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(54) **METHOD OF PURIFYING WATER, SUITABLE BACTERIA FOR THE METHOD AND USE THEREOF**

VERFAHREN ZUR REINIGUNG VON WASSER, DAFÜR GEEIGNETE BAKTERIEN UND DEREN VERWENDUNG

PROCEDE PERMETTANT DE PURIFIER DE L'EAU, BACTERIES ADAPTEES AUDIT PROCEDE ET LEUR UTILISATION

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- (56) References cited:
**EP-A- 0 915 061 US-A- 4 317 885
US-A- 5 679 568**

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Description

FIELD OF THE INVENTION

5 **[0001]** The invention relates to a method of purifying waste water biologically, and to bacteria and a mixed bacterial population suitable for the method and the use thereof. The invention further relates to a bioreactor comprising said bacteria or mixed population.

10 BACKGROUND OF THE INVENTION

[0002] Conventionally, water can be purified both by physical and chemical means, for example by sedimentation, filtration or flocculation (WO94/5866 and WO88/5334). In order to remove organic compounds and other compounds that are difficult to purify it is also preferable to use so-called biological purification wherein the water to be purified is brought into contact with microorganisms that decompose pollution agents. Biological water treatment methods are suited for use both in conventional water treatment plants and industrial waste water treatment plants. Biological water treatment has also been tested in systems where water is recycled (FI 964141). Biological water treatment is also needed to purify seep water of a dump, for example, before the seep water is discharged into the environment.

15 **[0003]** The biological purifying method is, however, more difficult to control than the physical or chemical purifying methods. Firstly, microorganisms to decompose pollution agents must be found. Secondly, the microorganisms must be capable of easily surviving and reproducing under conditions during the water treatment process. In other words, the microorganisms used for purifying water must be competitive ones so as to prevent other organisms in the water from overruling. In addition, the microorganisms used for purifying water must not be sensitive to the changes in their environment that often occur during water treatment processes when the load varies.

20 **[0004]** Many kinds of microorganisms have been used for purifying water, including bacteria and protozoa, such as the ciliates. Bacteria that have often been used include species of the *Pseudomas* genus, but also members of the *Alcagenes*, *Acinetobacter* or *Rhodococcus* genera are often used. Mixed populations, some identified and some unidentified, comprising a great number of different microorganisms are often used. Aerobic or facultative microorganisms are best suited to purifying water, in which case it is appropriate to pump air into the water to be purified so as to make the purification process more efficient.

25 **[0005]** US-A-5 679 568 discloses decomposition of a halogenated organic acid and/or of aliphatic organochlorine compounds by certain organisms including *Pseudomonas* and *Xanthobacter* and particularly a new *Renobacter* strain.

[0006] EP-A-915 061 relates to how to remove the detrimental effect of detergents on microorganism growth in order to improve e.g. industrial fermentation processes. The detergent's detrimental effect is removed by adding hydrolysing enzymes to the liquid i.e. the removal of the detergent from the wastewater is enzymatic not biological.

30 **[0007]** US-A-4 317 885 relates to the use of a particular strain of *Pseudomonas fluorescens* in removing detergents and other pollutants from wastewater. The strain used is an obligate aerobe, which means that it is not capable of denitrification, which is essential in removing nitrogenous compounds from wastewater.

35 **[0008]** When microorganisms, are cultivated, the growth medium should normally be sterilized so as to prevent the cultivation from becoming contaminated by external organisms. Since large amounts of water are processed while purifying waste water, the amount of necessary biomass for the biological purification is also large. To produce such biomass under sterile conditions is both laborious and expensive; hence, it would be most desirable if the biomass could be produced under non-sterile conditions without any danger of becoming contaminated. The present invention now provides a novel fermentation technology with no need to sterilize. This is possible when microorganisms particularly suitable for the method are used and these microorganisms are fed on nutrients suitable for them.

40 SUMMARY OF THE INVENTION

[0009] The present invention relates to microorganisms that are surprisingly well suited to biological purification of waste water. These microorganisms meet particularly well the aforementioned requirements set for microorganisms suitable for the biological purification of water. In addition, the microorganisms of the invention are so specific that their biomass can be produced under non-sterile conditions by using a growth medium where other microorganisms are unable to compete. This enables large savings in the costs and energy consumption of a biological water purification process, the purification results also being excellent. Water purified according to the invention is even recyclable.

45 **[0010]** The invention thus relates to the bacteria *Bacillus* sp. DT-1 having the deposit number DSM 12560, *Pseudomonas* sp. DT-2, subsequently identified as *Pseudomonas azelaica* having the deposit number DSM 12561, and the former *Pseudomonas* sp. now being *Rhizobium* sp. and having the deposit number DSM 12562. Later 16S rDNA analyses have shown that this bacterium most closely resembles the members of the *Rhizobium* genus, so hereafter, it will be considered as one of them. The invention further relates to the following bacterial strains promoting water

purification: *Pseudomonas azelaica* DT-6 having the deposit number DSM 13516, *Azospirillum* sp. DT-10 having the deposit number DSM 13517, *Ancylobacter aquaticus* DT-12 having the deposit number DSM 13518, and *Xanthobacter* sp. DT-13 having the deposit number DSM 13519. DSM 12560 - 12562 have been deposited at Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH on 1 December 1998, and DSM 13516 - 13519 on 29 May 2000.

5 [0011] The invention further relates to a bacterial mixed population characterized by comprising the bacterium *Bacillus* sp. DT-1 having the deposit number DSM 12560, *Pseudomonas azelaica* DT-2 having the deposit number DSM 12561, and/or *Rhizobium* sp. DT-5 having the deposit number DSM 12562.

10 [0012] The invention further relates to the use of the bacterial mixed population in waste water treatment and to a method of purifying waste water, characterized by purifying water biologically by a mixed population comprising the microorganisms *Bacillus* sp. DT-1 having the deposit number DSM 12560, *Pseudomonas azelaica* DT-2 having the deposit number DSM 12561, and *Rhizobium* sp. DT-5 having the deposit number DSM 12562.

15 [0013] The invention further relates to a bioreactor characterized by comprising the microorganisms *Bacillus* sp. DT-1 having the deposit number DSM 12560, *Pseudomonas azelaica* DT-2 having the deposit number DSM 12561, and *Rhizobium* sp. DT-5 having the deposit number DSM 12562. A bioreactor is a reactor in which a biological purification process is conducted.

DRAWINGS

[0014]

20 Figure 1 schematically shows a purification system for seep water, Figure 2a shows a profile of the fatty acids of bacterial strain DT-1, Figure 2b is a print of a fatty acid analysis of bacterial strain DT-1, Figure 3a shows a profile of the fatty acids of bacterial strain DT-2, Figure 3b is a print of a fatty acid analysis of bacterial strain DT-2, Figure 4 is a print of a fatty acid analysis of bacterial strain DT-5, Figure 5 is a print of a fatty acid analysis of bacterial strain DT-6, Figure 6 is a print of a fatty acid analysis of bacterial strain DT-10, Figure 7 is a print of a fatty acid analysis of bacterial strain DT-12, and Figure 8 is a print of a fatty acid analysis of bacterial strain DT-13.

DETAILED DESCRIPTION OF THE INVENTION

35 [0015] Microorganisms growing in a soap mixture were enriched from waste water of an industrial plant and then adapted by cultivating them in a bioreactor comprising waste water from a dump. Three bacterial strains were thus isolated that were superior to the others. Said bacterial strains are *Bacillus* sp. DT-1 having the deposit number DSM 12560, *Pseudomonas azelaica* DT-2 having the deposit number DSM 12561 and *Rhizobium* sp. DT-5 having the deposit number DSM 12562. These bacteria can be cultivated in tap water comprising about 1 - 4 g/l of soap. Extremely few microorganisms can actively grow under such conditions; therefore, this growth medium needs not be sterilized when biomass of said three bacteria is being produced. The strains tolerate as high amounts of soap as about 40 g/l. They grow best in a soap content of about 0.3 - 0.5 g/l.

40 [0016] In addition to being capable of growing in a growth medium where most other bacteria are incapable of reproducing, said bacterial strains are extremely efficient in removing the organic load of waste water. This is usually measured as total COD, which means the total chemical oxygen consumption (mg O₂/l). The isolated bacterial strains can particularly decompose compounds that do not decompose easily, such as chlorophenoles, polycyclic aromatic hydrocarbons (PAH compounds) and oils. They also remove heavy metals.

45 [0017] The bacteria *Bacillus* sp. DT-1, *Pseudomonas azelaica* DT-2 and *Rhizobium* sp. DT-5 further tend to flocculate, in which case they form a so-called bionetwork, which comprises lumps comprising microorganisms and other particles and which promotes the purification.

50 [0018] Particularly good waste water treatment results are achieved when biological water purification utilizes a bacterial mixed population comprising the bacteria *Bacillus* sp. DT-1, *Pseudomonas azelaica* DT-2 and *Rhizobium* sp. DT-5. In addition to these three strains, the bacterial mixed population may further comprise other microorganism strains that are useful in water treatment and that have a favourable combined effect on the purification capacity.

55 [0019] The best purification results are achieved when the microorganism strains DT-1, DT-2, and/or DT-5 are used together with one or more bacterial strains from the group *Pseudomonas azelaica* DT-6 having the deposit number DSM 13516, *Azospirillum* sp. DT-10 having the deposit number DSM 13517, *Ancylobacter aquaticus* DT-12 having the deposit number DSM 13518, and *Xanthobacter* sp. DT-13 having the deposit number DSM 13519. Said four strains were isolated from the biofilm of the last unit of a four cascade bioreactor for treating water containing a mixture of

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soaps. They can be grown in the same growth medium and under the same conditions as DT-1, DT-2 and DT-5. DT-6, DT-10, DT-12 and DT-13 improve the immobilization properties of the biofilm to supporting matrices when they are mixed with strains DT-1, DT-2 and DT-5. Association of the strains also improves the treatment process of waste water as a result of more tolerance of the biofilm formed against poisonous substances.

[0020] *Bacillus* sp. DT-1 is a rod which is about 1.0 - 1.2 μm in width and 3.0 - 6.0 μm in length. Partial sequencing of the 16S rDNA shows a similarity of 99.3% to *B. cereus* and 100% to *B. thuringiensis*. In identification tests DT-1 reacted as indicated below:

Anaerobic growth	+
VP reaction	+
pH in VP broth	4.8
Growth in medium pH 5.7	+
2% NaCl	+
5%	+
7%	-
10%	-
Lysozyme broth	+
Acid from	
L-arabinose	-
D-xylose	-
D-mannitol	-
D-fructose	+
Lecithinase	+
Hydrolysis of:	
casein	+
Tween 80	weak
aesculin	+
Use of propionate	-
Indol reaction	-
Phenylalanine deaminase	+
Hemolysis	+
Growth in penicillin 900U/ml	+

[0021] *Pseudomonas azelaica* DT-2 is a rod which is 0.5 - 0.7 μm in width and 1.5 - 3.0 μm in length with 1 - 3 polar flagella and lacking fluorescent pigments. The partial sequencing of the 16S rDNA is 99.8% similar to *Ps. azelaica*. It reacts as follows:

Lysis by 3% KOH	+
Amino peptidase (Cerny)	+
Lecithinase	-
Utilization of arabinose	-
adipat	+
mannitol	-
gluconat	+
caprat	+

[0022] *Rhizobium* sp. DT-5 is a rod which is 0.5 - 0.7 μm in width and 1.5 - 3.0 μm in length. Partial 16S rDNA sequencing shows a 98.6% similarity to *R. giardinii* and 98.6% similarity to *Phyllobacterium myrsinacearum*. Physiological test results are given below. They do not confirm any of these genera.

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Lysis by 3% KOH	+
Aminopeptidase (Cerny)	+
Anaerobic growth	-
Simmons citrate	+
Utilization of arabinose	+
mannose	+
mannitol	+
adipat	-

[0023] Other morphological, physiological and biochemical characteristics of bacterial strains DT-1, DT-2 and DT-5 are shown in Table 1.

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Table 1. Morphological, physiological and biochemical characteristics of the bacterial strains.

Characteristic	Strain reaction		
	DT-1	DT-2	DT-5
Cell morphology	Straight or slightly curved rod	Straight rod	Rod
Motility	+	+	+
Formation of endospores	+	-	-
Spore form	E	-	-
Spore position	T	-	-
Expanded sporangium	-	-	-
Gram's stain	P	N	N
Catalase	+	+	+
Oxidase	+	+	+
Reduction of nitrate to nitrite	+	+	-
Denitrification	-	+	-
Argininedihydrolase	+	+	-
Hydrolysis:			
- starch	+	-	-
- gelatin	+	-	-
- acetamide	-	-	+
Urease	-	-	+
Splitting up aromatic ring	-	Orto	-

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	Growth at temperature of:			
5	35°C	+	+	+
	39°C	+	+	-
	40°C	+	-	-
	41°C	+	-	-
10	43°C	-	-	-
	Utilization of:			
	Acetate	+	+	+
15	D-Alanine	-	+	-
	L-Alanine	-	+	+
	β-Alanine	-	+	-
20	L-Arginine	+	+	+
	L-Asparagine	±	+	±
	L-Aspartate	±	+	-
	Citrate	+	+	-
25	L-Cystein	-	-	+
	L-Cystin	-	-	-
	Ethanol	-	+	-
30	D-glucose	+	+	+
	Glutamate	+	+	±
	Glycerol	+	-	-
	Glycine	-	-	-
35	L-Histidine	-	+	+
	p-Hydroxybenzoate	-	+	-
	meso-inositol	-	-	+
40	Lactose	-	-	-
	L-Leucine	±	+	+
	L-Lysine	±	+	-
45	Malat	+	+	-
	Malonate	+	-	-
	Methanol	-	-	-
50	L-Methionine	-	-	-
	L-Proline	-	+	+
	DL-Serine	+	-	-
55	Succinate	+	+	+

Saccharose	±	-	+
DL-Threonine	-	-	-
D-Trehalose	+	-	+
DL-Tryptophan	±	-	-
L-Tyrosine	-	+	±

P = positive

N = negative

E = of elliptical shape

T = terminal

[0024] Furthermore, the profiles of the fatty acids of bacterial strains DT-1, DT-2 and DT-5 were determined and they are shown in Figures 2 to 4. The bacteria were grown 24 hours at 28°C on tryptic soy broth agar and methyl esters were prepared for the fatty acid analysis of the whole cell, as described in publication Structure and composition of biological slimes on paper and board machines. Appl. Environ. Microbiol. 60:641-653 by Väisänen, O.M., E-L. Nurmi-aho-Lassila, S.A. Marmo and M.S. Salkinoja-Salonen (1994). An aerobic TSBA library, version 3.9 (MIDI Inc., Newark, DE, USA), was used. The retention time (in minutes) is shown on the x-axis of Figures 2a and 3a, and the intensity of a peak is shown on the y-axis of the same figures. The corresponding prints of the fatty acid analyses are shown in Figures 2b, 3b and 4. The profile of the fatty acids of DT-1 is typical of the *B. cereus* group. The profile of DT-2 is typical of the RNA group I of the pseudomonads, and the profile of DT-5 points to the *Rhizobium* group.

[0025] *Pseudomonas azelaica* DT-6 is a 0.5 - 0.7 µm wide and 1.5 - 3.0 µm long gram-negative motile rod having 1 - 3 polar flagella and lacking fluorescent pigments. Its fatty acid analysis print (Figure 5) is typical of the RNA group I of the pseudomonads. The partial sequencing of the 16S rDNA shows a 99.8% similarity to *Ps. azelaica*. DT-6 has the following physiological reactions:

Lysis by 3% KOH	+
Aminopeptidase (Cerny)	+
Oxidase	+
Catalase	+
ADH	+
NO ₂ from NO ₃	+
Denitrification	weak
Urease	-
Hydrolysis of gelatin	-
Lecithinase	-
Utilization of (API 20NE)	
glucose	+
arabinose	-
adipat	+
malat	+
mannitol	-
gluconat	+
caprat	+

[0026] *Azospirillum* sp. DT-10 is a 0.8 - 1.2 µm wide and 2.0 - 4.0 µm long gram-negative rod. Its fatty acid analysis print (Figure 6) is typical of the α-subgroup of the proteobacteria and points to the genus *Azospirillum*. The partial

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sequencing of the 16S rDNA shows similarities between 92% and 97.4% to different members of the genus *Azospirillum*. The highest similarity 97.4% was found to *Azospirillum lipoferum*. The physiological reactions of DT-10 are shown below. They point to the genus *Azospirillum* but are not typical of *A. lipoferum*. DT-10 is possibly a new species of this genus.

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Lysis by 3% KOH	weak
Aminopeptidase (Cerny)	+
Oxidase	+
Catalase	+
NO ₂ from NO ₃	+
Urease	+
ADH	-
Hydrolysis of gelatin	-
esculin	-
Utilization of (sole carbon source) glucose	-
arabinose	-
adipat	-
malat	+
mannitol	-
phelyacetat	-
citrate	-
caprat	-
gluconat	-
maltose	-
n-acetylglucosamin	-
α-ketoglutarate	+
sucrose	-
m-inositol	-
D-fructose	+
rhamnose	-
arabitol	-
ribose	-
Growth at 41 °C	-
with 3% NaCl	-

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[0027] *Ancylobacter aquaticus* DT-12 is a gram-negative curved rod which is 0.5 - 0.7 μm in width and 1.5 - 2.0 μm in length. The partial sequence of the 16S rDNA shows a similarity of 98.8% to *Ancylobacter aquaticus*. *Thiobacillus novellus* shows a similarity of 97.8%. The fatty acids (Figure 7) point to the α-proteobacteria. The physiological tests as shown below clearly identify the species *Ancylobacter aquaticus*.

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Lysis by 3% KOH	weak
Aminopeptidase (Cerny)	+
Oxidase	+
Catalase	+
ADH	-
Urease	-
Hydrolysis of gelatin	-

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(continued)

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esculin	+
NO ₂ from NO ₃	-
Denitrification (24 h)	-
Utilization of glucose	+ (weak)
citrate	+
arabinose	+
mannose	-
mannitol	+
maltose	-
N-acetylglucosmin	-
gluconat	-
malat	+
phenylacetat	-
methanol	+
formiate	weak

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[0028] *Xanthobacter* sp. DT-13 is an irregular, motile, gram-negative rod which is 0.8 - 1.0 µm in width and 1.5 - 3.0 µm in length. The partial sequences of the 16S rDNA show similarities of 98.5% to 99.3% to different members of the genus *Xanthobacter*. *X. falvus* shows the highest similarity (99.3%). The profile of the fatty acids is typical of the subclass of α-proteobacteria. The physiological tests are not able to distinguish reliably between the species of this genus (i.e. no pigment production detected, no slime production, etc.). The physiological data are given below:

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Lysis by 3% KOH	+
Aminopeptidase (Cerny)	+
Oxidase	+
Catalase	+
ADH	-
Urease (24 h)	-
Hydrolysis of gelatin	-
esculine	-
NO ₃ utilization	-
Utilization of phenylacetate	-
citrate	-
malate	+
arabinose	-
mannose	-
mannit	-
caprat	-
maltose	-
adipate	+
malonate	+
methanol	-
m-inosit	-
m-tartrate	+
D-gluconate	+
phelylalanine	-

[0029] The above-described bacteria are suited for use in purifying waste water. The bacteria can then be first grown

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in a minimal salt medium (KSN) in a shaker. Soy pepton (0.5 g/l), trypton (0.1 g/l), glucose (0.2 g/l) and potassium acetate (0.3 g/l) may be added, if desired. The growing temperature of the bacteria is about 20 - 30°C. After this, the volume of the culture is then increased in order to produce the necessary biomass for purifying the water. This stage no longer needs to be conducted under sterile conditions, in which case tap water wherein about 0.5 - 4 g/l of soap has been added can be used as the growth medium. The soap used is preferably a mixture containing anionic, cationic, amphoteric and non-ionic tensides. It is preferable to use a mixture of different soaps, such as cleaning agents, fabric conditioners and detergents for clothes and dishes. The bacteria are grown as a submerged culture with air pumped thereto. The biomass can be produced as a batch culture, but preferably, it is produced as a continuous culture, or chemostat culture. It is preferable to use a carrier in the production of the biomass. Any common carrier, for example a plastic one, is suitable for this purpose. The produced biomass is then transferred into a water treatment reactor, into which the water to be purified is conveyed. A carrier for the bacteria is also used in the reactor, the carrier preferably being the same as used in the production of the biomass. The carrier is preferably one having a specific density lower than 1 g/cm³. The carrier is generally held in place in a tank by means of a net ('fixed carrier'), for example, but sometimes the carrier is allowed to float freely in the tank ('swimming carrier').

[0030] The method of the invention is suited particularly to purifying seep water of a dump, which is here described in closer detail with reference to Figure 1. A dump is usually surrounded by a ditch to collect the seep water. Seep water refers to water seeping from a dump due to rain and ground water. This seep water containing both surface water and cavity water is usually first conveyed to a tank wherefrom the water is conveyed through a purification process before being discharged into the environment. The seep water obtained both from deep and shallow ground is preferably first conveyed to a settlement basin, from which the water is filtered through an inlet pipe 1 to a filtrate well 2, and from there, through a transfer pipe 8 to a bioreactor 3 containing said bacteria and a carrier 5. The bacteria form a so-called biofilm around the carrier. The carrier with its bacteria is usually kept below the surface of the water by means of a net. The bioreactor preferably comprises one or more separating walls 6 arranged to force the water to circulate in the reactor. The separating walls may be arranged on opposite walls, for example, as shown in Figure 1. The reactor usually further comprises an aerator 9 for conveying air into the reactor through an aeration pipe 4. The bioreactor further comprises an outlet pipe 7, through which processed water is discharged from the reactor.

[0031] In addition to purifying seep water, the present invention is extremely well suited also to purifying household and industrial grey water. Grey water refers to waste water other than that originating from lavatories, e.g. water from showers, handbasins, bath tubs and laundry rooms. The purification method of the invention is also suited to purifying waste water from lavatories, which is called black water. The method of the invention can also be used to purify laundry and industrial waste water, which often contains a large amount of organic waste, such as oil, polycyclic aromatic hydrocarbons (PAH compounds) and/or heavy metals. The method is also suitable for purifying waste water originating from food industry and water in swimming pools.

Example 1

Production of biomass and start of a bioreactor

[0032] *Bacillus* sp. DT-1, *Pseudomonas azelaica* DT-2 and *Rhizobium* sp. DT-5 were each transferred to 200 ml of sterilized minimum salt medium (KSN) of the following composition (g/l of distilled water): K₂HPO₄×3H₂O - 1.0, NaH₂PO₄×2H₂O - 0.25, (NH₄)₂SO₄ - 0.1, MgSO₄×7H₂O - 0.04, Ca(NO₃)₂×4H₂O - 0.01, yeast extract - 0.05, pH 7.0 - 7.3, and soap mixture about 1 g/l. The soap mixture contained about equal amounts of the following detergents: laundry soap, Comfort, Cleani Family -fabric conditioner, Cleani Color, Serto Ultra, Bio Luvil, Ariel Futur, Omo Color, Tend Color, Tend Mega, Tend Total and Eko Kompakt (about 1g/l in total). The bacteria were grown in a shaker (150 - 200 rpm), at 28°C.

[0033] When the growth was dense, all three cultures were brought to one 500-litre fermenter in order to produce the necessary biomass. The fermenter contained unsterilized tap water and a total of 4 g/l of the aforementioned soap mixture, and a plastic carrier containing polyethene and having a specific density of about 0.8 g/cm³. The carrier was kept below the surface of the liquid by means of a net. The cultivation now continued under non-sterile conditions to a turbidity of about 2 (600 nm), and then as a chemostat culture. A first inoculum obtained from the fermenter was then introduced into a bioreactor (6 m³) according to Figure 1, diluted 1:10. The bioreactor contained seep water from a municipal dump which was first collected into a tank, wherefrom it was then transferred to a settlement basin for removal of solid matter and next, to a filtrate well, wherefrom it was pumped to the bioreactor. In principle, the system works by gravity, the only necessary pump being a submersible pump in the filtrate well. The bioreactor contained the same carrier as the fermenter used for producing the biomass. The carrier was kept below the liquid level by means of a net. The bacteria flocculated at the end of the bioreactor. The purification process was continuous, operating at a capacity of about 100 m³/24 hours. Air was pumped so as to keep the oxygen content of the water to be processed > 7 mg/l.

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Example 2

Purification of seep water

[0034] A bioreactor arranged according to Example 1 was used for purification of seep water from a municipal dump. The average COD of the waste water to be purified was about 800 mg - 6 g O₂/l. The waste water contained chlorophenoles, PAH compounds and oil, for example. The removal of these substances from the waste water was monitored. According to Nordtest's technical report no. 329 (accepted 9603), the compounds were defined by a gas chromatograph equipped with a mass-selective detector. The results are shown in Table 2.

Table 2

Detection	Before bioreactor	After bioreactor
COD	0.8 - 6 g/l	100 - 200 mg/l
chlorophenoles	> 1 mg/l	< 1 µg/l
PAH	1 mg/l	< 1 µg/l
oil	0.2 - 1 mg/l	200 µg/l

Example 3

Purification of municipal waste water (full scale)

[0035] Waste water from a municipal waste water plant was purified both in a manner conventionally used in the plant and by the method of the invention. Conventionally, waste water was purified by first conveying the waste water into a preliminary settlement basin in order to precipitate the solids onto the bottom. The preliminary settled water was then conveyed to an aerobic treatment basin, where ferrous sulphate for precipitating phosphate, and polyamine for precipitating biosludge were added. Herefrom, the water was further conveyed to a secondary settlement basin. The purification system of the invention comprised five tanks whose total volume was 7.5 m³, the tanks being interconnected in the following order: two anaerobic tanks, where bacteria DT-1, DT-2 and DT-5 were added without a carrier, one aerobic tank where a carrier was attached (by means of a net) on which the bacteria DT-1, DT-2 and DT-5 were immobilized, and two sedimentation tanks. The temperature was 8 - 15°C. The flow rate was 7.5 m³/24 hours of waste water. The aeration was conducted by recycling the water through the carrier. The results are shown in Table 3.

Table 3

Parameter	Before treatment	After conventional purification	After purification of the invention
BOD7 mg O ₂ /l	200 - 300	10 - 15	10 - 15
COD _{Cr} mg O ₂ /l	250 - 500	60 - 75	40 - 50
Total nitrogen mg N/l	35 - 55	15 - 25	15 - 25
Total phosphor mg P/l	5 - 10	0.6 - 1.8	0.5 - 1.8
Fec. streptococci cfu/100 ml	10 ⁸	2 x 10 ⁴ - 3 x 10 ⁴	2 x 10 ⁴ - 3 x 10 ⁴
Thermo-tolerant coliforms cfu/100 ml	3 x 10 ⁸	2 x 10 ⁴ - 4 x 10 ⁴	2 x 10 ⁴ - 4 x 10 ⁴

[0036] The purification results achieved by the method of the invention were either as good as or better than those achieved by the conventional method, and energy consumption was significantly lower. The energy consumption in treating one cubic metre of water was 0.23 kWh at the municipal waste water treatment plant, and 0.05 - 0.1 kWh when the method of the invention was used.

Example 4

Purification of household black water (full scale)

[0037] The system comprised five tanks whose total volume was 6.5 m³, the tanks being interconnected in the following order: two anaerobic tanks without a carrier into which the DT-1, DT-2 and DT-5 were added, one aerobic tank where a carrier was attached on which the bacteria DT-1, DT-2 and DT-5 were immobilized, and two sedimentation

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tanks. The temperature was 8 - 15°C. The flow rate was 0.5 - 5 m³ of waste water per 24 hours. The aeration was conducted by recycling the water through the carrier. The energy consumption was 0.05 - 0.5 kWh. The results are shown in Table 4.

Table 4

Parameter	Before treatment	After treatment
BOD ₇ mg O ₂ /l	400 - 5500	3 - 20
COD _{cr} mg O ₂ /l	400 - 6000	40 - 70
Total nitrogen mg N/l	100 - 300	1 - 5
Total phosphorus mg P/l	10 - 25	0.2 - 2
Fec. streptococci cfu/100 ml	10 ⁸ - 10 ⁹	< 20
Thermo-tolerant coliforms cfu/100 ml	10 ⁸ - 10 ⁹	< 20
pH	7 - 8	6.5-7

Example 5

Purification of industrial waste water containing soap and heavy metals (laboratory scale)

[0038] Waste water from a coating metal industry plant was purified by a system whose effective treatment part comprised six anaerobic and twelve aerobic tanks. The bacteria DT-1, DT-2 and DT-5, which were immobilized on a carrier attached by nets, were added to all anaerobic and aerobic tanks. Each tank held 2 l. The entire system comprised 23 tanks whose total volume was 70 l, the tanks being interconnected in the following order: six anaerobic tanks (effective treatment volume), one sedimentation tank, six aerobic tanks (effective treatment volume), one sedimentation tank, six aerobic tanks (effective treatment volume), and two tanks for calcium chloride and sodium hydroxide treatments to precipitate the biomass and heavy metals. Before the treatment, the original waste water was diluted five times by gray water. After the dilution, mineral salts were added as follows: NH₄⁺ 2 - 10 mg/l, NO₃⁻ 5 - 20 mg/l, Mg²⁺ 2 - 10 mg/l, Ca²⁺ 0.5 - 2 mg/l, SO₄²⁻ 1 - 10 mg/l and PO₄³⁻ 2 - 20. mg/l. The temperature was 20 - 35°C and the flow rate 12 l of water per 24 hours. The results are shown in Table 5.

Table 5

Parameter	Before treatment	After treatment
COD _{Cr} mg O ₂ /l	19 000 - 21 000	100 - 400
Total phosphorus mg P/l	19 - 25	0.3 - 0.7
Aluminium	5 - 6	0.01 - 0.02
Chrome	1.3 - 1.5	0.01 - 0.02
Copper	35 - 40	0.03 - 0.1
Iron	1 - 2	0.02 - 0.07
Lead	23 - 25	0.02 - 0.09
Nickel	2 - 3	0.05 - 0.09
Zinc	30 - 60	0.003 - 0.007
pH	8-9	7 - 7.5

Example 6

Purification of household grey water for recycling (pilot scale)

[0039] The effective part of the system comprised three aerobic tanks whose single volume was 0.2 m³. The entire system comprised six tanks whose total volume was 2.8 m³, the tanks being interconnected in the following order: one tank for collecting grey water, three aerobic tanks comprising a fixed carrier on which the bacteria DT-1, DT-2 and DT-5 were immobilized (effective treatment volume), one aerobic tank without a carrier and one sedimentation tank, and, subsequently, a filtering system and a UV-light treatment system. The temperature was 20 - 35°C. The flow rate was about 1 m³ per 24 hours. The results are shown in Table 6.

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Table 6

Parameter	Before treatment	After treatment
COD _{Cr} mg O ₂ /l	150-400	15 - 35
Total nitrogen mg N/l	10-15	< 0.5
Total phosphorus mg P/l	5 -10	< 0.1
Coliforms cfu/100 ml	1.4 - 2 x 10 ⁶	0
pH	7.5-8.5	6.5-7

Example 7

Purification of grey water of a laundry for recycling (pilot scale)

[0040] The effective treatment part of the system comprised two aerobic tanks having the volume of 1 m³, the tanks comprising a swimming carrier on which DT-1, DT-2 and DT-5 were immobilized. The entire system comprised ten tanks whose total volume was 23 m³, the tanks being interconnected in the following order: one tank for collecting grey water, two aerobic tanks comprising a swimming carrier (effective treatment volume), one sedimentation tank, three aerobic tanks comprising a fixed carrier with its bacteria (effective treatment volume), one aerobic tank without a carrier, and two sedimentation tanks. The temperature of the water was 20 - 35°C, the flow rate 1 m³ of waste water per 24 hours. The results are shown in Table 7.

Table 7

Parameter	Before treatment	After treatment
COD _{cr} mg O ₂ /l	200 - 450	25 - 35
Total phosphorus mg P/l	1 - 2	< 0.1
pH	8.5-9	7-8

Example 8

Increase of immobilized biomass

[0041] Biomass of strains DT-1, DT-2, DT-5, DT-6, DT-10, DT-12 and DT-13 was produced and immobilized on a carrier as set forth in Example 1, and the amount of biomass on the carrier was weighed. The weight of one disc of the carrier was 72 ± 1 g. When DT-1, DT-2 and DT-5 were immobilized on the carrier, the weight of one disc of the carrier was 119 ± 13, i.e. the wet weight of the biomass was 47 ± 11 g per disc. When all seven bacterial strains were immobilized on the carrier, the weight of one disc of carrier was 172 ± 16, i.e. the wet weight of the biomass was 91 ± 16. The results show that DT-6, DT-10, DT-12 and DT-13 increased the immobilized biomass about twofold.

Claims

1. A method of purifying waste water, **characterized in that** the water is biologically purified by a mixed population comprising the microorganisms *Bacillus* sp. DT-1 having the deposit number DSM 12560, *Pseudomonas azelaica* DT-2 having the deposit number DSM 12561, and *Rhizobium* sp. DT-5 having the deposit number DSM 12562.
2. A method as claimed in claim 1, **characterized by** purifying seep water, grey water, black water, industrial waste water and waste water from laundries.
3. A method as claimed in claim 1 or 2, **characterized in that** necessary biomass for the purification is produced in a non-sterilized growth medium comprising tap water and about 0.5 - 4 g/l of soap.
4. A method as claimed in claim 1, **characterized in that** the water is also purified by one or more microorganisms from the group *Pseudomonas azelaica* DT-6 having the deposit number DSM 13516, *Azospirillum* sp. DT-10 having the deposit number DSM 13517, *Ancylobacter aquaticus* DT-12 having the deposit number DSM 13518, and *Xanthobacter* sp. DT-13 having the deposit number DSM 13519.

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5. *Bacillus* sp. DT-1 having the deposit number DSM 12560.
6. *Pseudomonas azelaica* DT-2 having the deposit number DSM 12561.
- 5 7. *Rhizobium* sp. DT-5 having the deposit number DSM 12562.
8. *Pseudomonas azelaica* DT-6 having the deposit number DSM 13516.
9. *Azospirillum* sp. DT-10 having the deposit number DSM 13517.
- 10 10. *Ancylobacter aquaticus* DT-12 having the deposit number DSM 13518.
11. *Xanthobacter* sp. DT-13 having the deposit number DSM 13519.
- 15 12. A bacterial mixed population, **characterized by** comprising *Bacillus* sp. DT-1 having the deposit number DSM 12560, *Pseudomonas azelaica* DT-2 having the deposit number DSM 12561, and/or *Rhizobium* sp. DT-5 having the deposit number DSM 12562.
- 20 13. A bacterial mixed population as claimed in claim 12, **characterized by** further comprising *Pseudomonas azelaica* DT-6 having the deposit number DSM 13516, *Azospirillum* sp. DT-10 having the deposit number DSM 13517, *Ancylobacter aquaticus* DT-12 having the deposit number DSM 13518, and/or *Xanthobacter* sp. DT-13 having the deposit number DSM 13519.
- 25 14. Use of a bacterial mixed population as claimed in claim 1 or 4 in purifying waste water.
- 15 15. A bioreactor, **characterized by** comprising the microorganisms *Bacillus* sp. DT-1 having the deposit number DSM 12560, *Pseudomonas azelaica* DT-2 having the deposit number DSM 12561, and *Rhizobium* sp. DT-5 having the deposit number DSM 12562.
- 30 16. A bioreactor as claimed in claim 15, **characterized by** further comprising one or more microorganisms from the group *Pseudomonas azelaica* DT-6 having the deposit number DSM 13516, *Azospirillum* sp. DT-10 having the deposit number DSM 13517, *Ancylobacter aquaticus* DT-12 having the deposit number DSM 13518, and *Xanthobacter* sp. DT-13 having the deposit number DSM 13519.
- 35 17. A bioreactor as claimed in claim 16, **characterized by** comprising all said seven bacterial strains.
18. A bioreactor as claimed in claim 15, **characterized by** comprising one or more separating walls arranged so as to force water to circulate in the reactor.
- 40 19. A bioreactor as claimed in claim 18, **characterized in that** the bacteria are immobilized on a plastic carrier medium whose specific density is about 0.8 g/cm³,

Patentansprüche

- 45 1. Verfahren zur Reinigung von Abwasser, **dadurch gekennzeichnet, dass** das Wasser durch eine gemischte Population biologisch gereinigt wird, welche die Mikroorganismen *Bacillus* sp. DT-1 mit der Hinterlegungsnummer DSM 12560, *Pseudomonas azelaica* DT-2 mit der Hinterlegungsnummer DSM 12561 und *Rhizobium* sp. DT-5 mit der Hinterlegungsnummer DSM 12562 umfasst.
- 50 2. Verfahren nach Anspruch 1, **dadurch gekennzeichnet, dass** Sickerwasser, trübes Wasser, schmutziges Wasser, industrielles Abwasser und Abwasser von Wäschereien gereinigt wird.
3. Verfahren nach Anspruch 1 oder 2, **dadurch gekennzeichnet, dass** die notwendige Biomasse für die Reinigung in einem nicht sterilisierten Wachstumsmedium hergestellt wird, das Leitungswasser und etwa 0,5-4 g/l Seife umfasst.
- 55 4. Verfahren nach Anspruch 1, **dadurch gekennzeichnet, dass** das Wasser ebenso durch ein oder mehrere Mikro-

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organismen aus der Gruppe *Pseudomonas azelaica* DT-6 mit der Hinterlegungsnummer DSM 13516, *Azospirillum* sp. DT-10 mit der Hinterlegungsnummer DSM 13517, *Ancylobacter aquaticus* DT-12 mit der Hinterlegungsnummer DSM 13518 und *Xanthobacter* sp. DT-13 mit der Hinterlegungsnummer DSM 13519 gereinigt wird.

- 5 5. *Bacillus* sp. DT-1 mit der Hinterlegungsnummer DSM 12560.
6. *Pseudomonas azelaica* DT-2 mit der Hinterlegungsnummer DSM 12561.
7. *Rhizobium* sp. DT-5 mit der Hinterlegungsnummer DSM 12562.
- 10 8. *Pseudomonas azelaica* DT-6 mit der Hinterlegungsnummer DSM 13516.
9. *Azospirillum* sp. DT-10 mit der Hinterlegungsnummer DSM 13517.
- 15 10. *Ancylobacter aquaticus* DT-12 mit der Hinterlegungsnummer DSM 13518.
11. *Xanthobacter* sp. DT-13 mit der Hinterlegungsnummer DSM 13519.
- 20 12. Bakterielle gemischte Population, **dadurch gekennzeichnet, dass** sie *Bacillus* sp. DT-1 mit der Hinterlegungsnummer DSM 12560, *Pseudomonas azelaica* DT-2 mit der Hinterlegungsnummer DSM 12561 und/oder *Rhizobium* sp. DT-5 mit der Hinterlegungsnummer DSM 12562 umfasst.
- 25 13. Bakterielle gemischte Population wie beansprucht in Anspruch 12, **dadurch gekennzeichnet, dass** sie weiterhin *Pseudomonas azelaica* DT-6 mit der Hinterlegungsnummer DSM 13516, *Azospirillum* sp. DT-10 mit der Hinterlegungsnummer DSM 13517, *Ancylobacter aquaticus* DT-12 mit der Hinterlegungsnummer DSM 13518 und/oder *Xanthobacter* sp. DT-13 mit der Hinterlegungsnummer DSM 13519 umfasst.
- 30 14. Verwendung einer bakteriellen gemischten Population wie in Anspruch 1 oder 4 beansprucht zur Reinigung von Abwasser.
- 35 15. Bioreaktor, **dadurch gekennzeichnet, dass** er die Mikroorganismen *Bacillus* sp. DT-1 mit der Hinterlegungsnummer DSM 12560, *Pseudomonas azelaica* DT-2 mit der Hinterlegungsnummer DSM 12561 und *Rhizobium* sp. DT-5 mit der Hinterlegungsnummer DSM 12562 umfasst.
- 40 16. Bioreaktor nach Anspruch 15, **dadurch gekennzeichnet, dass** er weiterhin ein oder mehrere Mikroorganismen aus der Gruppe *Pseudomonas azelaica* DT-6 mit der Hinterlegungsnummer DSM 13516, *Azospirillum* sp. DT-10 mit der Hinterlegungsnummer DSM 13517, *Ancylobacter aquaticus* DT-12 mit der Hinterlegungsnummer DSM 13518 und *Xanthobacter* sp. DT-13 mit der Hinterlegungsnummer DSM 13519 umfasst.
- 45 17. Bioreaktor nach Anspruch 16, **dadurch gekennzeichnet, dass** er alle genannten sieben bakteriellen Stämme umfasst.
18. Bioreaktor nach Anspruch 15, **dadurch gekennzeichnet, dass** er eine oder mehrere Trennwände umfasst, die so angeordnet sind, dass sie die Zirkulation von Wasser in dem Reaktor erzwingen.
- 50 19. Bioreaktor nach Anspruch 18, **dadurch gekennzeichnet, dass** die Bakterien auf einem Plastikträgermedium immobilisiert sind, dessen spezifische Dichte etwa 0,8 g/cm³ beträgt.

50 Revendications

- 55 1. Procédé de purification des eaux usées, **caractérisé en ce que** l'eau est biologiquement purifiée par une population mixte comprenant les microorganismes *Bacillus* sp. DT-1 ayant le numéro de dépôt DSM 12560, *Pseudomonas azelaica* DT-2 ayant le numéro de dépôt DSM 12561, et *Rhizobium* sp. DT-5 ayant le numéro de dépôt DSM 12562.
2. Procédé selon la revendication 1, **caractérisé par** la purification des eaux d'infiltration, des eaux usées ménagères, des eaux usées sanitaires, des eaux usées industrielles et des eaux usées provenant des blanchisseries.

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3. Procédé selon la revendication 1 ou 2, **caractérisé en ce que** la biomasse nécessaire pour la purification est produite dans un milieu de croissance non stérilisé comprenant l'eau du robinet et environ de 0,5 à 4 g/l de savon.
- 5 4. Procédé selon la revendication 1, **caractérisé en ce que** l'eau est également purifiée par un ou plusieurs microorganismes provenant du groupe *Pseudomonas azelaica* DT-6 ayant le numéro de dépôt DSM 13516, *Azospirillum* sp. DT-10 ayant le numéro de dépôt DSM 13517, *Ancylobacter aquaticus* DT-12 ayant le numéro de dépôt DSM 13518, et *Xanthobacter* sp. DT-13 ayant le numéro de dépôt DSM 13519.
- 10 5. *Bacillus* sp. DT-1 ayant le numéro de dépôt DSM 12560.
6. *Pseudomonas azelaica* DT-2 ayant le numéro de dépôt DSM 12561.
7. *Rhizobium* sp. DT-5 ayant le numéro de dépôt DSM 12562.
- 15 8. *Pseudomonas azelaica* DT-6 ayant le numéro de dépôt DSM 13516.
9. *Azospirillum* sp. DT- 10 ayant le numéro de dépôt DSM 13517.
- 20 10. *Ancylobacter aquaticus* DT-12 ayant le numéro de dépôt DSM 13518.
- 25 11. *Xanthobacter* sp. DT-13 ayant le numéro de dépôt DSM 13519.
12. Population bactérienne mixte, **caractérisée en ce qu'**elle comprend *Bacillus* sp. DT-1 ayant le numéro de dépôt DSM 12560, *Pseudomonas azelaica* DT-2 ayant le numéro de dépôt DSM 12561, et *Rhizobium* sp. DT-5 ayant le numéro de dépôt DSM 12562.
- 30 13. Population bactérienne mixte selon la revendication 12, **caractérisée en ce qu'**elle comprend en outre *Pseudomonas azelaica* DT-6 ayant le numéro de dépôt DSM 13516, *Azospirillum* sp. DT-10 ayant le numéro de dépôt DSM 13517, *Ancylobacter aquaticus* DT-12 ayant le numéro de dépôt DSM 13518, et *Xanthobacter* sp. DT- 13 ayant le numéro de dépôt DSM 13519.
- 35 14. Utilisation d'une population bactérienne mixte selon la revendication 1 ou 4, dans la purification des eaux usées.
15. Bioréacteur, **caractérisé en ce qu'**il comprend les microorganismes *Bacillus* sp. DT-1 ayant le numéro de dépôt DSM 12560, *Pseudomonas azelaica* DT-2 ayant le numéro de dépôt DSM 12561, et *Rhizobium* sp. DT-5 ayant le numéro de dépôt DSM 12562.
- 40 16. Bioréacteur selon la revendication 15, **caractérisé en ce qu'**il comprend en outre un ou plusieurs microorganismes parmi le groupe *Pseudomonas azelaica* DT-6 ayant le numéro de dépôt DSM 13516, *Azospirillum* sp. DT-10 ayant le numéro de dépôt DSM 13517, *Ancylobacter aquaticus* DT-12 ayant le numéro de dépôt DSM 13518, et *Xanthobacter* sp. DT-13 ayant le numéro de dépôt DSM 13519.
- 45 17. Bioréacteur selon la revendication 16, **caractérisé en ce qu'**il comprend toutes lesdites sept souches bactériennes.
18. Bioréacteur selon la revendication 15, **caractérisé en ce qu'**il comprend une ou plusieurs parois de séparation agencées de façon à forcer l'eau à circuler dans le réacteur.
- 50 19. Bioréacteur selon la revendication 18, **caractérisé en ce que** les bactéries sont immobilisées sur un milieu de support en plastique dont la densité spécifique est d'environ 0,8 g/cm³.

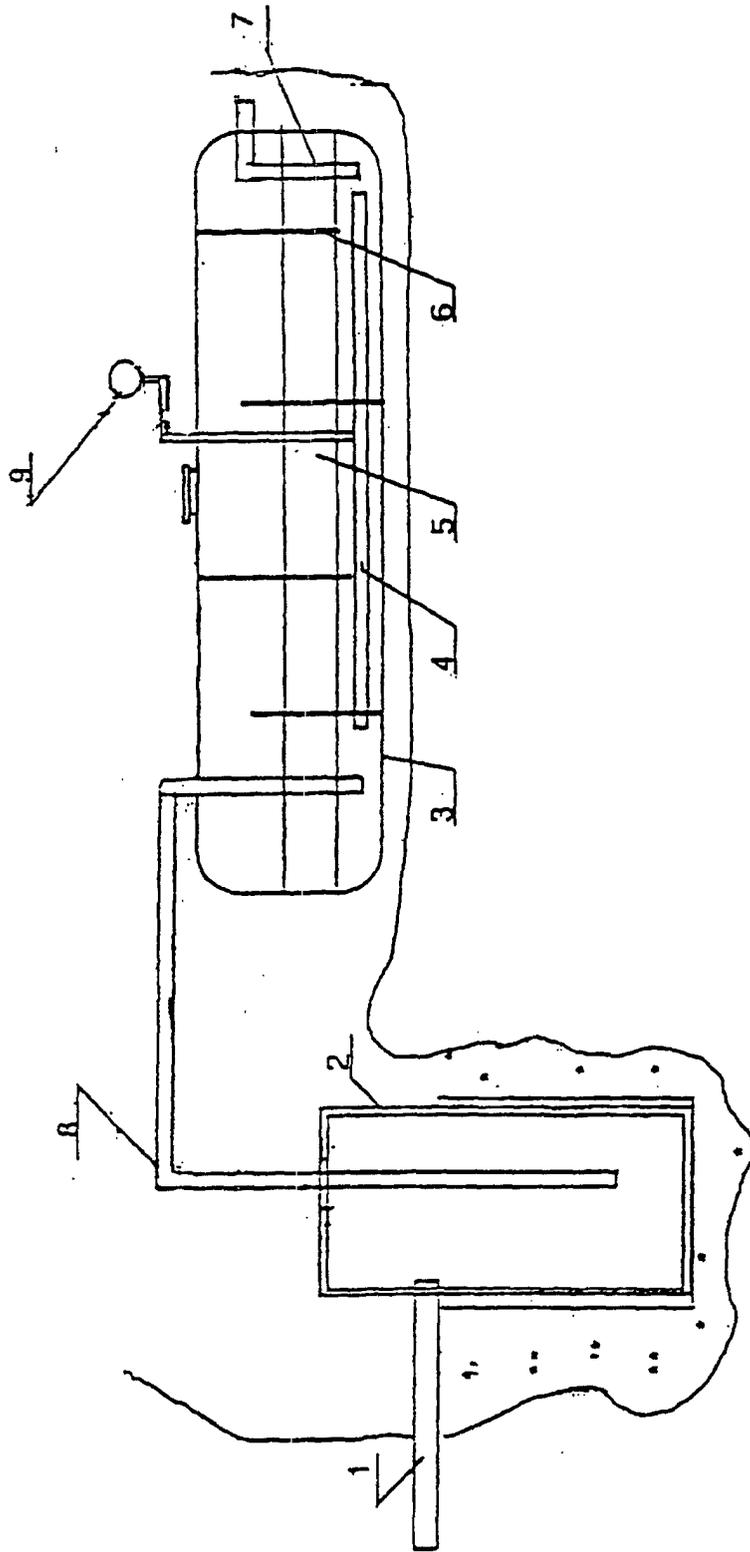


Fig. 1

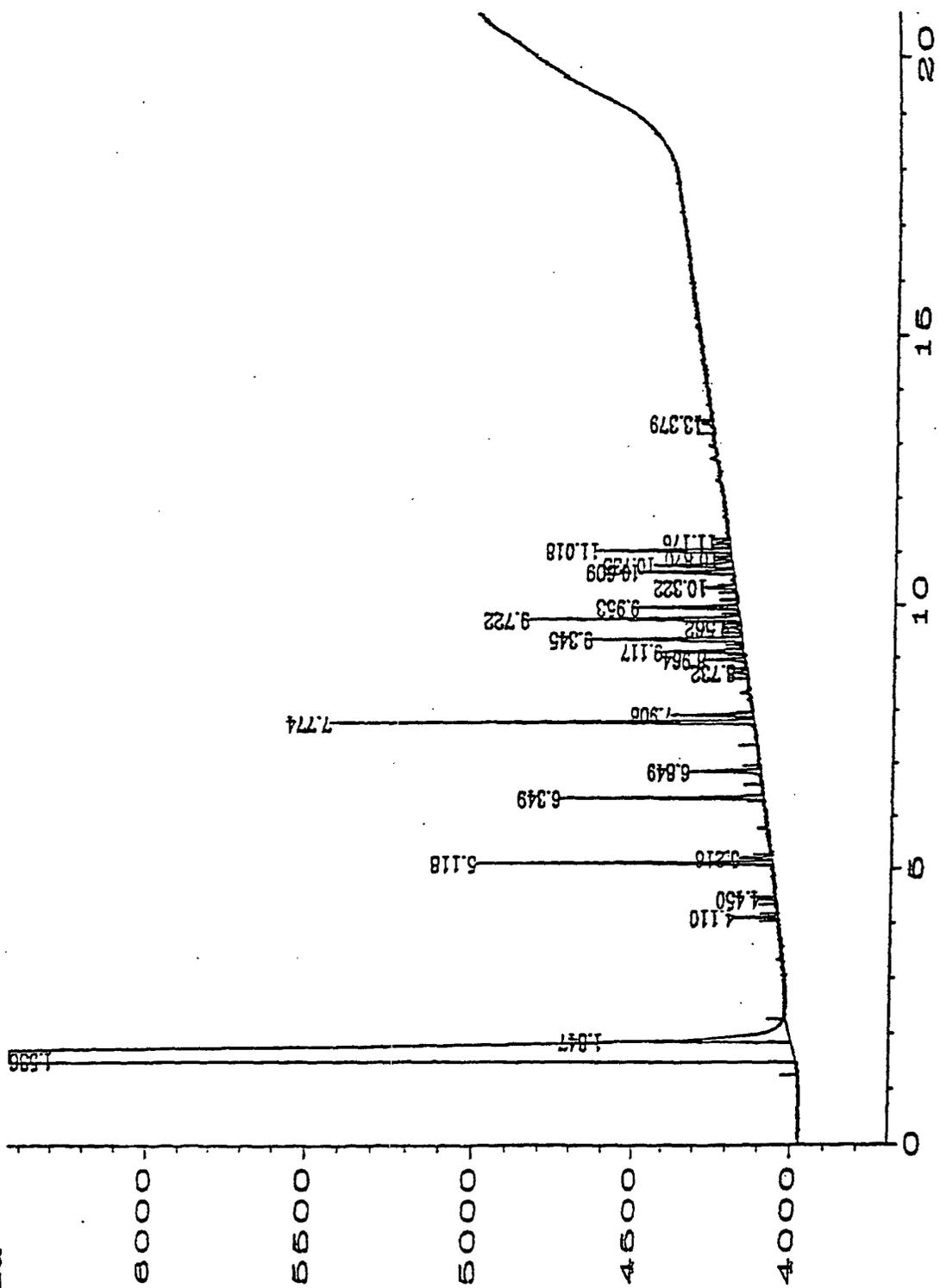


Fig. 2a

Fig. 2b

RT	Area	Ac/Ht	Respon	ECL	Name	W	Comment 1	Comment 2																
1.536	308581200	0.027		7.025	SOLVENT PEAK		< min rt																	
1.847	17778	0.083		7.607			< min rt																	
4.110	1440	0.028	1.084	11.607	12:0 ISO	1.65	ECL deviates -0.001	Reference 0.003																
4.450	606	0.031	1.069	12.000	12:0	0.69	ECL deviates -0.000	Reference 0.004																
5.118	10566	0.030	1.047	12.612	13:0 ISO	11.73	ECL deviates 0.000	Reference 0.003																
5.216	1182	0.033	1.044	12.702	13:0 ANTEISO	1.31	ECL deviates 0.001	Reference 0.004																
6.349	8064	0.033	1.014	13.618	14:0 ISO	8.68	ECL deviates -0.000	Reference 0.002																
6.849	3396	0.039	1.003	14.000	14:0	3.61	ECL deviates -0.000	Reference 0.002																
7.774	18384	0.037	0.986	14.622	15:0 ISO	19.23	ECL deviates 0.001	Reference 0.003																
7.908	3624	0.038	0.984	14.712	15:0 ANTEISO	3.78	ECL deviates 0.001	Reference 0.003																
8.732	684	0.042		15.245																				
8.964	1980	0.040	0.968	15.388	16:1 w/c alcohol	2.03	ECL deviates 0.002																	
9.117	3660	0.038	0.965	15.483	Sum In Feature 3	3.75	ECL deviates 0.001	16:1 ISO I/14:0 30																
9.345	8022	0.044	0.962	15.624	16:0 ISO	8.10	ECL deviates -0.002	Reference -0.001																
9.562	582	0.039	0.959	15.758	16:1 w/c	0.59	ECL deviates 0.001																	
9.722	10494	0.040	0.957	15.857	Sum In Feature 4	10.65	ECL deviates 0.010	15:0 ISO 20H/16:1W																
9.953	4800	0.040	0.954	15.999	16:0	4.86	ECL deviates -0.001	Reference 0.001																
10.322	1500	0.038	0.950	16.218	15:0 20H	1.51	ECL deviates 0.001																	
10.609	4914	0.041	0.946	16.387	ISO 17:1 w/c	4.93	ECL deviates 0.000																	
10.735	4188	0.043	0.945	16.462	ISO 17:1 w/c	4.20	ECL deviates 0.001																	
10.870	660	0.035	0.943	16.541	17:1 ANTEISO A	0.66	ECL deviates 0.000																	
11.018	6588	0.040	0.941	16.629	17:0 ISO	6.50	ECL deviates -0.000	Reference 0.002																
11.176	780	0.040	0.940	16.722	17:0 ANTEISO	0.70	ECL deviates 0.000	Reference 0.002																
13.379	624	0.044	0.918	18.001	18:0	0.61	ECL deviates 0.001	Reference 0.003																
*****	3660				SUMMED FEATURE 3	3.75	12:0 ALDE 7	unknown 10.928																
*****							16:1 ISO I/14:0 30H	14:0 30H/16:1 ISO																
*****	10494				SUMMED FEATURE 4	10.65	16:1 w/c/15 iso 20H	13:0 ISO 20H/16:1W																
<table border="1"> <thead> <tr> <th>Solvent Ac</th> <th>Total Area</th> <th>Named Area</th> <th>% Named</th> <th>Total Amt</th> <th>Nbr Ref</th> <th>ECL Deviation</th> <th>Ref ECL Shift</th> </tr> </thead> <tbody> <tr> <td>308581200</td> <td>96738</td> <td>96054</td> <td>99.29</td> <td>94302</td> <td>13</td> <td>0.002</td> <td>0.003</td> </tr> </tbody> </table>									Solvent Ac	Total Area	Named Area	% Named	Total Amt	Nbr Ref	ECL Deviation	Ref ECL Shift	308581200	96738	96054	99.29	94302	13	0.002	0.003
Solvent Ac	Total Area	Named Area	% Named	Total Amt	Nbr Ref	ECL Deviation	Ref ECL Shift																	
308581200	96738	96054	99.29	94302	13	0.002	0.003																	
<p>TSHA (Rev 3.90) Bacillus 0.265 (Bacillus cereus group)</p> <p>B. thuringiensis 0.265 (Bacillus cereus group)</p> <p>B. cereus 0.160</p> <p>CLIN (Rev 3.90) * NO MATCH *</p>																								

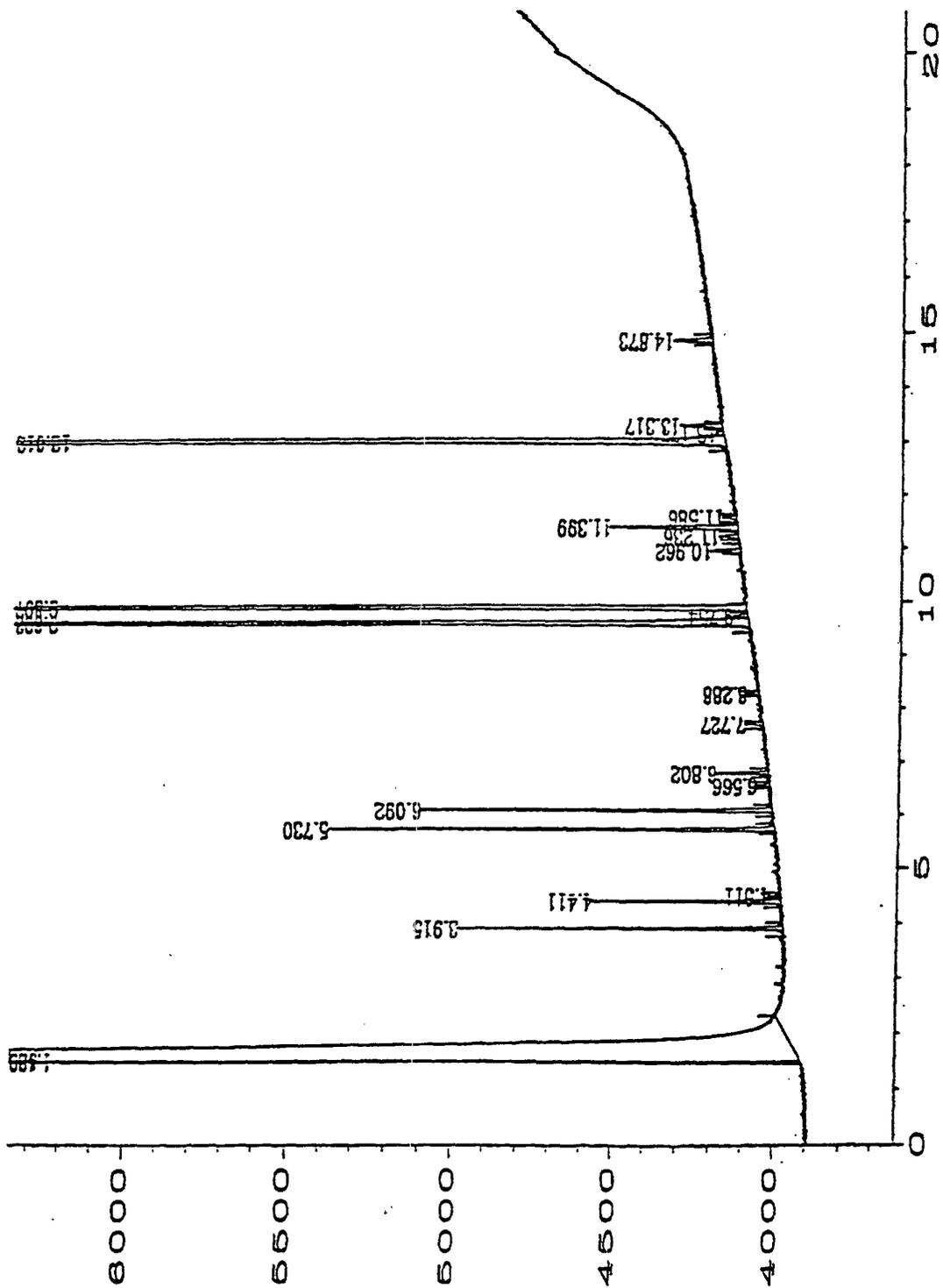


Fig. 3a

Fig. 3b

RT	Area	Ar/Ht	Respon	ECL	Name	W	Comment 1	Comment 2
1.489	150156	0.015		6.962			< min rt	
1.520	274442400	0.026		7.029	SOLVENT PEAK		< min rt	
3.915	10338	0.027	1.094	11.422	1010 30H	2.95	ECL deviates -0.001	Reference 0.000
4.411	6870	0.030	1.071	11.999	1210	1.92	ECL deviates -0.001	
4.511	408	0.031	1.067	12.091	1110 ISO 30H	0.11	ECL deviates 0.001	
5.730	16770	0.032	1.028	13.177	1210 20H	4.50	ECL deviates -0.001	
6.092	14094	0.034	1.019	13.455	1210 30H	3.75	ECL deviates -0.000	
6.566	558	0.035		13.818				
6.802	2136	0.034	1.002	13.999	1410	0.56	ECL deviates -0.001	Reference -0.001
7.727	846	0.041	0.984	14.624	1510 ISO	0.22	ECL deviates 0.003	Reference 0.002
8.288	630	0.045	0.974	15.002	1510	0.16	ECL deviates 0.002	Reference 0.002
9.603	86670	0.040	0.955	15.816	Sum In Feature 4	21.61	ECL deviates -0.001	16:1 W7c/15. Iso 20H
9.754	720	0.037	0.953	15.909	1611 W5c	0.18	ECL deviates 0.001	
9.897	85884	0.040	0.951	15.998	1610	21.32	ECL deviates -0.002	Reference -0.002
10.962	1596	0.042	0.938	16.629	1710 ISO	0.39	ECL deviates -0.000	Reference -0.001
11.236	984	0.043	0.935	16.791	1711 W8c	0.24	ECL deviates -0.001	
11.399	6552	0.044	0.933	16.887	1710 CYCLO	1.60	ECL deviates -0.001	Reference -0.002
11.586	744	0.045	0.931	16.998	1710	0.18	ECL deviates -0.002	Reference -0.002
13.012	163326	0.045	0.918	17.824	Sum In Feature 7	39.14	ECL deviates -0.001	18:1 W9c/W12t/W7c
13.177	570	0.054	0.916	17.919	1811 W5c	0.14	ECL deviates 0.000	
13.317	2106	0.042	0.915	18.001	1810	0.50	ECL deviates 0.001	Reference 0.000
14.873	2220	0.046	0.904	18.901	1910 CYCLO W8c	0.52	ECL deviates 0.001	Reference 0.000
*****	86670				SUMMED FEATURE 4	21.61	16:1 W7c/15 Iso 20H	15:10 ISO 20H/16:1 W7c
*****	163326				SUMMED FEATURE 7	39.14	18:1 W7c/W9t/W12t	18:1 W9c/W12t/W7c
*****							18:1 W12t/W9t/W7c	
Solvent Ar Total Area Named Area W Named Total Amt Nbr Ref ECL Deviation Ref ECL Shift								
274442400	404022	403164	99.86	382931	10	0.001	0.002	
TSBA (Rev 3.90) Pseudomonas 0.700								
P. aeruginosa 0.100								
Flavimonas 0.477 (Pseudomonas VE2)								
F. oryzae 0.477 (Pseudomonas VE2)								
Chryseomonas 0.387 (Pseudomonas VE1)								
C. luteola 0.307 (Pseudomonas VE1)								
CLIN (Rev 3.90) Pseudomonas 0.339								
P. aeruginosa 0.339								
P. stutzeri 0.242								
Chryseomonas 0.322 (Pseudomonas VE1*)								
C. luteola 0.322 (Pseudomonas VE1*)								
Flavimonas 0.205 (Pseudomonas VE2)								
F. oryzae 0.205 (Pseudomonas VE2)								

Fig. 4

RT	Area	Ar/Ht Respon	NCL	Name	%	Comment 1	Comment 2
1.665	241677184	0.032	7.033	SOVENT PEAK		< min rt	
1.946	536	0.030	7.563			< min rt	
10.502	1080	0.061	15.815	Sum In Feature 4	0.81	NCL deviates -0.002	16:1 Wc/13 iso 20H
10.814	9496	0.049	15.999	16:0	7.07	NCL deviates -0.001	Reference -0.001
11.974	6120	0.051	16.631	17:0 ISO	4.50	NCL deviates 0.002	Reference 0.002
13.653	3040	0.058	17.606				
14.043	119192	0.051	17.825	Sum In Feature 7	85.92	NCL deviates -0.000	18:1 Wc/w12t/w7c
14.354	2376	0.050	17.999	18:0	1.71	NCL deviates -0.001	Reference -0.001
14.498	4160	0.055	18.081				
14.615	2272	0.088	18.147				
*****	1080			SUMMED FEATURE 4	0.81	16:1 Wc/13 iso 20H	13:0 ISO 20H/16:1Wc
*****	119192			SUMMED FEATURE 7	85.92	18:1 Wc/w12t/w12t	18:1 Wc/w12t/w7c
*****						18:1 w12t/w2t/w7c	

Solvent Ar Total Area Named Area % Named Total Limit Nbr Ref NCL Deviation Ref NCL Shift

243677184	147736	138264	93.59	127054	3	0.001	0.001
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TSBA [Rev 3.90] Paracoccus

P. denitrificans	0.335
Bradyrhizobium	0.313 (4D, Rhis X medium)
B. japonicum	0.313 (4D, Rhis X medium)
B. j. CC subgroup A	0.313 (4D, Rhis X medium)
Methylobacterium	0.299 (48h, Pseudomonas mesophilica)
M. mesophilicum*	0.295 (48h, Pseudomonas mesophilica)
M. radiotolerans	0.246 (48h, Pseudomonas radiosa)
M. satmanii	0.186 (48h)

CLIN [Rev 3.90] Ochrobactrum

O. anthropi*	0.233
Sphingomonas	0.168 (Pseudomonas paucimobilia)
S. paucimobilia	0.168 (Pseudomonas paucimobilia)

Fig. 5

RT	Area	Ar/Rt	Respon	ECL	Name	%	Comment 1	Comment 2
1.665	239780224	0.032	. . .	7.033	SOLVENT PEAK	. . .	< min rt	
1.947	544	0.028	. . .	7.566	< min rt	
2.094	560	0.027	. . .	7.844	< min rt	
4.369	16792	0.034	1.095	11.420	10:0 3CH	4.14	ECL deviates -0.003	
4.870	2080	0.041	. . .	11.943		
4.923	6464	0.038	1.071	12.000	12:0	1.56	ECL deviates -0.000	Reference 0.000
5.235	1624	0.053	. . .	12.259		
5.370	23080	0.041	1.026	13.176	12:0 2CH	5.34	ECL deviates -0.002	
5.764	15360	0.041	1.015	13.455	12:0 3CH	3.52	ECL deviates -0.000	
7.535	3656	0.043	0.998	14.000	14:0	0.82	ECL deviates 0.000	Reference 0.000
10.309	109552	0.048	0.950	15.819	Sum In Feature 4	23.46	ECL deviates 0.002	16:1 w7c/15 iso 2CH
10.817	102120	0.048	0.946	16.001	16:0	21.78	ECL deviates 0.001	Reference 0.001
11.045	10608	0.053	0.943	16.130	15:0 ISO 3CH	2.26	ECL deviates -0.005	
11.330	10112	0.049	. . .	16.272		
12.376	6256	0.052	0.929	16.888	17:0 CYCLO	1.31	ECL deviates -0.000	Reference -0.000
14.045	169864	0.051	0.916	17.825	Sum In Feature 7	35.07	ECL deviates 0.000	18:1 w9c/w12t/w7c
14.355	1488	0.054	0.914	17.999	18:0	0.31	ECL deviates -0.001	Reference 0.000
14.603	16104	0.057	. . .	18.139		
15.951	2192	0.061	0.906	18.901	19:0 CYCLO w8c	0.45	ECL deviates 0.001	Reference 0.002
*****	109552	SUMMED FEATURE 4	23.46	16:1 w7c/15 iso 2CH	15:0 ISO 2CH/16:1w7c
*****	169864	SUMMED FEATURE 7	35.07	18:1 w7c/w9t/w12t	18:1 w9c/w12t/w7c
*****	18:1 w12t/w9t/w7c	

Solvent Ar	Total Area	Named Area	% Named	Total Amt	Kbr Ref	ECL Deviation	Ref ECL Shift
39780224	497352	467432	93.98	443648	6	0.002	0.001

TSRA [Rev 3.90]	Pseudomonas	0.457
	P. aeruginosa	0.457
CLM [Rev 3.90]	Pseudomonas	0.226
	P. aeruginosa*	0.226
	P. stutzeri	0.147
	P. putida	0.119
	P. p. biotype A*	0.119
	Chryseomonas	0.153 ("Pseudomonas VKI")
	C. luteola	0.153 ("Pseudomonas VKI")

Fig. 6

RT	Area	Ar/Ht	Respon	ECL	Name	%	Comment 1	Comment 2
1.660	248210304	0.031		7.034	SOLVENT PEAK		< min rt	
1.857	920	0.025		7.407			< min rt	
1.939	1296	0.029		7.562			< min rt	
9.919	1216	0.049	0.957	25.486	Sum In Feature 3	4.89	ECL deviates 0.004	16:1 ISO I/14:0 30K
10.480	3256	0.048	0.950	15.816	Sum In Feature 4	13.00	ECL deviates -0.001	16:1 W7c/15 iso 20K
10.789	1712	0.051	0.947	15.999	16:0	6.81	ECL deviates -0.001	Reference -0.003
13.469	1120	0.058	0.924	17.517	16:0 30K	4.35	ECL deviates -0.003	
14.009	16984	0.050	0.920	17.821	Sum In Feature 7	65.69	ECL deviates -0.001	18:1 W7c/W9t/w12t
16.249	1376	0.065	0.910	19.069	18:1 20K	9.26	ECL deviates 0.001	
*****	1216				SUMMED FEATURE 3	4.89	12:0 ALDH F	unknown 10.928
*****								14:0 30H/16:1 ISO I
*****	3256				SUMMED FEATURE 4	13.00	16:1 W7c/15 iso 20K	15:0 ISO 20H/16:1 W7c
*****	16984				SUMMED FEATURE 7	65.69	18:1 W7c/W9t/w12t	18:1 W9c/w12t/w7c
*****								18:1 w12t/w9t/w7c
Solvent Ar	Total Area	Named Area	% Named	Total Amt	Nbr Ref	ECL Deviation	Ref ECL Shift	
248210304	25664	25664	100.00	23797	1	0.002	0.003	
QUESTION ANALYSIS; TOTAL AREA LESS THAN 50000. CONCENTRATE AND RE-RUN.								
TSBA [Rev 3.90] Acospirillum 0.786								
A. brasiliense 0.786								
CLIN [Rev 3.90] Roseomonas 0.599								
R. fauriae** 0.890								

Fig. 8

RT	Area	Ar/Rt	Respon	ECL	Name	%	Comment 1	Comment 2
1.664	248735360	0.031	. . .	7.031	SOLVENT PEAK	. . .	< min rt	
1.770	6064	0.024	. . .	7.231	< min rt	
1.862	2552	0.027	. . .	7.405	< min rt	
1.945	1096	0.034	. . .	7.562	< min rt	
10.815	2752	0.046	0.946	15.999	16:0	2.81	ECL deviates -0.001	Reference -0.001
11.327	1448	0.054	. . .	16.291		
12.575	1712	0.058	0.927	17.002	17:0	1.72	ECL deviates 0.002	Reference 0.001
13.500	968	0.059	0.920	17.521	16:0 30E	0.96	ECL deviates 0.001	
14.041	90456	0.051	0.916	17.825	Sum In Feature 7	89.56	ECL deviates -0.000	18:1 w9c/w12t/w7c
14.352	3920	0.049	0.914	17.999	18:0	3.87	ECL deviates -0.001	Reference -0.001
14.499	760	0.044	. . .	18.082		
14.613	49552	0.055	. . .	18.147		
17.575	1096	0.057	0.902	19.834	20:1 w9t	1.07	ECL deviates 0.001	
*****	90456	SUMMED FEATURE 7	89.56	18:1 w7c/w9t/w12t	18:1 w9c/w12t/w7c
*****	18:1 w12t/w9t/w7c	

solvent	Ar	Total Area	Named Area	% Named	Total Area	Nbr Ref	ECL Deviation	Ref ECL Shift
248735360		152664	100904	66.10	92494	3	0.001	0.001

QUESTION ANALYSIS: PERCENT AREA NAMED IS LESS THAN 85. CHECK FOR CONTAMINATION.

TSBA [Rev 3.90]	Methylobacterium	0.782	(48h, Pseudomonas radiora)
	M. radiotolerans	0.782	(48h, Pseudomonas radiora)
	M. mesophilicum*	0.708	(48h, Pseudomonas mesophila)
	M. zatmanii	0.674	(48h)
	Rhodobacter	0.657	
	R. sphaeroides	0.657	
	R. capsulatus	0.454	
	Xanthobacter	0.647	
	X. flavus	0.647	
CLIN [Rev 3.90]	Methylobacterium	0.512	
	M. mesophilicum	0.512	
	Ochromobacter	0.403	
	O. anthropi*	0.403	