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Genome analysis of *Streptomyces nigra* PRNP1-1W reveals enzymes and metabolic pathways associated with mesophilic poly(butylene succinate) biodegradation

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ABSTRACT

Poly(butylene succinate) (PBS) is a biodegradable polyester that can degrade slowly in the environment, and mesophilic PBS-degrading bacteria remain insufficiently characterized. *Streptomyces nigra* PRNP1-1W, isolated from the Lower Mekong Basin, Thailand, formed a halo on emulsified PBS agar at 30°C ± 2°C. Its identity was supported by average nucleotide identity based on BLAST (ANIb) of 99.22%–99.37% and digital DNA–DNA hybridization of 95.9%. The 7.8-Mbp genome had 71.95 mol% G+C content and 7,440 predicted protein-coding sequences. Genome mining identified eight putative hydrolase genes, including OKIOMFPC_02247, a predicted secreted polyethylene terephthalate hydrolase-like protein sharing 51%–73% amino acid identity and a conserved catalytic triad with experimentally characterized PBS-hydrolyzing enzymes, proposed as a candidate PBS depolymerase. Among the conditions tested, the highest enzymatic activity index on PBS agar occurred at 35°C and initial pH 8.0. The isolate achieved 43.20% ± 5.40% net PBS weight loss after 10 days at 10 g/L. High-performance liquid chromatography and GC–MS/MS analyses provided preliminary indications of succinic acid and 1,4-butanediol, respectively, but their assimilation was not established. Scanning electron microscopy and Fourier-transform infrared spectroscopy provided qualitative information on PBS surface morphology and functional groups. These findings demonstrate the PBS-degrading potential of PRNP1-1W under mesophilic conditions.

1. INTRODUCTION

Poly(butylene succinate) (PBS) is a biodegradable aliphatic polyester increasingly recognized as a viable alternative to conventional petroleum-based plastics [1]. Its outstanding mechanical properties and biodegradability make it useful for a wide range of applications, including packaging materials, agricultural films, and disposable items [2]. Although PBS still represents a small fraction of the global plastics market, at approximately 368 million tonnes annually [2], its global production capacity was reported at approximately 30,000 metric tonnes in 2023 [1] and is expected to expand as new production facilities are established. Nevertheless, the accelerating production and disposal of PBS have contributed to its accumulation in the environment, as degradation under natural conditions proceeds slowly and incompletely [3,4].

Microbial degradation, in which bacteria and fungi enzymatically depolymerize synthetic polymers into simpler, non-toxic metabolites, represents a biologically and economically feasible approach to PBS waste remediation [5,6]. PBS is a polyester in which succinic acid and 1,4-butanediol are linked by ester bonds, and its breakdown is initiated by extracellular hydrolytic enzymes that cleave these bonds at the polymer surface. Several enzyme classes have been implicated in this process, including cutinases, lipases, esterases, and serine proteases [1]. Cutinases and lipases, produced by fungi and by bacteria such as actinomycetes, hydrolyze PBS chains into oligomers and monomers [1,3,6], while serine proteases have also been reported to degrade PBS and PBS/ polylactic acid (PLA) blends [4]. The resulting water-soluble products, mainly succinic acid and 1,4-butanediol, can then be taken up by the cells and assimilated as carbon and energy sources, ultimately being mineralized to water, carbon dioxide, and biomass [7]. Beyond mineralization, these hydrolysis products are valuable building blocks: succinic acid is used to produce biodegradable polymers, food additives, pharmaceuticals, and solvents, while 1,4-butanediol is an important precursor for polyesters, polyurethanes, and other industrial chemicals [1,8].

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Members of the genus *Streptomyces* are well-established producers of extracellular hydrolytic enzymes, and their versatile secondary metabolism positions them as strong candidates for polymer depolymerization [9]. Several studies have demonstrated the capacity of *Streptomyces* species to degrade biodegradable polyesters, including polycaprolactone (PCL) and PLA, through esterase- and lipase-mediated hydrolysis [10,11]. Despite this, evidence of PBS degradation by *Streptomyces* remains limited, and the underlying genetic determinants have not been characterized at the genomic level. The present study therefore isolated and characterized a PBS-degrading *Streptomyces* strain, employing whole-genome sequencing (WGS) and genome mining to identify putative degradative enzymes and metabolic pathways involved in PBS bioconversion.

Comprehensive identification and characterization of PBS-degrading microorganisms are essential for resolving the enzymatic and metabolic mechanisms underlying polymer bioconversion [11,12]. Whole-genome sequencing has emerged as a particularly powerful approach in this context, enabling the systematic identification of degradative genes, enzyme-coding sequences, and associated metabolic pathways in a single analytical framework [13,14].

The Lower Mekong Basin in Thailand harbors considerable microbial diversity shaped by prolonged exposure to organic substrates and environmental pollutants, including plastic debris. A previous study reported PBS-degrading bacteria isolated from this region, though degradation was demonstrated at 50°C, limiting practical applicability under ambient environmental conditions [15]. Whether mesophilic isolates from the same region possess comparable degradative capacity has not been established. In the present study, PBS-degrading bacteria were isolated from environmental samples collected in the Lower Mekong Basin and characterized for their ability to degrade PBS under mesophilic conditions. Whole-genome sequencing and genome mining were subsequently employed to elucidate the putative enzymatic machinery and metabolic pathways underlying PBS bioconversion in *Streptomyces nigra* PRNP1-1W.

2. MATERIALS AND METHODS

2.1. Preparation of PBS Substrates

PBS pellets (FZ91PD; Mitsubishi Chemical Corporation, Japan) at 2.0 g were solubilized in dichloromethane (10 ml; RCI Labscan, Thailand) to obtain a homogeneous polymer solution, which was slowly dispersed in 50 ml of sterile 0.1 M Tris–HCl buffer (Tris base, Vivantis, Malaysia) (pH 9.0). The mixture was emulsified using probe ultrasonication (Vibra-Cell Ultrasonic Processor) for 1 minute, and the suspension was left in a fume hood overnight to ensure complete evaporation of the organic solvent. The emulsified PBS material was recovered and stored at 4°C prior to subsequent experiments.

PBS powder was prepared by dissolving PBS granules (2.0 g) in chloroform (100 ml; RCI Labscan, Thailand), spreading the solution onto a flat tray, and allowing the solvent to evaporate overnight under a fume hood at ambient temperature. The dried PBS film was mechanically ground and sieved to obtain particles smaller than 4 mm.

2.2. Isolation and Primary Screening of PBS-Degrading Bacteria

Soil sediment was collected from the Lower Mekong Basin at Downtown Quayside, Nakhon Phanom Province, Thailand (17.3981° N, 104.7915° E), originating from the same sampling site and event as those described in our previous study but isolated under different conditions [15]. To isolate PBS-degrading bacteria, soil sediment (10 g) was homogeneously dispersed in 40 ml of sterile 0.85% (w/v) NaCl by vortexing. One hundred microliters of the suspension were spread onto emulsified PBS agar plates (2.0 g/L yeast extract (HiMedia, India), 2.0 g/L K_2HPO_4 (KemAus, Australia), 1.0 g/L KH_2PO_4 (KemAus, Australia), 0.5 g/L $MgSO_4 \cdot 7H_2O$ (KemAus, Australia), 15.0 g/L agar (Difco, USA), and 0.65% (v/v) emulsified PBS). Plates were incubated at room temperature (30°C ± 2°C) for 14 days, and colonies exhibiting a clear halo zone indicative of PBS hydrolysis were selected for further investigation [15].

Selected colonies were purified by repeated streaking on emulsified PBS agar plates and incubated at 30°C ± 2°C for 7 days. For long-term storage, cell suspensions or spore suspensions were mixed with 20% (v/v) sterile glycerol and stored at −80°C.

Selected isolates were screened for hydrolytic activity by single-point inoculation onto emulsified PBS agar plates, followed by incubation at 30°C for 7 days. Hydrolytic activity was quantified using the enzymatic activity index (EAI), calculated as the ratio of the clear halo zone diameter to the colony diameter, where both diameters were measured in millimeters (mm). The isolate exhibiting the largest and most distinct clear halo zone was selected for further examination of PBS degradation under submerged conditions.

2.3. Secondary Screening and Quantitative Assessment of PBS Degradation

PBS degradation was evaluated in 250 ml Erlenmeyer flasks containing 50 ml of minimal medium (MM) supplemented with 0.1% (w/v) PBS powder (particle size < 4 mm). The MM contained 2.0 g/L yeast extract, 2.0 g/L K_2HPO_4, 1.0 g/L KH_2PO_4, and 0.5 g/L $MgSO_4 \cdot 7H_2O$. Each flask was inoculated with 10% (v/v) of the selected isolate. Cultures were incubated at 30°C ± 2°C with orbital shaking at 150 rpm for 7 days. Uninoculated flasks containing PBS served as abiotic controls.

For inoculum preparation, one loopful of the culture was transferred into 50 ml of International *Streptomyces* Project medium 2 (ISP-2) containing yeast extract (4 g/L), malt extract (10 g/L), and dextrose (4 g/L) and incubated at 30°C ± 2°C with shaking at 150 rpm for 3 days. Following incubation, the cells were harvested and washed with sterile 0.85% (w/v) NaCl for 2 times to minimize the carryover of residual nutrients from the ISP-2 broth. The washed cells were subsequently resuspended in sterile 0.85% (w/v) NaCl and adjusted to an optical density at 600 nm (OD_{600}) of 1.0, corresponding to approximately 1.0×10^7 CFU/ml, and used as the inoculum for subsequent experiments at 10% (v/v), unless otherwise stated [11].

Following incubation, the culture was filtered through pre-weighed Whatman No. 3 filter paper (Cytiva, UK) to recover the solid fraction containing residual PBS particles and bacterial biomass. The retained material was washed with sterile 0.85% (w/v) NaCl and subsequently rinsed with distilled water to remove residual medium components and loosely attached bacterial cells.

Residual PBS particles and bacterial biomass were manually separated based on their distinct physical appearance and pigmentation. The PBS particles appeared as off-white flakes, whereas the bacterial biomass formed greenish-brown mycelial aggregates, allowing the two fractions to be visually distinguished and physically separated. The recovered PBS fraction was dried at 50°C for 6 hours to a constant weight and subsequently weighed for gravimetric determination

of residual PBS. The degree of PBS degradation was expressed as percentage weight loss, calculated as follows:

$$\text{Degradation (\%)} = \frac{W_i - W_f}{W_i} \times 100$$

where W_i and W_f denote the initial and final dry weights of PBS, respectively. Enzymatic activity of the culture supernatant was subsequently quantified by a modified turbidimetric assay as described by Phonlamai *et al.* [16]

An uninoculated control (MM containing PBS powder without the isolate) was incubated and processed under identical conditions to account for abiotic weight loss, including background hydrolysis during incubation. The weight loss of the control was calculated as follows:

$$\text{Abiotic weight loss (\%)} = \frac{W_{i,\,\text{ctrl}} - W_{f,\,\text{ctrl}}}{W_{i,\,\text{ctrl}}} \times 100$$

where $W_{i,\,\text{ctrl}}$ and $W_{f,\,\text{ctrl}}$ denote the initial and final dry weights of PBS in the uninoculated control, respectively. The net biodegradation attributable to the isolate was then obtained by subtracting the abiotic weight loss of the control from that of the inoculated sample.

2.4. PBS-Degrading Activity Assay

Enzymatic activity toward emulsified PBS was determined by a modified turbidimetric assay based on the method of Phonlamai *et al.* [16]. The reaction mixture contained 2.25 ml of 0.4% (w/v) emulsified PBS in 0.1 M Tris–HCl buffer (pH 9.0) and 0.25 ml of culture supernatant. Then, the reaction was incubated at 35°C for 30 minutes. The enzyme activity assay was performed at pH 9.0 following the conditions described in the previously established assay protocol [16]. This pH represents the assay condition and should not be interpreted as the optimum pH for enzyme production or PBS degradation.

Hydrolytic activity was monitored as the decrease in optical density at 630 nm (ΔOD_{630}) using a spectrophotometer with 1-cm pathlength cuvettes. Enzyme-free blanks were included in parallel to correct for non-enzymatic turbidity changes. One unit (U) of enzymatic activity was defined as the amount of enzyme causing a decrease in OD_{630} of 1.0 per minute under the assay conditions. All assays were performed in triplicate, and results are expressed as mean ± standard deviation.

2.5. Molecular Identification, Whole-Genome Sequencing, and Genomic Mining

Genomic DNA was extracted from the selected isolate using a commercial DNA extraction kit and purified according to the manufacturer's instructions. The 16S rRNA gene was amplified by PCR using the universal primers 8F (5′-AGAGTTTGATCCTGGCTCAG-3′) and 1492R (5′-GGTTACCTTGTTACGACTT-3′), and the amplified product was submitted for Sanger sequencing to Macrogen Inc. (Seoul, Republic of Korea). Obtained sequences were quality-checked and assembled in BioEdit [17]. Closely related reference sequences were retrieved from the EzBioCloud database [18], and multiple sequence alignment was performed using the ClustalW algorithm implemented in BioEdit prior to phylogenetic tree construction. A phylogenetic tree was subsequently constructed in MEGA11 [19] using the neighbor-joining method with bootstrap analysis (1,000 replicates).

Whole-genome sequencing was performed by Novogene Co., Ltd. on the MGI DNBSEQ-T7 platform with 150-bp paired-end reads. Raw sequencing reads were quality-filtered and adapter-trimmed using fastp v0.23.4 [20], and the resulting clean reads were assembled into contigs using Unicycler v0.5.1 in short-read mode [21]. Genome completeness and contamination were evaluated with CheckM v1.2.5 (lineage_wf) [22] and CheckM2 v1.1.0 [23], and 16S rRNA-based contamination was checked with ContEST16S [24]. Read depth was determined by mapping the raw reads to the assembly with minimap2 v2.31 [25] and calculating per-base depth with SAMtools v1.21 [26]. Genome size and G+C content were determined from the assembled genome sequence, while ANIb was calculated using JSpeciesWS [27]. Phylogenomic analysis and digital DNA–DNA hybridization (dDDH) estimation were performed using the Type Strain Genome Server [28], with dDDH values calculated using formula d_4. Genome annotation was performed with the RAST toolkit [29] through the comprehensive genome analysis service of the Bacterial and Viral Bioinformatics Resource Center (BV-BRC) [30]. The genome was additionally annotated with Prokka v1.15.6 [31] in Proksee [32], and the annotation was used to identify candidate genes and to construct the circular genome map. The deposited genome was also annotated by the NCBI Prokaryotic Genome Annotation Pipeline [33]. Candidate genes potentially involved in PBS degradation were identified based on their predicted functions and sequence annotations. Candidate hydrolases were screened for N-terminal signal peptides with SignalP 6.0 [34], and their conserved domains and transmembrane segments were identified with InterProScan [35], the latter using Phobius [36]. Each candidate was compared by BLASTp [37] with UniProtKB/Swiss-Prot to identify its closest characterized homolog and with polyester hydrolases experimentally reported to hydrolyze PBS. The polyethylene terephthalate (PET) hydrolase-like candidate and these reference enzymes were aligned with Clustal Omega [38] and visualized in Jalview v2.11.5.2 using the Clustal color scheme [39].

2.6. Effects of pH and Temperature on PBS Degradation on Agar Plates

The effects of pH and temperature on PBS-hydrolyzing activity were assessed by single-point inoculation of the selected isolate onto emulsified PBS agar plates. pH was adjusted across a range of 6.0–10.0 using 0.1 N HCl or NaOH, and plates were incubated at temperatures ranging from 30°C to 40°C for 7 days. Hydrolytic activity was quantified as the EAI as described above.

2.7. Effects of PBS Concentration on Degradation Efficiency

Cultivation was performed at 35°C with an initial medium pH of 8.0 and agitation at 150 rpm for 10 days. Corresponding uninoculated controls were prepared for each PBS concentration and incubated under the same conditions. Following incubation, the final culture pH was recorded, and residual PBS was recovered to determine PBS weight loss as described in Section 2.3. Net PBS weight loss (%) was calculated by correcting the weight loss observed in each inoculated treatment for that of its corresponding abiotic control. The absolute amount of PBS degraded (g/L) was calculated by multiplying the initial PBS concentration (g/L) by the net PBS weight loss fraction. The average PBS degradation rate (g/L/day) was determined by dividing the total amount of PBS degraded by the 10-day cultivation period. Bacterial biomass was estimated gravimetrically following manual separation from residual PBS particles, as described in Section 2.3. The biomass fraction, consisting predominantly of greenish-brown mycelial aggregates, was dried at 50°C for 12 hours and expressed as apparent cell dry weight (g/L).

2.8. Growth and Time-Course PBS Degradation

The selected isolate was inoculated at 10% (v/v) into MM medium containing 10 g/L PBS powder and incubated at the selected cultivation

conditions of 35°C and an initial pH of 8.0 with agitation at 150 rpm. The experiment was conducted using three independent biological replicates for each sampling time point (days 0, 1, 3, 5, 7, and 10). Separate cultivation flasks were prepared for each replicate and sampling time point, together with corresponding uninoculated abiotic controls. At each time point, the designated flasks were harvested to determine PBS weight loss, bacterial biomass, and culture pH. Residual PBS was recovered, and net PBS weight loss was calculated after correction for the corresponding abiotic control, as described in Section 2.3. Bacterial biomass was determined as cell dry weight (g/L), following the method described in Section 2.7. The pH of the culture supernatant was also measured at each sampling time point.

2.9. Analysis of PBS Hydrolysis Products and Surface Characterization

Culture samples collected after 10 days of cultivation were analyzed for potential PBS-related degradation products. Succinic acid was examined using high-performance liquid chromatography (HPLC; Agilent 1260 Infinity II, Agilent Technologies, USA) equipped with an Aminex HPX-87H column (300 × 7.8 mm). The column temperature was maintained at 50°C, and 5 mM H_2SO_4 was used as the mobile phase at a flow rate of 0.6 ml/minute. Detection was performed at 210 nm, with a total analysis time of 30 minutes. Chromatographic peaks were tentatively assigned to succinic acid by comparison of their retention times with those of an authentic reference standard.

Qualitative analysis of 1,4-butanediol was performed by an external analytical laboratory using gas chromatography–tandem mass spectrometry (GC–MS/MS; Shimadzu GC-MS-TQ8040 NX, Shimadzu, Japan) equipped with an AOC-20i+s autosampler. The compound was reported as identified by the analytical laboratory based on its GC–MS analysis. Because the analysis was qualitative, no concentration of 1,4-butanediol was reported.

The surface morphology of PBS particles was examined using scanning electron microscopy (SEM) (SEM; SU8020, Hitachi, Tokyo, Japan). PBS samples were collected after 10 days of cultivation with *S. nigra* PRNP1-1W. PBS particles incubated in uninoculated MM under the same conditions for 10 days were used as the abiotic control for SEM analysis. The samples were examined using a scanning electron microscope at an accelerating voltage of 10 kV and a magnification of 5000x.

Fourier-transform infrared spectroscopy (FTIR; Nicolet iS5, Thermo Scientific, USA) was used to examine the characteristic functional groups of PBS. Native PBS particles, which had not undergone cultivation or incubation, were used as the reference material, whereas PBS particles recovered after 10 days of cultivation with PRNP1-1W were used as the treated samples. Spectra were recorded over the range of 500–4,000 cm^{-1} [11].

2.10. Assessment of Enzymatic Activities Potentially Associated with PBS Biodegradation

Extracellular protease, esterase, and lipase activities were initially screened using skim milk agar, Tween 20 agar, and Tween 80 agar, respectively. The skim milk agar medium consisted of (g/L): peptone, 5.0; yeast extract, 2.5; glucose, 1.0; skim milk powder, 10.0; and agar, 15.0. The Tween 20 agar medium contained (g/L): peptone, 10.0; NaCl, 5.0; $CaCl_2 \cdot 2H_2O$, 0.1; and agar, 15.0, supplemented with 10 ml/L Tween 20 (1%, v/v). Similarly, the Tween 80 agar medium contained the same basal composition, with Tween 80 (10 ml/L; 1%, v/v) replacing Tween 20. The initial pH of all media was adjusted to 7.0 ± 0.2 before sterilization. Each agar plate was inoculated with a standardized inoculum of the bacterial isolate and incubated at 35°C for 7 days. Extracellular protease activity was determined by the formation of a clear hydrolysis zone surrounding the colonies on skim milk agar. Esterase and lipase activities were evaluated based on the appearance of opaque precipitation halos around the colonies on Tween 20 and Tween 80 agar, respectively, resulting from the formation of insoluble calcium salts of liberated fatty acids. The presence of distinct hydrolysis zones or precipitation halos was considered indicative of extracellular hydrolytic enzyme activity [11].

Protease and esterase activities in the culture supernatant (Day 7) were subsequently quantified using azocasein and p-nitrophenyl acetate as substrates, respectively, following the methods of Coêlho *et al.* [40] and Kademi *et al.* [41]. One unit (U) of protease activity was defined as the amount of enzyme required to digest 1 mg of substrate per minute under the specified assay conditions. One unit (U) of esterase activity was defined as the amount of enzyme releasing 1 µmol of p-nitrophenol per min under the assay conditions.

2.11. Statistical Analysis

Statistical analyses were performed using SPSS version 21.0 (SPSS Inc., USA). Experimental data were expressed as mean ± standard deviation ($n = 3$). One-way analysis of variance (ANOVA) was used to evaluate differences among treatment groups in experiments involving a single factor. For the effects of temperature and pH on the EAI, two-way ANOVA was used to assess the main effects of temperature and pH, as well as their interaction. Where appropriate, differences among treatment means were evaluated using Tukey's honestly significant difference post hoc test. Statistical significance was determined at $p < 0.05$.

3. RESULTS AND DISCUSSION

3.1. Isolation and Screening of PBS-Degrading Bacteria

Among all isolates screened in the agar plate assay, only isolate PRNP1-1W produced a distinct, clear halo zone on emulsified PBS agar, with an EAI of 1.16 ± 0.01 (dimensionless; clear zone diameter/colony diameter), indicating that the hydrolysis zone exceeded the colony diameter.

In the liquid MM assay containing 0.1% (w/v) PBS powder at 30°C ± 2°C, the culture supernatant of isolate PRNP1-1W exhibited extracellular PBS-degrading activity of 0.20 ± 0.04 U/ml after 7 days of cultivation. Under the same conditions, the inoculated cultures showed a net PBS weight loss of 53.01% ± 4.61% after 7 days, after correcting for the abiotic weight loss of the uninoculated control. This result corroborates the hydrolytic activity observed on agar. Together, these results (Table 1) confirm the capacity of isolate PRNP1-1W to degrade PBS through extracellular enzyme production.

The formation of a clear halo zone on emulsified PBS agar indicates the secretion of extracellular enzymes that hydrolyze the ester bonds in insoluble PBS particles, yielding soluble oligomers and monomers [15]. Halo formation on emulsified polyester agar has been employed as a primary screening criterion for polyester-degrading *Streptomyces* isolates [9,11] and for other PBS-degrading bacteria. For example, the marine bacterium *Terribacillus* sp. JY49 formed clear zones on PBS, PBAT, and PCL, and degraded 31.4% of PBS film within 10 days at 30°C [42]. In this study, an EAI above 1.0 shows that the hydrolytic activity extended beyond the colony boundary, consistent with the

secretion of extracellular depolymerases rather than cell-associated activity alone.

The liquid-medium results were consistent with the agar assay. Isolate PRNP1-1W showed extracellular PBS-degrading activity of 0.20 ± 0.04 U/ml and a net PBS weight loss of 53.01% ± 4.61% within 7 days, in a range comparable to that reported for *Terribacillus* sp. JY49 at the same temperature [42], although the substrate form and culture conditions differed. A variety of microbial hydrolases have been shown to act on PBS, including an extracellular esterase from *Pseudomonas mendocina* [43] and esterase-lipase superfamily (serine hydrolase) enzymes from the actinomycetes *Amycolatopsis, Actinomadura*, and *Streptomyces* [10], supporting the possibility that the enzymes of isolate PRNP1-1W act on polyester linkages. The concordance between the agar-based and liquid-medium assays strengthens the reliability of isolate PRNP1-1W as a PBS-degrading candidate and warrants further genomic and biochemical characterization.

Table 1. Summary of the degradation potential of PBS polymer by isolate PRNP1-1W.

Analysis	Result
Enzymatic activity index (EAI)	1.16 ± 0.01
PBS-degrading activity (U/ml)	0.20 ± 0.04
Degradation (%)	53.01 ± 4.61

Note: Values are expressed as mean ± SD (n = 3). EAI is dimensionless (ratio of total clear zone diameter to colony diameter). Enzyme activity was measured in the culture supernatant after 7 days. The reported PBS weight loss (53.01% ± 4.61%) represents the net weight loss after correction for the corresponding abiotic control (1.07% ± 0.16%) under the same experimental conditions.

3.2. Molecular Identification and Whole-Genome Analysis

Based on 16S rRNA gene sequencing, isolate PRNP1-1W shared 99.65% sequence similarity with *S. nigra* 452^T. The 16S rRNA gene sequence of isolate PRNP1-1W was deposited in the NCBI GenBank database under accession number PX106404, and phylogenetic analysis consistently placed the isolate within the *S. nigra* clade (Fig. 1). *Streptomyces* is a genus of filamentous actinobacteria widely recognized for its prolific secretion of extracellular hydrolytic enzymes and broad metabolic versatility, properties that underpin its capacity to degrade complex polymeric substrates, including biodegradable polyesters [9,44]. While several *Streptomyces* species have been reported to degrade PCL and PLA, reports of PBS degradation within this genus remain limited [10,45], and *S. nigra* in particular has not previously been characterized as a PBS degrader.

The assembled genome of isolate PRNP1-1W comprised 44 contigs totaling 7,849,260 bp, with an average G+C content of 71.95 mol%, and was deposited in the NCBI database under BioSample accession SAMN56400991 and BioProject PRJNA1434440. The assembly had a contig N50 of 495,497 bp and a mean read depth of 384.7×. CheckM and CheckM2 estimated 100% completeness with ≤0.21% contamination, indicating a high-quality genome from a pure culture (Table 2). ContEST16S could not assess contamination because the assembly contained only a single 16S rRNA gene fragment. Genome annotation predicted 7,440 protein-coding sequences (CDS), 74 tRNA

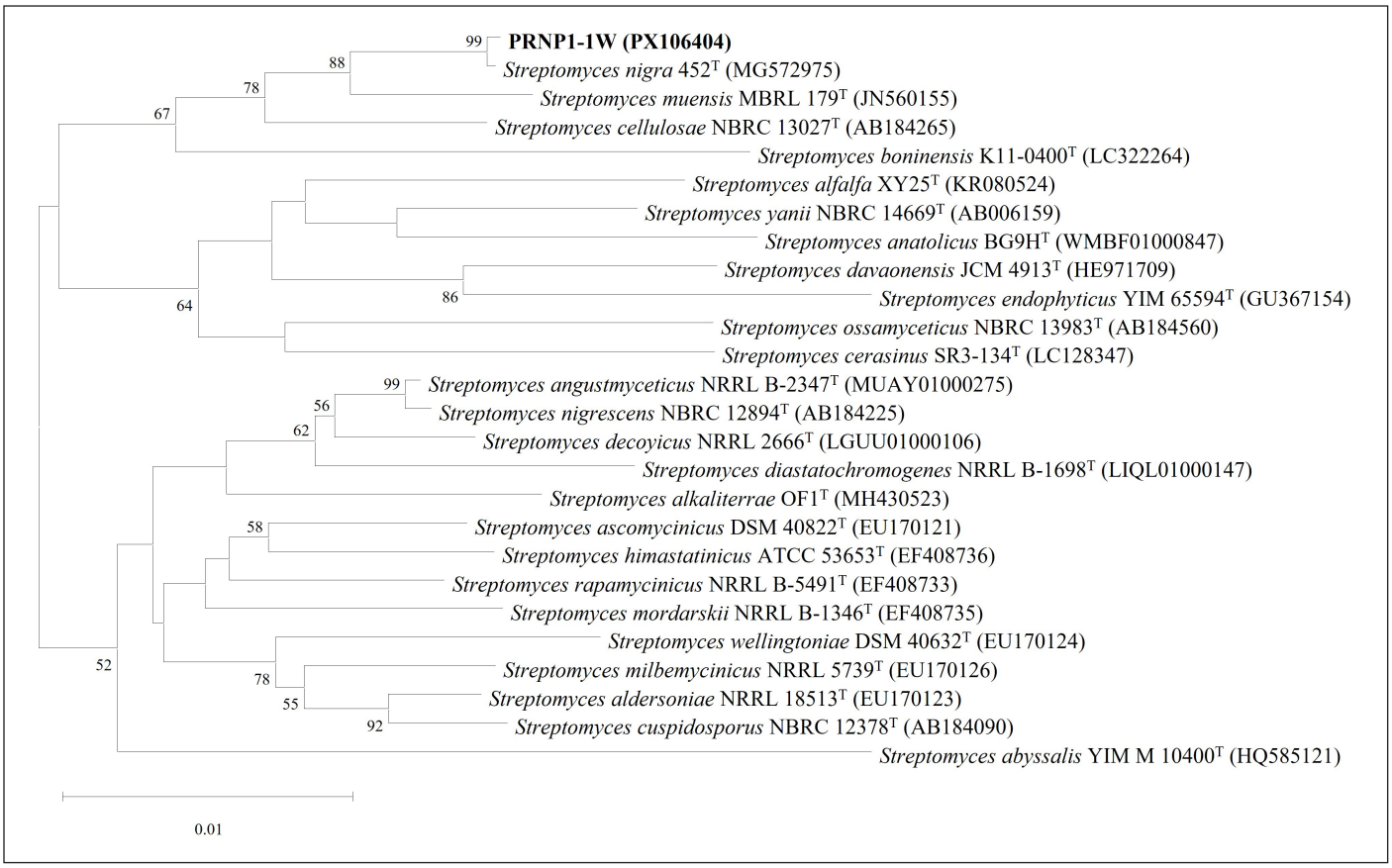

Figure 1. A phylogenetic tree of *Streptomyces nigra* PRNP1-1W and related type strains based on 16S ribosomal RNA (16S rRNA) gene sequences calculated using the neighbor-joining method in MEGA 11.

genes, and 4 rRNA genes. Genomic species boundaries were assessed using average nucleotide identity and digital dDDH, both established metrics for prokaryotic species delineation [46]. ANIb and dDDH values between isolate PRNP1-1W and *S. nigra* 452^T were 99.22%–99.37% and 95.9%, respectively, both exceeding the recognized species thresholds of 95% and 70%, confirming the assignment of isolate PRNP1-1W to *S. nigra*. In the phylogenomic tree, isolate PRNP1-1W clustered with *S. nigra* 452^T with 100% GBDP pseudo-bootstrap support (Fig. 2).

Table 2. Genomic features of *Streptomyces nigra* PRNP1-1W.

Feature	Value
Genome size	7,849,260 bp
G+C content	71.95 mol%
No. of contigs	44
Contig N50	495,497 bp
L50	7
Largest contig	848,434 bp
Mean read depth	384.7×
Completeness (CheckM / CheckM2)	100% / 100%
Contamination (CheckM / CheckM2)	0.21% / 0.03%
CDS	7,440
rRNA	4
tRNA	74

Functional annotation of the genome was performed using multiple databases, yielding 5,194 proteins with putative functional assignments and 1,347 proteins associated with Enzyme Commission numbers (Table 3). KEGG and GO annotations (1,056 and 1,167 proteins, respectively) captured well-curated functional roles [47], while PLfam and PGfam (7,056 and 7,084 proteins, respectively) provided broader domain-based predictions encompassing both characterized and hypothetical proteins [30]. Subsystem analysis revealed a genome dominated by metabolism-related functions (101 subsystems, 894 genes), with substantial representation of energy metabolism (33 subsystems, 355 genes) and protein processing subsystems (42 subsystems, 266 genes) (Fig. 3). This functional architecture is consistent with the known capacity of *Streptomyces* to secrete extracellular enzymes and assimilate structurally diverse carbon sources, supporting the genomic potential of isolate PRNP1-1W for PBS polymer degradation and monomer utilization.

Table 3. Protein features of *Streptomyces nigra* PRNP1-1W.

Feature	Value
KEGG	1,056
GO	1,167
PLfam	7,056
PGfam	7,084
Proteins with functional assignments	5,194
Proteins with EC number assignments	1,347

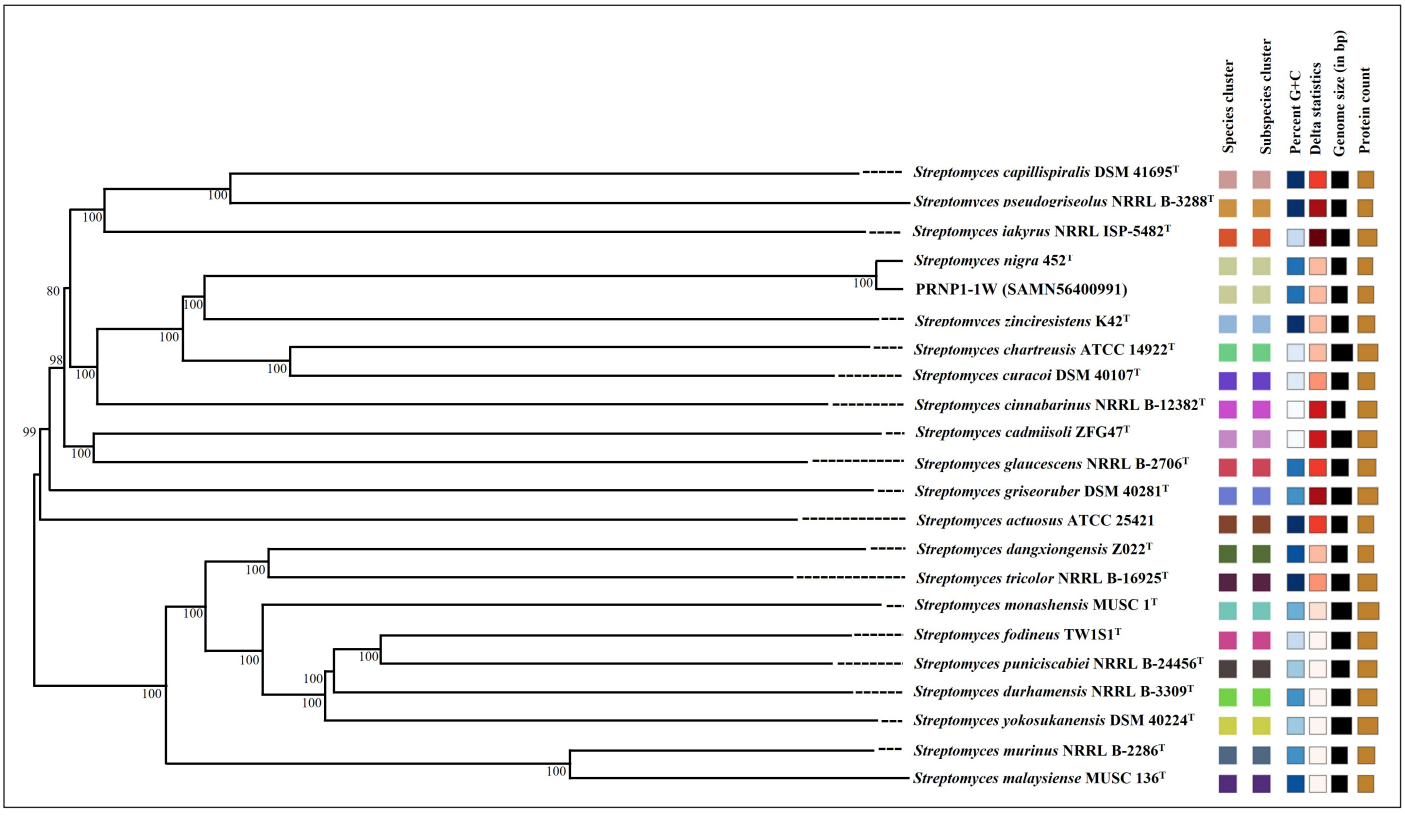

Figure 2. Phylogenomic tree based on the whole-genome sequence of PRNP1-1W and closely related strains. The colors represent species cluster, sub-species cluster, percent G + C, delta statistics, genome size (in bp), and protein count. The branch lengths are scaled in terms of the GBDP distance formula d5. The numbers above the branches are Genome BLAST Distance Phylogeny (GBDP) pseudo-bootstrap support values from 100 replications. Different colors indicate different species or subspecies clusters

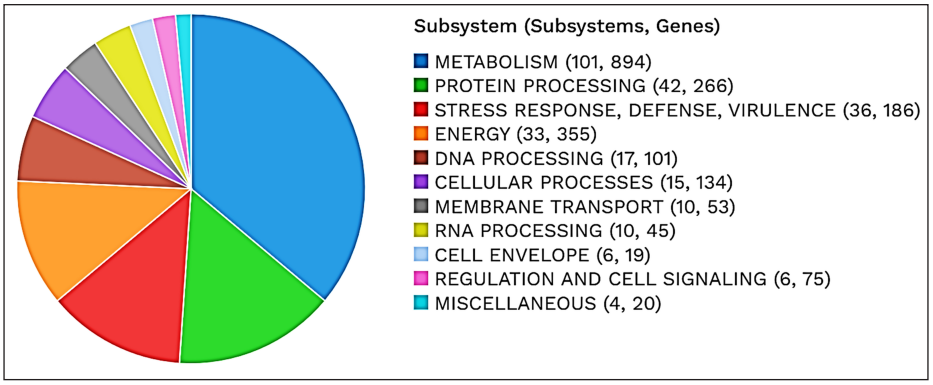

Figure 3. Distribution of predicted functional subsystems in the genome of *Streptomyces nigra* PRNP1-1W based on genome annotation using the RAST subsystem framework through the BV-BRC platform.

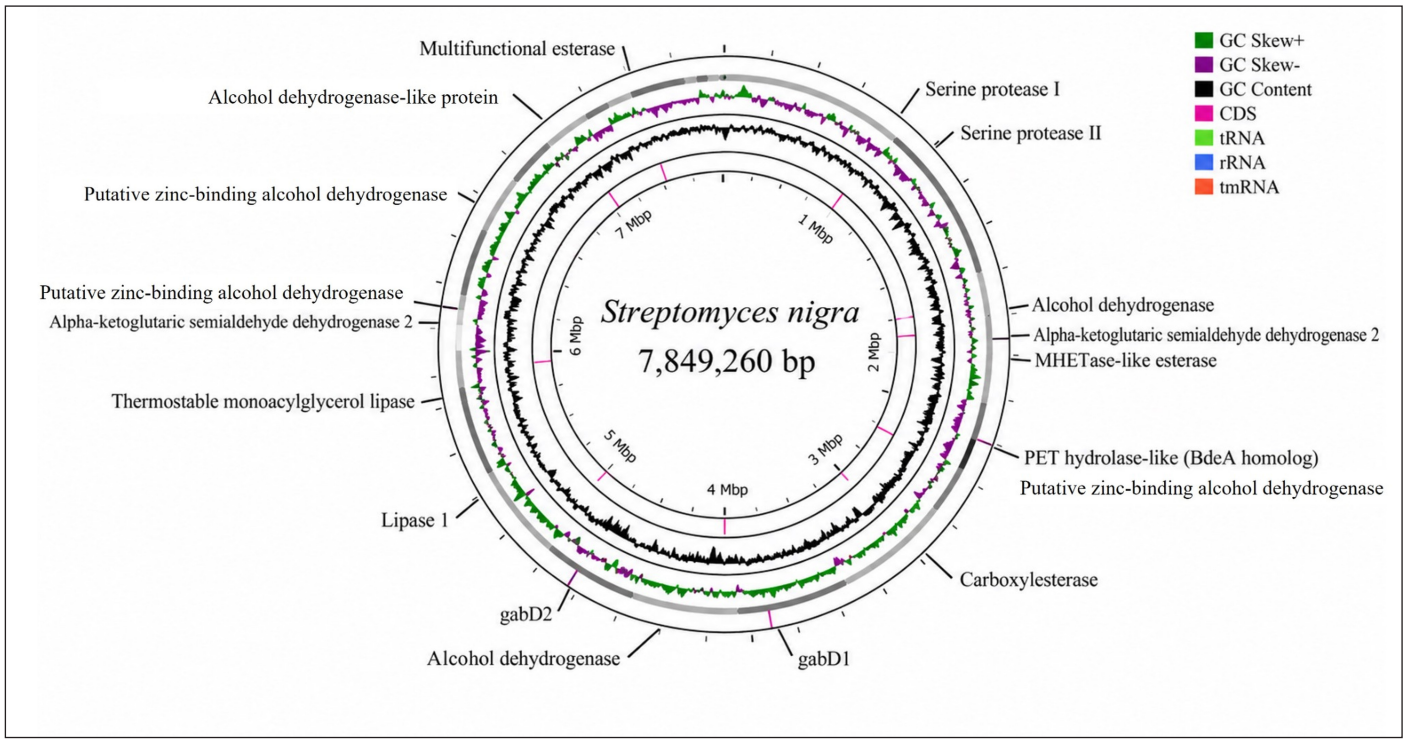

Figure 4. Circular map of the *Streptomyces nigra* PRNP1-1W genome showing candidate hydrolase genes and genes of the proposed downstream pathway. From the inside out: genome position (Mbp), GC content, GC skew, and coding sequences (CDS). Genes were annotated with Prokka v1.15.6 and visualized in Proksee.

3.3. Genome Mining for PBS-Degrading Genes and Potential Metabolic Pathways

Genome mining is a useful strategy for identifying genes that may be associated with plastic biodegradation [11]. Genome annotation of isolate PRNP1-1W revealed eight putative hydrolase genes, including two serine proteases, lipases, esterases, and PET hydrolase-like and MHETase-like proteins (Fig. 4; Table S1; Prokka locus tags with the prefix OKIOMFPC_). These enzyme classes have been associated with the degradation of aliphatic polyesters, in which esterases and lipases catalyze ester bond cleavage, generating lower-molecular-weight products [43,48]. SignalP 6.0 predicted N-terminal Sec signal peptides in four of these proteins, the MHETase-like protein OKIOMFPC_01852, the PET hydrolase-like protein OKIOMFPC_02247, lipase OKIOMFPC_04836, and multifunctional esterase OKIOMFPC_06885, indicating that they are probably exported *via* the general secretory (Sec) pathway (Table S2; Fig. S1). In contrast, both serine proteases lacked a signal peptide and contained three to four predicted transmembrane segments, consistent with membrane-associated proteases (Table S3). Most candidates shared moderate identity (35%–74%) with characterized proteins in UniProtKB/Swiss-Prot (Table S4). OKIOMFPC_02247 was most similar to the bis(2-hydroxyethyl) terephthalate (BHET)-hydrolyzing esterase BdeA of *Streptomyces coelicolor* A3(2) (87.9% identity) and shared 46.8% identity with the PET hydrolase of *Ideonella sakaiensis* (IsPETase) [49]. It also carried a PET hydrolase-like domain (PF12740) and a conserved Ser177–Asp223–His255 catalytic triad (Tables S3 and S5). OKIOMFPC_01852 shared only 30.2% identity with mono(2-hydroxyethyl) terephthalate hydrolase (MHETase), so its functional assignment remains tentative (Table S5). Neither protein has been tested on PET or its intermediates, and the degradation of PET by isolate PRNP1-1W was not examined. OKIOMFPC_02247 also shared

51%–73% amino acid identity across the mature protein with four polyester hydrolases experimentally shown to hydrolyze PBS (Table S6), and its catalytic triad aligned with the corresponding residues of all these enzymes (Fig. 5; Table S7). OKIOMFPC_02247 (NCBI locus tag AC0NME_RS11330; WP_474776732.1) is therefore proposed as a candidate extracellular PBS depolymerase of isolate PRNP1-1W. The remaining candidates showed weak or no significant similarity to these PBS-hydrolyzing enzymes (Table S6). These sequence-based predictions do not establish gene expression, secretion, or enzymatic activity, which require confirmation by heterologous expression and biochemical assays.

A hypothetical pathway for the degradation and potential metabolism of PBS-derived compounds was proposed based on genome annotation and previously reported metabolic routes (Fig. 6). Hydrolysis of PBS may generate succinic acid and 1,4-butanediol, which have been reported as products of PBS degradation [43]. Succinic acid can enter central carbon metabolism in the form of succinate, an intermediate of the tricarboxylic acid cycle. The metabolism of 1,4-butanediol is more complex and may proceed through several alternative routes. One proposed route involves its sequential oxidation to 4-hydroxybutyraldehyde and 4-hydroxybutyrate, followed by further conversion toward succinate through intermediate reactions [50]. However, previous studies have also described alternative metabolic processes, including CoA-dependent reactions and β-oxidation-related pathways [50,51]. Therefore, the route illustrated in Figure 6 represents one of the possible metabolic pathways proposed in the literature rather than a pathway experimentally demonstrated in isolate PRNP1-1W. In particular, the specific enzymes and genes responsible for the individual conversion steps have not been functionally verified in this isolate.

The potential entry of PBS-derived compounds into central carbon metabolism suggests a possible route for carbon utilization. Nevertheless, the presence of predicted metabolic genes does not establish that isolate PRNP1-1W can assimilate succinic acid or 1,4-butanediol as carbon and energy sources. The proposed pathway should therefore be interpreted as a working hypothesis requiring experimental validation. The hydrolytic gene repertoire identified in isolate PRNP1-1W is consistent with previous reports describing the ability of *Streptomyces* species to degrade aliphatic polyesters, including PCL and PLA, through extracellular hydrolytic activities [10,15]. However, the specific contribution of the annotated genes to PBS degradation remains unresolved. Taken together, the genome mining results identify candidate enzymes and metabolic functions that may be relevant to the observed PBS-degrading phenotype of isolate PRNP1-1W. Further investigations, including growth assays using succinate and 1,4-butanediol as sole carbon sources, direct enzyme characterization, and metabolite profiling, are required to validate the proposed pathway and establish the relationship between the predicted genes and PBS degradation.

3.4. Influence of pH and Temperature on PBS Degradation on Agar Plates

The effects of temperature and initial medium pH on the agar-based EAI of *S. nigra* PRNP1-1W were evaluated at 30°C, 35°C, and 40°C and at initial pH values ranging from 6.0 to 10.0 (Fig. 7). Among the conditions examined, the highest numerical EAI was observed at 35°C and pH 8.0. However, this observation does not necessarily indicate the optimal conditions for PBS-hydrolyzing enzyme activity, as EAI reflects clear-zone formation and may be influenced by bacterial growth, enzyme production, and diffusion through the agar medium.

At 30°C and 40°C, the highest numerical EAI values were observed at pH 10.0, suggesting that the EAI response varied across the tested temperature-pH combinations. Nevertheless, the relatively narrow temperature range (30°C–40°C) and the indirect nature of the agar-based assay limit the interpretation of these findings. Therefore, 35°C

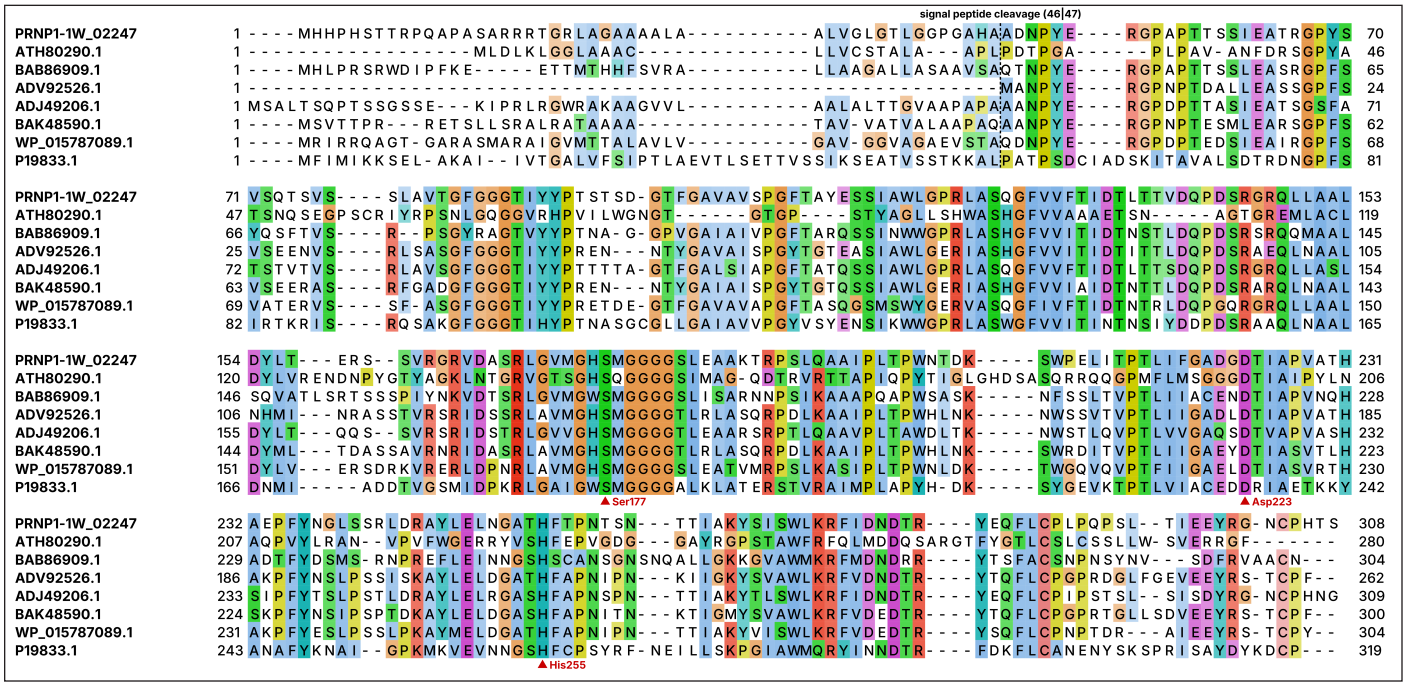

Figure 5. Multiple sequence alignment of PRNP1-1W_02247 (OKIOMFPC_02247) with polyester hydrolases reported to hydrolyze PBS and a reference lipase (sequence details in Table S7). Sequences were aligned with Clustal Omega and displayed in Jalview using the Clustal color scheme. Red triangles mark the catalytic triad (Ser177, Asp223, His255), and the dashed line marks the predicted signal-peptide cleavage site (positions 46–47).

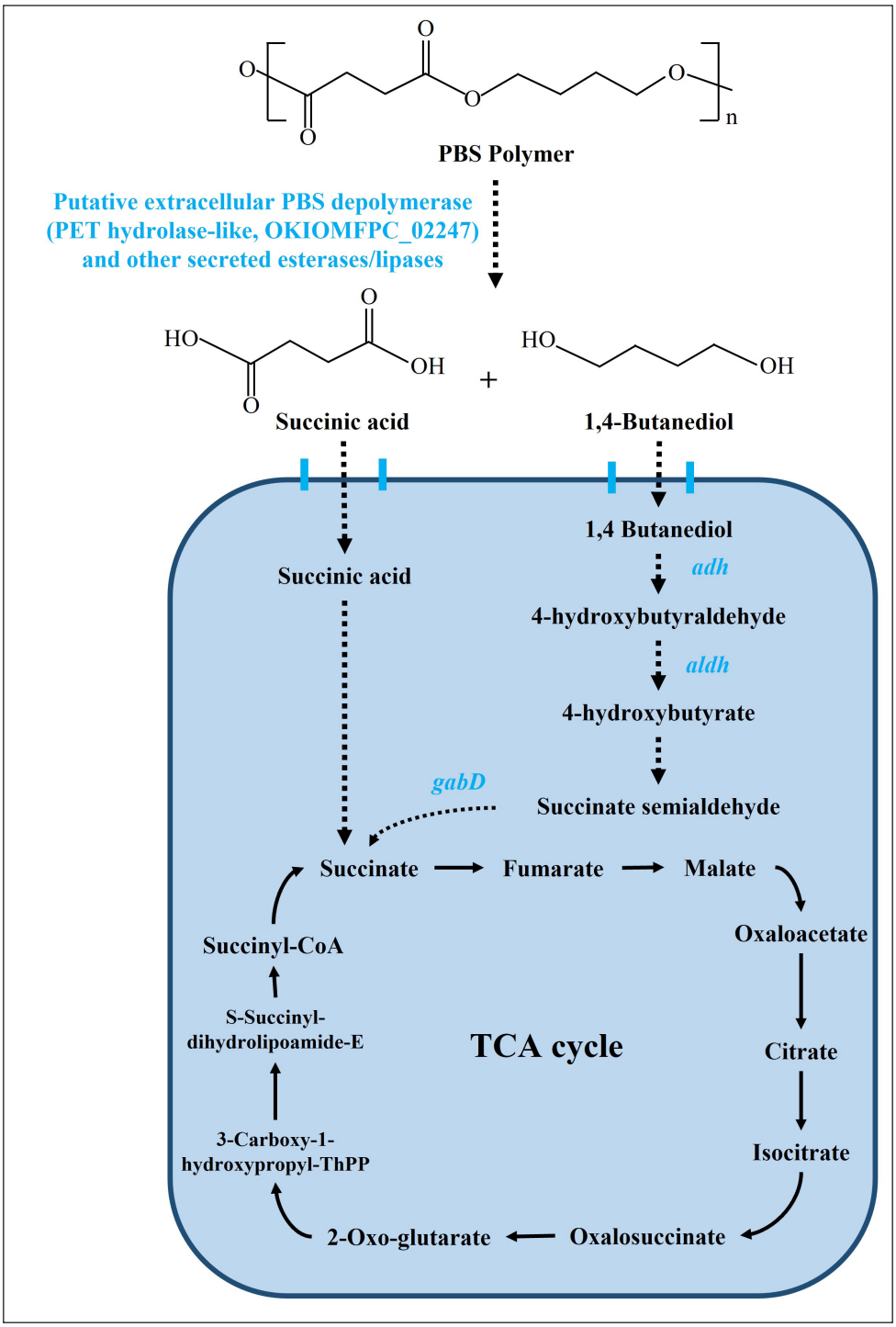

Figure 6. Proposed pathway for PBS degradation and metabolism of the released monomers in *Streptomyces nigra* PRNP1-1W, inferred from genome annotation and previously reported pathways [50,51]. Extracellular hydrolysis of PBS by putative secreted hydrolases, including the candidate PBS depolymerase OKIOMFPC_02247 (Fig. 5), releases succinic acid and 1,4-butanediol. 1,4-Butanediol may be oxidized by alcohol dehydrogenase (adh) and aldehyde dehydrogenase (aldh) to 4-hydroxybutyrate and, via succinate semialdehyde, to succinate by succinate-semialdehyde dehydrogenase (gabD), which enters the tricarboxylic acid (TCA) cycle. Dotted arrows indicate steps predicted from genome annotation. No candidate gene was assigned to the conversion of 4-hydroxybutyrate to succinate semialdehyde. Candidate genes are listed in Table S1.

and an initial pH of 8.0 were selected for subsequent PBS degradation experiments based on the highest observed EAI. Further studies involving direct measurements of PBS-hydrolyzing enzyme activity across broader temperature and pH ranges are required to determine the optimal enzymatic conditions.

The selected cultivation conditions of 35°C and an initial pH of 8.0, which yielded the highest numerical agar-based EAI among the conditions tested, fall within the moderate-temperature and neutral-to-mildly alkaline ranges reported for several PBS-degrading microorganisms. For example, the esterase JY35_02679 from *Bacillus*

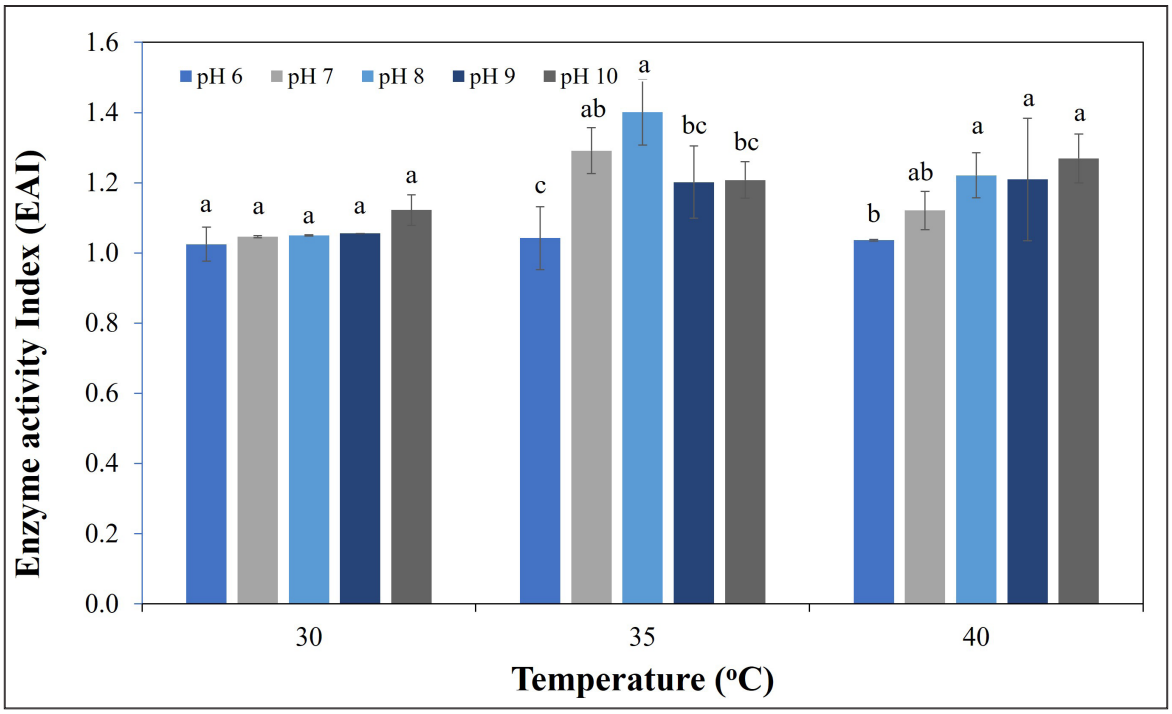

Figure 7. Effects of temperature and pH on the enzymatic activity index (EAI) of isolate PRNP1-1W on PBS-containing agar. Data are presented as mean ± standard deviation ($n = 3$). Statistical analysis was performed using two-way ANOVA, followed by Tukey's multiple comparison test. Different lowercase letters indicate significant differences among pH treatments within the same temperature ($p < 0.05$). Means sharing at least one letter are not significantly different.

sp. JY35 exhibited PBS-degrading activity at 30°C, with recombinant *Escherichia coli* expressing this enzyme achieving approximately 45.7% PBS film weight loss after 10 days [52]. More recently, an extracellular esterase from *P. mendocina* SA-1503 showed optimal PBS-degrading activity at pH 9.0 and 40 °C, with stability maintained over pH 8.0–9.0 and 30°C–40°C [43]. These findings indicate that PBS-degrading enzymes from mesophilic bacteria commonly exhibit activity within a relatively broad range of neutral-to-alkaline pH and moderate temperatures.

In contrast, enzymes produced by thermophilic microorganisms generally exhibit higher temperature optima. For instance, Microbispora rosea BS2-4 showed optimal PBS-degrading enzyme production at pH 9.0 and 50°C, whereas the enzyme exhibited optimal activity at pH 7.0 and 60°C [16]. Similarly, the serine protease produced by Laceyella sacchari LP175 degraded PBS efficiently at 50°C [4]. In the present study, 35°C and an initial pH of 8.0 were selected as cultivation conditions based on the highest numerical agar-based EAI. These conditions should not be interpreted as the temperature or pH optima of the PBS-degrading enzymes produced by PRNP1-1W. A recent study demonstrated that a recombinant marine fungal cutinase efficiently degraded PBS at 37°C [53], indicating that PBS hydrolysis can occur under moderate temperatures. However, direct measurements of PBS-hydrolyzing enzyme activity are required before the enzymatic properties of PRNP1-1W can be compared with those of previously characterized enzymes.

The enzymatic mechanism of PBS degradation involves hydrolytic cleavage of the ester bonds linking succinic acid to 1,4-butanediol units, and several enzyme classes contribute to this process through distinct mechanisms [43]. Esterases and lipases, which belong to the α/β-hydrolase family, hydrolyze ester bonds in the polymer chain, releasing oligomers and, upon further hydrolysis, the monomers succinic acid and 1,4-butanediol. The activity of esterases toward PBS has been demonstrated for the extracellular esterases of *P. mendocina* [43] and *Bacillus* sp. JY35 [52]. Among the candidates identified in isolate PRNP1-1W, OKIOMFPC_02247 is the most plausible contributor to the extracellular hydrolytic activity observed in this study, because it carries a predicted Sec signal peptide and shares 51%–73% amino acid identity, including the catalytic triad, with cutinase-type enzymes that hydrolyze PBS. The secreted lipase (OKIOMFPC_04836) and multifunctional esterase (OKIOMFPC_06885) may also contribute, whereas the two serine proteases lack signal peptides and are predicted to be membrane-anchored, so their contribution to extracellular PBS hydrolysis remains uncertain. However, these computational predictions do not establish the involvement of individual enzymes in PBS hydrolysis, which requires heterologous expression and activity assays.

Taken together, PBS degradation by PRNP1-1W likely proceeds in two stages: extracellular hydrolases first cleave the polymer at the surface, producing oligomers and monomers, and the resulting succinic acid and 1,4-butanediol may then be taken up and metabolized via routes predicted by the genome. This model is consistent with the PBS weight loss and the detection of the two monomers as hydrolysis products, whereas uptake and assimilation of the monomers remain to be demonstrated.

3.5. Effect of PBS Concentration on Degradation Efficiency

To evaluate the effect of substrate loading, PBS was added at initial concentrations of 10, 20, and 30 g/L, corresponding to 10–30 times the concentration used in the initial screening experiments (1 g/L). These concentrations were selected to investigate PBS degradation at higher substrate loadings, with 10 g/L based on a previous study [54]. The highest percentage of PBS degradation was observed at

10 g/L (42.60% ± 3.11%), followed by 20 g/L (28.30% ± 1.48%) and 30 g/L (21.06% ± 0.84%) (Table 4). However, when expressed as the absolute amount of PBS degraded, the values increased from 4.26 ± 0.31 g/L at 10 g/L to 5.66 ± 0.30 and 6.32 ± 0.25 g/L at 20 and 30 g/L, respectively. Similarly, the average PBS degradation rate increased from 0.426 ± 0.031 to 0.566 ± 0.030 and 0.632 ± 0.025 g/L/day, respectively. These results indicate that increasing the initial PBS concentration was associated with lower fractional degradation but greater absolute PBS removal. Therefore, the decrease in percentage degradation alone does not demonstrate substrate inhibition.

The final culture pH decreased from the initial value of 8.0 to 4.9, 4.5, and 4.0 at PBS concentrations of 10, 20, and 30 g/L, respectively (Table 4). The greater decrease in pH at higher PBS loadings may reflect changes in the culture medium during degradation and microbial growth. However, the contribution of PBS-derived products and other metabolites to acidification remains unclear. Previous studies have suggested that the accumulation of degradation products may affect microbial growth and enzymatic activity. For example, *Terribacillus* sp. JY49 exhibited a degradation plateau of 31.4% after 10 days, with monomer accumulation proposed as a possible contributing factor [42]. Nevertheless, the present results do not establish a comparable inhibitory mechanism in isolate PRNP1-1W. Other factors, including changes in medium pH, substrate accessibility, and nutrient availability, may influence the degradation response at different PBS loadings, but these possibilities require further investigation.

Although the percentage of PBS degradation was highest at 10 g/L, the absolute amount degraded was greater at 20 and 30 g/L. Therefore, 10 g/L was selected for subsequent experiments based on its highest percentage weight loss among the concentrations examined, rather than its maximum absolute PBS removal. The time-course experiment conducted at this concentration was used to further characterize changes in PBS weight loss, bacterial biomass, and culture pH during cultivation. Further studies involving pH-controlled cultivation, quantitative analysis of degradation products, and evaluation of

Table 4. Effects of PBS concentration on degradation efficiency, pH, and growth.

PBS concentration (g/L)	pH		Degradation (%)	PBS degraded (g/L)	Average rate (g/L/day)	Growth (g/L)
	Initial	Final				
10	8.0 ± 0.00	4.9 ± 0.00	42.60 ± 3.11^{a}	4.260 ± 0.311^{a}	0.426 ± 0.031^{a}	1.268 ± 0.26
20	8.0 ± 0.00	4.5 ± 0.00	28.30 ± 1.48^{b}	5.660 ± 0.296^{b}	0.566± 0.030^{b}	1.027 ± 0.17
30	8.0 ± 0.00	4.0 ± 0.00	21.06 ± 0.84^{c}	6.318 ± 0.252^{b}	0.632± 0.025^{b}	0.867 ± 0.14

Note: Values are expressed as mean ± SD (n = 3), except for pH values, which are reported as measured values at the indicated precision. PBS degradation (%) represents the net weight loss after correction for the corresponding abiotic control at each initial PBS concentration (10, 20, and 30 g/L). The absolute amount of PBS degraded (g/L) was calculated from the initial PBS concentration and net weight loss (%). The average degradation rate (g/L/day) was calculated by dividing the absolute amount degraded by the incubation period of 10 days. Different lowercase letters within the same column indicate significant differences ($p < 0.05$), where indicated.

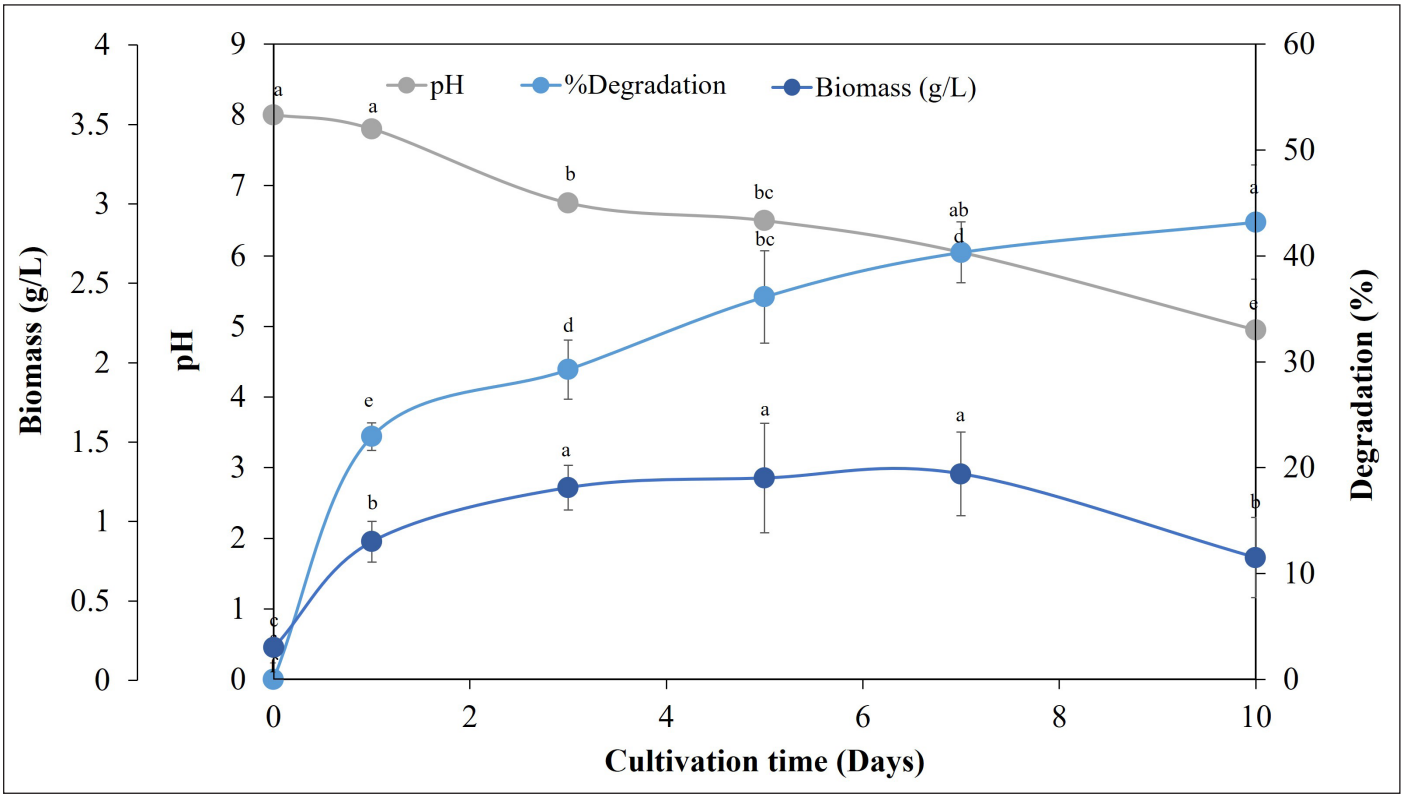

Figure 8. Growth and degradation efficiency of PBS powder by the PRNP1-1W strain at different cultivation times. Values are expressed as mean ± SD (n = 3). Different letters within the same condition indicate significant differences ($p < 0.05$)

substrate feeding strategies would be valuable for understanding and potentially improving PBS degradation at higher substrate loadings.

3.6. PBS Degradation and Characterization of Degradation Products

The time courses of cell growth, culture pH, and PBS degradation at 10 g/L PBS, 35°C, and initial pH 8.0 are shown in Figure 8. Biomass increased from about 0.2 g/L at day 0 to about 1.2 g/L by day 3, remained stable through day 7 (about 1.3 g/L), and then decreased to about 0.8 g/L at day 10. Culture pH decreased from 8.0 to 6.50 on day 5, 6.05 on day 7, and 4.95 on day 10. PBS degradation was already about 23% on day 1, increased to about 36% on day 5 and about 41% on day 7, and reached a maximum of 43.20% ± 5.40% on day 10, although the rate of increase slowed markedly after the first day.

A relatively high PBS weight loss was observed on the first day of cultivation, despite limited increases in biomass and only a small change in culture pH. Although the inoculum was washed before use to minimize carryover of extracellular enzymes and residual culture components, the possible contribution of cell-associated enzymes cannot be ruled out. In addition, physical fragmentation of PBS and the loss of fine particles during filtration may have influenced the measured weight loss. Therefore, the early weight loss should be interpreted with caution, as these potential contributions could not be distinguished without additional controls, such as heat-killed cell treatments.

During cultivation, an increase in bacterial biomass was observed together with a decrease in culture pH. These changes occurred alongside PBS weight loss and may reflect microbial growth and changes in the culture medium during incubation. However, biomass accumulation and pH reduction alone do not demonstrate the assimilation of PBS-derived monomers. Further experiments using individual degradation products as sole carbon sources, together with metabolite consumption analyses, would be required to confirm their metabolic utilization by isolate PRNP1-1W.

HPLC analysis revealed a chromatographic peak with a retention time corresponding to that of an authentic succinic acid standard, suggesting the presence of succinic acid in the culture sample (Fig. S2). However, the original calibration and peak-integration records were insufficient to independently verify the quantitative concentration. Therefore,

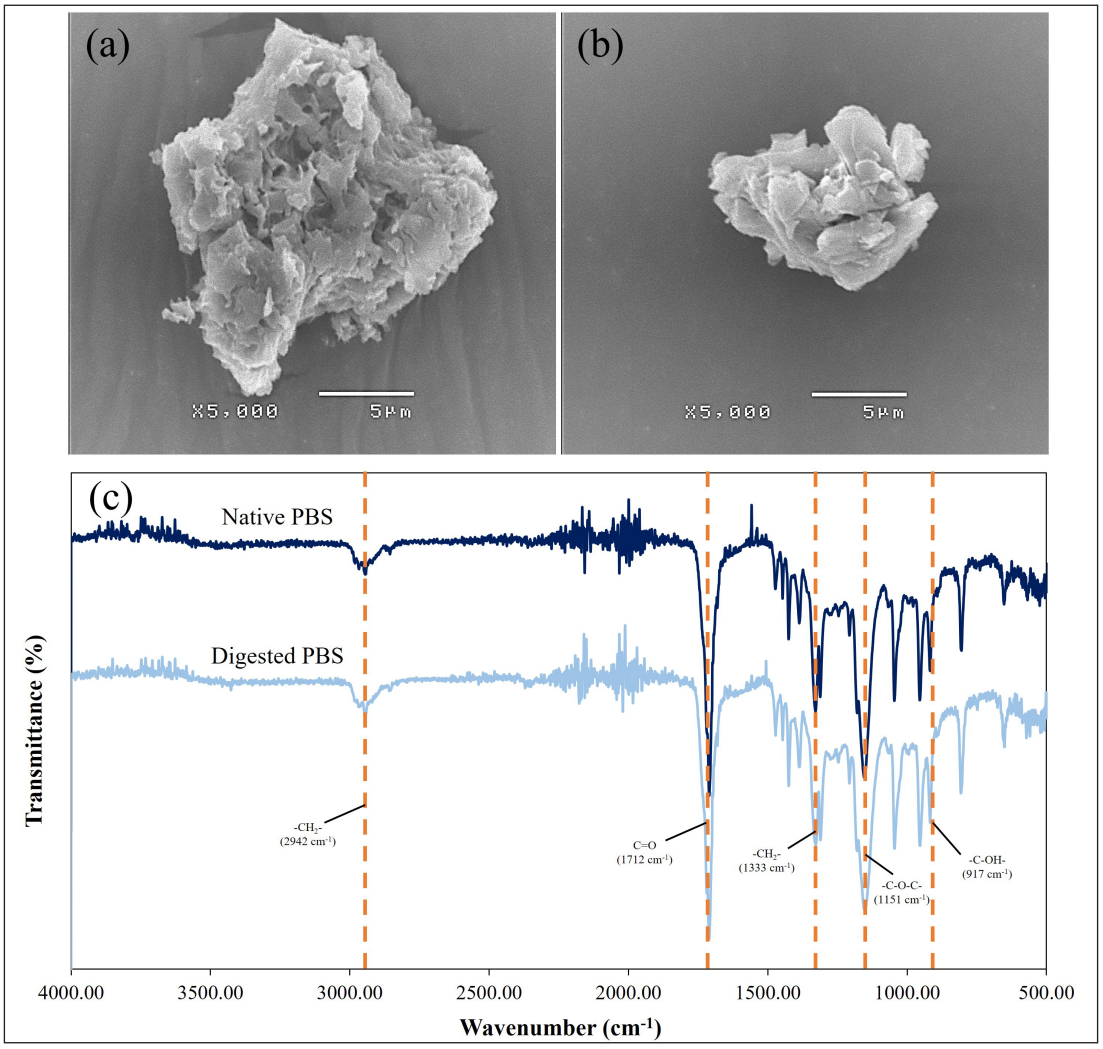

Figure 9. Scanning electron microscopy (SEM) images of PBS particles recovered after 10 days of incubation in MM medium: (a) uninoculated control and (b) PBS recovered after cultivation with isolate PRNP1-1W. (c) Fourier-transform infrared (FTIR) spectra of native PBS and PBS recovered after cultivation with isolate PRNP1-1W. The SEM images are representative and are presented for qualitative comparison of particle morphology. Scale bars represent 5 µm.

succinic acid was reported as a tentatively identified compound without quantitative estimation. In addition, 1,4-butanediol was qualitatively identified in the culture sample by an external analytical laboratory using GC–MS/MS (Fig. S2c). Although the laboratory reported identifying this compound, the available analytical documentation did not include the complete mass spectral identification records or a reference-standard chromatogram for independent verification. Therefore, this finding is presented as a qualitative analytical result. Furthermore, the detection of 1,4-butanediol does not establish its subsequent assimilation or contribution to bacterial growth by isolate PRNP1-1W.

The surface morphology of PBS particles was examined by SEM after 10 days of incubation in MM medium (Fig. 9a,b). PBS recovered from the uninoculated control exhibited an irregular, layered surface with visible cracks and folds (Fig. 9a). Similarly, PBS particles recovered after cultivation with isolate PRNP1-1W showed irregular surface features and apparent fragmentation (Fig. 9b). Although differences in particle appearance were observed, these representative micrographs do not provide sufficient evidence to establish a reduction in particle size or confirm enzymatic surface erosion. Quantitative analysis of particle-size distributions would be required to determine whether these morphological differences were consistent across the samples.

FTIR analysis was performed to examine the characteristic functional groups of PBS (Fig. 9c). Both the native PBS and PBS recovered after cultivation with isolate PRNP1-1W exhibited a prominent absorption band at approximately 1,712 cm^{-1}, corresponding to ester carbonyl (C=O) stretching [55]. Additional bands were observed near 2,942 cm^{-1}, associated with aliphatic C–H stretching, and at 1,333 and 1,151 cm^{-1} within the fingerprint region. These absorption bands are consistent with the characteristic chemical structure of PBS. However, the spectra were vertically offset and were not normalized for quantitative comparison. Therefore, differences in band intensity cannot be reliably interpreted as evidence of ester bond cleavage. Further analysis using baseline-corrected and normalized spectra, together with a suitable carbonyl index, would be necessary to assess chemical changes more conclusively.

Overall, the SEM and FTIR analyses provide qualitative information on the morphology and chemical characteristics of PBS following cultivation. Although these observations are relevant to the degradation process, they do not independently confirm polymer surface erosion or ester bond hydrolysis. The PBS weight loss measurements provide the primary experimental evidence of degradation by isolate PRNP1-1W, while the hydrolytic genes identified through genome mining suggest possible enzymatic mechanisms that require further functional validation.

3.7. Assessment of Enzymatic Activities Potentially Associated with PBS Biodegradation

Phenotypic assays were conducted to examine extracellular hydrolytic activities that may be associated with the PBS-degrading phenotype of isolate PRNP1-1W. The isolate exhibited extracellular protease and esterase activities, as indicated by clear-zone formation on skim milk agar and the appearance of an opaque precipitation halo on Tween 20 agar, respectively (Fig. 10). In the submerged cultivation system, the culture supernatant collected on day 7 exhibited protease and esterase activities of 2.67 ± 0.41 U/ml and 1.23 ± 0.13 U/ml, respectively, whereas lipase activity was not detected under the tested conditions. These results demonstrate the production of extracellular hydrolytic activities but do not directly establish their involvement in PBS depolymerization.

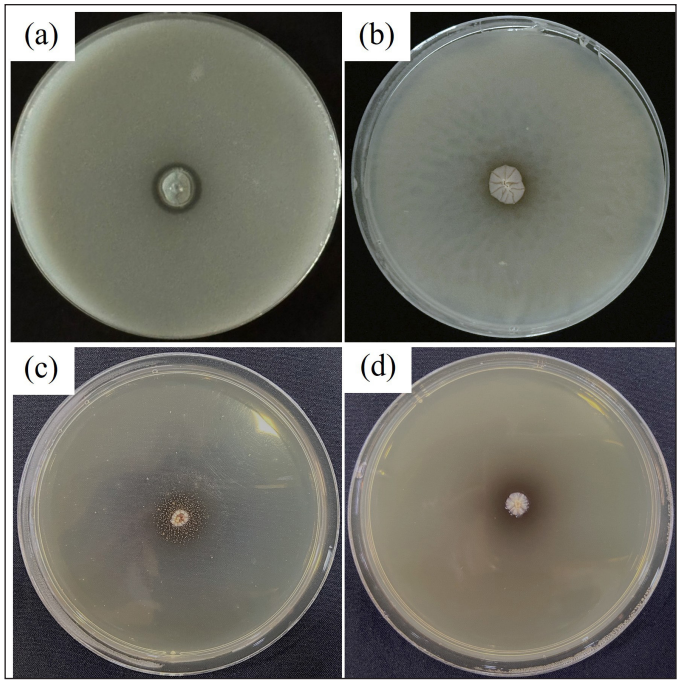

Figure 10. Hydrolytic enzyme production by the PRNP1-1W strain on agar plates at 35°C for 7 days. (a): PBS agar plate, (b): skim milk agar plate, (c): Tween 20 agar plate, and (d): Tween 80 agar plate.

The detection of esterase activity is relevant to investigating PBS biodegradation because the cleavage of ester bonds is an important step in the hydrolysis of aliphatic polyesters. Sriyapai *et al.* [10] reported PBS-degrading enzyme activities of up to 19.4 U/ml in culture broths of actinobacterial isolates, including *Streptomyces* sp. APL3, cultivated in PBS-containing medium supplemented with yeast extract. However, direct quantitative comparison between these studies is limited by differences in assay substrates, definitions of enzyme activity, cultivation conditions, and experimental procedures. Therefore, the esterase activity measured in the present study should not be interpreted as equivalent to PBS-specific hydrolytic activity. Although further optimization of cultivation conditions may influence extracellular enzyme production, this possibility remains to be investigated.

Extracellular protease activity was also detected. Previous studies have reported extracellular hydrolytic enzymes, including proteases, in microorganisms associated with polyester degradation [11]. Nevertheless, protease activity measured using a model substrate does not demonstrate direct hydrolysis of PBS or confirm that the annotated protease genes are responsible for the observed activity. Similarly, the detection of esterase activity does not establish a direct functional relationship with the predicted esterase-encoding genes.

Although putative lipase-encoding genes were identified in the genome of isolate PRNP1-1W, lipase activity was not detected on Tween 80 agar under the conditions examined. This observation may reflect differences in gene expression, enzyme secretion, substrate specificity, or assay sensitivity. However, the underlying explanation cannot be determined from the present results.

Taken together, the genome mining and phenotypic assays indicate a possible association between the predicted hydrolytic gene repertoire and the extracellular enzyme activities of isolate PRNP1-1W. However, these findings do not establish a direct genotype–phenotype relationship or identify the specific enzymes responsible

for PBS degradation. Further investigations involving PBS-specific enzyme assays, protein identification, and functional characterization of candidate genes are required to clarify the enzymatic mechanisms underlying PBS biodegradation by this isolate.

4. CONCLUSION

This study demonstrates the PBS-degrading potential of the mesophilic isolate *S. nigra* PRNP1-1W under the conditions investigated. Abiotic-control-corrected PBS weight loss provided the primary experimental evidence of PBS degradation. SEM observations provided qualitative information on PBS particle morphology, whereas FTIR analysis identified characteristic functional groups of PBS. However, the representative SEM micrographs did not establish enzymatic surface erosion, and the unnormalized FTIR spectra did not provide sufficient evidence to confirm degradation-related chemical changes or ester-bond cleavage. Genome mining identified eight putative hydrolase genes, among which the predicted secreted PET hydrolase-like protein OKIOMFPC_02247 shared 51%–73% amino acid identity and a conserved catalytic triad with experimentally characterized PBS-hydrolyzing enzymes, making it the most promising candidate PBS depolymerase. Extracellular esterase and protease activities were also detected in the culture supernatant. However, the specific enzymes responsible for PBS hydrolysis and their relationships with the predicted genes remain to be experimentally confirmed. Chromatographic analyses provided preliminary indications of succinic acid and 1,4-butanediol in the culture samples. Consequently, these observations should be considered preliminary and do not provide definitive evidence of PBS-derived monomer release or subsequent microbial assimilation. Among the conditions examined, the highest numerical EAI was observed at 35°C and pH 8.0, suggesting that PRNP1-1W may be suitable for PBS biodegradation under moderate cultivation conditions. Further studies involving functional characterization of candidate enzymes, validation of the proposed metabolic pathways, and optimization of cultivation conditions are required.

5. AUTHOR CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agree to be accountable for all aspects of the work. All the authors are eligible to be an author as per the International Committee of Medical Journal Editors (ICMJE) requirements/guidelines.

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7. CONFLICT OF INTERESTS

The authors report no financial or any other conflicts of interest in this work.

8. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

9. DATA AVAILABILITY

This Whole Genome Shotgun project of *Streptomyces nigra* PRNP1-1W has been deposited at DDBJ/ENA/GenBank under the accession JBWBCN000000000 (assembly GCA_056134365.1; BioProject PRJNA1434440; BioSample SAMN56400991). The version described in this paper is version JBWBCN010000000.

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11. USE OF ARTIFICIAL INTELLIGENCE (AI)-ASSISTED TECHNOLOGY

During the preparation of this work, the authors used Claude (Anthropic) in order to assist with language checking and writing arrangement. After using this tool/service, the authors reviewed and edited the content as needed and take full responsibility for the content of this work. AI-assisted text was used solely to support language editing and manuscript preparation. No AI-generated experimental data, analytical results, figures, or scientific findings were used in this study. All experimental data and results were obtained from the research conducted by the authors.

12. SUPPLEMENTARY MATERIAL

The supplementary material can be accessed at the journal's website: Link here [https://jabonline.in/admin/php/uploadss/1548_pdf.pdf]

REFERENCES

1. Mtibe A, Muniyasamy S, Mokhena TC, Ofosu O, Ojijo V, John M. Recent insight into the biomedical applications of polybutylene succinate and polybutylene succinate-based materials. Express Polym Lett 2023;17(1):2–8; doi: https://doi.org/10.3144/expresspolymlett.2023.2
2. Barletta M, Aversa C, Ayyoob M, *et al.* Poly(butylene succinate) (PBS): materials, processing, and industrial applications. Prog Polym Sci 2022;132:101579; doi: https://doi.org/10.1016/j.progpolymsci.2022.101579
3. Wierckx N, Narancic T, Eberlein C, *et al*. Plastic biodegradation: challenges and opportunities. In: Steffan RJ (ed.). Consequences of Microbial Interactions with Hydrocarbons, Oils, and Lipids: Biodegradation and Bioremediation. Springer, Cham, Switzerland, pp 1–29, 2018; doi: https://doi.org/10.1007/978-3-319-44535-9_23-1
4. Samaimai S, Krajangsang S, Kitpreechavanich V *et al.* Degradation of poly(butylene succinate) and poly(butylene succinate)/poly(lactide) blends using serine protease produced from *Laceyella sacchari* LP175. Trends Sci 2021; 18(20):37; doi: https://doi.org/10.48048/tis.2021.37
5. Tokiwa Y, Calabia BP, Ugwu CU, Aiba S. Biodegradability of plastics. Int J Mol Sci 2009;10(9):3722–42; doi: https://doi.org/10.3390/ijms10093722
6. Shah AA, Hasan F, Hameed A, Ahmed S. Biological degradation of plastics: a comprehensive review. Biotechnol Adv 2008;26(3):246–65; doi: https://doi.org/10.1016/j.biotechadv.2007.12.005
7. Aboelela D, Bassyouni MA. Biodegradable polymers converting environmental challenges into eco-friendly solutions. Egypt J Chem 2024;67(13):2015–32; doi: https://doi.org/10.21608/ejchem.2024.299280.10012
8. Jung H, Shin G, Park SB, Jegal J, Park SA, Park J, *et al.* Circular waste management: superworms as a sustainable solution for

biodegradable plastic degradation and resource recovery. Waste Manag 2023;171:568–79; doi: https://doi.org/10.1016/j.wasman.2023.09.027
9. Butbunchu N, Pathom-Aree W. Actinobacteria as promising candidate for polylactic acid type bioplastic degradation. Front Microbiol 2019;10:2834; doi: https://doi.org/10.3389/fmicb.2019.02834
10. Sriyapai P, Chansiri K, Sriyapai T. Isolation and characterization of polyester-based plastics-degrading bacteria from compost soils. Microbiology 2018;87(2):290–300; doi: https://doi.org/10.1134/S0026261718020157
11. Sujarit K, Pannim B, Kuakkhunthod N, Uywannang U, Sakdapetsiri C, Panyachanakul T, *et al.* Potential of Streptomyces rochei 8ER183 for poly(lactic acid)-degrading enzyme production, biodegradative capability, and its whole-genome sequence characterization. 3 Biotech 2025;15(3):55; doi: https://doi.org/10.1007/s13205-025-04219-3
12. Urbanek AK, Rymowicz W, Mirończuk AM. Degradation of plastics and plastic-degrading bacteria in cold marine habitats. Appl Microbiol Biotechnol 2018;102(18):7669–78; doi: https://doi.org/10.1007/s00253-018-9195-y
13. Danso D, Chow J, Streit WR. Plastics: environmental and biotechnological perspectives on microbial degradation. Appl Environ Microbiol 2019;85(19):e01095–19; doi: https://doi.org/10.1128/AEM.01095-19
14. Velo J, Caipang CM, Noblezada A, Banabatac LI, Tan NP, Ferriols VME. Whole genome sequence of *Arthrobacter* sp. from Iloilo City landfill soil unveils potential plastic biodegradation genes. Biodegradation 2025;36:72; doi: https://doi.org/10.1007/s10532-025-10168-8
15. Suphan S, Kunkhuntod N, Thimyaingam C, Khetkorn W, Sujarit K, Phonlamai A, *et al.* Unveiling bacterial diversity in the Lower Mekong Basin and biodegradation potential for polylactic acid (PLA), polybutylene succinate (PBS), and PLA/PBS blend polymers. Biocatal Agric Biotechnol 2025;69:103797; doi: https://doi.org/10.1016/j.bcab.2025.103797
16. Phonlamai A, Thongpool V, Sakdapetsiri C, Kitpreechavanich V, Lomthong T. Sustainable utilization of silk fibrous waste (SFW) for poly(butylene succinate) (PBS)-degrading enzyme production by Microbispora rosea BS2-4 and its degradative capability on PBS film polymer. Waste Biomass Valorization 2026;17:2317–27; doi: https://doi.org/10.1007/s12649-025-03247-7
17. Hall TA. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. In: Nucleic acids symposium series. Vol. 41. Oxford University Press, Oxford, UK, pp 95–8, 1999.
18. Yoon SH, Ha SM, Kwon S, Lim J, Kim Y, Seo H, *et al.* Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. Int J Syst Evol Microbiol 2017;67(5):1613–7; doi: https://doi.org/10.1099/ijsem.0.001755
19. Tamura K, Stecher G, Kumar S. MEGA11: molecular evolutionary genetics analysis version 11. Mol Biol Evol 2021;38(7):3022–7; doi: https://doi.org/10.1093/molbev/msab120
20. Chen S, Zhou Y, Chen Y, Gu J. Fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 2018;34(17):i884–90; doi: https://doi.org/10.1093/bioinformatics/bty560
21. Wick RR, Judd LM, Gorrie CL, Holt KE. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. PLoS Comput Biol 2017;13(6):e1005595; doi: https://doi.org/10.1371/journal.pcbi.1005595
22. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Res 2015;25:1043–55; doi: https://doi.org/10.1101/gr.186072.114
23. Chklovski A, Parks DH, Woodcroft BJ, Tyson GW. CheckM2: a rapid, scalable and accurate tool for assessing microbial genome quality using machine learning. Nature Methods 2023;20(8):1203–12; doi: https://doi.org/10.1038/s41592-023-01940-w
24. Lee I, Chalita M, Ha SM, *et al.* ContEst16S: an algorithm that identifies contaminated prokaryotic genomes using 16S rRNA gene sequences. Int J Syst Evol Microbiol 2017;67(6):2053–7; doi: https://doi.org/10.1099/ijsem.0.001872
25. Li H. Minimap2: pairwise alignment for nucleotide sequences. Bioinformatics 2018;34(18):3094–100; doi: https://doi.org/10.1093/bioinformatics/bty191
26. Danecek P, Bonfield JK, Liddle J, Marshall J, Ohan V, Pollard MO, *et al.* Twelve years of SAMtools and BCFtools. GigaScience 2021;10(2):8; doi: https://doi.org/10.1093/gigascience/giab008
27. Richter M, Rosselló-Móra R, Oliver Glöckner F, Peplies J. JSpeciesWS: a web server for prokaryotic species circumscription based on pairwise genome comparison. Bioinformatics 2016;32(6):929–31; doi: https://doi.org/10.1093/bioinformatics/btv681
28. Meier-Kolthoff JP, Göker M. TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. Nat Commun 2019;10(1):2182; doi: https://doi.org/10.1038/s41467-019-10210-3
29. Brettin T, Davis JJ, Disz T, Edwards RA, Gerdes S, Olsen GJ, *et al.* RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. Scientific Rep 2015;5(1):8365; doi: https://doi.org/10.1038/srep08365
30. Olson RD, Assaf R, Brettin T, Conrad N, Cucinell C, Davis JJ, *et al.* Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD and ViPR. Nucleic Acids Res 2023;51(1):D678–89; doi: https://doi.org/10.1093/nar/gkac1003
31. Seemann T. Prokka: rapid prokaryotic genome annotation. Bioinformatics 2014;30(14):2068–9; doi: https://doi.org/10.1093/bioinformatics/btu153
32. Grant JR, Enns E, Marinier E, Mandal A, Herman EK, Chen CY, *et al.* Proksee: in-depth characterization and visualization of bacterial genomes. Nucleic Acids Res 2023;51(W1):W484–92; doi: https://doi.org/10.1093/nar/gkad326
33. Li W, O'Neill KR, Haft DH, Dicuccio M, Chetvernin V, Badretdin A, *et al.* RefSeq: expanding the Prokaryotic Genome Annotation Pipeline reach with protein family model curation. Nucleic Acids Res 2021;49(1):D1020–8; doi: https://doi.org/10.1093/nar/gkaa1105
34. Teufel F, Almagro Armenteros JJ, Johansen AR, Gíslason MH, Pihl SI, Tsirigos KD, *et al.* SignalP 6.0 predicts all five types of signal peptides using protein language models. Nat Biotechnol 2022;2022(7):1023–5; doi: https://doi.org/10.1038/s41587-021-01156-3
35. Jones P, Binns D, Chang HY, Fraser M, Li W, Mcanulla C, *et al.* InterProScan 5: genome-scale protein function classification. Bioinformatics 2014;30(9):1236–40; doi: https://doi.org/10.1093/bioinformatics/btu031
36. Käll L, Krogh A, Sonnhammer ELL. A combined transmembrane topology and signal peptide prediction method. J Mol Biol 2004;338(5):1027–36; doi: https://doi.org/10.1016/j.jmb.2004.03.016
37. Altschul S. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res 1997;25(17):3389–402; doi: https://doi.org/10.1093/nar/25.17.3389
38. Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, et al. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Mol Syst Biol 2011;7:539; doi: https://doi.org/10.1038/msb.2011.75
39. Waterhouse AM, Procter JB, Martin DMA, Clamp M, Barton GJ. Jalview Version 2—a multiple sequence alignment editor and analysis workbench. Bioinformatics 2009;25(9):1189–91; doi: https://doi.org/10.1093/bioinformatics/btp033
40. Coêlho DF, Saturnino TP, Fernandes FF, Mazzola PG, Silveira E, Tambourgi EB. Azocasein substrate for determination of proteolytic activity: reexamining a traditional method using bromelain samples. BioMed Res Int 2016;1(1):8409183.
41. Kademi A, Aït-Abdelkader N, Fakhreddine L, Baratti JC. Characterization of a new thermostable esterase from the moderate

thermophilic bacterium *Bacillus circulans*. J Mol Catalysis B Enzymatic 2000;10(4):395–401.
42. Kim SH, Cho JY, Cho DH, *et al.* Acceleration of polybutylene succinate biodegradation by Terribacillus sp. JY49 isolated from a marine environment. Polym (Basel) 2022;14(19):3978; doi: https://doi.org/10.3390/polym14193978
43. Hu T, Wang Y, Ma L, *et al.* Biodegradation of polybutylene succinate by an extracellular esterase from *Pseudomonas mendocina*. Int Biodeterior Biodegrad 2024;195:105910; doi: https://doi.org/10.1016/j.ibiod.2024.105910
44. Penkhrue W, Khanongnuch C, Masaki K, *et al.* Isolation and screening of biopolymer-degrading microorganisms from northern Thailand. World J Microbiol Biotechnol 2015;31:1431–42; doi: https://doi.org/10.1007/s11274-015-1895-1
45. Savitha KS, Ravji Paghadar B, Senthil Kumar M, Jagadish RL. Polybutylene succinate, a potential biodegradable polymer: synthesis, copolymerization and biodegradation. Polym Chem 2022;13(24):3562–612; doi: https://doi.org/10.1039/D2PY00204C
46. Arahal DR. Whole-genome analyses: average nucleotide identity. In: Goodfellow M, Sutcliffe I, Chun J (eds.). Methods in Microbiology. Vol. 41: New Approaches to Prokaryotic Systematics. Academic Press, London, UK, pp 103–122, 2014; doi: https://doi.org/10.1016/bs.mim.2014.07.002
47. Kanehisa M, Furumichi M, Sato Y, Matsuura Y, Ishiguro-Watanabe M. KEGG: biological systems database as a model of the real world. Nucleic Acids Res 2025;53(D1):D672–7.
48. Shi K, Su T, Wang Z. Comparison of poly(butylene succinate) biodegradation by *Fusarium solani* cutinase and *Candida antarctica* lipase. Polym Degrad Stab 2019;164:55–60; doi: https://doi.org/10.1016/j.polymdegradstab.2019.04.005
49. Shehbas MC, Desai DS, Mathew TM, Nampoothiri KM. Microbial enzymes for plastic degradation: a comprehensive review of current status and emerging trends. Biodegradation 2026;37(2):30; doi: https://doi.org/10.1007/s10532-026-10248-3
50. Li WJ, Narancic T, Kenny ST, *et al.* Unraveling 1, 4-butanediol metabolism in *Pseudomonas putida* KT2440. Front Microbiol 2020;11:382; doi: https://doi.org/10.3389/fmicb.2020.00382
51. Qian X, Xin K, Zhang L, Zhou J, Xu A, Dong W, *et al.* Integration of ARTP mutation and adaptive laboratory evolution to reveal 1, 4-butanediol degradation in *Pseudomonas putida* KT2440. Microbiol Spectr 2023;11(3):4988; doi: https://doi.org/10.1128/spectrum.04988-22
52. Kim SH, Cho JY, Nara-Shin, Hwang JH, Kim HJ, Oh SJ, *et al.* Revealing the key gene involved in bioplastic degradation from superior bioplastic degrader Bacillus sp. JY35. Int J Biol Macromol 2023;244:125298; doi: https://doi.org/10.1016/j.ijbiomac.2023.125298
53. Lang F, Fei F, Sun C, Wu S. Highly efficient degradation of polybutylene succinate (PBS) and polycaprolactone (PCL) by a recombinant marine fungal cutinase. Appl Environ Microbiol 2025;91(9):833; doi: https://doi.org/10.1128/aem.00833-25
54. Phonlamai A, Khetkorn W, Thongpool V, Panyachanakul T, Suriyachadkun C, Kitpreechavanich V, *et al.* Profiling of the bacterial community and the degradative capability of newly isolated poly (lactic acid)(PLA)-and poly (butylene succinate)(PBS)-degrading bacteria from coastal samples. 3 Biotech 2025;15(10):352; doi: https://doi.org/10.1007/s13205-025-04521-0
55. Yao SF, Chen XT, Ye HM. Investigation of structure and crystallization behavior of poly (butylene succinate) by fourier transform infrared spectroscopy. J Phys Chem B 2017;2017(40):9476–85; doi: https://doi.org/10.1021/acs.jpcb.7b07954
56. Tan Y, Henehan GT, Kinsella GK, Ryan BJ. An extracellular lipase from Amycolatopsis mediterannei is a cutinase with plastic degrading activity. Comput Struct Biotechnol J 2021;19:869–79; doi: https://doi.org/10.1016/j.csbj.2021.01.019
57. Gamerith C, Vastano M, Ghorbanpour SM, *et al.* Enzymatic degradation of aromatic and aliphatic polyesters by P. pastoris expressed cutinase 1 from Thermobifida cellulosilytica. Front Microbiol 2017;8:938; doi: https://doi.org/10.3389/fmicb.2017.00938
58. Thumarat U, Nakamura R, Kawabata T, Suzuki H, Kawai F. Biochemical and genetic analysis of a cutinase-type polyesterase from a thermophilic Thermobifida alba AHK119. Appl Microbiol Biotechnol 2012;95(2):419–30; doi: https://doi.org/10.1007/s00253-011-3781-6
59. Uchida H, Shigeno-Akutsu Y, Nomura N, *et al.* Cloning and sequence analysis of poly(tetramethylene succinate) depolymerase from Acidovorax delafieldii strain BS-3. J Biosci Bioeng 2002;93(2):245–7; doi: https://doi.org/10.1263/jbb.93.245
60. Feller G, Thiry M, Gerday C. Sequence of a lipase gene from the antarctic psychrotroph Moraxella TA144. Nucleic Acids Res 1990;18(21):6431; doi: https://doi.org/10.1093/nar/18.21.6431
61. Kawai F, Oda M, Tamashiro T, *et al.* A novel Ca^{2+}-activated, thermostabilized polyesterase capable of hydrolyzing polyethylene terephthalate from Saccharomonospora viridis AHK190. Appl Microbiol Biotechnol 2014;98(24):10053–64; doi: https://doi.org/10.1007/s00253-014-5860-y

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