Minutes of the joint open meeting, 6 September 2011, Sapporo, Japan

International Committee on Systematics of Prokaryotes

Subcommittee on the taxonomy of Halobacteriaceae and Subcommittee on the taxonomy of Halomonadaceae

Minute 1. Call to order. The meeting was held at the Sapporo Convention Center, Sapporo, Japan. The chairman, Dr. A. Ventosa, opened the meeting at 09:40.

Minute 2. Record of attendance. The subcommittee members present were Drs. A. Ventosa (Chairman, Subcommittee on the taxonomy of Halobacteriaceae) and D. R. Arahal (Secretary, Subcommittee on the taxonomy of Halomonadaceae). Apologies were received from V. Bejar, R. R. Colwell, M. L. Dyall-Smith, A. Gambacorta, C. D. Litchfield, Y. Ma, R. Montalvo-Rodriguez, M. R. Mornile, E. Quesada, F. Rodriguez-Valera, H. Stan-Lotter, B. J. Tindall and R. H. Vreeland.

In addition, the meeting was attended by A. Echigo (Japan), P. Kämpfer (Germany), H. Minegishi (Japan), Y. Shimane (Japan) and H. Shimoshige (Japan).

Minute 3. Appointment of secretaries. D. R. Arahal (Secretary, Subcommittee on the taxonomy of Halomonadaceae) and A. Oren (Secretary, Subcommittee on the taxonomy of Halobacteriaceae) were appointed secretaries of the joint subcommittee meeting.

Minute 4. Approval of agenda. The agenda of the meeting was approved.

Minute 5. In memoriam Helge Larsen. Professor Emeritus Helge Larsen, who was a member of the Subcommittee on the taxonomy of Halobacteriaceae from 1986 until 1994, passed away in 2005. The subcommittee became aware of this only in 2010. A. Oren presented a short obituary in memory of Helge Larsen.

Minute 6. Report of the chairman. A. Ventosa explained the work of the subcommittees and stressed the importance of the participation of young scientists in the subcommittees’ work. A few members are approaching retirement age or have even retired in the recent years, making the recruitment of active people interested in the activities of the subcommittees more necessary.

Minute 7. New taxa within the family Halobacteriaceae. The new names associated with taxa within the family were reviewed by A. Oren. As of 31 August 2011, the family Halobacteriaceae contained 33 genera and 126 species. An updated list of taxa was prepared and will be uploaded on the home page of the subcommittee on the ICSP website. This list is to a large extent based on information from Professor Jean Euzéby’s List of Prokaryotic Names with Standing in Nomenclature (http://www.bacterio.cict.fr). The subcommittees thank Jean Euzéby for maintaining this important website.

Reports on the following new taxa and reclassification of existing taxa were presented, as published between July 2010 and August 2011:

Natronorubrum sediminis sp. nov. [Gutiérrez et al., Int J Syst Evol Microbiol 60 (2010), 1802–1806], with type strain CECT 7487T, CGMCC 1.8981T, JCM 15982T.

Haloplanus vescus sp. nov. [Cui et al., Int J Syst Evol Microbiol 60 (2010), 1824–1827], with type strain CGMCC 1.8712T, JCM 16055T.

An emended description of the genus Haloplanus was given [Cui et al., Int J Syst Evol Microbiol 60 (2010), 1824–1827].

Halopelagius gen. nov. [Cui et al., Int J Syst Evol Microbiol 60 (2010), 2089–2093], with type species Halopelagius inordinatus. Recommended three-letter abbreviation: Hpl.

Halopelagius inordinatus sp. nov. [Cui et al., Int J Syst Evol Microbiol 60 (2010), 2089–2093], with type strain CGMCC 1.7739T, JCM 15773T.

Haloterrigena daqingensis sp. nov. [Wang et al., Int J Syst Evol Microbiol 60 (2010), 2267–2271], with type strain CGMCC 1.8909T, NBRC 105739T.

Halosarcina limi sp. nov. [Cui et al., Int J Syst Evol Microbiol 60 (2010), 2462–2466], with type strain CGMCC 1.8711T, JCM 16054T.

An emended description of the genus Halosarcina was given [Cui et al., Int J Syst Evol Microbiol 60 (2010), 2462–2466].

Halarchaeum acidiphilum sp. nov. [Minegishi et al., Int J Syst Evol Microbiol 60 (2010), 2513–2516], with type strain JCM 16109^T, DSM 22442^T, CECT 7534^T.


Natronoarchaeum mannanilyticum sp. nov. [Shimane et al., Int J Syst Evol Microbiol 60 (2010), 2529–2534], with type strain JCM 16328^T, CECT 7563^T.

Halostagnicola kamekurae sp. nov. [Namwong et al., Int J Syst Evol Microbiol 61 (2011), 231–236], with type strain BCC 40029^T, JCM 15759^T, PCU 313^T.

Halostagnicola gelatinilyticum sp. nov. [Namwong et al., Int J Syst Evol Microbiol 61 (2011), 231–236], with type strain BCC 40030^T, JCM 15760^T, PCU 314^T.

Halogramum gelatinilyticum sp. nov. [Cui et al., Int J Syst Evol Microbiol 61 (2011), 911–915], with type strain CGMCC 1.10119^T, JCM 16426^T.

Halogramum amylyticum sp. nov. [Cui et al., Int J Syst Evol Microbiol 61 (2011), 911–915], with type strain CGMCC 1.10121^T, JCM 16428^T.

An emended description of the genus Halogramum was given [Cui et al., Int J Syst Evol Microbiol 61 (2011), 911–915].


Halomarina oriensis sp. nov. [Inoue et al., Int J Syst Evol Microbiol 61 (2011), 942–946], with type strain JCM 16495^T, KCTC 4074^T.

Haloplanus aerogenes sp. nov. [Cui et al., Int J Syst Evol Microbiol 61 (2011), 965–968], with type strain CGMCC 1.10124^T, JCM 16430^T.

Halorubrum aquaticum sp. nov. [Gutiérrez et al., Int J Syst Evol Microbiol 61 (2011), 1144–1148], with type strain CECT 7174^T, CGMCC 1.6377^T, JCM 1403^T.

Halostagnicola alkaliophila sp. nov. [Nagaoka et al., Int J Syst Evol Microbiol 61 (2011), 1149–1152], with type strain JCM 16592^T, CECT 7631^T.


Halolamina pelagica sp. nov. [Cui et al., Int J Syst Evol Microbiol 61 (2011), 1617–1621], with type strain CGMCC 1.10329^T, JCM 16809^T.

Descriptions of the following new taxa are in press in Int J Syst Evol Microbiol:

Haloarchaeobius gen. nov. (Makhdoumi-Kakhki et al.), with type species Haloarchaeobius iranensis. Recommended three-letter abbreviation: Hab.

Haloarchaeobius iranensis sp. nov. (Makhdoumi-Kakhki et al.), with type strain IBRC-M 10013^T, KCTC 4048^T.

Halobellus gen. nov. (Cui et al.), with type species Halobellus clavatus. Recommended three-letter abbreviation: Hbs.

Halobellus clavatus sp. nov. (Cui et al.), with type strain CGMCC 1.10118^T, JCM 16424^T.

Halorientalis gen. nov. (Cui et al.), with type species Halorientalis regularis. Recommended three-letter abbreviation: Hos.

Halorientalis regularis sp. nov. (Cui et al.), with type strain CGMCC 1.10123^T, JCM 16425^T.

Salarchaeum gen. nov. (Shimane et al.), with type species Salarchaeum japonicum. Recommended three-letter abbreviation: Sar.

Salarchaeum japonicum sp. nov. (Shimane et al.), with type strain JCM 16327^T, CECT 7563^T.

Halomicrobium zhouii sp. nov. (Yang & Cui), with type strain CGMCC 1.10457^T, JCM 17095^T.

Halovenus gen. nov. (Makhdoumi-Kakhki et al.), with type species Halovenus aranensis. Recommended three-letter abbreviation: Hvn.

Halovenus aranensis sp. nov. (Makhdoumi-Kakhki et al.), with type strain IBRC 10015^T, CGMCC 1.1101^T.

Two papers relevant to the taxonomy of Halobacteriaceae are in press in Int J Syst Evol Microbiol:

Minegishi et al.: Gene orders in the upstream of 16S rRNA genes divide genera of the family Halobacteriaceae into two groups.

Papke et al.: A multilocus sequence analysis (MLSA) approach to Halobacteriales phylogeny and taxonomy.

Minute 8. New taxa within the family Halomonadaceae. The new names associated with taxa within each individual family were reviewed by D. R. Arahal. As of 31 August 2011, the family Halomonadaceae contained 10 genera and 88 species.

The following taxa did not appear in the minutes of the previous meeting:
Aidingimonas gen. nov. [Wang et al., Int J Syst Evol Microbiol 59 (2009), 3088–3094], with type species Aidingimonas halophila.

Aidingimonas halophila sp. nov. [Wang et al., Int J Syst Evol Microbiol 59 (2009), 3088–3094], with type strain CCTCC AB 207002T, KCTC 12885T.

Reports on the following new taxa and reclassification of existing taxa were presented, as published between July 2010 and August 2011:

Kushneria sinocarnis sp. nov. [Zhou & Wang, Int J Syst Evol Microbiol 60 (2010), 1881–1886], with type strain CCTCC AB 209027T, NRRL B-59197T, DSM 23229T.

Halomonas titanicae sp. nov. [Sánchez-Porro et al., Int J Syst Evol Microbiol 60 (2010), 2768–2772], with type strain ATCC BAA-1257T, CECT 7585T, JCM 16411T, LMG 25388T.

Halomonas vilamensis sp. nov. [Menes et al., Int J Syst Evol Microbiol 61 (2011), 1211–1217], with type strain DSM 21020T, LMG 24332T.

Halomonas daqiaonensis sp. nov. [Qu et al., Int J Syst Evol Microbiol 61 (2011), 1612–1616], with type strain CGMCC 1.9150T, MCCC 1B00920T, NCCB 100305T.

Descriptions of the following new taxa are in press in Int J Syst Evol Microbiol:

Halomonas xianhensis sp. nov. (Zhao et al.), with type strain CGMCC 1.6848T, JCM 14849T.

Halomonas rifensis sp. nov. (Amjres et al.), with type strain CECT 7698T, LMG 25695T.

Halomonas stenophila sp. nov. (Llamas Company et al.), with type strain CECT 7744T, LMG 25812T.

The following paper relevant to the taxonomy of Halomonadaceae is in press in Int J Syst Evol Microbiol:

de la Haba et al.: Multilocus sequence analysis (MLSA) of the family Halomonadaceae.

Minute 9. Should the family Halobacteriaceae be split into two families? H. Minegishi presented his comparative studies of 165 rRNA gene sequences and the presence of the pyrD (coding for dihydroorotate oxidase) or lpdA (coding for dihydrolipoamide dehydrogenase) genes immediately upstream of the rRNA operon in 136 strains of the Halobacteriaceae. Two clusters can be recognized, which may warrant the splitting of the Halobacteriaceae into two families. The discussion that followed ended with the recommendation not to split the family as long as no phenotypic properties can be found to discriminate between the two clusters.

Minute 10. Recommended minimal standards. The recommended minimal standards for describing new taxa of the family Halobacteriaceae were published in 1997 [Oren et al., Int J Syst Bacteriol 47 (1997), 233–238] and the recommended minimal standards for describing new taxa of the family Halomonadaceae were published in 2007 [Arahali et al., Int J Syst Evol Microbiol 57 (2007), 2436–2446]. Although new methods, and notably multilocus type analysis, were introduced in recent years, it was felt that the current minimal standards documents are still adequate in combination with Notes on the characterization of prokaryote strains for taxonomic purposes [Tindall et al., Int J Syst Evol Microbiol 60 (2010), 249–266]. The need for updated recommended minimal standards should be discussed further at the next meeting(s) of the subcommittee(s).

Minute 11. Importance of chemotaxonomic information. A. Oren read a message received from B. J. Tindall, who stressed the importance of physiological/biochemical data and chemotaxonomy as descriptive and diagnostic characteristics. It is to be restated that useful information gathered at the chemical level will also be reflected at the genomic level.

Minute 12. Multilocus sequence analysis (MLSA) of the Halobacteriaceae. A. Oren read a statement to the subcommittee on the taxonomy of Halobacteriaceae by R. T. Papke on the usefulness of MLSA for the Halobacteriaceae. Dr Papke’s laboratory has collected extensive multilocus sequence data for the type strains of most of the species within the family as well as for many unclassified strains. He intends to set up an online database containing all of the sequence data for all members of the Halobacteriales and provide alignments for downloading. In return, he asks that any newly generated MLSA sequences be uploaded to the database, even if it is determined that the strain belongs to an existing species. To enhance and facilitate the usefulness of such a specialized repository, the inclusion of all phenotypic and other metadata such as collection site characteristics should also be a significant aspect of the database. The subcommittee congratulates Dr Papke for his initiative and will do all it can to support the effort by supplying sequence data and other information.

Minute 13. The taxonomic status of Halobacterium piscisalii. As a follow-up to Minute 11 of the joint meeting of the Subcommittee on the taxonomy of Halobacteriaceae and the Subcommittee on the taxonomy of Halomonadaceae held in Beijing, China, on 30 June 2010 [Oren & Ventosa, Int J Syst Evol Microbiol 60 (2010), 2257–2259], A. Oren inquired about the current status of Halobacterium piscisalii. H. Minegishi and A. Echigo replied that Halobacterium piscisalii JCM 14661T [Yachai et al., Int J Syst Evol Microbiol 58 (2008), 2136–2140] shares exactly the same 16S rRNA gene sequence and high DNA–DNA relatedness (more than 80%) with Halobacterium salinarum JCM 8978T, and this was confirmed by sequencing of the type strain obtained from different culture collections (HPC2-1T kept at BIOTEC, Thailand, as well as BCC 24372T) and DNA–DNA hybridization. The authors of the species description acknowledged that their published sequence and DNA–DNA relatedness values were incorrect. A formal proposal to
consider *Halobacterium piscisalsi* as a later heterotypic synonym of *Halobacterium salinarum* was submitted to *Int J Syst Evol Microbiol* and is currently under review.

**Minute 14. Next meeting of the subcommittees.** The next meetings of both subcommittees will be held in association with the international meeting on halophilic micro-organisms, scheduled to take place in Storrs, CT, USA, in July–August 2013.

**Minute 15. Adjournment.** The meeting was adjourned at 10:40 on 6 September 2011.