Efficient biodegradation of petroleum n-alkanes and polycyclic aromatic hydrocarbons by polyextremophilic Pseudomonas aeruginosa san ai with multidegradeative capacity†

Ana Medić,a Marija Lješević,b Hideyuku Inui,c,d Vladimir Beškoski,d Ivan Kojić,e Ksenija Stojanovićd and Ivanka Karadžićf,g,h

Pseudomonas aeruginosa san ai, an alkaliphilic, metal-tolerant bacterium, degraded individual selected petroleum compounds, i.e., n-alkanes (n-hexadecane, n-nonadecane) and polycyclic aromatic hydrocarbons (fluorene, phenanthrene, pyrene) with efficiency of 80%, 98%, 96%, 50% and 41%, respectively, at initial concentrations of 20 mg L⁻¹ and in seven days. P. aeruginosa san ai showed a high biodegradative capacity on complex hydrocarbon mixtures, the aliphatic and aromatic fractions from crude oil. The efficiency of P. aeruginosa san ai degradation of crude oil fractions in seven days reached stage 3–4 of the oil biodegradation scale, which ranges from 0 (no biodegradation) to 10 (maximum biodegradation). Identified metabolites concomitant with genomic and enzymatic data indicated the terminal oxidation pathway for the n-alkane degradation, and the salicylate and phthalate pathways for fluorene biodegradation. Polyextremophilic P. aeruginosa san ai, as a biosurfactant producer with multidegradeative capacity for hydrocarbons, can be used in an improved strategy for environmental bioremediation of hydrocarbon-contaminated sites, including extreme habitats characterized by low or elevated temperatures, acidic or alkaline pH or high concentrations of heavy metals.

1. Introduction

Widespread use of crude oil/petroleum causes serious environmental problems in the forms of effluents from oil refineries and accidental oil spills. While some crude oil compounds are readily degraded, long-chain alkanes, and particularly polycyclic aromatic hydrocarbons (PAHs), are relatively resistant to biodegradation. Because of their carcinogenic and mutagenic properties, some PAHs are classified by regulatory agencies as high-priority pollutants that pose risks to humans and wildlife. Bioremediation techniques based on the use of microorganisms capable of heterogeneous contaminant degradation have been developed as an alternative to chemical and physical techniques for cleaning up polluted environments, as they have a comparative advantage because they are economically viable and less harmful to the environment. During bioremediation, organic pollutants are transformed into compounds with reduced toxicity or are completely degraded/mineralized. These techniques do not generate any waste, and the cultivated land can recover its natural biological activity.

Several pseudomonads have been reported to degrade hydrocarbons with various chain lengths and structures. Pseudomonas putida was found to degrade n-alkanes,4 P. aeruginosa W10 preferentially utilized n-C₁₆₆, but also degraded naphthalene, phenanthrene, fluoranthene and pyrene,5 Pseudomonas F274 was found to utilize fluorene,6 Pseudomonas NCIB 9816-4 had the ability to degrade fluorene, dibenzofuran and dibenzothiophene,7 and P. aeruginosa DQ8, isolated from petroleum-contaminated soil, could degrade PAHs such as fluorene, phenanthrene, fluoranthene and pyrene.8 Being able to utilize a broad spectrum of hydrocarbons, Pseudomonas genus has a key role in the removal of these compounds from petroleum-polluted sites.9 This is particularly important because hydrocarbon-degrading extremophiles can tolerate a wide range of conditions and could be used for bioremediation of polluted extreme habitats.10

There are four oxidation pathways of n-alkane degradation: (i) the monoterminval/terminal pathway where terminal methyl
produces the primary alcohols further oxidized to fatty acid; (ii) the biterminal pathway in which the termini of the n-alkane undergo oxidation to the corresponding fatty acids; (iii) the subterminal pathway where the subterminal carbon is oxidized to an ester; and; (iv) a unique pathway postulated for Acinetobacter sp. where n-alkanes are oxidized to fatty acids through n-alkyl hydroperoxides and aldehydes. As pathways for n-alkane catabolism vary in different microorganisms, the genetic bases, enzymes and metabolites need to be elucidated in order to characterize the specific mechanism of n-alkane degradation in each specific microorganism.

Although there are plenty of PAH degradation pathways depending on the number of fused rings, catabolism of PAHs usually starts with hydroxylation to activate the ring, followed by ring-cleaving and several transformations that lead to formation of two key intermediates, phthalate or salicylate, which are further degraded into metabolites of the tricarboxylic acid cycle (TCA). However, in spite of extensive investigation of PAH catabolism, there is a lack of knowledge about the mechanisms involved in degradation of different PAHs, as well as about the whole metabolic network that includes metabolites and enzymes that mediate the reactions. Among the PAHs, bacterial degradation of fluorene (FLU) has been particularly well studied because of its environmental significance. Three major degradation pathways of FLU have been described via angular and lateral dioxygenation or monoxygenation as the upper catalytic intermediates such as protocatechuates and catechols that are further transformed into metabolites of the TCA.

P. aeruginosa san ai, primarily isolated from alkaline cutting oil as its natural habitat, grows well in laboratory conditions, with a growth temperature range of 15-40 °C. Under alkaline pH condition, it tolerates high concentrations of cadmium up to 7.3 mM and chromium up to 5.0 mM. Consequently, P. aeruginosa san ai is an alkaliphilic and metallotolerant bacterium.

Aliphatic and aromatic hydrocarbon fractions used in this study were isolated from non-biodegraded, paraffinic crude oil (Turija-Sever oil field, SE Pannonian Basin, Serbia) according to the procedure described by Bastow et al.

P. aeruginosa san ai was activated on nutrient agar (Torlak, Belgrade, Serbia) at 30 °C for 24 h and transferred to 500 mL Erlenmeyer flasks, containing 100 mL of minimal salt medium (MSM) as previously reported, supplemented with different sources of carbon and energy, to achieve initial counts (in colony-forming units; CFU mL^{-1}) of approximately 4 \times 10^7 mL^{-1}. n-C_{16}, n-C_{19}, FLU, PHE, PYR, and aliphatic and aromatic hydrocarbon fractions isolated from Turija-Sever crude oil were used as sole carbon sources, while sunflower oil was used as a control substrate for bacterial growth. An appropriate volume of a stock solution of each sole carbon source in n-hexane was injected individually into sterile 500 mL Erlenmeyer flasks to obtain 20 mg L^{-1} of the sole carbon source, after which n-hexane was allowed to evaporate under the air flow. After forming a thin film of n-C_{16}, n-C_{19}, FLU, PHE, PYR or crude oil fraction in the bottom of the flask, 100 mL of sterilized MSM was added into each flask to achieve the final concentration of the sole carbon source of 20 mg L^{-1}, and each flask was shaken at 150 cycles min^{-1} using a horizontal shaker (Kuhner, Basel, Switzerland) at 30 °C for 7 days.

Sterile MSM with n-C_{16}, n-C_{19}, FLU, PHE, PYR, or aliphatic and aromatic hydrocarbon fraction isolated from crude oil were utilized as controls of chemical decomposition, and inoculated sterile MSM without any of the hydrocarbon substrates were prepared as controls of microbial growth. All experiments were performed in three independent replicates and average values are given in the study. Differences in results between replicates in all experiments did not exceed 1.2%.

Production of biosurfactants, i.e. rhamnolipid and exopolysaccharide, was determined on MSM supplemented with crude oil as a sole C-source.

2. Materials and methods

Chemicals

n-C_{16}, n-C_{19}, FLU, PHE, PYR, and organic solvents were purchased from Sigma Aldrich (St. Louis, MO, USA) with purity above 99% and HPLC grade. All other chemicals used in this study were of pro analysis grade purchased from Merck (Darmstadt, Germany). Non-biodegraded, paraffinic crude oil used in this study was taken from the Turija-Sever oil field (South-East Pannonian Basin, Serbia).
Microbial growth was measured at 580 nm using a UV-2600 spectrophotometer (Shimadzu, Japan). As the intensities of microbial growth on n-C_{16}, n-C_{19}, FLU, PHE, PYR, and the hydrocarbon fractions from crude oil were similar to the measured growth intensity on sunflower oil,\textsuperscript{35} any increase of absorbance of >0.05 after 4 days was considered as culture growth.\textsuperscript{31}

**Gas chromatography-mass spectrometry analysis of degradation of individual n-alkanes, PAHs, and crude oil fractions**

Each whole flask culture was extracted with n-hexane three times. The extracts were dehydrated with anhydrous Na\textsubscript{2}SO\textsubscript{4}, and the solvents were evaporated under reduced pressure by a rotary evaporator (Senco GG17, Shanghai, China). The extraction residues were dissolved in n-hexane and analyzed by gas chromatography-mass spectrometry (GC-MS). A gas chromatograph Agilent 7890A GC (HP5-MS capillary column, 30 m × 0.25 mm, 0.25 μm film thickness, He carrier gas 1.5 cm\textsuperscript{3} min\textsuperscript{-1}) coupled to an Agilent 5975C mass selective detector (70 eV) was used. The column was heated from 80 to 300 °C at a rate of 2 °C min\textsuperscript{-1}, held at 300 °C for 20 minutes and then heated from 300 to 310 °C at a rate of 10 °C min\textsuperscript{-1}, and held at 310 °C for 1 minute. The injector temperature was 250 °C. The spectrometer was operated in the EI (electron ionization) mode over a scan range from m/z 45 to 550. The individual peaks for n-C\textsubscript{16}, n-C\textsubscript{19}, FLU, PHE, PYR and their degradation products, as well as the compounds in the aliphatic and aromatic fractions of crude oil, were identified on the basis of their mass spectra (library NIST11). Quantification of the compounds in standard series, controls (sterile MSM with n-C\textsubscript{16}, n-C\textsubscript{19}, FLU, PHE, and PYR) and inoculated samples (P. aeruginosa san ai inoculated into sterile MSM supplemented with n-C\textsubscript{16}, n-C\textsubscript{19}, FLU, PHE, and PYR) were performed by integration of peak areas (so-called GCMS Data Analysis). For the calculations, a standard series of commercial n-C\textsubscript{16}, n-C\textsubscript{19}, FLU, PHE, and PYR solutions in n-hexane concentrations from 2 to 20 mg L\textsuperscript{-1} (2, 5, 7, 10, 15 and 20 mg L\textsuperscript{-1}) were prepared and analyzed under the same GC-MS conditions as samples. The ratios of the peak areas to corresponding concentrations were linear, with very high correlations (r\textsuperscript{2} ≥ 0.991). The degradation efficiency of individual hydrocarbons was determined based on the concentrations of target compounds in control and inoculated samples, and is given in percent. The degradation efficiency of crude oil fractions was determined based on the mass loss of the fraction before and after microbial treatment and notable changes in distributions and abundances of individual compounds in total ion chromatograms (TICs) of control and inoculated aliphatic and aromatic fractions.

**Determinations of rhamnolipid and exopolysaccharide**

Concentrations of rhamnolipid (RL) and exopolysaccharide (EPS) were determined spectrophotometrically using the UV-2600 (Shimadzu, Japan). The concentration of RL in the culture broth was determined by the orcinol assay.\textsuperscript{29} The reaction mixture of 0.15 mL of sample and 1.35 mL of orcinol reagent (0.19% orcinol in 53% sulfuric acid) was heated for 30 min at 80 °C, then cooled to room temperature and the absorbance was measured at 421 nm. The RL concentration was calculated from standard curves prepared with rhamnose and expressed as a rhamnose equivalent, where 1 μg rhamnose is equivalent to 2.5 μg RL.

The concentration of EPS in the fermentation broth was determined by the phenol-sulfuric acid method.\textsuperscript{32} The reaction mixture consisted of 0.1 mL of supernatant, 0.9 mL of distilled water, 0.05 mL of 80% phenol solution and 2.5 mL of concentrated sulfuric acid. Reaction mixtures were vortexed and absorbances measured at 490 nm after 10 minutes. The EPS concentration was calculated from standard curves prepared with starch solution at concentrations from 0 to 100 mg L\textsuperscript{-1}.

**Respiration measurement**

Microbial respiration activity of P. aeruginosa san ai was measured using a twelve-channel Micro Oxymax® respirometer (Columbus, USA) connected to a PC. The experiments were performed in Micro Oxymax light-proof 500 mL bottles containing 100 mL of MSM supplemented with 20 mg L\textsuperscript{-1} of n-C\textsubscript{16}, n-C\textsubscript{19}, FLU, PHE or PYR and stirred constantly (150 rpm) with a magnetic stirrer at 27 °C for four days. Produced carbon dioxide (μL) was determined. Cell respiration was measured every 300 min for four days. Data were evaluated by Micro Oxymax® software.

**Genome analysis**

The databases Integrated Microbial Genomes (IMG)\textsuperscript{33} https://img.jgi.doe.gov/cgi-bin/m/main.cgi and Kyoto...
Enzyme assays

Total proteins were isolated from biomass grown in MSM supplemented with different C-sources (n-C16, n-C19, FLU, PHE, or PYR) to early stationary phase, by the method described by Medić et al. Crude protein extract was used for enzyme assays after determination of protein content by Bradford’s method.

The specific enzyme activity was calculated as enzyme activity per mg of protein.

1,2-Catechol dioxygenase (C12O) and 2,3-catechol dioxygenase (C23O) activities were measured spectrophotometrically at 260 nm and 375 nm, respectively, using the UV-2600, by a slightly modified procedure, and with FLU, PHE, or PYR as substrates. One unit of activity is defined as the amount of C12O and C23O enzyme, respectively, producing 1 μmol of cis,cis-muconate ([ε][260] = 1.6 × 10⁴ mol⁻¹ cm⁻¹), or 2-hydroxymuconic semialdehyde ([ε][375] = 4.4 × 10⁴ mol⁻¹ cm⁻¹), per minute at 25 °C.

Hydroxylase activity was measured spectrophotometrically as a decrease of absorbance of NADH at 340 nm by the slightly modified procedure of Jauhari et al.; therefore, we used 20 mM sodium phosphate instead of Tris–HCl buffer, pH 7.4.

Alcohol dehydrogenase was measured against ethanol, propanol and iso-propanol according to Jauhari et al.

Hydroxylase and alcohol dehydrogenase activities were calculated using the NADH extinction coefficient of ε₃₄₀ of 6220 mol⁻¹ cm⁻¹. One enzyme unit is defined as the amount of enzyme which in the presence of substrate causes the oxidation of 1 μmol NADH per min.

3. Results and discussion

Degradation of individual n-alkanes and PAHs by P. aeruginosa san ai

As Fig. 1a shows, P. aeruginosa san ai has a high capacity for degradation of n-alkanes (n-C₁₆, n-C₁₉) and PAHs (FLU, PHE, PYR). The degradation efficiency of individual hydrocarbons (initial concentrations of 20 mg L⁻¹) reached 80%, 98%, 96%, 50% and 41%, respectively, over a period of seven days. Therefore, P. aeruginosa san ai can be considered as a multi-degradative hydrocarbonoclastic bacterium with the ability to degrade n-alkanes and PAHs. PAHs with three rings (FLU, PHE) were significantly better degraded than PYR as a four-ring PAH (Fig. 1a), similar to the observation made by Zhang et al. FLU, as a naphthenoaromatic hydrocarbon (containing aromatic and methylenic moieties) was almost completely degraded. An increase in the number of fused rings results in increased hydrophobicity and decreased solubility that leads to reduced availability of such compounds for microbial degradation. FLU, the most soluble compound (1.992 mg L⁻¹), was completely exhausted, while almost 60% of PYR remained non-degraded as a result of its lower solubility (0.135 mg L⁻¹). Several other P. aeruginosa isolates were reported to degrade PAHs similarly to P. aeruginosa san ai. P. aeruginosa DQ8 completely degraded 40 mg L⁻¹ of FLU and PHE in 7 days, and 34% of PYR (40 mg L⁻¹) in 12 days. P. aeruginosa BZ-3 degraded 75% of PHE at an initial concentration of 50 mg L⁻¹ in 7 days. P. aeruginosa completely removed PHE in concentrations up to 200 mg L⁻¹ in 30 days. P. aeruginosa ATAI9 degraded 31% of PYR at an initial concentration of 50 mg L⁻¹ in 9 days.

Complete degradation of low soluble n-alkanes (hexadecane - 0.023 mg L⁻¹, nonadecane - 0.008 mg L⁻¹) seems to be a surfactant-mediated process in which alkane-degrading bacteria produce diverse surfactants. In addition, bio-surfactant producing P. aeruginosa S5 highly promoted the removal of PAHs, implying that hydrocarbons removal is a surfactant-mediated process. Indeed, P. aeruginosa san ai produces a mixture of the biosurfactants, rhamnolipids and exopolysaccharide, which could facilitate the emulsification of the hydrocarbons. Specifically, during P. aeruginosa san ai growth on medium supplemented with crude oil, both bio-surfactants were detected (37.4 mg L⁻¹ for RL and 39.7 mg L⁻¹ for EPS). A similar affinity for medium-chain alkanes was found for P. aeruginosa B1, while P. aeruginosa SJTD-1, RM1, S1 and D8 efficiently degraded medium- and long-chain n-alkanes. P. aeruginosa D8 completely removed n-C₁₂₂, n-C₁₉₀ and n-C₄₀₀, concentration 100 mg L⁻¹, in 7 days.

In spite of the limited bioavailability of n-alkanes and PAHs due to their low solubility, Pseudomonas has been regarded as critical for recycling organic carbon on the planet. Compared to other hydrocarbonoclastic bacteria, P. aeruginosa san ai has an additional advantage, as it has a particular ability to survive and to grow in extreme environments such as alkaline and heavy metal polluted sites. It seems that there are similarities in the efficacy and capacity to degrade hydrocarbons between extremophilic P. aeruginosa that have originated from different extreme conditions. So, for example, the thermophilic bacterium P. aeruginosa AP02-1 has a high multidegradative capacity, ranging from n-alkanes to PAH, while the halotolerant P. aeruginosa AspH2 successfully degrades different fractions of petroleum hydrocarbons similar to polyextremophilic P. aeruginosa san ai. Heavy metals (cadmium, chromium, lead, zinc and, particularly, nickel and vanadium) are present in crude oil, oil spills, and in alkaline oil refinery effluents. In conditions of crude oil pollution caused by spills or oil industry activity, the alkaliophilic, metallotolerant, hydrocarbonoclastic P. aeruginosa san ai could be an ideal microorganism that can be used for remediation of polluted environments.

Dynamics of n-nonadecane and fluorene degradation

To investigate the dynamics of degradation, n-C₁₉₀ and FLU were selected as representative of alkanes and PAHs, as these two classes of substances were efficiently degraded by P. aeruginosa san ai (98% and 96%, respectively; Fig. 1a). As depicted in Fig. 1c, the degradation of both hydrocarbons fits first order kinetics, being in agreement with degradation kinetics of other n-alkanes and PAHs. Biodegradation rate constants were
Fig. 1  Biodegradation of n-alkanes (n-C_{16}, n-C_{19}) and PAHs (FLU, PHE, PYR) by P. aeruginosa san ai. (a) The percent of biodegradation for each hydrocarbon. (b) KEGG map of n-alkane degradation. (c) Dynamics of n-C_{19} and FLU degradation. (d) Cumulative carbon dioxide production during biodegradation (controls were subtracted). The initial concentration of all substances was 20 mg L\(^{-1}\). Each data point represents the mean of three independent biodegradation studies. Some error bars are not visible because they are shorter than the symbol size. Legend: n-C_{16} (n-hexadecane), n-C_{19} (n-nonadecane), FLU (fluorene), PHE (phenanthrene), PYR (pyrene).

calculated to be 1.59 and 0.51 (per day) for n-C_{19} and FLU, respectively, using the following equation:  
\[
\ln[A] = \ln[A_0] - kt,
\]
where [A] is the residual concentration of hydrocarbon (n-C_{19} and FLU) at a specific time, [A_0] is the initial hydrocarbon concentration, k is the biodegradation rate constant, and t is time (days). The biodegradation rate constant for n-C_{19} by P. aeruginosa san ai of 1.59 per day is higher than that published for Pseudomonas BP10 (0.11 for n-C_{16}),\(^{29}\) indicating easier degradation of the shorter, odd number n-alkane. This result is in concordance with biodegradation in natural conditions, where both aerobic and anaerobic bacteria preferably utilize short-chain n-alkanes.\(^{31}\) Additionally, P. aeruginosa san ai has better capacity for PAH degradation (0.51 per day for FLU), than Pseudomonas BZ-3 (0.11 per day for PHE).\(^{34}\)

The half-life (\(t_1/2\)) of n-C_{19} and FLU was calculated using the equation \(t_1/2 = \ln 2/k\), and it was estimated as 0.43 and 1.36 days, respectively. The higher constant rate and lower \(t_1/2\) for n-C_{19} indicate the easier biodegradability of n-alkanes than PAHs. Apparently, P. aeruginosa san ai quickly removed both hydrocarbons from the growth medium that contained 20 mg L\(^{-1}\) of n-C_{19} or FLU, clearly demonstrating the excellent potential of this bacterium for aerobic biodegradation of n-alkanes and PAHs. Grifoll et al.\(^{4}\) revealed intensive FLU utilization within the first three days of growth and almost complete degradation of FLU by Pseudomonas F274, which is in good agreement with our data.

Respiration activity

P. aeruginosa san ai can use n-alkanes and PAHs in MSM as sole carbon and energy sources. The disappearance of hydrocarbons accompanied by CO\(_2\) production implies metabolic and respiratory activity of the microorganism during its growth on these carbon sources. Cumulative CO\(_2\) production, monitored continuously during the biodegradation of n-alkanes and PAHs, is given in Fig. 1d. All substrates caused intensive respiration, implying the active metabolism of the bacterium when growing on n-alkanes and PAHs. The most intensive respiration in all cases occurred in the first day, with cumulative CO\(_2\) production (\(\mu\)L of: 280 [PYR], 470 [n-C_{16}], 630 [n-C_{19}], 750 [PHE] and 820 [FLU]) The respiration levels did not entirely correlate with the degradation percentages from Fig. 1a, which is a result of differences in metabolism during the biodegradation of n-alkanes and PAHs. Salicylic and phthalic acids, as key intermediates of PAHs degradative pathways, both funnel into the \(\beta\)-ketoadipate pathway, the main products of which are succinate (C\(_4\)) and adipate (C\(_6\)) that go into central TCA metabolism.\(^{52}\) On the other hand, degradation of n-alkanes produces acetate (C\(_2\)) as a result of \(\beta\)-oxidation, which induces the glyoxylate cycle to bypass the steps in the TCA cycle and to prevent the loss of CO\(_2\). Therefore, there is a difference between the TCA and the glyoxylate pathways in carbon balance, which is C\(_2\) \(\rightarrow\) C\(_4\) for the TCA, while for the glyoxylate cycle, it is C\(_2\) + C\(_2\) \(\rightarrow\) C\(_4\).\(^{53}\) Besides, key enzymes of the glyoxylate cycle, isocitrate lyase and
Biodegradation of crude oil fractions by *P. aeruginosa* san ai

In order to study the degradation potential of *P. aeruginosa* san ai in complex hydrocarbon mixtures, experiments were carried out on aliphatic and aromatic fractions isolated from non-biodegraded, paraffinic crude oil. Oil was separated into the fractions since it contains a huge number of hydrocarbons, and without separation it is difficult to perform precise identification (particularly in TIC) due to the co-elution of more than one compound in the single GC-MS chromatographic peak. Moreover, some compounds that are present in lower amounts (particularly aromatic hydrocarbons) could be masked by compounds such as *n*-alkanes that are present in higher concentrations in crude oil. Nevertheless, both our aliphatic and aromatic fractions contained numerous hydrocarbons having different structures (Fig. 2a and b).

The mass of the aliphatic hydrocarbon fraction was reduced by 45%, whereas the mass of the aromatic hydrocarbon fraction was reduced by 25%. In controls, no mass change of oil fraction was detected. This result clearly shows the lower resistance of aliphatic than aromatic hydrocarbons against biodegradation by *P. aeruginosa* san ai, as we observed in experiments with individual hydrocarbons (Fig. 1a and c), and as was previously proven in natural conditions i.e. oil reservoirs that are located at low depths usually up to 800 m and where temperatures do not exceed 70–80 °C.

Comparison of TICs in control and inoculated aliphatic fraction revealed significant differences. The full series of *n*-alkanes from *C*₁₂ to *C*₁₉ which notably dominated the TIC of the aliphatic fraction in the control, was completely removed by *P. aeruginosa* san ai in 7 days (Fig. 2a and c). As a result, the inoculated aliphatic fraction was then dominated by isoprenoids, hopanes and steranes (Fig. 2c). Detailed examination of the inoculated aliphatic fraction using *m/z* 71 (the characteristic ion fragmentogram for *n*-alkanes) confirmed the complete absence of these hydrocarbons (Fig. S1, ESI†). *n*-Alkanols and fatty acids, which are possible products of *n*-alkane degradation, were not detected at all in our inoculated aliphatic fraction (non-derivatised *n*-hexane extract), even when using their specific ion fragmentograms, indicating complete mineralization of *n*-alkanes during microbial growth on complex hydrocarbon mixtures.

Comparison of TICs of the control and inoculated aromatic fractions showed that *P. aeruginosa* san ai completely degraded FLU and almost all the PHE in 7 days (Fig. 2b and d). This clearly confirms the high capability of *P. aeruginosa* for FLU degradation. The contents of methyl- and dimethyl-derivatives of FLU and PHE which prevailed in the control aromatic fraction were notably decreased in the inoculated crude oil aromatic fraction, whereas chrysene, methylchrysenes, triaromatic steroids, 8(14)-secohopanoid with fluorene moiety, and isorenieratane contents were unaltered (Fig. 2b and d). This is not surprising, since it is known that, for example, triaromatic steroids are the compounds that are most resistant to microbial attack in oil wells. More detailed inspection of ion chromatograms of naphthalene (*m/z* 142 + 156 + 170), FLU (*m/z* 166 + 180 + 194) and PHE (*m/z* 178 + 192 + 206) derivatives of control and inoculated aromatic fractions (Fig. S2, ESI†) shows that resistance of aromatic hydrocarbons against biodegradation increases in the following order: naphthalene derivatives < fluorene derivatives < phenanthrene derivatives. Furthermore, it is obvious that resistance of aromatic hydrocarbons to biodegradation increases with the degree of methylation. Both observations are in concordance with results from natural oil wells.

The changes detected in distributions of aliphatic and aromatic hydrocarbons in control and inoculated fractions indicate the hydrocarbon degradation efficiency of *P. aeruginosa* san ai during 7 days corresponds to stage 3–4 of the oil biodegradation scale (in oil reservoirs), which ranges from 0 to 10 (0 indicates no biodegradation, whereas stage 10 equates to removal of almost all hydrocarbons from oil with the exception of oleane, gammacerane, diasteranes, diapohanes and aromatic steroids, which are, however, also altered). For comparison, the same biodegradation degree (stage 3–4) in oil wells is attained after hundreds of thousands or millions of years. Therefore, the proven degradation capacity of *P. aeruginosa* san ai against complex hydrocarbon mixtures follows the biodegradation sequence in natural geological and environmental conditions.

Degradation of *n*-hexadecane and *n*-nonadecane

A collection of genes encoding for proteins involved in alkane degradation, i.e., alkane monooxygenase, rubredoxin, rubredoxin reductase and alcohol and aldehyde dehydrogenases, have been found in the *P. aeruginosa* san ai genome, as shown in Fig. 1b. In addition to extensively studied alkanes with an even number of carbon atoms, *P. aeruginosa* san ai has the ability to transform the odd number alkane *n*-C₁₉ that, to the best of our knowledge, has not been reported yet for *P. aeruginosa*. *P. aeruginosa* san ai efficiently degraded both of the analyzed *n*-alkanes (Fig. 1a). Based on GC-MS analysis, the following *n*-C₁₆ metabolites were identified: 1-hexadecanol (*Mₙ* = 242, characteristic *m/z* fragment ions: 55, 69, 83, 97, 111, 125) and *n*-hexadecanoic acid (*Mₙ* = 256, characteristic *m/z* fragment ions: 73, 60, 129, 213, 83, 97, 157, 171), unambiguously demonstrating a terminal oxidation metabolic pathway for *n*-alkane degradation in *P. aeruginosa* san ai. However, only 1-nonadecanol with *Mₙ* = 284 and fragment ions (*m/z*) 55, 69, 83, 97, 111, 125, 139 were found as a result of *n*-C₁₉ degradation transformation. In addition to the detected 1-nonadecanol-specific activity of the first, activating enzyme in the metabolic pathway, alkane monooxygenase/hydroxylase was determined: 0.234 U mg⁻¹ and 0.436 U mg⁻¹ for *n*-C₁₆ and *n*-C₁₉, respectively, signifying hydroxylation of both alkanes and even more intensive hydroxylation of *n*-C₁₉. Alcohol dehydrogenase activities towards ethanol, propanol and iso-propanol from biomass of *P. aeruginosa* san ai grown on *n*-C₁₆ (0.281, 0.225 and 0.348 U mg⁻¹) and *n*-C₁₉ (0.421, 0.251 and 0.204 U mg⁻¹) explicitly show
high enzyme activity against alcohols. In accordance, several genes coding for alcohol dehydrogenases were found in the P. aeruginosa san ai genome, including a propanol-preferring enzyme, for which very broad substrate specificity toward primary and secondary alcohols has been referred (https://www.brenda-enzymes).

Fig. 2 Total ion chromatograms of control (a and b) and inoculated (c and d) aliphatic and aromatic fractions from crude oil exposed to degradation by P. aeruginosa san ai for seven days. n-Alkanes are labeled according to their carbon number; Pr – pristane; Ph – phytane; NPR – nonpristane; i-C15 – regular C15 isoprenoid; i-C16 – regular C16 isoprenoid; i-C21 – regular C21 isoprenoid; C30αβ – C30αβ-21β(H)-30-norhopane; C30αβ – C30αβ-21β(H)-21β(H)-30-norhopane; C31αβ – C31αβ-21β(H)-21β(H)-bishomohopane; C32αβ – C32αβ-21β(H)-trishomohopane; C34αβ – C34αβ-21β(H)-pentakishomohopane; S and R designate configuration at C-22 in C31–C35 hopanes (S epimer elutes before R epimer in corresponding doublets); * – co-elution of branched alkane; the term branched alkanes herein includes all branched alkanes having one or more methyl groups in the side chain; F – fluorene; MFs – methylfluorenes; P – phenanthrene; MPs – methylphenanthrenes; DMPs – dimethylphenanthrenes; Py – pyrene; TMPs – trimethylphenanthrenes; C – chrysene; MCs – methylchrysenes; TASSs – triaromatic steroids; MTASSs – methylated triaromatic steroids; 8(14)-SH FM – 8(14)-secohopanoid with fluorene moiety.
Degradation of fluorene

In this research, the catabolic pathway of FLU degradation was studied, as FLU is the simplest naphthoaromatic, and bears structural relationships to carboxales, dibenzothiophenes, dibenzofurans and dibenzodioxins, so thus, it can be a useful model for biodegradation studies. Moreover, FLU is an important component of fossil fuels and is one of the compounds on the EPA Priority Pollutants List. In the present study using GC × GC-MS, six metabolites were identified during FLU degradation by P. aeruginosa san ai (Table 1 and Fig. S3, ESI†). The genes encoding for proteins involved in the catabolism of aromatic compounds were identified in P. aeruginosa san ai, implying the potential of this bacterium for PAH degradation.24,29

The presence of 9H-fluoren-9-ol (II) and 9H-fluoren-9-one (III) implied that ring activation starts with monooxygenation at C-9, which is then dehydrogenated to 9H-fluoren-9-one (Fig. 3). In addition, high specific activities of hydroxylases (0.420, 1.286, and 0.846 U mg⁻¹ for FLU, PHE and PYR, respectively), clearly demonstrated extensive enzymatic ring activation. Compounds IV (1, 1α-dihydroxy-1-hydro-9-fluoren) and V (2α-carboxy-2, 3-dihydroxybiphenyl)6,16 were not found in the present study, but the final product of upper pathway transformation − phthalate (VI) − was detected (Fig. 3). As Fig. 3 shows, most of the metabolites identified in this study support well the proposed FLU degradation by the phthalate pathway.6,16 Salicylic acid (X) was also detected (Fig. 3), suggesting the existence of an additional pathway which starts with dioxygenation of FLU (compound VIII) and proceeds through several derivatives of 1-indanone (compound IX†). Furthermore, the GC × GC-MS peak ratio of phthalic to salicylic acids was 1 : 3, implying an increased accumulation of salicylic acid over time, although metabolites of the salicylate pathway were not identified after 18 h of microbial growth. Substantial secretion and accumulation of intermediates in Pseudomonas growing on aromatic compounds were determined by the limited activity of some of the enzymes of the β-ketoadipate pathway24 − a central pathway to which many different peripheral pathways converge.29 Salicylate (X) funnels into catechol (XI), while phthalate (VI) funnels into protocatechuic acid (VII), both parts of the β-ketoadipate pathway (Fig. 3). Interestingly, catechol formation was identified as the bottleneck in the β-ketoadipate pathway,25 which is in good agreement with the amount of salicylic acid found in our study. The catechol and protocatechuic acid branches converge at the intermediate, β-ketoadipate enol-lactone, which gives 3-oxoadipate and succinyl that goes into the TCA cycle.28 All of the genes coding for proteins involved in the β-ketoadipate ortho degradation pathway, catABC of the catechol branch and pcaBCDG of the protocatechuic acid branch, have been identified in the P. aeruginosa san ai genome.29 Although it was believed that phthalate and salicylate pathways cannot exist simultaneously, recent study of PYR degradation by Mycobacterium sp. WY10 undoubtedly showed that both pathways simultaneously played roles in degradation.69 In addition, based on identified metabolites, Zhang et al.6 proposed two pathways for FLU degradation by P. aeruginosa DQ8, although key metabolites, phthalate and salicylate, were not detected. Consistent with reports of Sun et al.61 and Zhang et al.6 and on the basis of metabolites identified in this study, particularly phthalate and salicylate, we propose the simultaneous existence of two FLU degradation pathways.

Table 1 GC × GC retention times and mass spectral data of fluorene and its metabolites detected in this study

| Compound number referred to in Fig. 3 | Retention time (min) | m/z (% of relative intensity) | Metabolite identification according to NIST library | Duration of biodegradation by P. aeruginosa san ai |
|--------------------------------------|----------------------|-------------------------------|-------------------------------------------------|-----------------------------------------------|
|                                      |                      |                               |                                                  | 18 h  | 24 h  | 48 h  |
| I                                    | 34.80                | 166 (100), 165 (81), 167 (24), 164 (17), 82 (16), 163 (13) | Fluorene                                        | +     | +     | +     |
| II                                   | 35.70                | 182 (100), 181 (78), 166 (29), 165 (28), 183 (24), 152 (18) | 9H-Fluorene-9-ol                                | +     | +     | +     |
| III                                  | 38.20                | 180 (100), 152 (39), 181 (22), 151 (19), 76 (17), 150 (11), 153 (8) | 9H-Fluorene-9-one                               | +     | +     | +     |
| VI                                   | 37.30                | 147 (100), 73 (63), 148 (19), 295 (14), 149 (9) | 1,2-Benzene-dicarboxylic acid, bis(trimethylsilyl)ester (phthalic acid, di-TMS) | +     | +     | +     |
| VII                                  | 40.40                | 73 (100), 193 (84), 370 (23), 194 (18), 74 (13), 355 (13) | Benzoic acid, 3,4-bis[(trimethylsilyl)oxy]-trimethylsilyl ester (protocatechuic acid, di-TMS) | nd†   | nd†   | +     |
| X                                    | 36.00                | 73 (100), 267 (95), 268 (24), 74 (15), 91 (9) | Salicylic acid (2TMS)                           | +     | +     | +     |
| XII                                  | 32.90                | 73 (100%), 75 (38%), 111 (33%), 147 (25%) | Adipic acid (2TMS)                              | —     | —     | +     |
| XIII                                 | 27.70                | 147 (100%), 73 (65%), 148 (23%), 75 (18%) | Succinic acid (2TMS)                            | —     | —     | +     |

† + − present; nd − not detected.
pathways, phthalate and salicylate, in \textit{P. aeruginosa} san ai (Fig. 3).

Homology search analysis by blastp suite (https://blast.ncbi.nlm.nih.gov/Blast.cgi) of the proteins in \textit{Terrabacter} DBF63 (ref. 16) involved in FLU biodegradation to phthalate:

\textbf{Table 2} Enzyme activities of catechol dioxygenase from \textit{P. aeruginosa} san ai

| C-source | Substrate | 1,2-Catechol dioxygenase activity, U mg\(^{-1}\) | 2,3-Catechol dioxygenase activity, U mg\(^{-1}\) |
|----------|-----------|---------------------------------|---------------------------------|
| FLU      | FLU       | 0.275                           | 0.039                           |
|          | Catechol  | 0.150                           | 0.001                           |
| PHE      | PHE       | 0.285                           | 0.010                           |
|          | Catechol  | 0.274                           | <0.001                          |
| PYR      | PYR       | 0.151                           | <0.001                          |
|          | Catechol  | 0.371                           | <0.001                          |

4. Conclusion

Polyextremophile \textit{P. aeruginosa} san ai showed a high degradation capacity for \textit{n}-alkanes, PAHs and their complex mixture in crude oil hydrocarbon fractions over a period of seven days. PAHs have higher resistance to biodegradation than \textit{n}-alkanes, and the resistance increases with number of aromatic rings. \textit{n}-Alkanes were metabolized via the terminal oxidation pathway, while FLU was degraded by both the salicylate and phthalate pathways. Since heavy metals are present in oil spills and alkaline oil refinery effluent, alkaliphilic, metalotolerant, hydrocarbonoclastic \textit{P. aeruginosa} san ai is an ideal microorganism for remediation of hydrocarbon-contaminated sites, including extreme habitats. Additionally, this bacterium could be considered as an early biomarker of environmental pollution.

Conflicts of interest

There are no conflicts of interest to declare.

Acknowledgements

This research was supported by the Ministry of Education, Science and Technological Development of the Republic of Serbia (Projects III 43004 and 176006), the Japan International Cooperation Agency (JICA) partnership program “Environmental improvement in Pančevo, Serbia through the collaborations among Academia, Government, Industry and Citizens” and the Japan Society for the Promotion of Science (JSPS) Invitation Fellowship Program, ID no. S19013. The authors are
grateful to Dr Branka Lončarević for assistance with respiration experiments.

References

1 Z. Cui, G. Cui, W. Xu, Q. Gao, B. Li, G. Yang and L. Zheng, *Int. Biodeterior. Biodegrad.*, 2014, 91, 45–51.
2 V. Beškoski, G. Gojčić-Cvijović, J. Milić, M. Ilić, S. Miletić, T. Šolčević and M. Vrvić, *Chemosphere*, 2011, 83, 34–40.
3 M. Vidali, *Pure Appl. Chem.*, 2001, 73, 1163–1172.
4 J. B. van Beilen, S. Panke, S. Lucchini, A. G. Franchini, M. Rothlisberger and B. Witholt, *Microbiology*, 2001, 147, 1621–1630.
5 A. Chebbi, D. Hentati, H. Zaghdane, N. Baccar, F. Rezgui, M. Chalbi, S. Sayadi and M. Chamkha, *Int. Biodeterior. Biodegrad.*, 2017, 122, 128–140.
6 M. Grifoll, S. A. Selifonov and P. J. Chapman, *Appl. Environ. Microbiol.*, 1994, 60, 2438–2449.
7 S. M. Resnick and D. T. Gibson, *Appl. Environ. Microbiol.*, 1996, 62, 4073–4080.
8 Z. Zhang, Z. Hou, C. Yang, C. Ma, F. Tao and P. Xu, *Bioreourses. Technol.*, 2011, 102, 4111–4116.
9 S. Varjani, *Bioreourses. Technol.*, 2017, 223, 277–286.
10 R. Margetis and F. Schinner, *Appl. Microbiol. Biotechnol.*, 2001, 56, 650–663.
11 G. Mehetre, S. Dastager and M. Dharne, *Sci. Total Environ.*, 2019, 679, 52–60.
12 R. J. Watkinson and P. Morgan, *Biodegradation*, 1990, 1, 79–92.
13 T. Kotani, H. Yurimoto, N. Kato and Y. Sakai, *J. Bacteriol.*, 2007, 189, 886–893.
14 W. Finnerty, in *Proceedings of the World Conference on Biotechnology for the Fats and Oil Industry*, ed. A. H. Applevhite, 1988, pp. 184–188.
15 J. S. Seo, Y. S. Keum and Q. X. Li, *Int. J. Environ. Res. Public Health*, 2009, 6, 278–309.
16 H. Habe, J. S. Chung, H. Kato, Y. Ayabe, K. Kasuga, T. Yoshida, H. Nojiri, H. Yamane and T. Omori, *J. Bacteriol.*, 2004, 186, 5938–5944.
17 M. Grifoll, S. A. Selifonov, C. V. Gatlin and P. J. Chapman, *Appl. Microbiol. Biotechnol.*, 1995, 61, 3711–3723.
18 H. Nojiri, H. Habe and T. Omori, *J. Gen. Appl. Microbiol.*, 2001, 47, 279–305.
19 R. A. Kanaly and S. Harayama, *J. Bacteriol.*, 2000, 182, 2059–2067.
20 J. Nogales, J. L. García and E. Díaz, *Degradation of aromatic compounds in Pseudomonas: a systems biology view, in Aerobic utilization of hydrocarbons, oils and lipids, Handbook of hydrocarbon and lipid microbiology*, ed. F. Rojo, Springer, Cham, 2017, pp. 1–49.
21 S. K. Samanta, O. V. Singh and R. K. Jain, *Trends Biotechnol.*, 2002, 20, 243–248.
22 L. Izrael-Živković, M. Rkalović, G. Gojčić-Cvijović, S. Kazazić, M. Vrvić, I. Brčeski, V. Beškoski, B. Lončarević, K. Gočević and I. Karadžić, *RSC Adv.*, 2018, 8, 10549–10560.
23 I. Karadžić, A. Masui and N. Fujiwara, *J. Biosci. Bioeng.*, 2004, 98, 145–152.
24 L. Izrael-Živković, V. Beškoski, M. Rikalović, S. Kazazić, N. Shapiro, T. Woyke, G. Gojčić-Cvijović, M. Vrvić, N. Maksimović and I. Karadžić, *Extremophiles*, 2019, 23, 399–405.
25 M. Rikalović, A. M. Abdel-Mawgoud, E. Dzečel, G. Gojčić-Cvijović, Z. Nestorović, M. Vrvić and I. Karadžić, *J. Surfactants Deterg.*, 2013, 16, 673–682.
26 A. Dimitrijević, D. Veličković, M. Rikalović, N. Avramović, N. Milosavić, R. Jankov and I. Karadžić, *Carbohydr. Polym.*, 2011, 83, 1397–1401.
27 N. Avramović, S. Nikolić-Mandić and I. Karadžić, *J. Serb. Chem. Soc.*, 2013, 78, 639–652.
28 T. P. Bastow, B. G. K. van Aarssen and D. Lang, *Org. Geochem.*, 2007, 38, 1235–1250.
29 A. Medić, K. Stojanović, L. Izrael-Živković, V. Beškoski, B. Lončarević, S. Kazazić and I. Karadžić, *RSC Adv.*, 2019, 9, 23696–23710.
30 X. Tao, G. Lu, J. Liu, T. Li and L. Yang, *Int. J. Environ. Res. Public Health*, 2009, 6, 2470–2480.
31 M. Lin, X. Hu, W. Chen, H. Wang and C. Wang, *Int. Biodeterior. Biodegrad.*, 2014, 94, 176–181.
32 M. Dubois, K. A. Gilles, J. K. Hamilton, P. A. Rebers and F. Smith, *Anal. Chem.*, 1956, 28, 350–356.
33 I. A. Chen, K. Chu, K. Palaniappan, M. Pillay, A. Ratner, J. Huang, M. Huntemann, N. Varghese, J. R. White, R. Seshadri, T. Smirnova, E. Kirton, S. P. Jungbluth, T. Woyke, E. A. Eloe-Fadrosh, N. N. Ivanova and N. C. Kyrpides, *Nucleic Acids Res.*, 2019, 47, D666–D677.
34 M. Kanehisa, Y. Sato, M. Furumichi, K. Morishima and M. Tanabe, *Nucleic Acids Res.*, 2019, 47, D590–D595.
35 M. M. Bradford, *Anal. Biochem.*, 1976, 72, 248–254.
36 F. Briganti, E. Pessione, C. Giunta and A. Scozzafava, *FEBS Lett.*, 1997, 416, 61–64.
37 M. Mahiuddin, A. N. M. Fakhruddin and A. A. Mahin, *ISRN Microbiol.*, 2012, 741820.
38 I. Tsirogianni, M. Aivaliotis, M. Karas and G. Tsiotis, *Biochim. Biophys. Acta*, 2004, 1700, 117–123.
39 N. Jauhari, S. Mishra, B. Kumari and S. N. Singh, *Bioresour. Technol.*, 2014, 170, 62–68.
40 M. C. Romero, M. C. Cazau, S. Giorgieri and A. M. Arambarri, *Environ. Pollut.*, 1998, 101, 355–359.
41 I. Amini, A. Tahmourespour and A. Abdollahi, *Pollution*, 2017, 3, 9–19.
42 E. Z. Ron and E. Rosenberg, *Curr. Opin. Biotechnol.*, 2002, 13, 249–252.
43 S. Sun, Y. Wang, T. Zang, J. Wei, H. Wu., C. Wei, G. Qiu and F. Li, *Bioresour. Technol.*, 2019, 281, 421–428.
44 L. Tao, W. F. Hua, G. L. Ping, L. X. Liang, Y. X. Jin and L. A. Jun, *Chemistry*, 2012, 55, 1968–1975.
45 H. Liu, J. Xu, R. Liang and J. Liu, *PLoS One*, 2014, 9, e105506.
46 S. B. Salam, *J. Biotech.*, 2016, 6, 98.
47 R. S. Kahlon, *Biodegradation and bioremediation of organic chemical pollutants by Pseudomonas, in Pseudomonas: Molecular and Applied Biology*, ed. R. Kahlon, Springer International Publishing, Switzerland, 2016, pp. 343–417.
48 A. Perfumo, I. M. Banat, F. Canganella and R. Marchant, *Appl. Microbiol. Biotechnol.*, 2006, 72, 132.
49 H. R. Ali, D. A. Ismail and N. S. El-Gendy, *Energy Sources, Part A*, 2014, **36**, 1429–1436.
50 P. Censi, S. E. Spoto, F. Saiano, M. Sprovieri, S. Mazzola, G. Nardone and D. Ottonello, *Chemosphere*, 2006, **64**, 1167–1176.
51 K. E. Peters, C. C. Walters and J. M. Moldowan, *The biomarker guide: biomarkers and isotopes in the petroleum exploration and earth history*, Cambridge University Press, Cambridge, UK, vol. 2, 2005.
52 S. Sudarsan, L. M. Blank, A. Dietrich, O. Vielhauer, R. Takors, A. Schmid and M. Reuss, *Metab. Eng. Commun.*, 2016, **3**, 97–110.
53 D. White, *The Physiology and Biochemistry of Prokaryotes*, Oxford University Press, New York, 2nd edn, 2000, p. 198, 204.
54 C. Park and W. Park, *Front. Microbiol.*, 2018, **9**, 1081.
55 J. D. Wang, X. X. Li and C. T. Qu, *Curr. Microbiol.*, 2019, **76**, 1270–1277.
56 S. C. George, C. J. Boreham, S. A. Minifie and S. C. Teerman, *Org. Geochem.*, 2002, **33**, 1293–1317.
57 J. K. Volkman, R. Alexander, R. I. Kagi, S. J. Rowland and P. N. Sheppard, *Org. Geochem.*, 1984, **6**, 619–632.
58 I. M. Head, D. M. Jones and S. Larter, *Nature*, 2003, **426**, 344–352.
59 L. M. Wenger, C. L. Davis and G. H. Isaksen, *SPE Reservoir Eval. Eng.*, 2002, **5**, 375–383.
60 K. Stojanović, B. Jovančičević, A. Šajnović, T. Sabo, D. Vitorović, J. Schwarzbauer and A. Golovko, *Fuel*, 2009, **88**, 287–296.
61 S. Sun, H. Wang, Y. Chen, J. Lou, L. Wua and J. Xu, *J. Hazard. Mater.*, 2019, **364**, 509–518.