RESEARCH ARTICLE

Production, purification and evaluation of biodegradation potential of PHB depolymerase of Stenotrophomonas sp. RZS7

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Abstract

There are numerous reports on poly-β-hydroxybutyrate (PHB) depolymerases produced by various microorganisms isolated from various habitats, however, reports on PHB depolymerase production by an isolate from plastic rich sites scarce. Although PHB has attracted commercial significance, the inefficient production and recovery methods, inefficient purification of PHB depolymerase and lack of ample knowledge on PHB degradation by PHB depolymerase have hampered its large scale commercialization. Therefore, to ensure the biodegradability of biopolymers, it becomes imperative to study the purification of the biodegrading enzyme system. We report the production, purification, and characterization of extracellular PHB depolymerase from Stenotrophomonas sp. RZS7 isolated from a dumping yard rich in plastic waste. The isolate produced extracellular PHB depolymerase in the mineral salt medium (MSM) at 30˚C during 4 days of incubation under shaking. The enzyme was purified by three methods namely ammonium salt precipitation, column chromatography, and solvent purification. Among these purification methods, the enzyme was best purified by column chromatography on the Octyl-Sepharose CL-4B column giving optimum yield (0.7993 Umg⁻¹mL⁻¹). The molecular weight of purified PHB depolymerase was 40 kDa. Studies on the assessment of biodegradation of PHB in liquid culture medium and under natural soil conditions confirmed PHB biodegradation potential of Stenotrophomonas sp. RZS7. The results obtained in Fourier-Transform Infrared (FTIR) analysis, High-Performance Liquid Chromatography (HPLC) study and Gas Chromatography Mass-Spectrometry (GC-MS) analysis confirmed the biodegradation of PHB in liquid medium by Stenotrophomonas sp. RZS7. Changes in surface morphology of PHB film in soil burial as observed in Field Emission Scanning Electron Microscopy (FESEM) analysis confirmed the biodegradation of PHB under natural soil environment. The isolate was capable of degrading PHB and it resulted in 87.74% biodegradation. A higher rate of degradation under the...
natural soil condition is the result of the activity of soil microbes that complemented the biodegradation of PHB by *Stenotrophomonas* sp. RZS7.

**Introduction**

Poly-β-hydroxy alkanoates (PHAs) or PHB are accumulated as a source of food and energy by a wide variety of bacteria growing under nitrogen stress but carbon-rich conditions is utilized during starvation by the activity of PHB depolymerase [1–3]. PHAs/PHB are considered as the best environment-friendly and renewable option to the synthetics petrochemical plastics because of its similar properties to synthetic plastic [4–6] besides being thermoplastic and biodegradable in nature. Because of such useful properties, it has attracted commercial interest for use as the best alternative to the hazardous synthetic petrochemical polymers and hence it has been successfully commercialized [7–8]. During the last decades much research has been devoted towards the distribution and occurrence of PHB degraders and studies on different PHB depolymerases. Jendrossek and Handrick [9] reported that PHB depolymerases are responsible for extracellular PHB degradation. Extracellular PHB depolymerases of *Aspergillus fumigatus* Pdf1 [10], *Aureobacterium saperdae* [11], *Thermus thermophiles* HB8 [12], *Streptomyces bangladeshensis* 77T-4 [13], *Penicillium simplicissimum* LAR13 [14], *Acidovorax* sp. TP4 [15], *Streptomyces* KJ-72 [16] have been isolated and purified.

There are many different degradation mechanisms that are combined synergistically in nature to degrade polymers [17]. These mechanisms include biodeterioration, biofragmentation, assimilation, mineralization, and enzymatic degradation through extracellular and intracellular depolymerases that break the polymer to water-soluble products. [17]. PHB depolymerases produced by PHA degrading microorganism excrete under starved conditions, which degrade the polymer to water-soluble product forming clearing zones around the PHB depolymerase producing colonies. The action of PHB depolymerase breaks the ester bonds in PHB to produces PHB dimer and 3HB monomer. [18].

The bacterial isolate obtained from the plastic contaminated habitat that possess the ability to degrade PHB may be a potential source of commercially valuable PHB depolymerase, provided that the production, recovery, and purification protocols are properly optimized for large scale production of PHB depolymerase. Therefore, to ensure the biodegradability of biopolymers, it becomes imperative to study the purification of PHB biodegrading enzyme system [16]. PHB depolymerase of isolates obtained from plastic rich habitat is expected to have better relevance for its application in plastic/ bioplastic degradation.

The present paper reports the production, purification, and characterization of extracellular PHB depolymerase of *Stenotrophomonas* sp. RZS7 isolated from a plastic contaminated site in North Maharashtra region of India.

**Materials and methods**

**PHB**

PHB procured from Sigma-Aldrich, Germany was used as a standard for all experiments.

**Source of cultures**

Cultures of fungi; *Aspergillus niger* NCIM1025, *A. flavus* NCIM650, *Alternaria alternate* ARI715, and *Cercospora arachichola* were procured from NCIM, NCL, Pune, Maharashtra,
India. *Alcaligenes* sp RZS4 and *Pseudomonas* sp. RZS1 and *Streptomycetes* sp. were obtained from the culture depository of the Department. For present study, *Stenotrophomonas* sp. RZS7 that was previously identified [19] was used as PHB depolymerase producer.

**Production of PHB depolymerase**

Production of PHB depolymerase was carried out by shake flask method by growing *Stenotrophomonas* sp. RZS7 in MSM containing (gL⁻¹) PHB, 0.015 K₂HPO₄, 0.07 g; KH₂PO₄, 0.07 g; MgSO₄, 0.07 g; NH₄Cl, 0.1 g; NaNO₃, 0.1 g; NaCl, 0.5 mg; FeSO₄, 0.2 mg, ZnSO₄, 0.7 mg [14] at 120 rpm for 4 days at 30˚C.

**PHB depolymerase assay**

Following the incubation, MSM was centrifuged a 10,000 rpm for 15 min and the supernatant was used for PHB depolymerase assay [12]. The reaction mixture contained 150 μg ml⁻¹ PHB granules, (substrate for PHB depolymerase) and 2 mM CaCl₂ 50 mM Tris-HCl buffer (pH 7.0) and 0.5 mL of supernatant from MSM. Enzyme activity was spectrophotometrically measured at 650 nm as a decrease in the PHB turbidity. One unit of PHB depolymerase was defined as the quantity of enzyme required to decrease the absorbance by 0.1 min⁻¹.

**Purification of PHB depolymerase**

The cell-free supernatant of, MSM was subjected for purification of the enzyme as follows -

**Ammonium salt precipitation.** The cell-free supernatant was precipitated by adding increasing concentration (10–80%) w/v) of solid ammonium sulfate with continuous stirring at 4˚C for 1 h. The precipitate was dissolved in the Tris-HCl buffer (pH 7), supernatant and the dissolved precipitate was transferred in a separate dialysis bag and allowed for overnight dialysis in chilled phosphate buffer (pH 7.0) [13]. The protein content of dialyzed supernatant and dialyzed precipitate was measured as per Lowry et. al. method [20]. PHB depolymerase activity of dialyzed supernatant and dialyzed precipitate was measured [12].

**Solvent purification method.** The cell free supernatant was centrifuged at 10,000 rpm for 20 min. The residue obtained was dissolved in pre-chilled 1:1 acetone ethanol mixture, shaken well and kept in a water bath at 50˚C until all solvent is evaporated. The pellet obtained after evaporation was dissolved in Tris-HCl buffer (pH 7). PHB depolymerase activity of pellet and supernatant was measured [12].

**Column chromatography.** The cell-free supernatant obtained from MSM was loaded onto an Octyl-Sepharose CL-4B column pre-equilibrated with 50 mM glycine NaOH buffer (pH 9.0) followed by elution with 50% ethanol [12]. The eluting fractions were separately collected and subjected for PHB depolymerase [12].

**Determination of molecular weight of purified PHB depolymerase**

Determination of the molecular weight of purified PHB depolymerase was performed by Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis (SDS-PAGE). Purified fractions and standard protein marker (Ge-Nei, Bangaluru, India) were electrophoresed at 50 mv for 2 h. The separated bands were stained with Coomassie Brilliant Blue R-250 and visualized under UV transilluminator. The separated bands of test protein were compared with standard protein markers. The proteins content of bands was estimated by as per Lowry et al. [20].

**Assessment of biodegradation of PHB**

To evaluate the efficacy of degradation of biopolymer, the following methods were used
**PHB biodegradation under laboratory conditions.** Preparation of PHB film was done as per Linag et al. [21]. PHB powder (0.15 gm) was dissolved in 50 mL chloroform and vortexed for 10–15 min. The solution was poured into clean, dry Petri dishes and kept overnight at 30˚C. PHB film was obtained following the evaporation of chloroform. This film was used for the assessment of biodegradation.

PHB film was separately added as a sole carbon source into MSM and inoculated with *Stenotrophomonas* sp. RZS7 and incubated at 30˚C for 10 days at 120 rpm and observed for degradation of PHB film. Qualitative estimation involved the weight loss method. Quantitative estimation involved the measurement of change in optical density and crotonic acid concentration (μg mL⁻¹) at a different time intervals at 235 nm, [22]. The amount of crotonic acid was calculated from the calibration curve prepared with standard crotonic acid in the range of 10–100 μg mL⁻¹.

**PHB biodegradation under natural soil conditions.** Soil burial test gives an indication of the biodegradation of the polymer in a given soil under specific conditions. To check the biodegradability and durability of polymer sample under natural soil conditions, soil burial test was carried out. For this purpose garden soil was taken in different trays (1800 gm per tray) and the PHB film covered with the net was incorporated into the tray with *Stenotrophomonas* sp. RZS7 and trays were covered with moist thick paper [23]. Degradation of PHB film by *Stenotrophomonas* sp. RZS7 was observed in five different sets and was compared with negative control containing only sterile soil. The degradation of PHB film was measured in terms of weight loss and was expressed as percent reduction in the weight of PHB film.

**Fourier-transform infra red (FTIR) spectroscopy analysis**

Following the desired incubation period for degradation, the inoculated and incubated liquid culture medium of *Stenotrophomonas* sp. RZS7 was subjected to FTIR analysis on FTIR (FTIR Model 8400S, Shimadzu, Japan,) by using IR solution version 1.40 software. FTIR spectra were read between 4000 to 500 cm⁻¹ [24]. The functional groups present in degradation patterns were determined by FTIR and compared with the control.

**High-performance liquid chromatography (HPLC) analysis**

HPLC analysis of the preparation was analyzed on HPLC (Younglin, South Koria, ACME-9000) [25]. For this purpose, 20 μL of sample was injected into the C18 column as stationary phase and allowed to run 0.6 mL min⁻¹ on a mobile phase of acetonitrile: water (30:70 v/v) at 254 nm. The peaks were analyzed by using Autochro-3000 software.

**Gas chromatography-mass spectroscopic (GC-MS) analysis**

**Sample preparation.** The cell-free supernatant (2 mL) from a liquid medium was mixed with 2 mL chloroform and 2 mL of acidified methanol. For depolymerization and methanolysis of PHB, the mixture was heated at 100˚C for 3 h with occasional shaking followed by subsequently cooling at 30˚C followed by heating at 100˚C for 3 h and adding 1 mL of distilled water. The whole content was vortexed for 2 min and allowed to stand for 10 min to separate the phases. At the bottom layer, organic phase was obtained by a glass Pasteur pipette and it was subjected for spectral analysis [26].

**GC-MS analysis.** Monomers present in the degraded sample were identified by GC-MS (Model Autosystem XL, Perkin Elmer, USA) equipped with an SGE forte GC capillary column BP20 (Australia) and mass spectrophotometer. The mass spectra obtained were compared with the spectra of standard methyl esters of PHB available from mass spectra library of the National Institute of Standards and Technology (NIST), USA. The peak identities were initially
identified based on their matching of relative retention time with respect to standard sample extracted at time zero.

**GC-MS parameters.** One μL of sample was injected with a split ratio of 10:1. The rate of flow of carrier gas (helium) was 1 mL min⁻¹. The oven temperature of the column was programmed from 120°C for 2 min, increased at a rate of 20°C min⁻¹ to 230°C, and held at this temperature for 10 min. The temperature of the injector and detector was 225°C and 230°C respectively.

**Field emission scanning electron microscopy (FE SEM) analysis**

FE SEM was used to study the surface morphology and structural changes in PHB film following the biodegradation in soil burial test. PHB film from soil burial sample was thoroughly washed with sterile distilled water and mounted on stub using carbon tape it was made conducting by gold coating in vacuum by evaporation. The polymer film was dried in an Infrared (IR) lamp. The images of the treated test samples and untreated test samples were compared.

**Statistical analysis**

Three replicates of each experiment were run and the average value of triplicates was recorded. The data was analyzed by Student’s t-test and values of \( P \leq 0.05 \) were taken as statistically significant [27].

**Results and discussion**

**Production of PHB depolymerase**

After 4 days of incubation at 30°C at 120 rpm in MSM, *Stenotrophomonas* sp. RZS7 yielded 0.721 U mL⁻¹ PHB depolymerase. Similar enzyme activities have been reported by other researchers [21,28].

**Purification of PHB depolymerase**

**Ammonium salt precipitation.** Protein precipitation was increasing with increase in the concentrations of ammonium sulfate in the cell-free supernatant of *Stenotrophomonas* sp. RZS7, maximum proteins were precipitated with 70% ammonium sulfate concentration (Table 1). The protein concentration, specific activity and enzyme activity of PHB depolymerase in the dialyzed precipitate of *Stenotrophomonas* sp. RZS7 were 0.219 mgmL⁻¹, 0.7031 Umg⁻¹mL⁻¹ and 0.154 UmL⁻¹ respectively. Zhou et al. [28] have precipitated PHB depolymerase of *Escherichia coli*, and *Penicillium* sp. DS9701-D2 in 70 and 75% of ammonium sulfate respectively. Shivkumar et al. [29] have purified PHB depolymerase of *Penicillium citrinum* S2 in 80% of ammonium sulfate.

| Purification method            | Enzyme activity (Umg⁻¹mL⁻¹) |
|-------------------------------|-----------------------------|
| Salt precipitation            | 0.7031 (0.090)              |
| Solvent purification          | 0.1120 (0.022)              |
| Column chromatography         | 0.7993 (0.099)              |

Values are statistically significant at \( P \leq 0.05 \)
Values are the mean of triplicates
Values in the parenthesis are standard deviation

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Solvent purification method. Solvent purification of PHB depolymerase of *Stenotrophomonas* sp. RZS7 retained only 51.14% and 38.81% enzyme activity in pellet and supernatant (Table 1).

The protein concentration, specific activity and enzyme activity of PHB depolymerase in pellet and supernatant were 0.219 mgmL⁻¹, 0.5114 Umg⁻¹ mL⁻¹ and 0.3881 UmL⁻¹ respectively. The loss of enzyme activity in solvent system is due to the denaturation of proteins caused by the solvent system. Thus the solvent purification method proved an ineffective for purification of PHB depolymerase of *Stenotrophomonas* sp. RZS7.

Column chromatography. A total of five fractions were obtained from Octyl-Sepharose CL-4B. Among all the fractions analyzed for PHB depolymerase enzyme activity, the 3rd fraction showed maximum enzyme activity (Table 2). PHBV depolymerase of *Bacillus* sp. AF3 and *Streptoverticillium kashmirense* AF1 have also been purified on Sephadex G-75 [30]. Kim et al. [31] have also purified PHB depolymerase of *Emericellopsis minima* W2 and *Streptomyces* sp. KJ-72 on Sephadex G-100 and Sephadex G-150 respectively. Papanephtyotou et al. [12] and Hsu et al. [13] have isolated and purified extracellular PHB depolymerases of *Thermus thermophiles* HB8 and *Streptomyces bangladeshensis* 77T-4 respectively using column chromatography.

Among all three purification methods, purification on Octyl sepharose CL-4B column gave good purification yield (Table 1), more enzyme activity and more specific activity. The protein concentration, specific activity and enzyme activity of PHB depolymerase were 0.309 UmL⁻¹, 0.7993 Umg⁻¹ mL⁻¹ and 0.247 mgmL⁻¹ respectively.

Determination of molecular weight of purified PHB depolymerase

The protein fraction of *Stenotrophomonas* sp. RZS7 obtained from the octyl sepharose CL-4B column that exhibited maximum enzyme activity revealed a single protein band in SDS PAGE having a molecular mass of about 40 kDa Sadocco et al. [11] have also reported the molecular mass of 42.7 kDa PHB depolymerase in *Aureobacterium saperdae*. 

Assessment of biodegradation of PHB

Among the various reference cultures taken from our own departmental culture depository; all fungal and bacterial cultures were unable to degrade PHB when growing in PHB containing MSM. However, only *Streptomyces* sp. was found to degrade PHB on 10th day of incubation but the extent of PHB biodegradation in this case was less. Hence for further biodegradation studies *Stenotrophomonas* sp. RZS7 was used.

**Qualitative measurement.** A gradual reduction in the weight of PHB film was recorded after 8 days of incubation fragmentation in PHB film was observed while no changes occurred
in a control sample of PHB film (Table 3). Varda et al. [32] have recorded similar loss of weight of starch-based plastic by *S. epidermidis*.

**Quantitative estimation.** Isolate RZS7 caused the reduction in the amount of crotonic acid with an increase in the biomass. The maximum reduction in the amount of crotonic acid was recorded on 10th day of incubation at 37°C (Table 3). The reduction in crotonic acid concentration can be taken as the evidence of biodegradation of PHB film.

### Fourier transform infrared (FTIR) spectroscopy analysis

FTIR analysis of liquid culture medium containing PHB film and inoculated with *Stenotrophomonas* sp. RZS7 showed changes in the functional groups and significant shift of wavenumbers, indicating the biodegradation of polymer. It was observed that in case of control preparation (without inoculum) FTIR chromatogram peaks appearing at 3020.63 cm\(^{-1}\) changed to 3018.70, 2926.11, 2856.67 cm\(^{-1}\), 2399.53 cm\(^{-1}\) changed to 2360.95, 2333.94 cm\(^{-1}\), 2088.98 cm\(^{-1}\) changed to 2079.33 cm\(^{-1}\), 1641.48 cm\(^{-1}\) shifted to 1629.90 cm\(^{-1}\) and 1631.83 cm\(^{-1}\) shifted towards 1529.60, 1427.37, 1381.08 cm\(^{-1}\) (Figs 1 and 2). The major functional groups in control sample were found at wavelength frequency 1641.48 and 1631.83 denoted C = O stretch in ketone, frequency 3020.63 denoted C-H which stretch in alkane, wavelength frequency 1014.59 denoted C-O which stretch in ester and 756.12 denoted C-H which is rock alkane. However the major functional group frequency changes observed in degrading sample i.e. 1629.90 denoted C = O which stretch in ketone, 1215.19 which denote alkyl halide, 2399.53,2360.95 and 2333.94 denoted H-C = O group, 927.79 denoted C-O which stretch in ester, 769.62 denoted C-H which is rock alkane. These changes in wavelength frequency of major functional groups in degrading samples as compared to control give preliminary proof of biodegradation of polymer by *Stenotrophomonas* sp. RZS7.

### High performance liquid chromatography (HPLC) analysis

The spectra of the original polymer sample before degradation revealed six peaks at 254 nm (Fig 3). While polymer sample degradation by *Stenotrophomonas* sp. RZS7 revealed nine peaks having different retention time as compared to control (Fig 4) indicating the formation of monomers. The sum of the total area of peaks of the degraded sample was less than the sum of the total area of peaks of control (undegraded) preparation. This reduction in the peak area confirmed the degradation of the polymer.

### Gas chromatography-mass spectroscopic (GC-MS) analysis

The degradation pattern on the basis of removal or decrease in the retention time of the peaks and their comparison with the retention time of the peaks of reference demonstrated the

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**Table 3. Qualitative measurement of biodegradation of PHB film.**

| Weight of PHB film | Weight loss of PHB film (g) | OD  | Crotonic acid’ (μg/mL) |
|--------------------|----------------------------|-----|------------------------|
| Initial weight     | 0.159 (0.031)              | 0.000 | 1000.0030            |
| After 2 days       | 0.148 (0.029)              | 0.014 | 813 (0.026)           |
| After 4 days       | 0.109 (0.021)              | 0.019 | 794 (0.019)           |
| After 6 days       | 0.099 (0.017)              | 0.035 | 705 (0.018)           |
| After 8 days       | Fragmentation              | 0.050 | 686 (0.015)           |

Values were statistically significant at P ≤ 0.05

Values in the parenthesis are standard deviation

*Crotonic acid was as PHB standard for spectrophotometric estimation of PHB as when PHB is heated with concentrated sulphuric acid it gets converted into crotonic acid.

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**Fig 1.** FTIR chromatogram of PHB (Control) read between 4000 to 500 cm\(^{-1}\) and analyzed with 1.40 software.

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**Fig 2.** FTIR chromatogram of PHB after degradation by *Stenotrophomonas* sp. RZS7 read between 4000 to 500 cm\(^{-1}\) and analyzed with 1.40 software. The functional groups present in the spectra were compared with the functional groups in control preparation.

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disappearance of peaks indicating biodegradation of PHB components by *Stenotrophomonas* sp. RZS7 (Fig 5 and Fig 6). A significant decrease in area height and percentage in the degraded sample was clear over the control (undegraded) sample. The total area of peaks of degraded
Fig 5. Chromatogram of polymer sample before biodegradation (Standard). GC MS analysis was performed on gas chromatograph equipped with capillary column BP20 and mass spectrophotometer. The mass spectra obtained were recorded.

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sample was less as compared to the total area of peaks of control (undegraded) preparation. This reduction in the peak area confirmed the conversion of PHB due to its biodegradation into monomers.

The fragmentation patterns with GC-MS and the identities of peaks in the mass spectra were correlated to the carbonyl and hydroxyl ends of the represented hydroxyl alkanoates ethyl esters of PHB after degradation. Tridecanoic acid 12-methyl-methyl ester and heptacosanoic acid methyl ester in standard polymer sample were completely degraded whereas Decanoic acid methyl ester, undecanoic acid methyl ester, and nonanoic acid methyl ester were detected in the degraded sample (Table 4). McLafferty and Turecek [33] reported that the mass spectra of the methyl esters of PHB dominated by m/z = 74 represented the carbonyl end of the molecule and showed the characteristic of 3-hydroxyl functional groups. However, the peak at m/z = 59 indicated the release of the hydroxyl end during the cleavage of the molecule between C3 and C4.

The mass spectra of standard polymer sample and the characteristics signals were recorded at m/z = 29, 39, 41, 43, 55, 57, 59, 74, 75, 87, 101, 111, 131, 143, 157, 171, 185, 199, 219, 227, 239, 265, 270, 271, 314, 415. However in polymer degrading sample m/z = 29, 32, 41, 43, 44, 55, 57, 69, 74, 75, 87, 97, 111, 129, 143, 145, 169, 176, 199, 220, 227, 270 (Fig 7) which can be attributed to oligomers of PHB (Fig 8). Wennan et al. [34] reported that m/z = 29, 32, 41, 43, 55, 69, 75, 87, 97, 111, 143 denotes Pentadecanoic acid methyl ester, m/z = 29, 41, 55, 74, 75, 87, 97 denotes Decanoic acid, methyl ester, m/z = 41, 55, 74 denotes Dodecanoic acid methyl ester, m/z = 74 denotes Hexadecanoic acid methyl ester, m/z = 43, 55, 74 denotes Octadecanoic acid methyl ester.

### Table 4. GC MS analysis of methanolyse d polymer before degradation (Standard) and after degradation.

| Retention time | Methyl ester PHB monomers (before degradation) | MW | Methyl ester PHB monomers (after degradation) | MW |
|----------------|-----------------------------------------------|----|-----------------------------------------------|----|
| Pentadecanoic acid, 14-methyl-, methyl ester | Hexadecanoic acid, methyl ester | 270 | Tridecanoic acid, methyl ester | 228 |
| Tridecanoic acid, methyl ester | Hexadecanoic acid, methyl ester | 228 | Pentadecanoic acid, 14-methyl-, methyl ester | 270 |
| Hexadecanoic acid, 15-methyl-, methyl ester | Heptadecanoic acid, methyl ester | 284 | Hexadecanoic acid, 15-methyl-, methyl ester | 284 |
| Heneicosanoic acid, methyl ester | Decanoic acid, methyl ester | 340 | Tridecanoic acid, methyl ester | 186 |
| Docosanoic acid, methyl ester | Dodecanoic acid, methyl ester | 354 | Undecanoic acid, methyl ester | 214 |
| Eicosanoic acid, methyl ester | Hexacosanoic acid, methyl ester | 326 | Methyl tetradecanoate | 242 |
| Methyl tetradecanoate | Tridecanoic acid, 12-methyl-, methyl ester | 242 | Pentadecanoic acid, methyl ester | 256 |
| Octadecanoic acid, methyl ester | Eicosanoic acid, methyl ester | 298 | Dodecanoic acid, methyl ester | 326 |
| Dodecanoic acid, methyl ester | Heneicosanoic acid, methyl ester | 214 | Pentadecanoic acid, methyl ester | 340 |
| Pentadecanoic acid, methyl ester | Octadecanoic acid, methyl ester | 256 | Heptacosanoic acid, methyl ester | 298 |
| Heptacosanoic acid, methyl ester | Decosanoic acid, methyl ester | 424 | Tridecanoic acid, methyl ester | 354 |

### Fig 6. Chromatogram of polymer sample after biodegradation. GC MS analysis was performed by using gas chromatograph with turbomass GC capillary column BP20 and mass spectrophotometer. The mass spectra obtained were compared and identified with the library of spectra of standard methyl esters of PHB. The peaks were identified by matching relative retention time with respect to standard sample extracted at time zero.

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Fig 7. GC-MS spectra of polymer sample before degradation showing mass spectra of m/z = 29, 39, 41, 43, 45, 55, 57, 59, 74, 75, 87, 101, 111, 131, 143, 157, 171, 185, 199, 219, 227, 239, 265, 270, 271, 314, 415 indicating the presence of intact polymer of PHB.

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Fig 8. GC-MS spectra of polymer sample after degradation showing mass spectra of m/z 29, 32, 41, 43, 44, 55, 57, 69, 74, 75, 87, 97, 111, 129, 143, 145, 169, 176, 199, 220, 227, 270 indicating the presence of oligomers of PHB.

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Production of PHB depolymerase of Stenotrophomonas sp. RZS7
Field emission scanning electron microscopy (FE-SEM) analysis

Surface analysis of PHB film after soil burial experiment showed many differences in the morphology of PHB film as compared to control (Fig 9A) and PHB film buried in the soil (Fig 9B). Biodegradation of PHB film caused erosion and roughening of the surface of PHB film (Fig 9C). Gautam and Kaur [35] have also reported the morphological changes in polyethylene surface after degradation as compared with control. Calabia and Tokiwa [36] analyzed the degradation of PHB by SEM and observed the presence of holes on the surface of PHB film due to the growth of Streptomyces sp. SC-17 on the surface of PHB film causing biodegradation of PHB.

Conclusion

The present attempt provided PHB degrading Stenotrophomonas sp. RZS 7 which utilized PHB as a sole source of carbon under the influence of extracellular PHB depolymerase. The enzyme acted as a key enzyme responsible for the biodegradation of PHB. Purification of PHB depolymerase by solvent purification resulted in protein precipitation and denaturation of the enzyme. Column chromatography appeared as an efficient and best purification method as it yielded maximum protein, maximum enzyme activity, and maximum specific activity. The molecular weight of purified PHB depolymerase of Stenotrophomonas sp. RZS7 (40 kDa) matched with a molecular weight of Aureobacterium saperae.

Biodegradation of PHB in liquid culture medium and under natural soil conditions confirmed PHB biodegradation potential of Stenotrophomonas sp. RZS7. The results obtained in FTIR analysis, HPLC study and GC-MS analysis confirmed the biodegradation ability of Stenotrophomonas sp. RZS7 in liquid medium. Changes in surface morphology of PHB film in the soil burial as observed in FE SEM analysis confirmed the ability of isolate to degrade PHB under natural soil conditions. Higher rate of degradation under natural soil condition is the result of activity of soil microbes that complemented the degradation by Stenotrophomonas sp. RZS7.

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