

Request for an Opinion

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The status of the genus name *Halovibrio* Fendrich 1989 and the identity of the strains *Pseudomonas halophila* DSM 3050 and *Halomonas variabilis* DSM 3051. Request for an Opinion

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During the course of studies on halophilic, Gram-negative bacteria, a comparison of two strains of halophilic bacteria, *Pseudomonas halophila* DSM 3050 and *Halomonas variabilis* DSM 3051 (formerly *Halovibrio variabilis*) demonstrated that the characteristics of strain DSM 3050 corresponded to the original description of *Halovibrio variabilis* and those of DSM 3051 to *P. halophila*, both of which had been isolated from the Great Salt Lake in Utah [Fendrich, C. (1988). *Syst Appl Microbiol* **11**, 36–43]. It was concluded that these two strains did not correspond with their original descriptions, e.g. the original description of *Halovibrio variabilis* matched that of *Pseudomonas halophila* DSM 3050 and the original description of *Pseudomonas halophila* matched that of *Halovibrio variabilis* DSM 3051, which was subsequently transferred to the genus *Halomonas* as *Halomonas variabilis* DSM 3051. These findings raise the question of whether the genus name *Halovibrio*, with the type species *Halovibrio variabilis*, should be associated with type strain DSM 3050 and recognition of strain DSM 3051 as the type strain of *Pseudomonas halophila*.

In an accompanying publication (Sorokin *et al.*, 2006), three new, extremely halophilic, denitrifying bacteria isolated from hypersaline lakes in Central Asia have been described, which, on the basis of 16S rRNA gene sequence, phenotypic and chemotaxonomic data, clustered together with DSM 3050 (supplied as *Pseudomonas halophila*) in the *Gamma-proteobacteria*. The moderately halophilic species *P. halophila* and extremely halophilic species *Halovibrio variabilis* had been isolated from the Great Salt Lake in Utah by C. Fendrich (Fendrich, 1988) and the type and only strains were deposited in the DSMZ, in 1984, under the numbers DSM 3050 and DSM 3051, respectively. Subsequently, on the basis of 16S rRNA gene sequence (Dobson *et al.*, 1993; Dobson & Franzmann, 1996; Okamoto *et al.*, 2004) and chemotaxonomic (Franzmann & Tindall, 1990) analyses, *Halovibrio variabilis* was reclassified as *Halomonas variabilis* with DSM 3051 as the type strain, whereas *P. halophila* strain DSM 3050 was clearly allocated to another cluster of the *Gamma-proteobacteria* (Anzai *et al.*, 2000; Franzmann & Tindall,

1990). Despite high 16S rRNA gene sequence similarity, the isolates of Sorokin *et al.* (2006) clearly differed in their biochemistry and physiology from the original description of *P. halophila* (Fendrich, 1988). On the other hand, there was a striking resemblance to *Halovibrio variabilis*.

This prompted Sorokin *et al.* (2006) to undertake phenotypic cross-comparison of strains DSM 3050 and DSM 3051. The results (Sorokin *et al.*, 2006) confirmed the initial suspicion that the isolates deposited under these DSM numbers did not correspond to the original published descriptions. However, the description of DSM 3050 (catalogued as the type strain of *P. halophila*) corresponded with the original description of *Halovibrio variabilis*, whereas the original description of DSM 3051 (catalogued as the type strain of *Halovibrio variabilis*) corresponded with the original description of *P. halophila* (Table 1). Checking both the original publication and the accession forms also indicated that DSM 3050 had been deposited as 'strain 55', whereas DSM 3051 had been deposited as 'strain 65', both in 1984. However, neither strain designations appear in the publication of Fendrich (1988) and freeze-dried strains returned

Table 1. Comparison of the characteristics of *P. halophila* DSM 3050 and *Halomonas variabilis* DSM 3051 with their original descriptions (Fendrich, 1988)

Characteristic	DSM 3050	<i>Halovibrio variabilis</i> (original description)	DSM 3051	<i>P. halophila</i> (original description)
DNA G + C content (mol%)	61·6	61 ± 1	58	57 ± 1
NaCl range for growth (M)	1·5–4·5	1·2–4·9	0·05–3·0	0·02–3·3
pH range	6·7–8·5	6·5–8·4	5·5–9·0	4·5–9·6
Sugar utilization	—	—	+	+
Cell morphology	Vibrios or spirilla	Spirilla	Straight, fat rods	Rods

to Fendrich for confirmation of identity were confirmed as being identical to the original isolates. Notes in the DSMZ on the ability of these two strains to be freeze-dried and cultivated indicated that DSM 3050 was more difficult to handle than DSM 3051, a fact which easily allows these two strains to be distinguished from one another.

Based on the data collected to date, we can conclude that DSM 3051 is clearly a member of the genus *Halomonas*, a fact confirmed by both chemotaxonomic and 16S rRNA gene sequence data (Dobson *et al.*, 1993; Franzmann & Tindall, 1990). Physiologically and morphologically, the data published under the name *P. halophila* correspond to those of DSM 3051. In contrast, DSM 3050 clearly is not a member of the genus *Halomonas*, which also can be confirmed by 16S rRNA gene sequence and chemotaxonomic data (Dobson *et al.*, 1993; Franzmann & Tindall, 1990). Clearly the published descriptions of the type strains of these two species do not correspond with the characteristics of the currently available type strains. According to Rule 18g of the *Bacteriological Code* (Lapage *et al.*, 1992), this is a matter for the Judicial Commission.

There would appear to be three alternative solutions.

Firstly, the fact that the descriptions of the type strains do not correspond with the characteristics of the designated type strains may be taken to indicate that either neotypes should be designated or that both the genus name *Halovibrio* and the species names *P. halophila*, *Halovibrio variabilis* and its homotypic synonym *Halomonas variabilis* should be rejected. However, we do not believe that this serves the interest of stability of nomenclature.

Secondly, the Judicial Commission may rule that the description published under the name *P. halophila* be applied to *Halovibrio variabilis* and that the description published under the name *Halovibrio variabilis* be applied to *P. halophila*. However, this would appear to contradict the original intention of Fendrich (1988), when these names were proposed.

The third alternative, which we favour, would involve recognizing the fact that the strains DSM 3050 and DSM 3051 have been wrongly associated with names and descriptions. We also believe that this solution best retains the original intent of Fendrich (1988).

We propose that the following steps should be undertaken by the Judicial Commission.

- (i) The type of the name *Halovibrio variabilis* Fendrich 1989 is to be regarded as DSM 3050, not as currently published DSM 3051.
- (ii) The circumscription of the genus *Halovibrio* should be emended as proposed by Sorokin *et al.* (2006).
- (iii) This would also have the effect of placing members of the genus *Halovibrio* outside of the genus *Halomonas* and would mean that the names *Halovibrio variabilis* and *Halomonas variabilis* cannot be treated as synonyms.
- (iv) DSM 3051 should be recognized as the type strain of *P. halophila*.
- (v) The species name *Halomonas variabilis* (Fendrich 1989) Dobson and Franzmann 1996 is to be rejected, because it was created in the belief that *Halovibrio variabilis* was correctly represented by DSM 3051.
- (vi) Recognition of DSM 3051 as the type strain of *P. halophila* would mean that data collected for this strain indicate that it should be properly placed (at least at present) within the genus *Halomonas*. However, the name *Halomonas halophila* already exists and it would be necessary to create a new name (nomen novum) to reflect this taxonomic interpretation. We propose the combination *Halomonas utahensis* nom. nov. (homotypic synonym *P. halophila*) to accommodate strain DSM 3051, with the current authors (and date) being the authority of the name. The type strain is DSM 3051. The circumscription is emended, based on the original data of Fendrich (1988), together with the 16S rRNA gene sequence data of Dobson *et al.* (1993) and the chemotaxonomic data of Franzmann & Tindall (1990).
- (vii) Given the special circumstances under which the data were collected and published, we also request that the Judicial Commission recognize that the species name *Halovibrio denitrificans* was validly published by Sorokin *et al.* (2006).

This work further illustrates the necessity of carefully checking phenotypic (epigenetic) data against (genetic) molecular data and recognizing that correlation at both levels plays a vital role in biology and prokaryotic systematics.

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