

Rapid biodegradation of phenanthrene by a novel strain *Pseudomonas denitrificans* Fdl

ABSTRACT

Aims: The aim of the study was to find, isolate, identify and characterize a phenanthrene degrader strain, and examine its ability to degrade phenanthrene.

Place and Duration of Study: Faculty of Natural Sciences, Novosibirsk State University, between September 2013 and June 2014.

Methodology: Soil was sampled from the oil contaminated area in the Purov district of the Yamal-Nenetsk Autonomous region in Russia (63.00729 NL, 76.89418 EL), and the enriched culture of oil-degraders was spread on plates with polyaromatic hydrocarbons (PAH) to isolate PAH degraders. The isolated strain was characterized morphologically, biochemically, physiologically and genetically (16S rRNA gene nucleotide sequence).

Results: By using crude oil-contaminated soil to obtain a culture enriched with oil-degraders followed by plate cultivation on phenanthrene-amended agar a bacterial strain denoted Fdl was isolated. Its cells were Gram-negative motile rods 0.4-0.5 µm wide and 1.5-2.5 µm long with phenotypic traits common for the *Pseudomonas* genus. The 16S rRNA gene fragment nucleotide sequence showed 99% similarity with *Pseudomonas denitrificans*. The isolated *Pseudomonas denitrificans* Fdl strain was deposited into the GenBank under access number KM 436103. Incubation of the Fdl strain cells in the medium with phenanthrene as a sole carbon source resulted in phenanthrene concentration decrease, accumulation of corresponding metabolites and bacterial proliferation, which confirmed the strain's ability to utilize phenanthrene. Over 40 hours of incubation the phenanthrene concentration decreased from 100 to 1 ppm, proving the novel strain to be an effective phenanthrene degrader. Addition of Tween-20 non-ionic surfactant into the incubation medium accelerated phenanthrene degradation and cell proliferation as compared to phenanthrene degradation without a surfactant.

Conclusion: The isolated strain *Pseudomonas denitrificans* Fdl is capable of efficient phenanthrene degradation, especially in the presence of detergent, and hence can be a good candidate for biological preparations to be tested for bioremediation and sewage sludge treatment.

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Keywords: oil-contaminated soil, phenanthrene, phenanthrene degrading bacteria, Pseudomonas denitrificans, novel strain

1. INTRODUCTION

14 Polycyclic aromatic hydrocarbons (PAH) are very common organic pollutants that are toxic and often carcinogenic [1]. Sixteen PAH, including phenanthrene, are included into the priority list of pollutants by the US Environmental Protection Agency [2]. The search for effective and cheap ways to clean PAH polluted territories has been increasingly actual issue. Bioremediation, i.e. using microbes, capable to destruct effectively various organic pollutants and preferably isolated from the contaminated site [3], is one of the most effective methods to remove PAH from environment.

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Biodegradation of PAH has been quite intensively studied over the last years, and various bacterial strains, capable to degrade PAH in a broad range of environmental conditions, e.g. acidic and alkaline pH, low and high salinity, low and high temperatures, were isolated and characterized in detail [4-6]. Biodegradation of PAH is limited by their extremely low water solubility and hence low availability for bacterial degradation. To increase PAH bioavailability and intensify their biodegradation the addition of surfactants has been investigated [7]. However, surfactants are also known to negatively affect PAH biodegradation, as they can be more preferable carbon substrates for microbial utilization [8], exert toxic effect on microbial cells [9], inhibit biodegradation by blocking substrate access into the enzyme active

28 center by forming micelle [10], etc. Thus it is important to seek microorganisms, capable to degrade PAH
29 effectively in the presence of surfactants. Phenanthrene, a polycyclic aromatic hydrocarbon with three
30 benzene rings, is a dangerous organic pollutant, and due to its wide environmental occurrence and low
31 water solubility (1.29 g/l) it is often used as a model substrate in microbial degradation studies, including
32 isolation of novel PAH-degrading strains and estimating their potential for PAH biodegradation. The
33 metabolic pathways of low molecular weight PAH degradation, and in particular, phenanthrene, were
34 studied by many researchers, the established common intermediate being 1-hydroxy-2-naphthoic acid,
35 which is further metabolized via one of the two pathways [11].

36 The aim of our study was to find, isolate, identify and characterize a novel phenanthrene degrader strain,
37 and examine its ability to degrade phenanthrene in a liquid medium in the presence of non-ionic
38 detergent.

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40 2. MATERIAL AND METHODS

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42 2.1 Chemicals and media composition

43 Phenanthrene and other chemicals used in the study were of analytical grade. The liquid minimal basal
44 salts medium (MBS) contained the following (g/L): $(\text{NH}_4)_2\text{SO}_4$, 1.0; g KH_2PO_4 , 5.0; g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.1;
45 $\text{Fe}(\text{NH}_4)_2(\text{SO}_4)_2$, 0.005; and 1 ml of micronutrients' solution, containing 23 mg $\text{MnCl}_2 \cdot 2\text{H}_2\text{O}$, 31 mg H_3BO_3 ,
46 36 mg $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 10 mg $\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$, 20 mg $\text{NiCl}_2 \cdot 6\text{H}_2\text{O}$, 50 mg ZnCl_2 , 30 mg $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$. The
47 medium pH was adjusted to 7.0. The solid MBS was prepared by adding 30 g of bacteriological agar into
48 1 liter of liquid MBS. The standard agarised Luria broth (LB) medium was used for colony-forming units
49 (CFU) counting.

50 2.2 Isolation of a phenanthrene degrader strain and enrichment culture conditions

51 Soil was sampled from the long-term oil contaminated area the Purov district of the Yamal-Nenetsk
52 Autonomous region in Russia (63.00729 NL, 76.89418 EL). The enrichment culture approach was
53 employed to isolate the oil-degrading bacterial strains. Initially the enriched culture of oil-degraders was
54 obtained. Then the culture was spread on plates with PAH to isolate PAH degraders. To obtain a culture
55 enriched with oil-degraders 1 g of soil was put into the 250 ml Erlenmeyer flask with 100 ml of sterile
56 liquid MBS medium. The sterilized crude oil at the rate of 2.5 % (v/v) was added into the medium as a
57 sole carbon source. Flask cultivations were carried out in a rotary shaker at 150 rpm for 1 week at 35 °C.
58 After that a 1 ml aliquot of the enriched medium was transferred into the new flask with similar medium for
59 the next cultivation step. The process was repeated 3 times. After that a 100 µl aliquot of the enriched
60 medium was spread on MBS agar plates. The phenanthrene solution in diethyl ester (0.1 % w/v) was
61 pulverized over plates in a sterile box, the solvent being allowed to evaporate under regular laminar flux.
62 The plates were cultivated for 1 week at 35 °C. The presence of a ring around a colony was interpreted
63 as positive phenanthrene degradation. The colonies were sampled with a sterile loop and transferred onto
64 LB agar plates to obtain a pure culture.

65 2.3 Morphological and biochemical characterization of a strain

66 Cell morphology was studied by phase-contrasting microscopy using Axiscop 40 microscope (Carl Zeiss,
67 Germany). Biochemical and physiological traits, as well as **pathogenicity**, were determined by standard
68 techniques [12, 13]. The antibiotic testing was studied using the antibiotics-impregnated paper discs
69 produced by the Research Centre of Pharmacotherapy (Saint-Petersburg, Russia), the amount of
70 antibiotics per disc being as following (µg): rifampicin, 5; penicillin, oxacillin, ampicillin and gentamicin, 10
71 each; oleandomycin, erythromycin and lincomycin, 15 each; streptomycin, neomycin, kanamycin,
72 monomycin, tetracycline, levomycetin and ristomycin, 30 each; karbenicyllin, 100; and polymyxin, 100
73 unites.

74 2.4 Molecular identification of a bacterial strain

75 The isolated strain was identified by analyzing its 16S rRNA gene nucleotide sequence. A 1350 bp gene
76 fragment was amplified using the lyzate of the strain colonies. The oligonucleotides 16S-8-f-b 5'-
77 AGRGTTTGATCCTGGCTCA-3' and 16S-1350-r-B 5'-ACGGGCGGTGTGTACAAG-3' were used as
78 primers to identify bacteria by their 16S rRNA gene [14].

79 Sequencing of the obtained PCR-amplicons was performed with the same oligonucleotides and BigDye
80 v.3.1 reagent under standard conditions. The reaction products were analysed electrophoretically using
81 ABI Sequencing Analyzer 3500. The obtained nucleotide sequences were analysed using ABI Sequence
82 Scanner and Sequencher v.4.1.4 software and compared to the 16S rRNA gene sequences deposited in
83 GenBank using BLASTN software.

84 **2.5 Phenanthrene degradation**

85 Phenanthrene biodegradation was studied in 100 ml of liquid MBS medium in 250 ml Erlenmeyer flasks
86 with phenanthrene added at the rate of 100 mg/L. When studying the effect of a detergent on
87 phenanthrene degradation, Tween-20 was added into the flasks to the 0.5% concentration (v/v). The
88 medium was inoculated with 1 ml of suspension, containing 107 CFU/ml, obtained from colonies grown
89 on the phenanthrene-containing agar and washed 3 times by sterile liquid MBS. Then the flasks were
90 incubated at 35 °C in a rotary shaker at 150 rpm. When no detergent was added, the aliquots were
91 sampled after 8, 16, 24, 32, 40, 48 hours of incubation. When the detergent was added, the aliquots were
92 sampled after 2, 4, 6, 8, 16, 24, 48 hours of incubation. The pH of the aliquots was adjusted to 2.3 using
93 concentrated hydrochloric acid (HCl), and then extracted 3 times by 30 ml of dichloromethane. The
94 extracts were dried over anhydrous sodium sulphate and then evaporated in vacuum. The dried residue
95 was solved in acetonitrile for further analysis.

97 **2.6 Measurement of phenanthrene and 1-hydroxy-2-naphthoic acid concentration.**

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99 Concentrations of phenanthrene and 1-hydroxy-2-naphthoic acid in the obtained acetonitrile solutions
100 were analysed by reversed-phase HPLC. HPLC was performed on a Milichrome A-02 chromatograph
101 (Econova, Ltd., Russia), equipped with a ProntoSIL 120-5C18 AQ column (2 x 75 mm, B&W Separation
102 Technologies Pvt. Ltd.) under the following conditions: solvent A, 0,2 M LiClO₄ - 0.05 M HClO₄; solvent B,
103 acetonitrile; linear gradient of B in A from 0 to 100% in 40 min, flow rate of 100 µl/min, column
104 temperature of 400 C, detection at 210, 220, 230, 240, 250, 260, 280 and 300 nm; the sample volume 3
105 µl. The presence of 1-hydroxy-2-naphthoic acid (HNA) was determined by comparing the retention time
106 and spectrum of the analysed sample with the respective characteristics of the reference standard. The
107 HNA and phenanthrene concentrations were determined by measuring the areas of the respective peaks,
108 using the calibration curve with reference compounds.

110 **2.7 Cell growth during biodegradation**

111 Bacterial cell proliferation in course of biodegradation was estimated by counting the strain colonies
112 grown over 48 hours on the LB agar. When no detergent was added, the aliquots were sampled after 8,
113 16, 24, 32, 40, 48 hours of cultivation. When the detergent was added, the aliquots were sampled after 2,
114 4, 6, 8, 16, 24, 48 hours of cultivation. The aliquots thus sampled were titrated in 0.9 % solution of NaCl in
115 water and transferred onto LB agar plates to count CFU after 48 hours incubation at 35 °C.

116 117 **3. RESULTS AND DISCUSSION**

118 119 **3.1 Isolation and characterization of a novel strain of the phenanthrene-degrading** 120 **bacterium**

121 By using crude oil-contaminated soil to obtain a culture enriched with oil-degraders followed by plate
122 cultivation on phenanthrene-amended agar we isolated a bacterial strain denoted Fdl. To identify it we

123 studied its morphological, physiological and biochemical properties and performed 16S rRNA genes
 124 sequencing.

125 **3.2 Morphological and physiological characteristics of the isolated strain**

126 The cells of the isolated strain were found to be Gram-negative motile rods, mostly solitary, but
 127 sometimes paired cells 0.4-0.5 µm wide and 1.5-2.5 µm long cells without endospores. On the LB agar
 128 the strain produced transparent yellowish glance round-shaped colonies with an even or slightly curving
 129 edge; on the solid medium containing fish peptone the strain produces yellow-orange pigment. The strain
 130 was found to be aerobic with the optimum growth temperature of 28-30 °C, the moderate and weak
 131 growth rate being observed at 37 °C and 10 °C, respectively.

132 **3.3 Biochemical characteristics of the strain**

133 Standard biochemical characterization of the strain showed its negative reaction to indol, hydrogen
 134 sulphide, casein hydrolysis, as well as in Voges-Proskauer test reaction and in incubation with the methyl
 135 red dye. The strain was found to be able to reduce nitrates into nitrites and to utilize citrate as a carbon
 136 source. Under laboratory conditions the strain was not shown to secrete such enzymes as amylase,
 137 lipase, gelatinase, licitinase, urease, DNase, RNase, while positive reaction was displayed in oxidase
 138 and catalase tests (Tab.1). The isolated strain was found to be represented by a bacterium with a
 139 respiratory, rather than fermentation, metabolism as it does not hydrolyze sucrose, glucose, lactose,
 140 arabinose, ramnose, displaying weak acid-formation on media containing maltose and xylose (Tab.2).

141 **Table 1. Biochemical characteristics of the isolated strain Fdl B-1299**

Trait	Reaction	Trait	Reaction
<i>Amilase</i>	- *	<i>FP reaction</i>	-
<i>Lecitinase</i>	-	<i>MR reaction</i>	-
<i>Lipase</i>	-	<i>Oxidase</i>	+
<i>Casein hydrolysis</i>	-	<i>Catalase</i>	+
<i>Gelatinase</i>	-	<i>RNase</i>	-
<i>Indol production</i>	-	<i>DNase</i>	-
<i>H₂S production</i>	-	<i>Lysinedecarboxylase</i>	-
<i>Urease</i>	-	<i>Ornithinedecarboxylase</i>	-
<i>Citrate utilization</i>	+	<i>Argininedecarboxylase</i>	±
<i>Nitrate reduction</i>	+	<i>Phenylalaninnedesaminase</i>	-

142 * Symbols used: "+" means a positive reaction, and "-" means a negative one.

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144 **Table 2. Carbohydrates utilization by the isolated strain on the OF medium**

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Carbohydrate	Gas emission	Acid production
Sucrose	-	-
Mannitol	-	-
Glucose	-	+
Lactose	-	-

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Arabinose	-	-
Ramnose	-	-
Maltose	-	+
Xylose	-	±

150 Notably, the strain showed negative results as related to all four pathogenicity tests, i.e. hemolythic,
151 plasmocoagulating, fibrinolythic and gelatinolythic activities. The absence of pathogenic properties in the
152 isolated strain intended for bioremediation is very important as it shows its ecological safety. The strain
153 was also found to be resistant to ampicillin, benzylpeicillin, carbenicillin, oxaxillin, rifampicin, levomycetin
154 and lincomycin, (Tab.3).

155 **Table 3. Antibiotic activity (zones of the reduced growth of the isolated strain around the**
156 **antibiotic containing discs, mm)**

Antibiotic	Reduced growth, mm	Antibiotic	Reduced growth, mm
<i>polymyxin</i>	14	<i>tetracycline</i>	10
<i>amikacin</i>	25	<i>ciprofloxacin</i>	26
<i>vankomicyn</i>	15	<i>azlocilline</i>	21
<i>gentamycin</i>	15	<i>streptomycin</i>	18
<i>kanamycin</i>	20	<i>imipenem</i>	14
<i>ampicillin, benzylpenicillin,</i>		<i>neomycin</i>	11
<i>carbenicillin, oxaxillin, kanamycin,</i>	0	<i>cefotaxime</i>	12
<i>rifampicin, levomycetin, lincomycin</i>			

157

158 The isolated strain showed phenotypic traits common for the representatives of the *Pseudomonas* genus.
159 Further identification of the isolated Fd1 strain revealed its close relationship with *P. denitrificans* species
160 (Tab.4). Comparison of the 16S rRNA gene sequence of the novel strain with the respective sequences
161 stored in the international data base GenBank showed that the novel sequence had 99% similarity with
162 the sequences of the following bacteria: *Pseudomonas nitroreducens* (NR 113601), *P. denitrificans* (NR
163 102805) and *P. multiresinivorans* (NR 119225). These information, together with the results of the
164 phenotypic and genotypic analysis of the isolated strain Fd1 led us to identify it as representing
165 *Pseudomonas denitrificans* species. The 16S rRNA gene fragment nucleotide sequence of the
166 *Pseudomonas denitrificans* Fd1 strain was deposited into the GenBank under access number KM 436103.

167 **Table 4. Morphological, physiological and biochemical characteristics of the bacterial genus**
168 ***Pseudomonas*, its typical representative strain *P. denitrificans* and the novel strain Fd1 B-1299**

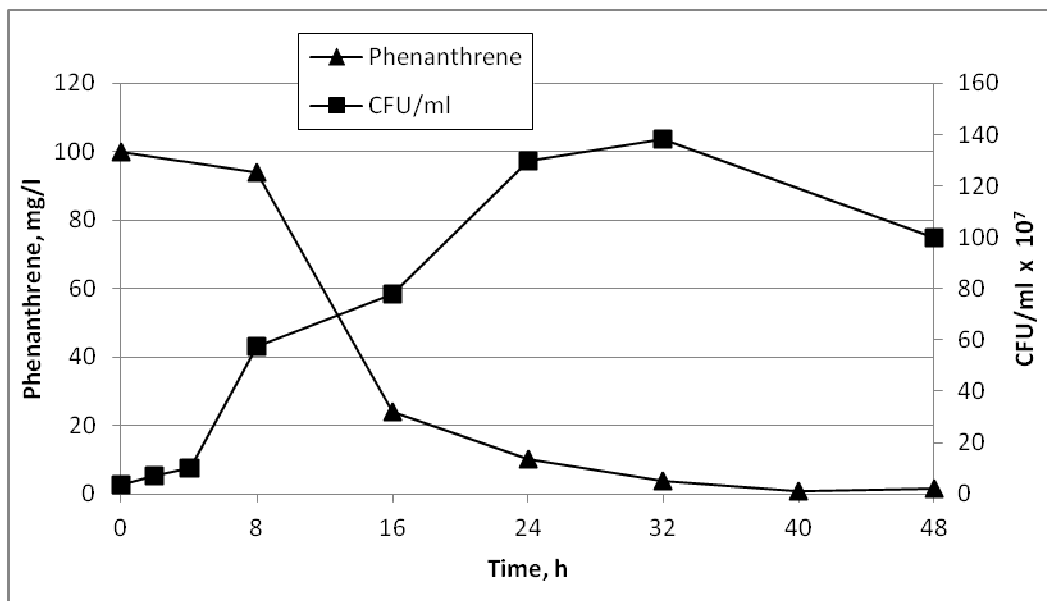
Trait	Genus <i>Pseudomonas</i>	<i>P. denitrificans</i> (reference strain KC1439 - ATCC 138667; [15])	Strain Fd1 B- 1299
Cell shape	rods	rods	rods
Cell dimensions, width x length, µm	(0.5-1.0) × 1.5-4.0	(0.5-1) × (1.5-4.0)	(0.4-0.5) × (1.5-2.5)
Cell motility	+ *	+	+
Gram reaction	-	-	-

Respiratory, not fermenting metabolism	+	+	+
Strictly aerobic	+	+	+
Catalase	+	+	+
Oxidase	+	+	+
Growth at +4 °C and lower	+		+
Growth at 25 °C	+	+	+
35 °C		+	+
up to 42 °C		[±]	±
pH 5.4	-	-	+
eskulin	-	-	n.d.
Lisinedecarboxylase	-	-	-
Ornitinedecarboxylase	-	-	-
Argininedecarboxylase	[±]	[±]	+
Glucose oxidation	[±]	[±]	+
Xylose oxidation	[±]	[±]	±
Sucrose oxidation	-	-	-
Maltose oxidation	[±]	+	+
Citrate utilization	+	+	+
Nitrate reduction into nitrite	[±]	[±]	+
Indol production	-	-	-
Hydrogen sulphide production	-	-	-
Gelatine	±	-	-
Hemolysis	[±]	[±]	- (rabbit blood)
G+C	58-70 mol %		n.d.
NaCl, 0 %	[±]	+	+
6 %	[±]	[±]	-
Water soluble pigment	+	[±]	+

* Symbols used: "+" denotes a positive reaction, "-" denotes a negative reaction; [±] means variable trait, while "±" means weak trait and "n.d." means no datum.

3.4 Phenanthrene degradation by the isolated strain

Incubation of the Fdl strain cells in the medium with phenanthrene as a sole carbon source was found to result in phenanthrene concentration decrease, accumulation of corresponding metabolites in the medium and bacterial cell proliferation, all together confirming the ability of the strain to utilize phenanthrene as a carbon source. The kinetic curve of phenanthrene biodegradation was characterized by three portions, coinciding with the main phases of cell proliferation and growth (Fig.1). After 4 hours of incubation the lag-phase ended, and the exponential growth started and continued up to 24 hours of incubation with the maximal degradation rate being observed between 8 and 16 hours. After 32 hours of incubation, when almost all phenanthrene in the medium was utilized, the number of living cells started to decrease correspondingly. Over 40 hours of incubation the phenanthrene concentration decreased from 100 ppm down to 1 ppm, proving the novel Fdl strain to be an effective phenanthrene degrader.

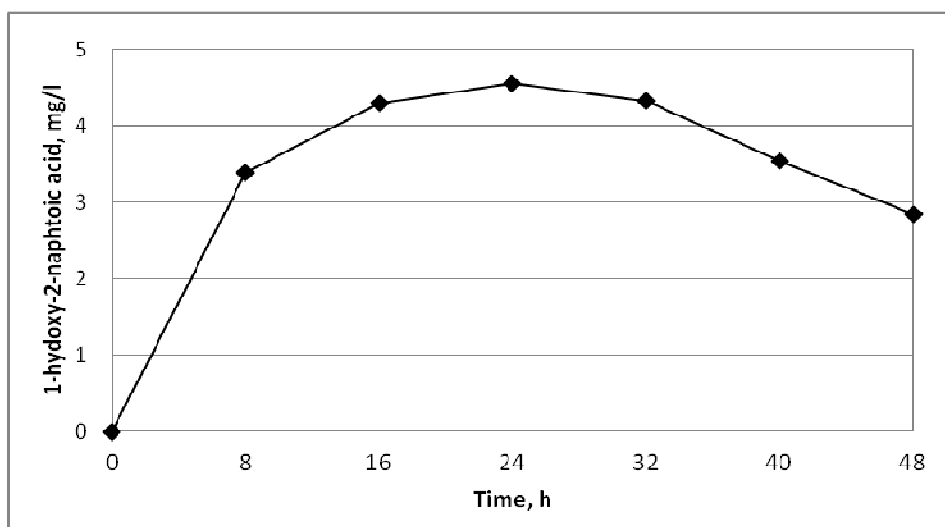


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184 **Fig. 1. Phenanthrene degradation and cell proliferation**

185 **3.5 Identification and accumulation of 1-hydroxy-2-naphthoic acid**

186 The HPLC analysis of phenanthrene degradation products in the incubation medium was found to contain
 187 significant amount of HNA known to be the key metabolite in phenanthrene degradation. Kinetic studies
 188 of the HNA accumulation (Fig.2) showed increase in HNA concentration during the first 24 hours of
 189 incubation. After 32 hours of incubation when phenanthrene concentration decreased below the HNA
 190 concentration, the latter started to decrease as well. The further degradation of HNA, as was reported
 191 earlier, goes via salicylic or phthalic acid production. However, HPLC analysis found no such compounds
 192 in the incubation medium, which may result from their extremely short life time in the medium. The fact
 193 that the strain was found to be able to proliferate on/in the medium containing salicylic acid as the sole
 194 carbon source and not on/in the medium with the phthalic acid as the sole carbon source (the data are
 195 not shown) can serve as indirect evidence in favour of the salicylic acid production pathway.

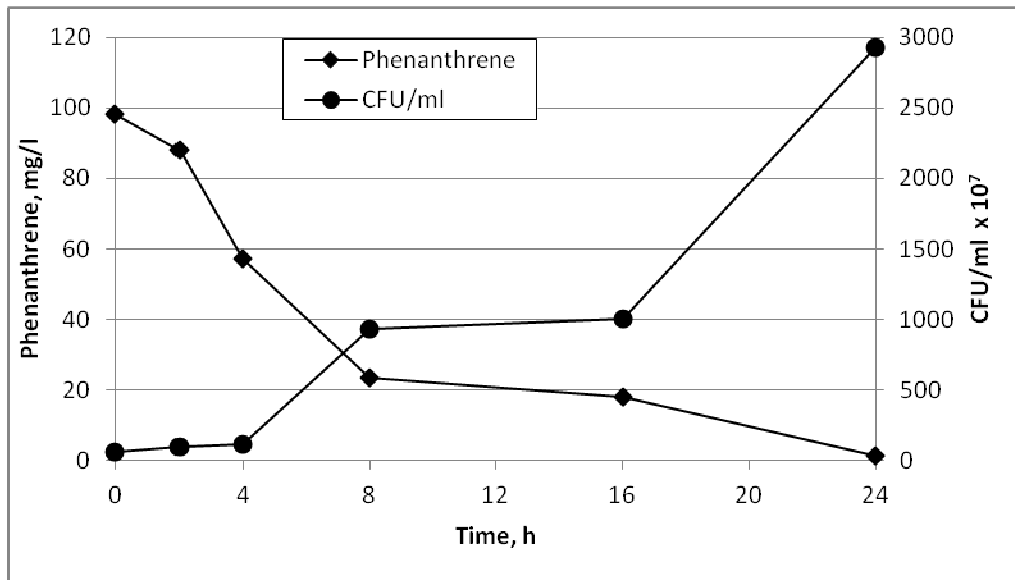


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197 **Fig. 2. Accumulation of 1-hydroxy-2-naphthoic acid in course of phenanthrene degradation**

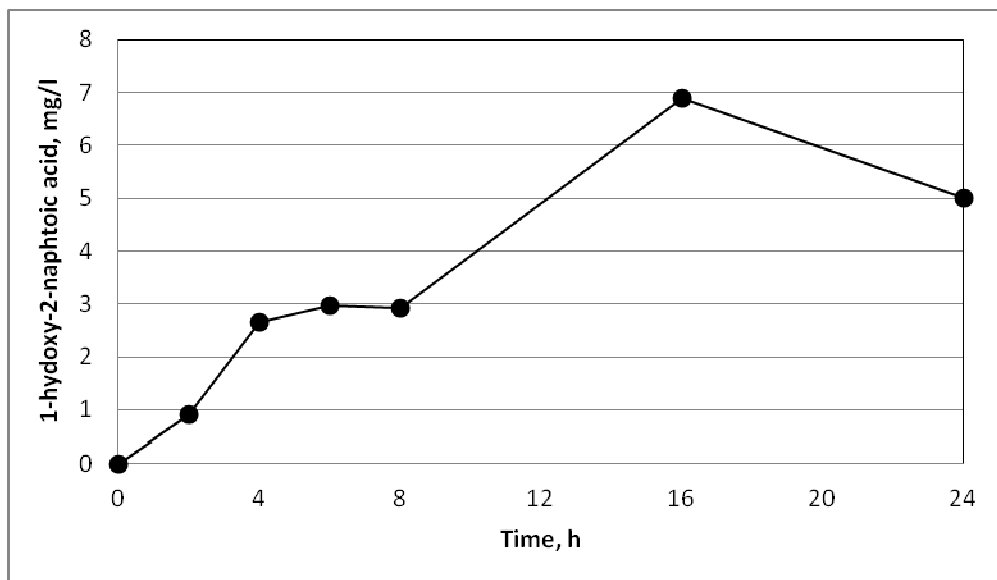
198 **3.6 The effect of Tween-20 surfactant on phenanthrene degradation**

199 Addition of Tween-20 non-ionic surfactant into the incubation medium accelerated phenanthrene
200 degradation and cell proliferation as compared to phenanthrene degradation without a surfactant (Fig.3).
201 When Tween 20 was added, the phenanthrene concentration was found to decrease already after 2
202 hours of incubation, decreasing to 1 ppm over 24 hours, with the maximal degradation rate being
203 recorded at 2-8 hours interval. Since Tween 20 is known as a good carbon source to be utilized by
204 bacterial cells, its effect on phenanthrene degradation may be due both to a facilitated assimilation/uptake
205 of phenanthrene by bacterial cells and/or increased cell biomass. Judging by the CFU counts, we may
206 conclude that after 4 hours of incubation cell proliferation is supported mostly by Tween 20 as a growth
207 substrate, with phenanthrene contributing not more than 10 %. However, as phenanthrene degradation
208 was observed to start already after 2 hours of incubation, i.e. before the end of the lag-phase, the
209 increased phenanthrene uptake by cells may be suggested to contribute into the accelerated degradation
210 as well.



211
212 **Fig. 3. Phenanthrene degradation and bacterial cell proliferation in the medium with Tween 20**
213 **added**

214 The presence of Tween 20 in the medium resulted in the accumulation of large amount of HNA, with a
215 pattern similar to the one without Tween 20 (Fig.4). The maximal HNA concentration was registered after
216 16 hours of incubation. Despite the fact that it is a less preferable substrate for bacterial utilization, as
217 compared with Tween 20, HNA did not accumulate in the medium in course of incubation.



218

219 **Fig. 4. The accumulation of 1-hydroxy-2-naphthoic acid in course of phenanthrene degradation in**
 220 **the medium with Tween 20 added**

221 Many bacteria, representing diverse genera such as *Bacillus* [16], *Nocardia* [17], *Pseudomonas* [18-21],
 222 *Sphingomonas* [22], *Sphingobium* [23], *Mycobacterium* [24], *Sinorhizobium* [25], *Rhizobium* [26],
 223 *Novosphingobium* [27] and others [28, 29] were reported to degrade phenanthrene. However, their
 224 degradation rate in liquid medium with 100 ppm phenanthrene ranged 96-99 % over 77-360 hours,
 225 whereas the *Pseudomonas denitrificans* Fdl strain isolated in this study was shown to degrade
 226 phenanthrene over 48 hours without any additions present, and twice as rapidly if phenanthrene
 227 assimilation/uptake was facilitated by the detergent present in the medium. The closest to our strain was
 228 a *Pseudomonas* strain, reported to degrade 100 % of 60 mg/L phenanthrene within 60 hours [30].

229 Some phenanthrene-degrading *Pseudomonas* strains were found to produce biosurfactants, facilitating
 230 PAH bioavailability [31]. Although we did not examine its capability to produce biosurfactants, the isolated
 231 strain may be quite likely to do so, which might enhance the strain's prospects as a potential
 232 bioremediator.

233 4. CONCLUSION

234
 235 The isolated strain *Pseudomonas denitrificans* Fdl is capable of efficient phenanthrene degradation,
 236 especially in the presence of detergent, and hence can be a good candidate for biological preparations to
 237 be tested for industrial bioremediation and sewage sludge treatment.
 238

239 REFERENCES

- 240
 241 1. Mastrangelo G, Fadda E, Marzia V. Polycyclic aromatic hydrocarbons and cancer in man. *Environ*
 242 *Health Perspect.* 1996;104:1166–1170. PMID: PMC1469515
 243 2. US Environmental Protection Agency. Priority Pollutants. Accessed 13 June 2017. Available:
 244 <http://water.epa.gov/scitech/methods/cwa/pollutants.cfm>
 245 3. Wu M, Chen L, Tian Y, Ding Y, Dick WA. Degradation of polycyclic aromatic hydrocarbons by microbial
 246 consortia enriched from three soils using two different culture media. *Environ Pollut.* 2013;78:152-158.
 247 doi:10.1016/j.envpol.2013.03.004
 248 4. Gerbeth A, Krause S, Gemende B, Muller RH. Search of microorganism that degrade PAHs under
 249 alkaline conditions. *Eng Life Sci.* 2004;20044:311-318. doi: 10.1002/elsc.200420034

250 5. Okere UV, Cabrerizo A, Dachs J, Jones KC, Semple KT. Biodegradation of phenanthrene by
251 indigenous microorganisms in soils from Livingstone Island, Antarctica. FEMS Microbiol Lett.
252 2004;329:69-77. doi: 10.1111/j.1574-6968.2012.02501.x

253 6. Viamajala S., Peyton BM, Richards LA, Petersen JN. Solubilization, solution equilibria, and
254 biodegradation of PAH's under thermophilic conditions. Chemosphere. 2007;66:1094-1106.
255 doi:10.1016/j.chemosphere.2006.06.059

256 7. Li J., Chen BH. Surfactant-mediated Biodegradation of Polycyclic Aromatic Hydrocarbons. Materials.
257 2009;2:76-94. doi:10.3390/ma2010076

258 8. Jin DY, Jiang X, Jing X, Ou ZQ. Effects of concentration, head group, and structure of surfactants on
259 the degradation of phenanthrene. J Hazard Mater. 2007;144:215-221. doi:10.1016/j.jhazmat.2006.10.012

260 9. Tiehm A. Degradation of polycyclic aromatic-hydrocarbons in the presence of synthetic surfactants.
261 Appl Environ Microbiol. 1994;60:258-263. PMID: PMC201297

262 10. Efroymsen RA, Alexander M. Biodegradation by an Arthrobacter species of hydrocarbons partitioned
263 into an organic-solvent. Appl Environ Microbiol. 1991;57:1441-1447.
264 <http://aem.asm.org/content/57/5/1441>

265 11. Gao S, Seo JS, Wang J, Keuma YS, Li J, Li QX. Multiple degradation pathways of phenanthrene by
266 *Stenotrophomonas maltophilia* C6. Int Biodeterior Biodegradation. 2013;79:98-104.
267 doi:10.1016/j.ibiod.2013.01.012

268 12. Holt J.G. Bergey's Manual of Systematic Bacteriology, V.2. Baltimore-London: Williams and Wilkins;
269 1986.

270 13. Gerhardt P. Methods for General and molecular bacteriology. Washington: ASM; 1994.

271 14. Wang Y, Qian P. Conservative Fragments in Bacterial 16S rRNA Genes and Primer Design for 16S
272 Ribosomal DNA Amplicons in Metagenomic Studies. PLoS ONE, 2009;4:e7401.
273 doi:10.1371/journal.pone.0007401

274 15. Weyant R, Moss CW, Weaver R.E, Hollis DG, Jordan JJ, Cook EC, et al. Identification of Unusual
275 Pathogenic Gram-Negative Aerobic and Facultative Anaerobic Bacteria. Baltimore: Williams & Wilkins;
276 1994.

277 16. Doddamani HP, Ninnekar HZ. Biodegradation of phenanthrene by a *Bacillus* sp. Curr Microbiol.
278 2000;41:11-14. doi:10.1007/s002840010083

279 17. Zeinali M, Vossoughi M, Ardestani SK. Degradation of phenanthrene and anthracene by *Nocardia*
280 *otitidiscaviarum* strain TSH1, a moderately thermophilic bacterium. J Appl Microbiol. 2008;105:398-406.
281 doi:10.1111/j.1365-2672.2008.03753.x.

282 18. Phale PS. Biodegradation of phenanthrene by *Pseudomonas* sp. strain PP2: novel metabolic
283 pathway, role of biosurfactant and cell surface hydrophobicity in hydrocarbon assimilation. Appl Microbiol
284 Biotechnol. 2003;61:342-351. doi:10.1099/mic.0.030460-0

285 19. Prabhu Y, Zeinali M, Vossoughi M, Ardestani SK. Degradation of phenanthrene and anthracene by
286 *Nocardia* *otitidiscaviarum* strain TSH1, a moderately thermophilic bacterium. J Appl Microbiol.
287 2008;105:398-406. doi:10.1111/j.1365-2672.2008.03753.x.

288 20. Deveryshetty J, Phale PS. Biodegradation of phenanthrene by *Pseudomonas* sp. strain PPD:
289 purification and characterization of 1-hydroxy-2-naphthoic acid dioxygenase. Microbiology.
290 2009;155:3083-3091. doi:10.1099/mic.0.030460-0

291 21. Sun K, Liu J, Gao Y, Jin L, Gu Y, Wang W. Isolation, plant colonization potential and phenanthrene
292 degradation performance of the endophytic bacterium *Pseudomonas* sp. Ph6-gfp. Scientific Reports.
293 2014;26:5462. doi:10.1038/srep05462

294 22. Hesham Ael-L, Mawad AM, Mostafa YM, Shoreit A. Biodegradation ability and catabolic genes of
295 petroleum-degrading *Sphingomonas koreensis* strain ASU-06 isolated from Egyptian oily soil. Biomed
296 Res Int. 2014;127674. doi: 10.1155/2014/127674

297 23. Wang C, Wang F, Hong Q, Zhang Y, Kengara FO, Li Z, et al. Isolation and characterization of a toxic
298 metal-tolerant Phenanthrene-degrader *Sphingobium* sp. in a two-liquid-phase partitioning bioreactor
299 (TPPB). Environ Earth Sci. 2013;70:1765-1773. doi:10.1007/s12665-013-2264-8

300 24. Moody JD, Freeman JP, Doerge DR, Cerniglia CE. Degradation of Phenanthrene and Anthracene by
301 Cell Suspensions of *Mycobacterium* sp. Strain PYR-1. Appl Environ Microbiol. 2001;67:1476-1483.
302 doi:10.1128/AEM.67.4.1476-1483.2001

303 25. Keum Y-S, Se J-S, Hu Y, Li QX. Degradation pathways of phenanthrene by *Sinorhizobium* sp. C4.
304 Applied Microbiology & Biotechnology. 2006;1:935-941. doi:10.1007/s00253-005-0219-z

305 26. González-Paredes Y, Alarcón A, Ferrera-Cerrato R, Almaraz JJ, Martínez-Romero E, Cruz-Sánchez
306 JS, et al. Tolerance, growth and degradation of phenanthrene and benzo[a]pyrene by *Rhizobium tropici*
307 CIAT 899 in liquid culture medium. *Appl Soil Ecol.* 2013;63:105-111. doi:10.1016/j.apsoil.2012.09.010
308 27. Lyu Y, Zheng W, Zheng T, Tian Y. Biodegradation of polycyclic aromatic hydrocarbons by
309 *Novosphingobium pentaromativorans* US6-1. *PLoS One.* 2014;9:e101438.
310 doi:10.1371/journal.pone.0101438
311 <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0101438>
312 28. Roy AS, Baruah R, Borah M, Singh AK, Boruah HPD, Saikia N, et al. Bioremediation potential of
313 native hydrocarbon degrading bacterial strains in crude oil contaminated soil under microcosm study. *Int*
314 *Biodeterior Biodegradation.* 2014;94:79-89. doi:10.1016/j.ibiod.2014.03.024
315 29. Wu M, Chen L, Tian Y, Ding Y, Dick WA. Degradation of polycyclic aromatic hydrocarbons by
316 microbial consortia enriched from three soils using two different culture media. *Environ Pollut.*
317 2013;178:152-158. doi:10.1007/s13205-017-0704-y
318 30. Feng T, Lin H, Tang J, Feng Y. Characterization of polycyclic aromatic hydrocarbons degradation and
319 arsenate reduction by a versatile *Pseudomonas* isolate. *Int Biodeterior Biodegradation.* 2014;90:79-87.
320 doi:10.1016/j.ibiod.2014.01.015
321 31. Xia W., Du Z, Cui Q, Dong H, Wang F, He P, Tang YC. Biosurfactant produced by novel
322 *Pseudomonas sp.* WJ6 with biodegradation of n-alkanes and polycyclic aromatic hydrocarbons. *J Hazard*
323 *Mater.* 2014;276:489-498. doi: 10.1016/j.jhazmat.2014.05.062.