Retrieval of the species *Alteromonas tetraodonis* Simidu *et al.* 1990 as *Pseudoalteromonas tetraodonis* comb. nov. and emendation of description

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A polyphasic taxonomy study was undertaken of three strains of *Pseudoalteromonas haloplanktis* subsp. *tetraodonis* (Simidu *et al.* 1990) Gauthier *et al.* 1995. DNA was prepared from each of the strains and genomic relatedness was measured by DNA–DNA hybridization. Strains KMM 458^T and IAM 14160^T shared 99% genetic relatedness, but were only 48–49% related to the type strain of *Pseudoalteromonas haloplanktis* subsp. *haloplanktis*, IAM 12915^T. The third strain, *P. haloplanktis* subsp. *tetraodonis* A-M, showed 83% genetic similarity with *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T and 32% with KMM 458^T. From these results, it is concluded that strains KMM 458^T and IAM 14160^T comprise a separate species, originally described as *Alteromonas tetraodonis*, whereas strain A-M belongs to the species *Pseudoalteromonas haloplanktis*. Based on phenotypic and chemotaxonomic data, genomic fingerprint patterns, DNA–DNA hybridization data and phylogenetic analysis of 16S rRNA, it is proposed that the species *Alteromonas tetraodonis* be retrieved and recognized as *Pseudoalteromonas tetraodonis* comb. nov. (type strain IAM 14160^T = KMM 458^T).

Keywords: retrieval, *Alteromonas tetraodonis*, *Pseudoalteromonas haloplanktis* subsp. *tetraodonis*, *Pseudoalteromonas tetraodonis*

INTRODUCTION

The genus *Pseudoalteromonas* Gauthier *et al.* 1995 currently comprises 17 validly described species originating from the *Alteromonas haloplanktis* rRNA branch (Van Landschoot & De Ley, 1983) of the former genus *Alteromonas* Baumann *et al.* 1972

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The GenBank accession numbers for the 16S rDNA sequences of *Pseudoalteromonas tetraodonis* KMM 458^T and strain IAM 14160^T are AF214729 and AF214730, respectively.

(Baumann *et al.*, 1984; Gauthier & Breittmayer, 1992). The type species of the genus *Pseudoalteromonas* is *Pseudoalteromonas haloplanktis*, which includes two subspecies, *P. haloplanktis* subsp. *haloplanktis* and *P. haloplanktis* subsp. *tetraodonis*. The latter was described as *Alteromonas tetraodonis* Simidu *et al.* 1990 to accommodate one of four marine bacterial isolates, strain GFC^T, that produces tetrodotoxin (Simidu *et al.*, 1990). This bacterium was isolated from the surface slime of a puffer fish (*Fugu poecilonotus*) shown to produce tetrodotoxin in association with the animals. A few years later, on the basis of DNA–DNA hybridization data, it was found that *A. tetraodonis*

Simidu *et al.* 1990 should be recognized as a junior subjective synonym of *A. haloplanktis* (ZoBell and Upham 1944) Reichelt and Baumann 1973 (Baumann *et al.*, 1984; Akagawa-Matsushita *et al.*, 1993). At present, and in accordance with results of phylogenetic and biochemical analyses and the level of genomic DNA relatedness, this bacterial taxon is recognized as *P. haloplanktis* subsp. *tetraodonis* (Simidu *et al.* 1990) Gauthier *et al.* 1995.

During the last decade, bacterial isolates in the Collection of Marine Micro-organisms, Vladivostok, Russia, that are related to *Alteromonas* have been subjected to extensive taxonomic investigation. Shortly after publication of the article describing the new species *Alteromonas tetraodonis*, strain GFC^T was subjected to DNA–DNA hybridization experiments to clarify the taxonomic position of the newly isolated bacteria. In 1991, K. Kita-Tsukamoto, on behalf of U. Simidu, kindly provided strain GFC^T, designated *A. tetraodonis* IAM 14160^T, and deposited it in our laboratory as strain KMM 458^T (KMM; Collection of Marine Micro-organisms, Pacific Institute of Bio-organic Chemistry). Results of DNA–DNA hybridization studies disagreed with those published by Akagawa-Matsushita *et al.* (1993). After consultation with M. Akagawa-Matsushita, DNA–DNA hybridization experiments were repeated using strains *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T, *P. haloplanktis* subsp. *tetraodonis* A-M (= KMM 3660), kindly provided by M. Akagawa-Matsushita, *P. haloplanktis* subsp. *tetraodonis* IAM 14160^T from the Collection of the Institute of Molecular and Cellular Biosciences (formerly Institute of Applied Microbiology), Japan, and strain KMM 458^T (formerly *A. tetraodonis* and provided by U. Simidu). Results showed that strains KMM 458^T and IAM 14160^T are identical and should be considered as a separate species, as described originally by Simidu *et al.* (1990). A polyphasic taxonomy study, including phenotypic, biochemical and genomic characteristics, together with phylogenetic study of the strains, was undertaken. Results given here have led to the conclusion that the species initially described as *Alteromonas tetraodonis* (Simidu *et al.*, 1990) is indeed a species separate from *P. haloplanktis* and should be retrieved as *Pseudoalteromonas tetraodonis* comb. nov.

METHODS

Bacterial strains. The strains employed in this study are as follows: *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T (= ATCC 14393^T); *P. haloplanktis* subsp. *tetraodonis* IAM 14160^T; *P. haloplanktis* subsp. *tetraodonis* A-M (= KMM 3660), obtained from M. Akagawa-Matsushita; strain KMM 458^T (= IAM 14160^T), originally provided in 1991 by K. Kita-Tsukamoto, on behalf of U. Simidu, as *Alteromonas tetraodonis* IAM 14160^T; *Pseudoalteromonas atlantica* IAM 12376^T; and *Pseudoalteromonas carrageenovora* IAM 12662^T. The strains were grown at 25 °C on Marine Agar 2216 (Difco) and stored frozen at –80 °C in Marine Broth (Difco) supplemented with 30 % (v/v) glycerol.

Phenotypic analysis. Unless otherwise indicated, the phenotypic properties employed to characterize *Alteromonas* and related species were obtained using procedures described by Baumann *et al.* (1972, 1984) and Smibert & Krieg (1994). Tests for utilization of various organic substrates (Table 1) as sole carbon sources, at concentrations of 0.1 % (w/v), were performed as described elsewhere (Ivanova *et al.*, 1996).

Sensitivity to antibiotics was tested by the disc-diffusion method using Marine Agar 2216 and discs impregnated with the following antibiotics: kanamycin (30 µg); ampicillin (10 µg); benzylpenicillin (10 µg); streptomycin (10 µg); erythromycin (15 µg); gentamicin (10 µg); oxacillin (20 µg); lincomycin (15 µg); carbenicillin (25 µg); vancomycin (30 µg); tetracycline (30 µg); oleandomycin (15 µg); and O/129 (150 µg).

Lipid analysis. Lipids were extracted from wet cells, according to the method of Bligh & Dyer (1953). Polar lipids were subjected to two-dimensional TLC using 10 × 10 cm silica gel plates (KSK). Following development in chloroform/methanol/ammonium hydrate/benzene (65:30:6:10) (first dimension) and chloroform/methanol/acetone/acetic acid/benzene/water (70:30:5:4:1:10) (second dimension), lipids were detected on chromatograms by spraying with both a non-specific reagent (50 % sulfuric acid in methanol and heating at 180 °C) and specific reagents (ninhydrin and Dragendorff's reagent). Quantification of phospholipids on two-dimensional chromatograms was done using the method of Vaskovsky *et al.* (1975).

Fatty acid methyl ester analysis. Analysis of fatty acid methyl esters was performed by GLC, as described previously by Svetashev *et al.* (1995).

Serology. ELISA was performed, according to the methods of Voller *et al.* (1979), as described elsewhere (Ivanova *et al.*, 1998). The level of antigen relatedness was estimated, as described by Conway de Macario *et al.* (1982), as the mean value of three independent experiments.

Genetic analysis. DNA was isolated according to the method of Marmur (1961). DNA G+C content (mol%) was determined by the thermal denaturation methods of Marmur & Doty (1962) and Owen *et al.* (1969). DNA–DNA hybridization was performed spectrophotometrically and initial renaturation rates were recorded as described by De Ley *et al.* (1970).

Genomic fingerprints: primers and PCR conditions. PCR genomic fingerprinting was carried out using specific primers and conditions as follows. REP-directed PCR (Louws *et al.*, 1994): REP1R-I, 5'-IIICGICGICATCIGGC-3'; REP2-I, 5'-ICGICTTATCIGGCCTAC-3'. ERIC-directed PCR (Judd *et al.*, 1993): ERIC 1 (reverse), 5'-ATGTAAGCTC-CTGGGGATTAC-3'; ERIC 2 (forward): 5'-AAGTA-AGTGACTGGGGTGAGCG-3'. BOX-directed PCR (Versalovic *et al.*, 1991; Louws *et al.*, 1994): 5'-CTACG-GCAAGGCGACGCTGACG-3'. PCRs were performed using the following programs: one initial cycle at 95 °C for 7 min, 35 cycles of denaturation at 94 °C for 1 min, annealing at 44, 52 or 53 °C for 1 min with REP, ERIC or BOX primers, respectively, and extension at 65 °C for 10 min, with a single final extension cycle at 65 °C for 20 min for REP, ERIC and BOX primers, and a final soak at 4 °C. PCR products were separated by horizontal electrophoresis on 2.2 % agarose gels, stained with SYBR Green I (FMC Bioproducts) and visualized by scanning at 500 nm in a Fluorimager scanner (Molecular Dynamics). To examine

Table 1. Phenotypic data for *P. haloplanktis* subsp. *haloplanktis* and strains of *P. haloplanktis* subsp. *tetraodonis*

All strains studied produced gelatinase and lipase, did not produce alginase or agarase, did not grow at 41 °C and utilized succinate and fumarate. +, Positive; –, negative; ND, no data available; D, 11–89% of strains positive; v, variable.

Characteristic	<i>P. haloplanktis</i> subsp. <i>haloplanktis</i> IAM 12915 [†]			<i>P. haloplanktis</i> subsp. <i>tetraodonis</i> IAM 14160 [†]		
	Baumann <i>et al.</i> (1984)	Akagawa-Matsushita <i>et al.</i> (1993)	This study	Akagawa-Matsushita <i>et al.</i> (1993)	Simidu <i>et al.</i> (1990)	This study
Production of:						
Amylase	D	–	–	–	–	–
Chitinase	D	ND	–	ND	–	–
Growth at:						
4 °C	–	+*	–	+*	+	+
35 °C	D	+	+	+	+	+
Utilization of:						
D-Glucose, pyruvate, ethanol, acetate	+	ND	+	ND	+	+
D-Mannose	+	–	+	–	+	–
D-Fructose	D	+	+	–	+	–
Sucrose	+	–	+	+	+	+
Trehalose	D	–	–	+	+	–
Maltose	+	ND	+	ND	+	+
Cellobiose	–	+	–	+	+	–
Lactose, D-ribose, D-xylose, D-arabinose, rhamnose, gluconate, salicin, ketoglutarate, glycerol	–	–	–	–	+	–
D-Galactose	D	–	v	–	+	+
Propionate	+	ND	+	ND	+	ND
Butyrate, valerate	D	+	v	+	+	+
Caproate	–	+	–	+	–	+
DL-Lactate	ND	–	–	–	+	+
Citrate	+	–	+	–	–	+
Aconitate	+	–	+	–	+	+
Caprylate	D	–	v	–	ND	–
D-Malate	–	–	–	+	–	–
Mannitol	D	–	v	–	+	–
D-Sorbitol	–	ND	–	ND	+	–
p-Hydroxybenzoate	–	–	–	–	+	ND
L-Alanine	–	ND	+	ND	+	+
L-Threonine	–	ND	–	ND	+	–
Aspartate	D	ND	ND	ND	–	–
Glutamate	D	ND	+	ND	+	+
L-Lysine	–	–	–	+	+	–
L-Arginine	D	–	–	+	+	–
L-Ornithine	–	–	–	–	+	–
L-Histidine	D	ND	+	ND	+	–
L-Proline	D	ND	+	ND	+	–
L-Tyrosine	+	–	+	–	+	+
L-Phenylalanine	–	–	–	–	+	–

* Growth tested at 5 °C.

the reproducibility of the results, the ERIC and BOX PCRs were repeated at least twice.

DNA amplification and sequencing. Bacterial DNAs for PCR were prepared using the Promega Wizard genomic DNA extraction kit according to the instruction manual. DNA templates (100 ng) were used in PCR to amplify small-subunit rRNA genes, as described previously by Sawabe *et al.* (1998a, b). PCR conditions were as follows: an initial denaturation step at 94 °C for 180 s, an annealing step at 55 °C for 60 s and an extension step at 72 °C for 90 s. The thermal profile then consisted of 30 cycles. The amplification primers used in this study gave a 1.5 kb PCR product and corresponded to positions 25–1521 of the *Escherichia coli* sequence. The PCR products were purified using a Promega Wizard PCR preps DNA purification kit and sequenced directly by using a *Taq* FS dye terminator sequencing kit (ABI) and the protocol recommended by the manufacturer. DNA sequencing was performed with an Applied Bio-

systems model 373S automated sequencer. Nine sequencing primers were used (Sawabe *et al.*, 1998a).

Phylogenetic analysis. Sequences were aligned and studied using a set of programs developed by R. Christen. In all phylogenetic analyses, the sequences determined in this study and small-subunit rDNA sequences obtained from the EMBL database were used. Domains used to construct the dendrogram shown in Fig. 2 were regions of the small-subunit rDNA sequences available for all sequences and excluding positions likely to show homoplasy: positions 101–181, 219–837, 850–1133, 1138–1205 (*E. coli* small-subunit rDNA sequence J01695 numbering). Phylogenetic analyses were performed using three different methods: distances were calculated using Kimura's two-parameter correction and a modified neighbour-joining method, BIONJ (Gascuel, 1997), maximum-likelihood (options QFYG, fastDNAmI program; Olsen *et al.*, 1994) and maximum-parsimony (PHYLIP, Phylogeny Inference Package, version

3.5c; distributed by J. Felsenstein, Department of Genetics, University of Washington, Seattle, WA, USA). The robustness of each topology was checked using the neighbour-joining method and 100 bootstrap replications. Trees were drawn using the NJPLOT program for the Macintosh (M. Gouy, CNRS URA 243, Université Claude Bernard, Lyon, France).

RESULTS AND DISCUSSION

The bacterial strain GFC^T (= KMM 458^T = IAM 14160^T), described originally as *Alteromonas tetraodonis*, had all the features characteristic for the genus *Pseudoalteromonas* (formerly an rRNA cluster of *Alteromonas haloplanktis*). The strain was motile by means of a single flagellum. It was a chemo-organotroph, with a respiratory metabolism. It did not form endospores or accumulate polyhydroxybutyrate as an intracellular reserve product. It did not possess arginine dihydrolase and was oxidase- and catalase-

positive. It required Na⁺ or sea water for growth; good growth was observed in media containing 1–7 % NaCl. The temperature range for growth was 4–35 °C, with an optimum between 25 and 30 °C. No growth was detected at 40 °C. The pH range for growth was 5.5–9.5, with optimum growth at pH 7.5–8.0. Amylase, agarase, chitinase and alginase were not produced. Tween 80, gelatin and DNA were decomposed. Many of these characteristics, and others listed in Table 1, are similar for *P. haloplanktis* subsp. *haloplanktis*, *P. haloplanktis* subsp. *tetraodonis* and strains A-M and KMM 458^T (= IAM 14160^T). On the other hand, differences in carbohydrate utilization were noted when comparing related data published by other investigators. Strain KMM 458^T utilized DL-lactate, caproate, valerate and butyrate, whereas *P. haloplanktis* subsp. *haloplanktis* did not utilize these compounds. In contrast, strain KMM 458^T did not utilize D-mannose, D-fructose, mannitol, L-histidine or

Table 2. Fatty acid composition of *P. haloplanktis* and *P. tetraodonis*

Data were from Svetashev *et al.* (1995) and this study.

Fatty acid	<i>P. haloplanktis</i> IAM 12915 ^T	<i>P. haloplanktis</i> A-M	<i>P. tetraodonis</i> KMM 458 ^T (= IAM 14160 ^T)
11:0 3-OH	0.3	0.24	0.4
12:0 3-OH	1.9	1.11	0.9
12:0	2.0	2.12	1.5
12:1	0.3	0.54	0.3
i13:0	0.1	0.00	0.0
13:0	0.2	0.26	0.5
13:1	0.3	0.26	0.5
i14:0	0.0	0.15	0.1
14:0	2.0	1.62	2.0
14:1(n-7)	0.6	1.13	1.2
i15:0	0.0	0.11	0.0
a15:0	0.2	0.58	0.4
15:0	3.3	3.47	8.0
15:1(n-8)	2.3	2.80	6.3
15:1(n-6)	0.2	0.36	0.6
i16:0	0.2	2.52	1.4
16:0	30.1	23.10	18.2
16:1(n-9)	0.0	0.82	0.0
16:1(n-7)	40.5	38.37	35.0
16:1(n-5)	0.0	0.39	0.2
i17:0	0.0	0.68	0.3
a17:0	0.0	1.15	0.6
17:0	3.9	3.76	5.5
17:1(n-8)	6.0	6.25	10.7
17:1(n-6)	0.2	0.52	0.8
i18:0	0.0	0.49	0.2
18:0	1.9	1.30	0.6
18:1(n-11)	0.1	0.34	0.4
18:1(n-9)	0.2	0.11	0.2
18:1(n-7)	2.4	4.28	2.5
19:1	0.2	0.28	0.2
Unidentified fatty acid	—	0.56	—
Total	99.5	99.67	99.6

Fig. 1. Comparative genomic fingerprinting of some *Pseudoalteromonas* species. REP (a), ERIC (b) and BOX (c) PCR patterns are shown. The fingerprints are as follows: M, 1 kb ladder (Gibco-BRL); 1, *P. tetraodonis* IAM 14160^T; 2, *P. haloplanktis* IAM 12915^T; 3, *P. tetraodonis* KMM 458^T; 4, *P. atlantica* IAM 12376^T; and 5, *P. carrageenovora* IAM 12622^T.

Table 3. DNA relatedness of *P. haloplanktis* and *P. tetraodonis*

Taxon	G + C content (mol %)	DNA relatedness (%)	
		<i>P. haloplanktis</i> IAM 12915 ^T	<i>P. tetraodonis</i> IAM 14160 ^T
<i>P. haloplanktis</i> IAM 12915 ^T	42.2	100	—
<i>P. haloplanktis</i> A-M	41.3	83	32
<i>P. tetraodonis</i> KMM 458 ^T	41.5	49	99
<i>P. tetraodonis</i> IAM 14160 ^T	41.8	48	100

L-proline (Table 1). The strain was susceptible to benzylpenicillin, carbenicillin, vancomycin and tetracycline.

Cellular fatty acids of strains A-M and KMM 458^T were characteristic for *Pseudoalteromonas* species (Table 2) and the dominant fatty acids were as follows: 16:1(n-7), 16:0, 17:1(n-8), 17:0 and 18:1(n-8). However, the fatty acid profiles of *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T and strain A-M were similar and they contrasted with that of strain KMM 458^T. For example, the amounts of 15:0, 15:1(n-8), 17:0 and 17:1(n-8) fatty acids for the latter strain were almost twice those in the other two strains.

Phospholipids were a significant component of the polar lipids (ca. 80–85%); the phospholipid composition was generally the same for all strains included in this study. Phosphatidyl ethanolamine and phosphatidyl glycerol were the major components: 73.2 and 23% for *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T, 75.1 and 23.7% for *P. haloplanktis* subsp. *tetraodonis* IAM 14160^T and 71.7 and 21.7% for strain KMM 458^T, respectively. The concentrations of the minor phospholipids varied slightly. In the three strains above, levels of bis-phosphatidic acid were 1.8, 2.2 and 1.7%, those of phosphatidic acid were 0.3, 0.7

and 1.2% and those of lyso-phosphatidyl ethanolamine were 1.9, 0.7 and 0.6%, respectively. Unidentified phospholipids (0.6%) were present in the lipid fractions of *P. haloplanktis* subsp. *tetraodonis* IAM 14160^T and KMM 458^T. Cardiolipin and glycolipids were not detected.

Genomic fingerprinting patterns obtained using primers corresponding to the REP, ERIC and BOX elements of *P. haloplanktis* subsp. *tetraodonis* IAM 14160^T and KMM 458^T were identical, whereas those of *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T were different. Since a dispersion of repetitive sequences in the bacterial genome reflects a strain-specific characteristic, the identity of the genomic profiles is interpreted as identity of strains IAM 14160^T and KMM 458^T (Fig. 1).

Results of DNA–DNA hybridizations showed that strains KMM 458^T and IAM 14160^T are 99% related to each other, but only 48–49% related to the type strain, *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T. Strain A-M showed 83% genetic similarity to *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T and 32% to KMM 458^T (Table 3). Thus, the two strains KMM 458^T and IAM 14160^T represent a distinct species, originally described as *Alteromonas tetraodonis* by

Fig. 2. Unrooted tree obtained using the neighbour-joining algorithm and Kimura's two-parameter correction for distance calculations. Branches also obtained in the maximum-likelihood analysis are indicated by asterisks ($P < 0.01$). +, Branches also found in maximum-likelihood and parsimony analysis; bootstrap percentages retrieved in 500 replicons bootstrap analysis using Kimura's two-parameter analysis are shown at the nodes. Bar, 0.02 accumulated changes per nucleotide.

Simidu *et al.* (1990), which is consistent with the criteria cited by Wayne *et al.* (1987). In contrast, it is concluded that strain A-M belongs to *P. haloplanktis*

and, on the basis of its high DNA–DNA hybridization value with strain IAM 12915^T (83 %), that it does not merit subspecies status. Results of the DNA–DNA

hybridization experiments were supported by serological data obtained using polyclonal antibodies to cell surface determinants. Antiserum to *P. haloplanktis* subsp. *haloplanktis* IAM 12915^T did not cross-react with surface antigens of KMM 458^T, even though it showed 50 % surface antigen similarity to strain IAM 14160^T.

In order to clarify the taxonomic affiliation of *P. haloplanktis* subsp. *tetraodonis* IAM 14160^T and KMM 458^T at the genus level, the 16S rDNA sequences were aligned by comparison to a database containing about 10000 already aligned eubacterial small-subunit rDNA sequences. The results of broad phylogenetic analyses showed clearly that the strains studied belonged to the γ -*Proteobacteria* of the *Bacteria* (data not shown) and, more precisely, to the γ -3 subgroup. More detailed analyses showed that these bacteria were included in the genus *Pseudoalteromonas* and formed a cluster with *P. haloplanktis*, *P. nigrifaciens*, '*P. gracilis*', *P. citrea* KMM 216 and *P. antarctica*. Sequence similarities between *P. haloplanktis* subsp. *haloplanktis* ATCC 14393^T and both *P. haloplanktis* subsp. *tetraodonis* IAM 14610^T and KMM 458^T were 99.9 % (Fig. 2). Rather low DNA homology values, about 50 %, against *P. haloplanktis* subsp. *haloplanktis* have enabled recognition of *P. haloplanktis* subsp. *tetraodonis* and *P. haloplanktis* subsp. *haloplanktis* as separate species of the genus *Pseudoalteromonas*. *Pseudoalteromonas tetraodonis* comb. nov. and an emended species *Pseudoalteromonas haloplanktis* are proposed.

Description of *Pseudoalteromonas tetraodonis* comb. nov.

Basonym *Pseudoalteromonas haloplanktis* subsp. *tetraodonis* (Simidu *et al.* 1990) Gauthier *et al.* 1995.

The description of *Pseudoalteromonas tetraodonis* comb. nov. is identical to that given by Simidu *et al.* (1990), with some additional characteristics, including growth in media containing 1–10 % NaCl, growth at pH 5.5–9.5, with optimum growth at 7.5–8.0, and utilization of D-glucose, sucrose, D-maltose, D-galactose, DL-lactate, caproate, valerate, butyrate, citrate, fumarate, succinate, caprylate, glutamate, acetate, pyruvate, ethanol and L-tyrosine. It does not utilize D-mannose, D-fructose, mannitol, L-histidine, L-proline or D-malate. It is susceptible to benzylpenicillin, carbenicillin, vancomycin and tetracycline. Cellular fatty acids include 16:1(n-7), 16:0, 17:1(n-8), 17:0 and 18:1(n-8). The 15:0, 15:1(n-8), 17:0 and 17:1(n-8) fatty acids are minor components. The major phospholipids, phosphatidyl ethanolamine and phosphatidyl glycerol, constitute 75.1 and 23.7 % of the total polar lipids. Cardiolipin and glycolipids are absent. The DNA G + C content of *P. tetraodonis* is 41.5 mol % (determined by thermal denaturation). The type strain is GFC^T (= KMM 458^T = IAM 14160^T), isolated from the surface slime of a puffer fish (*Fugu poecilonotus*).

Emended description of *Pseudoalteromonas haloplanktis*

The description of *Pseudoalteromonas haloplanktis* is identical to that of *Alteromonas haloplanktis* given by ZoBell & Upham (1944), with some additional characteristics. It is resistant to benzylpenicillin, vancomycin and tetracycline. Cellular fatty acids include 16:1(n-7), 16:0, 17:1(n-8), 17:0 and 18:1(n-8). The 15:0, 15:1(n-8), 17:0 and 17:1(n-8) fatty acids are minor components. The major phospholipids, phosphatidyl ethanolamine and phosphatidyl glycerol, constitute 73.2 and 23.0 % of the total polar lipids. Cardiolipin and glycolipids are absent. The type strain is IAM 12915^T (= ATCC 14393^T). Strain A-M (= KMM 3660), assigned previously to *P. haloplanktis* subsp. *tetraodonis*, is a strain of *P. haloplanktis*.

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