

7 The Family *Halobacteriaceae*

Aharon Oren

Department of Plant and Environmental Sciences, The Institute of Life Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel

Taxonomy, Historical and Current	42		
Family <i>Halobacteriaceae</i> Gibbons 1974, 269 ^{AL}	42		
Phylogenetic Structure of the Family and Its Genera	57		
Genome Analysis	57		
Phages	63		
Phenotypic Analyses	65		
The Properties of the Genera and Species of <i>Halobacteriaceae</i>	65		
Genus <i>Halobacterium</i> Elazari-Volcani 1957, 207 ^{AL} ; emend. Kamekura and Dyll-Smith 1995, 344; emend. Oren, Arahal, and Ventosa 2009, 638	81		
Genus <i>Haladaptatus</i> Savage, Krumholz, Oren, and Elshahed 2007, 23 ^{VP} ; emend. Cui, Sun, Gao, Dong, Xu, Zhou, Liu, Oren, and Zhou 2010a, 1087; emend. Roh, Lee, and Bae 2010, 1189	83		
Genus <i>Halalkalicoccus</i> Xue, Fan, Ventosa, Grant, Jones, Cowan, and Ma 2005, 2504 ^{VP}	85		
Genus <i>Halarchaeum</i> Minegishi, Echigo, Nagaoka, Kamekura, and Usami 2010, 2515 ^{VP}	85		
Genus <i>Haloarchaeobius</i> Makhdoumi-Kakhki, Amoozegar, Bagheri, Ramezani, and Ventosa 2012, 1024 ^{VP}	85		
Genus <i>Haloarcula</i> Torreblanca, Rodriguez-Valera, Juez, Kamekura, and Kates 1986b, 573 ^{VP} (Validation list 22); Effective Publication: Torreblanca, Rodriguez-Valera, Juez, Kamekura, and Kates 1986a, 98; emend. Oren, Arahal, and Ventosa 2009, 638	85		
Genus <i>Halobaculum</i> Oren, Gurevich, Gemmell, and Teske 1995, 752 ^{VP}	87		
Genus <i>Halobellus</i> Cui, Yang, Gao, and Xu 2011d, 2687 ^{VP}	89		
Genus <i>Halobiforma</i> Hezayen, Tindall, Steinbüchel, and Rehm 2002, 2278 ^{VP} ; emend. Oren, Arahal, and Ventosa 2009, 640	89		
Genus <i>Halococcus</i> Schoop 1935, 817 ^{AL} ; emend. Oren, Arahal, and Ventosa 2009, 639	89		
Genus <i>Haloferax</i> Torreblanca, Rodriguez-Valera, Juez, Kamekura, and Kates 1986b, 573 ^{VP} (Validation list 22); Effective Publication: Torreblanca, Rodriguez-Valera, Juez, Kamekura, and Kates 1986a, 98; emend. Oren, Arahal, and Ventosa 2009, 639	92		
		Genus <i>Halogeometricum</i> Montalvo-Rodríguez, Vreeland, Oren, Kessel, Betancourt, and López-Garriga 1998, 1310 ^{VP} ; emend. Cui, Yang, Gao, Li, Xu, Zhou, Liu, and Zhou 2010f, 2615	95
		Genus <i>Halogramum</i> Cui, Gao, Sun, Dong, Xu, Zhou, Liu, Oren, and Zhou 2010b, 1369 ^{VP} ; emend. Cui, Yang, Gao, and Xu 2011e, 913	95
		Genus <i>Halolamina</i> Cui, Gao, Yang, and Xu 2011b, 1619 ^{VP}	98
		Genus <i>Halomarina</i> Inoue, Itoh, Ohkuma, and Kogure 2011, 944 ^{VP}	98
		Genus <i>Halomicrobium</i> Oren, Elevi, Watanabe, Tamura, Ihara, and Corcelli 2002, 1834 ^{VP}	98
		Genus <i>Halonotius</i> Burns, Janssen, Itoh, Kamekura, Echigo, and Dyll-Smith 2010, 1198 ^{VP}	98
		Genus <i>Halopelagius</i> Cui, Li, Gao, Xu, Zhou, Liu, Oren, and Zhou 2010g, 2092 ^{VP}	98
		Genus <i>Halopenitus</i> Amoozegar, Makhdoumi- Kakhki, Shahzede Fazeli, Azarbaijani, and Ventosa 2012, 1935 ^{VP}	98
		Genus <i>Halopiger</i> Gutiérrez, Castillo, Kamekura, Xue, Ma, Cowan, Jones, Grant, and Ventosa 2007, 1404 ^{VP}	99
		Genus <i>Haloplanus</i> Elevi Bardavid, Mana, and Oren 2007, 782 ^{VP} ; emend. Cui, Gao, Li, Xu, and Zhou 2010c, 1826	99
		Genus <i>Haloquadratum</i> Burns, Janssen, Itoh, Kamekura, Li, Jensen, Rodríguez-Valera, Bolhuis, and Dyll-Smith 2007, 391 ^{VP}	99
		Genus <i>Halorhabdus</i> Wainø, Tindall, and Ingvorsen 2000, 188 ^{VP} ; emend. Antunes, Taborda, Huber, Moissl, Nobre, and Da Costa 2008, 218	99
		Genus <i>Halorientalis</i> Cui, Yang, Gao, and Xu 2011d, 2687 ^{VP}	99
		Genus <i>Halorubrum</i> McGenity and Grant 1996, 362 ^{VP} ; Effective Publication: McGenity and Grant 1995, 241; emend. Oren, Arahal, and Ventosa 2009, 639	99
		Genus <i>Halosarcina</i> Savage, Krumholz, Oren, and Elshahed 2008, 859 ^{VP} ; emend. Cui, Gao, Li, Xu, Zhou, Liu, and Zhou 2010d, 2464	100
		Genus <i>Halosimplex</i> Vreeland, Rosenzweig, Straight, Krammes, Dougherty, and Kamekura 2002, 450 (Validation list 92, 2003, 936 ^{VP})	100
		Genus <i>Halostagnicola</i> Castillo, Gutiérrez, Kamekura, Xue, Ma, Cowan, Jones, Grant, and Ventosa 2006, 1521 ^{VP}	100

Genus <i>Haloterrigena</i> Ventosa, Gutiérrez, Kamekura, and Dyall-Smith 1999b, 135 ^{VP} ; emend. Oren, Arahal, and Ventosa 2009, 640	100
Genus <i>Halovenus</i> Makhdoumi-Kakhki, Amoozegar, and Ventosa 2012a, 1334 ^{VP}	101
Genus <i>Halovivax</i> Castillo, Gutiérrez, Kamekura, Ma, Cowan, Jones, Grant, and Ventosa 2006, 767 ^{VP}	101
Genus <i>Natrialba</i> Kamekura and Dyall-Smith 1996, 625 ^{VP} ; Effective Publication: Kamekura and Dyall-Smith 1995, 347 (Validation list 57); emend. Oren, Arahal, and Ventosa 2009, 640	101
Genus <i>Natrinema</i> McGenity, Gemmell, and Grant 1998, 1194 ^{VP}	101
Genus <i>Natronoarchaeum</i> Shimane, Hatada, Minegishi, Mizuki, Echigo, Miyazaki, Ohta, Usami, Grant, and Horikoshi 2010, 2532 ^{VP}	102
Genus <i>Natronobacterium</i> Tindall, Ross, and Grant 1984b, 355 ^{VP} ; Effective Publication: Tindall, Ross, and Grant 1984a, 41 (Validation list 15)	102
Genus <i>Natronococcus</i> Tindall, Ross, and Grant 1984b, 355 ^{VP} ; Effective Publication: Tindall, Ross, and Grant 1984a, 41	102
Genus <i>Natronolimnobiuss</i> Itoh, Yamaguchi, Zhou, and Takashina 2005, 1744 ^{VP} (Validation list no. 105); Effective Publication: Itoh, Yamaguchi, Zhou, and Takashina 2005, 114	102
Genus <i>Natronomonas</i> Kamekura, Dyall-Smith, Upasani, Ventosa, and Kates 1997, 856 ^{VP} , emend. Burns, Janssen, Itoh, Minegishi, Usami, Kamekura, and Dyall-Smith 2010, 1175	103
Genus <i>Natronorubrum</i> Xu, Zhou, and Tian 1999, 265 ^{VP} ; emend. Cui, Tothy, Feng, Zhou, and Liu 2006, 1517; emend. Oren, Arahal, and Ventosa 2009, 641	103
Genus <i>Salarchaeum</i> Shimane, Hatada, Minegishi, Echigo, Nagaoka, Miyazaki, Ohta, Maruyama, Usami, Grant, and Horikoshi 2011, 2269 ^{VP}	103
Isolation, Enrichment, and Maintenance Procedures	103
Maintenance	104
Chemotaxonomic Properties	104
Surface Layers	104
Polar Lipids, Neutral Lipids, and Pigments	105
Respiratory Quinones and Polyamines	106
Physiological Properties	106
Sensitivity to Antibiotics	108
Halocins	108
Ecology	108

Pathogenicity: Clinical Relevance 109

Application 109

Abstract

The family *Halobacteriaceae*, first proposed by Gibbons in 1974, is affiliated with the archaeal phylum Euryarchaeota. Currently (August 2012) it encompasses 40 genera: *Halobacterium* [type genus], *Haladaptatus*, *Halalkalicoccus*, *Halarchaeum*, *Halarchaeobius*, *Haloarcula*, *Halobaculum*, *Halobellus*, *Halobiforma*, *Halococcus*, *Haloferax*, *Halogeometricum*, *Halogramum*, *Halolamina*, *Halomarina*, *Halomicrobium*, *Halonotius*, *Halopelagius*, *Halopenitus*, *Halopiger*, *Haloplanus*, *Haloquadratum*, *Halorhabdus*, *Halorientalis*, *Halorubrum*, *Halosarcina*, *Halosimplex*, *Halostagnicola*, *Haloterrigena*, *Halovenus*, *Halovivax*, *Natrialba*, *Natrinema*, *Natronoarchaeum*, *Natronobacterium*, *Natronococcus*, *Natronolimnobiuss*, *Natronomonas*, *Natronorubrum*, and *Salarchaeum*, with a total of 137 species. All members of the family have a high requirement for salt, and most grow optimally at salt concentrations above 150–200 g/l. Most species are pigmented red-pink by carotenoid pigments and have an aerobic chemoheterotrophic metabolism. Some have the ability to grow anaerobically by fermentation, anaerobic respiration, or using bacteriorhodopsin to absorb light as an energy source.

Taxonomy, Historical and Current

Family *Halobacteriaceae* Gibbons 1974, 269^{AL}

Ha.lo.bac.te.ri.a.ce'ae. N.L. neut. n. *Halobacterium*, type genus of the family; -*aceae*, ending to denote a family; N.L. fem. pl. n. *Halobacteriaceae*, the *Halobacterium* family.

Type genus: *Halobacterium*.

The mol% G + C of the DNA varies between 46.9 and 71.2.

The family *Halobacteriaceae* (order *Halobacteriales*; Grant et al. 2001a) was circumscribed on the basis of the high salt requirement of its members, their physiological and chemotaxonomic features, and their phylogenetic affiliation with the Euryarchaeota phylum of the Archaea (Grant et al. 2001b). At the time of writing (August 2012), the family contained 40 genera with a total of 137 species whose names have standing in the nomenclature (↪ [Tables 7.1](#), ↪ [7.2](#), ↪ [7.3](#), ↪ [7.4](#), ↪ [7.5](#), ↪ [7.6](#), ↪ [7.7](#), ↪ [7.8](#), ↪ [7.9](#), ↪ [7.10](#), ↪ [7.11](#), ↪ [7.12](#), ↪ [7.13](#), ↪ [7.14](#), ↪ [7.15](#), ↪ [7.16](#), ↪ [7.17](#), ↪ [7.18](#), ↪ [7.19](#), ↪ [7.20](#), ↪ [7.21](#), and ↪ [7.22](#)): *Halobacterium* [type genus; three-letter abbreviation *Hbt.*] (3 species), *Haladaptatus* (*Hap.*) (3 species), *Halalkalicoccus* (*Hac.*) (2 species), *Halarchaeum* (*Hla.*) (1 species), *Halarchaeobius* (*Hab.*) (1 species), *Haloarcula* (*Har.*) (9 species), *Halobaculum* (*Hbl.*) (1 species), *Halobellus*

Table 7.1

Comparison of selected characteristics of the members of the genera *Halobacterium*, *Haladaptatus*, and *Halalkalicoccus*

Genus	<i>Halobacterium</i> ^a		<i>Haladaptatus</i>		<i>Halalkalicoccus</i>	
Species	<i>Hbt. salinarum</i> ^a	<i>Hbt. jilantaiense</i> ^b	<i>Hbt. noricense</i> ^c	<i>Hap. pauchihalophilus</i> ^d	<i>Hap. litoreus</i> ^f	<i>Hac. tibetensis</i> ^g
Older names	<i>Halobacterium salinarium</i> ; includes <i>Halobacterium halobium</i> and <i>Halobacterium cutirubrum</i>					
Type strain	ATCC 33171 CIP 104033 DSM 3754 JCM 8978 NBRC 102687 NCIMB 764 NRC 34002 VKM B-1769	CGMCC 1.5337 JCM 13558	ATCC BAA-852 DSM 15987 JCM 15102 NCIMB 13967	ATCC BAA-1313 DSM 18195 JCM 13897 KCTC 4006	CGMCC 1.7737 JCM 15771	AS 1.3240 JCM 11890
Cell shape	Rods	Slender rods	Rods	Cocci-coccobacilli	Cocci	Cocci
Cell size (µm)	0.5–1.0 × 1.0–6.0	0.5–1.0 × 1.0–3.0	1.2–2.0	1.2	1.0–1.5	1.0–1.5
Motility	+	NR	+	–	–	–
Colony color	Pink	Red	Light red	Pink	Pink	Orange
NaCl range for growth and optimum (%)	18–30 (Opt. 20–25)	16–30 (Opt. 18–20)	>12.5 (Opt. 15.0–17.5)	5–30 (Opt. 18)	10–30 (Opt. 30)	8–30 (Opt. 20)
Lysis in distilled water	+	+	+	–	–	–
Magnesium requirement and optimum (M)	0.05–0.1	0.05–0.3 (Opt. 0.1–0.2)	Opt. 0.7–0.8	> 0.005	>0.005 (Opt. 0.02)	–
pH range for growth and optimum	5.5–8.0	5.5–8.5 (Opt. 7.0–7.5)	5.2–7.0	5.0–7.5 (Opt. 6.0–6.5)	6.0–8.5 (Opt. 7.0)	8.0–10.5 (Opt. 9.5–10.0)
Temperature range for growth and optimum (°C)	20–55 (Opt. 50)	22–55 (Opt. 40)	28–50 (Opt. 37–45)	25–45 (Opt. 25–30)	25–55 (Opt. 37–40)	23–47 (Opt. 40)
						21–50 (Opt. 37–45)

^aATCC, American Type Culture Collection; CIP, Chinese Institute of Pathology and Microbiology; DSM, Deutsche Sammlung von Mikroorganismen und Zellkulturen; JCM, Japan Collection of Micro-organisms and Cell Cultures; NBRC, National Institute of Advanced Industrial Science and Technology; NCIMB, National Collection of Industrial Microbiology and Cell Culture; NRC, National Reference Culture; VKM, Vsesoyuznyy Nauchno-Issledovatskiy Tsentr Mikroorganizmologii i Biokhimiya.

^bCGMCC, China General Microbiological Culture Collection; JCM, Japan Collection of Micro-organisms and Cell Cultures.

^cATCC, American Type Culture Collection; DSM, Deutsche Sammlung von Mikroorganismen und Zellkulturen; JCM, Japan Collection of Micro-organisms and Cell Cultures; NCIMB, National Collection of Industrial Microbiology and Cell Culture.

^dATCC, American Type Culture Collection; DSM, Deutsche Sammlung von Mikroorganismen und Zellkulturen; JCM, Japan Collection of Micro-organisms and Cell Cultures; KCTC, Korean Collection of Type Cultures.

^eDSM, Deutsche Sammlung von Mikroorganismen und Zellkulturen; JCM, Japan Collection of Micro-organisms and Cell Cultures.

^fCGMCC, China General Microbiological Culture Collection; JCM, Japan Collection of Micro-organisms and Cell Cultures.

^gAS, Institute of Botany, Chinese Academy of Sciences; JCM, Japan Collection of Micro-organisms and Cell Cultures.

Table 7.1 (continued)

Genus	<i>Halobacterium</i> ^a	<i>Hbt. jilantaiense</i> ^b	<i>Hbt. noricense</i> ^c	<i>Haladaptatus</i>	<i>Hap. citbarius</i> ^e	<i>Hap. litoreus</i> ^f	<i>Halalkalicoccus</i>	<i>Hac. jeotgalph</i>
Species	<i>Hbt. salinarum</i> ^a	<i>Hbt. jilantaiense</i> ^b	<i>Hbt. noricense</i> ^c	<i>Hap. pauchalophilus</i> ^d	<i>Hap. citbarius</i> ^e	<i>Hap. litoreus</i> ^f	<i>Hac. tibetensis</i> ^g	<i>Hac. jeotgalph</i>
Organic substrates used	Glyc	Glyc	Glyc (w) Star (w)	Acet Citr Fruc Fuma Gala Gluc Glyc Mala Manni Pyru Sucr Treh Xylo	Acet Form Fruct Lacto Gluc Sucr	Acet Fuma Gala Gluc Glyc Lact Malt Mann Manni Pyru Star Sucr	Acet Fruc Gluc Lacto Malt Manni Sorb Succ	Acet Citr Gluc Lacto Sucr
Acid produced from	–	–	–	Fruc Gala Gluc Glyc Manni Star Sucr Xylo	Gluc Sucr	Gala Gluc Glyc Malt Star Sucr	–	NR
Organic substrates not used	Gala Gluc Malt Sucr Xylo	Fruc Gala Gluc Lacto Malt Mann Manni Ribo Sorbi Sucr Xylo	Gala Gluc Malt Sucr Xylo	Dulc Lacto Sorbi Sucr	Citr Manni	Fruc Lacto Mala Sorb Succ Ribo Xylo	Arab Gala Mann Raff Rham Ribo Sucr Xylo	Fruc
Indole from typtophan	+	+	NR	+	+	+	–	NR
Starch hydrolysis	–	–	–	+	–	+	–	NR
Gelatin liquefaction	+	+	–	NR	+	+	–	NR
Nitrate reduction	–	+	–	–	–	+	+	–
Polar lipids	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-TGD-1, S-TeGD, TGD-1	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-TGD-1, S-TeGD, TGD-1	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-TeGD, TGD-1	PG, PGP-Me, PGS, two unidentified glycolipids	PG, PGP-Me, two unidentified glycolipids	PG, PGP-Me, PGS, three glycolipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me	PG, PGP- Me
Respiratory quinones	MK-8, MK-8(H ₂), traces of MK- 7(H ₂), MK-7, MK-6	NR	MK-8, MK-8(H ₂), traces of MK-7(H ₂), MK-9	NR	NR	NR	MK-8, small amounts of MK-8(H ₂)	NR

Sensitivity to antibiotics	Sensitive: Ani Nov	Sensitive: Ani Nov	Sensitive: Ani Nov	Sensitive: Ani Nov	Sensitive: Ani Aph Chl Rif	Sensitive: Bac Nov Rif	Sensitive: Chl (slight) Nov Rif	Sensitive: Ani Aph Nov
	Resistant: Amp Chl Gen Kan Str Tet Van	Resistant: Amp Bac Chl Ery Gen Kan Pen Rif Str Tet	Resistant: Amp Bac Chl Gen Kan Str Tet Van	Resistant: Amp Chl Ery Neo Pen	Resistant: Amp Chl Ery	Resistant: Amp Ery Kan Pol Str	Resistant: Amp Chl Cip Ery Kan Neo Pen Tet	Resistant: Amp Bac Neo Pen Pol Str Tet
G + C content of DNA (mol%)	66–70.9 (major component); 57–60 (minor component)	64.2	54.3–54.5	60.5	56.5	54.0	61.5	63.2
Sample source and site	Salt lakes, salted food products	Salt lake, Inner Mongolia	Permian rock salt, Austria	Low-salt sulfidic spring, Oklahoma	Korean salt-fermented shellfish	Saltern, China	Salt lake, Tibet	Shrimp jeotgal (Korean food)

Data taken from:

^aGrant (2001a)

^bYang et al. (2006)

^cGruber et al. (2004)

^dSavage et al. (2007)

^eRoh et al. (2010a)

^fCui et al. (2010a)

^gXue et al. (2005)

^hRoh et al. (2007a)

Additional data on growth substrates and other properties can be found in the original species descriptions

General notes:

Most data were derived from the original species descriptions as cited; other sources may provide different data

Abbreviations of sugars, organic acids and other growth substrates: *Acer* Acetate, *Arab* Arabinose, *Benz* Benzoate, *Bury* Butanol; *Bury* Butyrate; *Cell* Cellobiose, *Citr* Citrate, *Dulc* Dulcitol, *Etha* Ethanol, *Form* Formate, *Fruc* Fructose, *Fuco* Fucose, *Fuma* Fumarate, *Gala* Galactose, *Gluc* Glucose, *Glyc* Glycerol, *Lact* Lactate, *Lacto* Lactose, *Mala* Malate, *Malt* Maltose, *Mann* Mannose, *Manni* Mannitol, *Melli* Melibiose, *Oxal* Oxalate, *Prop* Propionate, *PyrU* Pyruvate, *Raff* Raffinose, *Ribo* Ribose, *Rham* Rhamnose, *Sorb* Sorbose, *Sorbi* Sorbitol, *Star* Starch, *Succ* Succinate, *Sucr* Sucrose, *Treh* Trehalose, *Xylo* Xylose

Abbreviation of lipids: *PG* phosphatidyl glycerol, *PGP-Me* methyl ester of phosphatidyl glycerophosphate, *PGS* phosphatidyl glycerosulfate, *DGD* diglycosyl diether lipid, *S-DGD* sulfated diglycosyl diether lipid, *S₂-DGD* bis-sulfated diglycosyl diether lipid, *TGD* triglycosyl diether lipid, *S-TGD* sulfated triglycosyl diether lipid, *S-TeGD* sulfated tetraglycosyl diether lipid.

Abbreviations of quinones: *DMK* dimethylated menaquinone, *MMK* monomethylated menaquinone, *MK* menaquinone

Abbreviations of antibiotics: *Amp* Ampicillin, *Ani* Anisomycin, *Aph* Aphidicolin, *Bac* Bacitracin, *Chi* Chloramphenicol, *Cip* Ciprofloxacin, *Ery* Erythromycin, *Gen* Gentamicin, *Kan* Kanamycin, *Neo* Neomycin, *Nor* Norfloxacin, *Nov* Novobiocin, *Pen* Penicillin, *Pol* Polymyxin, *Rif* Rifampicin, *Str* Streptomycin, *Tet* Tetracycline, *Van* Vancomycin

NR not reported; v, variable, depending on growth conditions; w, weakly positive

Table 7.2

Comparison of selected characteristics of the members of the genera *Halarchaeum*, *Haloarchaeobius*, *Halobaculum*, and *Halobellus*

Genus	<i>Halarchaeum</i>	<i>Haloarchaeobius</i>	<i>Halobaculum</i>	<i>Halobellus</i>		
Species	<i>Hla. acidiphilum</i> ^a	<i>Hab. iranensis</i> ^b	<i>Hbl. gomorrhense</i> ^c	<i>Hbs. clavatus</i> ^d	<i>Hbs. limi</i> ^e	<i>Hbs. salinus</i> ^e
Type strain	CECT 7534 DSM 22442 JCM 16109	IBRC-M 10013 KCTC 4048	ATCC 700876 DS2807 DSM 9297 JCM 9908	CGMCC 1.10118 JCM 16424	CGMCC 1.10331 JCM 16811	CGMCC 1.10710 DSM 18730 JCM 14359
Cell shape	Pleomorphic, discs and triangular shapes	Rods	Rods	Rods	Pleomorphic	Pleomorphic
Cell size (µm)	~2	1.5–2.0 × 3–7	0.5–1.0 × 5–10	~0.5 × 1.0–1.6	NR	NR
Motility	–	+	+ (w)	+	+	+
Colony color	Non-pigmented	Orange-red	Red	Red	Red	Red
NaCl range for growth and optimum (%)	18–30 (Opt. 21–24)	12–30 (Opt. 20)	> 6 (Opt. 9–12)	10–30 (Opt. 15)	8–30 (Opt. 15–23)	15–30 (Opt. 20)
Lysis in distilled water	+	+	+	NR	+	+
Magnesium requirement and optimum (M)	>0.001	–(Opt. 0.2)	Opt. 0.6–1.0	Opt. 0.05	–(Opt. 0–0.1)	>0.01 (Opt. 0.05)
pH range for growth and optimum	4.0–6.0 (Opt. 4.4–4.5)	6.0–8.0 (Opt. 7.5)	5.5–8.0 (Opt. 6.0–7.0)	5.5–9.0 (Opt. 7.0–7.5)	5.5–9.5 (Opt. 7.0)	5.5–9.5 (Opt. 7.0–7.5)
Temperature range for growth and optimum (°C)	15–45 (Opt. 37)	25–50 (Opt. 40)	Up to 45 (Opt. 40)	20–50 (Opt. 37)	25–55 (Opt. 45)	25–45 (Opt. 37)
Organic substrates used	Arab Cello Fruc Gala Gluc Glyc Raff Sucr Xylo	Fruc Gala Gluc Lacto Malt	Gala Gluc Glyc Lact Malt Sucr Star Treh Xylo	Fuma Gala Gluc Glyc Lact Lacto Mala Malt Mann Pyrus Succ Sucr	Gala Gluc Glyc Lact Lacto Malt Mann Manni Pyru Sorbi Sucr	Citr Gluc Glyc Lact Mala Pyru Sorbi Sucr
Acid produced from	NR	Gluc Malt	Gala Gluc Glyc Malt Star Sucr Treh Xylo	Gala Gluc Lacto Malt Mann Sucr	Gala Gluc Lacto Mann Sucr	Gala Gluc Lacto Mann Sucr
Organic substrates not used	Citr Lacto Malt Manni Ribo Sorbi Treh	Arab Manni Ribo Sucr	Acet Arab Citr Lacto Manni Prop Ribo Sorbi Succ	Fruc Manni Ribo Sorb Sorbi Xylo	Acet Citr Fruc Fuma Mala Ribo Sorb Succ Xylo	Acet Gala Fruc Fuma Lacto Malt Mann Ribo Sorb Succ Xylo
Indole from typtophan	–	–	–	–	–	–
Starch hydrolysis	–	–	+	–	–	–
Gelatin liquefaction	–	+	–	–	–	–
Nitrate reduction	–	–	+	+	+	–

■ Table 7.2 (continued)

Genus	<i>Halarchaeum</i>	<i>Haloarchaeobius</i>	<i>Halobaculum</i>	<i>Halobellus</i>		
Species	<i>Hla. acidiphilum</i> ^a	<i>Hab. iranensis</i> ^b	<i>Hbl. gomorreense</i> ^c	<i>Hbs. clavatus</i> ^d	<i>Hbs. limi</i> ^e	<i>Hbs. salinus</i> ^e
Polar lipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, and 4 unidentified glycolipids	PG, PGP-Me, PGS, 3 unidentified glycolipids, 1 minor phospholipid	PG, PGP-Me, S-DGD-1	PG, PGP-Me, PGS, S-DGD-1, minor amounts of other glycolipids	PG, PGP-Me, PGS, S-DGD-1, DGD-1 three minor unidentified glycolipids	PG, PGP-Me, PGS, S-DGD-1, DGD-1, one minor unidentified glycolipid
Respiratory quinones	NR	MK-8(II-H ₂)	NR	NR	NR	NR
Sensitivity to antibiotics	Sensitive: Ani Bac Nov Rif Tet	Sensitive: Bac Nov Rif	Sensitive: Ani Bac Nov	Sensitive: Ani Aph Bac Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Kan Nor Nov Rif
	Resistant: Amp Chl Ery Kan Neo Pen	Resistant: Amp Chl Ery Kan Neo Pen Str Tet	Resistant: Amp Chl Kan Neo Pen Str	Resistant: Amp Chl Ery Kan Neo Nor Pen Tet	Resistant: Amp Chl Cip Ery Kan Neo Nor Pen Str Tet	Resistant: Amp Chl Cip Ery Neo Pen Str Tet
G+C content of DNA (mol %)	61.4	67.7	70	61.5–62.4	69.2	67.0
Sample source and site	Australian solar salt imported to Japan	Salt lake, Iran	The Dead Sea	Solar saltern, China	Solar saltern, China	Solar saltern, Australia

Data taken from:

^aMinegishi et al. (2010b)

^bMakhdoumi-Kakhki et al. (2012b)

^cOren (2001), Oren et al. (1995)

^dCui et al. (2011d)

^eCui et al. (2012a)

Additional data on growth substrates and other properties can be found in the original species descriptions

(*Hbs.*) (3 species), *Halobiforma* (*Hbf.*) (3 species), *Halococcus* (*Hcc.*) (7 species), *Haloferax* (*Hfx.*) (11 species), *Halogeometricum* (*Hgm.*) (2 species), *Halogramum* (*Hgn.*) (4 species), *Halolamina* (*Hlm.*) (1 species), *Halomarina* (*Hmr.*) (1 species), *Halomicrobium* (*Hmc.*) (3 species), *Halonotius* (*Hns.*) (1 species), *Halopelagius* (*Hpl.*) (1 species), *Halopenitus* (*Hpt.*) (1 species), *Halopiger* (*Hpg.*) (2 species), *Haloplanus* (*Hpn.*) (3 species), *Haloquadratum* (*Hqr.*) (1 species), *Halorhabdus* (*Hrd.*) (2 species), *Halorientalis* (*Hos.*) (1 species), *Halorubrum* (*Hrr.*) (25 species), *Halosarcina* (*Hsn.*) (2 species), *Halosimplex* (*Hsx.*) (1 species), *Halostagnicola* (*Hst.*) (3 species), *Haloterrigena* (*Htg.*) (9 species), *Halovenus* (*Hvn.*) (1 species), *Halovivax* (*Hvx.*) (2 species), *Natrialba* (*Nab.*) (7 species), *Natrinema* (*Nnm.*) (7 species), *Natronoarchaeum* (*Nac.*) (1 species), *Natronobacterium* (*Nbt.*) (1 species), *Natronococcus* (*Ncc.*) (3 species), *Natronolimnobiis* (*Nln.*) (2 species), *Natronomonas* (*Nmn.*) (2 species), *Natronorubrum* (*Nrr.*) (5 species), and *Salarchaeum* (*Sar.*) (1 species). The three-letter abbreviations for the genus names within the family have been endorsed by the International Committee on Systematics of Prokaryotes Subcommittee on the Taxonomy of Halobacteriaceae (<http://www.the-icsp.org/taxa/halobacterlist.htm>; accessed October 29, 2012). At the time of writing,

descriptions were in press of *Hla. salinum* sp. nov. (Yamauchi et al. 2012) and *Hbl. magnesiophilum* (Shimoshige et al. 2012). The names *Hrr. sfaxense* (Trigui et al. 2011) and *Salinarchaeum laminariae* gen. nov., sp. nov. (Cui et al. 2011c) were effectively published, but were not yet validated. These taxa were not included in ► Tables 7.1, ► 7.2, ► 7.3, ► 7.4, ► 7.5, ► 7.6, ► 7.7, ► 7.8, ► 7.9, ► 7.10, ► 7.11, ► 7.12, ► 7.13, ► 7.14, ► 7.15, ► 7.16, ► 7.17, ► 7.18, ► 7.19, ► 7.20, ► 7.21, and ► 7.22.

DasSarma and DasSarma (2008) proposed to rename the family as “*Haloarchaeaceae*.” This name is not validly published, and the proposed change is in violation of the General Considerations, Principles, and Rules of the International Code of Nomenclature of Prokaryotes (Oren 2008).

When in the late 1970s 16S rRNA sequence information was first used to obtain phylogenetic information on the prokaryotes, it was quickly realized that the Halobacteriaceae belong to the newly defined group of the Archaea (Magrum et al. 1978). A short history of the taxonomy of the family, documenting how our concepts on the systematics of the group have changed over the years with the advance of new methods for the characterization of prokaryotes, was given by Oren (2012). Until the late 1970s, the diversity of the group was considered to be low

Table 7.3
Comparison of selected characteristics of the members of the genus *Haloarcula*

Genus	<i>Haloarcula</i> ^{a,b}	<i>Har. amylyolytica</i> ^d	<i>Har. argentinensis</i> ^e	<i>Har. hispanica</i> ^f	<i>Har. japonica</i> ^g	<i>Har. marismortui</i> ^h	<i>Har. quadrata</i> ⁱ	<i>Har. salaria</i> ^j	<i>Har. tradensis</i> ^k
Species	<i>Har. vallismortis</i> ^c								
Older names	Basonym: <i>Halobacterium vallismortis</i>					Synonyms: "Halobacterium marismortui" "Flavobacterium marismortui"			
Type strain	ATCC 29715 DSM 3756 IFO (now NBRC) 14741 JCM 8877 VKM B-1791	CGMCC 1.5335 JCM 13557	ATCC 700875 CIP 105173 DSM 12282 JCM 9737	ATCC 33960 DSM 4426 JCM 8911 NBRC 102182 VKM B-1755	ATCC 49778 DSM 6131 JCM 7785 NBRC 101032 VKM B-2009	ATCC 43049 CGMCC 1.1784 DSM 3752 JCM 8966 VKM B-1809	ATCC 700850 DSM 11927 JCM 11048	BCC 40029 JCM 15759 PCU 313	BCC 40030 JCM 15760 PCU 314
Cell shape	Pleomorphic rods	Rods	Triangular flat discs	Short rods	Triangular, with asymmetric division	Pleomorphic flat	Square to pleomorphic flat	Pleomorphic	Pleomorphic rods
Cell size (µm)	0.6–1.0 × 3.0–5.0	0.6–0.8 × 2.0–2.5	1.0 × 3.0	0.3 × 0.5–1.0	0.2–0.3 × 1.0–2.0	1.0–2.0 × 2.0–3.0	2.0–3.0	0.6–0.8 × 1.0–2.0	0.8–1.2 × 1.0–2.5
Motility	+	+	+	+	+	+(w)	+	–	–
Colony color	Pink	Red	Orange-red	Red-orange	Red	Red	Red-orange	Red	Red
NaCl range for growth and optimum (%)	>15 (Opt. 25)	12–30 (Opt. 17–19)	12–26 (Opt. 15–18)	15–30 (Opt. 20–25)	10–25 (Opt. 15–25)	10–30 (Opt. 20–23)	16–25 (Opt. 20–25)	> 15 (Opt. 20–25)	> 15 (Opt. 20–25)
Lysis in distilled water	+	+	NR	NR	NR	NR	+	+	+
Magnesium requirement and optimum (M)	NR	0.005–0.7 (Opt. 0.1–0.3)	>0.03 (Opt. 0.1)	> 0.005	0.04–0.65 (Opt. 0.16)	NR	> 0.05 (Opt. 0.1–0.5)	0.08–0.4	0.08–0.4
pH range for growth and optimum	5.5–8.5 (Opt. 7.4–7.5)	6.5–9.0 (Opt. 7.0–7.5)	NR	6.0–> 8.0 (Opt. 7.0)	6.0–8.0 (Opt. 7.0–7.5)	NR	5.9–8.0 (Opt. 6.5–7.0)	6.0–8.0 (Opt. 7.0)	6.0–8.0 (Opt. 7.0)

Table 7.3 (continued)

Genus	<i>Halobaculum</i> ^{a,b}	<i>Har. amylyolytica</i> ^d	<i>Har. argentinensis</i> ^e	<i>Har. hispanica</i> ^f	<i>Har. japonica</i> ^g	<i>Har. marismortui</i> ^h	<i>Har. quadrata</i> ⁱ	<i>Har. salaria</i> ^j	<i>Har. tradensis</i> ^j
Species	<i>Har. vallismortis</i> ^c	<i>Har. amylyolytica</i> ^d	<i>Har. argentinensis</i> ^e	<i>Har. hispanica</i> ^f	<i>Har. japonica</i> ^g	<i>Har. marismortui</i> ^h	<i>Har. quadrata</i> ⁱ	<i>Har. salaria</i> ^j	<i>Har. tradensis</i> ^j
Sensitivity to antibiotics	Sensitive: Bac Nov Resistant: Chl Ery Kan Pen Str Tet Van	Sensitive: Bac Nov Resistant: Amp Chl Cip Ery Kan Neo Pen Rif Str Tet Van	Sensitive: Ani Nov Resistant: Chl Kan Pen	Sensitive: Nov Resistant: Amp Bac Chl Ery Gen Kan Neo Pen Str Tet	Sensitive: Ani Bac Nov	Sensitive: Bac Nov	Sensitive: Ani Bac Nov Resistant: Amp Chl Ery Neo Pen Rif	Sensitive: Bac Resistant: Amp Chl Gen Nov Rif Str	Sensitive: Bac Nov Resistant: Amp Chl Gen Rif Str Tet
G + C content of DNA (mol%)	61.8 ^k	62.4	62	62.7	63.3	61.1 ^k	60.1	61.6	62.2
Sample source and site	Dearth Valley, CA, USA	Salt Lake, China	Salt flat, Argentina	Saltern, Spain	Saltern, Japan	The Dead Sea	Brine pool, Sinai, Egypt	Fish sacuce, Thailand	Fish sacuce, Thailand

Data taken from:

^aVentosa (2001a)^bTorreblanca et al. (1986)^cGonzalez et al. (1978)^dYang et al. (2007)^eIhara et al. (1997)^fJuez et al. (1986)^gHorikoshi et al. (1993)^hOren et al. (1990)ⁱOren et al. (1999)^jNamwong et al. (2011)^kCalculated from the genome sequence (see Table 7.21)

Additional data on growth substrates and other properties can be found in the original species descriptions

Table 7.4

Comparison of selected characteristics of the members of the genera *Halobiforma*, *Halogeometricum*, and *Halogramum*

Genus	<i>Halobiforma</i>		<i>Hbf. lacisalsi</i> ^b		<i>Hbf. nitratireducens</i> ^{a,c}	<i>Halogeometricum</i> ^d		<i>Hgm. rufum</i> ^f	<i>Halogramum</i>		<i>Hgn. amyolyticum</i> ^h	<i>Hgn. gelatinolyticum</i> ^h	<i>Hgn. salarium</i>
Species	<i>Hbf. haloterrestri</i> ^a				<i>Hbf. nitratireducens</i> ^{a,c}	<i>Hgm. bovinquense</i> ^e							
Older names					Basonym: <i>Natronobacterium nitratireducens</i>								
Type strain	DSM 13078 JCM 11627	CGMCC 1.3738 JCM 12983			AS 1.1980 JCM 10879	ATCC 700274 DSM 11551 JCM 10706	CGMCC 1.17738 JCM 15772	CGMCC 1.7736 JCM 15770	CGMCC 1.10121 JCM 16428	CGMCC 1.10119 JCM 16426	DSM 23171 KCTC 4066		
Cell shape	Rods, pleomorphic cells, cocci	Rods, pleomorphic cells, cocci			Rods	Pleomorphic	Pleomorphic	Pleomorphic	Pleomorphic	Pleomorphic	Pleomorphic		
Cell size (µm)	0.5–1.5 × 2–8 (rods), 1.25–2.0 diameter (cocci)	0.5–0.8 × 3.0–5.0 (rods), 0.5–1.5 diameter (cocci)			0.4–0.8 × 3–7	1–2 × 1–3	NR	NR	1–2	1–2	0.5–2.0		
Motility	+	+			+	+	+	+	–	+	+	+	+
Colony color	Red	Reddish			Red	Pink	Red	Red	Red	Red	Red	Red	Red
NaCl range for growth and optimum (%)	13–30 (Opt. 20)	>10 (Opt. 15–25)			15–30 (Opt. 20)	>8 (Opt. 20–25)	12–30 (Opt. 23)	15–25 (Opt. 23)	8–30 (Opt. 20–23)	10–30 (Opt. 20–23)	8–30 (Opt. 15–20)		
Lysis in distilled water	+	+			+	NR	NR	NR	+	+	+	+	+
Magnesium requirement and optimum (M)	–	0–0.5			NR	Opt. 0.04–0.08	0.05–0.7 (Opt. 0.3)	Opt. 0.3	– (Opt. 0.05)	Opt. 0.1	– (Opt. 0.05–0.15)		
pH range for growth and optimum	6.0–9.2 (Opt. 7.5)	6.5–9.0 (Opt. 7.5)			8.0–10.5 (Opt. 8.5)	6.0–8.0 (Opt. 7.0)	6.0–8.5 (Opt. 7.0)	6.0–8.0 (Opt. 7.5)	5.5–9.0 (Opt. 6.5)	5.5–9.0 (Opt. 7.0)	5.0–8.0 (Opt. 7.0)		
Temperature range for growth and optimum (°C)	Opt. 42 Max 58	24–57 (opt 42–45)			26–44 (Opt. 36–41)	22–50 (Opt. 40)	25–55 (Opt. 42)	20–50 (Opt. 37)	20–50 (Opt. 37)	20–50 (Opt. 37)	15–50 (Opt. 37)		

Table 7.4 (continued)

Genus	<i>Halobiforma</i>	<i>Hbf. haloterrestris</i> ^a	<i>Hbf. laclisalsi</i> ^b	<i>Hbf. nitratreducens</i> ^{a,c}	<i>Halogeometricum</i> ^d	<i>Hgm. rufum</i> ^f	<i>Halogramum</i>	<i>Hgn. amylolyticum</i> ^h	<i>Hgn. gelatinolyticum</i> ^h	
Organic substrates used	Arab Acet Buty Gluc Glyc Malt Pyru Sucr	Acet (w) Fruc Gluc (w) Pyru Manni (w)	Acet Fruc Gluc Glyc Lact Pyru	Acet (w) Fruc Gluc (w) Pyru Manni (w)	Cell Fruc Gluc Glyc Malt Mann Raff Treh Xylo	Acet Gala Gluc Glyc Lact Lacto Mann Malt Pyru Sorb Sucr	Acet Fuma Gala Gluc Glyc Lact Lacto Mala Malt Mann Manni Pyru Star Sucr	Acet Fuma Gala Gluc Glyc Lact Lacto Mala Malt Mann Manni Pyru Sorb Sucr	Acet Gala Gluc Glyc Lact Lacto Mann Pyru Sorb Sucr	Acet Arab Fruc Fuco Gala Gluc Glyc Lact Malt Mann Manni Meli Pyru Ribo Sorb Sorbi Star Sucr Xylo
Acid produced from	Arab Gluc Malt Sucr Xylo	–	Gluc Glyc	–	Arab Fruc Lacto Ribo Sucr Xylo	Carbohydrates	Gala Gluc Glyc Malt Sucr	Arab Gala Gluc Lacto Mann Sucr Xylo	Gala Gluc Lacto Mann Sucr	Arab Fruc Gluc Glyc Malt Mann Sucr Xylo
Organic substrates not used	Citr Fruc Gala Lacto Manni Sorb Xylo	–	Arab Citr Fuma Gala Lacto Mala Malt Manni Prop Rham Ribo Sorbi Sucr Xyl	Arab Fuma Gala Glyc Lacto Mala Malt Mann Prop Raff Rham Ribo Sorb Sucr Sucr Xylo	NR	Citr Fruc Fuma Mala Manni Ribo Sorb Sucr Xylo	Citr Fuma Mala Manni Rham Ribo Sorb Sucr Xylo	Citr Fuma Fruc Mala Malt Manni Ribo Rham Sorb Sucr Xylo	Citr Fuma Fruc Mala Malt Manni Ribo Rham Sorb Sucr Xylo	Citr Fuma Lacto Mala Rham Sucr
Indole from typtophan	NR	–	–	–	+	+	–	+	+	–
Starch hydrolysis	–	–	–	+	–	–	w	+ or w	+	–
Gelatin liquefaction	+	+	+	+	+	–	+	–	+	+
Nitrate reduction	+	+	–	+	+	–	+	+	–	–
Polar lipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, S-TGD, TGD	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ diether derivatives of PG, PGP-Me, glycolipid	–	PG, PGP-Me, a minor phospholipid PL1	PG, PGP-Me, 1 glycolipid resembling TGD-2	PG, PGP-Me, S- DGD-1, DGD-1	PG, PGP-Me, S- DGD-1, DGD-1, 1 unidentified phospholipid	PG, PGP-Me, trace of PGS S-DGD-1, DGD-1, 2 unidentified glycolipids	PG, PGP-Me, trace of PGS S- DGD-1, DGD-1, 3 unidentified glycolipids	PG, PGP-Me, S-DGD-1, DGD-1, 1 unidentified phospholipid

Respiratory quinones	MK-8 MK-8[VIII-H ₂]	NR	NR	NR	NR	NR	NR	NR	NR
Sensitivity to Antibiotics	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif
	Resistant: Chl Ery Pen Str Tet	Resistant: Amp Chl Neo Pen	Resistant: Amp Chl Ery Kan Pen Tet Van	Resistant: Amp Chl Ery Gen Kan Neo Nor Pen Str Tet	Resistant: Amp Chl Cip Ery Gen Kan Neo Nor Pen Str Tet	Resistant: Amp Chl Cip Ery Gen Kan Neo Nor Pen Str Tet	Resistant: Amp Chl Cip Ery Gen Kan Neo Nor Pen Str Tet	Resistant: Amp Chl Ery Gen Kan Neo Nor Pen Str Tet	Resistant: Amp Chl Ery Gen Kan Neo Nor Pen Str Tet
G + C content of DNA (mol %)	66.9	63.8	59.9 ^j	64.9	55.7	62.0	64.0	63.7–64.4	
Sample source and site	Hypersaline soil, Egypt	Salt lake, Inner Mongolia	Solar Saltern, Puerto Rico	Solar saltern, China	Soil from solar saltern, China	Solar saltern, China	Solar saltern, China	Salt on seashore, Korea	

Data taken from:

^aHezayen et al. (2002)

^bXu et al. (2005a)

^cXin et al. (2001)

^dOren et al. (2001)

^eMontalvo-Rodriguez et al. (1998)

^fCui et al. (2010f)

^gCui et al. (2010b)

^hCui et al. (2011e)

ⁱKim et al. (2011)

^jCalculated from the genome sequence (see [Table 7.21](#))

Additional data on growth substrates and other properties can be found in the original species descriptions

Table 7.5
Comparison of selected characteristics of the members of the genus *Halococcus*

Genus	<i>Halococcus</i> ^a	<i>Hcc. dombrowskii</i> ^c	<i>Hcc. hamelinensis</i> ^d	<i>Hcc. qingdaonensis</i> ^e	<i>Hcc. saccharolyticus</i> ^f	<i>Hcc. salifodinae</i> ^g	<i>Hcc. thailandensis</i> ^h
Species	<i>Hcc. morrhuae</i> ^b	<i>Hcc. dombrowskii</i> ^c	<i>Hcc. hamelinensis</i> ^d	<i>Hcc. qingdaonensis</i> ^e	<i>Hcc. saccharolyticus</i> ^f	<i>Hcc. salifodinae</i> ^g	<i>Hcc. thailandensis</i> ^h
Type strain	ATCC 17082 DSM 1307 IFO (now NBRC) 14719 JCM 8876 VKM B-1772	ATCC BAA-364 DSM 14522 JCM 12289 NCIMB 13803	ACM 5227 JCM 12892	CGMCC 1.4243 JCM 13587	ATCC 49257 CCM 4147 DSM 5350 JCM 8878 VKM B-1770	ATCC 51437 DSM 8989 JCM 9578 VKM B-2108	BCC 20213 JCM 13552 PCU 278
Cell shape	Cocci	Cocci	Cocci	Cocci	Cocci	Cocci	Cocci
Cell size (µm)	0.8–1.5	0.8–1.2	0.8–1.2	0.6–1.5	0.8–1.5	0.8–1.2	0.8–1.2
Motility	–	–	–	–	–	–	–
Colony color	NR	Light-red	Orange-pink	Red	Red-orange	Pink (colorless at pH 9.5)	Red
NaCl range for growth and optimum (%)	20–30	20–30 (Opt. 20–25)	12.5–30 (Opt. 15)	>10 (Opt. 18)	20–30	20–30	>15 (Opt. 20–30)
Lysis in dist. water	–	–	NR	–	–	–	–
Magnesium requirement and optimum (M)	0.005	+ (Opt. 0.02–0.06)	+ (Opt. 0.0005–0.05)	Opt. 0.04	>0.4	< 0.0001	–
pH range for growth and optimum	5.5–8.0 (Opt. 7.2)	5.2–8.0	4.0–9.0	4.0–9.0 (Opt. 6.0)	6.0–8.0 (Opt. 7.2)	>6.0– < 10.5 (Opt. 6.8–9.5)	6–10 (Opt. 6–8)
Temperature range for growth and optimum (°C)	Opt. 37	Opt. 37	Opt. 37	Opt. 35–40	28–42 (Opt. 37–40)	28–50 (Opt. 40)	15–45 (Opt. 37)
Organic substrates used	Buty Treh	Arab Fruc Gala Xylo	Etha Gluc Glyc Malt Manni Sucr Treh, Xylo	Gluc	Etha Fruc Gala Gluc Glyc Lact Lacto Malt Manni Manni Prop Sorbi Treh	Arab Fruc Gala Gluc Glyc Lacto Raff Rham Treh Xylo	Arab Fruc Gluc Xylo
Acid produced from	–	–	Gluc (w) Glyc (w) Malt Sucr Treh Xylo	NR	Gluc	Gluc	Arab Cell Gluc Lacto Manni Sucr Treh
Organic substrates not used	Arab Etha Fuma Lact Lacto Mann Raff Rham Sorbi	Gala Gluc Lacto Raff	Fuma Lacto Mann Sorbi Raff	Lacto	Meli Raff Ribo Rham Sucr Treh Xylo	NR	Gala

Indole from typtophan	+	NR	–	NR	+	NR	–	NR	–
Starch hydrolysis	v (type strain: –)	–	+	+	–	–	–	–	–
Gelatin liquefaction	v (type strain: +)	+	–	–	v	–	–	–	–
Nitrate reduction	+	+	+	–	+	–	+	+	+
Polar lipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ diether derivatives of PG, PGP-Me, S-DGD-1	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ diether derivatives of PG, PGP-Me, S-DGD-1	PG, PGP-Me, S-DGD-1	PG, PGP-Me, S-DGD-1	PG, PGP-Me, S-DGD-1, unidentified phospholipids and glycolipids	PG, PGP-Me, S-DGD-1, unidentified glycolipids present	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ diether derivatives of PG, PGP-Me, S-DGD-1, unidentified glycolipids present	PG, PGP-Me, S-DGD-1, unidentified glycolipids	
Respiratory quinones	"Normal menaquinones"	MK-8(H ₂), MK-7(H ₂), MK-8	NR	NR	NR	NR	MK-8(H ₂), MK-8	MK-8(H ₂)	
Sensitivity to antibiotics	Sensitive: Bac Nov	Sensitive: Ani (w) Chl (w) Bac Nov Rif Tet (w)	Sensitive: Bac Nov Rif	Sensitive: Bac Chl (w) Neo (w) Rif	Sensitive: Ani Bac	Sensitive: Bac Chl (w) Neo (w) Rif	Sensitive: Ani Aph Bac Nov	Sensitive: Bac Nov Rif	
	Resistant: Pen Str Tet	Resistant: Amp Chl Kan Pen Str Tet	Resistant: Kan Neo Pen Str Tet	Resistant: Ery Kan Pen Str Tet	Resistant: Chl Neo Nov Pen Str Tet	Resistant: Chl (w) Pen Str Tet (w)	Resistant: Amp Chl Kan Str Tet		
G + C content of DNA (mol%)	61–66	61.3 ± 1	60.1 ⁱ	61.2	59.5	62 ± 1	60.2–61.8		
Sample source and site	Saline lakes, salterns, salted products	Permian rock salt, Austria	Shark Bay, W. Australia	Crude sea salt, China	Saltern, Spain	Permian rock salt, Austria	Fish sauce fermentation, Thailand		

Data taken from:

^aGrant (2001b)

^bKocur and Hodgkiss (1973)

^cStan-Lotter et al. (2002)

^dGoh et al. (2006)

^eWang et al. (2007)

^fMontero et al. (1989)

^gDenner et al. (1994)

^hNamwong et al. (2007)

ⁱCalculated from the genome sequence (see [Table 7.21](#))

Additional data on growth substrates and other properties can be found in the original species descriptions

Table 7.6

Comparison of selected characteristics of the members of the genus *Haloferax* (part A)

Genus	<i>Haloferax</i> ^{a,b}					
Species	<i>Hfx. volcanii</i> ^c	<i>Hfx. alexandrinus</i> ^d	<i>Hfx. denitrificans</i> ^{e,f}	<i>Hfx. elongans</i> ^g	<i>Hfx. gibbonsii</i> ^h	<i>Hfx. larsenii</i> ⁱ
Older names	Basonym: <i>Halobacterium volcanii</i>		Basonym: <i>Halobacterium denitrificans</i>			
Type strain	ATCC 29605 DSM 3757 IFO (now NBRC) 14742 JCM 8879 NCCB 85050 NCIMB 2012 VKM B-1768	CIP 107620 JCM 10717 KCTC 12962 NBRC 16590	ATCC 35960 DSM 4425 JCM 8864 VKM B-1754	ATCC BAA-1513 JCM 14791 UNSW 104100	ATCC 33959 DSM 4427 JCM 8863 NBRC 102184 VKM B-1756	CGMCC 1.5347 JCM 13917
Cell shape	Disc-shaped, pleomorphic	Pleomorphic	Pleomorphic and disc-shaped	Pleomorphic rods, elongating during exponential growth	Pleomorphic discs, triangular forms, bulging rods	Pleomorphic
Cell size (µm)	1–2 × 2–3	1.1–1.5 × 3.4–4.0	0.8–1.0 × 2.0–3.0	up to 12	0.4 × 2.0–2.5	0.8 × 1.5
Motility	+	–	–	+	+	+
Colony color	Pink	Red	Orange-red	Red	Orange-red	Orange-red
NaCl range for growth and optimum (%)	9–26 (Opt. 10–15)	10–30 (Opt. 25)	9– > 26 (Opt. 12–18)	10–30 (Opt. 15–20)	Opt. 20–25 (40 °C) 15–20 (30 °C)	6–28 (Opt. 13–20)
Lysis in distilled water	+	+	+	+	NR	+
Magnesium requirement and optimum (M)	Opt. 0.2	+ (Opt. 0.3)	NR	>0.2 M (Opt. 0.4)	0.01–0.02	>0.005 (Opt. 0.2–0.5)
pH range for growth and optimum	NR	5.5–7.5 (Opt. 7.2)	6.0–8.0 (Opt. 6.7)	7.0–9.0 (Opt. 7.4)	5.0–8.0 (Opt. 6.5–7.0)	6.0–8.5 (Opt. 6.5–7.0)
Temperature range for growth and optimum (°C)	Opt. 30–40	ND (grown at 37)	30–55 (Opt. 50)	30–55 (Opt. 53)	25–55 (Opt. 35–40)	25–55 (Opt. 42–45)
Organic substrates used	NR	Gluc Glyc Succ	Acet Citr Fuma Fruc Gala Gluc Glyc Lact Mala Malt Pyru Succ Sucr	Gluc Glyc Malt Sucr Treh	NR	Fuma Gluc Glyc Lact Mala Mann Malt Pyru Star Succ Sucr
Acid produced from	NR	Arab Fruc Gluc Glyc Malt Rham Ribo Sucr Xylo	Fruc Gala Gluc Malt Sucr	Gluc Glyc Malt Sucr Treh	Arab Fruc Gala Gluc Malt Mann, Sucr Xylo	Fruc (w) Gluc (w) Glyc Malt Sucr (w)
Organic substrates not used	NR	Citr Gala Lacto Mann	Lacto Mann Ribo	Etha Fuma Lacto Mann Manni Raff Sorbi Xylo	NR	Acet Arab Citr Gala Lacto Manni Prop Rham Ribo Sorbi Xylo
Indole from typtophan	+	+	–	+	+	+
Starch hydrolysis	–	–	–	+	–	+

■ Table 7.6 (continued)

Genus	<i>Haloferax</i> ^{a,b}					
Species	<i>Hfx. volcanii</i> ^c	<i>Hfx. alexandrinus</i> ^d	<i>Hfx. denitrificans</i> ^{e,f}	<i>Hfx. elongans</i> ^g	<i>Hfx. gibbonsii</i> ^h	<i>Hfx. larsenii</i> ⁱ
Gelatin liquefaction	—	+	+	+	—	+
Nitrate reduction	+	+	+	—	v	+
Polar lipids	PG, PGP-Me, S-DGD-1, DGD-1	PG, PGP-Me, S-DGD-1, DGD-1	PG, PGP-Me, S-DGD-1, DGD-1	PG, PGP-Me, S-DGD-1, DGD-1	PG, PGP-Me, S-DGD-1	PG, PGP-Me, S-DGD-1, DGD-1
Respiratory quinones	NR	NR	MK-8, MK-8(VIII-H ₂)	NR	NR	NR
Sensitivity to antibiotics	NR	Sensitive: Bac (high conc) Nov	Sensitive: Aph Bac Chl (high conc.) Ery Nov	Sensitive: Nov	Sensitive: Nov	Sensitive: Ani Aph Bac Nov Rif
		Resistant: Bac (up to 20 µg/ml) Chl Ery Neo Rif Tet	Resistant: Pen Str	Resistant: Amp Bac Chl Ery Gen Neo Pen Rif Str Tet	Resistant: Amp Bac Chl Ery Gen Kan Neo Pen Str Tet	Resistant: Amp Chl Ery Kan Neo Pen Pen Str Tet
G + C content of DNA (mol%)	63.4	59.5 ± 0.3	66.3 ⁿ	61.4	61.8	62.2 ± 0.8
Sample source and site	The Dead Sea	Saltern, Egypt	Saltern, California, USA	Hamelin Pool, W. Australia	Saltern, Spain	Saltern, China

(Colwell et al. 1979), but the use of more varied growth media and culture conditions, together with improved methods for the taxonomic characterization of strains, has led to our current insight that a great physiological and chemotaxonomic diversity exists within the family.

Phylogenetic Structure of the Family and Its Genera

Phylogenetically the family *Halobacteriaceae* is affiliated with the *Euryarchaeota*. ► *Figure 7.1a* shows a grouped neighbor-joining tree based on 16S rRNA sequence comparisons, showing the genera of the family; an unfolded tree showing the type strains of species of the family is shown in ► *Fig. 7.1b*.

Most genera are well separated within the tree. A major exception is formed by the genera *Haloterrigena*, *Natrialba*, *Natrinema*, and *Natronorubrum* (see also Tindall 2003 and Wright 2006). The genus *Halomicrobium* may require a taxonomic reassessment. Alkaliphilic genera are found throughout the tree; there is no single haloalkaliphilic lineage such as was proposed in an early 16S RNA sequencing study (McGenity and Grant 1993).

A major problem encountered when constructing 16S rRNA-based phylogenetic trees of the family *Halobacteriaceae* is the fact that many species contain multiple 16S rRNA genes, and their sequences can differ by as much as 5 % or more. Mylvaganam and Dennis (1992) first documented the phenomenon for the *rrnA* and *rrnB* genes of *Har. marismortui*, which showed substitutions in 74 positions. Both genes can be expressed in each individual cell (Amann et al. 2000). *rrnB*

appears to be preferentially expressed at higher growth temperatures (López-López et al. 2007). *Har. marismortui* has three divergent rRNA genes. Other *Haloarcula* species also show 16S rRNA polymorphism, and so do the members of the genus *Halomicrobium* (Cui et al. 2009). *Halosimplex carlsbadense* possesses three different 16S rRNA genes (Vreeland et al. 2002).

Genes encoding 23S rRNA have seldom been used for the reconstruction of the phylogenetic relationships within the *Halobacteriaceae*. In a study of six species for which both 16S and 23S rRNA gene sequences were known at the time, Briones and Amils (2000) obtained trees with different topologies for the two phylogenetic markers.

Other genetic markers have been proposed in recent years for phylogenetic tree reconstruction for the members of the family by multilocus sequence analysis (Dennis and Shimmin 1997; Enache et al. 2007a; Minegishi et al. 2010a, 2012a; Papke et al. 2007). Use of the markers *atpB*, EF-2, *radA*, *rpoB*, and *secY* enabled differentiation of individual strains within species, as well as the delineation of species and genera, including the identification of potential novel species and even family-like relationships (Papke et al. 2011).

Genome Analysis

At the time of writing (August 2012), information was available on the genome sequences of 27 isolates of *Halobacteriaceae*, 21 of which are type strains of species (► *Table 7.21*). Detailed information can be found in the specialized databases HaloLex (<http://www.halolex.mpg.de>;) (Pfeiffer et al. 2008b) and HaloWeb (<http://halo4.umbi.umd.edu>) (DasSarma et al. 2010),

Table 7.7

Comparison of selected characteristics of the members of the genus *Haloferax* (part B)

Genus	<i>Haloferax</i>				
Species	<i>Hfx. lucentense</i> ^j	<i>Hfx. mediterranei</i> ^k	<i>Hfx. mucosum</i> ^g	<i>Hfx. prahovense</i> ^l	<i>Hfx. sulfurifontis</i> ^m
Older names	Corrig. from <i>Haloferax lucentensis</i>	Basonym: <i>Halobacterium mediterranei</i>			
Type strain	CCM 7023 CECT 5871 CIP 107410 DSM 14919 JCM 9276 NCIMB 13854	ATCC 33500 CCM 3361 DSM 1411 IFO (now NBRC) 14739 JCM 8866 VKM B-1748	ATCC BAA-1512 JCM 14792 UNSW 104200 UNSW	DSM 18310 JCM 13924	CCM 7217 CIP 108334 DSM 16227 JCM 12327
Cell shape	Pleomorphic rods	Pleomorphic rods	Pleomorphic	Rods	Pleomorphic irregular shaped cells and rods
Cell size (µm)	0.6 × 2.5	0.5–2.0	NR	NR	1.0–1.5
Motility	+	+ (w)	–	NR	–
Colony color	Pink	Pink	Pink-red	Beige-orange	Pink
NaCl range for growth and optimum (%)	10–30 (Opt. 25)	Up to 30 (Opt. 17)	10–30 (Opt. 15–20)	15–30 (Opt. 20)	6– > 30
Lysis in distilled water	+	+	+	+	+
Magnesium requirement and optimum (M)	NR	0.02–0.04	>0.2	Opt. 0.4	>0.001
pH range for growth and optimum	5.0–9.0 (Opt. 7.5)	Opt. 6.5	6.0–10.0 (Opt. 7.4)	6.0–8.5 (Opt. 7.0–7.5)	4.5–9.0 (Opt. 6.4–6.8)
Temperature range for growth and optimum (°C)	10–45 (Opt. 37)	Up to 45 (Opt. 35)	30–55 (Opt. 53)	23–51 (Opt. 38–48)	18–50 (Opt. 32–37)
Organic substrates used	Acet Arab Buty Cell Fruc Fuma Gluc Glyc Rham Sucr Treh Xylo	Acet Citr Gluc Glyc Lact Lacto Mala Manni Pyru Sorbi Star Sucr Succ	Gluc Glyc Malt Sucr Treh	Acet Arab Citr Fuma Fruc Gala Gluc Glyc Lact Lacto Mala Malt Prop Pyru Raff Rham Star Succ Sucr Xylo	Acet Arab Benz Citr Fruc Fuma, Gala Gluc Glyc Mala Malt Succ Sucr Xylo
Acid produced from	Arab Fruc Gluc Glyc Malt Xylo	Arab (w) Fruc Gluc Malt Sucr Xylo	Gluc Glyc Malt Sucr Treh	Fruc, Lacto	Arab Fruc Gala Gluc Glyc Malt Sucr Xylo
Organic substrates not used	Citr Etha Gala Lacto Mala Malt Mann Manni Prop Raff Ribo Sorbi	NR	Etha Fuma Gala Lacto Mann Manni Raff Sorbi Xylo	Mann Manni Ribo Sorbi	Lacto Manni Ribo Sorbi Star
Indole from typtophan	+	+	+	+	+
Starch hydrolysis	–	+	–	+	–
Gelatin liquefaction	–	+	+	–	+
Nitrate reduction	–	+	–	–	+
Polar lipids	PG, PGP-Me, S-DGD-1, DGD-1	PG, PGP-Me, S-DGD-1, DGD-1	PG, PGP-Me, S-DGD-1, DGD-1	PG, PGP-Me, S-DGD-1	PG, PGP-Me, S-DGD-1

■ Table 7.7 (continued)

Genus	<i>Haloferax</i>				
Species	<i>Hfx. lucentense</i> ^j	<i>Hfx. mediterranei</i> ^k	<i>Hfx. mucosum</i> ^g	<i>Hfx. prahovense</i> ^l	<i>Hfx. sulfurifontis</i> ^m
Respiratory quinones	NR	NR	NR	NR	NR
Sensitivity to antibiotics	NR	Sensitive: Ani Bac (high conc) Nov Resistant: Amp Bac (up to 40 µg/ml) Chl Ery Gen Kan Neo Pen Str Tet	Sensitive: Nov Resistant: Amp Bac Chl Cip Ery Gen Neo Pen Rif Str Tet	Sensitive: Aph Ani Nov Rif Resistant: Amp Bac Chl Ery Neo Pen	Sensitive: Aph Ani Bac (high conc) Nov Resistant: Amp Bac (up to 100 µg/ml) Chl Ery Gen Kan Pen Rif
G + C content of DNA (mol%)	64.5	60.3 ⁿ	61.8 ⁿ	63.7	66.3 ⁿ
Sample source and site	Saltern, Spain	Saltern, Spain	Hamelin Pool, W. Australia	Salt lake, Romania	Saline sulfur spring, Oklahoma

Data taken from:

^aVentosa (2001b)

^bTorreblanca et al. (1986)

^cMullakhanbhai and Larsen (1975)

^dAsker and Ohta (2002a)

^eTomlinson et al. (1986)

^fTindall et al. (1989)

^gAllen et al. (2008)

^hJuez et al. (1986)

ⁱXu et al. (2007a)

^jGutierrez et al. (2002)

^kRodriguez-Valera et al. (1983)

^lEnache et al. (2007b)

^mElshahed et al. (2004)

ⁿCalculated from the genome sequence (see Table 7.21)

Additional data on growth substrates and other properties can be found in the original species descriptions

as well as in the UCSC Archaeal Genome Browser <http://archaea.ucsc.edu> (all accessed November 1, 2012). Based on genomic information, comparative studies are possible, e.g., of carbohydrate and amino acid degradation pathways (Anderson et al. 2011).

The chromosomes are between 2.0 and 4.5 Mbp in length and contain between 2,630 and 4,682 protein-coding genes. The number of rRNA operons encoded by these genomes varies between 1 and 3. Many species of *Halobacteriaceae* contain, in addition to the main chromosome, additional DNA in “minichromosomes,” “megaplasmids,” or plasmids. An extreme case is *Har. marismortui* with nine circular replicons: two “chromosomes” (3.1 and 0.28 MBp) and 7 plasmids. In many species 25–30 % of the genetic material is found outside the main chromosome. The presence of more than one kind of DNA in representatives of the family was first reported in a CsCl density gradient centrifugation of *Hbt. salinarum* DNA, which yielded two fractions with 67–68 % and 58–59 % mol% G+C (Joshi et al. 1963). The distinction between minichromosomes, megaplasmids, and plasmids, to be based on copy number, replication control, and evolutionary history, is not always clear (DasSarma et al. 2008; Ng et al. 1998). Out of 65 strains of haloarchaea tested, 75 % had at least one megaplasmid (Gutiérrez et al. 1986).

The paper describing the *Hrd. utahensis* genome (Bakke et al. 2009) is of special interest as it shows how three different genome annotation services (IMG, Joint Genome Institute Integrated Microbial Genome system; RAST, Rapid Annotation using Subsystems Technology server of the National Microbial Pathogen Data Resource NMPDR; and JCVI, J. Craig Venter Institute Annotation Service) differ considerably in gene calls and different other features. Based on the same raw sequence data, the number of predicted genes ranged from 2,898 to 3,254, and the average gene length ranged between 845 and 942 bp.

At the time of writing, the type strain of the type species of the family (*Hbt. salinarum*) had not yet been sequenced. For two related strains, the complete genome sequences are available: *Halobacterium* strain NRC-1, a strain that can be classified within the species (Gruber et al. 2004), and strain R1 (Pfeiffer et al. 2008a). The *Halobacterium* strain NRC-1 genome was the first complete *Halobacteriaceae* genome sequenced (Ng et al. 2000), and the data have been extensively used for computational analysis and functional genomics and transcriptomics studies (Kennedy et al. 2001; Soppa et al. 2008). The chromosome of strain R1 is completely colinear and virtually identical to that of NRC-1,

Table 7.8

Comparison of selected characteristics of the members of the genera *Halolamina*, *Halomarina*, *Halomicrobium*, *Halonotius*, and *Halopelagius*

Genus	<i>Halolamina</i>	<i>Halomarina</i>	<i>Halomicrobium</i> ^c			<i>Halonotius</i>	<i>Halopelagius</i>
Species	<i>Hlm. pelagica</i> ^a	<i>Hmr. oriensis</i> ^b	<i>Hmc. mukohataei</i> ^d	<i>Hmc. katesii</i> ^e	<i>Hmc. zhoui</i> ^f	<i>Hns. pteroides</i> ^g	<i>Hpl. inordinatus</i> ^h
Older names			Basonym: <i>Haloarcula mukohataei</i>				
Type strain	CGMCC 1.10329 JCM 16809	JCM 16495 KCTC 4074	ATCC 700874 CIP 105174 DSM 12286 JCM 9738 NCIMB 13541	CECT 7257 DSM 19301	CGMCC 1.10457 JCM 17095	CECT 7525 DSM 18729 JCM 14355	CGMCC 1.7739 JCM 15773
Cell shape	Pleomorphic	Irregular cocci or discs	Rods and pleomorphic cells	Rods	Pleomorphic	Flat rods with rounded ends	Pleomorphic
Cell size (µm)	NR	0.6 × 2.0	0.5 × 1–8	1.8–2.2 × 2.2–2.8	NR	0.7–1.5 × 2–6	NR
Motility	–	–	+	–	+	+	+
Colony color	Red	Pink	Red-orange	Orange	Red	Red	Red
NaCl range for growth and optimum (%)	8–30 (Opt. 20–23)	10–30 (Opt. 15)	15–26 (Opt. 18–20)	20–30 (Opt. 25)	8–30 (Opt. 15)	16–36 (Opt. 20–24)	15–28 (Opt. 20–23)
Lysis in distilled water	+	–	NR	NR	NR	+	+
Magnesium requirement and optimum (M)	0–0.7 (Opt. 0.01–0.05)	0.01–1.0 (Opt. 0.2–0.5)	>0.003	–	0–1 (Opt. 0.05)	+ (Opt. 0.2–0.6)	0.03–0.7 (Opt. 0.5)
pH range for growth and optimum	5.5–9.5 (Opt. 7.0–7.5)	7.0–9.0 (Opt. 7.0–8.0)	6.2–8.0	6.5–10.0 (Opt. 7.0–7.5)	5.5–9.5 (Opt. 7.0)	5.5–8.5 (Opt. 7.0–7.5)	5.5–8.0 (Opt. 6.5–7.0)
Temperature range for growth and optimum (°C)	25–50 (Opt. 37)	20–42 (Opt. 37)	Opt. 40–45	35–50 (Opt. 37–40)	20–55 (Opt. 42)	25–45 (Opt. 37–40)	20–50 (Opt. 37)
Organic substrates used	Acet Gala Gluc Lact Mann Pyru Star	Fruc Gala Gluc Glyc Lacto Malt Mann Pyru Ribo Star Sucr Xylo	Gala Gluc Glyc Malt Mann Ribo Sucr	Acet Cell Fruc Gala Gluc Glyc Malt Manni Pyru Sorbi Star Treh	Acet Gala Gluc Glyc Lacto Mann Pyru Sucr	Gluc Glyc Pyru	Acet Fruc Fuma Gala Gluc Glyc Lact Lacto Mala Malt Mann Pyru Sorbi Succ Sucr
Acid produced from	Gala Gluc Mann	Fruc Gala Gluc Glyc Lacto Malt Mann Pyru Ribo Star Xylo	Gala Gluc Glyc Malt Mann Ribo Sucr	Arab Fruc	Gala Gluc Lacto Mann Sucr	–	Fruc Gala Gluc Glyc Lacto Malt Mann Sorbi Sucr
Organic substrates not used	Citr Fruc Fuma Glyc Lacto Mala Malt Manni Ribo Sorb Sorbi Succ Sucr Xylo	Acet Citr Fuma Lact Mala Manni Sorbi Succ	Acet Ribo Succ	Arab Benz Citr Lacto Mala Mann Prop Raff Rham Sorb Succ Sucr Xylo	Citr Fruc Fuma Mala Malt Manni Sorb, Ribo Sorbi Star Succ Xylo	Acet Buty Cell Citr Fruc Fuma Gala Lact Lacto Mala Mann Mann Ribo Succ Sucr Xylo	Citr Manni Ribo Sorb Star Xylo

Table 7.8 (continued)

Genus	<i>Halolamina</i>	<i>Halomarina</i>	<i>Halomicrobium</i> ^c			<i>Halonotius</i>	<i>Halopelagius</i>
Species	<i>Hlm. pelagica</i> ^a	<i>Hmr. oriensis</i> ^b	<i>Hmc. mukohataei</i> ^d	<i>Hmc. katesii</i> ^e	<i>Hmc. zhouii</i> ^f	<i>Hns. pteroides</i> ^g	<i>Hpl. inordinatus</i> ^h
Indole from typtophan	—	—	—	—	—	—	+
Starch hydrolysis	+ (w)	—	+	+	—	—	—
Gelatin liquefaction	—	+	—	v	—	NR	—
Nitrate reduction	+ (v)	+	+	+	+	—	—
Polar lipids	PG, PGP-Me, PGS, S-DGD-1, DGD-1, TGD-1, 4 unknown glycolipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ diether derivatives of PG, PGP-Me, a glycolipid identical to TGD-2, 1 unknown glycolipid	PG, PGP-Me, PGS, S-DGD	PG, PGP-Me, a glycolipid resembling S-DGD-1, DGD-1	PG, PGP-Me, PGS, a glycolipid resembling S-DGD-1, DGD-1	PG, PGP-Me, a glycolipid resembling S-DGD-1	PG, PGP-Me, two glycolipids resembling S-DGD-1 and DGD-1
Respiratory quinones	NR	NR	NR	NR	NR	NR	NR
Sensitivity to antibiotics	Sensitive: Ani Aph Bac Nov Rif	Sensitive: Ani Aph Bac Rif	Sensitive: Ani Nov	Sensitive: Bac Nov	Sensitive: Bac Nov Rif	Sensitive: Ani Nov Rif	Sensitive: Ani Aph Bac Nov Rif
	Resistant: Amp Chl Cip Ery Gen Kan Neo Pen Str Tet Van	Resistant: Amp Chl Ery Neo Nov Pen Str Tet	Resistant: Chl Kan Pen	Resistant: Amp Chl Ery Gen Kan Neo Pen Str Tet	Resistant: Amp Chl Ery Gen Kan Neo Pen Str Tet	Resistant: Amp Bac Chl Ery Kan Neo Str Tet	Resistant: Amp Cip Chl Ery Gen Kan Neo Pen Str Tet Van
G+C content of DNA (mol%)	64.8	67.7	65.5 ⁱ	52.4–52.9	69.1	58.4–58.7	59.9–61.0
Sample source and site	Solar saltern, China	Seawater aquarium, Tokyo, Japan	Salt flat, Argentina	Salt lake, Chile; Sabkha, Algeria	Solar saltern, China	Saltern crystallizer Ponds, Australia	Solar saltern, China

Data taken from:

^aCui et al. (2011b)

^bInoue et al. (2011)

^cOren et al. (2002)

^dIhara et al. (1997)

^eKharroub et al. (2008)

^fYang and Cui (2012)

^gBurns et al. (2010b)

^hCui et al. (2010g)

ⁱCalculated from the genome sequence (see Table 7.21)

Additional data on growth substrates and other properties can be found in the original species descriptions

but in addition, it possesses not 2 but 4 megaplasmids. A portion of 210 kb of sequence occurs only in strain R1. Pfeiffer et al. (2008a) concluded that the two strains were descendents of one isolate and that the differences observed were the result of rapid evolution in the laboratory. Further information about the origin and the relations between the two strains was provided by Ng et al. (2008) and Pfeiffer et al. (2008b).

The genome of *Hqr. walsbyi*, an unusually shaped square archaeon, which also has the lowest G+C content of all (47.9 mol%), is of special interest because of its low coding density (76 %) as compared to 86–91 % in other haloarchaea, a phenomenon caused by a very large average intergenic spacing (average 289 bp) and a high number (>1,000) intergenic regions. It also encodes the largest protein identified in the group: the 9,159 amino acid long halomucin.

Table 7.9

Comparison of selected characteristics of the members of the genera *Halopenitus*, *Halopiger*, *Haloplanus*, and *Haloquadratum*

Genus	<i>Halopenitus</i>	<i>Halopiger</i>		<i>Haloplanus</i>			<i>Haloquadratum</i>
Species	<i>Hpt. persicus</i> ^a	<i>Hpg. xanaduensis</i> ^b	<i>Hpg. aswanensis</i> ^c	<i>Hpn. natans</i> ^d	<i>Hpn. aerogenes</i> ^e	<i>Hpn. vescus</i> ^f	<i>Hqr. walsbyi</i> ^g
Type strain	IBRC 10041 KCTC 4046	CECT 7173 CGMCC 1.6379	DSM 13151 JCM 11628	DSM 17983 JCM 14081	CGMCC 1.10124 JCM 16430	CGMCC 1.8712 JCM 16055	DSM 16854 JCM 12705
Cell shape	Pleomorphic rods, triangles, disc-shaped	Pleomorphic rods	Pleomorphic rods	Flat pleomorphic	Flat pleomorphic	Flat pleomorphic	Flat squares
Cell size (µm)	0.6–1.5 × 4.9–8.7	0.5–1.0 × 3.0–13.0	0.6–0.9 × 1.25–6.5	2.5–8.0	1.0–2.0	1.0–2.0	0.2 × 2 × 2
Motility	–	NR	+	–	+	+	–
Colony color	Pale pink	Red	Pink	Light pink	Pink	Pink	Pink
NaCl range for growth and optimum (%)	10–25 (Opt. 17)	15–30 (Opt. 25)	>10 (Opt. 22.5–25)	15–25 (Opt. 18)	15–25 (Opt. 18)	8–30 (Opt. 12)	14–36 (Opt. 18)
Lysis in distilled water	+	+	+	+	+	+	+
Magnesium requirement and optimum (M)	>0.05	–	–	NR	0–1 (Opt. 0.01)	0.03–0.5 (Opt. 0.03)	–
pH range for growth and optimum	6.5–8.5 (Opt. 7.5)	6.0–11.0 (Opt. 7.5–8.0)	6.0–9.2 (Opt. 7.5)	6.5–8.0 (Opt. 7.0)	6.0–9.0 (Opt. 7.5)	5.5–7.5 (Opt. 6.0–6.5)	6.0–8.5
Temperature range for growth and optimum (°C)	25–50 (Opt. 40)	28–45 (Opt. 37)	<55 (Opt. 40)	37–52 (Opt. 40)	25–50 (Opt. 37–40)	30–50 (Opt. 40)	25–45
Organic substrates used	Fruc Gala Gluc Malt	Acet Gala Gluc Xylo	Some carbohydrates Acet Pyru	Acet Gluc Ribo	Acet Gala Gluc Lact Mann Pyru Sucr	Acet Gluc Lact Lacto Malt Mann Manni Pyru Sorbi	Pyru
Acid produced from	Gluc Malt	Arab Gluc Xylo	Arab Fruc Gluc Malt Star Sucr Xylo	NR	NR	NR	–
Organic substrates not used	Arab Manni Ribo Sucr	Fruc Fuma Glyc Lacto, Mala Malt Mann Manni Prop Raff Ribo, Sorbi Succ Treh	NR	Gala Glyc Malt Succ Sucr	Fruc Glyc Lacto Malt Manni Sorb Ribo Sorbi Star Succ Xylo	Citr Fruc Fuma Gala Glyc Mala Ribo Sorb Star Succ Sucr Xylo	Acet Arab Benz Cell Citr Fruc Fuma Gala Gluc Glyc Lact Lacto Mala Malt Mann Manni Prop Ribo, Succ Sucr Xylo
Indole from typtophan	–	–	+	v (type +)	+	+	–
Starch hydrolysis	–	–	+	–	–	–	–
Gelatin liquefaction	–	+	–	–	–	–	–

■ Table 7.9 (continued)

Genus	<i>Halopenitus</i>	<i>Halopiger</i>		<i>Haloplanus</i>			<i>Haloquadratum</i>
Species	<i>Hpt. persicus</i> ^a	<i>Hpg. xanaduensis</i> ^b	<i>Hpg. aswanensis</i> ^c	<i>Hpn. natans</i> ^d	<i>Hpn. aerogenes</i> ^e	<i>Hpn. vesicus</i> ^f	<i>Hqr. walsbyi</i> ^g
Nitrate reduction	—	—	+	+	+	+	—
Polar lipids	PG, PGP-Me, 1 unidentified glycolipid, 3 minor phospholipids	PG, PGP-Me, S ₂ -DGD-1	PG, PGP-Me, S ₂ -DGD-1	PG, PGP-Me, PGS, 1 glycolipid resembling S-DGD-1	PG, PGP-Me, PGS, 1 glycolipid resembling S-DGD-1	PG, PGP-Me, PGS, 1 glycolipid resembling S-DGD-1	PG, PGP-Me, PGS, S-DGD-1 ^h
Respiratory quinones	MK-8(II-H ₂)	NR	MK-8 MK-8(VIII-H ₂)	NR	NR	NR	NR
Sensitivity to antibiotics	Sensitive: Ani Bac Nov	Sensitive: Bac Nov	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov	Sensitive: Ani Aph Bac Nov Rif	Sensitive: Ani Aph Bac Nov Rif	Sensitive: Ani Aph Bac Chl Ery Nov Rif Tet
	Resistant: Amp Chl Ery Kan Neo Pen Rif Str Tet	Resistant: Amp Chl Ery Kan Neo Pen Rif Str Tet Van	Resistant: Chl Ery Pen Str Tet Van	Resistant: Amp Chl Neo Pen Rif	Resistant: Amp Chl Ery Kan Neo Pen Rif Str Tet Van	Resistant: Amp Chl Ery Kan Neo Pen Rif Str Van	Resistant: Amp Bac Kan Neo Str
G + C content of DNA (mol%)	66.0	65.2 ⁱ	67.1	66.1–66.4	64.1	62.1	46.9–47.9 ⁱ
Sample source and site	Salt lake, Iran	Salt lake, Inner Mongolia	Hypersaline soil, Egypt	Experimental mesocosm, the Dead Sea	Solar saltern, China	Solar saltern, China	Solar salterns, Spain, Australia

Data taken from:

^aAmoozegar et al. (2012)

^bGutiérrez et al. (2007)

^cHezayen et al. (2010)

^dElevi Bardavid et al. (2007)

^eCui et al. (2011a)

^fCui et al. (2010c)

^gBurns et al. (2007)

^hLobasso et al. (2008)

ⁱCalculated from the genome sequence (see ▶ Table 7.21)

Additional data on growth substrates and other properties can be found in the original species descriptions

In some cases, phage-like elements were encountered within the sequenced genomes. Thus, the *Nab. magadii* genome contains a phage-like element—halovirus ΦCh1.

Phages

Since the first viruses lysing *Halobacterium* strains were described (Torsvik and Dundas 1974; Wais et al. 1975), a large number of viruses targeting different members of the *Halobacteriaceae* have been isolated and characterized in greater or lesser depth (Dyall-Smith et al. 2003; Pina et al. 2011). They have been classified within the Myoviridae, Siphoviridae, Fuselloviridae, and “Pleolipoviruses.” ▶ Table 7.22 summarizes

their properties. These viruses show different morphologies including head-tail, lemon-shaped, and pleomorphic types, and they may contain circular or linear double-stranded or single-stranded DNA. *Halorubrum* sp. virus HRPV-3 has double-stranded DNA with single-stranded interruptions (Senčilo et al. 2012). *Nab. magadii* halovirus ΦCh1 contains both linear double-stranded 55 kbp DNA and several RNA species (80–700 nt) (Witte et al. 1997). The recently discovered pleomorphic “Pleolipoviruses” are of special interest as they contain lipids derived from the host, as well as glycolipid spikes (Bamford et al. 2005; Pietilä et al. 2012a). Restriction and modification, known from bacteriophages of the Bacteria, have been identified for haloviruses as well (Daniels and Wais 1984).

Table 7.10

Comparison of selected characteristics of the members of the genera *Halorhabdus*, *Halorientalis*, *Halosarcina*, and *Halosimplex*

Genus	<i>Halorhabdus</i>		<i>Halorientalis</i>	<i>Halosarcina</i>		<i>Halosimplex</i>
Species	<i>Hrd. utahensis</i> ^a	<i>Hrd. tiamatea</i> ^b	<i>Hos. regularis</i> ^c	<i>Hsn. pallida</i> ^d	<i>Hsn. limi</i> ^e	<i>Hsx. carlsbadense</i> ^f
Type strain	DSM 12940 JCM 11049	DSM 18392 JCM 14471	CGMCC 1.10123 JCM 16425	JCM 14848 KCTC 4017	CGMCC 1.8711 JCM 16054	ATCC BAA-75 JCM 11222
Cell shape	Pleomorphic	Pleomorphic	Pleomorphic rods	Cocci	Pleomorphic	Pleomorphic rod
Cell size (µm)	0.5–1.0 × 2–10	0.5–1.0 × 1–8	~0.5 × 1.0–1.6	0.8–1.0	NR	~0.95 × 5
Motility	+	–	+	–	+	+
Colony color	Red	Non-pigmented	Red	Pink	Red	Pink-red
NaCl range for growth and optimum (%)	9–30 (Opt. 27)	10–30 (Opt. 27)	15–30 (Opt. 18–20)	10–25 (Opt 18)	12–30 (Opt. 23)	20–30 (Opt. 25)
Lysis in distilled water	+	+	+	+		+
Magnesium requirement and optimum (M)	0.002–0.8	– (Opt. 0–1)	Opt. 0.01–0.03	>0.001	0.05–0.7 (Opt 0.3)	>0.2 (Opt. 0.4–0.8)
pH range for growth and optimum	5.5–8.5 (Opt. 6.7–7.1)	5.5–8.5 (Opt. 6.5–7.0)	6.0–9.0 (Opt. 7.0–7.5)	5.0–8.5 (Opt. 6.5)	6.5–8.0 (Opt. 7.0)	7.0–8.0 (Opt. 7.5)
Temperature range for growth and optimum (°C)	17–55 (Opt. 50)	15–55 (Opt. 45)	20–50 (Opt. 37)	25–45 (Opt. 30)	20–50 (Opt. 37)	22–50 (Opt. 37–40)
Organic substrates used	Fruc Gluc Xylo	Fruc (w) Gala (w) Gluc (w) Malt Xylo (w)	Acet Fuma Gala Gluc Lact Mala Mann Pyru Succ	Acet Fruc Fuma Gala Gluc Glyc Lact Mala Pyru Sorbi Succ Sucr	Acet Gala Gluc Glyc Lact Lacto Mann Pyru Sucr	Acet Glyc Pyru
Acid produced from	Gluc and other carbohydrates	Malt	NR	Fruc Gala Gluc Glyc Lacto Sorbi Star Sucr	Gala Gluc Glyc Lacto Mann Sucr	–
Organic substrates not used	Acet Arab Citr Gala Glyc Lact Lacto Malt Pyru Sorbi Sucr	Acet Arab Citr Glyc Lact Lacto Pyru Sorbi	Fruc Lacto Malt Ribo Sorb Xylo	Citr Manni Xylo	Citr Fruc Fuma Mala Malt Manni Ribo Sorb Sorbi Succ Xylo	Arab Buta Citr Fruc Gala Gluc Lact Lacto Mala Mann Raff Rham Xylo Succ Sucr Treh
Indole from typtophan	–	–	+	+	–	–
Starch hydrolysis	–	w	w	–	w	–
Gelatin liquefaction	–	+	–	–	–	–
Nitrate reduction	–	+	+	+	+	–
Polar lipids	PG, PGP-Me, TGD, S-TGD, 1 unknown component	PG, PGP-Me, TGD, S-TGD, 1 unknown component	PG, PGP-Me, S-DGD-1, 3 unidentified glycolipids	PG, PGP-Me, S-DGD-1, DGD	PG, PGP-Me, S-DGD-1, S ₂ -DGD	PG, PGP-Me, S-TeGD, S ₂ -DGD, S-DGD-1, 1 unidentified glycolipid
Respiratory quinones	MK-8 MK-8(VIII-H ₂)	MK-8 MK-8(VIII-H ₂)	NR	NR	NR	NR

■ Table 7.10 (continued)

Genus	<i>Halorhabdus</i>		<i>Halorientalis</i>	<i>Halosarcina</i>		<i>Halosimplex</i>
Species	<i>Hrd. utahensis</i> ^a	<i>Hrd. tiamatea</i> ^b	<i>Hos. regularis</i> ^c	<i>Hsn. pallida</i> ^d	<i>Hsn. limi</i> ^e	<i>Hsx. carlsbadense</i> ^f
Sensitivity to antibiotics	Sensitive: Bac Nov	Sensitive: Ani Aph Bac Chl (50 µg/ml) Nov Rif	Sensitive: Ani Aph Bac Nov Rif	Sensitive: Ani Aph Bac Nov Rif	Sensitive: Ani Aph Bac Nov Rif	Sensitive: Bac Nov Rif
	Resistant: Amp Chl Ery Gen Neo Pen Rif Str Tet	Resistant: Amp Chl (25 µg/ml) Ery Pen Tet	Resistant: Amp Chl Cip Ery Kan Neo Pen Str Tet	Resistant: Amp Chl Ery Neo Pen	Resistant: Amp Chl Cip Ery Kan Neo Nor Pen Tet	Resistant: Ani Amp Aph Chl Ery Kan Neo Pen Tet
G + C content of DNA (mol%)	62.9 ^g	62.0 ^g	61.5.61.9	65.4	61.2	64.4
Sample source and site	Great Salt Lake, Utah	Deep-sea brine, Red Sea	Solar saltern, China	Saline sulfur spring, Oklahoma	Solar saltern, China	Salt crystals, Salado formation, New Mexico

Data taken from:

^aWainø et al. (2000)

^bAntunes et al. (2008)

^cCui et al. (2010d)

^dSavage et al. (2008)

^eCui et al. (2010d)

^fVreeland et al. (2002)

^gCalculated from the genome sequence (see ► Table 7.21)

Additional data on growth substrates and other properties can be found in the original species descriptions

Comparisons of haloviral genomes have shown that HHPV-1, a pleomorphic double-stranded DNA *Har. hispanica* virus that is released from the host without cell lysis, has remarkable synteny and amino acid sequence similarity to the single-stranded DNA *Halorubrum* sp. HRPV-1 virus. A provirus identified in the *Hfx. volcanii* chromosome is also a member of this group (Roine et al. 2010). Analysis of the genomes of haloviruses HF1 and HF2 yielded evidence for a recent and large recombination event. HF1, a virus with a broad host range (*Hbt. salinarum*, *Hfx. volcanii*, *Hfx. lucentense*), is 94.4 % identical to the *Hrr. coriense* HF2 genome but about 1.8 kb shorter. Except for a single base change, the first 48 kb are identical. Then there is an abrupt change, suggesting a recent recombination event between either HF1 or HF2 and another HF-like halovirus that has swapped most of the right-end 28 kb (Tang et al. 2004).

The true diversity of haloviruses in hypersaline ecosystem is probably much larger than that suggested in ► Table 7.22. A transmission electron microscopy study of the hypersaline Lake Retba, Senegal, showed a tremendous variety of virus like particle morphologies including spindle-shaped, spherical, and linear particles, chains of small globules, hook-shaped particles, reed-shaped particles consisting of a cylindrical body and thin tail, “tadpole” shape, and branched filaments. All these are likely archaeal viruses, although association with bacteria or with eukaryotes cannot be excluded. All these novel types are waiting to be isolated and further characterized. Less than 1 % of the viruslike particles observed had a head-and-tail morphology (Sime-Ngando et al. 2010).

Phenotypic Analyses

The Properties of the Genera and Species of Halobacteriaceae

► Tables 7.1, ► 7.2, ► 7.3, ► 7.4, ► 7.5, ► 7.6, ► 7.7, ► 7.8, ► 7.9, ► 7.10, ► 7.11, ► 7.12, ► 7.13, ► 7.14, ► 7.15, ► 7.16, ► 7.17, ► 7.18, ► 7.19, ► 7.20, ► 7.21, and ► 7.22 summarize the properties of the species of *Halobacteriaceae* whose names have been validly published until August 2012. A number of additional genus and species names have been effectively published but were not yet validated. These include the genus *Halorubellus* with species *Hrb. salinus* and *Hrb. litoreus* (Cui et al. 2012b) and the genus *Halorussus* with the species *Hrs. rarus* (Cui et al. 2010e).

The tables provide a general overview only of the properties of the organisms, and do not list all characters that have been documented in the original species descriptions and in later studies. For example, a positive reaction for nitrate reduction as listed in ► Tables 7.1, ► 7.2, ► 7.3, ► 7.4, ► 7.5, ► 7.6, ► 7.7, ► 7.8, ► 7.9, ► 7.10, ► 7.11, ► 7.12, ► 7.13, ► 7.14, ► 7.15, ► 7.16, ► 7.17, ► 7.18, ► 7.19, ► 7.20, ► 7.21, and ► 7.22 can signify reduction of nitrate to nitrite only or true denitrification with production of N₂ and/or N₂O coupled to anaerobic growth. The entry “Organic substrates used” may list compounds that stimulate growth or compounds that can be used as sole carbon and energy source. The species descriptions are not always clear in this respect. Some species are indeed able to grow on single carbon sources without amino acid supplement,

Table 7.11
Comparison of selected characteristics of the members of the genus *Halorubrum* (part A)

Genus	<i>Halorubrum</i> ^{a,b}	<i>Hrr. aidingense</i> ^a	<i>Hrr. alkaliphilum</i> ^e	<i>Hrr. aquaticum</i> ^f	<i>Hrr. arcis</i> ^g	<i>Hrr. californiense</i> ^h	<i>Hrr. chaoviator</i> ⁱ	<i>Hrr. cibirj</i>	<i>Hrr. coriense</i> ^{k,l}
Species	<i>Hrr. saccharovorum</i> ^c								
Older names	Basonym: <i>Halobacterium saccharovorum</i> ; <i>Halorubrobacterium saccharovorum</i> is a later homotypic synonym								<i>Halorubrobacterium coriense</i> is a later homotypic synonym
Type strain	ATCC 29252 CIP 105329 DSM 1137 IFO (now NBRC) 14717 JCM 8865 NCIMB 2081 VKM B-1747	CGMCC 1.2670 JCM 13560	AS 1.3528 JCM 12358	CECT 7174 CGMCC 1.6377 JCM 14031	CGMCC 1.5343 JCM 13916	CECT 7256 DSM 19288 JCM 14715	ATCC BAA-1602 DSM 19316 NCIMB 14426	DSM 19504 JCM 15757 KCTC 4026	ACM 3911 CIP 105331 DSM 10284 JCM 9275
Cell shape	Rods	Rods	Short rods	Rods	Rods	Rods	Rod-shaped to pleomorphic	Rods	Pleomorphic
Cell size (µm)	0.6–1.2 × 2.5	0.9–1.0 × 3.6–6.4	0.8–1.0 × 1.8–2.0	1.0–1.2 × 2.0–6.0	0.5–1.0 × 2.0–4.0	0.5–1.0 × 1.5	0.5–0.8 × 2.0–5.0	0.4–0.5 × 0.8–1.1	0.5–5
Motility	+	+	+	–	+	+	+	+	+
Colony color	Red-orange	Red	Red	Red	Red	Pink	Red	Red	Red-orange
NaCl range for growth and optimum (%)	9–30 (Opt. 20–26)	10–25 (Opt. 15)	10–30 (Opt. 23–25)	15–30 (Opt. 20)	13–30 (Opt. 20–23)	15–30 (Opt. 20–26)	12–30 (Opt. 25)	15–30 (Opt. 23–25)	> 13 (Opt. 13–16)
Lysis in distilled water	+	NR	NR	+	+	NR	+	+	NR
Magnesium requirement and optimum (M)	> 0.005	–	–	–	– (Opt. 0.02–0.2)	0.17–1.7 (Opt. 0.2)	v (0–0.05)	+	> 0.005

pH range for growth and optimum	NR	7.0–9.0 (Opt. 7.5)	6.0–8.5 (Opt. 7.5)	6.8–8.5 (Opt. 7.3)	7.0–8.5 (Opt. 7.4)	7.0–8.5 (Opt. 7.5)	NR
Temperature range for growth and optimum (°C)	30–56 (Opt. 50)	25–52 (Opt. 40–42)	20–44 (Opt. 38)	25–50 (Opt. 35–40)	25–55 (Opt. 42)	25–55 (Opt. 42)	30–60 (Opt. 50)
Organic substrates used	Fruc Gala Gluc Lacto Malt Mann Ribo Sucr	Fruc Gala Gluc Malt Mann Manni Sucr	Fruc Gluc Glyc Lact Malt Mann	Arab Fruc Fuma Gluc Glyc Lacto Malt Manni Star Sucr Treh	Gluc Glyc Malt Star	Gala Gluc Lacto	Gluc Glyc Lacto Sucr
Acid produced from	Fruc Gala Gluc Lacto Sucr Xyl	Fruc Gala Gluc Malt Mann Manni Sucr	Fruc Gluc Malt Mann	–	Gluc Glyc Malt	Gala Gluc Lacto Malt	NR
Organic substrates not used	NR	Lacto Ribo Sorb Sorbi Xylo	Gala Lacto Manni Raff Rham Ribo Sorbi Sucr	Acet Mala Mann Prop Raff Ribo Sorbi Succ Xylo	Acet Arab Citr Fruc Fuma Gala Lact Lacto Mala Mann Manni Prop Pyru Rham Ribo Sorbi Succ Sucr Xylo	Acet Fruc Mann	NR
Indole from typtophan	–	+	–	–	NR	–	–
Starch hydrolysis	–	–	–	–	+	+	NR
Gelatin liquefaction	–	–	–	–	–	–	NR
Nitrate reduction	+	+	+	+	+	+	NR
Polar lipids	C ₂₀ –C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD	C ₂₀ –C ₂₀ derivatives of PG, PGP-Me, PGS	C ₂₀ –C ₂₀ and C ₂₀ –C ₂₅ derivatives of PG and PGP-Me	PG, PGP-Me, S-DGD, unidentified glycolipids	C ₂₀ –C ₂₀ derivatives of PGP-Me, PGS, S-DGD	C ₂₀ –C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD	C ₂₀ –C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD
Respiratory quinones	NR	NR	NR	NR	NR	NR	NR

Table 7.11 (continued)

Genus	<i>Halorubrum</i> ^{a,b}	<i>Hrr. aidingense</i> ^a	<i>Hrr. alkalphilum</i> ^e	<i>Hrr. aquaticum</i> ^f	<i>Hrr. arcis</i> ^g	<i>Hrr. californiense</i> ^h	<i>Hrr. chaoviator</i> ⁱ	<i>Hrr. cibji</i>	<i>Hrr. coriense</i> ^{k,l}
Species	<i>Hrr. saccharovororum</i> ^c	<i>Hrr. aidingense</i> ^a	<i>Hrr. alkalphilum</i> ^e	<i>Hrr. aquaticum</i> ^f	<i>Hrr. arcis</i> ^g	<i>Hrr. californiense</i> ^h	<i>Hrr. chaoviator</i> ⁱ	<i>Hrr. cibji</i>	<i>Hrr. coriense</i> ^{k,l}
Sensitivity to antibiotics	Sensitive: Pol	Sensitive: Bac Nov Rif	Sensitive: NR	Sensitive: Bac Ery Nov Str	Sensitive: Ani Bac Nov Rif	Sensitive: Bac Kan	Sensitive: Bac Nov	Sensitive: Ani Amp Aph Bac Nov	Sensitive: Bac Nov
G + C content of DNA (mol %)	71.2	64.2	62.1	62.1	65.7	69.4	66.5	61.7	NR
Sample source and site	Saltern, California, USA	Salt lake, China	Soda lake, China	Saline lake, Inner Mongolia	Salt lake, Tibet	Saltern, California, USA	Evaporitic salt, Baja California, Mexico, Salt pools, Australia and Greece	Salt-fermented seafood, Korea	Saltern, Australia

Data taken from:

^aMcGenity and Grant (2001)^bMcGenity and Grant (1995)^cTomlinson and Hochstein (1976)^dCui et al. (2006a)^eFeng et al. (2005)^fGutiérrez et al. (2011)^gXu et al. (2007b)^hPesenti et al. (2008)ⁱMancinelli et al. (2008)^jRoh and Bae (2009)^kNuttall and Dyal-Smith (1993b)^lKamekura and Dyal-Smith (1995)

Additional data on growth substrates and other properties can be found in the original species descriptions

Table 7.12
Comparison of selected characteristics of the members of the genus *Halorubrum* (part B)

Genus	<i>Halorubrum</i>	<i>Hrr. ejinorense</i> ^e	<i>Hrr. ezzemoulense</i> ^f	<i>Hrr. kocuriji</i> ^g	<i>Hrr. lacusprofundum</i> ^{h,i}	<i>Hrr. lipolyticum</i> ^j	<i>Hrr. litoreum</i> ^k	<i>Hrr. luteum</i> ^l
Species	<i>Hrr. distributum</i> ^{a,b,c,d}							
Older names	Basonym: <i>Halobacterium distributum</i> ; <i>Halorubrobacterium distributum</i> is a later homotypic synonym				Basonym: <i>Halobacterium lacusprofundi</i> ; <i>Halorubrobacterium lacusprofundi</i> is a later homotypic synonym			
Type strain	ATCC 51197 CIP 105238 JCM 9100 JCM 10118 VKM B-1733	CECT 7194 CGMCC 1.6782 JCM 14265	CECT 7099 DSM 17463	CECT 7322 CGMCC 1.7018 JCM 14978	ACAM 34 ATCC 49239 CIP 105334 DSM 5036 JCM 8891 UQM 3107 VKM B-1753	CGMCC 1.5332 JCM 13559	CGMCC 1.5336 JCM 13561	CECT 7303 CGMCC 1.6783
Cell shape	Pleomorphic	Rods	Rods	Rods	Rods and pleomorphic	Rods	Rods	Pleomorphic
Cell size (µm)	0.8–1.0 × 2.5–7.0	1.0–1.5 × 5.0–8.0	0.6 × 1.5–3.0	0.9–1.1 × 2.0–5.0	Up to 12	0.9–1.2 × 1.8–5.5	0.3–0.5 × 2.0–5.0	0.5–0.9 × 0.6–1.5
Motility	+	–	+	–	+	+	+	+
Colony color	Orange-red	Red	Red	Red	Red	Red	Red	Orange
NaCl range for growth and optimum (%)	10–30 (Opt. 15–25)	15–30 (Opt. 20)	15–25 (Opt. 20)	>15 (Opt. 20)	9–26 (Opt. 15–20)	10–28 (Opt. 15)	12–30 (Opt. 20)	15–30 (Opt. 23–25)
Lysis in distilled water	NR	NR	+	+	+	NR	NR	+
Magnesium requirement and optimum (M)	NR	–	+	–	NR	+	0.03–0.7	–
pH range for growth and optimum	NR	6–10 (Opt. 7.5)	6.5–9.0 (Opt. 7.0–7.5)	6.0–9.0 (Opt. 7.5)	NR	7.0–9.0 (Opt. 7.5)	6.5–9.0 (Opt. 7.0–7.5)	7.5–10.5 (Opt. 9.5–10.0)

Table 7.12 (continued)

Genus	<i>Halorubrum</i>		<i>Hrr. ezzemoulense</i> ^f	<i>Hrr. kocurij</i> ^g	<i>Hrr. lacusprofund</i> ^{h,i}	<i>Hrr. lipolyticum</i> ^j	<i>Hrr. litoreum</i> ^k	<i>Hrr. luteum</i> ^l
Species	<i>Hrr. distributum</i> ^{a,b,c,d}	<i>Hrr. ejinorensense</i> ^e	<i>Hrr. ezzemoulense</i> ^f	<i>Hrr. kocurij</i> ^g	<i>Hrr. lacusprofund</i> ^{h,i}	<i>Hrr. lipolyticum</i> ^j	<i>Hrr. litoreum</i> ^k	<i>Hrr. luteum</i> ^l
Temperature range for growth and optimum (°C)	26–50 (Opt. 37–45)	25–50 (Opt. 37)	22–50 (Opt. 37–40)	25–55 (Opt. 37)	4– < 45 (Opt. 31–37)	25–58 (Opt. 45–48)	20–55 (Opt. 37–42)	17–41 (Opt. 33–37)
Organic substrates used	NR	Treh	Acet Arab Citr Gluc, Glyc Mala Malt Manni Oxal Sucr	Xylo	Acet Etha Form Gala Gluc Glyc Lact Lacto Mann Prop Ribo Succ	Fruc Gala Gluc Malt Mann Sucr	Acet Fuma Gala Gluc Glyc Lacto Mala Malt Pyru Sucr	Citr Fuma Gluc Glyc Lact Lacto Mala Malt Mann Manni Pyru Sorbi Succ
Acid produced from	Gala Gluc Glyc Sucr	–	Gala Gluc Lacto Rham Xylo	NR	–	Fruc Gala Gluc Malt Mann Sucr	NR	–
Organic substrates not used	Gala Gluc Sucr	Acet Arab Fuma Fruc Glyc Lacto Manni Prop Raff Ribo Sorbi Succ Xylo	Cell Fruc Fuma Gala Lacto Mann Raff Rham Xylo	Acet Arab Fruc Fuma Gala Gluc Glyc Lacto Mala Malt Mann Manni Prop Raff Ribo Sorbi Succ Star Treh	–	Acet Lacto Manni Ribo Sorbi Sorb Succ Xylo	Citr Fruc Lact Mann Manni Ribo Sorb Sorbi Star Succ Xylo	Acet Fruc Gala Ribo Sorb Sucr Xylo
Indole from typtophan	–	–	–	–	–	–	–	+
Starch hydrolysis	NR	–	–	–	–	+	–	–
Gelatin liquefaction	–	–	–	–	–	+	–	–
Nitrate reduction	NR	+	+	+	w	+	+	+
Polar lipids	C ₂₀ C ₂₀ derivatives of PGP, PGP-Me, PGS, S-DGD	PG, PGP-Me	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD	PG, PGP-Me, S-DGD	C ₂₀ C ₂₀ derivatives of PGP, PGP-Me, PGS, S-DGD	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD	PG, PGP-Me

Respiratory quinones	NR	NR	NR	NR	NR	NR	NR	NR	NR
Sensitivity to antibiotics	NR	Sensitive: Bac Nov Resistant: Amp Chl Ery Gen Kan Neo Pen Pol Rif Str Van	Sensitive: Bac Nov Resistant: Amp Chl Ery Gen Kan Neo Rif Str	Sensitive: Bac Nov Rif Resistant: Amp Chl Ery Gen Neo Rif Str Tet	Sensitive: Bac Nov Resistant: Amp Chl Ery Gen Neo Rif Str Tet	Sensitive: Bac Nov Rif Resistant: Amp Chl Ery Gen Neo Rif Str Tet	Sensitive: Nov Rif Resistant: Amp Bac Chl Cip Ery Kan Neo Pen Str Tet Van	Sensitive: Nov Rif Resistant: Amp Bac Chl Cip Ery Kan Neo Pen Str Tet Van	Sensitive: Ery Nov Resistant: Amp Bac Chl Kan Neo Pen Pol Rif Str Tet Van
G + C content of DNA (mol %)	63.6 (major comp.); 54.6 (minor)	64.0	61.9	69.4	65.3–65.8 (major comp.); 54.8–56.5 (minor)	65.9	64.9	60.2	
Sample source and site	Salinie soil, USSR	Salt lake, China	Sabkha, Algeria	Salt lake, Inner Mongolia	Deep Lake, Antarctica	Salt lake, China	Saltern, China	Salt lake, Inner Mongolia	

Data taken from:

^aZvyagintseva and Tarasov (1987)

^bZvyagintseva et al. (1996)

^cVentosa et al. (2004)

^dOren and Ventosa (1996)

^eCastillo et al. (2007a)

^fKharroub et al. (2006)

^gGutiérrez et al. (2008a)

^hFranzmann et al. (1988)

ⁱMcGenity and Grant (1995)

^jCui et al. (2006a)

^kCui et al. (2007a)

^lHu et al. (2008)

Additional data on growth substrates and other properties can be found in the original species descriptions

Table 7.13
Comparison of selected characteristics of the members of the genus *Halorubrum* (part C)

Genus	<i>Halorubrum</i>	<i>Hrr. sodomense</i> ^{b,c}	<i>Hrr. tebenquichense</i> ^d	<i>Hrr. terrestre</i> ^{e,f}	<i>Hrr. tibetense</i> ^g	<i>Hrr. trapanicum</i> ^c	<i>Hrr. vacuolatum</i> ^{h,i}	<i>Hrr. xinjiangense</i> ^j
Species	<i>Hrr. orientale</i> ^a	<i>Hrr. sodomense</i> ^{b,c}	<i>Hrr. tebenquichense</i> ^d	<i>Hrr. terrestre</i> ^{e,f}	<i>Hrr. tibetense</i> ^g	<i>Hrr. trapanicum</i> ^c	<i>Hrr. vacuolatum</i> ^{h,i}	<i>Hrr. xinjiangense</i> ^j
Older names		Basonym: <i>Halobacterium sodomense</i> ; <i>Halorubrobacterium sodomense</i> is a later homotypic synonym		Formerly classified as a strain of <i>Hrr. distributum</i>		Basonym: <i>Halobacterium trapanicum</i>	Basonym: <i>Natronobacterium vacuolatum</i> corrig.	
Type strain	CECT (7145) CGMCC 1.6295 JCM 13889	ATCC 33755 CIP 105330 DSM 3755 IFO (now NBRC) 14740 JCM 8880 NCIMB 2197 VKM B-1771	CECT 5371 DSM 14210 JCM 12290	JCM 10247 VKM B-1739	AS 1.3239 JCM 11889	NCCB 71076 NRC 34021 VKM B-2026	CIP 104547 DSM 8800 JCM 9060 NCIMB 13189	AS 1.3527 JCM 12388
Cell shape	Pleomorphic	Rods	Irregular discs	Pleomorphic, flat and disc-shaped	Irregular rods	Pleomorphic rods	Short rods; spherical in the stationary phase	Short rods
Cell size (µm)	1.0–2.0 × 1.5–2.0	0.5 × 2.5–5.0	0.8–1.2 × 1.0–1.5	1.0–1.5 × 1.5–2.5	0.5–1.0 × 1.5–2.5	0.7–1.0 × 1.5–3.0	0.5–0.7 × 1.5–3.0	0.8–1.2 × 1.8–2.6
Motility	+	+	NR	+	–	–	–	+
Colony color	Red	Red-orange	Red-orange	Orange-red	Red	Pale orange to almost colorless	Pink	Red
NaCl range for growth and optimum (%)	15–30 (Opt. 20)	3–25 (Opt. 10–15)	15–30	15–30 (Opt. 25)	10–30 (Opt. 18–20)	15–30	15–30 (Opt. 20)	12–30 (Opt. 18–20)
Lysis in distilled water	NR	+	NR	NR	+	NR	+	NR
Magnesium requirement and optimum (M)	–	+	–	NR	–	NR	–	–

pH range for growth and optimum	NR	7.0–10.0	5.0–9.0 (Opt. 7.5)	8.0–10.5 (Opt. 9.0–9.5)	NR	8.5–10.5 (Opt. 9.5)	6.0–10.0 (Opt. 7.0–7.5)
Temperature range for growth and optimum (°C)	20–50 (Opt. 40)	35–50	28–50 (Opt. 37–45)	22–45 (Opt. 37–40)	Opt. 37	20–50 (Opt. 35–40)	10–54 (Opt. 40)
Organic substrates used	Fruc Gluc Glyc Malt Sucr	Acet Fruc Gala Glyc Mann Pyru Treh	NR	Acet Gluc Lacto Malt Mann Manni Sorb Succ Sucr Star	Fruc Gala Gluc Glyc Mann Malt Sucr Treh	Acet Citr Fuma Gala Gluc Succ Sucr	Fruc Gluc Malt Sucr
Acid produced from	Fruc Gluc Glyc Malt Sucr	–	Glyc	–	Fruc Gala Gluc Glyc Mann Malt Sucr Treh	–	Fruc Malt Gluc Sucr
Organic substrates not used	Gala Lacto Mann Ribo	NR	Cell Etha Manni Raff Rham Sorbi Treh	Gala	Arab Lacto Manni Raff Rham Ribo Sorb Star Xyl	Fruc Manni Pyru	Gala Glyc Lacto Mann Manni Raff Rham Ribo Sorbi organic acids
Indole from typtophan	–	–	–	–	–	NR	–
Starch hydrolysis	+	–	–	–	–	–	–
Gelatin liquefaction	–	–	–	–	–	–	NR
Nitrate reduction	+(w)	+	–	+	+	+	–
Polar lipids	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, S-DGD	PG, PGP-Me, S-DGD-3, 2 minor unidentified lipids	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ diether derivatives of PG and PGP, 5 minor phospholipids	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ diether derivatives of PG and PGP	C ₂₀ C ₂₀ derivatives of PG, PGP-Me, PGS, S-DGD
Respiratory quinones	NR	NR	NR	NR	NR	MK-8	NR

Table 7.13 (continued)

Genus	<i>Halorubrum</i>									
Species	<i>Hrr. orientale</i> ^a	<i>Hrr. sodomense</i> ^{b,c}	<i>Hrr. tebenquichense</i> ^d	<i>Hrr. terrestre</i> ^{e,f}	<i>Hrr. tibetense</i> ^g	<i>Hrr. trapanicum</i> ^c	<i>Hrr. vacuolatum</i> ^{h,i}	<i>Hrr. xinjiangense</i> ^j		
Sensitivity to antibiotics	Sensitive: Amp Bac Chl Ery Gen Neo Nov Rif Str Resistant: Pen Rif	Sensitive: Bac Nov Resistant: Chl Ery Kan Neo Kan Pen Str Tet	Sensitive: Bac Nov Resistant: Chl Kan Pen Tet	Sensitive: Ani Bac Nov Resistant: Amp Chl Kan Pen Pol Str Tet	Sensitive: Nov Pol Resistant: Bac Chl Ery Neo Pen Rif Str Tet		Sensitive: Ery (w) Nov Resistant: Amp Chl Str Tet	NR		
G + C content of DNA (mol%)	64.2	68	63.2	64.2–64.9	63.3	64.3	62.7	68.0		
Sample source and site	Salt lake, Inner Mongolia	The Dead Sea	Hypersaline lake, Atacama Desert	Saline soil	Soda lake, Tibet	Solar salt, Italy	Lake Magadi, Kenya	Salt lake, China		

Data taken from:

^aCastillo et al. (2006a)^bOren (1983)^cMcGenity and Grant (1995)^dLizama et al. (2002)^eVentosa et al. (2004)^fZvyagintseva et al. (1996)^gFan et al. (2004)^hMwatha and Grant (1993)ⁱKamekura et al. (1997)^jFeng et al. (2004)

Additional data on growth substrates and other properties can be found in the original species descriptions

Table 7.14
Comparison of selected characteristics of the members of the genus *Haloterrigena*

Genus	<i>Haloterrigena</i> ^a	<i>Htg. daqingensis</i> ^d	<i>Htg. hispanica</i> ^e	<i>Htg. jeotgali</i> ^f	<i>Htg. limicola</i> ^g	<i>Htg. longae</i> ^g	<i>Htg. saccharovitans</i> ^h	<i>Htg. salina</i> ⁱ	<i>Htg. thermotolerans</i> ^j
Species	<i>Htg. turkmenica</i> ^{b,c}	<i>Htg. daqingensis</i> ^d	<i>Htg. hispanica</i> ^e	<i>Htg. jeotgali</i> ^f	<i>Htg. limicola</i> ^g	<i>Htg. longae</i> ^g	<i>Htg. saccharovitans</i> ^h	<i>Htg. salina</i> ⁱ	<i>Htg. thermotolerans</i> ^j
Older names	Basonym: <i>Halococcus turkmenicus</i>								
Type strain	ATCC 51198 CIP 106419 DSM 5511 JCM 9101 NCIMB 13204 VKM B-1734	CGMCC 1.8909 NCRB 105739	ATCC BAA-1310 DSM 18328	CECT 7218 DSM 18794 JCM 14585 KCTC 4020	CGMCC 1.5333 JCM 13563	CGMCC 1.5334 JCM 13562	AS 1.3730 JCM 12889	CGMCC 1.6203 JCM 13891	ATCC 700275 DSM 11552 JCM 11050 NBRC 102635
Cell shape	Cocci to oval	Cocci	Cocci	Rods	Rods	Rods	Rods; cocci in stationary cultures	Cocci	Rods
Cell size (µm)	1.5–2.0	0.8–1.3	1.5–2.0	0.4 × 1.0	0.6–0.8 × 1.8–3.6	0.5–0.6 × 2.8–11	0.4–1.0 × 3–10	1.2 × 1.6	0.7–1.0 × 4–13
Motility	–	–	NR	–	+	–	+	–	–
Colony color	Red	Orange	Light red	Light red	Red	Red	Light red	Light-red	Pale red
NaCl range for growth and optimum (%)	Opt. 15–25	10–30 (Opt. 12–15)	13–23 (Opt. 20)	10–30 (Opt. 15–20)	10–30 (Opt. 18)	10–30 (Opt. 18)	> 10 (Opt. 18–20)	15–30 (Opt. 20)	> 12 (Opt. 18–20)
Lysis in distilled water	–	–	+	+	NR	NR	NR	NR	+
Magnesium requirement and optimum	NR	NR	0–0.4 (Opt. 0.2)	–	0.005–0.7 (Opt. 0.05)	0–1 (Opt. 0.1)	Opt. 0–0.2.	–	0.005
pH range for growth and optimum	NR	8.0–10.5 (Opt. 10.0)	6.5–8.5 (Opt. 7.0)	6.5–8.5 (Opt. 7.0–7.5)	6.5–9.0 (Opt. 7.0)	6.5–9.0 (Opt. 7.0–7.5)	6.5–8.5 (Opt. 7.5)	6.0–9.0 (Opt. 7.0–8.0)	6.5–8.2 (Opt. 7.0–7.5)
Temperature range for growth and optimum (°C)	Opt. 45	20–50 (Opt. 35)	37–60 (Opt. 50)	17–50 (Opt. 37–45)	30–61 (Opt. 45–50)	30–56 (Opt. 41–45)	24–58 (Opt. 42–45)	25–50 (Opt. 37)	< 60 (Opt. 50)

Respiratory quinones	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR
Sensitivity to antibiotics	NR	Sensitive: Cip Ery Nov Rif	Sensitive: Bac Nov	Sensitive: Ani Aph Nov	Sensitive: Nov Rif	Sensitive: Nov Rif	Sensitive: Nov Rif	Sensitive: Nov Rif	Sensitive: Tet			Sensitive: Ani Bac Nov
		Resistant: Amp Bac Chl Kan Neo Pen Str Tet Van	Resistant: Amp Chl Ery Kan Neo Pen Str Tet Van	Resistant: Amp Bac Chl Ery Pen	Resistant: Amp Bac Chl Ery Kan Neo Pen Str Tet Van	Resistant: Amp Bac Chl Ery Kan Neo Pen Str Tet Van	Resistant: Amp Bac Chl Ery Kan Neo Pen Str Tet Van	Resistant: Amp Bac Chl Ery Kan Neo Pen Str Tet Van	Resistant: Amp Kan Str Van	Resistant: Amp Chl Ery Neo Pen Str Tet	Resistant: Amp Chl Ery Neo Pen Str Tet	Resistant: Amp Chl Ery Kan Neo Pen Str Tet Van
G + C content of DNA (mol %)	59.8	59.3	62.0	62.3	61.9	63.2	66.6	67.0	63.3			
Sample source and site	Saline soil, Turkmenia	Saline alkaline soil, China	Salt lake, Spain	Fermented food, Korea	Salt lake, China	Salt lake, China	Salt lake, China	Salt lake, Inner Mongolia	Saltern, Puerto Rico			

Data taken from:

- ^aVentosa and Kamekura (2001)
^bZvyagintseva and Tarasov (1987)
^cVentosa et al. (1999)
^dWang et al. (2010)
^eRomano et al. (2007)
^fRoh et al. (2009)
^gCui et al. (2006c)
^hXu et al. (2005c)
ⁱGutiérrez et al. (2008b)
^jMontalvo-Rodríguez et al. (2000)

Additional data on growth substrates and other properties can be found in the original species descriptions

Table 7.15

Comparison of selected characteristics of the members of the genera *Halostagnicola*, *Halovenus*, and *Halovivax*

Genus	<i>Halostagnicola</i>			<i>Halovenus</i>	<i>Halovivax</i>	
Species	<i>Hst. larsenii</i> ^a	<i>Hst. alkaliphila</i> ^b	<i>Hst. kamekurae</i> ^c	<i>Hvn. aranensis</i> ^d	<i>Hvx. asiaticus</i> ^e	<i>Hvx. ruber</i> ^f
Type strain	CECT 7116 CGMCC 1.5338 DSM 17691 JCM 13463	CECT 7631 JCM 16592	CECT 7536 DSM 22427 JCM 16110	CGMCC 1.11001 IBRC-M 10015	CECT 7098 CGMCC 1.4248 JCM 14624	CGMCC 1.6204 DSM 18193 JCM 13892
Cell shape	Pleomorphic rods	Pleomorphic rods	Pleomorphic rods	Pleomorphic: rods to triangles, squares or disc-shaped	Pleomorphic rods	Pleomorphic rods and irregular cells
Cell size (µm)	0.5–1.0 × 1.0–3.0	0.8–1.0 × 2.0–2.5	0.8–1.0 × 2.0–2.5	0.6–1.3 × 4.9– 10.7	0.4–0.5 × 4.0–5.0	0.6–0.8 × 3.5–4.5
Motility	–	+	+	–	–	–
Colony color	Pink	White-pink	White, later pink	Red	Pale pink	Red
NaCl range for growth and optimum (%)	15–30 (Opt. 20)	20–30 (Opt. 25)	10–30 (Opt. 15)	15–30 (Opt. 23)	15–25 (Opt. 20)	>15 (Opt. 20)
Lysis in distilled water	+	+	+	+	+	+
Magnesium requirement and optimum (M)	–	NR	– (Opt. 0.06)	0.2–1.0 (Opt. 0.5)	–	>0.005 (Opt. 0.15)
pH range for growth and optimum	Opt. 7.0–8.0	8.0–10.0 (Opt. 8.5– 9.0)	6.0–9.0 (Opt. 6.5–7.0)	6.0–8.0 (Opt. 7.5)	6.0–9.0 (Opt. 7.0– 7.5)	6.0–9.0 (Opt. 7.0– 7.5)
Temperature range for growth and optimum (°C)	<50 (Opt. 37)	20–55 (Opt. 37)	20–45 (Opt. 30)	25–50 (Opt. 40)	25–45 (Opt. 37)	25–45 (Opt. 37)
Organic substrates used	Acet Arab Fruc Gala Gluc Glyc Lacto Malt Prop Ribo Star Treh Xylo	Fruc Fuma Gala Gluc Glyc Lact Malt Mann Prop Pyrul Sucr Treh Xylo	Acet Arab Gala Gluc Glyc Lacto Mala Malt Mann Prop Treh	Gala Gluc	Acet Lacto Prop Raff Treh Xylo	Fuma Lacto Mann Prop Raff Ribo Starc Treh Xylo
Acid produced from	Sucr	NR	Arab Mann	Gluc	Xylo	NR
Organic substrates not used	Fuma Mala Raff Sorbi Succ	Acet Arab Cell Citr Lacto Mala Manni Ribo Raff Succ	Cell Fruc Fuma Manni Ribo Sorbi Succ Sucr Xylo	Lacto	Arab Fruc Fuma Gala Gluc Glyc Mala Malt Manni Ribo Sorbi Star Succ Sucr	Acet Arab Fruc Gala Gluc Glyc, Mala Malt Manni Sorbi Succ
Indole from typtophan	–	–	+	–	–	–
Starch hydrolysis	+	–	–	–	–	–
Gelatin liquefaction	–	–	–	–	+	+

■ Table 7.15 (continued)

Genus	<i>Halostagnicola</i>			<i>Halovenus</i>	<i>Halovivax</i>	
Species	<i>Hst. larsenii</i> ^a	<i>Hst. alkaliphila</i> ^b	<i>Hst. kamekurae</i> ^c	<i>Hvn. aranensis</i> ^d	<i>Hvx. asiaticus</i> ^e	<i>Hvx. ruber</i> ^f
Nitrate reduction	+	+	+	–	–	–
Polar lipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, 2 unidentified glycolipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me	PG, PGP-Me, 2 major unknown glycolipids, several minor unknown glycolipids	PG, PGP-Me, 2 minor phospholipids	PG, PGP-Me, 2 major and 1 minor glycolipids, 1 unidentified glycolipid	PG, PGP-Me, 2 major and 1 minor glycolipids, 1 unidentified glycolipid
Respiratory quinones	NR	NR	NR	MK-8(II-H ₂)	NR	NR
Sensitivity to antibiotics	Sensitive: Bac Nov	Sensitive: Ani Bac Ery Nov Rif	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Nov Rif Str	Sensitive: Bac Nov	Sensitive: Amp Bac Gen Neo Nov Rif
	Resistant: Amp Chl Ery Neo Pen Rif Str Tet	Resistant: Amp Chl Ery Kan Neo Pen Str Tet Van	Resistant: Amp Chl Ery Gen Kan Neo Pen Str Tet	Resistant: Amp Chl Ery Gen Kan Neo Pen Tet	Resistant: Amp Chl Ery Gen Neo Pen Rif Str Tet	Resistant: Chl Ery Pen
G + C content of DNA (mol %)	61.0	60.7	59.8	61.0	60.3	65.0
Sample source and site	Salt lake, Inner Mongolia	Rock salt imported to Japan from China	Solar salt important to Japan from the Philippines	Salt lake, Iran	Salt lake, Inner Mongolia	Salt lake, Inner Mongolia

Data taken from:

^aCastillo et al. (2006d)

^bNagaoka et al. (2011)

^cNagaoka et al. (2010)

^dMakhdoumi-Kakhki et al. (2012a)

^eCastillo et al. (2006b)

^fCastillo et al. (2007b)

Additional data on growth substrates and other properties can be found in the original species descriptions

examples being *Har. hispanica*, *Hfx. volcanii*, *Hmn. pharaonis*, and *Hrd. utahensis* (Feng et al. 2012). The list of organic compounds given here is limited to sugars, sugar alcohols, and organic acids. Some species descriptions give information on the use of different amino acids as well. Properties such as the Gram stain are not listed in the tables as, with very few exceptions, all members of the *Halobacteriaceae* stain Gram negative, when using the special modification of the Gram stain protocol developed for halophilic prokaryotes. Exceptions are *Hrr. vacuolatum* and *Htg. daquinensis*, reported as Gram variable. Nearly all members of the family were reported to display catalase activity, exceptions being *Hla. acidiphilum*, *Hns. pteroides*, *Hst. alkaliphila*, *Hst. kamekurae*, and *Nac. mannanyliticum*. The oxidase reaction is also generally positive, but in some species, no oxidase activity could be detected: *Hbt. noricense*, *Hac. jeotgali*, *Hla. acidiphilum*, *Hcc. hamelinensis*, *Hcc. qingdaonensis*, *Hfx. mucosum*, *Hns. pteroides*, *Hrd. tiamatea* (a rare case of a member of the *Halobacteriaceae* with an anaerobic life style), *Hrr. aquaticum*, *Hrr. cibi*, *Hst. kamekurae*, *Nnm. pellirubrum*,

Nac. mannanyliticum, and *Ncc. jeotgali*. When evaluating such results, it should be taken into account that different protocols may have been used in different laboratories. A comparative study using comparable methods and culture of similar age was never yet performed.

A critical evaluation of the tables shows some problematic data published in the species descriptions. For example, the growth of *Hmr. oriensis*, *Hrr. aquaticum*, *Hrr. kocurii*, *Hrr. orientale*, *Hrr. tibetense*, *Htg. salina*, and *Hvx. ruber* was reported to be stimulated by starch, but amylase activity could not be detected in these species. Also some of the published data on sensitivity to antibiotics need a renewed evaluation. For example, the described sensitivity of *Hvx. ruber* to ampicillin, an antibiotic that inhibits the formation of the bacterial cell wall but not of the wall of the Archaea, needs to be reassessed.

The short descriptions of the different genera given below only list their distinctive phenotypic and chemotaxonomic properties. Since in recent years many new genera have been proposed mainly on the basis of 16S rRNA gene sequences, it has become

Table 7.16

Comparison of selected characteristics of the members of the genus *Natrialba*

Genus	<i>Natrialba</i> ^a					
Species	<i>Nab. asiatica</i> ^b	<i>Nab. aegyptiaca</i> ^c	<i>Nab. chagannaensis</i> ^d	<i>Nab. hulunbeirensis</i> ^d	<i>Nab. magadii</i> ^{e,f}	<i>Nab. taiwanensis</i> ^c
Older names		<i>Nab. aegyptia</i>			Basonym: <i>Natronobacterium magadii</i>	<i>Natrialba asiatica</i> B1T
Type strain	ATCC 700177 CIP 105332 DSM 12278 JCM 9576 NBRC 102637	DSM 13077 JCM 11194 NBRC 102636	AS 1.1977 JCM 10990 NBRC 102638	AS 1.1986 JCM 10989 NBRC 102639	ATCC 43099 CIP 104546 JCM 8861 NBRC 102185 NCIMB 2190	DSM 12281 JCM 9577 NBRC 102640
Cell shape	Rods-coccobacilli	Rods, cocci, tetrads	Rods	Rods	Rods	Rods-coccobacilli
Cell size (µm)	0.5–1.0 × 1.0–5.0	0.5–1.2 × 1.5–6	0.4–0.6 × 1.0–2.5	0.4–0.6 × 1.0–2.5	0.7–0.9 × 2–4	0.3–0.5 × 1.0–1.5
Motility	+	+ (rods)	–	–	+	+
Colony color	Non-pigmented	Non-pigmented to slightly pigmented	Red	Red	Orange-red	Non-pigmented
NaCl range for growth and optimum (%)	12–30 (Opt. 23)	10–30 (Opt. 15–18)	10–30 (Opt. 15)	12–30 (Opt. 20)	12–30 (Opt. 20)	12–30 (Opt. 20)
Lysis in distilled water	+	+	+	+	+	+
Magnesium requirement and optimum (M)	–	–	NR	NR	NR	–
pH range for growth and optimum	6.0–8.0 (Opt. 6.6–7.0)	6.0–9.0 (Opt. 7.0–8.0)	8.5–10.5 (Opt. 9.0)	8.5–10.0 (Opt. 9.0)	8.5–11.0 (Opt. 9.5)	5–10 (Opt. 7.5–7.8)
Temperature range for growth and optimum (°C)	<50 (Opt. 30–40)	<60 (Opt. 37–42)	20–55 (Opt. 45)	20–55 (Opt. 50)	20–50 (Opt. 37–40)	Up to 55 (Opt. 35–40)
Organic substrates used	NR	NR	Acet Fruc Gluc Malt	Fruc Malt	Acet	NR
Acid produced from	NR	Arab Gluc Lacto (w) Malt Sucr Star Xylo	NR	NR	NR	Arab Gluc (w) Malt (w) Sucr Star Xylo
Organic substrates not used	NR	NR	Lacto Manni Sucr	Acet Gluc Lacto Manni Sucr	Carbohydrates	NR
Indole from typtophan	+	+	NR	NR	NR	+
Starch hydrolysis	–	+	+	–	NR	+
Gelatin liquefaction	+	+	+	+	–	–
Nitrate reduction	+	+	+	+	–	+

Table 7.16 (continued)

Genus	<i>Natrialba</i> ^a					
Species	<i>Nab. asiatica</i> ^b	<i>Nab. aegyptiaca</i> ^c	<i>Nab. chagannaensis</i> ^d	<i>Nab. hulunbeirensis</i> ^d	<i>Nab. magadii</i> ^{e,f}	<i>Nab. taiwanensis</i> ^c
Polar lipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, S ₂ -DGD	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, S ₂ -DGD	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, 1 uncharacterized lipid	NR	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, S ₂ -DGD
Respiratory quinones	NR	NR	NR	NR	MK-8, MK-8(H ₂)	NR
Sensitivity to antibiotics	Sensitive: Ani Bac Nov Rif	Sensitive: Ani Bac Rif Nov	Sensitive: Bac Ery Rif	Sensitive: Bac Ery Rif	Sensitive: Ani Bac Ery Nov	Sensitive: Ani Bac Rif Nov
	Resistant: Chl Ery Pen Str Tet	Resistant: Chl Ery Pen Str Tet	Resistant: Tet	Resistant: Tet	Resistant: Amp Chl Pol Str Tet	Resistant: Chl Ery Pen Str Tet
G + C content of DNA (mol%)	60.3–63.1	61.5	63.7	64.3	63.0 (major component) 49.5 (minor component)	62.3
Sample source and site	Beach sand, Japan	Salt soil, Egypt	Soda lake, China	Soda lake, China	East-African alkaline lakes	Solar salt, Taiwan

Data taken from:

^aKamekura (2001a)

^bKamekura and Dyll-Smith (1995)

^cHezayen et al. (2001)

^dXu et al. (2001b)

^eTindall et al. (1984)

^fKamekura et al. (1997)

Additional data on growth substrates and other properties can be found in the original species descriptions

more difficult to find morphological, physiological, or chemotaxonomic traits that can be used to unequivocally assign a strain to one of these genera. An example can be found in the description below of the genus *Halomicrobium*, a genus established only on the basis of 16S rRNA gene comparisons, which now contains organisms with greatly different G+C contents of their DNA, with some species possessing and some lacking phosphatidylglycerol sulfate in their polar lipids. Full descriptions of the genera can be found in the original descriptions as cited. A number of emended genus descriptions were given by Oren et al. (2009).

Genus *Halobacterium* Elazari-Volcani 1957, 207^{AL}; emend. Kamekura and Dyll-Smith 1995, 344; emend. Oren, Arahal, and Ventosa 2009, 638

Ha.lo.bac.te'ri.um. Gr. n. *hals*, halos, salt; L. neut. n. *bacterium*, a small rod; N.L. neut. n. *Halobacterium*, salt (-requiring) bacterium.

Cells are motile rods of varying length and lyse in distilled water. Colonies are red or pink due to the presence of

bacterioruberin carotenoids; purple retinal pigments may be present as well. Some strains possess gas vesicles. Magnesium requirement is moderate (5–50 mM). Amino acids are required for growth. Many strains grow anaerobically in the dark by fermentation of arginine. Sugars are poorly used, and no acid is formed in the presence of sugars. The optimum salt concentration for growth is 3.5–4.5 M NaCl. Neutrophilic. Characteristic lipids are PG, PGP-Me, PGS, and sulfated triglycosyl- and tetraglycosyl diethers.

The mol% G+C of the DNA is 54.3–70.9.

The genus *Halobacterium* currently contains three species: *Hbt. salinarum* (type species), *Hbt. jilantaiense*, and *Hbt. noricense*.

The main features of the members of the genus are summarized in Table 7.1.

Additional comments:

- *Hbt. piscisalsi* (Yachai et al. 2008) is not included in the table, as it is now considered a later heterotypic synonym of *H. salinarum* (Minegishi et al. 2012b).
- *Hbt. cutirubrum*, *Hbt. halobium*, and *Hbt. salinarium* were renamed as *Hbt. salinarium* nom. corrig. (Ventosa and Oren 1996).

Table 7.17

Comparison of selected characteristics of the members of the genus *Natrinema*

Genus	<i>Natrinema</i> ^a					
Species	<i>Nnm. pellirubrum</i> ^b	<i>Nnm. altunense</i> ^c	<i>Nnm. ejinorensis</i> ^d	<i>Nnm. gari</i> ^e	<i>Nnm. pallidum</i> ^b	<i>Nnm. versiforme</i> ^f
Type strain	CIP 106293 JCM 10476 NCIMB 786	AS 1.31731 JCM 12890	CECT 7144 CGMCC 1.6202 JCM 13890	BCC 24370 JCM 14663 PCU 303	CIP 106292 JCM 8980 NCIMB 777	ANMR 0149 AS 1.2365 JCM 10478
Cell shape	Rods	Rods	Pleomorphic	Rods	Rods	Pleomorphic
Cell size (µm)	0.6–1.0 × 1–4	0.8–1.2 × 3–7	0.8–2.0 × 1.5–4.0	0.5–0.8 × 2.0–3.0	0.7–1.0 × 1.5–6	0.6–1.5 × 1–5
Motility	+	+	–	+	+	–
Colony color	Pale orange	Orange-red	Pale red	Pale orange	Pale orange	Light red
NaCl range for growth and optimum (%)	>12 (Opt. 20–25)	> 10 (Opt. 18–25)	>10 (Opt. 20)	Opt. 15–20	>10 (Opt. 20–25)	> 9 (Opt. 20–25)
Lysis in distilled water	+	+	+	+	+	+
Magnesium requirement and optimum (M)	0.1–0.2	>0.005 (Opt. 0.050–0.2)	–	– (Opt. 0.1–0.2)	0.1–0.2	>0.005 (Opt. 0.15)
pH range for growth and optimum	6.0–8.6 (Opt. 7.2–7.8)	6.0–8.0 (Opt. 7.0–7.7)	6.0–8.5 (Opt. 7.0)	5.5–8.5 (Opt. 6.0–6.5)	6.0–8.4 (Opt. 7.2–7.6)	6.0–8.0 (Opt. 6.5–7.0)
Temperature range for growth and optimum (°C)	20–45	20–40	25–50 (Opt. 37)	20–60 (Opt. 37–40)	25–60 (Opt. 37–40)	20–53 (Opt. 37–46)
Organic substrates used	Fruc Gluc Lacto Ribo	Acet Fuma Gluc Glyc, Mala Malt Prop Pyru Succ	Acet Fruc Fuma Gluc Glyc Malt Prop Treh	Arab Gluc Glyc	Fruc Gluc Lacto	Fruc Gala Gluc Glyc Malt Mann Ribo Sucr Xylo
Acid produced from	NR	Gluc Glyc Malt Mann	NR	Arab, Glyc	NR	Glyc
Organic substrates not used	NR	Fruc Gala Lacto Ribo Sucr Xylo	Arab Gala Mala Mann Lacto Manni Raff Ribo, Sorbi Succ Xylo	Citr Lacto Malt Manni Mann, Meli Rham Ribo Sorbi Sucr Xylo	Ribo	Lacto
Indole from typtophan	–	–	–	–	–	+
Starch hydrolysis	–	–	+	–	–	w
Gelatin liquefaction	+	+	+	+	+	–
Nitrate reduction	+	+	+	–	+	+
Polar lipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, PGS (trace), unidentified glycolipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, PGS, unidentified glycolipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, S ₂ -DGD-1	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, PGS, 2 glycolipids, 1 unidentified lipid	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, PGS, unidentified glycolipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, PGS, 2 unidentified glycolipids

■ Table 7.17 (continued)

Genus	<i>Natrinema</i> ^a					
Species	<i>Nnm. pellirubrum</i> ^b	<i>Nnm. altunense</i> ^c	<i>Nnm. ejinorensis</i> ^d	<i>Nnm. gari</i> ^e	<i>Nnm. pallidum</i> ^b	<i>Nnm. versiforme</i> ^f
Respiratory quinones	MK-8, MK-8(H ₂)	NR	NR	MK-8	MK-8, MK-8(H ₂)	NR
Sensitivity to antibiotics	Sensitive: Ani Bac Nov	Sensitive: NR	Sensitive: Bac Nov	Sensitive: Bac Nov Rif	Sensitive: Ani Bac Nov Rif (w)	Sensitive: Ani Bac Nov Rif
	Resistant: Amp Chl Rif Str Tet	Resistant: Amp Cip Ery Kan Neo Str	Resistant: Amp Chl Ery Pen Rif Str Tet	Resistant: Amp Chl Kan Neo. Str Tet	Resistant: Amp Chl Str Tet	Resistant: Amp Chl Ery Neo Pen
G + C content of DNA (mol %)	69.9 (major component), 60.0 (minor component)	65.6	64.7	65.4	NR	64.2
Sample source and site	Salted hides	Salt lake, China	Salt lake, Inner Mongolia	Fermented fish sauce, Thailand	Salted fish, hides	Salt lake, China

Data taken from:

^aMcGenity et al. (2001)

^bMcGenity et al. (1998)

^cXu et al. (2005b)

^dCastillo et al. (2006c)

^eTapingkae et al. (2008)

^fXin et al. (2000)

Additional data on growth substrates and other properties can be found in the original species descriptions

- *Hbt. denitrificans* (Tomlinson et al. 1986) was reclassified as *Hfx. denitrificans* comb. nov. (Tindall et al. 1989).
- *Hbt. distributum* (Zvyagintseva et al. 1987) was reclassified as *Hrr. distributum* comb. nov. (Oren and Ventosa 1996).
- *Hbt. lacusprofundi* (Franzmann et al. 1988) was reclassified as *Hrr. lacusprofundi* comb. nov. (McGenity and Grant 1995; Validation List 57, 1996).
- *Hbt. mediterranei* (Rodriguez-Valera et al. 1983) was reclassified as *Hfx. mediterranei* (Torreblanca et al. 1986).
- *Hbt. pharaonis* (Soliman and Trüper 1982) was reclassified first as *Nbt. pharaonis* comb. nov. (Tindall et al. 1984) and later as *Nmn. pharaonis* comb. nov. (Kamekura et al. 1997).
- *Hbt. saccharovororum* (Tomlinson and Hochstein 1976) was reclassified as *Hrr. saccharovororum* comb. nov. (McGenity and Grant 1995; Validation List 57, 1996).
- *Hbt. sodomense* (Oren 1983) was reclassified as *Hrr. sodomense* comb. nov. (McGenity and Grant 1995; Validation List 57, 1996).
- *Hbt. trapanicum* (Petter 1931) (Elazari-Volcani 1957) was reclassified as *Hrr. trapanicum* comb. nov. (McGenity and Grant 1995).
- *Hbt. vallismortis* (Gonzalez et al. 1978) was reclassified as *Har. vallismortis* comb. nov. (Torreblanca et al. 1986).

Genus *Haladaptatus* Savage, Krumholz, Oren, and Elshahed 2007, 23^{VP}; emend. Cui, Sun, Gao, Dong, Xu, Zhou, Liu, Oren, and Zhou 2010a, 1087; emend. Roh, Lee, and Bae 2010, 1189

Hal.a.dap.ta'tus. Gr. n. *hals*, *halos*, salt; L. part. adj. *adaptatus*, adapted to a thing; N.L. masc. n. *Haladaptatus*, a bacterium adapted to salt.

Cells are cocci or coccobacilli occurring singly or in pairs and do not lyse in distilled water. Some species possess more than one different 16S rRNA gene sequences. Grow on a wide range of substrates, including single and complex carbon sources. Acid is produced from carbohydrates. Grow at a wide range of NaCl concentrations. Cells contain PG and PGP-Me and two or three glycolipids may be present, one of which is chromatographically identical to S-DGD-1. The presence of PGS is variable.

The mol% G+C of the DNA is 54.0–60.5.

The genus *Haladaptatus* currently contains three species: *Hap. paucihalophilus* (type species), *Hap. cibarius*, and *Hap. litoreus*.

The main features of the members of the genus are summarized in ► Table 7.1.

Table 7.18

Comparison of selected characteristics of the members of the genera *Natronoarchaeum*, *Natronobacterium*, and *Natronococcus*

Genus	<i>Natronoarchaeum</i>	<i>Natronobacterium</i> ^b	<i>Natronococcus</i> ^d		
Species	<i>Nac. mannanilyticum</i> ^a	<i>Nbt. gregoryi</i> ^c	<i>Ncc. occultus</i> ^b	<i>Ncc. amylolyticus</i> ^e	<i>Ncc. jeotgali</i> ^f
Type strain	CECT 7565 JCM 16328	ATCC 43098 CIP 104747 DSM 3393 JCM 8860 NBRC 102187 NCIMB 2189 VKM B-1750	ATCC 43101 CIP 104548 DSM 3396 JCM 8859 NBRC 102186 NCIMB 2192 VKM B-1752	ATCC 51971 CIP 10533 DSM 10524 JCM 9655	CECT 7216 DSM 18795 JCM 14583 KCTC 4018
Cell shape	Extremely pleomorphic	Rods	Cocci	Cocci	Cocci
Cell size (µm)	1–5	0.5–1.0 × 2–15	1.0–2.0	1.0–2.0	1.0–2.0
Motility	–	–	–	–	–
Colony color	Red	Red	Pale brown	Orange-red	Orange-red
NaCl range for growth and optimum (%)	12–30 (Opt. 23–26)	12–30 (Opt. 17.5)	8–30 (Opt. 20–22)	8–30 (Opt. 15–20)	7.5–30 (Opt. 23–25)
Lysis in distilled water	+	+	–	–	–
Magnesium requirement and optimum (M)	+ (Opt. 0.005)	–	–	–	–
pH range for growth and optimum	5.8–9.5 (Opt. 8.0–9.0)	>8.5 (Opt. 9.5)	8.5–11.0 (Opt. 9.5)	8.0–10.0 (Opt. 9.0)	7.0–9.5 (Opt. 7.5)
Temperature range for growth and optimum (°C)	20–55 (Opt. 37)	25–40 (Opt. 37)	20–50 (Opt. 35–40)	22–50 (Opt. 40–45)	21–50 (Opt. 37–45)
Organic substrates used	Cell Gluc Lacto Mann Pyru Raff	Fruc Gluc Mann Ribo Sucr	Gluc Ribo Sucr	Citr Lacto	Acet Fruc Gluc Lacto Sucr
Acid produced from	NR	NR	NR	NR	NR
Organic substrates not used	NR	NR	Citr Lacto	NR	Citr
Indole from typtophan	+	NR	NR	NR	NR
Starch hydrolysis	+	–	–	+	NR
Gelatin liquefaction	–	+	+	–	NR
Nitrate reduction	–	–	+	+	+
Polar lipids	PG, PGP-Me, S ₂ -DGD, 1 unknown glycolipid	PG, PGP-Me, minor unidentified phospholipids	PG, PGP-Me, a phosphatidylglycero-(cyclo-)-phosphate (PL2)	PG, PGP-Me	PG, PGP-Me
Respiratory quinones	NR	MK-8, MK-8(VIII-H ₂), MMK-8, MMK-8(VIII-H ₂), DMMK-8, DMMK-8(VIII-H ₂)	MK-8, MK-8(H ₂)	NR	NR
Sensitivity to antibiotics	Sensitive: Bac Nov Rif	Sensitive: Ani Bac Cip Ery Nov	Sensitive: Ani Bac Eri Nov	Sensitive: Ani Bac Eri Nov Tet	Sensitive: Ani Aph Bac (w) Nov
	Resistant: Amp Chl Ery Gen Kan Neo Pen Str Tet Van	Resistant: Amp Chl Pol Str Tet	Resistant: Amp Chl Pol Str Tet	Resistant: Amp Chl Pol Str	Resistant: Amp Chl Ery Pen

Table 7.18 (continued)

Genus	<i>Natronoarchaeum</i>	<i>Natronobacterium</i> ^b	<i>Natronococcus</i> ^d		
Species	<i>Nac. mannanyliticum</i> ^a	<i>Nbt. gregoryi</i> ^c	<i>Ncc. occultus</i> ^b	<i>Ncc. amylolyticus</i> ^e	<i>Ncc. jeotgali</i> ^f
G + C content of DNA (mol%)	63	63.2–65.0	64.0 (major component) 55.7 (minor component)	63.5	NR
Sample source and site	Commercial salt, Japan	East-African soda lakes	Soda lakes, East Africa	Lake Magadi, Kenya	Shrimp jeotgal, Korea

Data taken from:

^aShimane et al. (2010)

^bTindall (2001a)

^cTindall et al. (1984)

^dTindall (2001b)

^eKanai et al. (1995)

^fRoh et al. (2007b)

Additional data on growth substrates and other properties can be found in the original species descriptions

Genus *Halalkalicoccus* Xue, Fan, Ventosa, Grant, Jones, Cowan, and Ma 2005, 2504^{VP}

Hal.al.ka.li.coc'cus. Gr. n. *hals*, *halos*, salt; Arabic n. alkali (al-qaliy), the ashes of saltwort; N.L. masc. *coccus* (from Gr. masc. n. *kokkos*, grain, seed), coccus; N.L. masc. n. *Halalkalicoccus*, coccus existing in salted and alkaline environment.

Cells are cocci occurring singly, in pairs, or irregular clusters. Stain mainly Gram negative with some cells Gram positive in young cultures. Cells do not lyse in distilled water. Alkaliphilic. Possesses C₂₀C₂₀ and C₂₀C₂₅ diethers. No glycolipids or PGS detected. Isoprenoid quinones are MK-8 and MK-8(H₂).

The mol% G+C of the DNA is 61.5–63.2.

The genus *Halalkalicoccus* currently contains two species: *Hac. tibetensis* (type species) and *Hac. jeotgali*.

The main features of the members of the genus are summarized in Table 7.1.

Genus *Halarchaeum* Minegishi, Echigo, Nagaoka, Kamekura, and Usami 2010, 2515^{VP}

Hal.ar.chae'um. Gr. n. *hals*, *halos*, salt; N.L. neut. n. *archaeum* (from Gr. adj. *archaios*, ancient), ancient one, archaeon; N.L. neut. n. *Halarchaeum*, a saline archaeon.

Cells are nonmotile, pleomorphic, with triangular and disk morphology. Lipids are C₂₀C₂₀ and C₂₀C₂₅ derivatives of PG and PGP-Me, and four unidentified glycolipids. Cells lyse in distilled water. Cells grow on a wide range of substrates, including simple and complex carbon sources.

The mol% G+C of the DNA is 61.4.

Type species and currently only species: *Hla. acidiphilum*.

The main features of the members of the genus are summarized in Table 7.2.

Genus *Haloarchaeobius* Makhdoumi-Kakhki, Amoozegar, Bagheri, Ramezani, and Ventosa 2012, 1024^{VP}

Ha.lo.ar.chae.o'bi.us. Gr. n. *hals*, *halos*, salt; N.L. adj. *archaeos* from Gr. adj. *archaios* ancient; N.L. masc. n. *bios* from Gr. masc. n. *bios* life; N.L. masc. n. *Haloarchaeobius*, halophilic ancient (archaeal) life.

Cells are motile strictly aerobic rods, pigmented orange-red. Neutrophilic and mesophilic. Magnesium is not required for growth. Polar lipids include PG, PGP-Me, PGS, three unidentified glycolipids, and one minor phospholipid. MK-8(II-H₂) is the only respiratory lipoquinone present.

The mol% G+C of the DNA is 67.7.

Type species and currently only species: *Hab. iranensis*.

The main features of the members of the genus are summarized in Table 7.2.

Genus *Haloarcula* Torreblanca, Rodriguez-Valera, Juez, Kamekura, and Kates 1986b, 573^{VP} (Validation list 22); Effective Publication: Torreblanca, Rodriguez-Valera, Juez, Kamekura, and Kates 1986a, 98; emend. Oren, Arahai, and Ventosa 2009, 638

Ha.lo.ar'cu.la. Gr. n. *hals*, *halos*, salt; L. fem. n. *arcula* small box; N.L. fem. n. *Haloarcula*, salt (-requiring) small box.

Table 7.19

Comparison of selected characteristics of the members of the genera *Natronolimnobius*, *Natronomonas*, and *Salarchaeum*

Genus	<i>Natronolimnobius</i>		<i>Natronomonas</i> ^b		<i>Salarchaeum</i>
Species	<i>Nln. baerhuensis</i> ^a	<i>Nln. innermongolicus</i> ^a	<i>Nmn. pharaonis</i> ^{c,d}	<i>Nmn. moolapensis</i> ^e	<i>Sar. japonicum</i> ^f
Older names			Basonym: <i>Halobacterium pharaonis</i> Other synonym: <i>Natronobacterium pharaonis</i>		
Type strain	CGMCC 1.3597 JCM 12253	CGMCC 1.2124 JCM12255	ATCC 35678 CIP 103997 DSM 2160 IFO (now NBRC) 14720 JCM 8858 NCIMB 2260 VKM B-1749	CECT 7526 DSM 18674 JCM 14361	CECT 7563 JCM 16327
Cell shape	Rods	Pleomorphic, flat	Rods	Short rods, flat tetragonal shapes, cocci	Short rods
Cell size (µm)	0.5 × 3.0–5.0	0.6 × 3.0–6.0	0.8 × 2–3	0.7–1.7	0.5–1.0 × 0.5–2.0
Motility	+	–	+	+	+
Colony color	Red	Light red	Red	Red	Red
NaCl range for growth and optimum (%)	>15 (Opt. 20)	>10 (Opt. 15–20)	12–30 (Opt. 20)	14–36 (Opt. 18–20)	9–30 (Opt. 15–18)
Lysis in distilled water	+	+	+	+	+
Magnesium requirement and optimum (M)	NR	NR	–	Opt. 0.2–0.4	+ (Opt. 0.2–0.3)
pH range for growth and optimum	7.0–10.0 (Opt. 9.0)	7.5–10.0 (Opt. 9.5)	Opt. 8.5–9.0	5.5–8.5 (Opt. 7.0–7.5)	5.0–8.8 (Opt. 5.2–6.3)
Temperature range for growth and optimum (°C)	30–46 (Opt. 37)	19–54 (Opt. 45)	25–50 (Opt. 45)	25–45	20–55 (Opt. 40)
Organic substrates used	Acet Arab Fruc Fuma Gala Gluc Glyc Lacto Malt Mann Pyru Rham Raff Xylo	Acet Arab Fuma Gala Gluc Glyc Lact Mala Prop Pyru Raff Sorbi	Buty Fuma Pyru	Acet Buta Buty Etha Gluc (v) Glyc Lact Prop Pyru	Fuma Mala Succ
Acid produced from	NR	NR	NR	–	NR
Organic substrates not used	Citr Prop Sorbi	Fruc Lacto Malt Mann Rham Succ Sucr Xylo	Sugars	Arab, Benz Cell Citr Fruc Fuma Gala Gluc (v) Lacto Mala Manni Mann Ribo Succ Sucr Xylo	Acet Arab Cell Citr Fruc Gala Gluc Glyc Lact Lacto Malt Mann Pyru Raff Ribo Sorbi Sucr Treh Xylo
Indole from typtophan	+	+	+	–	–
Starch hydrolysis	–	–	–	–	–

■ Table 7.19 (continued)

Genus	<i>Natronolimnobius</i>		<i>Natronomonas</i> ^b		<i>Salarchaeum</i>
Species	<i>Nln. baerhuensis</i> ^a	<i>Nln. innermongolicus</i> ^a	<i>Nmn. pharaonis</i> ^{c,d}	<i>Nmn. moolapensis</i> ^e	<i>Sar. japonicum</i> ^f
Gelatin liquefaction	–	+	+	NR	–
Nitrate reduction	–	+	–	v	–
Polar lipids	PG, PGP-Me, 1 minor unidentified phospholipid	PG, PGP-Me	PG, PGP-Me, phosphatidic acid, 1 unknown phospholipid	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, 1 unknown glycolipid, 1 other unknown lipid	PG, PGP-Me, S-DGD-1, 5 unidentified glycolipids
Respiratory quinones	NR	NR	MK-8, MK-8(H ₂)	NR	NR
Sensitivity to antibiotics	Sensitive: Aph Ani Bac Ery Nov Rif	Sensitive: Aph Ani Bac Ery Nov Rif	Sensitive: Ani Bac Nov Tet	Sensitive: Nov Rif	Sensitive: Nov
	Resistant: Amp Chl Neo Pen	Resistant: Amp Chl Neo Pen	Resistant: Amp Chl Ery Str	Resistant: Amp Ani Bac Chl Ery Kan Neo Str Tet	Resistant: Amp Ani Bac Chl Ery Gen Kan Neo Pen Rif Str Tet Van
G + C content of DNA (mol %)	59–60	63	61.2–64.3 (major component); 51.9 (minor component)	63.4–63.8	64
Sample source and site	Soda lake, Inner Mongolia	Soda lake, Inner Mongolia	Alkaline lake, Wadi Natrun, Egypt	Saltern, Australia	Marine salt, Japan

Data taken from:

^aItoh et al. (2005)

^bKamekura (2001b)

^cSoliman and Trüper (1982)

^dKamekura et al. (1997)

^eBurns et al. (2010a)

^fShimane et al. (2011)

Additional data on growth substrates and other properties can be found in the original species descriptions

Cells are extremely pleomorphic and lyse in distilled water. Irregular disks, flat triangles, and other irregular shapes are commonly found. Some species are motile. Magnesium requirement is moderate (5–50 mM). Amino acids are not required for growth. The optimum salt concentration for growth is 2–3 M NaCl. Neutrophilic. Characteristic lipids are PG, Me-PGP, and a triglycosyl diether lipid (S-TGD-2).

The mol% G+C of the DNA is 60.1–64.7.

The genus *Haloarcula* currently contains 9 species: *Har. vallismortis* (type species), *Har. amylyolytica*, *Har. argentinensis*, *Har. hispanica*, *Har. japonica*, *Har. marismortui*, *Har. quadrata*, *Har. salaria*, and *Har. tradensis*.

The main features of the members of the genus are summarized in ◀ Table 7.3.

Additional comments:

- *Har. mukohataei* (Ihara et al. 1997) has been transferred to the genus *Halomicrobium* as *Hmc. mukohataei* comb. nov. (Oren et al. 2002).

Genus *Halobaculum* Oren, Gurevich, Gemmell, and Teske 1995, 752^{VP}

Ha.lo.ba'cu.lum. Gr. n. *hals*, *halos*, salt; L. neut. n. *baculum* stick; N.L. neut. n. *Halobaculum*, salt stick.

Cells are motile rods of varying length and lyse in distilled water. Magnesium requirement is moderate (5–50 mM). Amino acids are required for growth. The optimum salt concentration for growth is 3.5–4.5 M NaCl. Neutrophilic. Characteristic lipids are PG, Me-PGP, and a sulfated diglycosyl diether. PGS is absent.

The mol% G+C of the DNA is 70.

Type species and currently only species: *Hbl. gomorreense*.

The main features of the members of the genus are summarized in ◀ Table 7.2.

Additional comment:

- The description of *Hbl. magnesiophilum*, a species that grows optimally at 5 % NaCl only and can grow at salt concentrations as low as 1 % is currently in press (Shimoshide et al. 2012).

Table 7.20

Comparison of selected characteristics of the members of the genus *Natronorubrum*

Genus	<i>Natronorubrum</i> ^a				
Species	<i>Nrr. bangense</i> ^b	<i>Nrr. aibiense</i> ^c	<i>Nrr. sediminis</i> ^d	<i>Nrr. sulfidifaciens</i> ^e	<i>Nrr. tibetense</i> ^b
Type strain	AS 1.1984 CIP 107015 JCM 10635	CGMCC 1.4299 JCM 13488	CECT 7487 CGMCC 1.8981 JCM 15982	CGMCC 1.6307 JCM 14089	AS 1.2123 CIP 107016 JCM 10636
Cell shape	Pleomorphic flat	Rods	Pleomorphic rods	Pleomorphic rods, triangular disc-shaped	Pleomorphic flat
Cell size (μm)	NR	0.8–1.0 × 1.4–3.6	0.8–1.0 × 4.0–6.0	NR	NR
Motility	–	+	–	+	–
Colony color	Red	Red	Pink	Red	Red
NaCl range for growth and optimum (%)	12–25 (Opt. 22.5)	12–25 (Opt. 15–18)	15–30 (Opt. 20)	12–28 (Opt. 18)	12–30 (Opt. 20)
Lysis in distilled water	+	+	+	NR	+
Magnesium requirement and optimum (M)	NR	0–0.5 (Opt. 0.05)	–	–	NR
pH range for growth and optimum	8.0–11 (Opt. 9.0–9.5)	6.5–9.5 (Opt. 8.0)	8.0–11.0 (Opt. 9.0)	8.0–1.0 (Opt. 8.7–9.2)	8.5–11 (Opt. 9.0)
Temperature range for growth and optimum (°C)	25–55 (Opt. 45)	20–50 (Opt. 45)	25–50 (Opt. 37)	20–55 (Opt. 44–47)	25–55 (Opt. 45)
Organic substrates used	Acet Fruc Gluc Malt Sucr	Gala Gluc Malt Sucr	Arab Fruc Gluc Mann Xylo	Acet Fuma Gluc Glyc Lact Mala Malt Pyru Succ Sucr	Acet Fruc Gluc Lacto Malt, Sucr
Acid produced from	NR	Gala Gluc Malt Sucr	NR	NR	NR
Organic substrates not used	Manni	Fruc Lacto Mann Manni Ribo Sorb Sorbi Xylo	Acet Fuma Gala Glyc Lacto Mala Malt Manni Prop Raff Ribo Sorbi Succ Treh	Citr Fruc Gala Lacto Mann Manni Ribo Sorb Sorbi Xylo	Manni
Indole from typtophan	+	+	–	+	+
Starch hydrolysis	–	–	–	–	–
Gelatin liquefaction	–	–	–	–	+
Nitrate reduction	–	+	+	+	–
Polar lipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, 2 minor uncharacterized phospholipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, TGD-1, 2 unidentified glycolipids	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me	PG, PGP-Me	C ₂₀ C ₂₀ and C ₂₀ C ₂₅ derivatives of PG, PGP-Me, 2 minor uncharacterized phospholipids
Respiratory quinones	NR	NR	NR	NR	NR

Table 7.20 (continued)

Genus	<i>Natronorubrum</i> ^a				
Species	<i>Nrr. bangense</i> ^b	<i>Nrr. aibiense</i> ^c	<i>Nrr. sediminis</i> ^d	<i>Nrr. sulfidifaciens</i> ^e	<i>Nrr. tibetense</i> ^b
Sensitivity to antibiotics	Sensitive: Ery	Sensitive: Nov Rif	Sensitive: Nov	Sensitive: Cip Ery Nov Rif Tet	Sensitive: Ery
		Resistant: Amp Bac Chl Cip Ery Kan Neo Pen Tet	Resistant: Amp Bac Chl Ery Neo Pen Rif Str Tet	Resistant: Amp Bac Chl Neo Pen Str	
G + C content of DNA (mol%)	59.9	61.2	61.9–62.5	60.9	60.1
Sample source and site	Soda lake, Tibet	Salt lake, China	Salt lake, Inner Mongolia	Salt Lake, China	Soda lake, Tibet

Data taken from:

^aXu et al. (2001a)

^bXu et al. (1999)

^cCui et al. (2006b)

^dGutiérrez et al. (2010)

^eCui et al. (2007b)

Additional data on growth substrates and other properties can be found in the original species descriptions

Genus *Halobellus* Cui, Yang, Gao, and Xu 2011d, 2687^{VP}

Ha.lo.bel'lus. Gr. n. *hals*, *halos*, salt; L. masc. adj. *bellus*, beautiful; N.L. masc. n. *Halobellus*, beautiful salt organism.

Cells are rod shaped under optimal growth conditions and lyse in distilled water. Sugars are metabolized, in some cases with formation of acids. The major polar lipids are PG, PGP-Me, PGS, and one major glycolipid chromatographically identical to S-DGD-1.

The mol% G+C of the DNA is 61.5–69.2.

The genus *Halobellus* currently contains three species: *Hbs. clavatus* (type species), *Hbs. limi*, and *Hbs. salinus*.

The main features of the members of the genus are summarized in Table 7.2.

Genus *Halobiforma* Hezayen, Tindall, Steinbüchel, and Rehm 2002, 2278^{VP}; emend. Oren, Arahal, and Ventosa 2009, 640

Ha.lo.bi.for'ma. Gr. n. *hals*, *halos*, salt; L. adv. num. *bis*, twice; L. fem. n. *forma*, form; N.L. fem. n. *Halobiforma*, the halophile with two different shapes.

Cells are rod shaped, coccoid or pleomorphic, motile. Cells are red or pink and lyse in distilled water. Neutrophilic or alkaliphilic with growth up to pH 10.5. Grow by aerobic respiration; some species grow also by anaerobic respiration in the presence of nitrate. No growth on single substrates. Some species produce acids from sugars. The major polar lipids are

C₂₀C₂₀ and C₂₀C₂₅ glycerol diether derivatives of PG and PGP-Me. Glycolipids may be present in some species; when present, the glycolipids are a triglycosyl diether and its sulfated derivative.

The mol% G+C of the DNA is 63.8–66.9.

The genus *Halobiforma* currently contains three species: *Hbf. haloterrestriis* (type species), *Hbf. lacisalsi*, and *Hbf. nitratireducens*.

The main features of the members of the genus are summarized in Table 7.4.

Genus *Halococcus* Schoop 1935, 817^{AL}; emend. Oren, Arahal, and Ventosa 2009, 639

Ha.lo.coc'cus. Gr. n. *hals*, *halos*, salt; N.L. masc. n. *coccus* (from Gr. masc. n. *kokkos* a berry), coccus; N.L. masc. n. *Halococcus*, salt (-requiring) coccus.

Cells are coccoid, nonmotile, occurring in pairs, tetrads, or irregular clusters. Most cells stain Gram negative. Do not lyse in distilled water. Oxidase positive or negative. Magnesium requirement is moderate (1–40 mM). The optimum salt concentration for growth is 3.5–4.5 M NaCl. Neutrophilic. Some species require amino acids for growth. Possess both C₂₀C₂₀ and sometimes C₂₀C₂₅ core lipids. Characteristic lipids are PG, Me-PGP, and a sulfated diglycosyl diether.

The mol% G+C of the DNA is 59.5–66.

The genus *Halococcus* currently contains seven species: *Hcc. morrhuae* (type species), *Hcc. dombrowskii*, *Hcc. hamelinensis*, *Hcc. qingdaonensis*, *Hcc. saccharolyticus*, *Hcc. salifodinae*, and *Hcc. thailandensis*.

Table 7.21

Properties of the sequenced genomes of members of the *Halobacteriaceae* (as of August 2012)

Species, strain	Length	G + C content	Predicted protein genes	Predicted RNA genes	16S rRNA genes	Accession no.	References
<i>Halalkalicoccus jeotgali</i> B3 ^T	3,698,650 (chromosome) 2,809,118 406,285 363,534 44,576 23,727 6,951 (plasmids)	65.0 55.3 54.2 58.9 54.9 47.6 60.0	3860	52	1	CP002062.1– CP002068.1	Roh et al. (2010b)
" <i>Haloarcula californiae</i> " ATCC 22799	4,420,514	60.8	4627	69	NR	PubSEED 662475.4	Lynch et al. (2012)
<i>Haloarcula hispanica</i> ATCC 33869	2,995,271 (chromosome I) 488,918 (minichromosome II) 405,816 (megaplasmid)	63.7 57.0 59.9	3859	58	3	CP002921– CP002923	Liu et al. (2011)
<i>Haloarcula marismortui</i> ATCC 43049	3,131,724 288,050 (chromosomes) 410,554 155,300 132,678 50,060 39,521 33,452 33,303 (plasmids)	61.1	4242 ^a ; 4348 ^b	62	3	AY596290.1 – AY596298.1	Baliga et al. (2004) ^a , Anderson et al. (2011) ^b
" <i>Haloarcula sinaiensis</i> " ATCC 33800	4,525,388	60.8	4538	55	NR	PubSEED 662478.5	Lynch et al. (2012)
<i>Haloarcula vallismortis</i> ATCC 29715	3,930,055	61.8	4084	84	NR	PubSEED 662477.4	Lynch et al. (2012)
<i>Halobacterium salinarum</i> R1	2,000,962 (chromosome) 147,963 194,963 284,332 40,894 (plasmids)	68.0 57.4 58.6 59.8 57.9	2878	52	NR	AM774415.1– AM774419.1	Pfeifer et al. (2008) ^a
<i>Halobacterium</i> sp. NRC–1	2,014,239 (chromosome) 191,346 365,425 (minichromosomes)	67.9 57.9 59.2	2630	52	1	AE004437.1, AF016485.1 AE004438.1	Ng et al. (2000)
<i>Halobiforma lacisalsi</i> AJ5	4,398,155 (draft)	65.4	4682	49	2	AGFZ01000000	Jiang et al. (2011)
<i>Halococcus hamelinensis</i> strain 100A6 ^T	3,133,046	60.1	3150	48	1	PRJNA80845	Burns et al. (2012)

■ Table 7.21 (continued)

Species, strain	Length	G + C content	Predicted protein genes	Predicted RNA genes	16S rRNA genes	Accession no.	References
<i>Haloferax denitrificans</i> ATCC 35960	3,848,468	66.3	3809	58	NR	PubSEED 662478.4	Lynch et al. (2012)
<i>Haloferax mediterranei</i> ATCC 33500	2,948,884 129,210 321,908 504,705 3,905,749	61.1 57.6 57.9 57.5 60.3	3864 3942	63 63	2	CP001868– CP001871 PubSEED 523841.6	Han et al. (2012), Lynch et al. (2012)
<i>Haloferax mucosum</i> ATCC BAA-1512	3,371,699	61.8	3455	61	NR	PubSEED 662479.5	Lynch et al. (2012)
<i>Haloferax sulfurifontis</i> ATCC BAA-897	3,816,558	66.3	3856	59	NR	PubSEED 662480.4	Lynch et al. (2012)
<i>Haloferax volcanii</i> DS2 ^T	2,847,757 (main chromosome) 635,786 (small chromosome) 437,906 85,092 6,359 (plasmids)	66.6 61.7 65.5 55.5 56 65	4063	57	2	CP001953–1– CP001957.1	Hartman et al. (2010)
<i>Halogeometricum borinquense</i> DSM 11551	3,944,467 (chromosome and 5 plasmids)	59.9	3937	57	2	CP01690.1– CP01695.1	Malfatti et al. (2009)
<i>Halomicrobium mukohataei</i> DSM 12286	3,332,349 (chromosome of 3.11 Mbp and one 219kbp plasmid)	65.5	3416	56	3	CP001688.1 CP001689.1	Tindall et al. (2009)
<i>Halopiger xanaduensis</i> SH-6	3,668,009 (chromosome) 436,718 181,778 68,763 (plasmids)	65.2	4310	60	3	CP002839.1– CP002842.1	Anderson et al. (2012)
<i>Haloquadratum walsbyi</i> DSM 16790	3,132,949 (chromosome) 46,867 (plasmid)	47.9 47.7	2738 + 39	51	2	AM180088.1 AM180089.1	Bolhuis et al. (2006)
<i>Halorhabdus tiamatea</i> strain SARL4B ^T	NR	62	4034	NR	NR	66979 – AFNT00000000	Antunes et al. (2011)
<i>Halorhabdus utahensis</i> DSM 12940	3,129,561	62.9	3027 (or 3097, 2898 or 3254, depending on the annotation service used)	48	1	CP001687.1	Anderson et al. (2009), Bakke et al. (2009)
<i>Halorubrum lacusprofundi</i>	2,735,295 525,943 431,338	NR	3665	NR	3	CP001365.1– CP001367.1	Anderson et al. (2011), Shukla et al. (2006)

Table 7.21 (continued)

Species, strain	Length	G + C content	Predicted protein genes	Predicted RNA genes	16S rRNA genes	Accession no.	References
<i>Haloterrigena turkmenica</i> DSM 5511	5,540,782 (3,889,038 [chromosome] and 6 plasmids of 15.8–698.5 kbp)	64.3	5287	63	3	CP001860–CP001866	Saunders et al. (2010)
<i>Natrialba magadii</i> ATCC 43099 ^T	3,751,858 (large chromosome) 378,348 (small chromosome) 254,950 (plasmid) 58,487 (virus Φ Ch1)	61.4 60.1 56.8 61.9	4212	60	3	CP001932.1–CP001935.1	Sidderamappa et al. (2012)
<i>Natrinema pellirubrum</i> DSM 15624 (Draft)	NR	NR	4555	NR	NR	AGIN01000000	Feng et al. (2012)
<i>Natrinema</i> sp. J7-2	3,687,626 (chromosome) 95,989 (plasmid)	64 59	4302	56	3	CP003412 CP003413	Feng et al. (2012)
<i>Natronomonas pharaonis</i> DSM 2160	2,595,221 (chromosome) 130,989 23,486 (plasmids)	63.4 57.2 60.6	2843	51	1	CR936257.1–CR936259.1	Falb et al. (2005)

The main features of the members of the genus are summarized in Table 7.5.

Additional comments:

- *Hcc. turkmenicus* (Zvyagintseva and Tarasov 1987; Validation List 31, 495, 1989) was reclassified as *Htg. turkmenica* comb. nov. (Ventosa et al. 1999).

Genus *Haloferax* Torreblanca, Rodriguez-Valera, Juez, Kamekura, and Kates 1986b, 573^{VP} (Validation list 22); Effective Publication: Torreblanca, Rodriguez-Valera, Juez, Kamekura, and Kates 1986a, 98; emend. Oren, Arahall, and Ventosa 2099, 639

Ha.lo.fe'rax. Gr. n. *hals*, halos, salt; L. neut. adj. *ferax* fertile; N.L. neut. n. *Haloferax*, salt (-requiring) and fertile.

Cells are extremely pleomorphic and lyse in distilled water. Flat disks and pleomorphic rods are commonly found. Colonies have a mucoid appearance. Pigmentation often depends on the salinity of the medium. Some species are motile; some possess

gas vesicles. Most species are oxidase positive, but oxidase-negative and oxidase-variable species have been reported. Magnesium requirement is high (20–50 mM). Amino acids are not required for growth. Acids are produced from sugars. The optimum salt concentration for growth is 2–3 M NaCl. Neutrophilic. Characteristic lipids are PG, Me-PGP, and a sulfated diglycosyl diether. PGS is absent.

The mol% G+C of the DNA is 59.5–66.3.

The genus *Haloferax* currently contains 11 species: *Hfx. volcanii* (type species), *Hfx. alexandrinus*, *Hfx. denitrificans*, *Hfx. elongans*, *Hfx. gibbonsii*, *Hfx. larsenii*, *Hfx. lucentense*, *Hfx. mediterranei*, *Hfx. mucosum*, *Hfx. prahovense*, and *Hfx. sulfurifontis*.

The main features of the members of the genus are summarized in Tables 7.6 and 7.7.

Additional comments:

- The name *Hfx. alexandrinus* is illegitimate because the epithet must be in the neuter gender (*alexandrinum*).
- The original spelling of the specific epithet *lucentensis* (Gutierrez et al. 2002) has been corrected to *lucentense* on validation.

■ Table 7.22

List of Haloviruses described as of August (2010)^a

Name	Host organism	Morphology	Classification	Nucleic acid type	Genome size	Life style	Reference
B10	<i>Halobacterium</i> sp.	Head -tail	Myovirus	NR	NR	NR	Torsvik (1982), Dyall-Smith et al. (2003)
BJ1	<i>Halorubrum saccharovorum</i>	Head-tail	Siphovirus	C dsDNA	42,271	Virulent	Pagaling et al. (2007)
HATV-1	<i>Haloarcula</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HATV-2	<i>Haloarcula</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HCTV-1	" <i>Haloarcula californiae</i> "	Head-tail	Siphovirus	NR	NR	NR	Kukkaro and Bamford (2009)
HCTV-2	" <i>Haloarcula californiae</i> "	Head-tail	Siphovirus	NR	NR	NR	Atanasova et al. (2012)
HCTV-5	" <i>Haloarcula californiae</i> "	Head-tail	Siphovirus	NR	NR	NR	Atanasova et al. (2012)
HGPV-1	<i>Halogeometricum</i> sp.	Pleomorphic	"Pleolipovirus"	C dsDNA with short stretches of ssDNA	9,694	Released without cell lysis	Atanasova et al. (2012), Senčilo et al. (2012), Pietilä et al. (2012a)
HF1	<i>Halorubrum saccharovorum</i> , <i>Haloferax volcanii</i>	Head-tail	Myovirus	L dsDNA	75,898	Virulent	Nuttall and Dyall-Smith (1993a), Tang et al. (2002)
HF2	<i>Halorubrum coriense</i>	Head-tail	Myovirus	L dsDNA	77,670	Virulent	Nuttall and Dyall-Smith (1993a), Tang et al. (2002)
HGTV-1	<i>Halogramum</i> sp.	Head-tail	<i>Myoviridae</i>	NR	NR	NR	Atanasova et al. (2012)
Hh-1	<i>Halobacterium salinarum</i>	Head-tail	Siphovirus	dsDNA	37.6 kpb	Temperate	Rohrmann et al. (1983), Pauling (1982), Dyall-Smith et al. (2003)
Hh-3	<i>Halobacterium salinarum</i>	Head-tail	Siphovirus	dsDNA	29.6 kpb	Temperate	Rohrmann et al. (1983), Pauling (1982), Dyall-Smith et al. (2003)
HHIV-2	<i>Haloarcula hispanica</i>	Icosaedral with inner membrane	Unclassified	L dsDNA	30,578	Virulent	Jaakkola et al. (2012)
HHPV-1	<i>Haloarcula hispanica</i>	Pleomorphic	"Pleolipoviruses"	C dsDNA	8,082	Released without cell lysis	Roine et al. (2010), Pietilä et al. (2012a)
HHTV-1	<i>Haloarcula hispanica</i>	Head-tail	Siphovirus	NR	NR	NR	Kukkaro and Bamford (2009)
HHTV-2	<i>Haloarcula hispanica</i>	Head-tail	Siphovirus	NR	NR	NR	Atanasova et al. (2012)
His1	<i>Haloarcula hispanica</i>	Lemon-shaped	Salterprovirus (<i>Fuselloviridae</i>)	L dsDNA	14.9 kbp	Released without cell lysis	Bath and Dyall-Smith (1998), Pietilä et al. (2012b)
His2	<i>Haloarcula hispanica</i>	Pleomorphic	Salterprovirus ("Pleolipovirus")	L dsDNA	16,067	Released without cell lysis	Bath et al. (2006), Pietilä et al. (2012a)
HJTV-1	<i>Haloarcula japonica</i>	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HJTV-2	<i>Haloarcula japonica</i>	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRPV-1	<i>Halorubrum</i> sp.	Pleomorphic	"Pleolipovirus"	C ssDNA	7,048 nt	Released without cell lysis, persistent in host cells	Pietilä et al. (2009, 2010, 2012a); Senčilo et al. (2012)

Table 7.22 (continued)

Name	Host organism	Morphology	Classification	Nucleic acid type	Genome size	Life style	Reference
HRPV-2	<i>Halorubrum</i> sp.	Pleomorphic	"Pleolipovirus"	C ssDNA	10,656	Released without cell lysis	Senčilo et al. (2012), Pietilä et al. (2012a)
HRPV-3	<i>Halorubrum</i> sp.	Pleomorphic	"Pleolipovirus"	C dsDNA with short stretches of ssDNA	8,770	Released without cell lysis	Senčilo et al. (2012), Pietilä et al. (2012a)
HRPV-6	<i>Halorubrum</i> sp.	Pleomorphic	"Pleolipovirus"	C ssDNA	8,549	Released without cell lysis	Senčilo et al. (2012), Pietilä et al. (2012a)
HRTV-1	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Kukkaro and Bamford (2009)
HRTV-2	<i>Halorubrum</i>	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-3	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-4	<i>Halorubrum</i> sp.	Head-tail	Siphovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-5	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-6	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-7	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-8	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-9	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-10	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-11	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HRTV-12	<i>Halorubrum</i> sp.	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
Hs1	<i>Halobacterium salinarum</i>	Head-tail	Bradley Gp A (Myovirus)	NR	NR	Temperate?	Torsvik and Dundas (1974, 1980), Torsvik (1982)
HSTV-1	" <i>Haloarcula sinaiensis</i> "	Head-tail	Podovirus	NR	NR	NR	Atanasova et al. (2012)
HSTV-2	<i>Halorubrum sodomense</i>	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HSTV-3	<i>Halorubrum sodomense</i>	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HTV-1	NR	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HVTV-1	<i>Haloarcula vallismortis</i>	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
HVTV-2	<i>Haloarcula vallismortis</i>	Head-tail	Myovirus	NR	NR	NR	Atanasova et al. (2012)
Ja. 1	<i>Halobacterium salinarum</i>	Head-tail	Bradley Gp A (Myovirus)	dsDNA	NR	Virulent	Wais et al. (1975)
S41	<i>Halobacterium salinarum (curtirubrum)</i>	Head-tail	Bradley A1 (Myovirus)	NR	NR	Virulent	Daniels and Wais (1998)
S4100	<i>Halobacterium salinarum (curtirubrum)</i>	Head-tail	Bradley A1 (Myovirus)	NR	NR	Virulent	Daniels and Wais (1998)
S45	<i>Halobacterium salinarum</i>	Head-tail Group B1	Siphovirus	dsDNA	NR	Virulent	Daniels and Wais (1984)
S50.2	<i>Halobacterium salinarum (curtirubrum)</i>	Head-tail	Bradley A1 (Myovirus)	NR	NR	Virulent	Daniels and Wais (1998)

■ Table 7.22 (continued)

Name	Host organism	Morphology	Classification	Nucleic acid type	Genome size	Life style	Reference
S5100	<i>Halobacterium salinarum</i>	Head-tail	Bradley A1 (Myovirus)	NR	NR	Temperate	Daniels and Wais (1990)
SH1	<i>Haloarcula hispanica</i>	Icosahedral, with inner membrane	Unclassified	L dsDNA	30,898	Virulent	Porter et al. (2005), Kivelä et al. (2006), Bamford et al. (2005), Jääliñoja et al. (2008)
SNJ1	<i>Natrinema</i> sp.	(Head-tail), icosahedral with inner membrane	Unclassified	C dsDNA	16,341	Temperate	Mei et al. (2007), Zhang et al. (2012)
ΦCh1	<i>Natrialba magadii</i>	Head-tail	Myovirus	L, dsDNA, RNA	58,498 Several RNA of 80–700 nt	Temperate	Witte et al. (1997), Klein et al. (2002, 2012)
φH	<i>Halobacterium salinarum</i>	Head-tail isometric head, contractile tail	<i>Myoviridae</i>	L	59	Temperate	Schnabel et al. (1982), Dyall-Smith et al. (2003)
ΦN	<i>Halobacterium salinarum</i>	Head-tail isometric head, contractile tail	Siphovirus	L dsDNA	56 kbp	Not critically tested, most probably lytic	Vogelsang-Wenke and Oesterhelt (1988)

^aThe author thanks Dr. Elina Roine, University of Helsinki, Finland, for valuable comments

Genus *Halogeometricum* Montalvo-Rodríguez, Vreeland, Oren, Kessel, Betancourt, and López-Garriga 1998, 1310^{VP}; emend. Cui, Yang, Gao, Li, Xu, Zhou, Liu, and Zhou 2010f, 2615

Ha.lo.ge.o.me'tri.cum. Gr. n. *hals*, *halos*, salt; L. neut. adj. *geometricum* geometrical; N.L. neut. n. *Halogeometricum*, salty geometrical shape.

Cells are extremely pleomorphic (short and long rods, squares, triangles, ovals, and irregular cocci) under optimal growth conditions, motile, and lyse in distilled water. Sugars are metabolized, in some cases with formation of acids. Neutrophilic. Cells contain PG and Me-PGP. In some species, a yet unidentified non-sulfate-containing glycolipid and S-DGD-1 may be present as a minor component. In other species, the major glycolipid is chromatographically identical to S-DGD-1, and DGD-1 may be present as a minor component. PGS is absent.

The mol% G + C of the DNA is 59.9–64.9

The genus *Halogeometricum* currently contains two species: *Hgm. borinquense* (type species), and *Hgm. rufum*.

The main features of the members of the genus are summarized in ● Table 7.4.

Genus *Halogramum* Cui, Gao, Sun, Dong, Xu, Zhou, Liu, Oren, and Zhou 2010b, 1369^{VP}, emend. Cui, Yang, Gao, and Xu 2011e, 913

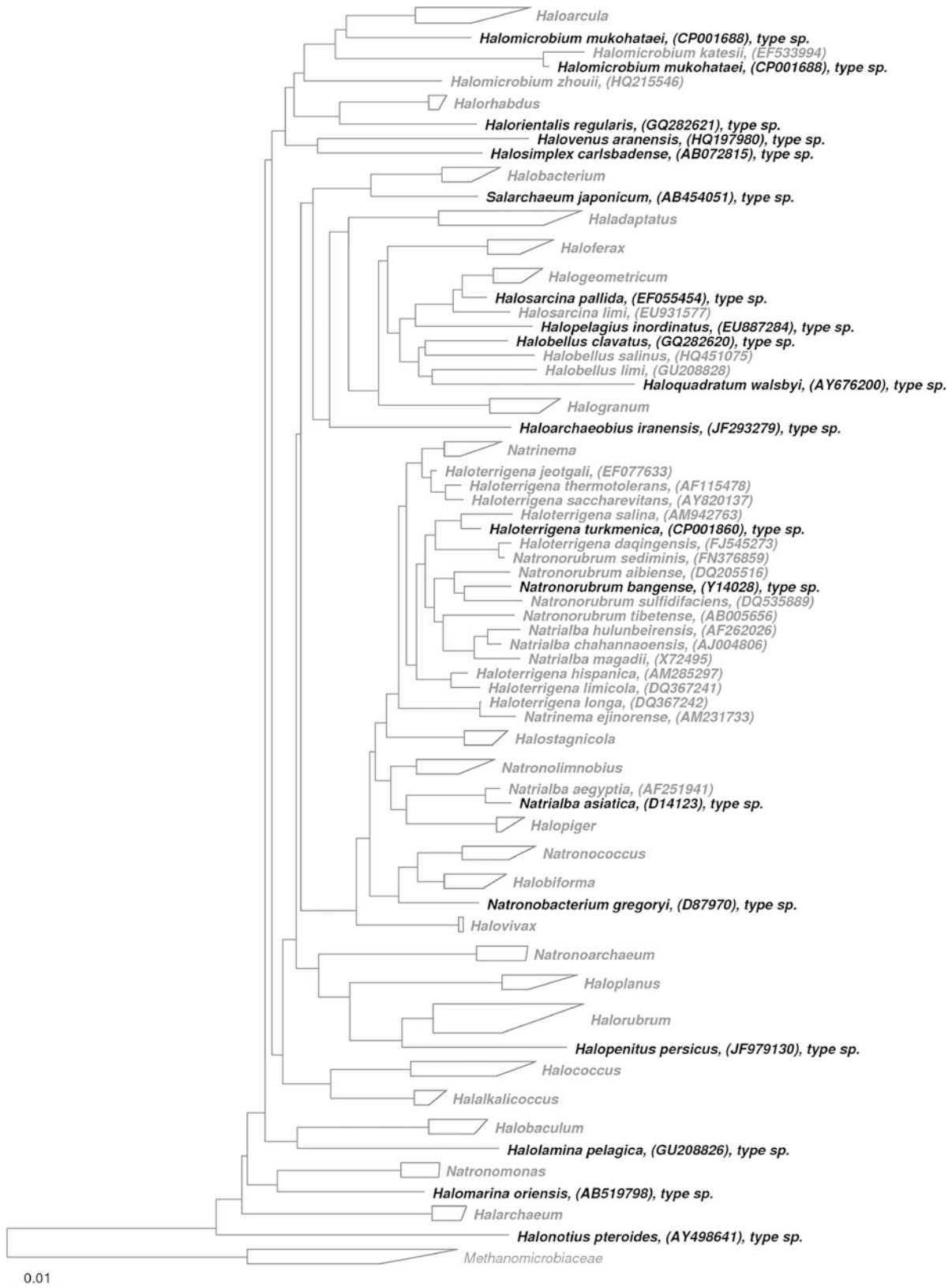
Ha.lo.gra'num. Gr. n. *hals*, *halos*, salt; L. neut. n. *granum*, granule; N.L. neut. n. *Halogramum*, salty granule shape.

Cells are pleomorphic under optimal growth conditions and lyse in distilled water. Sugars are metabolized with the formation of acids. The polar lipids are PG, PGP-Me, traces of PGS, and one major glycolipid and one minor glycolipid chromatographically identical to S-DGD-1 and DGD-1, respectively. Other minor glycolipids may be present.

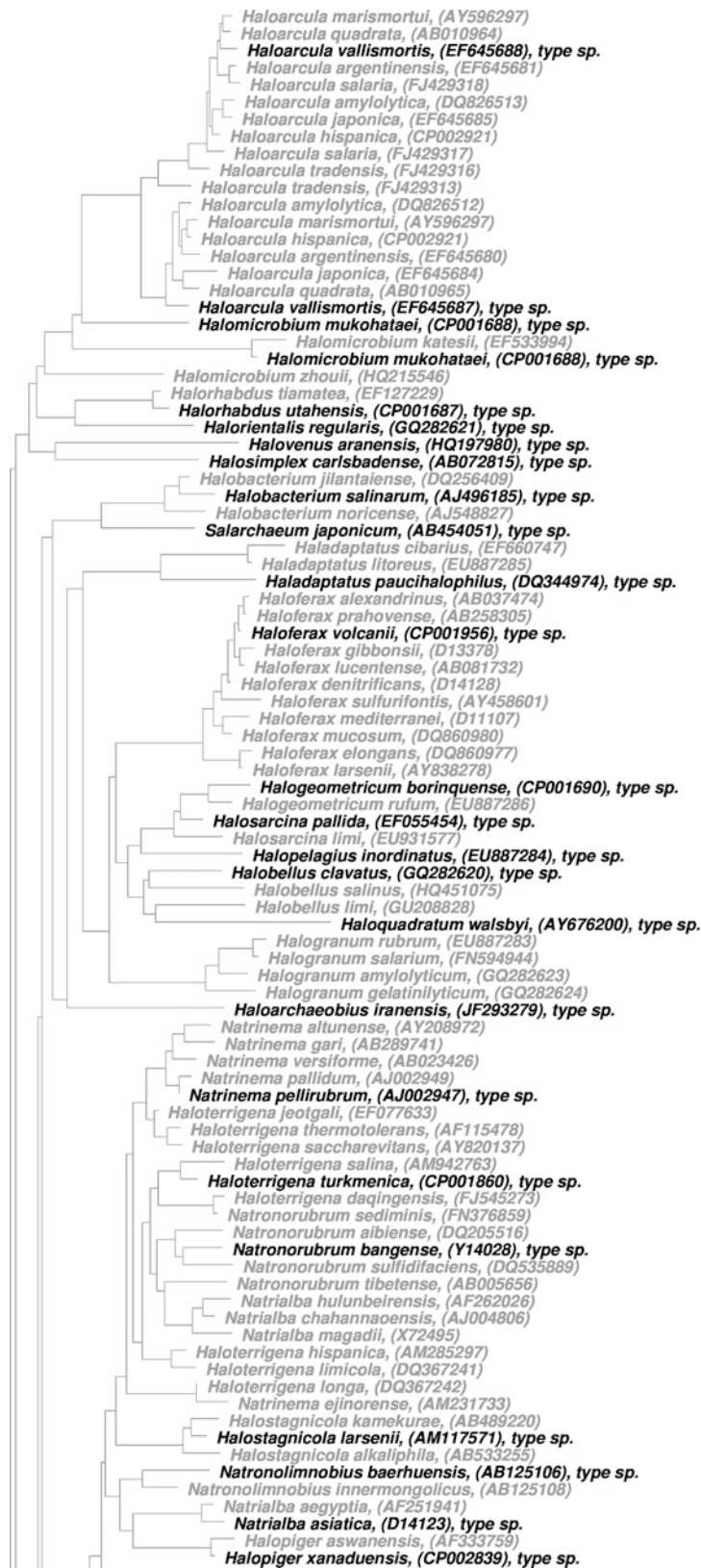
The mol% G + C of the DNA is 55.7–64.4.

The genus *Halogramum* currently contains 4 species: *Hgn. rubrum* (type species), *Hgn. amylolyticum*, *Hgn. gelatinilyticum*, and *Hgn. salarium*.

The main features of the members of the genus are summarized in ● Table 7.4.



■ Fig. 7.1 (continued)



■ Fig. 7.1 (continued)

Genus *Halolamina* Cui, Gao, Yang, and Xu 2011b, 1619^{VP}

Ha.lo.la'mi.na. Gr. n. *hals*, *halos*, salt; L. fem. n. *lamina*, a thin slice; N.L. fem. n. *Halolamina*, thin-slice-shaped salt (organism).

Cells are pleomorphic and thin-slice-shaped. Sugars are metabolized, sometimes with the formation of acids. Polar lipids include PGS and 8 yet uncharacterized glycolipids.

The mol% G + C of the DNA is 64.8.

Type species and currently only species: *Hlm. pelagica*.

The main features of the members of the genus are summarized in [Table 7.7](#).

Genus *Halomarina* Inoue, Itoh, Ohkuma, and Kogure 2011, 944^{VP}

Ha.lo.ma.ri'na. Gr. n. *hals*, *halos*, salt; L. adj. *marinus*, marine; N. L. fem. n. *Halomarina*, a halophile existing in the marine environment.

Cells are mesophilic and neutrophilic. Lipids are C₂₀C₂₀ and C₂₀C₂₅ diether derivatives of PG, PGP-Me, triglycosyl diether, and at least one unidentified glycolipid. Grows on a wide range of substrates, including single and complex carbon sources. Survives at low salt concentrations and can recover after prolonged exposure to distilled water.

The mol% G + C of the DNA is 67.7.

Type species and currently only species: *Hmr. oriensis*.

The main features of the members of the genus are summarized in [Table 7.8](#).

Genus *Halomicrobium* Oren, Elevi, Watanabe, Tamura, Ihara, and Corcelli 2002, 1834^{VP}

Ha.lo.mi.cro'bi.um. Gr. n. *hals*, *halos*, salt; N.L. neut. n. *microbium* (from Gr. adj. *micros*, small and Gr. n. *bios*, life), a microbe; N.L. neut. n. *Halomicrobium*, small, salt life-form.

Cells are rod shaped or pleomorphic, aerobic, or facultatively anaerobic in the presence of nitrate. Some species are motile.

The mol% G + C of the DNA is 52.4–69.1.

The genus *Halomicrobium* currently contains three species: *Hmc. mukohataei* (type species), *Hmc. katesii*, and *Hmc. zhouii*.

The main features of the members of the genus are summarized in [Table 7.8](#).

Additional comment:

- *Har. mukohataei* (Ihara et al. 1997) has been transferred to the genus *Halomicrobium* as *Hmc. mukohataei* comb. nov. (Oren et al. 2002).

Genus *Halonotius* Burns, Janssen, Itoh, Kamekura, Echigo, and Dyall-Smith 2010, 1198^{VP}

Ha.lo.no'ti.us. Gr. n. *hals*, *halos*, salt; L. masc. n. *notius*, southern; N.L. masc. n. *Halonotius*, a salty southern one.

Cells are flat rods, often with rounded ends. Oxidase and catalase tests are negative.

The mol% G + C of the DNA is 58.4–58.7.

Type species and currently only species: *Hns. pteroides*.

The main features of the members of the genus are summarized in [Table 7.8](#).

Genus *Halopelagius* Cui, Li, Gao, Xu, Zhou, Liu, Oren, and Zhou 2010g, 2092^{VP}

Ha.lo.pe.la'gi.us. Gr. n. *hals*, *halos*, salt; L. masc. adj. *pelagius*, of or pertaining to the sea; N.L. masc. n. *Halopelagius*, salt organism from the sea.

Cells are pleomorphic under optimal growth conditions and lyse in distilled water. Sugars are metabolized, in some cases with formation of acid. Lipids are PG, PGP-Me, and two main glycolipids chromatographically identical to S-DGD-1 and DGD-1. PGS is absent.

The mol% G + C of the DNA is 59.9–61.0.

Type species and currently only species: *Hpl. inordinatus*.

The main features of the members of the genus are summarized in [Table 7.8](#).

Genus *Halopenitus* Amoozegar, Makhdoumi-Kakhki, Shahzede Fazel, Azarbaijani, and Ventosa 2012, 1935^{VP}

Ha.lo.pe'ni.tus. Gr. n. *hals*, *halos*, salt; L. masc. adj. *penitus* inner, interior; N.L. masc. n. *Halopenitus*, intended to mean an archaeon isolated from an inland salt lake.

Cells are pleomorphic rods, triangular, or disk-shaped, nonmotile. Neutrophilic. Polar lipids include PG, PGP-Me, one unidentified glycolipid, and three minor phospholipids.

The mol% G + C of the DNA is 66.0.

Fig. 7.1

Phylogenetic reconstruction of the family *Halobacteriaceae* based on 16S rRNA and created using the neighbor-joining algorithm with the Jukes-Cantor correction. (a) presents the genera in a grouped tree, and (b) is an unfolded tree showing the type strains of species of the family. The sequence datasets and alignments were used according to the All-Species Living Tree Project (LTP) database (Yarza et al. 2010; <http://www.arb-silva.de/projects/living-tree>). The tree topology was stabilized with the use of a representative set of nearly 750 high-quality type strain sequences proportionally distributed among the different bacterial and archaeal phyla. In addition, a 40 % maximum frequency filter was applied in order to remove hypervariable positions and potentially misplaced bases from the alignment. Scale bar indicates estimated sequence divergence

Type species and currently only species: *Hpt. persicus*.

The main features of the members of the genus are summarized in [Table 7.9](#).

Genus *Halopiger* Gutiérrez, Castillo, Kamekura, Xue, Ma, Cowan, Jones, Grant, and Ventosa 2007, 1404^{VP}

Ha.lo.pi'ger. Gr. n. *hals*, *halos*, salt; L. masc. adj. *piger*, lazy; N.L. masc. n. *Halopiger*, lazy halophile, referring to the slow growth under laboratory conditions.

Cells are strictly anaerobic pleomorphic rods. Polar lipids include C₂₀C₂₀ and C₂₀C₂₅ glycerol diethers of PG, PGP-Me, and the bis-sulfated glycolipid S₂-DGD-1. PGS is absent.

The mol% G + C of the DNA is 65.2–67.1.

The genus *Halopiger* currently contains two species: *Hpg. xanaduensis* (type species) and *Hpg. aswanensis*.

The main features of the members of the genus are summarized in [Table 7.9](#).

Genus *Haloplanus* Eleri Bardavid, Mana, and Oren 2007, 782^{VP}; emend. Cui, Gao, Li, Xu, and Zhou 2010c, 1826

Ha.lo.pla'nus. Gr. n. *hals*, *halos*, salt; L. adj. *planus*, flat; N.L. masc. n. *Haloplanus*, flat salt-life form.

Cells are pleomorphic and flat and contain gas vesicles. In static liquid culture, cells float to the surface. Strictly aerobic. Cells lyse in distilled water. Cells contain PG, PGP-Me, PGS, and one major glycolipid that is chromatographically identical to S-DGD-1.

The mol% G + C of the DNA is 62.1–66.4.

The genus *Haloplanus* currently contains three species: *Hpn. natans* (type species), *Hpn. aerogenes*, and *Hpn. vesicus*.

The main features of the members of the genus are summarized in [Table 7.9](#).

Genus *Haloquadratum* Burns, Janssen, Itoh, Kamekura, Li, Jensen, Rodríguez-Valera, Bolhuis, and Dyal-Smith 2007, 391^{VP}

Ha.lo.qua.dra'tum. Gr. n. *hals*, *halos*, salt; L. neut. n. *quadratum*, square; N.L. neut. n. *Haloquadratum*, salt square.

Cells are flat and square and usually contain gas vesicles and PHA storage granules. Oxidase and catalase tests are negative.

The mol% G + C of the DNA is 46.9–47.9.

Type species and currently only species: *Hqr. walsbyi*.

The main features of the members of the genus are summarized in [Table 7.9](#).

Genus *Halorhabdus* Wainø, Tindall, and Ingvorsen 2000, 188^{VP}; emend. Antunes, Taborda, Huber, Moissl, Nobre, and Da Costa 2008, 218

Ha.lo.rhab.dus. Gr. n. *hals*, *halos*, salt; Gr. fem. n. *rhabdos*, rod, stick; N.L. fem. n. *Halorhabdus*, salt (-loving) rod.

Cells are extremely pleomorphic, although most are rod shaped. Pigmented red or unpigmented. Motile by a single flagellum or nonmotile. Cells lyse in distilled water. Ferments glucose. Amino acids are not required for growth; grows under aerobic or anaerobic conditions in defined media; some species prefer anaerobic conditions. PHA is produced. Acid is produced from carbohydrates. A limited number of organic substrates are used for growth. The polar lipids are PG, PGP-Me, TGD, S-TGD, and an unknown component. PGS is absent. MK-8 and MK-8(VIII-H₂) are the respiratory lipoquinones.

The mol% G + C of the DNA is 62.0–64.0.

The genus *Halorhabdus* currently contains two species: *Hrd. utahensis* (type species), and *Hrd. tiamatea*.

The main features of the members of the genus are summarized in [Table 7.10](#).

Genus *Halorientalis* Cui, Yang, Gao, and Xu 2011d, 2687^{VP}

Hal.ori.en.ta'lis. Gr. n. *hals*, *halos*, salt; L. fem. adj. *orientalis*, of the east; N.L. fem. n. *Halorientalis*, salt-loving organism from the orient.

Cells are pleomorphic and rod shaped under optimal growth conditions and lyse in distilled water. Sugars are metabolized, in some cases with the formation of acids. The polar lipids are PG, PGP-Me, one major glycolipid, chromatographically identical to S-DGD-1, and 3–4 minor unidentified glycolipids.

The mol% G + C of the DNA is 61.5–61.9.

Type species and currently only species: *Hos. regularis*.

The main features of the members of the genus are summarized in [Table 7.10](#).

Genus *Halorubrum* McGenity and Grant 1996, 362^{VP}; Effective Publication: McGenity and Grant 1995, 241; emend. Oren, Arahal, and Ventosa 2009, 639

Ha.lo.ru'brum. Gr. n. *hals*, *halos*, salt; L. neut. adj. *rubrum* red; N.L. neut. n. *Halorubrum*, salt (-requiring) and red.

Cells are rod shaped or pleomorphic under optimal growth conditions, motile or nonmotile, and lyse in distilled water. Short and long rods, triangles, squares, and oval cells are found. Some species may be almost colorless. Some species possess gas vesicles. Magnesium requirement is moderate (5–50 mM) or low. Amino acids are not required for growth.

Some species grow on single carbon sources. Most species use sugars, some with the production of acids. The optimum salt concentration for growth is 2.5–4.5 M NaCl. Neutrophilic and alkaliphilic species exist. The major polar lipids are C₂₀C₂₀ or C₂₀C₂₅ glycerol diether derivatives of PG, PGP-Me, PGS, and a sulfated diglycosyl diether. Alkaliphilic species lack PGS and glycolipids.

The mol% G + C of the DNA is 60.2–71.2.

The genus *Halorubrum* currently contains 26 species: *Hrr. saccharovorum* (type species), *Hrr. aidingense*, *Hrr. alkaliphilum*, *Hrr. aquaticum*, *Hrr. arcis*, *Hrr. californiense*, *Hrr. chaoviator*, *Hrr. cibi*, *Hrr. coriense*, *Hrr. distributum*, *Hrr. ejinorensense*, *Hrr. ezzemoulense*, *Hrr. kocurii*, *Hrr. lacusprofundi*, *Hrr. lipolyticum*, *Hrr. litoreum*, *Hrr. luteum*, *Hrr. orientale*, *Hrr. sodomense*, *Hrr. tebenquichense*, *Hrr. terrestre*, *Hrr. tibetense*, *Hrr. trapanicum*, *Hrr. vacuolatum*, and *Hrr. xinjiangense*.

The main features of the members of the genus are summarized in ► [Table 7.10](#).

Additional comments:

- *Halorubrobacterium* (Kamekura and Dyal-Smith 1995) (Validation list 57, 1996) is a later synonym of *Halorubrum* (McGenity and Grant 1995). *Halorubrobacterium coriense*, *Halorubrobacterium distributum*, and *Halorubrobacterium sodomense* were transferred to *Halorubrum* (Oren and Ventosa 1996).
- Strain VKM B-1733 was originally designated as the type strain of *Hrr. distributum* (Zvyagintseva and Tarasov 1987). Zvyagintseva et al. (1996) later proposed VKM B-1739 as the new type. However, strain VKM B-1733 and JCM 9100 which was derived from it must remain the type strain of the species (Oren et al. 1997).
- NCIMB 13488 was proposed as a neotype of *Hrr. trapanicum* (basonym: *Hbt. trapanicum*) as the original isolate is no longer available (Grant et al. 1998). However, the Judicial Commission of the ICSP ruled that strain NCIMB 13488 is derived from strain NRC 34021, which in turn is derived from Petter's original isolate (Judicial Commission 2003). Therefore NCIMB 13488 may serve as the type strain of the species.
- The name *Hrr. sfaxense* (Trigui et al. 2011) has been effectively but not yet validly published. The species was therefore not included in ► [Table 7.11](#), ► [7.12](#), and ► [7.13](#).

Genus *Halosarcina* Savage, Krumholz, Oren, and Elshahed 2008, 859^{VP}; emend. Cui, Gao, Li, Xu, Zhou, Liu, and Zho 2010d, 2464

Ha.lo.sar.ci'na. Gr. n. *hals*, *halos*, salt; L. fem. n. *sarcina* a package; N.L. fem. n. *Halosarcina*, a salt (-loving) package.

Cells are cocci (sarcina-like clusters) or pleomorphic (rods and deformed cocci) under optimal growth conditions. Cells are motile or nonmotile and lyse in distilled water. Sugars are metabolized, sometimes with formation of acids. Polar lipids are PG and

PGP-Me; PGS is absent. The major glycolipid is chromatographically identical to S-DGD-1. DGD-1 or another glycolipid may be present in some species as a minor component.

The mol% G + C of the DNA is 61.2–65.4.

The genus *Halosarcina* currently contains two species: *Hsn. pallida* (type species) and *Hsn. limi*.

The main features of the members of the genus are summarized in ► [Table 7.10](#).

Genus *Halosimplex* Vreeland, Rosenzweig, Straight, Krammes, Dougherty, and Kamekura 2002, 450 (Validation list 92, 2003, 936^{VP})

Ha.lo.sim'plex. Gr. n. *hals*, *halos*, salt; L. adj. *simplex*; simple, uncomplicated; N.L. neut. n. *Halosimplex*, the simple halophile.

Cells are rod shaped or pleomorphic, pink to red. Cannot use nitrate or other alternate electron acceptors. Neutrophilic and mesophilic. Extremely fastidious: grows only on pyruvate, pyruvate plus glycerol, or glycerol plus acetate as carbon sources in defined medium. Unable to grow on any other organic carbon compounds tested. Lipids are PG, PGP-Me, and four sulfated glycolipids, two of which have been identified as TeGD and S₂-DGD.

The mol% G + C of the DNA is 64.4.

Type species and currently only species: *Hsx. carlsbadense*.

The main features of the members of the genus are summarized in ► [Table 7.10](#).

Genus *Halostagnicola* Castillo, Gutiérrez, Kamekura, Xue, Ma, Cowan, Jones, Grant, and Ventosa 2006, 1521^{VP}

Ha.lo.stag.ni'co.la. Gr. n. *hals*, *halos*, salt; L. neut. n. *stagnum*, a piece of standing water, pond, lake; L. suff. *-cola* (from L. n. *incola*), inhabitant, dweller; N.L. fem. n. *Halostagnicola*, a dweller of a saline lake.

Cells are pleomorphic, although most are rod shaped. Strictly aerobic. Polar lipids include C₂₀C₂₀ and C₂₀C₂₅ diethers of PG, PGP-Me, and two unidentified glycolipids.

The mol% G + C of the DNA is 59.8–61.0.

The genus *Halostagnicola* currently contains three species: *Hst. larsenii* (type species), *Hst. alkaliphila*, and *Hst. kamekurae*.

The main features of the members of the genus are summarized in ► [Table 7.15](#).

Genus *Haloterrigena* Ventosa, Gutiérrez, Kamekura, and Dyal-Smith 1999b, 135^{VP}; emend. Oren, Arahal, and Ventosa 2009, 640

Ha.lo.ter.ri'ge.na. Gr. n. *hals*, *halos*, salt; L. fem. adj. *terrigena* born from the earth; N.L. fem. n. *Haloterrigena*, salt (-requiring) and born from the earth.

Cells are coccoid or oval or rod shaped under optimal growth conditions. Some species become coccoid in stationary cultures. Cells lyse in distilled water. The optimum salt concentration for growth is 3.5–4.5 M NaCl. Magnesium requirement is moderate (5–50 mM) or low. Amino acids are required for growth. Some species grow on single carbon sources. Most species use sugars, some with the production of acids. Possess both C₂₀C₂₀ and C₂₀C₂₅ core lipids. Characteristic lipids are PG, Me-PGP, and a glycolipid (S₂-DGD in most species or S-DGD). PGS is absent.

The mol% G + C of the DNA is 59.3–67.0.

Type species: *Haloterrigena turkmenica*.

The genus *Haloterrigena* currently contains nine species: *Htg. turkmenica* (type species), *Htg. daqingensis*, *Htg. hispanica*, *Htg. jeotgali*, *Htg. limicola*, *Htg. longa*, *Htg. saccharevitans*, and *Htg. salina*.

The main features of the members of the genus are summarized in [Table 7.14](#).

Additional comment:

- Phylogenetically the genera *Haloterrigena* and *Natrinema* are not well separated (Tindall 2003; see also [Fig. 7.1](#)). Based on other phylogenetic markers such as the RNA polymerase subunit B' (*rpoB'*) gene, the genera *Natrinema* (McGenity et al. 1998) and *Haloterrigena* (Ventosa et al. 1999) might constitute a single genus (Minegishi et al. 2010a).

Genus *Halovenus* Makhdoumi-Kakhki, Amoozgar, and Ventosa 2012a, 1334^{VP}

Ha.lo.ve'nus. Gr. n. *hals*, *halos*, salt; L. fem. n. *venus* beauty, grace, elegance; N.L. fem. n. *Halovenus*, a salt-loving beauty, reflecting the attractive appearance of colonies.

Cells are nonmotile and pleomorphic (rods to triangles, squares, or disk shaped) and lyse in distilled water. Strictly aerobic, growing on a wide range of substrates, including single and complex carbon sources. Polar lipids are PG, PGP-Me, and two minor phospholipids. MK-8(II-H₂) is the only lipoquinone present.

The mol% G + C of the DNA is 61.0.

Type species and currently only species: *Hvn. aranensis*.

The main features of the members of the genus are summarized in [Table 7.15](#).

Genus *Halovivax* Castillo, Gutiérrez, Kamekura, Ma, Cowan, Jones, Grant, and Ventosa 2006, 767^{VP}

Ha.lo.vi'vax. Gr. n. *hals*, *halos*, salt; L. adj. *vivax*, long-lived, tenacious of life; N.L. masc. n. *Halovivax*, long-living halophile.

Cells are extremely pleomorphic, although most are rod shaped. Colonies are pale pink pigmented. Strictly aerobic. Polar lipids include PG, PGP-Me, two major and one minor glycolipids similar to those of *Nnm. pellirubrum*, and an unidentified glycolipid.

The mol% G + C of the DNA is 60.3–65.0.

The genus *Halovivax* currently contains two species: *Hvx. asiaticus* (type species) and *Hvx. ruber*.

The main features of the members of the genus are summarized in [Table 7.15](#).

Genus *Natrialba* Kamekura and Dyall-Smith 1996, 625^{VP}; Effective Publication: Kamekura and Dyall-Smith 1995, 347 (Validation list 57); emend. Oren, Arahall, and Ventosa 2009, 640

Na.tri.al'ba. N.L. neut. n. *natron* (arbitrarily derived from the Arabic n. *natrun* or *natron*) soda, sodium carbonate; L. fem. adj. *alba*, white; N.L. fem. n. *Natrialba*, sodium white, referring to the high sodium ion requirement and the pigmentless colonies of the type species.

Cells are rods, cocci, or coccobacilli, sometimes occurring in tetrads. Some species lack pigmentation, while others are pigmented red by bacterioruberin carotenoids. Cells lyse in distilled water. Salt concentration for growth is 1.6–5.3 M NaCl. Neutrophilic or alkaliphilic with growth up to pH 10.5–11. Magnesium requirement is moderate (5–50 mM) or low. No growth on single substrates. Neutrophilic species produce acids from sugars. Amino acids are required for growth. Possess both C₂₀C₂₀ and C₂₀C₂₅ core lipids. Polar lipids are PG and PGP-Me. Neutrophilic species contain S₂-DGD in addition. Unidentified phospholipids found in alkaliphilic species. Glycolipids are absent in alkaliphilic species.

The mol% G + C of the DNA is 61.5–64.3 CHECK.

The genus *Natrialba* currently contains six species: *Nab. asiatica* (type species), *Nab. aegyptiaca*, *Nab. chagannaensis*, *Nab. hulunbeirensis*, *Nab. magadii*, and *Nab. taiwanensis*.

The main features of the members of the genus are summarized in [Table 7.16](#).

Additional comments:

- *Nab. taiwanensis* was originally described as a strain of *Nab. asiatica* (Hezayen et al. 2001).
- The name *Nab. aegyptiaca* was changed to *Nab. aegyptia* by the List Editor of Int. J. Syst. Evol. Microbiol. (Notification List, Int. J. Syst. Evol. Microbiol. 51, 1233, 2001), but *Nab. aegyptiaca* is correct as well. The International Committee on Systematics of Prokaryotes Subcommittee on the Taxonomy of Halobacteriaceae recommends use of *Nab. aegyptiaca*.

Genus *Natrinema* McGenity, Gemmell, and Grant 1998, 1194^{VP}

Na.tri.ne'ma. N.L. neut. n. *natron* (arbitrarily derived from the Arabic n. *natrun* or *natron*) soda, sodium carbonate; Gr. neut. n. *nema*, a thread; N.L. neut. n. *Natrinema*, sodium (-requiring) thread.

Cells are rods of varying length that lyse in distilled water. The optimum salt concentration for growth is 3.4–4.3 M NaCl. Magnesium requirement is moderate (5–50 mM) or low. Amino acids are required for growth. Neutrophilic and slightly alkaliphilic species exist. Possess both C₂₀C₂₀ and C₂₀C₂₅ core lipids, as well as several unidentified glycolipids.

The mol% G + C of the DNA is 64.2–69.9.

The genus *Natrinema* currently contains 6 species: *Nnm. pelli-rubrum* (type species), *Nnm. altunense*, *Nnm. ejinorensis*, *Nnm. gari*, *Nnm. pallidum*, *Nnm. pelli-rubrum*, and *Nnm. versiforme*.

The main features of the members of the genus are summarized in [Table 7.17](#).

Additional comments:

- Phylogenetically the genera *Haloterrigena* and *Natrinema* are not well separated (Tindall 2003; see also [Fig. 7.1](#)). Based on other phylogenetic markers such as the RNA polymerase subunit B' (*rpoB'*) gene, the genera *Natrinema* (McGenity et al. 1998) and *Haloterrigena* (Ventosa et al. 1999) might constitute a single genus (Minegishi et al. 2010a).

Genus *Natronoarchaeum* Shimane, Hatada, Minegishi, Mizuki, Echigo, Miyazaki, Ohta, Usami, Grant, and Horikoshi 2010, 2532^{VP}

Na.tro.no.ar.chae'um. N.L. neut. n. *natron* (arbitrarily derived from the Arabic n. *natrun* or *natron*) soda, sodium carbonate; N.L. neut. n. *archaeum* (from Gr. adj. *archaios*, ancient), ancient one, archaeon; N.L. neut. n. *Natronoarchaeum*, the soda archaeon.

Cells are nonmotile and extremely pleomorphic. Aerobic and slightly alkaliphilic. The major polar lipids are PG, PGP-Me, and a disulfated diglycosyl diether (S₂-DGD).

The mol% G + C of the DNA is 63.

Type species and currently only species: *Nac. mannanylyticum*.

The main features of the members of the genus are summarized in [Table 7.18](#).

Genus *Natronobacterium* Tindall, Ross, and Grant 1984b, 355^{VP}; Effective Publication: Tindall, Ross, and Grant 1984a, 41 (Validation list 15)

Na.tro.no.bac.te'ri.um. N.L. neut. n. *natron* (arbitrarily derived from the Arabic n. *natrun* or *natron*) soda, sodium carbonate; N.L. pref. *natrono-*, pertaining to soda; L. neut. n. *bacterium*, a small rod; N.L. neut. n. *Natronobacterium*, soda rod.

Cells are rods of varying length that lyse in distilled water. Motile or nonmotile. The optimum salt concentration for growth is 3.5–4.5 M NaCl. Alkaliphilic, with a very low magnesium requirement. Possess both C₂₀C₂₀ and C₂₀C₂₅ core

lipids. Unidentified phospholipids are present; glycolipids and PGS are absent.

The mol% G + C of the DNA is 65.

Type species and currently only species: *Nbt. gregoryi*.

The main features of the members of the genus are summarized in [Table 7.18](#).

Additional comments:

- *Nbt. magadii* (Tindall et al. 1984) was transferred to the genus *Natrialba* as *Nab. magadii* comb. nov. (Kamekura et al. 1997).
- *Nbt. nitratreducens* (Xin et al. 2001) was transferred to the genus *Halobiforma* as *Hbf. nitratreducens* comb. nov. (Hezayen et al. 2002).
- *Nbt. pharaonis* (Soliman and Trüper 1982) was transferred to the genus *Natronomonas* as *Nmn. pharaonis* comb. nov. (Kamekura et al. 1997).
- *Nbt. vacuolatum* (Mwatha and Grant 1993) was transferred to the genus *Halorubrum* as *Hrr. vacuolatum* comb. nov. (Kamekura et al. 1997).

Genus *Natronococcus* Tindall, Ross, and Grant 1984b, 355^{VP}; Effective Publication: Tindall, Ross, and Grant 1984a, 41

Na.tro.no.coc'cus. N.L. neut. n. *natron* (arbitrarily derived from the Arabic n. *natrun* or *natron*) soda, sodium carbonate; N.L. pref. *natrono-*, pertaining to soda; N.L. masc. n. *coccus* (from Gr. n. *kokkos*, grain, seed), coccus; N.L. masc. n. *Natronococcus*, soda berry.

Cells are coccoid, nonmotile, occurring in pairs, tetrads, or irregular clusters, and do not lyse in distilled water. Alkaliphilic, with a very low magnesium requirement. The optimum salt concentration for growth is 3.0–4.0 M NaCl. Neutrophilic. Possess both C₂₀C₂₀ and C₂₀C₂₅ core lipids. Unidentified phospholipids are present; glycolipids and PGS are absent.

The mol% G + C of the DNA is 63.5–64.0

Type species: *Natronococcus occultus*.

The genus *Natronococcus* currently contains three species: *Ncc. occultus* (type species), *Ncc. amylolyticus*, and *Ncc. jeotgali*.

The main features of the members of the genus are summarized in [Table 7.18](#).

Genus *Natronolimnobius* Itoh, Yamaguchi, Zhou, and Takashina 2005, 1744^{VP} (Validation list no. 105); Effective Publication: Itoh, Yamaguchi, Zhou, and Takashina 2005, 114

Na.tro.no.lim.no'bi.us. N.L. neut. n. *natron* (arbitrarily derived from the Arabic n. *natrun* or *natron*) soda, sodium carbonate; N.L. pref. *natrono-*, pertaining to soda; Gr. n. *limnos*, a pool of

standing water, lake; Gr. masc. n. *bios*, life; N.L. masc. n. *Natronolimnobi*, organism living in a soda lake.

Cells are rod shaped or pleomorphic flat shaped and strictly aerobic. Cells lyse in distilled water. Mesophilic or thermotolerant. C₂₀C₂₀ and C₂₀C₂₅ core lipids are present; glycolipids are not detected.

The mol% G + C of the DNA is 59–63.

The genus *Natronolimnobi* currently contains two species: *Nln. baerhuensis* (type species) and *Nln. innermongolicus*.

The main features of the members of the genus are summarized in [Table 7.19](#).

Genus *Natronomonas* Kamekura, Dyall-Smith, Upasani, Ventosa, and Kates 1997, 856^{VP}, emend. Burns, Janssen, Itoh, Minegishi, Usami, Kamekura, and Dyall-Smith 2010, 1175

Na.tro.no.mo'nas. N.L. neut. n. *natron* (arbitrarily derived from the Arabic n. *natrun* or *natron*) soda, sodium carbonate; N.L. pref. *natrono-*, pertaining to soda; L. fem. n. *monas*, monad, unit; N.L. fem. n. *Natronomonas*, the soda unit.

Cells are rods or pleomorphic shapes of varying length, motile, and lyse in distilled water. Amino acids are required for growth. Alkaliphilic or non-alkaliphilic. Alkaliphilic strains grow at pH 7–10, while non-alkaliphilic strains grow at pH 5.5–8.5. Possess both C₂₀C₂₀ and C₂₀C₂₅ core lipids. PG, PGP-Me, and phosphatidic acid. Unidentified phospholipids or glycolipids are present; PGS are absent, and alkaliphilic strains lack glycolipids.

The mol% G + C of the DNA is 61.2–64.3.

The genus *Natronomonas* currently contains two species: *Nmn. pharaonis* (type species) and *Nmn. moolapensis*.

The main features of the members of the genus are summarized in [Table 7.19](#).

Additional comment:

- *Nbt. pharaonis* (Soliman and Trüper 1982) was transferred to the genus *Natronomonas* as *Nmn. pharaonis* comb. nov. (Kamekura et al. 1997).

Genus *Natronorubrum* Xu, Zhou, and Tian 1999, 265^{VP}; emend. Cui, Tothy, Feng, Zhou, and Liu 2006, 1517; emend. Oren, Arahai, and Ventosa 2009, 641

Na.tro.no.ru'brum. N.L. neut. n. *natron* (arbitrarily derived from the Arabic n. *natrun* or *natron*) soda, sodium carbonate; N.L. pref. *natrono-*, pertaining to soda; L. neut. adj. *rubrum*, red; N.L. neut. n. *Natronorubrum*, the red of soda.

Cells are pleomorphic nonmotile rods or pleomorphic flat shaped, which lyse in distilled water. Cells are nonmotile or motile. Amino acids are required for growth. The optimum salt concentration for growth is 3.4–3.8 M NaCl. Alkaliphilic, with a very low magnesium requirement, or neutrophilic. Many

sugars are utilized, sometimes with acid production. Possess both C₂₀C₂₀ and C₂₀C₂₅ core lipids. Unidentified phospholipids are present; glycolipids absent in some species; others may contain TGD-1 and additional unidentified glycolipids. PGS is absent.

The mol% G + C of the DNA is 59.9–62.5.

The genus *Natronorubrum* currently contains 5 species: *Nrr. bangense* (type species), *Nrr. aibiense*, *Nrr. sediminis*, *Nrr. sulfidifaciens*, and *Nrr. tibetense*.

The main features of the members of the genus are summarized in [Table 7.20](#).

Genus *Salarchaeum* Shimane, Hatada, Minegishi, Echigo, Nagaoka, Miyazaki, Ohta, Maruyama, Usami, Grant, and Horikoshi 2011, 2269^{VP}

Sal.ar.chae'um. L. n. *sal*, salt; N.L. neut. n. *archaeum* (from Gr. adj. *archaios*, ancient), ancient one, archaeon; N.L. neut. n. *Salarchaeum*, salt-requiring archaeon.

Cells are motile short rods. Does not use sugars as a single carbon source. Slightly acidophilic. The major polar lipids are PG, PGP-Me, S-DGD-1, and five unidentified glycolipids.

The mol% G + C of the DNA is 64.

Type species and currently only species: *Sar. japonicum*.

The main features of the members of the genus are summarized in [Table 7.19](#).

Isolation, Enrichment, and Maintenance Procedures

A variety of media have been recommended for the growth of different members of the *Halobacteriaceae*. Useful information can be found in the original papers with the species descriptions and in earlier reviews (Tindall 1991; Oren 2006). The web site of the Deutsche Sammlung von Mikroorganismen und Zellkulturen mbH (DSMZ, <http://www.dmsz.de>) lists many protocols for the preparation of media. Another useful online resource providing descriptions of growth media and laboratory procedures for use with the halophilic Archaea is the “Halohandbook” prepared by Dyall-Smith (2008) http://www.haloarchaea.com/resources/halohandbook/halohandbook_2008_v7.pdf. For solid media, higher than usual agar concentrations should be used as the high salt concentration of the medium interferes with the solidification of the agar. A concentration of 20 g agar/l generally gives satisfactory results. For the preparation of agar media for the haloalkaliphiles, the agar should be sterilized separately from the sodium carbonate and the other alkaline components of the media.

Media used differ greatly in total salt concentration, ionic composition (e.g., high magnesium concentrations of up to 0.8 M for species isolated from the Dead Sea), and pH (9.5 and higher for the alkaliphilic species, using media very low in divalent cation concentrations). Members of the *Halobacteriaceae* are

generally grown in complex media containing high concentrations of yeast extract, casamino acids, and similar rich sources of nutrients. The use of media with high concentrations of peptides and amino acids reflects environments such as salted fish and hides from which many isolates were obtained. Not all members of the family prefer such rich media; the use of low-nutrient media and a restricted range of organic compounds has in the past decade led to the isolation of a number of interesting species such as *Hqr. walsbyi* and *Hsx. carlsbadense*. Notably the use of pyruvate, whether or not combined with the use of agarose instead of agar, has enabled the isolation of the elusive square flat *Haloquadratum* (Bolhuis et al. 2004; Burns et al. 2004a; Walsby 1980, 2005) and is one of the few substrates that enable growth of *Hsx. carlsbadense* (Vreeland et al. 2002).

Several brands of peptone, notably Bacto peptone (Difco), are unsuitable for the cultivation of members of the *Halobacteriaceae* as they cause lysis of the cells. The toxic factor present in Bacto peptone was identified as bile acids (Kamekura et al. 1988), known since 1956 to cause lysis of halophilic Archaea when present at very low concentrations (Dussault 1956a, b). Sugars may stimulate growth of many species. When adding sugars, proper buffering may be required to avoid acidification of the medium to values inhibitory for growth. Though light can be used as an energy source in species containing bacteriorhodopsin, no absolute requirement for light has been demonstrated for any strain, and all known members of the *Halobacteriaceae* grow well in the dark.

One of the key factors important when trying to recover as many species of *Halobacteriaceae* as possible as colonies on agar plates is the incubation time. Combined use of cultivation-dependent and cultivation-independent methods showed that members of most haloarchaeal groups in an Australian crystallizer pond are cultivable. Out of the 1.2×10^7 cells/ml detected by microscopy, up to 1.9×10^6 were recovered as colonies on plates containing 0.01 % nutrient broth and salts after 8 weeks of incubation (Burns et al. 2004b). Drying out of agar plates with the formation of salt crystals on the surface of the agar may present a serious problem in view of the often long incubation times required for colonies to appear. Incubation and storage of petri dishes in plastic bags is then recommended.

Recovery of colonies of halophilic Archaea from samples collected from nature may sometimes be enhanced by the addition of natural brine from the sampling site and a whole cell extract of *Halobacterium salinarum* as a source of stimulatory growth factors (Wais 1988). For the selective isolation of Archaea from natural sources, inclusion of antibiotics such as penicillin or ampicillin has been recommended.

Few procedures have been described for the selective isolation of specific genera and species belonging to the family *Halobacteriaceae*. *Halobacterium* can be selectively enriched under anaerobic conditions in medium containing L-arginine (Oren and Litchfield 1999). *Halococcus* species may possibly be selectively isolated by suspension of the sample in medium with a salt concentration sufficiently low to kill other neutrophilic halophilic Archaea, followed by cultivation in a suitable high-salinity medium. Viable *Halococcus* cells could even be recovered

from seawater: 2–35 *Halococcus* colonies were obtained from 5 l portions of Mediterranean seawater sampled 5 km off the coast of Spain (Rodríguez-Valera et al. 1979). Members of the genera *Haloferax* and *Haloarcula* grow on inorganic media amended with a suitable single carbon and energy source (Rodríguez-Valera et al. 1980).

Maintenance

Cold maintenance at -20 C to -70 C in 10–15 % glycerol + salts in stab cultures kept under liquid paraffin at 4–8 C are sometimes used for preservation of cultures of *Halobacteriaceae*. For long-term preservation, suspensions can be frozen in liquid nitrogen in salt solutions + 5 % DMSO or by lyophilization with the pre-dried milk method (Tindall 1991).

Chemotaxonomic Properties

The *Halobacteriaceae* show many interesting chemotaxonomic traits, part of which are connected to their phylogenetic affiliation with the archaeal domain.

Surface Layers

The non-cocoid representatives of the *Halobacteriaceae* possess an S-layer cell wall, whose main constituent is a high-molecular-weight glycoprotein. This glycoprotein cell wall is responsible for maintaining the native cell shape. The S-layer glycoprotein of *Hbt. salinarum* (molecular mass ~ 120 kDa) consists of a 87 kDa core protein rich in acidic amino acids, containing attached acidic and neutral saccharide chains. The primary structure of the protein backbone and the mode of glycosylation vary among the species. The glycoprotein cell wall requires high NaCl concentrations for stability. Similar to most other proteins of halophilic Archaea (see below), the wall protein denatures when suspended in distilled water, and as a result, the cells of most species lyse in the absence of salt due to the denaturation and dissolution of the cell wall. In some species, relatively high concentrations of magnesium or other divalent cations are required in addition to high NaCl concentrations to maintain the structural stability of the glycoprotein cell wall.

Halococcus species possess a thick sulfated heteropolysaccharide cell wall that does not require high salt concentrations to maintain its rigidity. The polysaccharide wall of *Hcc. morrhuae* contains glucose, galactose, mannose, N-acetylglucosamine, N-acetylgalactosamine, and different uronic acids; part of the sugar residues are sulfated (Schleifer et al. 1982). The cocoid *Ncc. occultus* also has a thick cell wall that retains its shape in the absence of salt. Its structure is unlike

that of the cell wall polymer of *Halococcus*, and it consists of repeating units of a poly(L-glutamine) glycoconjugate (Niemetz et al. 1997).

Some species excrete exopolysaccharides that form a slime layers around the cells. This feature is especially prominent in some *Haloferax* species. The *Hfx. mediterranei* exopolysaccharide is built of glucose, mannose, and sulfated glucose units; the *Hfx. gibbonsii* polymer is composed of mannose, galactose, glucose, and rhamnose. *Hfx. denitrificans* has an exopolysaccharide composed of 2,3-diacetamido-2,3-dideoxy-D-glucopyranosiduronic acid and galactose (Parolis et al. 1999). Further information about the structure of these polysaccharides was reviewed by Oren (2006). Other types of extracellular polymers may occur as well; an interesting example is the poly-(γ -glutamate) layer found outside the cell wall of *Nab. aegyptiaca* (Hezayen et al. 2001).

Polar Lipids, Neutral Lipids, and Pigments

The *Halobacteriaceae* possess lipids based on branched 20-carbon (phytanyl) and in some genera also 25-carbon (sesterterpanyl) chains, bound to glycerol by ether bonds. This unusual lipid structure was elucidated long before the Archaea were recognized as the third domain of life (Sehgal et al. 1962; Kates et al. 1966). A variety of polar lipids, including phospholipids, sulfolipids, and glycolipids, can be encountered in the different representatives of the group. The types of polar lipids present are an important characteristic in the taxonomic classification of genera and species (see [Tables 7.1](#), [7.2](#), [7.3](#), [7.4](#), [7.5](#), [7.6](#), [7.7](#), [7.8](#), [7.9](#), [7.10](#), [7.11](#), [7.12](#), [7.13](#), [7.14](#), [7.15](#), [7.16](#), [7.17](#), [7.18](#), [7.19](#), [7.20](#), [7.21](#), and [7.22](#)). The diether core lipid that forms the basis for most of the polar lipid structures is 2,3-di-O-phytanyl-*sn*-glycerol (C₂₀,C₂₀). Many genera (*Halalkalicoccus*, *Halarchaeum*, *Halobiforma*, *Halococcus*, *Halomarina*, *Haloterrigena*, *Natrialba*, *Natrinema*, and others) contain in addition 2-O-sesterterpanyl-3-O-phytanyl-*sn*-glycerol (C₂₅,C₂₀). Sometimes 2,3-di-O-sesterterpanyl-*sn*-glycerol (C₂₅,C₂₅) is encountered as a minor component as well (De Rosa et al. 1982, 1983). The ratio between C₂₀,C₂₀ and C₂₅,C₂₀ lipids may depend on growth conditions: increasing medium salinity leads to an increased proportion of C₂₅,C₂₀ in the alkaliphiles *Nbt. gregoryi* and *Nab. magadii* (Morth and Tindall 1985). In most cases, the hydrophobic chains are fully saturated, but the occurrence of unsaturated phytanyl ("phytenyl") side chains was documented in *Hrr. lacusprofundi* isolated from Deep Lake, Antarctica, and able to grow at temperatures down to 4 C (Franzmann et al. 1988). Introduction of double bonds in the carbon chains is important in the regulation of membrane fluidity in this cold-adapted species. When grown at 25 C, the polar lipids (PG, PGP-Me, PGS, sulfated and non-sulfated glycolipids; see below) have fully saturated hydrophobic chains; cells grown at 12 C have unsaturated analogues with up to six double bonds (Gibson et al. 2005).

All *Halobacteriaceae* contain diether derivatives of phosphatidyl glycerol (PG) and the methyl ester of phosphatidyl glycerophosphate (PGP-Me) (Kates et al. 1993). The diether derivatives of phosphatidyl glycerosulfate (PGS) is present in many species. Its presence or absence is an important chemotaxonomic property that can be used to discriminate between different genera and species. Cardiolipins (bis-phosphatidyl glycerol) with different combinations of C₂₀ and C₂₅ isoprenoid chains were found in the membranes of the haloalkaliphiles *Ncc. occultus* and *Ncc. amylolyticus* (Angelini et al. 2012). Other yet unidentified phospholipids have been detected in the genus *Natrinema* (McGenity et al. 1998). In *Ncc. occultus*, a phospholipid with a cyclic phosphate group has been identified: 2,3-di-O-phytanyl-*sn*-glycero-1-phosphoryl-3'-*sn* glycerol-1,2-cyclic phosphate (Lanzotti et al. 1989).

Glycolipids are present in most neutrophilic species, but are generally absent in the alkaliphilic members of the family. Di-, tri-, and tetraglycosyl diether lipids occur, part of them carrying one or more sulfate groups bound to the sugar moieties. Not all have yet been fully characterized. Some of the better known and widespread glycolipids are:

- S-DGD-1 (1-O-[α -D-mannose-(6'-SO₃H)-(1' \rightarrow 2')- α -D-glucose]-2,3-di-O-phytanyl-*sn*-glycerol), the major glycolipid in the genus *Haloferax*. Chromatographically identical sulfated diglycosyl diether lipids have been identified in many other genera.
- DGD-1 (1-O-[α -D-mannose-(1' \rightarrow 2')- α -D-glucose]-2,3-di-O-phytanyl-*sn*-glycerol), found in minor amounts in *Haloferax* species.
- DGD-2, a minor diglyceride lipid of unknown structure, containing mannose and glucose, found as a minor component in *Haloarcula* species.
- S-DGD-3 (1-O-[α -D-mannose-(2'-SO₃H)- α -D-(1 \rightarrow 4)-glucose]-2,3-di-O-phytanyl-*sn*-glycerol), the glycolipid of some *Halorubrum* species.
- S₂-DGD-1, a bis-sulfated glycolipid (1-O-[α -D-mannose-(2',6'-SO₃H)- α -D-(1' \rightarrow 2')-glucose]-2,3-di-O-phytanyl- or phytanyl sesterterpanyl-*sn*-glycerol), first characterized from *Natrialba asiatica*.
- TGD-1 (1-O-[β -D-galactose-(1' \rightarrow 6')- α -D-mannose-(1' \rightarrow 2')- α -D-glucose]-2,3-di-O-phytanyl-*sn*-glycerol), a minor glycolipid of *Hbt. salinarum*.
- TGD-2 (1-O-[β -D-glucose-(1' \rightarrow 6')- α -D-mannose-(1' \rightarrow 2')- α -D-glucose]-2,3-di-O-phytanyl-*sn*-glycerol), the sole or major glycolipid of most *Haloarcula* species.
- S-TGD-1 (1-O-[β -D-galactose-(3'-SO₃H)-(1' \rightarrow 6')- α -D-mannose-(1' \rightarrow 2')- α -D-glucose]-2,3-di-O-phytanyl-*sn*-glycerol), found in the genus *Halobacterium*.
- TeGD (1-O-[β -D-galactose-(1' \rightarrow 6')- α -D-mannose-(3' \leftarrow 1')- α -D-galactofuranose-(1' \rightarrow 2')- α -D-glucose]-2,3-di-O-phytanyl-*sn*-glycerol), a minor glycolipid of *Hbt. salinarum*.
- S-TeGD (1-O-[β -D-galactose-(3'-SO₃H)-(1' \rightarrow 6')- α -D-mannose-(3' \leftarrow 1')- α -D-galactofuranose)-(1' \rightarrow 2')- α -D-glucose]-2,3-di-O-phytanyl-*sn*-glycerol), found in *Halobacterium*.

The chemical structures of many of the above-listed lipids were given by Kamekura and Kates (1999) and Oren (2006).

Neutral lipids may represent about 10 % of the total lipid content of the *Halobacteriaceae* (Kamekura and Kates 1988; Kushwaha and Kates 1979). They include:

- C₂₀ isoprenoid lipids: geranylgeraniol.
- Neutral phytanyl ethers of glycerol: DL-O-phytanyl-*sn*-glycerol and 2,3-di-O-phytanyl-*sn*-glycerol.
- C₃₀-isoprenoid compounds: squalene, dihydrosqualene, tetrahydrosqualene, and dehydrosqualene.
- Carotenoids. Most species are pigmented red-orange due to a high content of carotenoid pigments in their cell membrane. Rare exceptions are *Nab. asiatica* and *Hrb. tiamatea*, which lack substantial amounts of carotenoids. The pigment content of the cells may depend on their nutritional status (Gochnauer et al. 1972; Kushwaha and Kates 1979) and on the salinity of the growth medium: certain *Haloferax* species are pigmented when grown at low salinity (e.g., 15 %), while at higher salt concentrations (e.g., 25 %), they may be almost colorless (Kushwaha et al. 1982; Rodriguez-Valera et al. 1980). The most abundant carotenoids of the *Halobacteriaceae* are the 50-carbon compounds α -bacterioruberin and its derivatives monoanhydrobacterioruberin and bis-anhydrobacterioruberin (Kelly et al. 1970; Kushwaha et al. 1974, 1975). C₄₀ carotenoids may be present in small amounts, lycopene and β -carotene being the most abundant (Kushwaha et al. 1982; Tindall 1992). Accumulation of canthaxanthin, in addition to bacterioruberin carotenoids, was reported in *Hfx. alexandrinus* (Asker and Ohta 2002b). Carotenoid pigments protect the cells against photodamage as shown in competition experiments in which wild-type cells of *Hbt. salinarum* and a carotenoidless mutant were incubated at high light intensities (Dundas and Larsen 1962).

Respiratory Quinones and Polyamines

The major respiratory quinones in the *Halobacteriaceae* are MK-8 and MK-8(VIII-H₂) (Collins et al. 1981; Tindall and Collins 1986). Quinones may amount to about 9 % of the total neutral lipid content of the cells (Kamekura and Kates 1988). The relative abundance of MK-8 and MK-8(VIII-H₂) depend on the growth conditions (Tindall 1992; Tindall et al. 1991). *Nbt. gregoryi* also contains monomethylated and dimethylated menaquinones (Collins and Tindall 1987).

Polyamines are found in the *Halobacteriaceae* in very small amounts, if at all. If present, agmatine appears to be the most common polyamine (Hamana et al. 1995; Kamekura et al. 1987).

Physiological Properties

To provide osmotic balance of the cytoplasm with the extremely high salt concentrations in their environment, the

Halobacteriaceae accumulate molar concentrations of KCl. Organic osmotic solutes are generally not used. An exception is the accumulation of 2-sulfotrehalose in *Ncc. occultus* (Martin et al. 1999). Most proteins require high salt for structural stability and activity and are characterized by an exceptionally high content of the acidic amino acids glutamate and aspartate. Accordingly they have a large net negative charge at the physiological pH (Mevarch et al. 2000; Lanyi 1974; Reistad 1970). In addition to the high salinity required by all species, many are obligate alkaliphiles. Some have temperature optima above 50 °C (Bowers and Wiegel 2011; Robinson et al. 2005).

Most species lead an aerobic heterotrophic life style (Tindall and Trüper 1986). They generally prefer complex media with amino acids as main organic nutrient. *Hbt. salinarum*, the type species of the type genus of the family, is unable to grow on sugars, but carbohydrates can be used by a variety of other species. Carbohydrate utilization was first demonstrated in *Hrr. saccharovororum* (Tomlinson and Hochstein 1972a, b; Tomlinson and Hochstein 1976). Breakdown of glucose follows a modified Entner-Doudoroff pathway in which the phosphorylation step is postponed: glucose is oxidized via gluconate to 2-keto-3-deoxygluconate, followed by phosphorylation to 2-keto-3-deoxy-6-phosphogluconate, which is then split into pyruvate and glyceraldehyde-3-phosphate (Tomlinson et al. 1974). Use of carbohydrates is often associated with the production of acids, as oxidation of such substrates is incomplete. When grown on glucose, *Hrr. saccharovororum* excretes acetic acid and pyruvic acid; galactose, lactose, and other sugars are converted to the corresponding aldonic acids (Tomlinson and Hochstein 1972b; Tomlinson et al. 1978). Acetate, pyruvate, and D-lactate were identified in cultures of several *Haloferax* and *Haloarcula* species grown in the presence of glycerol (Oren and Gurevich 1994).

While the species of *Halobacterium* and many other genera require complex media for growth, other members of the family can grow on defined media with single organic compounds (simple sugars, organic acids, amino acids) as carbon and energy source (Rodriguez-Valera et al. 1980). Many species produce exoenzymes (proteases, amylases, lipases, nucleases) enabling them to use proteins, starch, lipids, and nucleic acids as sources of nutrients.

Recent advances in genomic and systems biology have enabled an in-depth reconstruction of the metabolism of model organisms, notably strains of *Hbt. salinarum*, *Har. marismortui*, *Hqr. walsbyi*, and *Nmn. pharaonis* (Falb et al. 2008; Gonzalez et al. 2008). Recently a novel anaerobic pathway for the incorporation of acetate into cellular carbon was identified in *Har. marismortui* and *Hfx. volcanii*: rather than the classic glyoxylate cycle, a methylaspartate cycle is operative (Khomyakova et al. 2011).

Some isolates can degrade aliphatic hydrocarbons (tetradecane, hexadecane, heptadecane, eicosane, heneicosane), aromatic hydrocarbons (acenaphthene, phenanthrene, anthracene, 9-methylanthracene), and other aromatic compounds (benzoate, cinnamate, 3-phenylpropionate, *p*-hydroxybenzoate). Most hydrocarbon and aromatic

compounds degrading isolates belong to the genera *Haloferax* and *Haloarcula* (Bertrand et al. 1990; Cuadros-Orellana et al. 2006.; Emerson et al. 1994; Fu and Oriol 1999; Kulichevskaya et al. 1991; Tapilatu et al. 2010).

Due to the low solubility of oxygen in salt-saturated brines, oxygen may easily become a limiting factor for development of halophilic Archaea. One possible strategy to avoid oxygen limitation is the use of gas vesicles to buoy the cells toward the surface of the brine. *Hbt. salinarum*, *Hfx. mediterranei*, *Hgm. borinquense*, *Hpn. aerogenes*, *Hpn. natans*, *Hpn. vesicus*, *Hqr. walsbyi*, and *Hrr. vacuolatum* can form gas vesicles. How effective gas vacuoles are to enable the cells to reach layer richer in oxygen is uncertain; for a critical discussion of this topic, see Oren et al. (2006).

One member of the family preferentially leads an anaerobic life style: *Hrd. tiamatea*, found in deep brines near the bottom of the Red Sea. It probably obtains its energy by fermentation (Antunes et al. 2008). Many other species have limited possibilities to survive and even grow in the absence of molecular oxygen, strategies based on anaerobic respiration with different electron acceptors, fermentation, or the use of light as an energy source when respiration cannot supply sufficient energy.

The ability to reduce nitrate is widespread among the members of the *Halobacteriaceae*. A few species (e.g., *Hfx. denitrificans*, *Har. marismortui*, *Har. vallismortis*, *Hgm. borinquense*) can grow anaerobically using nitrate as electron acceptor. Nitrate is generally reduced to N_2 , but N_2O formation has also been observed in several cases (Hochstein and Tomlinson 1985; Mancinelli and Hochstein 1986; Tomlinson et al. 1986). The ecological relevance of anaerobic growth on nitrate has never yet been ascertained.

Other alternative electron acceptors for respiration are dimethylsulfoxide (DMSO), trimethylamine *N*-oxide (TMAO), and fumarate. Reduction of DMSO and TMAO is coupled with growth in several species. *Hbt. salinarum*, *Hfx. mediterranei*, *Har. marismortui*, and *Har. vallismortis* grew anaerobically in the presence of DMSO or TMAO; in *Hfx. volcanii*, DMSO supported anaerobic growth, while TMAO did not (Oren and Trüper 1990). The genes enabling *Halobacterium* strain NRC-1 to grow on DMSO and TMAO have been characterized (Müller and DasSarma 2005). Fumarate-driven anaerobic growth was reported in some *Hbt. salinarum* strains, in *Hfx. denitrificans*, and in *Hfx. volcanii* (Oren 1991). The ecological relevance of anaerobic growth of members of the *Halobacteriaceae* on DMSO, TMAO, or fumarate is unknown. However, TMAO may be available as an electron acceptor in salted fish, a well-known habitat for species of *Halobacterium* and *Halococcus*. TMAO can be present in high concentrations within fish tissues as an osmotic solute. A recent addition to the list of electron acceptors that can drive anaerobic respiration in members of the *Halobacteriaceae* is thiosulfate. It is used by the pleomorphic rod-shaped strain HG, isolated from hypersaline lakes in the Kulunda steppe, Altai, Russia, phylogenetically affiliated with the genus *Natronorubrum*. It grows on acetate with reduction of thiosulfate to tetrathionate (Sorokin et al. 2005).

An entirely different strategy for anaerobic energy generation is fermentation of *L*-arginine to citrulline, ammonia, and CO_2 . This process can drive anaerobic growth in *Hbt. salinarum* (Hartmann et al. 1980; Ruepp and Soppa. 1996). Anaerobic growth on arginine is not widespread among the haloarchaea; a wide variety of neutrophilic strains tested belonging to genera other than *Halobacterium* gave negative results (Oren 1994; Oren and Litchfield 1999). A specific enrichment procedure for members of the genus *Halobacterium* could thus be developed, based on their ability to grow anaerobically in the presence of *L*-arginine (Oren and Litchfield 1999).

Light can be used as an energy source to drive anaerobic growth in *Hbt. salinarum*, provided the cells contain the light-driven proton pump bacteriorhodopsin, a membrane-bound 27 kDa protein carrying retinal as a prosthetic group (Hartmann et al. 1980; Oesterhelt 1982; Oesterhelt and Krippahl 1983). As the biosynthesis of retinal from β -carotene is oxygen-dependent, either trace concentrations of oxygen must still be present, or retinal or retinaloxime should be supplied to the medium to enable sustained light-driven anaerobic growth (Oesterhelt and Krippahl 1983). Four retinal-containing proteins have been identified in members of the family: bacteriorhodopsin, an outward light-driven proton pump; halorhodopsin, an inward light-driven chloride pump; and two sensory rhodopsins, involved in light sensing for phototaxis. Bacteriorhodopsin was first identified in *Hbt. salinarum*, where it is localized in specialized patches of the cell membrane ("purple membrane") (Oesterhelt and Stoeckenius 1971; for a historic overview, see also Grote and O'Malley 2011). Upon excitation by light (absorption maximum 570 nm), protons are extruded from the cytoplasm to the outside of the cell (for a review, see Lanyi 2004). The proton gradient thus formed is used to drive energy-requiring processes in the cell, including the phosphorylation of ADP to ATP (Danon and Stoeckenius 1974). Not all members of the family produce bacteriorhodopsin; among those that do are *Hrr. sodomense* and *Hqr. walsbyi*. Studies of the bacteriorhodopsin gene cluster of *Hbt. salinarum* have shown that expression of the protein is induced by low oxygen tension and by light (Betlach et al. 1986; Shand and Betlach 1991). A second retinal protein, also first discovered in *Hbt. salinarum*, is halorhodopsin. The structure of this protein is similar to that of bacteriorhodopsin, but it acts as a chloride pump: excitation by light (absorption maximum 580 nm) causes the inward transport of chloride ions (Schobert and Lanyi 1982). Chloride transport is important to maintain the proper ionic balance and is essential for cell growth. Halorhodopsin was also found in several haloalkaliphilic Archaea, and the halorhodopsin of *Nmn. pharaonis* has been studied in detail (Lanyi et al. 1990). *Hbt. salinarum* contains two sensory rhodopsins, involved in light sensing for phototaxis. Sensory rhodopsin I is a green light receptor (light to which the cells are attracted), and sensory rhodopsin II, also termed phoborhodopsin, is a blue light receptor (light that acts as a repellent).

Sensitivity to Antibiotics

Members of the *Halobacteriaceae* typically are resistant to such Bacteria-specific antibiotics as penicillin, ampicillin, cycloserine, kanamycin, neomycin, polymyxin, and streptomycin (Bonelo et al. 1984; Hilpert et al. 1981; Pecher and Böck 1981). Sensitivity to chloramphenicol is variable (see also ▶ [Tables 7.1](#), ▶ [7.2](#), ▶ [7.3](#), ▶ [7.4](#), ▶ [7.5](#), ▶ [7.6](#), ▶ [7.7](#), ▶ [7.8](#), ▶ [7.9](#), ▶ [7.10](#), ▶ [7.11](#), ▶ [7.12](#), ▶ [7.13](#), ▶ [7.14](#), ▶ [7.15](#), ▶ [7.16](#), ▶ [7.17](#), ▶ [7.18](#), ▶ [7.19](#), ▶ [7.20](#), ▶ [7.21](#), and ▶ [7.22](#)). Most species are sensitive to novobiocin and bacitracin. Novobiocin is a DNA gyrase inhibitor (Gadelle and Forterre 1994, Sioud et al. 1988) and acts on the same target in the Archaea as in sensitive Bacteria. Bacitracin inhibits incorporation of the high-molecular-weight saccharide into the cell wall glycoprotein of non-cocoid halophilic Archaea and may also inhibit lipid biosynthesis in these organisms.

Members of the *Halobacteriaceae* are sensitive to a number of additional antibiotics and other antibacterial compounds:

- Anisomycin, a protein synthesis inhibitor of ribosomes of eukaryotes, also inhibits protein synthesis of nearly all members of the *Halobacteriaceae* tested, both in vivo and in vitro (Pecher and Böck 1981). Four species were reported as resistant: *Hrr. chaoviator*, *Hsx. carlsbadense*, *Nmm. moolapensis*, and *Sar. japonicum*.
- Cerulenin, an inhibitor of the synthesis of the straight-chain fatty acids by the fatty acid synthetase complex, inhibits *Hbt. salinarum* (and possibly other members of the order as well) (Dees and Oliver 1977). This finding suggests that the production of straight-chain fatty acids is essential even in an organism possessing archaeal type lipids. It is now known that fatty acids are used to acylate certain membrane proteins (Pugh and Kates 1994).
- Rifampicin inhibits many members of the *Halobacteriaceae* (Bonelo et al. 1984; Hilpert et al. 1981; Pecher and Böck 1981). The target of rifampicin action in the halophilic Archaea is probably not the DNA-dependent RNA polymerase, but the inhibition may be due to its detergent effect on the cell membrane, causing cell lysis.
- The DNA polymerase inhibitor aphidicolin prevents cell division and often causes the formation of elongated cells (Forterre et al. 1984, 1986; Schinzel and Burger 1984).
- Inhibition of halophilic Archaea by coumarin and quinolone antibacterial compounds presented evidence for the presence of DNA gyrase-like enzymes (Sioud et al. 1988). The quinolone compound ciprofloxacin inhibited most *Haloferax* and *Haloarcula* species at concentrations between 25 and 60 µg/ml. *Halobacterium* cells proved less sensitive. Sensitivity to ciprofloxacin and other quinolone derivatives (norfloxacin, perfloxacin) was decreased at increased magnesium concentrations (Oren 1996; Sioud et al. 1988). *Hfx. volcanii* became more resistant when the magnesium concentration in the growth medium was increased. Alkaliphiles such as *Nmn. pharaonis* are very sensitive (Oren 1996).

- Bile acids at low concentrations cause lysis of the cell envelopes of non-cocoid halophilic Archaea and are potent growth inhibitors (Dussault 1956a, b; Kamekura et al. 1988).

Halocins

Many species of *Halobacteriaceae* excrete “halocins,” protein antibiotics that inhibit the growth of other related species (Meseguer and Rodriguez-Valera 1986; Meseguer et al. 1986; Rodriguez-Valera et al. 1982; Torreblanca et al. 1989, 1990, 1994). Different modes of action have been suggested for different halocins (Shand et al. 1999). Halocin H4, excreted by the type strain of *Hfx. mediterranei* and halocin H1 of *Hfx. mediterranei* strain Xai3 cause membrane permeability changes and ionic imbalance in *Hbt. salinarum* (Meseguer and Rodriguez-Valera 1986; Meseguer et al. 1991; O’Connor and Shand 2002). Halocin H7, excreted by *Hfx. gibbonsii*, targets the Na⁺/H⁺ antiporter activity of sensitive strains (Alberola et al. 1998; Meseguer et al. 1995). More than 10 halocins have been wholly or partially characterized (Li et al. 2003; O’Connor and Shand 2002). The size of the mature proteins (after cleavage of signal sequence of the pre-protein) varies between 3.6 kDa, the 36-amino acid long “microhalocin” S8 excreted by a further uncharacterized strain isolated from Great Salt Lake, Utah (Price and Shand 2000), and 34.9 kDa—halocin H4 of *Hfx. mediterranei* (Cheung et al. 1997). Although the ability to excrete halocins may be expected to be of considerable ecological advantage, no data are available as yet that prove that halocins are excreted by natural communities of halophilic Archaea in concentrations sufficient to inhibit the development of competitor strains, thus substantiating their ecological role (see Kis-Papo and Oren 2000).

Ecology

Members of the *Halobacteriaceae* can be found worldwide in hypersaline environments with salt concentrations above 10–15 % (Norton 1992; Oren 1994, 2011). As most species lyse when exposed to lower salinities even for short times, a stable high-salt environment is a prerequisite for their development. We find selected species at high pH in soda lakes, and an acidophilic species (*Hla. acidiphilum*) that grows optimally at pH 4.4 was recently characterized (Minegishi et al. 2008). Curiously, it was isolated from a sample of Chinese salt imported to Japan, that in saturated solution yielded an alkaline pH. Some can grow at low temperatures (*Hrr. lacusprofundi* from Deep Lake, Antarctica) (Franzmann et al. 1988), and temperatures up to 55 °C are tolerated by many species. Thus, as long as the salinity is suitably high, members of the *Halobacteriaceae* can be expected to grow.

Lakes with salt concentrations approaching saturation may show red hues, such as documented for the north arm of the

Great Salt Lake, the Dead Sea, and hypersaline alkaline lakes such as Lake Magadi, Kenya. Red-colored brines are also typically present during the final stages of the evaporation of seawater in solar saltern ponds (Oren 1994). Archaea are generally responsible for most of the color of the saltern brines. Numbers of 10^7 to 10^8 cells and higher per ml of brine are not unusual. Members of the *Halobacteriaceae* have also been recovered from saline and hypersaline soils (Zvyagintseva and Tarasov 1987).

The concentration of divalent cations, especially magnesium and calcium, in the environment is of considerable ecological importance. Thus, the Dead Sea is dominated by divalent cations (presently around 2 M Mg^{2+} and 0.5 M Ca^{2+} , in addition to about 1.5 M Na^+ and 0.2 M K^+). Halophilic Archaea isolated from the Dead Sea are characterized by a relatively low requirement for Na^+ and an extraordinarily high tolerance toward and often also a requirement for high Mg^{2+} concentrations, such as was shown for *Hfx. volcanii* (Mullakhanbhai and Larsen 1975), *Hrr. sodomense* (Oren 1983), and *Hbc. gomorrhense* (Oren et al. 1995).

Alkaliphilic members of the family such as *Hrr. vacuolatum* (Mwatha and Grant 1993), *Nmn. pharaonis* (Soliman and Trüper 1982), *Nab. magadii*, *Nbt. gregoryi*, *Ncc. occultus* (Tindall et al. 1984), and *Ncc. amylolyticus* (Kanai et al. 1995) are characteristic inhabitants of hypersaline soda lakes in which the pH reaches 9–10 and higher. In accordance with the low solubility of the divalent cations Mg^{2+} and Ca^{2+} at high pH, the alkaliphilic halophiles do not require significant concentrations of magnesium for growth (Tindall et al. 1980).

Halobacteriaceae were also recovered from rock salt deposited millions of years ago. Such isolates include the type strains of *Hsx. carlsbadense*, *Hcc. dombrowskii*, *Hcc. salifodinae*, and *Nbt. noricense*. Much has been speculated about the longevity of such organisms within salt crystals. Sequences of haloarchaeal 16S rRNA fragments have been retrieved from salt samples as ancient as the Permian or the Triassic era (Fish et al. 2002; McGenity et al. 2000; Radax et al. 2001).

The first isolates of *Halobacteriaceae* described—strains of *Hbt. salinarum* and *Hcc. morrhuae*—were obtained from red growth on salted food products (fish, meat) and salted hides, nutrient-rich environments where colonization by haloarchaea may cause economic damage.

In view of the extremely high salt requirement of most species of *Halobacteriaceae*, it is somewhat surprising to find reports of their isolation (and/or the recovery of their 16S rRNA genes in culture-independent studies) from low-salt environments. The isolation of *Halococcus* sp. from seawater (Rodriguez-Valera et al. 1979) was possible due to the fact that in contrast to most other genera that lyse at low salt concentrations, *Halococcus* has a rigid cell wall. *Halococcus* cells may be dispersed by birds: strains of *Hcc. morrhuae* and *Hcc. dombrowskii* could be cultivated from the salt-excreting glands in the nostrils of the seabird *Calonectris diomedea* (Brito-Echeverria et al. 2007). A strain related to *Haladaptatus*, isolated from a traditional Japanese-style salt field, showed a high

survival rate after 9 days incubation in 0.5 % seawater salts (Fukushima et al. 2007). In recent years, several reports were published on the existence of strains of *Halobacteriaceae* with a relatively low salt requirement for growth. Isolates of haloarchaea were obtained from a salt marsh in Essex, UK, an environment containing ~2.5 % salt only. One isolate designated strain HA Gp1 (unfortunately not characterized further) was reported to grow optimally at 10 % salt with growth being even possible at 2.5–3 % salt (Purdy et al. 2004). *Hap. paucihalophilus* was isolated from a low-salt sulfur spring in Oklahoma, and it grows at salt concentrations as low as 4.7 % NaCl with an optimum at 15–18 % (Savage et al. 2007). The recovery of *Haloarcula* sp. 16S rRNA gene sequences from a deep-sea black smoker chimney at a hydrothermal vent area near Papua New Guinea (Takai et al. 2001) is interesting as well. Whether hypersaline areas may be present within such chimney structures remains to be ascertained. An intriguing environment from which *Haloarcula*-related strains were recovered is the geothermal steam vent aerosols emerging from fumaroles in Kamchatka, Hawaii, New Mexico, California, and Wyoming. A single fumarole was estimated to emit $>10^9$ cells of haloarchaea per year (Ellis et al. 2008). The finding of 16S rRNA gene sequences of *Halobacteriaceae* within the intestine of humans is discussed in the next section.

Pathogenicity: Clinical Relevance

As the *Halobacteriaceae* require high salt concentrations for growth, much higher than the physiological salt concentration of ~9 g/l of the body fluids, members of the family cannot be expected to be associated with the human body. Still there are two interesting observations showing that some species may indeed colonize humans. A culture-independent study of the intestinal microflora of Korean people yielded 16S rRNA gene sequences related to *Halorubrum* and *Halococcus* (Nam et al. 2008). The finding may be related to the local diet: species such as *Hrr. alimentarium* and *Hrr. koreense* were isolated from salt-fermented seafood based on shrimps. Haloarchaeal 16S rRNA gene sequences were also recovered from the intestinal mucosa of patients with inflammatory bowel disease in the UK. Eight out of the 39 biopsy samples gave positive PCR results. Some phylotypes were affiliated to the genera *Halobacterium* and *Halorubrum*; others belonged to a new lineage not yet represented by cultures. Thus, members of the *Halobacteriaceae* may under certain conditions be present in the mucosal microbiota (Oxley et al. 2010).

Application

Members of the *Halobacteriaceae* have a number of useful applications, and potential new applications in biotechnological processes are being investigated (Galinski and Tindall 1992; Litchfield 2011; Margesin and Schinner 2001; Oren 2010;

Rodriguez-Valera 1992; Ventosa and Nieto 1995). The following list presents some of the current and potential future applications of the group:

- The positive effect of the presence of dense communities of red halophilic Archaea in saltern crystallizer ponds has been recognized for a long time. By trapping solar radiation, they raise the temperature of the brine and the rate of evaporation, thereby increasing salt production. To improve salt production in salterns that do not develop a sufficiently dense archaeal community, fertilization with nutrients may increase the red color of the ponds (Jones et al. 1981).
- Production of fermented fish sauce in the Far East (e.g., nam pla in Thailand) involves participation of halophilic Archaea. The product is traditionally made by adding two parts of fish and one part of marine salts. The mixture is covered with concentrated brine (4.4–5.1 M NaCl) and left to ferment for about a year. Red halophilic Archaea (identified as *Halobacterium* and *Halococcus*) reach their maximum density in the liquor after 3 weeks and persist throughout the fermentation period. The halobacterial proteases probably take part in the fermentation process (Thongthai and Siritwongpairat 1990; Thongthai and Suntinanalert 1991; Thongthai et al. 1992). Addition of starter cultures of *Halobacterium* sp. SP1(1) may accelerate fish sauce fermentation (Akolkar et al. 2010). Use of different strains of halophilic Archaea could improve the safety and quality of salted anchovies by reducing the content of histamine (Aponte et al. 2010). Immobilized cells of *Natrinema gari* strain BCC 24369 may be highly effective for the removal of histamine from salted food products (Tapingkae et al. 2010a, b).
- Different species of halophilic Archaea synthesize potentially useful products such as bacteriorhodopsin, exopolysaccharides, and poly- β -hydroxyalkanoate (PHA). Halophilic Archaea have distinct advantages in biotechnological processes as they are relatively easy to grow, danger of contamination is minimal, and culture size can be upscaled to the use of large fermenters (Kushner 1966). However, because of the low solubility of gases in concentrated brines, the supply of sufficient amounts of oxygen may cause problems. In addition, the aggressive nature of the salts should be taken into account when planning the construction of large fermenters with metal parts exposed to the medium. A corrosion-resistant bioreactor made of polyether-etherketone was developed for the production of PHA and poly(γ -glutamic acid) by *Natrialba* sp. (Hezayen et al. 2000).
- Bacteriorhodopsin, the light-driven proton pump of *Hbt. salinarum*, has considerable biotechnological potential (Oesterhelt et al. 1991). It may be used as a biological material for information processing. Other suggested uses include conversion of sunlight to electricity, ATP generation, desalination of seawater, use in chemo- and biosensors, and ultrafast light detection. The photochromic effect—shifts between the purple ground state of the molecule (the “B state”) and the yellow “M state”—may be used for information storage, including holographic storage, and may enable development of powerful computer memories and processors (Birge et al. 1999). Bacteriorhodopsin offers many advantages since it is a very stable molecule, functioning well between 0 °C and 45 °C and pH 1–11 (Chen and Birge 1993), is easy to immobilize on solid substrates, and produces very reproducible photoelectric signals. Holographic bacteriorhodopsin films are suitable for the construction of computer memories enabling parallel processing, and the developing technology may lead to a new generation of computers (Hong 1986). To turn bacteriorhodopsin into a light sensor, it is spread in a thin film sandwiched between an electrode and an electrically conductive gel. Changes in the shape of the molecule create a displacement of charge, generating an electrical signal. The suitability of bacteriorhodopsin for all these applications can be greatly enhanced by mutation; using genetically engineered bacteriorhodopsin, up to 700-fold improvement has been realized in volumetric data storage (Hampp 2002a, b; Wise et al. 2002). Bacteriorhodopsin-based photo-electrochemical cells can be constructed (Chu et al. 2010). Use of *Hbt. salinarum* for light-driven hydrogen production was also explored (Lata et al. 2007; Zabut et al. 2006).
- A microbial fuel cell operating at high ionic strength conditions was designed, using *Nab. magadii* or *Hfx. volcanii* as biocatalyst at the fuel cell anode. Such a system may be favorable as high-salt media have a high electrical conductivity so that the internal resistance is diminished (Abrevaya et al. 2011).
- The extracellular polysaccharide produced by *Haloferax* has considerable biotechnological potential (Antón et al. 1988; Rodriguez-Valera et al. 1991). The bacterium produces up to 3–8 g/l of an acidic heteropolysaccharide with a high apparent viscosity at relatively low concentrations and resistance to extremes of salts, temperature, and pH. The structure of this polymer was elucidated (Parolis et al. 1996). *Hfx. volcanii* and *Hfx. gibbonsii* also produce exopolysaccharides. Such polymers may be used to modify rheological properties of aqueous systems, for viscosity stabilization as thickening agents, gelling agents, and emulsifiers, and may find applications in microbially enhanced oil recovery (Ventosa and Nieto 1995). Here, a salt-resistant surfactant is advantageous as high-salinity brines are often encountered associated with oil deposits. Whole cell preparations may be used, as the lipids liberated upon lysis of halophilic Archaea may also act as surfactants to improve the oil-carrying properties (Post and Al-Harjan 1988).
- Use of *Haloferax* species (*Hfx. mediterranei*, *Hfx. denitrificans*) was proposed for the bioremediation of saline and hypersaline waters containing nitrate (Cyplik et al. 2007, 2010) or chlorate and perchlorate (Martinez-Espinosa and Bonete 2007). *Hbt. salinarum* ATCC 43214 (misnamed as *Halobacter* (sic) *halobium*) was used to supplement activated sludge in a rotating biological disk system for COD removal

from saline wastewater (Dinçer and Kargi 2001; Kargi 2002; Kargi and Dinçer 1996). However, the salinity of the wastewater treated (up to 5 % or 10 % salt) is too low for growth or even for survival of the halophilic Archaea, and therefore, the mechanism of the reported improvement in performance of the system is not clear.

- *Hfx. mediterranei* cells may contain considerable amounts of poly- β -hydroxyalkanoate (PHA) (Fernandez-Castillo et al. 1986; Rodriguez-Valera et al. 1991). PHA is used for the production of biodegradable plastics. Though halophilic Archaea are not yet being used commercially for PHA production, they have certain obvious advantages over an organism such as *Alcaligenes eutrophus*, which is already being exploited for the purpose. *Hfx. mediterranei* can be grown on a cheap substrate such as starch. Moreover, downstream processing and purification of the product should be relatively simple as the cells are easily lysed in water (Ventosa and Nieto 1995). Also the high genomic stability of the organism and the reduced danger of contamination are clear assets. PHA production is maximal when grown on sugars (glucose or starch) and in the presence of low phosphate concentrations (Lillo and Rodriguez-Valera 1990; Rodriguez-Valera and Lillo 1992). PHA production was demonstrated in certain other halophilic Archaea as well, such as *Hfx. volcanii* and *Har. marismortui*. It has been argued that *Hfx. mediterranei* is economically better than several non-halophilic producers for the production of PHA from whey: the strain is robust and stable, and danger of contamination is minimal (Koller et al. 2007). Processes for the use of crude oil, petrochemical wastewater, or glycerol for the production of PHA by *Haloarcula* sp. IRU1 were recently described (Taran 2011a, b, c). However, the proposed addition of 0.8 % tryptone or 0.4 or 0.8 % yeast extract as source of nitrogen and other nutrients will make such a process economically unfeasible.
- Exoenzymes such as amylases, amyloglucosidases, proteases, and lipases that function at high salinity may be useful in biotechnological processes requiring degradation of macromolecules in the presence of high salt concentrations (Chaga et al. 1993; Eichler 2001; Ventosa and Nieto 1995).
- Canthaxanthin can be produced using *Hfx. alexandrinus* (Asker and Ohta 1999, 2002b).
- Halophilic Archaea degrading aliphatic and aromatic hydrocarbons may prove useful for the reduction of the chemical oxygen demand of hypersaline petroleum-produced water and the bioremediation of oil spills (Bertrand et al. 1990; Bonfá et al. 2011; Kulichevskaya et al. 1991).
- Members of the *Halobacteriaceae* growing on brine-cured hides (a phenomenon known as “red heat”) negatively affect the quality of the product (Bailey and Birbir 1996). To prevent damage of brine-cured hides by growth of proteolytic halophilic Archaea, gelatinase-negative halocin producers could be applied against damaging proteolytic strains (Birbir et al. 2004).
- A 84 kDa protein from *Hbt. salinarum* has been used as an antigen to detect antibodies against the human *c-myc* oncogene product in the sera of cancer patients, and therefore, the protein may be useful for the detection of certain forms of cancer (Ben-Mahrez et al. 1988, 1991).
- Gas vesicles of *Halobacterium* can be used as a *Chlamydia* vaccine display and delivery system. Haptens incorporated in recombinant GvpC protein showed strong antibody response in mice in the absence of further adjuvants (Childs and Webley 2012; Stuart et al. 2001). Lipid vesicles (“archaeosomes”) made of *Hrr. tebenquichense* total polar lipids can be developed into vaccine delivery vehicles (Gonzalez et al. 2009).
- Site-specific endonucleases of halophilic Archaea (Schinzel and Burger 1986) may find uses in molecular biological research.

References

- Abrevaya XC, Sacco N, Mauas PJD, Cortón E (2011) Archaea-based microbial fuel cell operating at high ionic strength conditions. *Extremophiles* 15:633–642
- Akolkar AV, Durai D, Desai AJ (2010) *Halobacterium* sp. SP1(1) as a starter culture for accelerating fish sauce fermentation. *J Appl Microbiol* 109:44–53
- Alberola A, Meseguer I, Torreblanca M, Moya A, Sancho S, Polo B, Soria B, Such L (1998) Halocin H7 decreases infarct size and ectopic beats after myocardial reperfusion in dogs. *J Physiol* 509P:148P
- Allen MA, Goh F, Leuko S, Echigo A, Mizuki T, Usami R, Kamekura M, Neilan BA, Burns BP (2008) *Haloferax elongans* sp. nov. and *Haloferax mucosum* sp. nov., isolated from microbial mats from Hamelin pool, Shark Bay, Australia. *Int J Syst Evol Microbiol* 58:798–802
- Amann G, Stetter KO, Llobet-Brossa E, Amann R, Antón J (2000) Direct proof for the presence and expression of two 5 % different 16S rRNA genes in individual cells of *Haloarcula marismortui*. *Extremophiles* 4:373–376
- Amoozegar MA, Makhdoumi-Kakhki A, Shahzede Fazeli SA, Azarbaijani R, Ventosa A (2012) *Halopenitus persicus* gen. nov., sp. nov. an archaeon from an inland salt lake. *Int J Syst Evol Microbiol* 62:1932–1936
- Anderson I, Tindall BJ, Pomrenke H, Göker M, Lapidus A, Nolan M, Copeland A, Glavina del Rio T, Chen F, Tice H, Chen JF, Lucas S, Chertkov O, Bruce D, Brettin T, Detter JC, Han C, Goodwin L, Land M, Hauser L, Chang YJ, Jeffries CD, Pitluck S, Pati A, Mavromatis K, Ivanova N, Ovchinnikova G, Chen A, Palaniappan K, Chain P, Rohde M, Bristow J, Eisen JA, Markowitz V, Hugenholtz P, Kyrpides NC, Klenk HP (2009) Complete genome sequence of *Halorhabdus utahensis* type strain (AX-2^T). *Stand Genomic Sci* 1:218–225
- Anderson I, Scheuner C, Göker M, Mavromatis K, Hooper SD, Porat I, Klenk H-P, Ivanova N, Kyrpides N (2011) Novel insights into the diversity of catabolic metabolism from ten haloarchaeal genomes. *PLoS One* 6:e20237
- Anderson I, Tindall BJ, Rohde M, Lucas S, Han J, Lapidus A, Cheng J-F, Goodwin L, Pitluck S, Peters L, Pati A, Mikhailova N, Pagani I, Teshima H, Han C, Tapia R, Land M, Woyke T, Klenk H-P, Kyrpides N, Ivanova N (2012) Complete genome sequence of *Halopiger xanaduensis* type strain (SH-6^T). *Stand Genomic Sci* 6:31–42
- Angelini R, Corral P, Lopalco P, Ventosa A, Corcelli A (2012) Novel ether lipid cardiolipins in archaeal membranes of extreme haloalkaliphiles. *Biochim Biophys Acta* 1818:1365–1373
- Antón J, Meseguer I, Rodríguez-Valera F (1988) Production of an extracellular polysaccharide by *Haloferax mediterranei*. *Appl Environ Microbiol* 54:2381–2386
- Antunes A, Tiborda M, Huber R, Moissl C, Nobre MF, da Costa MS (2008) *Halorhabdus tiamatea* sp. nov., a non-pigmented, extremely

- halophilic archaeon from a deep-sea, hypersaline anoxic basin of the Red Sea, and emended description of the genus *Halorhabdus*. *Int J Syst Evol Microbiol* 58:215–220
- Antunes A, Alam I, Bajic VB, Stingl U (2011) Genome sequence of *Halorhabdus tiamatea*, the first archaeon isolated from a deep-sea anoxic brine lake. *J Bacteriol* 193:4553–4554
- Aponte M, Blaiotta G, Francesca N, Moschetti G (2010) Could halophilic archaea improve the traditional salted anchovies (*Engraulis encrasicolus* L.) safety and quality? *Lett Appl Microbiol* 51:697–703
- Asker D, Ohta Y (1999) Production of canthaxanthin by extremely halophilic bacteria. *J Biosci Bioeng* 88:617–621
- Asker D, Ohta Y (2002a) *Haloferax alexandrinus* sp. nov., an extremely halophilic canthaxanthin-producing archaeon from a solar saltern in Alexandria (Egypt). *Int J Syst Evol Microbiol* 52:729–738
- Asker D, Ohta Y (2002b) Production of canthaxanthin by *Haloferax alexandrinus* under non-aseptic conditions and a simple, rapid method for its extraction. *Appl Microbiol Biotechnol* 58:743–750
- Atanasova NS, Roine E, Oren A, Bamford DH, Oksanen HM (2012) Global network of specific virus-host interactions in hypersaline environments. *Environ Microbiol* 14:426–440
- Bailey DG, Birbir M (1996) The impact of halophilic organisms on the grain quality of brine cured hides. *J Am Leather Chem Assoc* 91:47–51
- Bakke P, Carney N, DeLoache W, Gearing M, Ingvorsen K, Lotz M, McNair J, Penumetcha P, Simpson S, Voss L, Win M, Heyer LJ, Campbell AM (2009) Evaluation of three automated genome annotations for *Halorhabdus utahensis*. *PLoS One* 4:e6291
- Baliga NS, Bonneau R, Facciotti MT, Pan M, Glusman G, Deutsch EW, Shannon P, Chiu Y, Sting Weng R, Richie Gan R, Hung P, Date SV, Marcotte E, Hood L, Ng WV (2004) Genome sequence of *Haloarcula marismortui*: a halophilic archaeon from the Dead Sea. *Genome Res* 14:2221–2234
- Bamford DH, Ravantti JJ, Rönnholm G, Laurinavičius S, Kukkaro P, Dyll-Smith M, Somerharju P, Kalkkinen N, Bamford JKH (2005) Constituents of SH1, a novel lipid-containing virus infecting the halophilic euryarchaeon *Haloarcula hispanica*. *J Virol* 79:9097–9107
- Bath C, Dyll-Smith ML (1998) His1, an archaeal virus of the *Fuselloviridae* family that infects *Haloarcula hispanica*. *J Virol* 72:9392–9395
- Bath C, Cukalac T, Porter K, Dyll-Smith ML (2006) His1 and His2 are distantly related, spindle-shaped haloviruses belonging to the novel virus group, Salterprovirus. *Virology* 350:228–239
- Ben-Mahrez K, Thierry D, Sorokine I, Danna-Muller A, Kohiyama M (1988) Detection of circulating antibodies against *c-myc* protein in cancer patient sera. *Br J Cancer* 57:529–534
- Ben-Mahrez K, Sorokine I, Thierry D, Kawasumi T, Ishii S, Salmon R, Kohiyama M (1991) An archaeobacterial antigen used to study immunological human response to *c-myc* oncogen product. In: Rodriguez-Valera F (ed) General and applied aspects of halophilic microorganisms. Plenum, New York, pp 367–372
- Bertrand JC, Almallah M, Acquaviva M, Mille G (1990) Biodegradation of hydrocarbons by an extremely halophilic archaeobacterium. *Lett Appl Microbiol* 11:260–263
- Betlach MC, Leong D, Boyer HW (1986) Bacterio-opsin gene expression in *Halobacterium halobium*. *Syst Appl Microbiol* 7:83–89
- Birbir M, Eryilmaz S, Ogan A (2004) Prevention of halophilic microbial damage on brine cured hides by extremely halophilic halocin producer strains. *J Soc Leather Technol Chem* 88:99–104
- Birge RR, Gillespie NB, Izaguirre EW, Kusnetzow A, Lawerence AF, Singh D, Song QW, Schmidt E, Stuart JA, Seetharaman S, Wise KJ (1999) Biomolecular electronics: protein-based associative processors and volumetric memories. *J Phys Chem B* 103:10746–10766
- Bolhuis H, te Poele EM, Rodriguez-Valera F (2004) Isolation and cultivation of Walsby's square archaeon. *Environ Microbiol* 6:1287–1291
- Bolhuis H, Palm P, Wende A, Falb M, Rampp M, Rodriguez-Valera F, Pfeiffer F, Oesterhelt D (2006) The genome of the square archaeon *Haloquadratum walsbyi*: life at the limits of water activity. *BMC Genomics* 7:169
- Bonelo C, Ventosa A, Megias M, Ruiz-Berraquero F (1984) The sensitivity of halobacteria to antibiotics. *FEMS Microbiol Lett* 21:341–345
- Bonfá MRL, Grossman MJ, Mellado E, Durrant LR (2011) Biodegradation of aromatic hydrocarbons by Haloarchaea and their use for the reduction of the chemical oxygen demand of hypersaline petroleum produced water. *Chemosphere* 84:1671–1676
- Bowers KJ, Wiegel J (2011) Temperature and pH optima of extremely halophilic archaea: a mini-review. *Extremophiles* 15:119–128
- Briones C, Amils R (2000) Nucleotide sequence of the 23S rRNA from *Haloferax mediterranei* and phylogenetic analysis of halophilic archaea based on LSU rRNA. *Syst Appl Microbiol* 23:124–131
- Brito-Echeverría J, López-López A, Yarza P, Antón J, Rosselló-Mora R (2007) Occurrence of *Halococcus* spp. in the nostrils salt glands of the seabird *Calonectris diomedea*. *Extremophiles* 13:557–565
- Burns DG, Camakaris HM, Janssen PH, Dyll-Smith ML (2004a) Cultivation of Walsby's square haloarchaeon. *FEMS Microbiol Lett* 238:469–473
- Burns DG, Camakaris HM, Janssen PH, Dyll-Smith ML (2004b) Combined use of cultivation-dependent and cultivation-independent methods indicates that members of most haloarchaeal groups in an Australian crystallizer pond are cultivable. *Appl Environ Microbiol* 70:5258–5265
- Burns DG, Janssen PH, Itoh T, Kamekura M, Li Z, Jensen G, Rodríguez-Valera F, Bolhuis H, Dyll-Smith ML (2007) *Haloquadratum walsbyi* gen. nov., sp. nov., the square haloarchaeon of Walsby, isolated from saltern crystallizers in Australia and Spain. *Int J Syst Evol Microbiol* 57:387–392
- Burns DG, Janssen PH, Itoh T, Minegishi H, Usami R, Kamekura M, Dyll-Smith ML (2010a) *Natronomonas moolapensis* sp. nov., non-alkaliphilic isolates recovered from a solar saltern crystallizer pond, and emended description of the genus *Natronomonas*. *Int J Syst Evol Microbiol* 60:1173–1176
- Burns DG, Janssen PH, Itoh T, Kamekura M, Echigo A, Dyll-Smith ML (2010b) *Halonotius pteroides* gen. nov., sp. nov., an extremely halophilic archaeon recovered from a saltern crystallizer. *Int J Syst Evol Microbiol* 60:1196–1199
- Burns B, Gudhka RK, Neilan BA (2012) Genome sequence of the halophilic archaeon *Halococcus hamelinensis*. *J Bacteriol* 194:2100–2101
- Castillo AM, Gutiérrez MC, Kamekura M, Xue Y, Ma Y, Cowan DA, Jones BE, Grant WD, Ventosa A (2006a) *Halorubrum orientale* sp. nov., a halophilic archaeon isolated from Lake Ejinor, Inner Mongolia, China. *Int J Syst Evol Microbiol* 56:2559–2563
- Castillo AM, Gutiérrez MC, Kamekura M, Ma Y, Cowan DA, Jones BE, Grant WD, Ventosa A (2006b) *Halovivax asiaticus* gen. nov., sp. nov., a novel extremely halophilic archaeon isolated from inner Mongolia, China. *Int J Syst Evol Microbiol* 56:765–770
- Castillo AM, Gutiérrez MC, Kamekura M, Xue Y, Ma Y, Cowan DA, Jones BE, Grant WD, Ventosa A (2006c) *Natrinema ejinorensis* sp. nov., isolated from a saline lake in inner Mongolia, China. *Int J Syst Evol Microbiol* 56:2683–2687
- Castillo AM, Gutiérrez MC, Kamekura M, Xue Y, Ma Y, Cowan DA, Jones BE, Grant WD, Ventosa A (2006d) *Halostagnicola larsenii* gen. nov., sp. nov., an extremely halophilic archaeon from a saline lake in inner Mongolia, China. *Int J Syst Evol Microbiol* 56:1519–1524
- Castillo AM, Gutiérrez MC, Kamekura M, Xue Y, Ma Y, Cowan DA, Jones BE, Grant WD, Ventosa A (2007a) *Halorubrum ejinorensis* sp. nov., isolated from Lake Ejinor, inner Mongolia, China. *Int J Syst Evol Microbiol* 57:2538–2542
- Castillo AM, Gutiérrez MC, Kamekura M, Xue Y, Ma Y, Cowan DA, Jones BE, Grant WD, Ventosa A (2007b) *Halovivax ruber* sp. nov., an extremely halophilic archaeon isolated from Lake Xilinhot, inner Mongolia, China. *Int J Syst Evol Microbiol* 57:1024–1027
- Chaga G, Porath J, Illíni T (1993) Isolation and purification of amyloglucosidase from *Halobacterium sodomense*. *Biomed Chromatogr* 7:256–261
- Chen Z, Birge RR (1993) Protein-based artificial retinas. *Trends Biotechnol* 11:292–300
- Cheung J, Danna KJ, O'Connor EM, Price LB, Shand RF (1997) Isolation, sequence, and expression of the gene encoding halocin H4, a bacteriocin from the halophilic archaeon *Haloferax mediterranei* R4. *J Bacteriol* 179:548–551
- Childs TS, Webley WC (2012) In vitro assessment of halobacterial gas vesicles as a *Chlamydia* vaccine display and delivery system. *Vaccine* 30:5942–5948

- Chu L-K, Yen C-W, El-Sayed MA (2010) Bacteriorhodopsin-based photo-electrochemical cell. *Biosens Bioelectron* 26:620–626
- Collins MD, Tindall BJ (1987) Occurrence of menaquinones and some novel methylated menaquinones in the alkaliphilic, extremely halophilic archaeobacterium *Natronobacterium gregoryi*. *FEMS Microbiol Lett* 43:307–312
- Collins MD, Ross HNM, Tindall BJ, Grant WD (1981) Distribution of isoprenoid quinones in halophilic bacteria. *J Appl Bacteriol* 50:559–565
- Colwell RR, Litchfield CD, Vreeland RH, Kiefer LA, Gibbons NE (1979) Taxonomic studies of red halophilic bacteria. *Int J Syst Bacteriol* 29:379–399
- Cuadros-Orellana S, Pohlschröder M, Durrant LR (2006) Isolation and characterization of halophilic archaea able to grown in aromatic compounds. *Int Biodeter Biodegr* 57:151–154
- Cui H-L, Tohty D, Zhou P-J, Liu S-J (2006a) *Halorubrum lipolyticum* sp. nov. and *Halorubrum aidingense* sp. nov., isolated from two salt lakes in Xin-Jiang, China. *Int J Syst Evol Microbiol* 56:1631–1634
- Cui H-L, Tohty D, Feng J, Zhou P-J, Liu S-J (2006b) *Natronorubrum aibiense* sp. nov., an extremely halophilic archaeon isolated from Aibi salt lake in Xin-Jiang, China, and emended description of the genus *Natronorubrum*. *Int J Syst Evol Microbiol* 56:1515–1517
- Cui H-L, Tohty D, Zhou P-J, Liu S-J (2006c) *Haloterrigena longa* sp. nov. and *Haloterrigena limicola* sp. nov., extremely halophilic archaea isolated from a salt lake. *Int J Syst Evol Microbiol* 56:1837–1840
- Cui H-L, Lin Z-Y, Dong Y, Zhou P-J, Liu S-J (2007a) *Halorubrum litoreum* sp. nov., an extremely halophilic archaeon from a solar saltern. *Int J Syst Evol Microbiol* 57:2204–2206
- Cui H-L, Tohty D, Liu H-C, Liu S-J, Oren A, Zhou P-J (2007b) *Natronorubrum sulfidifaciens* sp. nov., an extremely haloalkaliphilic archaeon isolated from Aiding salt lake in Xin-Jiang, China. *Int J Syst Evol Microbiol* 57:738–740
- Cui H-L, Zhou P-J, Oren A, Liu S-L (2009) Intraspecific polymorphism of 16S rRNA genes in two halophilic archaeal genera, *Haloarcula* and *Halomicrobium*. *Extremophiles* 13:31–37
- Cui H-L, Sun F-F, Gao X, Dong Y, Xu X-W, Zhou Y-G, Liu H-C, Oren A, Zhou P-J (2010a) *Haladaptatus litoreus* sp. nov., an extremely halophilic archaeon from a marine solar saltern, and emended description of the genus *Haladaptatus*. *Int J Syst Evol Microbiol* 60:1085–1089
- Cui H-L, Gao X, Sun F-F, Dong Y, Xu X-W, Zhou Y-G, Liu H-C, Oren A, Zhou P-J (2010b) *Halogramum rubrum* gen. nov., sp. nov., a halophilic archaeon isolated from a marine solar saltern. *Int J Syst Evol Microbiol* 60:1366–1371
- Cui H-L, Gao X, Li X-Y, Xu X-W, Zhou Y-G, Liu H-C, Zhou P-J (2010c) *Haloplanus vescus* sp. nov., an extremely halophilic archaeon from a marine solar saltern, and emended description of the genus *Haloplanus*. *Int J Syst Evol Microbiol* 60:1824–1827
- Cui H-L, Gao X, Li X-Y, Xu X-W, Zhou Y-G, Liu H-C, Zhou P-J (2010d) *Halosarcina limi* sp. nov., a halophilic archaeon from a marine solar saltern, and emended description of the genus *Halosarcina*. *Int J Syst Evol Microbiol* 60:2462–2466
- Cui H-L, Gao X, Yang X, Xu X-W (2010e) *Halorussus rarus* gen. nov., sp. nov., a new member of the family *Halobacteriaceae* isolated from a marine solar saltern. *Extremophiles* 14:493–499
- Cui H-L, Yang X, Gao X, Li X-Y, Xu X-W, Zhou Y-G, Liu H-C, Zhou P-J (2010f) *Halogeometricum rufum* sp. nov., a halophilic archaeon from a marine solar saltern, and emended description of the genus *Halogeometricum*. *Int J Syst Evol Microbiol* 60:2613–2617
- Cui H-L, Li X-Y, Gao X, Xu X-W, Zhou Y-G, Liu H-C, Oren A, Zhou P-J (2010g) *Haloplagius inordinatus* gen. nov., sp. nov., a new member of the family *Halobacteriaceae* isolated from a marine saltern. *Int J Syst Evol Microbiol* 60:2089–2093
- Cui H-L, Gao X, Yang X, Xu X-W (2011a) *Haloplanus aerogenes* sp. nov., an extremely halophilic archaeon from a marine solar saltern. *Int J Syst Evol Microbiol* 61:965–968
- Cui H-L, Gao X, Yang X, Xu X-W (2011b) *Halolamina pelagica* gen. nov., sp. nov., a new member of the family *Halobacteriaceae*. *Int J Syst Evol Microbiol* 61:1617–1621
- Cui H-L, Yang X, Mou Y-Z (2011c) *Salinarchaeum laminariae* gen. nov., sp. nov.: a new member of the family *Halobacteriaceae* isolated from salted brown alga *Laminaria*. *Extremophiles* 15:625–631
- Cui H-L, Yang X, Gao X, Xu X-W (2011d) *Halobellus clavatus* gen. nov., sp. nov. and *Halorientalis regularis* gen. nov., sp. nov., two new members of the family *Halobacteriaceae*. *Int J Syst Evol Microbiol* 61:2682–2689
- Cui H-L, Yang X, Gao X, Xu X-W (2011e) *Halogramum gelatinilyticum* sp. nov. and *Halogramum amylolyticum* sp. nov., isolated from a marine solar saltern, and emended description of the genus *Halogramum*. *Int J Syst Evol Microbiol* 61:911–915
- Cui H-L, Yang X, Zhou Y-G, Liu H-C, Zhou P-J, Dyll-Smith ML (2012a) *Halobellus limi* sp. nov. and *Halobellus salinus* sp. nov., isolated from two marine solar salterns. *Int J Syst Evol Microbiol* 62:1307–1313
- Cui H-L, Mou Y-Z, Yang X, Zhou Y-G, Liu H-C, Zhou P-J (2012b) *Halorubellus salinus* gen. nov., sp. nov. and *Halorubellus litoreus* sp. nov., novel halophilic archaea isolated from a marine solar saltern. *Syst Appl Microbiol* 35:30–34
- Cyplik P, Grajek W, Marecik R, Króliczak P, Dembczyński R (2007) Application of a membrane bioreactor to denitrification of brine. *Desalination* 207:134–143
- Cyplik P, Czaczuk K, Piotrowska-Cyplik A, Marecik R, Grajek W (2010) Removal of nitrates from brine using *Haloferax mediterranei* archaeon. *Environ Prot Eng* 36:5–16
- Daniels LL, Wais AC (1984) Restriction and modification of halophage S45 in *Halobacterium*. *Curr Microbiol* 10:133–136
- Daniels LL, Wais AC (1990) Ecophysiology of bacteriophage S5100 infecting *Halobacterium cutirubrum*. *Appl Environ Microbiol* 56:3605–3608
- Daniels JJ, Wais AC (1998) Virulence in phage populations infecting *Halobacterium cutirubrum*. *FEMS Microbiol Ecol* 25:129–134
- Danon A, Stoeckenius W (1974) Photophosphorylation in *Halobacterium halobium*. *Proc Natl Acad Sci USA* 71:1234–1238
- DasSarma P, DasSarma S (2008) On the origin of prokaryotic “species”: the taxonomy of halophilic Archaea. *Saline Systems* 4:5
- DasSarma S, Capes M, DasSarma P (2008) Haloarchaeal megaplasmids. *Microbiol Monogr* 11:3–30
- DasSarma SL, Capes MD, DasSarma P, DasSarma S (2010) HaloWeb: the haloarchaeal genomes database. *Saline Systems* 6:12
- De Rosa M, Gambacorta A, Nicolaus B, Ross HNM, Grant WD, Bu'Lock JL (1982) An asymmetric archaeobacterial diether lipid from alkaliphilic halophiles. *J Gen Microbiol* 128:343–348
- De Rosa M, Gambacorta A, Nicolaus B, Grant WD (1983) A C25, C25 diether core lipid from archaeobacterial haloalkaliphiles. *J Gen Microbiol* 129:2333–2337
- Dees C, Oliver JD (1977) Growth inhibition of *Halobacterium cutirubrum* by cerulenin, a potent inhibitor of fatty acid synthesis. *Biochem Biophys Res Commun* 78:36–44
- Denner EBM, McGenity TJ, Busse HJ, Grant WD, Wanner G, Stan-Lotter H (1994) *Halococcus salifodinae* sp. nov., an archaeal isolate from an Austrian salt mine. *Int J Syst Bacteriol* 44:774–780
- Dennis PB, Shimmin LC (1997) Evolutionary divergence and salinity-mediated selection in halophilic archaea. *Microbiol Mol Biol Rev* 61:90–114
- Danon A, Stoeckenius W (1974) Photophosphorylation in *Halobacterium halobium*. *Proc Natl Acad Sci USA* 71:1234–1238
- Dinçer AR, Kargı F (2001) Performance of rotating biological disc system treating saline wastewater. *Process Biochem* 36:901–906
- Dundas ID, Larsen H (1962) The physiological role of the carotenoid pigments of *Halobacterium salinarium*. *Arch Microbiol* 44:233–239
- Dussault HP (1956a) Study of red halophilic bacteria in solar salt and salted fish: I. effect of Bacto-oxgall. *J Fish Res Bd Canada* 13:183–194
- Dussault HP (1956b) Study of red halophilic bacteria in solar salt and salted fish: II. Bacto-oxgall as a selective agent for differentiation. *J Fish Res Bd Canada* 13:195–199
- Dyll-Smith ML (2008) The halo handbook: protocols for halobacterial genetics. Version 7, March 2008. http://www.haloarchaea.com/resources/halohandbook/halohandbook_2008_v7.pdf
- Dyll-Smith M, Tang S-L, Bath C (2003) Haloarchaeal viruses: how diverse are they? *Res Microbiol* 154:309–313
- Eichler J (2001) Biotechnological uses of archaeal extremozymes. *Biotechnol Adv* 19:261–278

- Elazari-Volcani B (1957) Genus XII. *Halobacterium*. In: Breed RS, Murray EGD, Smith NR (eds) *Bergey's manual of determinative bacteriology*, 7th edn. Williams & Wilkins, Baltimore, pp 207–212
- Elevi Bardavid R, Mana L, Oren A (2007) *Haloplanus natans* gen. nov., sp. nov., an extremely halophilic gas-vacuolate archaeon from Dead Sea—Red Sea water mixtures in experimental mesocosms. *Int J Syst Evol Microbiol* 57:780–783
- Ellis DG, Bizzoco RW, Kelley ST (2008) Halophilic archaea isolated from geothermal steam vent aerosols. *Environ Microbiol* 10:1582–1590
- Elshahed MS, Savage KN, Oren A, Gutierrez MC, Ventosa A, Krumholz LR (2004) *Haloferax sulfurifontis* sp. nov., a halophilic archaeon isolated from a sulfide- and sulfur-rich spring. *Int J Syst Evol Microbiol* 54:2275–2279
- Emerson D, Chauhan S, Oriel P, Breznak JA (1994) *Haloferax* sp. D1227, a halophilic archaeon capable of growth on aromatic compounds. *Arch Microbiol* 161:445–452
- Enache M, Itoh T, Fukushima T, Usami R, Dumitru L, Kamekura M (2007a) Phylogenetic relationships within the family *Halobacteriaceae* inferred from *rpoB* gene and protein sequences. *Int J Syst Evol Microbiol* 57:2289–2295
- Enache M, Itoh T, Kamekura M, Teodosiu G, Dumitru L (2007b) *Haloferax prahovense* sp. nov., an extremely halophilic archaeon isolated from a Romanian salt lake. *Int J Syst Evol Microbiol* 57:393–397
- Falb M, Pfeiffer F, Palm P, Rodewald K, Hickmann V, Tittor J, Oesterhelt D (2005) Living with two extremes: conclusions from the genome sequence of *Natronomonas pharaonis*. *Genome Res* 15:1336–1343
- Falb M, Müller K, Königsmäier L, Oberwinkler T, Horn P, von Gronau S, Gonzalez O, Pfeiffer F, Bornberg-Bauer E, Oesterhelt D (2008) Metabolism of halophilic archaea. *Extremophiles* 12:177–196
- Fan H, Xue Y, Ma Y, Ventosa A, Grant WD (2004) *Halorubrum tibetense* sp. nov., a novel haloalkaliphilic archaeon from Lake Zabuye in Tibet, China. *Int J Syst Evol Microbiol* 54:1213–1216
- Feng J, Zhou P-J, Liu S-J (2004) *Halorubrum xinjiangense* sp. nov., a novel halophile isolated from saline lakes in China. *Int J Syst Evol Microbiol* 54:1789–1791
- Feng J, Zhou P, Zhou Y-G, Liu S-J, Warren-Rhodes K (2005) *Halorubrum alkaliphilum* sp. nov., a novel haloalkaliphile isolated from a soda lake in Xinjiang, China. *Int J Syst Evol Microbiol* 55:149–152
- Feng J, Liu B, Zhang Z, Ren Y, Li Y, Gan F, Huang Y, Chen X, Shen P, Wang L, Tang B, Tang X-F (2012) The complete genome sequence of *Natrialba* sp. J7-2, a haloarchaeon capable of growth on synthetic media without amino acid supplements. *PLoS One* 7:e41621
- Fernandez-Castillo R, Rodriguez-Valera F, Gonzales-Ramos J, Ruiz-Berraquero F (1986) Accumulation of poly(β -hydroxybutyrate) by halobacteria. *Appl Environ Microbiol* 51:214–216
- Fish SA, Shepherd TJ, McGenity TJ, Grant WD (2002) Recovery of 16S ribosomal RNA gene fragments from ancient halite. *Nature* 417:432–436
- Forterre P, Elie C, Kohiyama M (1984) Aphidicolin inhibits growth and DNA synthesis in halophilic archaeobacteria. *J Bacteriol* 159:800–802
- Forterre P, Nadal M, Elie C, Mirambeau G, Jaxel C, Duguet M (1986) Mechanisms of DNA synthesis and topoisomerisation in archaeobacteria—reverse gyration *in vitro* and *in vivo*. *Syst Appl Microbiol* 7:67–71
- Franzmann PD, Stackebrandt E, Sanderson K, Volkman JK, Cameron DE, Stevenson PL, McMeekin TA, Burton HR (1988) *Halobacterium lacusprofundi* sp. nov., a halophilic bacterium isolated from Deep Lake, Antarctica. *System Appl Microbiol* 11:20–27
- Fu WJ, Oriel P (1999) Degradation of 3-phenylpropionic acid by *Haloferax* sp. D1227. *Extremophiles* 3:45–53
- Fukushima T, Usami R, Kamekura M (2007) A traditional Japanese-style salt field is a niche for haloarchaeal strains that can survive in 0.5% salt solution. *Saline Syst* 3:2
- Gadelle D, Forterre P (1994) DNA intercalating drugs inhibit positive supercoiling induced by novobiocin in halophilic archaea. *FEMS Microbiol Lett* 123:161–166
- Galinski EA, Tindal BJ (1992) Biotechnological prospects for halophiles and halotolerant micro-organisms. In: Herbert RA, Sharp RJ (eds) *Molecular biology*. Blackie Glasgow/Chapman, New York, p 114
- Gibbons NE (1974) Family V. *Halobacteriaceae* fam. nov. In: Buchanan RE, Gibbons NE (eds) *Bergey's manual of determinative bacteriology*, 8th edn. Williams & Wilkins, Baltimore, pp 269–270
- Gibson JAE, Miller MR, Davies NW, Neill GP, Nichols DS, Volkmann JK (2005) Unsaturated diether lipids in the psychrotrophic archaeon *Halorubrum lacusprofundi*. *System Evol Microbiol* 28:19–26
- Gochner MB, Kushwaha SC, Kates M, Kushner DJ (1972) Nutritional control of pigment and isoprenoid compound formation in extremely halophilic bacteria. *Arch Mikrobiol* 84:339–349
- Goh F, Leuko S, Allen MA, Bowman JP, Kamekura M, Neilan BA, Burns BP (2006) *Halococcus hamelinensis* sp. nov., a novel halophilic archaeon isolated from stromatolites in Shark Bay, Australia. *Int J Syst Evol Microbiol* 56:1323–1329
- Gonzalez C, Gutierrez C, Ramirez C (1978) *Halobacterium vallismortis* sp. nov. an amyolytic and carbohydrate-metabolizing, extremely halophilic bacterium. *Can J Microbiol* 24:710–715
- Gonzalez O, Groanau S, Falb M, Pfeiffer F, Mendoza E, Zimmer R, Oesterhelt D (2008) Reconstruction, modeling & analysis of *Halobacterium salinarum* R-1 metabolism. *Mol Biosyst* 4:148–159
- Gonzalez RO, Higa LH, Cutrullis RA, Bilen M, Morelli I, Roncaglia DI, Corral RS, Morilla MJ, Petray PB, Romero EL (2009) Archaeosomes made of *Halorubrum tebenquichense* total polar lipids: a new source of adjuvancy. *BMC Biotechnol* 9:71
- Grant WD (2001a) Genus I. *Halobacterium* Elazari-Volcani 1957, 207^{AL} emend. Larsen and Grant 1989, 2222. In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 301–305
- Grant WD (2001b) Genus IV. *Halococcus* Schoop 1935^a, 817^{AL}. In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 311–314
- Grant WD, Kamekura M, McGenity TJ, Ventosa A (2001a) Order I. *Halobacteriales* Grant and Larsen 1989b, 495^{VP} (Effective publication: Grant and Larsen 1989a, 2216). In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 294–299
- Grant WD, Kamekura M, McGenity TJ, Ventosa A (2001b) Family I. *Halobacteriaceae* Gibbons 1974a, 269^{AL}. In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 299–301
- Grant WD, Oren A, Ventosa A (1998) Proposal of strain NCBI 13488 as neotype of *Halorubrum trapanicum*: request for an opinion. *Int J Syst Bacteriol* 48:1077–1078
- Grote M, O'Malley MA (2011) Enlightening the life sciences: the history of halobacterial and microbial rhodopsin research. *FEMS Microbiol Rev* 35:1082–1099
- Gruber C, Legat A, Pfaffenhuemer M, Radax C, Weidler G, Busse H-J, Stan-Lotter H (2004) *Halobacterium noricense* s. nov., an archaeal isolate from a bore core of an alpine Permian salt deposit, classification of *Halobacterium* sp. NRC-1 as a strain of *Halobacterium salinarum* and emended description of *Halobacterium salinarum*. *Extremophiles* 8:431–439
- Gutiérrez MC, García MT, Ventosa A, Nieto JJ, Ruiz-Berraquero F (1986) Occurrence of megaplasmids in halobacteria. *J Appl Bacteriol* 61:67–71
- Gutiérrez MC, Kamekura M, Holmes ML, Dyll-Smith ML, Ventosa A (2002) Taxonomic characterization of *Haloferax* sp. (“*H. alicantei*”) strain Aa2.2: description of *Haloferax lucentensis* sp. nov. *Extremophiles* 6:479–483
- Gutiérrez MC, Castillo AM, Kamekura M, Xue Y, Ma Y, Cowan DA, Jones BE, Grant WD, Ventosa A (2007) *Halopiger xanaduensis* gen. nov., sp. nov., an extremely halophilic archaeon isolated from saline Lake Shangmatala in inner Mongolia, China. *Int J Syst Evol Microbiol* 57:1402–1407
- Gutiérrez MC, Castillo AM, Pagaling E, Heaphy S, Kamekura M, Xue Y, Ma Y, Cowan DA, Jones BE, Grant WD, Ventosa A (2008a) *Halorubrum kocurii* sp. nov., an archaeon isolated from a saline lake. *Int J Syst Evol Microbiol* 58:2031–2035

- Gutiérrez MC, Castillo AM, Kamekura M, Ventosa A (2008b) *Haloterrigena salina* sp. nov., an extremely halophilic archaeon isolated from a salt lake. *Int J Syst Evol Microbiol* 58:2880–2884
- Gutiérrez MC, Castillo AM, Corral P, Minegishi H, Ventosa A (2010) *Natronorubrum sediminis* sp. nov., an archaeon isolated from a saline lake. *Int J Syst Evol Microbiol* 60:1802–1806
- Gutiérrez MC, Castillo AM, Corral P, Kamekura M, Ventosa A (2011) *Halorubrum aquaticum* sp. nov., an archaeon isolated from hypersaline lakes. *Int J Syst Evol Microbiol* 61:1144–1148
- Hamana K, Hamana H, Itoh T (1995) Ubiquitous occurrence of agmatine as the major polyamine within extremely halophilic archaeobacteria. *J Gen Appl Microbiol* 41:153–158
- Hamp N (2000a) Bacteriorhodopsin as a photochromic retinal protein for optical memories. *Chem Rev* 100:1755–1776
- Hamp NA (2000b) Bacteriorhodopsin: mutating a biomaterial into an optoelectronic material. *Appl Microbiol Biotechnol* 53:633–639
- Han J, Zhang F, Liu X, Li M, Liu H, Cai L, Zhang B, Chen Y, Zhou J, Hu S, Xiang H (2012) Complete genome sequence of the metabolically versatile halophilic archaeon *Haloferax mediterranei*, a poly(3-hydroxybutyrate-co-3-hydroxyvalerate) producer. *J Bacteriol* 194:4463–4464
- Hartman AL, Norais C, Badger JH, Delmas S, Haldenby S, Madupu R, Robinson J, Khouri H, Ren Q, Lowe TM, Maupin-Furlow J, Pohlschroder M, Daniels C, Pfeiffer F, Allers T, Eisen JA (2010) The complete genome sequence of *Haloferax volcanii* DS2, a model archaeon. *PLoS One* 5:e9605
- Hartmann R, Sicking H-D, Oesterheld D (1980) Anaerobic growth of halobacteria. *Proc Natl Acad Sci USA* 77:3821–3825
- Hezayen FF, Rehm BHA, Eberhardt R, Steinbüchel A (2000) Polymer production by two newly isolated extremely halophilic archaea: application of a novel corrosion-resistant bioreactor. *Appl Microbiol Biotechnol* 54:319–325
- Hezayen FF, Rehm BHA, Tindall BJ, Steinbüchel A (2001) Transfer of *Natrialba asiatica* BIT to *Natrialba taiwanensis* sp. nov. and description of *Natrialba aegyptiaca* sp. nov., a novel extremely halophilic, non-pigmented member of the Archaea from Egypt that produces extracellular poly(glutamic acid). *Int J Syst Evol Microbiol* 51:1133–1142
- Hezayen FF, Tindall BJ, Steinbüchel A, Rehm BHA (2002) Characterization of a novel halophilic archaeon, *Halobiforma haloterrestriis* gen. nov., sp. nov., and transfer of *Natronobacterium nitratireducens* to *Halobiforma nitratireducens* comb. nov. *Int J Syst Evol Microbiol* 52:2271–2280
- Hezayen FF, Gutiérrez MC, Steinbüchel A, Tindall BJ, Rehm BHA (2010) *Halopiger aswanensis* sp. nov., a polymer-producing and extremely halophilic archaeon isolated from hypersaline soil. *Int J Syst Evol Microbiol* 60:633–637
- Hilpert R, Winter J, Hammes W, Kandler O (1981) The sensitivity of archaeobacteria to antibiotics. *Zbl Bakt Hyg, I Abt Orig C* 2:11–20
- Hochstein LI, Tomlinson GA (1985) Denitrification by extremely halophilic bacteria. *FEMS Microbiol Lett* 27:329–331
- Horikoshi K, Aono R, Nakamura S (1993) The triangular halophilic archaeobacterium *Haloarcula japonica* strain TR-1. *Experientia* 49:497–502
- Hong FT (1986) The bacteriorhodopsin model membrane system as a prototype molecular computing element. *Biosystems* 19:223–236
- Hu L, Pan H, Xue Y, Ventosa A, Cowan DA, Jones BE, Grant WD, Ma Y (2008) *Halorubrum luteum* sp. nov., isolated from Lake Chagannor, inner Mongolia, China. *Int J Syst Evol Microbiol* 58:1705–1708
- Ihara K, Watanabe S, Tamura T (1997) *Haloarcula argentinensis* sp. nov. and *Haloarcula mukohataei* sp. nov., two new extremely halophilic archaea collected in Argentina. *Int J Syst Bacteriol* 47:73–77
- Inoue K, Itoh T, Ohkuma M, Kogure K (2011) *Halomarina oriensis* gen. nov., sp. nov., a halophilic archaeon isolated from a seawater aquarium. *Int J Syst Evol Microbiol* 61:942–946
- Itoh T, Yamaguchi T, Zhou P, Takashina T (2005) *Natronolimnobius baerhuensis* gen. nov., sp. nov. and *Natronolimnobius innermongolicus* sp. nov., novel haloalkaliphilic archaea isolated from soda lakes in Inner Mongolia, China. *Extremophiles* 9:111–116
- Jaakkola ST, Penttinen RK, Vilen ST, Jalasvuori M, Rönholm G, Bamford JKH, Bamford DH, Oksanen HM (2012) Closely related archaeal *Haloarcula hispanica* icosahedral viruses HHIV-2 and SH1 have nonhomologous genes encoding host recognition functions. *J Virol* 86:4734–4742
- Jääliñoja HT, Roine E, Laurinmäki P, Kivelä HM, Bamford DH, Butcher SJ (2008) Structure and host-cell interaction of SH1, a membrane-containing, halophilic euryarchaeal virus. *Proc Natl Acad Sci USA* 105:8008–8013
- Jiang X, Wang S, Cheng H, Huo Y, Zhang X, Zhu X, Han X, Ni P, Wu M (2011) Genome sequence of *Halobiforma lacisalsi* AJ5, an extremely halophilic archaeon which harbors a *bop* gene. *J Bacteriol* 193:7023–7024
- Jones AG, Ewing CM, Melvin MV (1981) Biotechnology of solar salt fields. *Hydrobiologia* 82:391–406
- Joshi JG, Guild WR, Handler P (1963) The presence of two species of DNA in some halobacteria. *J Mol Biol* 6:34–38
- Judicial Commission of the International Committee on Systematics of Prokaryotes (2003) Strain NCIMB 13488 may serve as the type strain of *Halorubrum trapanicum*. Opinion 74. *Int J Syst Evol Microbiol* 53:933
- Juez G, Rodríguez-Valera F, Ventosa A, Kushner DJ (1986) *Haloarcula hispanica* spec. nov. and *Haloferax gibbonsii* spec. nov., two new species of extremely halophilic archaeobacteria. *System Appl Microbiol* 8:75–79
- Kamekura M (2001a) Genus IX. *Natrialba* Kamekura and Dyal-Smith 1996, 625^{VP} (Effective publication: Kamekura and Dyal-Smith 1995, 347). In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol 1. The Archaea and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 325–327
- Kamekura M (2001b) Genus XIII. *Natronomonas* Kamekura, Dyal-Smith, Upasani, Ventosa and Kates 1997, 856^{VP}. In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol 1. The Archaea and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 332–333
- Kamekura M, Dyal-Smith ML (1995) Taxonomy of the family *Halobacteriaceae* and the description of two new genera *Halorubrobacterium* and *Natrialba*. *J Gen Appl Microbiol* 41:333–350
- Kamekura M, Kates M (1988) Lipids of halophilic archaeobacteria. In: Rodríguez-Valera F (ed) *Halophilic bacteria*, vol II. CRC Press, Boca Raton, pp 25–54
- Kamekura M, Kates M (1999) Structural diversity of membrane lipids in members of *Halobacteriaceae*. *Biosci Biotechnol Biochem* 63:969–972
- Kamekura M, Hamada K, Matsuzaki S (1987) Polyamine contents and amino acid decarboxylation activities of extremely halophilic archaeobacteria and some eubacteria. *FEMS Microbiol Lett* 43:301–305
- Kamekura M, Oesterheld D, Wallace R, Anderson P, Kushner DJ (1988) Lysis of halobacteria in bacto-peptone by bile acids. *Appl Environ Microbiol* 54:990–995
- Kamekura M, Dyal-Smith ML, Upasani V, Ventosa A, Kates M (1997) Diversity of alkaliphilic halobacteria: proposals for transfer of *Natronobacterium vacuolatum*, *Natronobacterium magadii*, and *Natronobacterium pharaonis* to *Halorubrum*, *Natrialba*, and *Natronomonas* gen. nov., respectively, as *Halorubrum vacuolatum* comb. nov., *Natrialba magadii* comb. nov., and *Natronomonas pharaonis* comb. nov., respectively. *Int J Syst Bacteriol* 47:853–857
- Kanai H, Kobayashi T, Aono R, Kudo T (1995) *Natronococcus amylolyticus* sp. nov., a haloalkaliphilic archaeon. *Int J Syst Bacteriol* 45:762–766
- Kargi F (2002) Enhanced biological treatment of saline wastewater by using halophilic bacteria. *Biotechnol Lett* 24:1569–1572
- Kargi F, Dinçer AR (1996) Enhancement of biological treatment performance of saline wastewater by halophilic bacteria. *Bioproc Eng* 15:51–58
- Kates M, Palameta B, Jo CN, Kushner DJ, Gibbons NE (1966) Aliphatic diether analogs of glyceride-derived lipids. IV. The occurrence of di-O-dihydrophytylglycerol ether containing lipids in extremely halophilic bacteria. *Biochemistry* 5:4092–4099
- Kates M, Moldoveanu N, Stewart LC (1993) On the revised structure of the major phospholipid of *Halobacterium salinarum*. *Biochim Biophys Acta* 1169:46–53
- Kelly M, Norgård S, Liaaen-Jensen S (1970) Bacterial carotenoids. XXXI. C₅₀ carotenoids 5. Carotenoids of *Halobacterium salinarum*, especially bacterioruberin. *Acta Chem Scand* 24:2169–2182
- Kennedy SP, Ng WV, Salzberg SL, Hood L, DasSarma S (2001) Understanding the adaptation of *Halobacterium* species NRC-1 to its extreme environment

- through computational analysis of its genome sequence. *Genome Res* 11:1641–1650
- Kharroub K, Quesada T, Ferrer R, Fuentes S, Aguilera M, Boulahrouf A, Ramos-Cormenzana A, Monteoliva-Sanchez M (2006) *Halorubrum ezemoulense* sp. nov., a halophilic archaeon isolated from Ezzemoul sabkha, Algeria. *Int J Syst Evol Microbiol* 56:1583–1588
- Kharroub K, Lizama C, Aguilera M, Boulahrouf A, Campos V, Ramos-Cormenzana A, Monteoliva-Sanchez M (2008) *Halomicrobium katesii* sp. nov., an extremely halophilic archaeon. *Int J Syst Evol Microbiol* 58:2354–2358
- Khomyakova M, Bükmez O, Thomas LK, Erb TJ, Berg IA (2011) A methylaspartate cycle in haloarchaea. *Science* 331:334–337
- Kim KK, Lee KC, Lee J-S (2011) *Halogramma salarium* sp. nov., a halophilic archaeon isolated from sea salt. *Syst Appl Microbiol* 34:576–580
- Kis-Papo T, Oren A (2000) Halocins: are they important in the competition between different types of halobacteria in saltern ponds? *Extremophiles* 4:35–41
- Kivelä HM, Roine E, Kukkaro P, Laurinavičius S, Somerharju P, Bamford DH (2006) Quantitative dissociation of archaeal virus SH1 reveals distinct capsid proteins and a lipid core. *Virology* 356:4–11
- Klein R, Baranyi U, Rössler N, Greineder B, Scholz H, Witte A (2002) *Natrialba magadii* virus Φ Ch1: first complete nucleotide sequence and functional organization of a virus infecting a haloalkaliphilic archaeon. *Mol Microbiol* 45:851–863
- Klein R, Rössler N, Iro M, Scholz H, Witte A (2012) Haloarchaeal myovirus Φ Ch1 harbours a phase variation system for the production of protein variants with distinct cell surface adhesion specificities. *Mol Microbiol* 83:137–150
- Kocur M, Hodgkiss W (1973) Taxonomic status of the genus *Halococcus* Schoop. *Int J Syst Bacteriol* 23:151–156
- Koller M, Hesse P, Bona R, Kutschera C, Atlíć A, Braunegg G (2007) Potential of various archae- and eubacterial strains as industrial polyhydroxyalkanoate producers from whey. *Macromol Biosci* 7:218–226
- Kukkaro P, Bamford DH (2009) Virus-host interactions in environments with a wide range of ionic strengths. *Environ Microbiol Rep* 1:71–77
- Kulichevskaya IS, Milekhina EI, Borezinkov IA, Zvyagintseva IS, Belyaev SS (1991) Oxidation of petroleum hydrocarbons by extremely halophilic archaeobacteria. *Microbiol (Russ)* 60:596–601
- Kushner DJ (1966) Mass-culture of red halophilic bacteria. *Biotechnol Bioeng* 8:237–245
- Kushwaha SC, Kates M (1979) Effect of glycerol on carotenogenesis in the extreme halophile, *Halobacterium cutirubrum*. *Can J Microbiol* 25:1288–1291
- Kushwaha SC, Gochnauer MB, Kushner DJ, Kates M (1974) Pigments and isoprenoid compounds in extremely and moderately halophilic bacteria. *Can J Microbiol* 20:241–245
- Kushwaha SC, Kramer JKG, Kates M (1975) Isolation and characterization of C₅₀ carotenoid pigments and other polar isoprenoids from *Halobacterium cutirubrum*. *Biochim Biophys Acta* 398:303–313
- Kushwaha SC, Juez-Pérez G, Rodríguez-Valera F, Kates M, Kushner DJ (1982) Survey of lipids of a new group of extremely halophilic bacteria from salt ponds in Spain. *Can J Microbiol* 28:1365–1372
- Lanyi JK (1974) Salt-dependent properties of proteins from extremely halophilic bacteria. *Bacteriol Rev* 38:272–290
- Lanyi JK (2004) Bacteriorhodopsin. *Ann Rev Physiol* 66:665–688
- Lanyi JK, Duschl A, Hatfield GW, May K, Oesterhelt D (1990) The primary structure of a halorhodopsin from *Natronobacterium pharaonis*. *J Biol Chem* 265:1253–1260
- Lanzotti V, Nicolaus B, Trincon A, De Rosa M, Grant WD, Gambacorta A (1989) A complex lipid with a cyclic phosphate from the archaeobacterium *Natronococcus occultus*. *Biochim Biophys Acta* 1001:31–34
- Lata DB, Chandra R, Kumar A, Misra A (2007) Effect of light on generation of hydrogen by *Halobacterium halobium*. *Int J Hydrogen Energy* 32:3293–3300
- Li Y, Xiang H, Liu J, Zhou M, Tan H (2003) Purification and biological characterization of halocin C8, a novel peptide antibiotic from *Halobacterium* strain AS7092. *Extremophiles* 7:401–407
- Lillo JG, Rodríguez-Valera F (1990) Effects of culture conditions on poly(β -hydroxybutyric acid) production by *Haloferax mediterranei*. *Appl Environ Microbiol* 56:2517–2521
- Litchfield CD (2011) Potential for industrial products from the halophilic *Archaea*. *J Ind Microbiol Biotechnol* 38:1635–1647
- Liu H, Wu Z, Li M, Zhang F, Zheng H, Han J, Liu J, Zhou J, Wang S, Xiang H (2011) Complete genome sequence of *Haloarcula hispanica*, a model haloarchaeon for studying genetics, metabolism, and virus-host interaction. *J Bacteriol* 193:6086–6087
- Lizama C, Monteoliva-Sánchez M, Suárez-García A, Roselló-Mora R, Aguilera M, Campos V, Ramos-Cormenzana A (2002) *Halorubrum tebequichense* sp. nov., a novel halophilic archaeon isolated from the Atacama Saltern, Chile. *Int J Syst Evol Microbiol* 52:149–155
- Lobasso S, Lopalco P, Mascolo G, Corcelli A (2008) Lipids of the ultra-thin square halophilic archaeon *Haloquadratum walsbyi*. *Archaea* 2:1778–1783
- López-López A, Benlloch S, Bonfá M, Rodríguez-Valera F, Mira A (2007) Intragenomic 16S rDNA divergence in *Haloarcula marismortui* is an adaptation to different temperatures. *J Mol Evol* 65:687–696
- Lynch EA, Langille MGI, Darling A, Wilbanks EG, Haltiner C, Shao KSY, Starr MO, Teiling C, Harkins TT, Edwards RA, Eisen JA, Facciotti MT (2012) Sequencing of seven haloarchaeal genomes reveals patterns of genomic flux. *PLoS One* 7:e41389
- Magrum LJ, Luehrsen KR, Woese CR (1978) Are extreme halophiles actually “bacteria”? *J Mol Evol* 11:1–8
- Makhdoumi-Kakhki A, Amoozegar MA, Ventosa A (2012a) *Haloavenus aranensis* gen. nov., sp. nov., an extremely halophilic archaeon from Aran-Bidgol salt lake. *Int J Syst Evol Microbiol* 62:1331–1336
- Makhdoumi-Kakhki A, Amoozegar MA, Bagheri M, Ramezani M, Ventosa A (2012b) *Haloarchaeobius iranensis* gen. nov., sp. nov., an extremely halophilic archaeon isolated from a saline lake. *Int J Syst Evol Microbiol* 62:1021–1026
- Malfatti S, Tindall BJ, Schneider S, Fahnrich R, Lapidus A, LaButtiti K, Copeland A, Glavina Del Rio T, Nolan M, Chen F, Lucas S, Tice H, Cheng J-F, Bruce D, Goodwin L, Pitluck S, Anderson I, Pati A, Ivanova N, Mavromatis K, Chen A, Palaniappan K, D’haeseleer P, Göker M, Bristow J, Eisen JA, Marowitz V, Hugenholtz P, Kyrpides NC, Klenk H-P, Chain P (2009) Complete genome sequence of *Haloquadratum walsbyi* type strain (PR3^T). *Stand Genomic Sci* 1:150–158
- Mancinelli RL, Hochstein LI (1986) The occurrence of denitrification in extremely halophilic bacteria. *FEMS Microbiol Lett* 35:55–58
- Mancinelli RL, Landheim R, Sánchez-Porro C, Dornmayr-Pfaffenhuemer M, Gruber C, Legat A, Ventosa A, Radax C, Ihara K, White MR, Stan-Lotter H (2008) *Halorubrum chaoviator* sp. nov., a haloarchaeon isolated from sea salt in Baja California, Mexico, Western Australia and Naxos, Greece. *Int J Syst Evol Microbiol* 59:1908–1913
- Margesin R, Schinner F (2001) Potential of halotolerant and halophilic microorganisms for biotechnology. *Extremophiles* 5:73–83
- Martin DD, Ciulla RA, Roberts MF (1999) Osmoadaptation in Archaea. *Appl Environ Microbiol* 65:1815–1825
- Martinez-Espinosa RM, Bonete MJ (2007) Bioremediation of chlorate and perchlorate salted water using *Haloferax mediterranei*. *J Biotechnol* 131S: S227
- McGenity TJ, Grant WD (1993) The haloalkaliphilic archaeon (archaeobacterium) *Natronococcus occultus* represents a distant lineage within the *Halobacteriales*, most closely related to the other haloalkaliphilic lineage (*Natronobacterium*). *System Appl Microbiol* 16:239–243
- McGenity TJ, Grant WD (1995) Transfer of *Halobacterium saccharovororum*, *Halobacterium sodomense*, *Halobacterium trapanicum* NRC 34021 and *Halobacterium lacusprofundi* to the genus *Halorubrum* gen. nov., as *Halorubrum saccharovororum* comb. nov., *Halorubrum sodomense* comb. nov., *Halorubrum trapanicum* comb. nov., and *Halorubrum lacusprofundi* comb. nov. *System Appl Microbiol* 18:237–243
- McGenity TJ, Grant WD (2001) Genus VII. *Halorubrum* McGenity and Grant 1996, 362^{VP} (Effective publication: McGenity and Grant 1995, 241). In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey’s manual of systematic bacteriology*, vol. 1. The *Archaea* and the deeply branching and phototrophic bacteria. Springer, New York, pp 320–324
- McGenity TJ, Gemmell RT, Grant WD (1998) Proposal of a new halobacterial genus *Natrinema* gen. nov., with two species *Natrinema pellirubrum*

- nom. nov. and *Natrinema pallidum* nom. nov. *Int J Syst Bacteriol* 48:1187–1196
- McGenity TJ, Gemmell RT, Grant WD, Stan-Lotter H (2000) Origins of halophilic microorganisms in ancient salt deposits. *Environ Microbiol* 2:243–260
- McGenity TJ, Grant WD, Kamekura M (2001) Genus X. *Natrinema* McGenity, Gemmell and Grant 1998, 1194^{VP}. In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol. 1. The *Archaea* and the deeply branching and phototrophic bacteria. Springer, New York, pp 327–329
- Mei YJ, Chen D, Sun DC, Chen D, Yang Y, Shen P, Chen XD (2007) Induction and preliminary characterization of a novel halophage SNJ1 from lysogenic *Natrinema* sp. F5. *Can J Microbiol* 53:1106–1110
- Meseguer I, Rodríguez-Valera F (1986) Effect of halocin H4 on cells of *Halobacterium halobium*. *J Gen Microbiol* 132:3061–3068
- Meseguer I, Rodríguez-Valera F, Ventosa A (1986) Antagonistic interactions among halobacteria due to halocin production. *FEMS Microbiol Lett* 36:177–182
- Meseguer I, Torreblanca M, Rodríguez-Valera F (1991) Mode of action of halocins H4 and H6: are they effective against the adaptation to high salt environments? In: Rodríguez-Valera F (ed) *General and applied aspects of halophilic microorganisms*. Plenum, New York, pp 157–164
- Meseguer I, Torreblanca M, Konishi T (1995) Specific inhibition of the halobacterial Na⁺/H⁺ antiporter by halocin H6. *J Biol Chem* 270:6450–6455
- Mevarech M, Frolow F, Gloss LM (2000) Halophilic enzymes: proteins with a grain of salt. *Biophys Chem* 86:155–164
- Minegishi H, Mizuki T, Echigo A, Fukushima T, Kamekura M, Usami R (2008) Acidophilic haloarchaeal strains are isolated from various solar salts. *Saline Systems* 4:16
- Minegishi H, Kamekura M, Itoh T, Echigo A, Usami R, Hashimoto T (2010a) Further refinement of the phylogeny of the *Halobacteriaceae* based on the full-length RNA polymerase subunit B' (*rpoB'*) gene. *Int J Syst Evol Microbiol* 60:2398–2408
- Minegishi H, Echigo A, Nagaoka S, Kamekura M, Usami R (2010b) *Halarchaeum acidiphilum* gen. nov., sp. nov., a moderately acidophilic haloarchaeon isolated from commercial solar salt. *Int J Syst Evol Microbiol* 60:2513–2516
- Minegishi H, Kamekura M, Kitajima-Ihara T, Nakasone K, Echigo A, Shimane Y, Usami R, Itoh T, Ihara K (2012a) Gene orders in the upstream of 16S rRNA genes divide genera of the family *Halobacteriaceae* into two groups. *Int J Syst Evol Microbiol* 62:188–195
- Minegishi H, Echigo A, Shimane Y, Kamekura M, Tanasupawat S, Visessanguan W, Usami R (2012b) *Halobacterium piscisalsi* Yachai *et al.* 2008 is a later heterotypic synonym of *Halobacterium salinarum* Elazari-Volcani 1957. *Int J Syst Evol Microbiol* 62:2160–2162
- Montalvo-Rodríguez R, Vreeland RH, Oren A, Kessel M, Betancourt C (1998) *Halogeometricum borinquense* gen. nov., sp. nov., a novel halophilic archaeon from Puerto Rico. *Int J Syst Evol Microbiol* 48:1305–1312
- Montalvo-Rodríguez R, Lopez-Garriga J, Vreeland RH, Oren A, Ventosa A, Kamekura M (2000) *Haloterrigena thermotolerans* sp. nov., a halophilic archaeon from Puerto Rico. *Int J Syst Evol Microbiol* 50:1065–1071
- Montero CG, Ventosa A, Rodríguez-Valera F, Kates M, Moldoveanu N, Ruiz-Berraquero F (1989) *Halococcus saccharolyticus* sp. nov., a new species of extremely halophilic non-alkaliphilic cocci. *Syst Appl Microbiol* 12:167–171
- Morth S, Tindall BJ (1985) Variation of polar lipid composition within haloalkaliphilic archaeobacteria. *Syst Appl Microbiol* 6:247–250
- Mullakhanbhai MF, Larsen H (1975) *Halobacterium volcanii* spec. nov., a Dead Sea halobacterium with a moderate salt requirement. *Arch Microbiol* 104:207–214
- Müller JA, DasSarma S (2005) Genomic analysis of anaerobic respiration in the archaeon *Halobacterium* sp. strain NRC-1: dimethyl sulfoxide and trimethylamine N-oxide as terminal electron acceptors. *J Bacteriol* 187:1659–1667
- Mwatha WE, Grant WD (1993) *Natronobacterium vacuolata* sp. nov., a haloalkaliphilic archaeon isolated from Lake Magadi, Kenya. *Int J Syst Bacteriol* 43:401–404
- Mylvaganam S, Dennis PP (1992) Sequence heterogeneity between the two genes encoding 16S rRNA from the halophilic archaeobacterium *Haloarcula marismortui*. *Genetics* 130:399–410
- Nagaoka S, Minegishi H, Echigo A, Usami R (2010) *Halostagnicola kamekurae* sp. nov., an extremely halophilic archaeon from solar salt. *Int J Syst Evol Microbiol* 60:2828–2831
- Nagaoka S, Minegishi H, Echigo A, Shimane Y, Kamekura M, Usami R (2011) *Halostagnicola alkaliphila* sp. nov., an alkaliphilic haloarchaeon from commercial rock salt. *Int J Syst Evol Microbiol* 61:1149–1152
- Nam Y-D, Chang H-W, Kim K-H, Roh SW, Kim M-S, Jung M-J, Lee S-W, Kim J-Y, Yoon J-H, Bae J-W (2008) Bacterial, archaeal, and eukaryal diversity in the intestines of Korean people. *J Microbiol* 46:491–501
- Namwong S, Tanasupawat S, Visessanguan W, Kudo T, Itoh T (2007) *Halococcus thailandensis* sp. nov., from fish sauce in Thailand. *Int J Syst Evol Microbiol* 57:2199–2203
- Namwong S, Tanasupawat S, Kudo T, Itoh T (2011) *Haloarcula salaria* sp. nov. and *Haloarcula tradensis* sp. nov., isolated from salt in Thai fish sauce. *Int J Syst Evol Microbiol* 61:231–236
- Ng WV, Ciuffo SA, Smith TM, Bumgarner RE, Baskin D, Faust J, Hall B, Lorentz C, Seto J, Slagel J, Hood L, DasSarma S (1998) Snapshot of a large dynamic replicon in a halophilic archaeon: megaplasmid or minichromosome? *Genome Res* 8:1131–1141
- Ng WV, Kennedy SP, Mahairas GG, Berquist B, Pan M, Shukla HD, Lasky SR, Baliga NS, Thorsson V, Sbrogna J, Swartzell S, Weir D, Hall J, Dahl TA, Welti R, Goo YA, Leithausen B, Keller K, Cruz R, Danson MJ, Hough DW, Maddocks DG, Jablonski PE, Krebs MP, Angevine GM, Dale H, Isenbarger TA, Peck RF, Pohlschroder M, Spudich JL, Jung K-H, Alam M, Freitas T, Hou S, Daniels CJ, Dennis PP, Omer AD, Ebhardt H, Lowe TM, Liang P, Riley M, Hood L, DasSarma S (2000) Genome sequence of *Halobacterium* species NRC-1. *Proc Natl Acad Sci USA* 97:12176–12181
- Ng WV, Wu TH, Berquist BR, Coker JA, Capes M, DasSarma P, DasSarma S (2008) Letter to the editor. Genome sequences of *Halobacterium* species. *Genomics* 91:548–552
- Niemetz R, Kärcher U, Kandler O, Tindall BJ, König H (1997) The cell wall polymer of the extremely halophilic archaeon *Natronococcus occultus*. *Eur J Biochem* 249:905–911
- Norton CF (1992) Rediscovering the ecology of halobacteria. *ASM News* 58:363–367
- Nuttall SD, Dyall-Smith ML (1993a) HF1 and HF2: novel bacteriophages of halophilic archaea. *Virology* 197:678–684
- Nuttall SD, Dyall-Smith ML (1993b) Ch. 2, a novel halophilic archaeon from an Australian solar saltern. *Int J Syst Bacteriol* 43:729–734
- O'Connor EM, Shand RF (2002) Halocins and sulfolobocins: the emerging story of archaeal protein and peptide antibiotics. *J Ind Microbiol Biotechnol* 28:23–31
- Oesterhelt D (1982) Anaerobic growth of halobacteria. *Meth Enzymol* 88:417–420
- Oesterhelt D, Krippahl G (1983) Phototrophic growth of halobacteria and its use for isolation of photosynthetically-deficient mutants. *Ann Microbiol* 134B:137–150
- Oesterhelt D, Stoekenius W (1971) Rhodopsin-like protein from the purple membrane of *Halobacterium halobium*. *Nature* 233:149–152
- Oesterhelt D, Bräuchle C, Hampp N (1991) Bacteriorhodopsin: a biological model for information processing. *Quart Rev Biophys* 24:425–478
- Oren A (1983) *Halobacterium sodomense* sp. nov., a Dead Sea halobacterium with an extremely high magnesium requirement. *Int J Syst Bacteriol* 33:381–386
- Oren A (1991) Anaerobic growth of halophilic archaeobacteria by reduction of fumarate. *J Gen Microbiol* 137:1387–1390
- Oren A (1994) The ecology of the extremely halophilic archaea. *FEMS Microbiol Rev* 13:415–440
- Oren A (1996) Sensitivity of selected members of the family *Halobacteriaceae* to quinolone antimicrobial compounds. *Arch Microbiol* 165:354–358
- Oren A (2001) Genus III. *Halobaculum* Oren, Gurevich, Gemmell and Teske 1995, 752^{VP}. In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, 2nd ed., vol. 1. The *Archaea* and the deeply branching and phototrophic bacteria. Springer, New York, pp 309–311
- Oren A (2006) The order *Halobacteriales*. In: Dworkin M, Falkow S, Rosenberg E, Schleifer K-H, Stackebrandt E (eds) *The prokaryotes. A handbook on the biology of bacteria: ecophysiology and biochemistry*, vol 3. Springer, New York, pp 113–164

- Oren A (2008) Nomenclature and taxonomy of halophilic archaea—comments on the proposal by DasSarma and DasSarma for nomenclatural changes within the order *Halobacteriales*. *Int J Syst Evol Microbiol* 58:2245–2246
- Oren A (2010) Industrial and environmental applications of halophilic microorganisms. *Environ Technol* 31:825–834
- Oren A (2011) Ecology of halophiles. In: Horikoshi K (ed) *Extremophiles handbook*. Springer, Tokyo, pp 343–361
- Oren A (2012) Taxonomy of the family *Halobacteriaceae*: a paradigm for changing concepts in prokaryote systematics. *Int J Syst Evol Microbiol* 62:263–271
- Oren A, Gurevich P (1994) Production of D-lactate, acetate, and pyruvate from glycerol in communities of halophilic archaea in the Dead Sea and in saltern crystallizer ponds. *FEMS Microbiol Ecol* 14:147–156
- Oren A, Litchfield CD (1999) A procedure for the enrichment and isolation of *Halobacterium*. *FEMS Microbiol Lett* 173:353–358
- Oren A, Trüper HG (1990) Anaerobic growth of halophilic archaeobacteria by reduction of dimethylsulfoxide and trimethylamine N-oxide. *FEMS Microbiol Lett* 70:33–36
- Oren A, Ventosa A (1996) A proposal for the transfer of *Halorubrobacterium distributum* and *Halorubrobacterium coriense* to the genus *Halorubrum* as *Halorubrum distributum* comb. nov. and *Halorubrum coriense* comb. nov., respectively. *Int J Syst Bacteriol* 46:1180
- Oren A, Ginzburg M, Ginzburg BZ, Hochstein LI, Volcani BE (1990) *Haloarcula marismortui* (Volcani) sp. nov., nom. rev., an extremely halophilic bacterium from the Dead Sea. *Int J Syst Bacteriol* 40:209–210
- Oren A, Gurevich P, Gemmill RT, Teske A (1995) *Halobaculum gomorrense* gen. nov., sp. nov., a novel extremely halophilic archaeon from the Dead Sea. *Int J Syst Bacteriol* 45:747–754
- Oren A, Kamekura M, Ventosa A (1997) Confirmation of strain VKM B-1733 as the type strain of *Halorubrum distributum*. *Int J Syst Bacteriol* 47:231–232
- Oren A, Ventosa A, Gutiérrez MC, Kamekura M (1999) *Haloarcula quadrata* sp. nov., a square, motile archaeon isolated from a brine pool in Sinai (Egypt). *Int J Syst Bacteriol* 49:1149–1155
- Oren A, Montalvo-Rodríguez R, Vreeland RH (2001) Genus VI. *Halo geometricum* Montalvo-Rodríguez, Vreeland, Oren, Kessel, Betancourt and López-Garriga 1998, 1310^{VP}. In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 318–319
- Oren A, Eleví R, Watanabe S, Tamura T, Ihara K, Corcelli A (2002) *Halomicrobium mukohataei* gen. nov., comb. nov., and emended description of *Halomicrobium mukohataei*. *Int J Syst Evol Microbiol* 52:1831–1835
- Oren A, Pri-El N, Shapiro O, Siboni N (2006) Buoyancy studies in natural communities of square gas-vacuolate archaea in saltern crystallizer ponds. *Saline Systems* 2:4
- Oren A, Arahal DR, Ventosa A (2009) Emended descriptions of genera of the family *Halobacteriaceae*. *Int J Syst Evol Microbiol* 59:637–642
- Oxley APA, Lanfrancconi MP, Würdemann D, Ott S, Schreiber S, McGenity TJ, Timmis KN, Nogales B (2010) Halophilic archaea in the human intestinal mucosa. *Environ Microbiol* 12:2398–2410
- Pagaling E, Haigh RH, Grant WD, Cowan DA, Jones BE, Ma Y, Ventosa A, Heaphy S (2007) Sequence analysis of an archaeal virus isolated from a hypersaline lake in Inner Mongolia, China. *BMC Genomics* 8:410
- Papke RT, Zhaxybayeva O, Feil EJ, Sommerfeld K, Muise D, Doolittle WF (2007) Searching for species in haloarchaea. *Proc Natl Acad Sci USA* 104:14092–14097
- Papke RT, White E, Reddy P, Weigel G, Kamekura M, Minegishi H, Usami R, Ventosa A (2011) A multilocus sequence analysis approach to the phylogeny and taxonomy of the *Halobacteriales*. *Int J Syst Evol Microbiol* 61:2984–2995
- Parolis LAS, Parolis H, Paramonov NA, Boán IF, Antón J, Rodríguez-Valera F (1999) Structural studies on the acidic exopolysaccharide from *Haloferax denitrificans* ATCC 35960. *Carbohydr Res* 319:133–140
- Parolis H, Parolis LAS, Boán IF, Rodríguez-Valera F, Widmalm G, Manca MC, Jansson P-E, Sutherland IW (1996) The structure of the exopolysaccharide produced by the halophilic archaeon *Haloferax mediterranei* strain R4 (ATCC 33500). *Carbohydr Res* 295:147–156
- Pauling C (1982) Bacteriophages of *Halobacterium halobium*. Isolation from fermented fish sauce and primary characterization. *Can J Microbiol* 28:916–921
- Pecher T, Böck A (1981) In vivo susceptibility of halophilic and methanogenic organisms to protein synthesis inhibitors. *FEMS Microbiol Lett* 10:295–297
- Pesenti PT, Sikaroodi M, Gillivet PM, Sánchez-Porro C, Ventosa A, Litchfield CD (2008) *Halorubrum californiense* sp. nov., an extreme archaeal halophile isolated from a crystallizer pond at a solar salt plant in California, USA. *Int J Syst Evol Microbiol* 58:2710–2715
- Petter HFM (1931) On bacteria of salted fish. *Proc Kon Akad Wetensch Amsterdam B* 34:1417–1423
- Pfeifer F, Schuster SC, Broicher A, Falb M, Palm P, Rodewald K, Ruepp A, Soppa J, Tittor J, Oesterheld D (2008) Evolution in the laboratory: the genome of *Halobacterium salinarum* strain R1 compared to that of strain NRC-1. *Genomics* 91:335–346
- Pfeifer F, Broicher A, Gillich T, Klee K, Mejía J, Rampp M, Oesterheld D (2008a) Genome information management and integrated data analysis with HaloLex. *Arch Microbiol* 190:281–299
- Pfeifer F, Schuster SC, Broicher A, Falb M, Palm P, Rodewald K, Tittor J, Oesterheld D, Ruepp A, Soppa J (2008b) Genome sequences of *Halobacterium salinarum*: a reply. *Genomics* 91:553–554
- Pietilä MK, Laurinavičius S, Sund J, Roine E, Bamford DH (2010) The single-stranded DNA genome of novel archaeal virus *Halorubrum* pleomorphic virus 1 is enclosed in the envelope decorated with glycoprotein spikes. *J Virol* 84:788–798
- Pietilä MK, Atanasova NS, Manole V, Liljeroos L, Butcher SJ, Oksanen HM, Bamford DH (2012a) Virion architecture unifies globally distributed pleolipoviruses infecting halophilic archaea. *J Virol* 86:5067–5079
- Pietilä MK, Atanasova NS, Oksanen HM, Bamford DH (2012b) Modified coat protein forms the flexible spindle-shaped virion of haloarchaeal virus His1. *Environ Microbiol* 15:1674–1686
- Pietilä MK, Roine E, Paulin L, Kalkkinen N, Bamford DH (2009) An ssDNA virus infecting archaea: a new lineage of viruses with a membrane envelope. *Mol Microbiol* 72:307–319
- Pina M, Bize A, Forterre P, Prangishvili D (2011) The archeoviruses. *FEMS Microbiol Rev* 35:1035–1054
- Porter K, Kukkaro P, Bamford JKH, Bath C, Kivela HM, Dyall-Smith ML, Bamford DH (2005) SH1: a novel, spherical halovirus isolated from an Australian hypersaline lake. *Virology* 335:22–33
- Post FJ, Al-Harjan FA (1988) Surface activity of halobacteria and potential use in microbially enhanced oil recovery. *Syst Appl Microbiol* 11:97–101
- Price LB, Shand RF (2000) Halocin S8: a 36 amino acid microhalocin from the haloarchaeal strain S8a. *J Bacteriol* 182:4951–4958
- Pugh EL, Kates M (1994) Acylation of proteins of the archaeobacteria *Halobacterium cutirubrum* and *Methanobacterium thermoautotrophicum*. *Biochim Biophys Acta* 1196:38–44
- Purdy KJ, Cresswell-Maynard TD, Nedwell DB, McGenity TJ, Grant WD, Timmis KN, Embley TM (2004) Isolation of haloarchaea that grow at low salinities. *Environ Microbiol* 6:591–595
- Radax C, Gruber C, Stan-Lotter H (2001) Novel haloarchaeal 16S rRNA gene sequences from Alpine Permo-Triassic rock salt. *Extremophiles* 5:221–228
- Reistad R (1970) On the composition and nature of the bulk protein of extremely halophilic bacteria. *Arch Mikrobiol* 71:353–360
- Robinson JL, Pyzyrna B, Atrasz RG, Henderson CA, Morrill KL, Burd AM, DeSoucy E, Fogleman RE III, Nayolor JB, Steele SM, Elliott DR, Leyva KJ, Shand RF (2005) Growth kinetics of extremely halophilic *Archaea* (family *Halobacteriaceae*) as revealed by Arrhenius plots. *J Bacteriol* 187:923–929
- Rodríguez-Valera F (1992) Biotechnological potential of halobacteria. In: Danson MJ, Hough DW, Lunt GG (eds) *The archaeobacteria: biochemistry and biotechnology*. Biochemical society symposium no. 58. Biochemical Society, High Holborn, London, pp 135–147
- Rodríguez-Valera F, Ruiz-Berraquero F, Ramos-Cormenzana A (1979) Isolation of extreme halophiles from seawater. *Appl Environ Microbiol* 38:164–165
- Rodríguez-Valera F, Ruiz-Berraquero F, Ramos-Cormenzana A (1980) Isolation of extremely halophilic bacteria able to grow in defined inorganic media with single carbon sources. *J Gen Microbiol* 119:535–538

- Rodriguez-Valera F, Juez G, Kushner DJ (1982) Halocins: salt-dependent bacteriocins produced by extremely halophilic rods. *Can J Microbiol* 28:151–154
- Rodriguez-Valera F, Juez G, Kushner DJ (1983) *Halobacterium mediterranei* spec. nov., a new carbohydrate-utilizing extreme halophile. *Syst Appl Microbiol* 4:369–381
- Rodriguez-Valera F, Lillo JAG, Antón J, Meseguer I (1991) Biopolymer production by *Haloferax mediterranei*. In: Rodriguez-Valera F (ed) General and applied aspects of halophilic microorganisms. Plenum, New York, pp 373–380
- Rodriguez-Valera F, Lillo JAG (1992) Halobacteria as producers of polyhydroxyalkanoates. *FEMS Microbiol Rev* 103:181–186
- Roh SW, Bae J-W (2009) *Halorubrum cibi* sp. nov., an extremely halophilic archaeon from salt-fermented seafood. *J Microbiol* 47:162–166
- Roh SW, Nam Y-D, Chang H-W, Sung Y, Kim K-H, Oh H-M, Bae J-W (2007a) *Halalkalicoccus jeotgali* sp. nov., a halophilic archaeon from shrimp jeotgal, a traditional Korean fermented seafood. *Int J Syst Evol Microbiol* 57:2296–2298
- Roh SW, Nam Y-D, Chang H-W, Sung Y, Kim K-H, Lee H-J, Oh H-M, Bae J-W (2007b) *Natronococcus jeotgali* sp. nov., a halophilic archaeon from shrimp jeotgal, a traditional fermented seafood from Korea. *Int J Syst Evol Microbiol* 57:2129–2131
- Roh SW, Nam Y-D, Chang H-W, Kim K-H, Sung Y, Kim M-S, Oh H-M, Bae J-W (2009) *Haloterrigena jeotgali* sp. nov., an extremely halophilic archaeon from salt-fermented food. *Int J Syst Evol Microbiol* 59:2359–2363
- Roh SW, Lee M-L, Bae J-W (2010a) *Haladaptatus cibarius* sp. nov., an extremely halophilic archaeon from seafood, and emended description of the genus *Haladaptatus*. *Int J Syst Evol Microbiol* 60:1187–1190
- Roh SW, Nam Y-D, Nam S-H, Choi S-H, Park H-S, Bae J-W (2010b) Complete genome sequence of *Halalkalicoccus jeotgali* B3T, an extremely halophilic archaeon. *J Bacteriol* 192:4528–4529
- Rohrmann GF, Cheney R, Pauling C (1983) Bacteriophages of *Halobacterium halobium*: virion DNAs and proteins. *Can J Microbiol* 29:627–629
- Roine E, Kukkaro P, Paulin L, Laurinavičius S, Domanska A, Somerharju P, Bamford DH (2010) New, closely related haloarchaeal viral elements with different nucleic acid types. *J Virol* 84:3682–3689
- Romano I, Poli A, Finore I, Huertas FJ, Gambacorta A, Pelliccione S, Nicolaus G, Lama L, Nicolaus B (2007) *Haloterrigena hispanica* sp. nov., an extremely halophilic archaeon from Fuente de Piedra, southern Spain. *Int J Syst Evol Microbiol* 57:1499–1503
- Ruepp A, Soppa J (1996) Fermentative arginine degradation in *Halobacterium salinarium* (formerly *Halobacterium halobium*): genes, gene products, and transcripts of the *arcRACB* gene cluster. *J Bacteriol* 178:4942–4947
- Saunders E, Tindall BJ, Fährnich R, Lapidus A, Copeland A, Glavina Del Rio T, Lucas S, Chen F, Tice H, Cheng J-F, Han C, Detter JC, Bruce D, Goodwin L, Chain P, Pitluck S, Pati A, Ivanova N, Mavromatis K, Chen A, Palaniappan K, Land M, Hauser L, Chang Y-J, Jeffries CD, Brettin T, Rohde M, Göker M, Bristow J, Eisen JA, Markowitz V, Hugenholtz P, Klenk H-P, Kyrpides NC (2010) Complete genome sequence of *Haloterrigena turkmenica* type strain (4k^T). *Stand Genomic Sci* 2:107–116
- Savage KN, Krumholz LR, Oren A, Elshahed MS (2007) *Haladaptatus paucihalophilus* gen. nov., sp. nov., a halophilic archaeon isolated from a low-salt sulfide-rich spring. *Int J Syst Evol Microbiol* 57:19–24
- Savage KN, Krumholz LR, Oren A, Elshahed MS (2008) *Halosarcina pallida* gen. nov., sp. nov., a halophilic archaeon from a low-salt, sulfide-rich spring. *Int J Syst Evol Microbiol* 58:856–860
- Schinzler R, Burger KJ (1986) A site-specific endonuclease activity in *Halobacterium halobium*. *FEMS Microbiol Lett* 37:325–329
- Schinzler R, Burger KJ (1984) Sensitivity of halobacteria to aphidicolin, an inhibitor of eukaryotic α -type DNA polymerases. *FEMS Microbiol Lett* 25:187–190
- Schleifer KH, Steber J, Mayer H (1982) Chemical composition and structure of the cell wall of *Halococcus morrhuae*. *Zentralbl Bakt Hyg 1 Abt Orig C3*:171–178
- Schnabel H, Zillig W, Pfäffle M, Schnabel R, Michel H, Delius H (1982) *Halobacterium halobium* phage Φ H. *EMBO J* 1:87–92
- Schobert B, Lanyi JK (1982) Halorhodopsin is a light-driven chloride pump. *J Biol Chem* 257:10306–10313
- Sehgal SN, Kates M, Gibbons NE (1962) Lipids of *Halobacterium cutirubrum*. *Can J Biochem Physiol* 40:69–81
- Senčilo A, Paulin L, Kellner S, Helm M, Roine E (2012) Related haloarchaeal pleomorphic viruses contain different genome types. *Nucleic Acids Res* 40:5523–5534
- Shand RF, Betlach MC (1991) Expression of the *bop* gene cluster of *Halobacterium halobium* is induced by low oxygen tension and by light. *J Bacteriol* 173:4692–4699
- Shand RF, Price LB, O'Connor EM (1999) Halocins: protein antibiotics from hypersaline environments. In: Oren A (ed) Microbiology and biogeochemistry of hypersaline environments. CRC Press, Boca Raton, pp 295–306
- Shimane Y, Hatada Y, Minegishi H, Mizuki T, Echigo A, Miyazaki M, Ohta Y, Usami R, Grant WD, Horikoshi K (2010) *Natronoarchaeum mannanilyticum* gen. nov., sp. nov., an aerobic, extremely halophilic archaeon isolated from commercial salt. *Int J Syst Evol Microbiol* 60:2529–2534
- Shimane Y, Hatada Y, Minegishi H, Echigo A, Nagaoka S, Miyazaki M, Ohta Y, Maruyama T, Usami R, Grant WD, Horikoshi K (2011) *Salarchaeum japonicum* gen. nov., sp. nov., an aerobic, extremely halophilic member of the *Archaea* isolated from commercial salt. *Int J Syst Evol Microbiol* 61:2266–2270
- Shimoshige H, Yamada T, Minegishi H, Echigo A, Shimane Y, Kamekura M, Itoh T, Usami R (2012) *Halobaculum magnesiophilum* sp. nov., a magnesium dependent haloarchaeon, capable of growth in 1% (w/v) NaCl, isolated from commercial salt. *Int J Syst Evol Microbiol* 63:861–866
- Shukla HD, Reid IN, DasSarma S (2006) Genomic and proteomic analysis of the cold-adapted Antarctic halophile, *Halorubrum lacusprofundi*. *Astrobiology* 6:249–250
- Sidderamappa S, Challacombe JF, DeCastro RE, Pfeiffer F, Sastre DE, Giménez MI, Paggi RA, Dettler JC, Davenport KW, Goodwin LA, Kyrpides N, Tapia R, Pitluck S, Lucas S, Woyke T, Maupin-Furlow JA (2012) A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon *Natrialba magadii* ATCC 43099^T. *BMC Genomics* 13:165
- Sime-Ngando T, Lucas S, Robin A, Pause Tucker K, Colombet J, Bettarel Y, Desmond E, Gribaldo S, Forterre P, Breitbart M, Prangishvili D (2010) Diversity of virus–host systems in hypersaline Lake Retba, Senegal. *Environ Microbiol* 13:1956–1972
- Sioud M, Possot O, Elie C, Sibold L, Forterre P (1988) Coumarin and quinolone action in archaeobacteria: evidence for the presence of a DNA gyrase-like enzyme. *J Bacteriol* 170:946–953
- Soliman GSH, Trüper HG (1982) *Halobacterium pharaonis* sp. nov., a new, extremely haloalkaliphilic archaeobacterium with low magnesium requirement. *Zbl Bakt Hyg, I Abt Orig* 3:318–329
- Soppa J, Baumann A, Brenneis M, Dambeck M, Hering O, Lange C (2008) Genomics and functional genomics with haloarchaea. *Arch Microbiol* 190:197–215
- Sorokin DY, Tourova TP, Muyzer G (2005) Oxidation of thiosulfate by an haloarchaeon isolated from hypersaline habitat. *Extremophiles* 9:501–504
- Stan-Lotter H, Pfaffenhuemer M, Legat A, Busse H-J, Radax C, Gruber C (2002) *Halococcus dombrowskii* sp. nov., an archaeal isolate from a Permian alpine salt deposit. *Int J Syst Evol Microbiol* 52:1807–1814
- Stuart ES, Morshed F, Sremac M, DasSarma S (2001) Antigen presentation using novel particulate organelles from halophilic archaea. *J Biotechnol* 88:119–128
- Takai K, Komatsu T, Inagaki F, Horikoshi K (2001) Distribution of archaea in a black smoker chimney structure. *Appl Environ Microbiol* 67:3618–3629
- Tang S-L, Nuttall S, Ngui K, Fisher C, Lopez P, Dyall-Smith M (2002) HF2: a double-stranded DNA tailed haloarchaeal virus with a mosaic genome. *Mol Microbiol* 44:283–296
- Tang S-L, Nuttall S, Dyall-Smith M (2004) Haloviruses HF1 and HF2: evidence for a recent and large recombination event. *J Bacteriol* 186:2810–2817
- Tapilatu YH, Grossi V, Acquaviva M, Milton C, Bertrand J-C, Cuny P (2010) Isolation of hydrocarbon-degrading extremely halophilic archaea from an uncontaminated hypersaline pond (Camargue, France). *Extremophiles* 14:225–231
- Tapingkae W, Tanasupawat S, Itoh T, Parkin KL, Benjakul S, Visessanguan W, Valyasevi R (2008) *Natrinema gari* sp. nov., a halophilic archaeon isolated from fish sauce in Thailand. *Int J Syst Evol Microbiol* 58:2378–2383

- Tapingkae W, Tanasupawat S, Parkin KL, Benjakul S, Visessanguan W (2010a) Degradation of histamine by extremely halophilic archaea isolated from high salt-fermented fishery products. *Enzyme Microb Technol* 46:92–99
- Tapingkae W, Parkin KL, Tanasupawat S, Krueenate J, Benjakul S, Visessanguan W (2010b) Whole cell immobilization of *Natrinema gari* BCC 24369 for histamine degradation. *Food Chem* 120:842–849
- Taran M (2011a) Poly (3-hydroxybutyrate) polymer production from glycerol: optimization by Taguchi methodology. *J Polym Environ* 19:750–754
- Taran M (2011b) Poly (3-hydroxybutyrate) production from crude oil by *Haloarcula* sp. IRU1: optimization of culture conditions by Taguchi method. *Petrol Sci Tech* 29:1264–1269
- Taran M (2011c) Utilization of petrochemical wastewater for the production of poly(3-hydroxybutyrate) by *Haloarcula* sp. IRU1. *J Hazard Mater* 188:26–28
- Thongthai C, Siriwongpairat M (1990) The sequential quantitation of microorganisms in traditionally fermented fish sauce (nam pla). In: Reilly PJA, Parry RWH, Barile LE (eds) Post-harvest technology, preservation and quality of fish in Southeast Asia. International Foundation for Science, Stockholm, pp 51–59
- Thongthai C, Suintanaler P (1991) Halophiles in Thai fish sauce (nam pla). In: Rodriguez-Valera F (ed) General and applied aspects of halophilic microorganisms. Plenum, New York, pp 381–388
- Thongthai C, McGenity TJ, Suintanaler P, Grant WD (1992) Isolation and characterization of an extremely halophilic archaeobacterium from traditionally fermented Thai fish sauce (nam pla). *Lett Appl Microbiol* 14:111–114
- Tindall BJ (1991) Cultivation and preservation of members of the family *Halobacteriaceae*. *World J Microbiol Biotechnol* 7:95–98
- Tindall BJ (1992) The family *Halobacteriaceae*. In: Balows A, Trüper HG, Dworkin M, Harder W, Schleifer K-H (eds) The prokaryotes. A handbook on the biology of bacteria: ecophysiology, isolation identification, applications, vol 1. Springer, New York, pp 768–808
- Tindall BJ (2001a) Genus XI *Natronobacterium* Tindall, Ross and Grant 1984b, 355^{VP} (Effective publication: Tindall, Ross and Grant 1984a, 41) emend. In: Boone DR, Castenholz RW, Garrity GM (eds) Bergey's manual of systematic bacteriology, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 329–330
- Tindall BJ (2001b) Genus XII *Natronococcus* Tindall, Ross and Grant 1984b, 355^{VP} (Effective publication: Tindall, Ross and Grant 1984a, 41) emend. In: Boone DR, Castenholz RW, Garrity GM (eds) Bergey's manual of systematic bacteriology, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 330–332
- Tindall BJ (2003) Taxonomic problems arising in the genera *Haloterrigena* and *Natrinema*. *Int J Syst Evol Microbiol* 53:1697–1698
- Tindall BJ, Collins MD (1986) Structure of 2-methyl-3-VIII-dihydrooctaprenyl-1,4-naphthoquinone from *Halococcus morrhuae*. *FEMS Microbiol Lett* 37:117–119
- Tindall BJ, Trüper HG (1986) Ecophysiology of the aerobic halophilic archaeobacteria. *Syst Appl Microbiol* 7:202–212
- Tindall BJ, Mills AA, Grant WD (1980) An alkaliphilic red halophilic bacterium with a low magnesium requirement from a Kenyan soda lake. *J Gen Microbiol* 116:257–260
- Tindall BJ, Ross HNM, Grant WD (1984) *Natronobacterium* gen. nov. and *Natronococcus* gen. nov., two new genera of haloalkaliphilic archaeobacteria. *Syst Appl Microbiol* 5:41–57
- Tindall BJ, Tomlinson GA, Hochstein LI (1989) Transfer of *Halobacterium denitrificans* (Tomlinson, Jahnke, and Hochstein) to the genus *Haloferax* as *Haloferax denitrificans* comb. nov. *Int J Syst Bacteriol* 39:359–360
- Tindall BJ, Amendt B, Dahl C (1991) Variations in the lipid composition of aerobic, halophilic archaeobacteria. In: Rodriguez-Valera F (ed) General and applied aspects of halophilic microorganisms. Plenum, New York, pp 199–205
- Tindall BJ, Schneider S, Lapidus A, Copeland A, Glavina Del Rio T, Nolan M, Lucas S, Chen F, Tice H, Cheng J-F, Saunders E, Bruce D, Goodwin L, Pitluck S, Mikhailova N, Patti A, Ivanova N, Mavrommatis K, Chen A, Palaniappan K, Chain P, Land M, Hauser L, Chang Y-J, Jeffries CD, Brettin T, Han C, Rohde M, Göker M, Bristow J, Eisen JA, Markowitz V, Hugenholtz P, Klenk H-P, Kyrpides NC, Detter JC (2009) Complete genome sequence of *Halomicrobium mukohataei* type strain (arg-2^T). *Stand Genomic Sci* 1:270–277
- Tomlinson GA, Hochstein LI (1972a) Isolation of carbohydrate-metabolizing, extremely halophilic bacteria. *Can J Microbiol* 18:698–701
- Tomlinson GA, Hochstein LI (1972b) Studies on acid production during carbohydrate metabolism by extremely halophilic bacteria. *Can J Microbiol* 18:1973–1976
- Tomlinson GA, Hochstein LI (1976) *Halobacterium saccharovororum* sp. nov., a carbohydrate-metabolizing, extremely halophilic bacterium. *Can J Microbiol* 22:587–591
- Tomlinson GA, Koch TK, Hochstein LI (1974) The metabolism of carbohydrates by extremely halophilic bacteria: glucose metabolism via a modified Entner-Doudoroff pathway. *Can J Microbiol* 20:1085–1091
- Tomlinson GA, Strohm MP, Hochstein LI (1978) The metabolism of carbohydrates by extremely halophilic bacteria: the identification of lactobionic acid as a product of lactose metabolism by *Halobacterium saccharovororum*. *Can J Microbiol* 24:898–903
- Tomlinson GA, Jahnke LL, Hochstein LI (1986) *Halobacterium denitrificans* sp. nov., an extremely halophilic denitrifying bacterium. *Int J Syst Bacteriol* 36:66–70
- Torreblanca M, Rodriguez-Valera F, Juez G, Ventosa A, Kamekura M, Kates M (1986) Classification of non-alkaliphilic halobacteria based on numerical taxonomy and polar lipid composition, and description of *Haloarcula* gen. nov. and *Haloferax* gen. nov. *Syst Appl Microbiol* 8:89–99
- Torreblanca M, Meseguer I, Rodriguez-Valera F (1989) Halocin H6, a bacteriocin from *Haloferax gibbonsii*. *J Gen Microbiol* 135:2655–2661
- Torreblanca M, Meseguer I, Rodriguez-Valera F (1990) Effects of halocin H6 on the morphology of sensitive cells. *Biochem Cell Biol* 68:396–399
- Torreblanca M, Meseguer I, Ventosa A (1994) Production of halocin is a practically universal feature of archaeal halophilic rods. *Lett Appl Microbiol* 19:201–205
- Torsvik T (1982) Characterization of four bacteriophages for *Halobacterium*, with special emphasis on phage Hs1. In: Kandler O (ed) Archaeobacteria. Fischer, Stuttgart, pp 407–414
- Torsvik T, Dundas ID (1974) Bacteriophage of *Halobacterium salinarum*. *Nature* 248:680–681
- Torsvik T, Dundas ID (1980) Persisting phage infection in *Halobacterium salinarum* str. 1. *J Gen Virol* 47:29–36
- Trigui H, Masmoudi S, Brochier-Armanet C, Maalej S, Ducan S (2011) Characterization of *Halorubrum sfaxense* sp. nov., a new halophilic archaeon isolated from the solar saltern of Sfax in Tunisia. *Int J Microbiol* 2011:240191
- Ventosa A (2001a) Genus II. *Haloarcula* Torreblanca, Rodriguez-Valera, Juez, Ventosa, Kamekura and Kates 1986b, 573^{VP} (Effective publication: Torreblanca, Rodriguez-Valera, Juez, Ventosa, Kamekura and Kates 1986a, 98). In: Boone DR, Castenholz RW, Garrity GM (eds) Bergey's manual of systematic bacteriology, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 305–309
- Ventosa A (2001b) Genus V. *Haloferax* Torreblanca, Rodriguez-Valera, Juez, Ventosa, Kamekura and Kates 1986b, 573^{VP} (Effective publication: Torreblanca, Rodriguez-Valera, Juez, Ventosa, Kamekura and Kates 1986a, 98). In: Boone DR, Castenholz RW, Garrity GM (eds) Bergey's manual of systematic bacteriology, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 315–318
- Ventosa A, Kamekura M (2001) Genus VIII. *Haloterrigena* Ventosa, Gutiérrez, Kamekura and Dyll-Smith 1999b, 135^{VP}. In: Boone DR, Castenholz RW, Garrity GM (eds) Bergey's manual of systematic bacteriology, vol 1. The *Archaea* and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 324–325
- Ventosa A, Nieto JJ (1995) Biotechnological applications and potentialities of halophilic microorganisms. *World J Microbiol Biotechnol* 11:85–94
- Ventosa A, Oren A (1996) *Halobacterium salinarum* nom. corrig., a name to replace *Halobacterium salinarum* (Elazari-Volcani) and to include *Halobacterium halobium* and *Halobacterium cutirubrum*. *Int J Syst Bacteriol* 46:347
- Ventosa A, Gutiérrez MC, Kamekura M, Dyll-Smith ML (1999) Proposal to transfer *Halococcus turkmenicus*, *Halobacterium trapanicum* JCM 9743 and

- strain GSL-11 to *Haloterrigena turkmenica* gen. nov., comb. nov. *Int J Syst Bacteriol* 49:131–136
- Ventosa A, Gutiérrez MC, Kamekura M, Zvyagintseva IS, Oren A (2004) Taxonomic study of *Halorubrum distributum* and proposal of *Halorubrum terrestre* sp. nov. *Int J Syst Bacteriol* 54:389–392
- Vogelsang-Wenke H, Oesterhelt D (1988) Isolation of a halobacterial phage with a fully cytosine-methylated genome. *Mol Gen Genet* 211:407–417
- Vreeland RH, Straight S, Krammes J, Dougherty K, Rosenzweig WD, Kamekura M (2002) *Halosimplex carlsbadense* gen. nov., sp. nov., a unique halophilic archaeon, with three 16S rRNA genes, that grows only in defined medium with glycerol and acetate or pyruvate. *Extremophiles* 6:445–452
- Wainø M, Tindall BJ, Ingvorsen K (2000) *Halorhabdus utahensis* gen. nov., sp. nov., an aerobic, extremely halophilic member of the Archaea from Great Salt Lake, Utah. *Int J Syst Evol Microbiol* 50:183–190
- Wais AC (1988) Recovery of halophilic archaeobacteria from natural environments. *FEMS Microbiol Ecol* 53:211–216
- Wais AC, Kon M, MacDonald RE, Stollar BD (1975) Salt-dependent bacteriophage infecting *Halobacterium cutirubrum* and *H. halobium*. *Nature* 256:314–315
- Walsby AE (1980) A square bacterium. *Nature* 283:69–71
- Walsby AE (2005) Archaea with square cells. *Trends Microbiol* 13:193–195
- Wang Q-f, Li W, Yang H, Y-l L, H-h C, Dornmayr-Pfaffenhuemer M, Stan-Lotter H, G-q G, G-q G (2007) *Halococcus qingdaonensis* sp. nov., a halophilic archaeon isolated from a crude sea-salt sample. *Int J Syst Evol Microbiol* 57:600–604
- Wang S, Yang Q, Liu Z-H, Sun L, Wei D, Zhang J-Z, Song J-Z, Yuan H-F (2010) *Haloterrigena daqingensis* sp. nov., an extremely haloalkaliphilic archaeon isolated from a saline-alkaline soil. *Int J Syst Evol Microbiol* 60:2267–2271
- Wise KJ, Gillespie NB, Stuart JA, Krebs MP, Birge RR (2002) Optimization of bacteriorhodopsin for bioelectronic devices. *Trends Biotechnol* 20:387–394
- Witte A, Baranyi U, Klein R, Sulzner M, Luo C, Wanner G, Krüger DH, Lubitz W (1997) Characterization of *Natronobacterium magadii* phage Φ Ch1, a unique archaeal phage containing DNA and RNA. *Mol Microbiol* 23:603–616
- Wright A-DG (2006) Phylogenetic relationships within the order *Halobacteriales* inferred from 16S rRNA gene sequences. *Int J Syst Evol Microbiol* 56:1223–1227
- Xin H, Itoh T, Zhou P, Suzuki K-i, Kamekura M, Nakase T (2000) *Natrinema versiforme* sp. nov., an extremely halophilic archaeon from Aibi salt lake, Xinjiang, China. *Int J Syst Evol Microbiol* 50:1297–1303
- Xin H, Itoh T, Zhou P, Suzuki K-i, Nakase T (2001) *Natronobacterium nitrareducens* sp. nov., a haloalkaliphilic archaeon isolated from a soda lake in China. *Int J Syst Evol Microbiol* 51:1825–1829
- Xu Y, Zhou P, Tian X (1999) Characterization of two novel haloalkaliphilic archaea *Natronorubrum bangense* gen. nov., sp. nov. and *Natronorubrum tibetense* gen. nov., sp. nov. *Int J Syst Bacteriol* 49:261–266
- Xu Y, Zhou P, Tian X, Oren A (2001a) Genus XIV. *Natronorubrum* Xu, Zhou and Tian 1999, 261^{VP}. In: Boone DR, Castenholz RW, Garrity GM (eds) *Bergey's manual of systematic bacteriology*, vol 1. The Archaea and the deeply branching and phototrophic bacteria, 2nd edn. Springer, New York, pp 333–334
- Xu Y, Wang Z, Xue Y, Zhou P, Ventosa A, Grant WD (2001b) *Natricalba hulunbeirensis* sp. nov. and *Natricalba chahannaensis* sp. nov., novel haloalkaliphilic archaea from soda lakes in Inner Mongolia Autonomous Region, China. *Int J Syst Evol Microbiol* 51:1693–1698
- Xu X-W, Wu M, Zhou P-J, Liu S-J (2005a) *Halobiforma lacisalsi* sp. nov., isolated from a salt lake in China. *Int J Syst Evol Microbiol* 55:1949–1952
- Xu X-W, Ren P-G, Liu S-J, Wu M, Zhou P-J (2005b) *Natrinema altunense* sp. nov., an extremely halophilic archaeon isolated from a salt lake in Altun Mountain in Xinjiang, China. *Int J Syst Evol Microbiol* 55:1311–1314
- Xu X-W, Liu S-J, Tothy D, Oren A, Wu M, Zhou P-J (2005c) *Haloterrigena saccharevitans* sp. nov., an extremely halophilic archaeon from Xin-Jiang, China. *Int J Syst Evol Microbiol* 55:2539–2542
- Xu X-W, Wu Y-H, Wang C-S, Oren A, Zhou P-J, Wu M (2007a) *Haloferax larsenii* sp. nov., an extremely halophilic archaeon from a solar saltern. *Int J Syst Evol Microbiol* 57:717–720
- Xu X-W, Wu Y-H, Zhang H-b, Wu M (2007b) *Halorubrum arcis* sp. nov., an extremely halophilic archaeon isolated from a saline lake on the Qinghai-Tibet Plateau, China. *Int J Syst Evol Microbiol* 57:1069–1072
- Xue Y, Fan H, Ventosa A, Grant WD, Jones BE, Cowan DA, Ma Y (2005) *Halalkalicoccus tibetensis* gen. nov., sp. nov., a novel genus of haloalkaliphilic archaea. *Int J Syst Evol Microbiol* 55:2501–2505
- Yachai M, Tanasupawat S, Itoh T, Benjakul S, Visessanguan W, Valyasevi R (2008) *Halobacterium piscisalsi* sp. nov., from fermented fish (*pla-ra*) in Thailand. *Int J Syst Evol Microbiol* 58:2136–2140
- Yamauchi Y, Minegishi H, Echigo A, Shimane Y, Shimoshige H, Kamekura M, Itoh T, Doukyu N, Inoue A, Usami R (2012) *Halarchaenum salinum* sp. nov., a moderately acidophilic haloarchaeon isolated from commercial sea salt. *Int J Syst Evol Microbiol* 63(Pt 3):1138–42. doi:10.1099/ijms.0.040584-0
- Yang X, Cui H-L (2012) *Halomicrobium zhouii* sp. nov., a halophilic archaeon from a marine solar saltern. *Int J Syst Evol Microbiol* 62:1235–1240
- Yang Y, Cui H-L, Zhou P-J, Liu S-J (2006) *Halobacterium jilantaiense* sp. nov., a halophilic archaeon isolated from a saline lake in Inner Mongolia, China. *Int J Syst Evol Microbiol* 56:2353–2355
- Yang Y, Cui H-L, Zhou P-J, Liu S-J (2007) *Haloarcula amylolytica* sp. nov., an extremely halophilic archaeon isolated from Aibi salt lake in Xin-Jiang, China. *Int J Syst Evol Microbiol* 57:103–106
- Yarza P, Ludwig W, Euzéby J, Amann R, Schleifer KH, Glöckner FO, Rosselló-Móra R (2010) Update of the all-species living tree project based on 16S and 23S rRNA sequence analyses. *Syst Appl Microbiol* 33:291–299
- Zabut B, El-Kahlout K, Yücel M, Gündüz U, Türker L, Eroğlu I (2006) Hydrogen gas production by combined systems of *Rhodobacter sphaeoides* O.U. 001 and *Halobacterium salinarum* in a photobioreactor. *Int J Hydrogen Energy* 31:1553–1562
- Zhang Z, Liu Y, Wang S, Yang D, Cheng Y, Hu J, Chen J, Mei Y, Shen P, Bamford DH, Chen X (2012) Temperate membrane-containing halophilic archaeal virus SNJ1 has a circular dsDNA genome identical to that of plasmid. *Virology* 434(2):233–241. doi:10.1016/j.virol.2012.05.036, pHH205
- Zvyagintseva IS, Tarasov AL (1987) Extreme halophilic bacteria from saline soils. *Microbiol (Russ)* 56:664–669
- Zvyagintseva IS, Kudryashova EB, Bulygina ES (1996) Proposal of a new type strain of *Halobacterium distributum*. *Microbiol (Russ)* 65:352–354