



Biodegradation and Bioremediation

William Chang

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Biodegradation and Bioremediation

About the Book

This book on biodegradation and bioremediation focuses on environmental pollution, phytoremediation and rate of degradation in differing ecosystems. The assessment of the quality of biodegradability provides for better recycling processes as well as waste management techniques. Biodegradation is the process by which microorganisms decompose materials. Bioremediation is a waste management technique based on the principles of biodegradation. Both these processes are extremely significant for environmental sustainability. Some of the diverse topics covered in this text address the varied branches that fall under this category. The various advancements in this discipline are glanced at and their applications as well as ramifications are looked at in detail. This book on biodegradation and bioremediation would prove helpful for students and teachers in the field of ecological sciences, waste management and environmental engineering. A number of latest researches have been included to keep the readers up-to-date with the global concepts in this area of study.

About the Editor

William Chang received his Ph.D. in Environmental Health from Boston University, United States of America. He is a research professor in the department of earth and environmental health at a university of America. Chang's interests lie in the management and remediation of adverse effects of biodegradation and conserving nature through sustainability measures. He has been a part of numerous programmes related to biodegradation and has headed many campaigns for the sustainability of the environment.

Changes Biodegradation and Bioremediation

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Edited by William Chang

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New York

Published by Syrawood Publishing House,
750 Third Avenue, 9th Floor,
New York, NY 10017, USA
www.syrawoodpublishinghouse.com

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Edited by William Chang

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International Standard Book Number: 978-1-68286-452-4 (Hardback)

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Cataloging-in-publication Data

Biodegradation and bioremediation / edited by William Chang.

p. cm.

Includes bibliographical references and index.

ISBN 978-1-68286-452-4

1. Biodegradation. 2. Bioremediation. 3. Pollutants--Biodegradation. 4. Environmental management. I. Chang, William.

QH530.5 .B56 2017

577.16--dc23

Printed in China.

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PREFACE

This book on biodegradation and bioremediation focuses on environmental pollution, phytoremediation and rate of degradation in differing ecosystems. The assessment of the quality of biodegradability provides for better recycling processes as well as waste management techniques. Biodegradation is the process by which microorganisms decompose materials. Bioremediation is a waste management technique based on the principles of biodegradation. Both these processes are extremely significant for environmental sustainability. Some of the diverse topics covered in this text address the varied branches that fall under this category. The various advancements in this discipline are glanced at and their applications as well as ramifications are looked at in detail. This book on biodegradation and bioremediation would prove helpful for students and teachers in the field of ecological sciences, waste management and environmental engineering. A number of latest researches have been included to keep the readers up-to-date with the global concepts in this area of study.

This book has been a concerted effort by a group of academicians, researchers and scientists, who have contributed their research works for the realization of the book. This book has materialized in the wake of emerging advancements and innovations in this field. Therefore, the need of the hour was to compile all the required researches and disseminate the knowledge to a broad spectrum of people comprising of students, researchers and specialists of the field.

At the end of the preface, I would like to thank the authors for their brilliant chapters and the publisher for guiding us all-through the making of the book till its final stage. Also, I would like to thank my family for providing the support and encouragement throughout my academic career and research projects.

Editor

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List of Contributors

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Biodegradation of Polycyclic Aromatic Hydrocarbons by *Novosphingobium pentaromativorans* US6-1

Yihua Lyu^{1,2}, Wei Zheng^{1,2}, Tianling Zheng^{1,2}, Yun Tian^{1,2*}

¹ Key Laboratory of the Ministry of Education for Coastal and Wetland Ecosystems, Xiamen University, Xiamen, China, ² State Key Laboratory of Marine Environmental Science, Xiamen University, Xiamen, China

Abstract

Novosphingobium pentaromativorans US6-1, a marine bacterium isolated from muddy sediments of Ulsan Bay, Republic of Korea, was previously shown to be capable of degrading multiple polycyclic aromatic hydrocarbons (PAHs). In order to gain insight into the characteristics of PAHs degradation, a proteome analysis of *N. pentaromativorans* US6-1 exposed to phenanthrene, pyrene, and benzo[a]pyrene was conducted. Several enzymes associated with PAHs degradation were identified, including 4-hydroxybenzoate 3-monooxygenase, salicylaldehyde dehydrogenase, and PAH ring-hydroxylating dioxygenase alpha subunit. Reverse transcription and real-time quantitative PCR was used to compare RHD α and 4-hydroxybenzoate 3-monooxygenase gene expression, and showed that the genes involved in the production of these two enzymes were upregulated to varying degrees after exposing the bacterium to PAHs. These results suggested that *N. pentaromativorans* US6-1 degraded PAHs via the metabolic route initiated by ring-hydroxylating dioxygenase, and further degradation occurred via the *o*-phthalate pathway or salicylate pathway. Both pathways subsequently entered the tricarboxylic acid (TCA) cycle, and were mineralized to CO₂.

Editor: Stephen J. Johnson, University of Kansas, United States of America

Funding: This work was supported by the National Natural Science Foundation of China (40976069, 41176093). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

* Email: tianyun@xmu.edu.cn

Introduction

Polycyclic aromatic hydrocarbons (PAHs) are aromatic hydrocarbons with two or more fused benzene rings, and originate from natural as well as anthropogenic sources. They are widely distributed environmental contaminants that have detrimental biological effects, including toxicity, mutagenicity, and carcinogenicity [1,2]. PAHs in the environment are degraded via volatilization, photo-oxidation, chemical oxidation, bioaccumulation, and adsorption to soil particles; however, the principal removal processes are thought to be microbial transformation and degradation [3–4]. In several microorganisms, metabolic pathways have been identified that lead to complete mineralization of aromatic hydrocarbons or partial transformation to dead end intermediates. As bioremediation efforts aggressively attempt to employ microorganisms to biostimulate or bioaugment degradation of aromatic hydrocarbons on a practical scale [5], the enzymes involved in the degradation of PAHs should be fully characterized as part of a risk assessment of this process.

PAHs are thermodynamically stable and resistant to microbial degradation due to their aromatic nature, which includes stabilization by multiple rings and low aqueous solubility. Despite these properties, a variety of bacterial species can degrade PAHs. Most research on the enzymes involved in PAH metabolism and genetic regulation is focused on *Pseudomonas* and *Sphingomonas* species [6–11], but *Mycobacterium*, *Rhodococcus*, *Nocardioideis*, and *Novosphingobium* species can also mineralize PAHs [12,13]. Proposed pathways for pyrene biodegradation by mycobacteria have been reported [14], including the complete pathway to the

tricarboxylic acid (TCA) cycle proposed for *Mycobacterium vanbaalenii* PYR-1, but little is known about the genetic and enzymatic processes involved in the PAHs degradative pathways used by *Novosphingobium* species.

Novosphingobium pentaromativorans US6-1, is a marine bacterium that was isolated from muddy sediments of Ulsan Bay, Republic of Korea. Prior research has shown that it can degrade or transform phenanthrene, pyrene, chrysene, benz[a]anthracene, benzo[b]-fluoranthene and benzo[a]pyrene. Because of its metabolic versatility, this bacterium was proposed to be a potential candidate for the bioremediation of PAH-contaminated areas [15]. In the current study, a proteomic analysis of cells exposed to phenanthrene, pyrene, and benzo[a]pyrene was conducted using one-dimensional gel electrophoresis in combination with liquid chromatography-tandem mass spectrometry to identify the proteins involved in the degradation. These analyses documented protein composition profiles in response to exposure to three different PAHs, and identified specific proteins that characterize the physiological state of *Novosphingobium pentaromativorans* US6-1. A culture-independent method using reverse transcription and real-time quantitative PCR showed that gene expression of these different proteins was important in the biodegradation of PAHs. The results presented here comprise the foundation of a protein index for *N. pentaromativorans* US6-1, and provide fundamental information on PAH degradation as well as other metabolic characteristics in environmental strains of *Novosphingobium* sp.

Materials and Methods

1 Bacterial strain and culture conditions

Novosphingobium pentaromativorans US6-1 used in this study was provided by Dr. Kim Sangjin (Korean Ocean Research and Development Institute). All chemicals used were purchased from Sigma-Aldrich unless otherwise specified, and were of high-performance liquid chromatography grade. The PAH compounds (phenanthrene, pyrene, and benzo[a]pyrene) were of >97.0% purity, and stock solutions of each PAH were prepared in cyclohexane at a concentration of 5 mg mL⁻¹. *Novosphingobium pentaromativorans* US6-1 was cultured in Zobell 2216E broth (5 g L⁻¹ peptone, 1 g L⁻¹ yeast extract, 0.01 g L⁻¹ FePO₄, at pH 7.6–7.8) for 36 h at 25°C until exponential growth was achieved. Cells were collected via centrifugation and washed twice with MM2 medium [18 mM (NH₄)₂SO₄, 1 μM FeSO₄·7H₂O, 100 μL 1 M KH₂PO₄/Na₂HPO₄ buffer solution and 10% MCD (mixed-cyclodextrin), per liter of aged sea water, at pH 7.2]. The cyclohexane was allowed to volatilize by storing it in the fume hood for 2–3 days at room temperature, then the bacterial inocula were added to 100 mL MM2 with 10 ppm phenanthrene, pyrene, and benzo[a]pyrene, at a final optical density of approximately OD value 0.3 (measured spectrophotometrically at 600 nm). The cultures were incubated at 30°C in the dark, and mixed using a rotary shaker at 150 rpm. The media containing the same amount of PAHs but without the bacterial inoculation was used as the control to determine any abiotic loss of PAHs. Triplicate samples were collected from the experimental system every 12 h for two days.

2 Analysis of PAH biodegradation

The residual PAHs were extracted using the liquid-liquid extraction method, followed by GC-MS determination. Fluoranthene was used as an internal standard to adjust the percent extracted. These samples were treated with equivalent dichloromethane for 15 min in an ultrasonic bath, filtered through anhydrous sodium sulfate, and concentrated by rotary evaporation to 1 mL under a gentle stream of nitrogen. PAH analysis was performed with a CP3800 gas chromatograph with a split/splitless injection port. The GC was equipped with a CP5860 silica capillary column (30 m×0.25 mm i.d., 0.25 μm film thickness) and helium carrier gas. The injection temperature was 300°C with an injection volume of 1 μL (splitless). The temperature program was as follows: isothermal at 100°C for 1 min, with 20°C/min to 200°C, 10°C/min to 320°C, and a final isothermal cycle at 320°C for 3 min. Quantification of PAH concentration was assessed with a GC/HRMS using a Varian 1200 (Palo Alto, USA) in the EI positive ion setting, with an electron energy of 70 eV. Transfer line temperature and ion source temperature were maintained at 250°C and 200°C, respectively, and the mass spectra obtained were compared to the NIST library.

3 Measurement of electron transport system activity (ETSA)

The measurement procedure for bacterial ETSA followed established methods [16]: 0.5 mL of culture was combined with 1 mL of 2-p-iodophenyl-3-p-nitrophenyl-5-phenyl tetra-zolium chloride, and allowed to interact for 30 min at room temperature (25°C) in the dark, then 100 μL of formalin was added to stop the reaction. The mixture was centrifuged (10,000×g for 5 min) in a Hitachi SCR20BC centrifuge, the supernatant was removed, and 1 mL methanol was added to the reaction tube. After the mixture was homogenized, centrifugation for 5 min at 10,000×g with a micro-12 centrifuge was repeated, and the reaction tube was

placed in an ice bath. Absorbance was measured at 495 nm using a spectrophotometer. The ETSA in μgO₂/mL/min was calculated using the following formula:

$$\text{ETSA} = (\text{Ab}/15.9) \times V \times 32/2 \times 1/S \times t$$

where Ab is absorbance; V is final reaction volume (mL) (methanol volume); S is the sample amount (mL); t is the incubation time (min); 32/2 is a constant (relative molecular weight of oxygen); and 15.9 is the molar absorbance of formazan.

4 Extraction of total proteins

After incubation for 24, 36, or 48 h, the medium dosed with phenanthrene, pyrene, or benzo[a]pyrene was carefully removed by centrifugation at 4,000×g for 5 min at room temperature. Cells were washed twice with 30 mL of PBS (pH 7.6) and pelleted by centrifugation under the same conditions. For protein extraction, the cell pellets were resuspended in 2 mL lysate (7 M urea, 2 M thiourea, 4% w/v 3-[3-cholamidopropyl dimethylammonio]-1-propanesulfonate [CHAPS], 60 mM dithiothreitol, 2% v/v Pharmalyte 3–10, and a protease inhibitor cocktail) and sonicated on ice for 10 min using a 500 ms/s pulse at 40 W. The sonicated cell suspensions were then centrifuged at 10,000×g for 30 min at 4°C. Protein concentration was estimated using the 2-D Quant Kit (Amersham, USA).

5 Electrophoresis and protein identification

SDS-PAGE was carried out using the tris-glycine-SDS buffer system (25 mM Tris, 192 mM glycine, and 0.1% SDS) on the SE600 electrophoresis apparatus (GE Healthcare, USA), at 24 mA/gel, until the dye front reached the bottom edge of the gel. A protein MW marker (Takara, China) was used in the gel, which was stained with Coomassie Brilliant Blue G-250 (GE Healthcare, USA), and scanned using an Amersham Biosciences image scanner (GE Healthcare, USA).

Three specific bands differently expressed under phenanthrene, pyrene, and benzo[a]pyrene were excised from the gel and used for in-gel tryptic digestion [17]. The gel pieces were destained and washed, and, after dithiothreitol reduction and iodoacetamide alkylation, the proteins were digested with trypsin for 20 h at 37°C. The resulting tryptic peptides were extracted from the gel pieces with 60% acetonitrile, 0.1% trifluoroacetic acid, and 100% acetonitrile. Extracts were dried completely for nano-liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis. After resuspension in 20 μL 0.1% formic acid, the peptide samples were injected onto a Zorbax 300SB C18 peptide trap (Agilent Technologies, USA), and desalted with 0.2% formic acid at a flow rate of 10 μL min⁻¹ for 20 min. Peptides were eluted from the trap and separated on a reverse phase C18 column (0.15 mm×150 mm, Column Technology), with a linear gradient of 4% to 50% mobile phase B (0.1% formic acid-84% acetonitrile) in mobile phase A (0.1% formic acid), over 30 min at 65 μL min⁻¹. LC-MS/MS measurements were made with a linear trap quadrupole (LTQ) mass spectrometer (Thermo Finnigan, USA) equipped with a microspray source. The LTQ mass spectrometer operated in the data-dependent mode with the following parameters: spray voltage (3.4 kV), spray temperature 170°C, full scan m/z range (400–1800). The twenty most intense ions in every full scan were automatically selected for MS/MS.

6 Extraction of total RNA

At each of the aforementioned sampling times, total RNA was extracted from 100 mL of bacterial culture using Trizol (Invitro-

gen, USA), according to the manufacturer's instructions. Residual DNA was digested for 2 h at 37°C in a total volume of 200 µL using 100 U of DNase I in 40 mM Tris-HCl (pH 7.5) containing 6 mM MgCl₂. DNase I was removed using standard phenolization and precipitation procedures [18]. The RNA pellet was dissolved in 200 µL RNase-free H₂O and stored at -20°C. Extract concentrations were measured spectroscopically and were adjusted for optimal reverse transcription (RT)-PCR amplification.

7 RT-PCR and real-time quantitative PCR

For reverse transcription PCR (RT-PCR) of the isolated RNA, amplification reactions contained the following: 2 µg RNA template, 1 µL random hexamer primer (150 ng/µL), and 12 µL of nuclease-free water. Reactions were denatured for 5 min at 65°C, then 2 µL dNTP (10 mM), 4 µL 5×reaction buffer, 1 µL (20 U) RNase inhibitor, and 1 µL (25 U) RevertAid Reverse Transcriptase were added to obtain a total reaction volume of 20 µL. After centrifugation, the reaction was incubated for 5 min at 25°C followed by 60 min at 42°C, then terminated by heating the samples at 70°C for 5 min. RT-PCR analyses were completed using a Rotor-Gene 6000 (Corbett Research, Australia).

The sequences of the studied proteins, PAH ring-hydroxylating dioxygenase alpha subunit (RHDα) and 4-hydroxybenzoate 3-monooxygenase, were obtained from the GenBank nucleotide database (<http://www.ncbi.nlm.nih.gov/nucleotide/>) [19]. Primer Premier5 software (Premier Biosoft, Canada) was used to design a series of oligonucleotides from which three sets of specific primers (Table 1) were selected. The 16S ribosomal RNA (rRNA) gene was used as an internal standard. The relative quantification of genes by real-time quantification PCR was performed in a 12 µL reaction, which contained 2 µL of cDNA, 6 µL SYBR Premix ExTaq (TaKaRa, China), and 0.5 µL (10 µM) primer. Amplifications were carried out with the following temperature profiles: activation for 20 s at 95°C, followed by 40 cycles of 10 s at 95°C, 20 s at 60°C, and elongation at 72°C. Data was collected during each annealing step. Analyses of the dissociation curve and electrophoresis products were used to determine the specificity of the real-time PCR product. Each run included a negative control and a cDNA reaction without reverse transcriptase. Melt curve analysis was conducted at the end of each RT-PCR program, which measured signal intensity every 10 s as temperatures increased in 0.5°C increments from 51°C to 95°C.

The relative expression ratio of each target gene was calculated using the PAHs-treated group signal intensity divided by the control group signal intensity, after normalization to the levels of the standard gene. All analyses were based on the threshold cycle (C_t), defined as the PCR cycle at which the fluorescence signal crossed a threshold line in the exponential phase of the

amplification curve. Melting curve analysis of amplification products was performed at the end of each PCR reaction to ensure that only one product was amplified and detected. To maintain consistency, the baseline was set automatically by the software. A comparative C_t method was used to analyze the expression level of target genes, and the C_t for the target amplification of genes and the internal standard (16S rRNA gene) were determined for each sample. Differences between the C_t of the target and the internal standard, called ΔC_t, were calculated to normalize the differences in the amount of total nucleic acid added to each reaction, and the efficiency of the RT-PCR. The control group (without PAHs exposure) was used as the reference sample, and was referred to as the calibrator. The ΔC_t for each sample was subtracted from the ΔC_t of the calibrator; this difference was called the ΔΔC_t value. The expression level of target genes could be calculated by 2-ΔΔC_t, which represented the n-fold difference relative to the calibrator. In addition, template quantitation of test cDNA using the 16S rRNA gene was attempted. These analyses confirm the efficiency of the qPCR analysis.

Results and Discussion

1 Biodegradation of PAHs by *Novosphingobium pentaromativorans* US6-1

To gain a better understanding of the metabolic capabilities of *N. pentaromativorans* US6-1, the ETSA and biodegradation rates of phenanthrene, pyrene and benzo(a)pyrene were measured. The ETSA value provides an accurate measure of the actual respiratory rate of *N. pentaromativorans* US6-1 under different PAHs induction, and is positively correlated with cell activity. As shown in Fig. 1, the residual rate of PAHs decreased at different levels. After only 24 h of incubation, US6-1 degraded almost 86.62% of the phenanthrene. After 36 h of incubation, US6-1 degraded 31.81% of the pyrene, and after 48 h incubation degraded 22.18% of the benzo(a)pyrene. Along with the decrease in these residues, we observed an increase in ETSA to 2.95 µgO₂/mL/min, 3.92 µgO₂/mL/min, and 4.21 µgO₂/mL/min at incubation times of 24 h, 36 h, and 48 h, respectively. However, in the control, which contained these three PAHs but no bacteria, phenanthrene, pyrene, and benzo(a)pyrene residues only decreased by 1.5%, 1.3%, and 1.4%, respectively.

HMW-PAHs, such as pyrene, benzo(a)anthracene, chrysene, and benzo(a)pyrene, are resistant to microbial attack. Most reported microbial degradation rates of pyrene and benzo(a)pyrene are quite modest in comparison to certain reported strains; e.g., *Mycobacterium* sp. strain PYR-1 degraded 90% phenanthrene after 14 days of incubation [21]. In previous reports, pyrene and benzo(a)pyrene were degraded by *Sphingomonas aromaticivorans* B0695 after incubation times of 28–32 h [22], *Burkholderia cepacia*

Table 1. Characteristics of PCR primer sets used in this study.

Primer	Target gene	Sequence 5'-3'	Amplicon size (bp)	Reference
PAH-RHDα Fw	RHDα	GGA AAG GCT TGT GGG TGT CG	252	gi 494073952
PAH-RHDα Re	RHDα	GTG GCA TCA TCG CAT CGT GT	252	gi 494073952
HBMO Fw	4-hydroxybenzoate 3-monooxygenase	GCG TGT GCC GCC TTG TAA TCA	157	gi 494072487
HBMO Re	4-hydroxybenzoate 3-monooxygenase	ACG CCA GTT CGT CCC AGA TGC	157	gi 494072487
968R	16S rRNA	AAC GCG AAG AAC CTT AC	433	Felske A [20]
1401F	16S rRNA	CGG TGT GTA CAA GAC CC	433	Felske A [20]

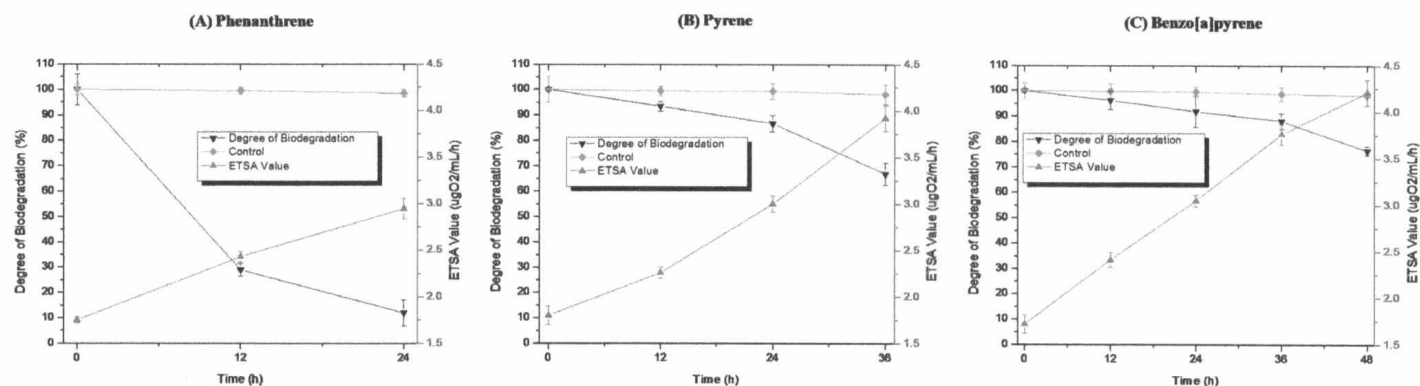


Figure 1. ETSA values and biodegradation rate of phenanthrene (A), pyrene (B), and benzo[a]pyrene (C) by *Novosphingobium pentaromativorans* US6-1 (mean and standard deviation of triplicate samples are shown.).

degraded 20–30% of benzo(a)pyrene in the presence of a pyrene substrate after 63 days of incubation time [23], and consortium BL co-metabolized 44.07% of 10 ppm benzo(a)pyrene after an incubation time of 14 days [24]. PAHs biodegradation pathways in bacteria are induced by the presence of either the parent compound or one of the pathway intermediates. In our study, *N. pentaromativorans* US6-1 degraded phenanthrene, pyrene, and benzo(a)pyrene after 24 h, 36 h, and 48 h, respectively, suggesting that the degradation pathways were active in US6-1 during all treatments.

2 Comparison of the overall proteome profile in *N. pentaromativorans* US6-1

In order to characterize the molecular characteristics involved in the biodegradation of PAHs, the proteome profiles of *N. pentaromativorans* US6-1 induced by phenanthrene, pyrene, and benzo(a)pyrene were compared. The total protein profile of strain US6-1 (separated by SDS-PAGE) is shown in Fig. 2. Many enzymes involved in PAH degradation are likely to be expressed constitutively with so-called housekeeping proteins, and are not necessarily induced; therefore, the proteome profiles and band intensities were similar between the PAH-induced groups and the control. However, three specific bands were expressed differently after exposure to the three different PAH compounds. Compared with the control, Band 1 was upregulated only in the benzo[a]pyrene induced culture, Band 2 was intensified in both the pyrene and benzo[a]pyrene induced cultures, and Band 3 was expressed in the cultures treated with each of the three PAH compounds. As indicated by MW markers, the approximate MWs of Bands 1 and 2 were 29 KDa and 50 KDa, respectively, while that of Band 3 was about 200 KDa.

These three differential protein bands (Bands 1, 2, and 3) were excised and identified (Table 2). Unique proteins were found, but the peptide counts and percent cover were low; thus, it is possibly that although there were peptides in the bands, the integrated proteins were broken during the sample treatment. In Band 1, site-specific DNA-methyltransferase (adenine-specific), 3-oxoacyl-(acyl-carrier-protein) reductase, 4-hydroxybenzoate 3-monooxygenase, and homoserine kinase were identified. The site-specific DNA-methyltransferase (adenine-specific) is a type of transferase enzyme that transfers a methyl group from an S-adenosyl methionine to adenine to form N6-methyladenine. DNA methylation plays a key role in DNA stability, and is linked to the regulation of cell growth and gene expression [25]. Benzo(a)pyrene is a moderately potent carcinogen, and its reactive intermediates can covalently bind to cellular macromolecules (i.e., DNA) leading to mutations, thus, it is

reasonable to hypothesize that this DNA-methyltransferase may be related to self-protection against mutation of the microorganism.

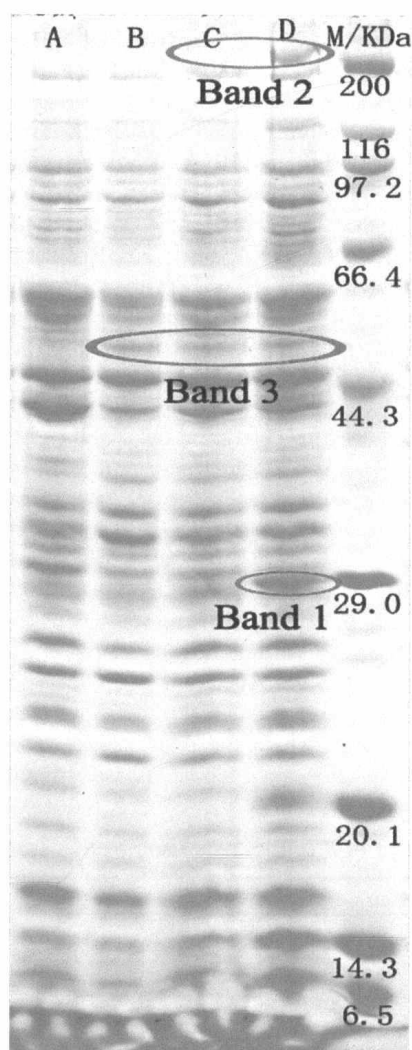


Figure 2. Separation of the total proteins of *Novosphingobium pentaromativorans* US6-1 using SDS-polyacrylamide gel electrophoresis. M, marker; A, control; B, phenanthrene-induced; C, pyrene-induced; D, benzo[a]pyrene-induced.