Minutes

International Committee on Systematics of Prokaryotes

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

Aharon Oren, *Secretary*
Antonio Ventosa, *Chairman*

Minutes of the meeting 30 June 2010, Beijing, China

Minute 1. Call to order. The meeting was held at the Grand Skylight Catic Hotel, Beijing, China. The chairman, A. Ventosa, opened the meeting at 17:10 on 30 June 2010.

Minute 2. Record of attendance. The subcommittee members present were A. Ventosa (Chairman – Subcommittee on the Taxonomy of *Halobacteriaceae* and Subcommittee on the Taxonomy of *Halomonadaceae*), A. Oren (Secretary – Subcommittee on the Taxonomy of *Halobacteriaceae*), M. Dyal-Smith, M. Kamekura, Y. Ma and M. Mormile. Apologies were received from D. R. Arahall, V. Bejar, R. R. Colwell, A. Gambacorta, C. D. Litchfield, R. Montalvo-Rodriguez, E. Quesada, F. Rodríguez-Valera, H. Stan-Lotter, B. J. Tindall and R. H. Vreeland.

In addition, the meeting was attended by M. A. Amoozegar (Tehran, Iran), A. Antunes (Thuwal, Saudi Arabia), Z. Cai (Beijing, China), J. A. Coker (Baltimore, USA), P. Corral (Sevilla, Spain), P. DasSarma (Baltimore, USA), S. DasSarma (Baltimore, USA), R. R. de la Haba (Sevilla, Spain), A. Echigo (Saitama, Japan), M. Enache (Bucharest, Romania), A. B. Fernandez (Sevilla, Spain), W. D. Grant (Leicester, UK), K. Inoue (Tokyo, Japan), B. E. Jones (Leiden, the Netherlands), F. Kong (China), W.-J. Li (Kunming, China), W. Lu (China), A. Makhdoumi-Kakhaki (Tehran, Iran), T. J. McGenity (Colchester, UK), H. Minegishi (Saitama, Japan), R. T. Papke (Storrs, USA), A. A. Pourbabaee (Tehran, Iran), J. Quillaguaman (Cochabamba, Bolivia), L. Rao (Beijing, China), C. Sánchez-Porro (Sevilla, Spain), Y. Shimane (Saitama, Japan), Y. Song (Beijing, China), E. White (Storrs, USA), Y. F. Xue (Beijing, China), Y. Zheng (Beijing, China) and C. Zhou (Beijing, China).

Minute 3. Appointment of a secretary. A. Oren was appointed secretary of the joint subcommittee meeting.

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

Minute 5. Minutes of previous meetings. The minutes of the meetings of the Subcommittee on the Taxonomy of *Halobacteriaceae* held in Istanbul, Turkey, 7 August 2008 [Oren & Ventosa, *Int J Syst Evol Microbiol* **58** (2008), 2465–

2467], and of the Subcommittee on the Taxonomy of *Halomonadaceae* held in Istanbul, Turkey, 7 August 2008 [Arahall & Ventosa, *Int J Syst Evol Microbiol* **58** (2008), 2670–2671], were discussed. P. DasSarma commented that the wording of Minute 17 of the minutes of the meetings of the Subcommittee on the Taxonomy of *Halobacteriaceae* was not appropriate. The words ‘the nomenclature changes proposed in the paper are unacceptable’ should therefore be replaced by ‘the nomenclature changes proposed in the paper cannot be approved’. There were no further comments on these minutes, and they will be submitted for approval by the upcoming closed meetings of both subcommittees.

Minute 6. New taxa within the family *Halobacteriaceae*.

The new names associated with taxa within the family were reviewed by A. Oren. As of 14 June 2010, the family *Halobacteriaceae* contained 29 genera and 110 species. An updated list of taxa was prepared and will be uploaded to the home page of the subcommittee on the ICSP website. Reports on the following new taxa and reclassification of existing taxa were presented, as published between August 2008 and June 2010:

Halorubrum kocurii sp. nov. [Gutiérrez *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2031–2035], with type strain CECT 7322^T, CGMCC 1.7018^T, JCM 14978^T.

Halobacterium piscisalsi sp. nov. [Yachai *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2136–2140], with type strain BCC 24372^T, JCM 14661^T, PCU 302^T.

Halomicrobium katesii sp. nov. [Kharroub *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2354–2358], with type strain CECT 7257^T, DSM 19301^T.

Natrinema gari sp. nov. [Tapingkae *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2378–2383], with type strain BCC 24370^T, JCM 14663^T, PCU 303^T.

Halorubrum californiense sp. nov. [Pesenti *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2710–2715], with type strain CECT 7256^T, DSM 19288^T, JCM 14715^T.

Haloterrigena salina sp. nov. [Gutiérrez *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2880–2884], with type strain CGMCC 1.6203^T, JCM 13891^T.

Emended descriptions of the genera *Halobacterium*, *Haloarcula*, *Halococcus*, *Haloferax*, *Halorubrum*, *Haloterrigena*, *Natrialba*, *Halobiforma* and *Natronorubrum* were published [Oren *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 637–642].

Halorubrum chaoviator sp. nov. [Mancinelli *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 1908–1913], with type strain ATCC BAA-1602^T, DSM 19316^T, NCIMB 14426^T.

Halorubrum cibi sp. nov. [effective publication: Roh & Bae, *J. Microbiol.* **47** (2009), 162–166; Validation List no. 129, *Int J Syst Evol Microbiol* **59** (2009), 2129–2130], with type strain JCM 15757^T, KCTC 4026^T.

Haloterrigena jeotgali sp. nov. [Roh *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 2359–2363], with type strain CECT 7218^T, DSM 18794^T, JCM 14585^T, KCTC 4020^T.

Halopiger aswanensis sp. nov. [Hezayen *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 633–637], with type strain DSM 13151^T, JCM 11628^T.

Haladaptatus litoreus sp. nov. [Cui *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1085–1089], with type strain CGMCC 1.7737^T, JCM 15771^T.

An emended description of the genus *Haladaptatus* was given [Cui *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1085–1089].

Natronomonas moolapensis sp. nov. [Burns *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1173–1176], with type strain JCM 14361^T, CECT 7526^T, DSM 18674^T.

An emended description of the genus *Natronomonas* was given [Burns *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1173–1176].

Haladaptatus cibarius sp. nov. [Roh *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1187–1190], with type strain DSM 19505^T, JCM 15962^T.

An emended description of the genus *Haladaptatus* was given [Roh *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1187–1190].

Halonotius gen. nov. [Burns *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1196–1199], with type species *Halonotius pteroides*. Recommended three-letter abbreviation: *Hns*.

Halonotius pteroides sp. nov. [Burns *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1196–1199], with type strain JCM 14355^T, CECT 7525^T, DSM 18729^T.

Halogramum gen. nov. [Cui *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1366–1371], with type species *Halogramum rubrum*. Recommended three-letter abbreviation: *Hgn*.

Halogramum rubrum sp. nov. [Cui *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 1366–1371], with type strain CGMCC 1.7738^T, JCM 15772^T.

Descriptions of the following new taxa are in press in IJSEM: *Halostagnicola alkaliphila*, *Halorubrum aquaticum*, *Haloplanus aerogenes*, *Halomarina oriensis*, *Halogramum gelatinilyticum*, *Halogramum amylolyticum*, *Haloarcula sa-*

laria, *Haloarcula tradensis*, *Halostagnicola kamekurae*, *Halogeometricum rufum*, *Natronoarchaeum mannanilyticum*, *Halarchaeum acidiphilum*, *Halosarcina limi*, *Haloterrigena daqingensis*, *Halopelagius inordinatus*, *Haloplanus vescus* and *Natronorubrum sediminis*.

Minute 7. New taxa within the family *Halomonadaceae*.

The new names associated with taxa within the family were reviewed by A. Ventosa. As of 14 June 2010 the family *Halomonadaceae* contained 10 genera and 84 species. Reports on the following new taxa and reclassification of existing taxa were presented, as published between August 2008 and June 2010:

Halomonas lutea sp. nov. [Wang *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2065–2069], with type strain KCTC 12847^T, CCTCC AB 206093^T.

Halomonas korlensis sp. nov. [Li *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2582–2588], with type strain CGMCC 1.6981^T, DSM 19633^T.

Halomonas salifodinae sp. nov. [Wang *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2855–2858], with type strain CGMCC 1.6774^T, JCM 14803^T.

Halomonas daqingensis sp. nov. [Wu *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2859–2865], with type strain CGMCC 1.6443^T, LMG 23896^T.

Kushneria gen. nov. [Sánchez-Porro *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 397–405], with type species *Kushneria aurantia*.

Kushneria aurantia sp. nov. [Sánchez-Porro *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 397–405], with type strain CCM 7415^T, CECT 7220^T.

Kushneria marisflavi comb. nov. (basonym: *Halomonas marisflavi*) [Sánchez-Porro *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 397–405].

Kushneria indalinina comb. nov. (basonym: *Halomonas indalinina*) [Sánchez-Porro *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 397–405].

Kushneria avicenniae comb. nov. (basonym: *Halomonas avicenniae*) [Sánchez-Porro *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 397–405].

Halomonas ilicicola sp. nov. [Arenas *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 578–582], with type strain CECT 7331^T, CCM 7522^T, DSM 19980^T.

Halomonas fontilapidosi sp. nov. [González-Domenech *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 1290–1296], with type strain CECT 7341^T, LMG 24455^T.

Halomonas zhanjiangensis sp. nov. [Chen *et al.*, *Int J Syst Evol Microbiol* **59** (2009), 2888–2893], with type strain CCTCC AB 208031^T, DSM 21076^T, KCTC 22279^T.

Halomonas xinjiangensis sp. nov. [Guan *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 349–352], CCTCC AB 208329^T, KCTC 22608^T.

Halomonas stevensii sp. nov. [Kim *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 369–377], with type strain KCTC 22148^T, DSM 21198^T.

Halomonas hamiltonii sp. nov. [Kim *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 369–377], with type strain KCTC 22154^T, DSM 21196^T.

Halomonas johnsoniae sp. nov. [Kim *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 369–377], with type strain KCTC 22157^T, DSM 21197^T.

Cobetia crustatorum sp. nov. [Kim *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 620–626], with type strain KCTC 22486^T, JCM 15644^T.

Salinicola salarii comb. nov. (basonym *Halomonas salaria*) [de la Haba *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 963–971].

Salinicola halophilus nom. nov. (basonym *Chromohalobacter salarii*) [de la Haba *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 963–971].

Halomonas andesensis sp. nov. [Guzmán *et al.*, *Int J Syst Evol Microbiol* **60** (2010), 749–753], with type strain CCUG 54844^T, LMG 24243^T, DSM 19434^T.

Descriptions of the following new taxa are in press in *Int J Syst Evol Microbiol*: *Kushneria sinocarnis* and *Halomonas titanicae*.

Two additional papers of importance for the taxonomy of the family *Halomonadaceae* were discussed: de la Haba *et al.*, Phylogenetic relationships within the family *Halomonadaceae* based on comparative 23S and 16S rRNA gene sequence analysis [*Int J Syst Evol Microbiol* **60** (2010), 737–748], and González-Domenech *et al.*, Denitrification as an important taxonomic marker within the genus *Halomonas* [*Syst Appl Microbiol* **33** (2010), 85–93].

Minute 8. Report of the ad-hoc committee for the Multilocus Sequence Analysis of *Halobacteriaceae*. R. T. Papke summarized the results presented in a lecture by E. White preceding the subcommittee meeting. The following genes are recommended for MLSA of the family *Halobacteriaceae*: *atpB*, *EF-2*, *radA*, *rpoB* and *secY*. PCR primers are now available for all these genes. It should be stressed that MLSA should be used as part of the polyphasic characterization of strains, and should not be used as the sole criterion for the establishment of new taxa. Further analyses are ongoing.

Minute 9. Multilocus Sequence Analysis of the family *Halomonadaceae*. R. R. de la Haba and A. Ventosa presented the results of their recent MLSA studies of the family *Halomonadaceae*. The genes *gyrB* and *rpoD* in combination with the 16S rRNA gene were found to be suitable markers for molecular phylogeny studies of the family *Halomonadaceae*, and PCR primers have been developed for these genes. Further studies of MLSA for the family *Halomonadaceae* are in progress.

Minute 10. *Halobacterium salinarum* strain MMD047 is a member of the genus *Halobacillus*. A. Oren presented the case of the description of an isolate from a marine sponge, designated *Halobacterium salinarum* strain MMD047, which was reported to grow in the absence of salt [Shanmughapriya *et al.*, *Biotechnol Bioprocess Engin* **14** (2009) 67–75]. Following a number of unsuccessful attempts to obtain the strain from the authors for further taxonomic study, a Letter to the Editor was published [Oren and Ventosa, *Biotechnol Bioprocess Engin* **14** (2009) 869–870]. The authors subsequently published an erratum stating that the strain was misidentified and is a *Halobacillus* sp. [Shanmughapriya *et al.*, *Biotechnol Bioprocess Engin* **14** (2009) 871]. The GenBank database still gives two 16S rRNA gene sequences for this strain, one with high similarity to the genus *Halobacterium* EU602318.1) and a second sequence (EU602318.2) closely affiliated with the genus *Halobacillus*.

Minute 11. Taxonomic status of *Halobacterium piscisalsi*. H. Minegishi and A. Echigo presented evidence that the recently described *Halobacterium piscisalsi* JCM 14661^T [Yachai *et al.*, *Int J Syst Evol Microbiol* **58** (2008), 2136–2140] shares high 16S rRNA gene similarity and high DNA–DNA relatedness with *Halobacterium salinarum*. It was recommended to also obtain cultures of the type strain of *Halobacterium piscisalsi* from other culture collections (BCC 24372^T, PCU 302^T). If these cultures are identical to JCM 14661^T, a taxonomic note should be published proposing *Halobacterium piscisalsi* as a later synonym of *Halobacterium salinarum*.

Minute 12. 16S rRNA gene sequences and DNA–DNA hybridization information in descriptions of novel species of the family *Halobacteriaceae*. H. Minegishi and A. Echigo stressed that future papers proposing new taxa of the order *Halobacteriales* should use 16S rRNA gene sequences that are as complete as possible, as described by Tindall *et al.* [*Int J Syst Evol Microbiol* **60** (2010), 249–266], and that appropriate controls should be used in DNA–DNA hybridization experiments.

Minute 13. Other matters. R. T. Papke presented the idea of splitting the family *Halobacteriaceae* into two families on the basis of multilocus gene comparison studies and other genomic information. Further studies are recommended before a formal proposal should be made for the establishment of a new family.

Minute 14. Next meetings of the subcommittees. The next meetings of both subcommittees will be held in association with the International Union of Microbiological Societies meetings to be held in Sapporo, Japan, 6–10 September 2011.

Minute 15. Adjournment. The meeting was adjourned at 19:05 on 30 June 2010.