the environment. In addition, the characteristics, optimization of degradation conditions, and degradation mechanism of different MP-degrading bacteria can also be studied in a follow-up of this study to further improve the degradation efficiency of MP-degrading bacteria.

4. Conclusions

According to our results, the biomass of the microbial culture medium after acclimation ranged from 88 to 699 mg/L. The bacterial growth on different MPs ranged from 0.03 to 0.09 OD 600 for the first generation to 0.009 to 0.081 OD 600 for the third generation. The weight loss method detected that the mass losses of PHB, PE, and PHA with large weight losses were 13.4%, 13.0%, and 12.7% after 30 days of degradation, respectively. The mass losses of PVC and PS were relatively low, at 8.90% and 9.10%, respectively. The degradation cycle $t_{1/2}$ for the 11 kinds of MPs ranged from 67 to 116 days. As domestication progressed, *Pseudomonas* sp., *Pandoraea* sp., and *Dyella* sp. were able to grow well in the mixed strains. The possible mechanism of degradation is that microbial aggregates can adhere to the surface of MPs and form complex biofilms, secrete extracellular and intracellular enzymes, break the hydrolyzable chemical bonds or ends of molecular chains by attacking the molecular chains of the MPs, and produce monomers, dimers, and other oligomers, leading to a reduction in the molecular weight of the MPs. In the future, screening high degradation efficiency microbial communities and verifying degradation mechanisms should be given more attention.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/toxics11050432/s1, Table S1: Comparison of degradation and screening microorganisms of different microplastics. References [65–81] are cited in the supplementary materials.

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