

Minutes

Peter Kuhnert, *Secretary*
Henrik Christensen, *Chairman*

International Committee on Systematics of Prokaryotes

Subcommittee on the taxonomy of *Pasteurellaceae*

Minutes of the meetings, 15 May 2014, Prato, Italy

Session 1 – Open meeting

Minute 1. Call to order. The open meeting was held on 15 May 2014 on the occasion of the International *Pasteurellaceae* Conference at Monash University, Prato, Italy. The Chairman, Henrik Christensen, opened the meeting at 13:40. He introduced the ICSP and the role of subcommittees.

Minute 2. Record of attendance. The members present were Henrik Christensen (Chairman), Peter Kuhnert (Secretary), Pat Blackall, Niels Nørskov-Lauritsen and Tom Inzana. Apologies were received from Magne Bisgaard, Robert Davies and Hans-Jürgen Busse. Fifteen guests were present.

Minute 3. Approval of agenda. An agenda was circulated electronically. No additional points to the agenda were made.

Minute 4. Last subcommittee meeting. The minutes of the previous subcommittee meetings in Elsinore, Denmark, 25 August 2011 have been published [*Int J Syst Evol Microbiol* **62** (2012), 257–258].

Tom Inzana gave an update on the work proposed at the last meeting on reclassification of [*Haemophilus*] *ducreyi*. Since it is very difficult to mail live bacterial strains any more, and since infection due to [*H.*] *ducreyi* in the USA is very rare, he still does not have any strains. Therefore, owing to the lack of field strains this initiative had to be stopped. However, he proposed changing efforts to take up reclassifying [*Haemophilus*] *parasuis*.

At the last meeting, Paul Langford initiated genome sequencing of *Actinobacillus pleuropneumoniae* serotype 8 reference strains from several laboratories in order to solve confusion on various strains obviously circulating. This is still ongoing but will soon be finished.

Minute 5. Taxonomic changes. Changes in taxonomy since the last meeting were summarized by Henrik Christensen. Three new genera each with one species have been validly published: *Otariodibacter oris* by Hansen *et al.* [*Int J Syst Evol Microbiol* **62** (2012), 2572–2578], *Frederiksenia canicola* by Korczak *et al.* [*Antonie van Leeuwenhoek* **105** (2014), 731–741; and *Int J Syst Evol*

Microbiol **64** (2014), 2184–2187], *Vespertiliibacter pulmonis* (and two genomospecies) by Mühldorfer *et al.* [*Int J Syst Evol Microbiol* **64** (2014), 2424–2430]. The genus and species ‘*Seminibacterium arietis*’ by Vela *et al.* [*Syst Appl Microbiol* **36** (2013), 166–170] has not been validly published and its description is *de facto* based on a single strain.

One new species has been validly published: *Haemophilus sputorum* by Nørskov-Lauritsen *et al.* [*Int J Med Microbiol* **302** (2012), 78–83; and *Int J Syst Evol Microbiol* **62** (2012), 1443–1445].

The species *Pasteurella lymphangitidis* has been proposed to be reclassified as *Yersinia pseudotuberculosis* by Gaillot *et al.* [*Int J Syst Evol Microbiol* **63** (2013), 3927–3929].

Minute 6. Use of MALDI-TOF MS for taxonomy. Matrix assisted laser desorption/ionization time-of-flight (MALDI-TOF) MS has proved useful for identification and differentiation of members of the family *Pasteurellaceae* [Alispahic *et al.*, *Int J Med Microbiol* **301** (2011), 513–522; Kuhnert *et al.*, *J Microbiol Methods* **89** (2012), 1–7]. It has also been applied in the description of the species *H. sputorum* by Nørskov-Lauritsen *et al.* [*Int J Med Microbiol* **302** (2012), 78–83] and *F. canicola* by Korczak *et al.* [*Antonie van Leeuwenhoek* **105** (2014), 731–741]. The members agreed that this technique should be included whenever possible and wherever useful for the description and (re)classification of taxa.

Minute 7. Publishing in IJSEM. Members expressed their concern that there are no general and transparent guidelines for the evaluation of manuscripts submitted to IJSEM. The review is often subject to arbitrariness and forcing of specific and commercial methods. The ‘minimal standards’ published for the family *Pasteurellaceae* have not improved the situation. Some reviewers and editors will always find yet another method necessary of being included, while for other taxa single strain descriptions, not taking into account biodiversity, are accepted. Of course this is minimizing variable characteristics, simplifying descriptions, but generating massive future problems. Members agreed to write a letter of concern to the editorial board raising these points.

Minute 8. Varia. The need for whole genome sequences was discussed both in the context of a comprehensive

phylogeny as well as in the framework as a tool for description of new taxa. Paul Planet presented an update on whole genome phylogeny of the family *Pasteurellaceae* at the conference in Prato. He proposed a plan for generating and analysing whole genome sequences of more members of the family *Pasteurellaceae*. There was agreement that as many species as possible, from as many places and temporal spaces as possible should be included in such an approach. In all cases type strains should be incorporated. Genomic DNA could be sent to Paul Planet, wrapped in aluminium foil to prevent nicking from X-ray scans during transport. In a first step a selection of strains should be done, then sending of strains should be coordinated and finally financing of such a collaborative project should be secured. A letter of support from members or the subcommittee to Paul Planet would be needed.

Minute 9. Adjournment. The open meeting was adjourned at 15:05 on 15 May 2014.

Session 2 – Closed meeting

Minute 10. Call to order. The closed meeting planned to be held at the IUMS meeting in Montreal 2014 was cancelled beforehand on the occasion of the open meeting in Italy since only two members of the subcommittee were supposed to attend IUMS 2014. Issues for the closed meeting were therefore communicated by email.

Minute 11. Current membership. There were no changes in membership since the last meeting in 2011. The current membership of the subcommittee is as follows: Henrik Christensen (Copenhagen, Denmark) (chairman); Peter Kuhnert (Bern, Switzerland) (secretary); Magne Bisgaard (Copenhagen, Denmark); Hans-Jürgen Busse (Wien, Austria); Pat Blackall (Moorooka, Australia); Tom Inzana

(Blacksburg, VA, USA); Robert Davies (Glasgow, UK); Olivier Gaillot (Lille, France) and Niels Nørskov-Lauritsen (Århus, Denmark).

Minute 12. Use of whole genome sequences. There was an email inquiry sent out to taxonomists by Ramon Roselló-Morá in June 2014. He raised the question of whether genome sequences should be compulsory for description of new taxa. This question was discussed on the occasion of a PhD defence in Copenhagen and by email by the chair, the secretary and Magne Bisgaard also in light of the recent publication by Vandamme & Peeters [*Antonie van Leeuwenhoek* **106** (2014), 57–65]. In this paper, Peter Vandamme, significantly involved in defining the polyphasic taxonomy approach, recognizes exactly this as ‘one of the main reasons ... why we have a ridiculously short list of ... bacterial species named today’. As a consequence, he advocates for ‘a full genome sequence and a minimal description of phenotypic characteristics’ as being appropriate for species description. The chair and secretary agreed that whole genome sequences should not become compulsory for description of new taxa at the moment, in particular not as yet another method and dataset added to the polyphasic approach. However, the proposal of Peter Vandamme formulated in his paper should be discussed in more detail within the subcommittee and a consensus should be found to overcome outdated approaches and to eventually advance taxonomy of the family *Pasteurellaceae*.

Minute 13. Next meeting. The next meeting is planned to be held in 2017 either at the IUMS meeting in Singapore or alternatively at the *Pasteurellaceae* conference in Brazil.

Minute 14. Adjournment. No other matters were raised. Email communication on issues normally dealt with in the closed meeting was adjourned on 1 August 2014.