Kinneretia asaccharophila gen. nov., sp. nov., isolated from a freshwater lake, a member of the *Rubrivivax* branch of the family *Comamonadaceae*

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A strictly aerobic, Gram-negative bacterium, strain KIN192^T, isolated from fresh water from Lake Kinneret, Israel, was examined using a polyphasic approach to characterize and clarify its phylogenetic and taxonomic position. Sequences of the 16S rRNA and *gyrB* genes and ITS1 revealed close relationships to species of the genera *Pelomonas*, *Mitsuaria* and *Roseateles*, in the *Rubrivivax* branch of the family *Comamonadaceae* of the *Betaproteobacteria*. Physiological and biochemical tests, cellular fatty acid analysis and DNA–DNA hybridizations indicated that this strain should be assigned to a new genus and species in the *Rubrivivax* phylogenetic branch, for which the name *Kinneretia asaccharophila* gen. nov., sp. nov., is proposed. The type strain of *Kinneretia asaccharophila* is strain KIN192^T (=CCUG 53117^T =CECT 7319^T).

Strain KIN192^T (=CCUG 53117^T) was isolated from surface waters of the freshwater Lake Kinneret, Israel, by Pinhassi & Berman (2003). This strain was one of the dominant colony-forming bacteria in an enrichment culture experiment, with additions of glucose, ammonium and phosphate, carried out on 11 September 2000. Strain KIN192^T accounted for approximately 42 % of colony-forming units (total 54 000 c.f.u. ml⁻¹), suggesting that it is an organism that prefers eutrophic growth conditions. At the time of the experiment, with a lake water temperature of 29 °C, close to the annual maximum recorded for the lake, bacterial growth in the lake was markedly limited by low levels of phosphorus. Isolate KIN192^T was provisionally ascribed to the *Pelomonas*–*Roseateles*–*Mitsuaria* phylogenetic branch, based on 16S rRNA gene sequence analysis. The relative branching order of most species within the group is difficult to determine because of the limited

number of variable positions available for estimating the phylogenetic distances between strains (Spring, 2006). However, molecular techniques have recently enabled better discrimination of the different species in the *Rubrivivax* line of descent (Gomila *et al.*, 2007, 2008). Comprehensive molecular analyses together with phenotypic and biochemical characterizations have enabled the elucidation of the taxonomic affiliations for organisms within this group (Amakata *et al.*, 2005; Gomila *et al.*, 2007, 2008; Kalmbach *et al.*, 1999; Suyama *et al.*, 1999; Xie & Yokota, 2005). In the present study, strain KIN192^T is concluded to represent a new genus and species.

Strains used in this study included the type strains of all species with validly published names belonging to the closely related genera *Aquabacterium*, *Mitsuaria*, *Pelomonas* and *Roseateles*: *Aquabacterium citratiphilum* CCUG 53899^T, *Aquabacterium commune* CCUG 48318^T, *Aquabacterium parvum* CCUG 48317^T, *Mitsuaria chitosanotabida* IAM 14711^T, *Pelomonas aquatica* CCUG 52575^T, *Pelomonas puraquae* CCUG 52769^T, *Pelomonas saccharophila* CCUG 32988^T, *Roseateles aquatilis* CCUG 48205^T, *Roseateles depolymerans* CCUG 52219^T, and *Roseateles terrae* CCUG 52222^T (=MC12^T, isolated by Suyama *et al.*, 1998). All strains used in this study were cultivated on Reasoner's R2A medium (Reasoner & Geldreich, 1985) and incubated

The GenBank/EMBL/DDBJ accession numbers for the sequences determined in this study are AY136099 (16S rRNA gene sequence of strain KIN192^T), FM945414–FM945427 (*gyrB* sequences) and FM945412 and FM945413 (ITS1 sequences).

An electron micrograph of a cell of strain KIN192^T, ITS1- and *gyrB*-based dendrograms, ITS1 and *gyrB* sequence similarities and detailed Biolog and DNA–DNA hybridization results are available as supplementary material with the online version of this paper.

for 3–4 days at 30 °C prior to analyses, if not otherwise stated.

Cell size, morphology and flagella insertion were determined by transmission electron microscopy of cells from the exponential growth phase in R2A broth. A Hitachi model H600 electron microscope was used at 75 kV. Negative stains of cells were prepared with phosphotungstic acid [1 % (w/v), pH 7.0], as described by Lalucat (1988). The following phenotypic tests were used: API 20NE (identification system for Gram-negative, non-enterobacterial rods), API 50CH, API ZYM enzyme and assimilation tests, according to the instructions of the manufacturer (bioMérieux). Biolog analyses were also carried out, essentially according to the instructions of the manufacturer, as described previously (Gomila *et al.*, 2007, 2008). Conventional phenotypic tests were done according to the methods of Cowan (1974). Growth rates in R2A medium were determined at different temperatures (4, 10, 20, 30, 37 and 45 °C).

Colonies of strain KIN192^T were small, approximately 2–3 mm in width, cream-coloured and translucent with irregular and undulate margins. Cells were Gram-negative, rod-shaped (approx. 2 µm long) and motile by means of a single polar flagellum (Supplementary Fig. S1, available in IJSEM Online). Differential phenotypic characteristics and substrates assimilated or utilized as sole carbon and energy sources are indicated in Table 1. Strain KIN192^T grew well between 20 and 37 °C, but was not able to grow at 4, 10 or 45 °C. Strain KIN192^T exhibited a phenotypic profile different from that of any of the other strains studied. Phenylacetic acid assimilation, β-glucosidase activity and nitrate reduction are characteristic and differential for strain KIN192^T. It was not able to assimilate any sugar that was tested, allowing its differentiation from the species of the genus *Pelomonas* and from the species of the closely related genera *Mitsuaria* and *Roseateles*. Differential phenotypic characteristics from species in closely related genera are the inability of strain KIN192^T to grow chemolithoautotrophically, to grow as a diazotroph or to produce photosynthetic pigments. It shows positive reactions for a few hydrolytic enzymes: alkaline phosphatase, esterase lipase (C8), esterase (C4) and leucyl arylamidase. The positive reaction for alkaline phosphatase observed for strain KIN192^T might be expected, given the phosphorus limitation in the ecosystem from which the strain was isolated. Biolog substrates utilized as electron donors are indicated in Supplementary Table S1.

Genomic DNA was prepared, 16S rRNA genes were amplified by PCR and PCR products were sequenced as described previously (Gomila *et al.*, 2005). Sequence data were edited manually and primer sequences were removed. Gene sequences were aligned with reference sequences of the closest relatives, retrieved using the BLAST analysis tool and the NCBI nucleotide sequence database (Altschul *et al.*, 1990). A hierarchical method for multiple alignments, implemented in the CLUSTAL_X program (Thompson *et al.*,

Table 1. Differential phenotypic characteristics between strain KIN192^T and species of the closely related genera *Mitsuaria*, *Pelomonas* and *Roseateles*

Strains: 1, KIN192^T (*Kinneretia asaccharophila* gen. nov., sp. nov.); 2, *P. saccharophila* CCUG 32988^T; 3, *P. aquatica* CCUG 52575^T; 4, *P. puraquae* CCUG 52769^T; 5, *M. chitosanotabida* IAM 14711^T; 6, *R. depolymerans* CCUG 52219^T; 7, *R. terrae* CCUG 52222^T; 8, *R. aquatilis* CCUG 48205^T. +, Positive; –, negative; w, weak; v, variable; ND, not determined. Data were obtained in this study unless indicated. All strains exhibit polar flagella (flagellation data for *R. depolymerans* CCUG 52219^T from Suyama *et al.*, 1999) and are oxidase-positive.

Characteristic	1	2	3	4	5	6	7	8
Flagella	1	1	1	1	1	Several	1	1
Growth at:								
10 °C	–	–	–	+	+	+	w	–
37 °C	+	–	+	+	+	+	+	–
Pigmentation	–	–	–	–	–	+	+	–
Autotrophic growth with H ₂	ND	+	–	+	–	–	–	–
Amplification product for:								
<i>cbbL</i>	–	+	–	+	–	–	–	–
<i>hox</i>	–	ND	–	+	–	–	ND	ND
<i>nifH</i>	–	+	–	+	–	+	+	–
<i>puf</i>	–	–	–	–	–	+	+	–
Catalase	–	–	–	–	–	+	+	–
Nitrate reduction	+	+	+	v	+	–	–	–
Urease	–	–	–	–	–	+	–	–
β-Glucosidase	–	+	+	+	+	+	+	–
Gelatin hydrolysis	+	–	–	+	+	+	+	+
β-Galactosidase	–	+	–	+	+	+	+	–
Assimilation of:								
D-Glucose	–	+	–	+	+	+	+	+
L-Arabinose	–	+	–	+	–	+	+	–
D-Mannose	–	v	–	–	–	+	+	–
D-Mannitol	–	–	–	–	–	+	+	–
N-Acetylglucosamine	–	+	–	–	–	–	–	–
Maltose	–	+	–	+	+	+	+	+
Gluconate	+	+	–	–	+	+	+	+
Capric acid	–	–	–	–	+	w	+	–
Adipic acid	w	–	–	–	–	w	–	–
Malic acid	–	v	–	+	+	w	w	+
Citrate	–	–	–	w	+	w	–	–
Phenylacetic acid	+	–	–	–	w	–	–	–
DNA G + C content (mol%)	69.3	70.9	72.7	70.0	71.3	68.0	68.0	70.1

*Pigmented under some conditions, according to Suyama *et al.* (1999).

1997), was used to create sequence alignments. Automatically aligned sequences were checked manually and all positions of ambiguous identity were removed for subsequent analyses. Sequence similarities and evolutionary distances were calculated using programs implemented in PHYLIP version

3.5c (Felsenstein, 1989). The 16S rRNA gene sequence of strain KIN192^T exhibited similarities between 98.0 and 98.9% with sequences of the type strains of described species from the genera *Mitsuaria*, *Pelomonas* and *Roseateles*. Similarities were distinctly lower, 95.6–96.0%, between the 16S rRNA gene sequence of KIN192^T and those of species of the closely related genera *Aquabacterium* and *Rubrivivax* (Fig. 1; Supplementary Table S2). The 16S rRNA gene phylogenetic tree clusters strain KIN192^T within the *Pelomonas* and *Mitsuaria* phylogenetic branch, although the position of the *Mitsuaria chitosanotabida* branch exhibited a relatively low bootstrap confidence (539/1000 replications). Although comparative 16S rRNA gene sequence analysis is able to place strain KIN192^T within the *Rubrivivax* lineage, closely related to the species of *Pelomonas* and *Mitsuaria*, it is not able to determine with confidence whether strain KIN192^T represents a novel species of *Pelomonas* or of *Mitsuaria* or a novel species of a new genus.

The sequence of the spacer region between the 16S and 23S rRNA genes, ITS1, of strain KIN192^T was analysed as a marker for higher-resolution differentiation than is possible by comparative 16S rRNA gene sequence analyses. Additionally, ITS1 sequence analyses have been shown to correlate well with genomic DNA–DNA hybridization results in delineating bacterial genotypic species or genomovars (Guasp *et al.*, 2000). ITS1 regions were amplified and sequenced, using the methods described by

Gomila *et al.* (2007), and the sequence data were handled as described for the 16S rRNA gene sequence. ITS1 sequences of KIN192^T and reference organisms for which ITS1 could be amplified by PCR were aligned and pairwise similarities (Supplementary Table S2) and cluster analyses (Supplementary Fig. S2) were calculated. While the ITS1 sequence similarities did not provide definitive evidence, in the case of the genera of the *Rubrivivax* phylogenetic lineage, the ITS1 sequence similarities of the species of *Pelomonas* ranged from 93.3 to 93.5%. The ITS1 sequence similarities between the species of the genera *Pelomonas*, *Roseateles* and *Mitsuaria* and the species of any different genus ranged from 74.3 to 88.8%.

Analysis of the housekeeping gene *gyrB* (encoding the gyrase β -subunit) was performed for all strains, amplifying genomic DNA with the forward primer M13Ral-*gyrB*1F (5'-CAGTCAGGAAACAGCTATGACCGCACACGGCCGCGGSATTCC-3'), modified from primer *gyrB*1F of Tayeb *et al.* (2008), and the reverse primer M13-U*gyrB*R (5'-CTGATGTAAAACGACGGCCAGTCCGCNGGRTCY-TTYTCYTGRCA-3'), modified from primer APu of Yamamoto *et al.* (2000). M13 linkers (underlined) were added to the 5' ends of the PCR primers to generate hybridization sites for sequencing primers on the termini of the amplification products. Primers M13F (5'-TCAGGAAACAGCTATGACCGC-3') and M13R (5'-ATGTAAAACGACGGCCAGTCC-3') and the internal primers Ral-*gyrB*422 (5'-TSTCGTTCCTGAACAATGGCG-3') and Ral-*gyrB*599 (5'-AGCTGTCTGTTCCACTGCATCG-3') were used to determine the primary sequences. The internal primers Ral-*gyrB*422 and Ral-*gyrB*599 were designed from the alignment of *gyrB* gene sequences in complete genomes as follows: *Cupriavidus metallidurans* CH 34^T (GenBank accession no. CP000352), *Acidovorax avenae* subsp. *citrii* AAC00-1 (CP000512), *Bordetella pertussis* Tohamal (NC_002929), *Burkholderia cenocepacia* AU1054 (CP000378) and *Burkholderia pseudomallei* K96243 (NC_006350). Strain KIN192^T represented a distinct phylogenetic branch related to the *Pelomonas* species, albeit with a low bootstrap value (less than 500/1000 replications) (Supplementary Fig. S3). Four other genes, *hox* (a hydrogenase), *nifH* (nitrogenase component), *cbbL* (ribulose-1,5-bisphosphate carboxylase/oxygenase) and *puf* (photosynthetic reaction centre component), were analysed as genotypic markers for better definition of the position of the novel strain. However, no amplification products were produced using the PCR primers and conditions described previously for *Pelomonas* and *Roseateles* species (Gomila *et al.*, 2007, 2008).

Gas chromatography of fatty acid methyl esters was performed in a standardized protocol, similar to that of the MIDI Sherlock MIS system (<http://www.midi-inc.com/>; further details at <http://www.ccug.se/>). Cellular fatty acids were identified and quantified, and the relative amount of each fatty acid was expressed in terms of the percentage of total fatty acids (Table 2). As in other species of related genera, the major cellular fatty acids detected were

Fig. 1. Phylogenetic tree, based on 16S rRNA gene sequence comparisons over 1341 aligned bases, showing estimated relationships between strain KIN192^T (*Kinneretia asaccharophila* gen. nov., sp. nov.) and the type strains of species of the closely related genera *Mitsuaria*, *Pelomonas* and *Roseateles* in the *Betaproteobacteria*. The tree was constructed using the neighbour-joining method, following distance analysis calculated by the method of Jukes & Cantor (1969). The topology of the tree was visualized by means of the TreeView program (Page, 1996). Bootstrap values greater than 500, based on 1000 replications, are indicated at branching nodes. Accession numbers are given in parentheses. Bar, 0.01 nucleotide substitutions per site.

Table 2. Cellular fatty acid compositions of strain KIN192^T and type strains of species of closely related genera

Strains: 1, KIN192^T (*K. asaccharophila*); 2, *P. saccharophila* CCUG 32988^T; 3, *P. aquatica* CCUG 52575^T; 4, *P. puraquae* CCUG 52769^T; 5, *M. chitosanotabida* IAM 14711^T; 6, *R. depolymerans* CCUG 52219^T; 7, *R. terrae* CCUG 52222^T; 8, *R. aquatilis* CCUG 48205^T. Values are percentages of total fatty acids; —, not detected. Abbreviations are exemplified by: 8:0 3-OH, 3-hydroxy-octanoic acid; 12:0, dodecanoic acid; 15:1 ω 6c, *cis*-9-pentadecenoic acid; 16:1 ω 7c/15:0 iso 2-OH, *cis*-9-hexadecenoic acid and/or 2-hydroxy-13-methyl-tetradecanoic acid; 18:2 ω 6,9c/18:0 anteiso, *cis*-9,12-octadecadienoic acid and/or 15-methyl-heptadecanoic acid; 18:1 ω 7c/12t/9t, one or more of *cis*-11-, *trans*-6- or *trans*-9-octadecenoic acid.

Fatty acid	1	2	3	4	5	6	7	8
8:0 3-OH	2.5	—	—	—	—	—	—	—
10:0 3-OH	—	9.2	9.4	7.1	3.8	5.8	7.2	4.1
12:0	2.6	7.4	7.4	4.9	—	0.9	2.5	—
12:0 2-OH	1.5	3.8	1.8	2.7	2.1	2.2	1.7	2.0
14:0	2.0	1.3	1.8	1.0	0.8	1.2	1.7	0.5
15:1 ω 6c	0.4	—	—	—	—	—	—	—
15:0	0.8	1.0	1.4	0.6	0.2	1.3	—	0.3
16:1 ω 7c	45.5	41.9	43.1	47.7	44.1	42.8	45.5	44.9
16:1 ω 7c/15:0 iso 2-OH	7.3	—	—	—	—	—	—	—
16:0	23.5	32.0	32.0	30.1	31.0	24.0	25.9	27.7
17:1 ω 8c	0.7	—	—	—	—	—	—	—
17:1 ω 6c	0.5	—	—	—	—	—	—	—
17:0	0.6	—	—	—	—	—	—	—
18:2 ω 6,9c/18:0 anteiso	0.3	—	—	—	—	0.3	—	—
18:1 ω 9c	0.4	—	—	—	—	0.3	—	—
18:1 ω 7c/12t/9t	11.1	3.3	3.2	3.7	12.9	13.0	11.0	15.5
18:0	0.3	—	—	0.5	0.5	0.4	—	0.6
Unidentified	—	—	—	—	—	0.1	—	0.6

cis-9-hexadecenoic (16:1 ω 7c) and hexadecanoic (16:0) acids. However, distinct differences in the relative proportions of the less-dominant fatty acids were apparent in differentiating KIN192^T from the species of *Pelomonas*, as well as species of the related genera *Mitsuaria* and *Roseateles*. The presence of 3-hydroxy-octanoic acid (8:0 3-OH), *cis*-9-pentadecenoic acid (15:1 ω 6c), *cis*-9-hexadecenoic acid and/or 2-hydroxy-13-methyl-tetradecanoic acid (16:1 ω 7c/15:0 iso 2-OH), *cis*-9-heptadecenoic acid (17:1 ω 8c), *cis*-11-heptadecenoic acid (17:1 ω 6c) and heptadecanoic acid (17:0), as well as the absence of 3-hydroxy-decanoic acid (10:0 3-OH), indicated significant differences in overall cellular fatty acid compositions in cells of KIN192^T in comparison with species of related genera. The relative amounts of dodecanoic acid (12:0), hexadecanoic acid (16:0) and one or more of *cis*-11-, *trans*-6- or *trans*-9-octadecenoic acid (18:1 ω 7c/12t/9t) further differentiated strain KIN192^T chemotaxonomically from *Pelomonas* species. The relative amounts of 3-hydroxy-octanoic acid and *cis*-9-hexadecenoic acid and/or 2-hydroxy-13-methyl-tetradecanoic acid, as well as the absence of 3-hydroxy-decanoic acid, allow good

discrimination of KIN192^T from the species of the genus *Pelomonas* and the closely related genera *Mitsuaria* and *Roseateles*.

Genomic DNA was isolated according to the method of Marmur (1961). DNA–DNA hybridizations were performed in duplicate using a non-radioactive method, as described by Ziemke *et al.* (1998). DNAs of strain KIN192^T, *A. commune* CCUG 48318^T and *P. saccharophila* CCUG 32988^T were double-labelled with DIG–11-dUTP and biotin–16-dUTP using a nick translation kit (Boehringer Mannheim). Each labelled DNA was hybridized against itself as well as DNAs of the strains *M. chitosanotabida* IAM 14711^T, *P. aquatica* CCUG 52575^T, *P. puraquae* CCUG 52769^T, *R. aquatilis* CCUG 48205^T, *R. depolymerans* CCUG 52219^T and *R. terrae* CCUG 52222^T. Genomic DNA–DNA relatedness between KIN192^T and the type strains of the species of the genera *Pelomonas*, *Mitsuaria* and *Roseateles* was less than 51 % in all cases when the DNA of strain KIN192^T was labelled, and less than 55 % when the DNAs of the complementary strains were labelled, indicating that strain KIN192^T could be delineated as representing a novel species in the *Rubrivivax* branch (Supplementary Table S3).

Determination of G + C content was performed for strain KIN192^T as well as for the type strains of the species of the closest related genera according to Urdiain *et al.* (2008) (Table 1). The G + C content of the genomic DNA of KIN192^T is 69.3 mol%.

The *Rubrivivax* line of descent includes the genera *Aquabacterium*, *Mitsuaria*, *Roseateles* and *Pelomonas*, constituting an interesting group of micro-organisms for their metabolic capabilities and their relevance in the ecological niches that they occupy. A relevant example is the investigation of the evolution of prokaryotic aerobic phototrophy initiated by Suyama *et al.* (2002). Unfortunately, the number of strains described for the 10 species of these genera is low, which does not allow good phylogenetic or taxonomic definition. In our opinion, the polyphasic characterization (chemotaxonomic, biochemical and phylogenetic) of more isolates will enable a better understanding and recognition of the species in this phylogenetic branch and, possibly, the unification of the three genera. Strain KIN192^T is clearly affiliated phylogenetically to this branch, but does not fit within the spectrum of species described and does not present characteristic phenotypic traits that allow its conclusive adscription to a described genus. Therefore, based on genotypic and phylogenetic analyses, as well as phenotypic and chemotypic characteristics, we conclude that strain KIN192^T represents a novel genus and species in the *Rubrivivax* phylogenetic branch, for which the name *Kinneretia asaccharophila* gen. nov., sp. nov. is proposed.

Description of *Kinneretia* gen. nov.

Kinneretia (Kin.ne.re'ti.a. N.L. fem. n. *Kinneretia* pertaining to Kinneret Lake, where the type strain of the type species was isolated).

Cells are Gram-negative, rod-shaped (approx. 2 µm long) and motile by means of a single polar flagellum. Oxidase-positive and catalase-negative. Not able to assimilate sugars. The major fatty acids are 16:1ω7c, 16:0 and 18:1ω7c/12t/9t. Phylogenetically, the genus belongs to the family Comamonadaceae. The type species is *Kinneretia asaccharophila*.

Description of *Kinneretia asaccharophila* sp. nov.

Kinneretia asaccharophila (a.sac.cha.ro'phi.la. Gr. pref. *a-* not; Gr. n. *saccharon* sugar; Gr. adj. *philos* loving; N.L. fem. adj. *asaccharophila* not sugar loving).

Displays the following properties in addition to those given in the genus description. Colonies are small, approximately 2–3 mm in width, cream in colour, translucent, with irregular and undulate margins. Good growth occurs in R2A medium between 20 and 37 °C; no growth at 10 or 45 °C. Positive for nitrate reduction. Tryptophanase, glucose fermentation, aesculin hydrolysis, PNPG test and arginine dihydrolase, β-galactosidase and urease activities are negative, but positive for gelatinase. Negative for growth with D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetylglucosamine, maltose, caprate, L-malate and citrate; good growth with D-gluconate and phenylacetate and extremely weak growth with adipate. Good growth in the presence of 0.5 % NaCl. Positive reactions for alkaline phosphatase, esterase lipase (C8), esterase (C4) and leucyl arylamidase. Negative reactions for lipase (C14), trypsin, chymotrypsin, phosphoamidase, acid phosphatase, α-fucosidase, α-mannosidase, N-acetyl-β-glucosaminidase, α-glucosidase, β-glucosidase, β-glucuronidase, β-galactosidase, α-galactosidase and cystine and valine arylamidases. The following compounds are assimilated during growth: acetic acid, D- and L-alanine, L-alaninamide, L-asparagine, 2,3-butanediol, α-cyclodextrin, dextrin, i-erythritol, L-glutamic acid, glycerol, DL-α-glycerol phosphate, glycogen, glycyl L-glutamic acid, α-, β- and γ-hydroxybutyric acids, inosine, α-ketovaleric acid, DL-lactic acid, L-phenylalanine, pyruvic acid methyl ester, L-proline, hydroxy-L-proline, L-serine, succinic acid monomethyl ester, L-threonine, thymidine, Tweens 40 and 80, uridine and urocanic acid. The following compounds are not assimilated: *cis*-aconitic acid, adonitol, L-alanyl glycine, γ-aminobutyric acid, 2-aminoethanol, L-arabinose, D-arabitol, L-aspartic acid, glycyl L-aspartic acid, bromosuccinic acid, DL-carnitine, cellobiose, citric acid, formic acid, D-fructose, L-fucose, D-galactonic acid lactone, N-acetyl-D-galactosamine, D-galactose, D-galacturonic acid, gentiobiose, D-gluconic acid, N-acetyl-D-glucosamine, D-glucosaminic acid, α-D-glucose, α-D-glucose 1-phosphate, D-glucose 6-phosphate, methyl β-D-glucoside, glucuronamide, D-glucuronic acid, L-histidine, *myo*-inositol, itaconic acid, α-ketobutyric acid, α-ketoglutaric acid, α-lactose, lactulose, L-leucine, malonic acid, maltose, D-mannitol, D-mannose, melibiose, L-ornithine, *p*-hydroxyphenylacetic acid, phenylethylamine, propionic acid, D-psicose, putrescine, L-pyroglutamic acid, quinic acid, raffinose, L-rham-

nose, D-saccharic acid, sebacic acid, D-serine, D-sorbitol, succinamic acid, succinic acid, sucrose, trehalose, turanose and xylitol. The G + C content of the genomic DNA of the type strain is 69.3 mol%.

The type strain, KIN192^T (=CCUG 53117^T =CECT 7319^T), was isolated from fresh water of Lake Kinneret, Israel.

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