Transfer of Acetobacter oboediens Sokollek et al. 1998 and Acetobacter intermedius Boesch et al. 1998 to the genus Gluconacetobacter as Gluconacetobacter oboediens comb. nov. and Gluconacetobacter intermedius comb. nov.

Yuzo Yamada

Tel: +81 54 635 2316. Fax: +81 54 635 2316. e-mail: yamada-yuzo@mub.biglobe.ne.jp

Acetobacter oboediens Sokollek et al. 1998 and Acetobacter intermedius Boesch et al. 1998 are transferred to the genus Gluconacetobacter as Gluconacetobacter oboediens comb. nov. and Gluconacetobacter intermedius comb. nov. because, on the basis of their 16S rRNA gene sequences, the type strains of both species are located in the cluster of the genus Gluconacetobacter along with those of Gluconacetobacter xylinus, Gluconacetobacter europaeus, Gluconacetobacter hansenii, Gluconacetobacter liquefaciens (the type species) and Gluconacetobacter diazotrophicus. The significance of growth on mannitol agar and the presence of a ubiquinone isoprenologue composed of Q-10 is discussed for characterization of the genus Gluconacetobacter.

Keywords: Gluconacetobacter oboediens comb. nov., Gluconacetobacter intermedius comb. nov., acetic acid bacteria, new combination

Recently, Sokollek et al. (1998) described Acetobacter oboediens and Boesch et al. (1998) described Acetobacter intermedius. Acetobacter oboediens LTH 2460\(^T\) and Acetobacter intermedius TF2\(^T\) were actually included within the cluster of the genus Gluconacetobacter in phylogenetic trees constructed on the basis of complete or near-complete 16S rRNA gene sequences reported by Sokollek et al. (1998), Boesch et al. (1998) and Yamada et al. (2000). The type strains of both species constituted a subcluster along with those of Gluconacetobacter xylinus, Gluconacetobacter hansenii and Gluconacetobacter europaeus. This subcluster 1 was different from subcluster 2, in which Gluconacetobacter liquefaciens and Gluconacetobacter diazotrophicus were located.

The genus Gluconacetobacter [sic] was introduced for acetate- and lactate-oxidizing acetoclastic bacteria equipped with Q-10 as the major ubiquinone (Yamada et al., 1997a). The generic name was validated and corrected as Gluconacetobacter nom. corrig. in accordance with Rule 61 of the Bacteriological Code (Yamada et al., 1998).

Boesch et al. (1998) stated that the name Gluconacetobacter was not valid on the basis of the note of Stackebrandt & Goebel (1994), because Yamada et al. (1997a) proposed the new genus without a complete or near-complete 16S rRNA gene sequence analysis. However, Stackebrandt & Goebel (1994) did not mention that such a proposal cannot be ‘valid’, though they noted that careful evaluation of the partial 16S rRNA sequence is required. In addition, Yamada et al. (1997a, b) discussed the phylogenetic and taxonomic positions of the species to be accommodated in the genus Gluconacetobacter by the use of their partial 16S rRNA sequences and the complete 16S rRNA gene sequences reported by Sievers et al. (1994a, b). The phylogenetic trees constructed by Sievers et al. (1994a, b) and by Yamada et al. (1997a, b, 2000) gave comparable results.

Franke et al. (1999) recognized the genus Gluconacetobacter and proposed a new species, Gluconacetobacter sacchari. In their paper, they mentioned “some newly sequenced and misidentified species, [Acetobacter] oboediens and ‘[Acetobacter] intermedius’, which should be reassigned to the genus Gluconacetobacter.”

Yamada et al. (2000) calculated the 16S rRNA gene sequence similarities between the type strains of Gluconacetobacter subcluster 1 to be 98.3–99.9 % and those between the type strains of species belonging to
**Gluconacetobacter** subcluster 1 and 2 to be 96.5–97.3%. In contrast, 16S rRNA gene sequence similarities of the type strains within the genera *Acetobacter* and *Gluconobacter* were 96.7–99.4% and 98.1–98.9%, respectively. The 16S rRNA gene sequence similarities of *Acetobacter oboediens* LTH 2460\(^{3}\) and *Acetobacter intermedius* TF2\(^{3}\) to the type strains of *Acetobacter aceti*, *Gluconobacter oxydans*, *Acidomonas methanolica* and *Asaia bogorensis* were 95.6–95.7, 95.2–95.3, 95.7–95.9 and 96.6–96.7%, respectively.

Sokollek *et al.* (1998) and Boesch *et al.* (1998) reported similarities that were similar to those proposed by Yamada *et al.* (2000). These data all support the classification of *Acetobacter oboediens* and *Acetobacter intermedius* in the genus *Gluconacetobacter*.

Boesch *et al.* (1998) mentioned neither the quinone system of *Acetobacter intermedius* nor the usefulness of the ubiquinone isoprenologue for differentiation of the genus *Gluconacetobacter* from the genus *Acetobacter*, which had already been described by Yamada *et al.* (1969, 1997a,b). The genus *Gluconacetobacter* is characterized by Q-10 and the genus *Acetobacter* is characterized by Q-9. The type strain (LTH 2458\(^{3}\)) of *Acetobacter pomorum* is actually equipped with Q-9 as the major ubiquinone (Sokollek *et al.*, 1998) and is located phylogenetically within the cluster of the genus *Acetobacter* along with *Acetobacter aceti* and *Acetobacter pasteurianus* in the trees constructed by Sokollek *et al.* (1998) and by Yamada *et al.* (2000).

Boesch *et al.* (1998) mentioned in their paper that “one of the characteristics that differentiates the four proposed genera, growth on mannitol agar only for the genera *Gluconobacter* and *Gluconacetobacter*, is definitely wrong.” In addition, they cited ‘YPM agar’ from the BCCM LMG List of Cultures Bacteria 1989, which corresponds to medium 13 (mannitol/yeast extract/peptone agar). Medium 13 or medium 17 (glucose/yeast extract/CaCO\(_3\) agar) is suggested by Janssens *et al.* (1998) for the cultivation of *Acetobacter*, *Gluconobacter* and *Frateria* strains. But this does not mean that all *Acetobacter* strains can indeed grow on mannitol agar. In fact, Asai *et al.* (1964) reported that *Gluconobacter* strains and the peripherally flagellated intermediate strains (i.e. strains of *Gluconacetobacter liquefaciens*) grew on mannitol agar, but *Acetobacter* strains showed scanty growth on this medium with the exception of two strains. In addition, Gosselé *et al.* (1983) described that 90% of strains of Phenon 2 (*Acetobacter liquefaciens*, 10 strains used), 50% of strains of Subphenon C (*Acetobacter hansenii*, 12 strains used), 100% of strains of Subphenon D (*Acetobacter aceti*, 7 strains used) and 15% of strains of Subphenon E (*Acetobacter pasteurianus*, 66 strains used) grew on mannitol medium. Of 98 strains that they examined, only 36% of strains (about 35 strains) grew on mannitol medium. Since *Acetobacter liquefaciens*, *Acetobacter hansenii* and *Acetobacter xylinus* were transferred to the genus *Gluconacetobacter* (Yamada *et al.*, 1997a), only Subphenon D and Subphenon E can be regarded as *Acetobacter* species.

Therefore, of 73 strains tested, only 17 (23%) grew on mannitol medium. Thus, the statement of Boesch *et al.* (1998) that all *Acetobacter* strains can grow on mannitol agar has lost standing.

Members of the genus *Gluconacetobacter* can be characterized by the combination of the ubiquinone isoprenologue composed of Q-10 as the major quinone, growth on mannitol agar for the majority of members and their 16S rRNA gene sequence. As a consequence, *Acetobacter oboediens* and *Acetobacter intermedius* should be transferred to the genus *Gluconacetobacter* as new combinations.

### Description of *Gluconacetobacter oboediens*

**(Sokollek, Hertel & Hammes 1998)** comb. nov.

*Gluconacetobacter oboediens* Sokollek, Hertel & Hammes. The description of the species was provided by Sokollek *et al.* (1998). The type strain is LTH 2460\(^{3}\) (= DSM 11826\(^{T}\)).

### Description of *Gluconacetobacter intermedius*

**(Boesch, Trček, Sievers & Teuber 1998)** comb. nov.

*Gluconacetobacter intermedius* Boesch, Trček, Sievers & Teuber. The description of the species was provided by Boesch *et al.* (1998). The type strain is TF2\(^{3}\) (= DSM 11804\(^{T}\)).

### References


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Transfer of two Acetobacter sp. to Gluconacetobacter


