

## Short Communication

# Description of *Komagataeibacter* gen. nov., with proposals of new combinations (*Acetobacteraceae*)

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The genus *Gluconacetobacter* Yamada et al. 1998 (*Gluconoacetobacter* [sic]) was introduced as the type species of *Gluconacetobacter liquefaciens* (Asai 1935) Yamada et al. 1998 by the elevation of the subgenus *Gluconacetobacter* (ex Asai 1935) Yamada and Kondo 1985 (Yamada et al., 1997, 1998). To date, 17 species have been accommodated to the genus (Yamada et al., 2012).

Franke et al. (1999) found a phylogenetic duality in the new genus *Gluconacetobacter*. Yamada et al.

(2000) divided the genus *Gluconacetobacter* into two subclusters, i.e., Subclusters 1 and 2. Subsequently, Dellaglio et al. (2005) and Lisdiyanti et al. (2006) recognized respectively two groups and two subclusters as well. Yamada and Yukphan (2008) suggested that the *Gluconacetobacter liquefaciens* group and the *Gluconacetobacter xylinus* group in the genus *Gluconacetobacter* can be phylogenetically, phenotypically and ecologically distinguished from each other at the generic level.

Yamada et al. (2012) proposed the new genus *Komagataeibacter* (*Komagatabacter* [sic]) with 12 new combinations on the basis of these taxonomic characteristics. However, the new name of the genus and the new combinations were not recognized in their validations, since the proposals that were done without any indications of the deposits in the type strains in at least two different collections in two different countries were not in accordance with Rule 27 of the Bacteriological

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Code (Tindall et al., 2006).

This paper newly gives the descriptions of *Komagataeibacter* gen. nov. and *Komagataeibacter xylinus* comb. nov., the type species of the genus, along with the new combinations of the remaining species.

Upon the proposals of the new genus and the new combinations for the second time, discussion is briefly made as follows, since it was already done in detail (Yamada and Yukphan, 2008; Yamada et al., 2012).

All the 16S rRNA gene sequences were obtained from the GenBank/EMBL/DDBJ databases. A phylogenetic tree based on 16S rRNA gene sequences of 1,216 bases was constructed by the neighbor-joining method (Saitou and Nei, 1987), as described previously (Yamada and Yukphan, 2008; Yamada et al., 2012). The confidence values of individual branches in the phylogenetic tree were calculated by use of the bootstrap analysis of Felsenstein (1985) based on 1,000 replications. The 16S rRNA gene sequence similarity was calculated for 1,446 bases.

In a 16S rRNA gene sequence phylogenetic tree constructed by the neighbor-joining method, the members of the *Gluconacetobacter xylinus* group and the *Gluconacetobacter liquefaciens* group constituted separate clusters (Fig. 1). The calculated bootstrap value at the branching point of the two clusters was 45%. This indicated that the two groups were not so tightly coupled phylogenetically. The calculated 16S rRNA gene sequence similarity was 96.9% between the type strains of *Gluconacetobacter liquefaciens* and *Gluconacetobacter xylinus*.

The two groups were differentiated from each other phenotypically (Table 1). The members of the *Gluconacetobacter liquefaciens* group were motile equipped with peritrichous flagella. On the other hand, the members of the *Gluconacetobacter xylinus* group were non motile without any flagellation. The former produced a water soluble-brown pigment, when grown on glucose/yeast extract/calcium carbonate medium, but the latter did not. The former produced 2,5-diketo-D-gluconate and  $\gamma$ -pyrone compounds from D-glucose, but the latter did not. The former was plant-associated, but the latter was not necessarily plant-associated (Yamada and Yukphan 2008; Yamada et al., 2012).

Cleenwerck et al. (2010) recognized that the genus *Gluconacetobacter* should not remain as a single genus on the basis of multilocus sequence analyses of the three housekeeping genes of *dnaK*, *groEL* and *rpoB*, as already suggested by Yamada and Yukphan (2008).

However, they stated that some of phenotypic features were of little use for the differentiation of acetic acid bacteria and that for this reason other differentiating features should be looked for before splitting the genus.

In contrast to their opinion, the above-mentioned phenotypic features were practically utilized without any exceptions to differentiate the two groups from each other and from the members of the genera *Acetobacter*, *Gluconobacter*, *Asaia*, *Swaminathania*, *Saccharibacter*, *Neoasaia*, *Granulibacter*, *Tanticharoenia*, *Ameyamaea*, and *Neokomagataea* in combination of other phenotypic features (Yamada and Yukphan, 2008; Yamada et al., 2012).

The phylogenetic and phenotypic characteristics obtained make it possible to separate the *Gluconacetobacter xylinus* group from the *Gluconacetobacter liquefaciens* group at the generic level, and the species of the former group can appropriately be classified under a separate new genus. The name of the genus is *Komagataeibacter* gen. nov.

Description of *Komagataeibacter* gen. nov.

*Komagataeibacter* [Ko.ma.ga.ta.e.i.bac'ter. N.L. fem. n. *Komagataea* Komagata (the name of a famous Japanese microbiologist); N.L. masc. n. *bacter* a rod; N.L. masc. n. *Komagataeibacter* a rod, which is named in honor of Dr. Kazuo Komagata, Professor, The University of Tokyo, Bunkyo-ku, Tokyo, Japan, who contributed to the bacterial systematics, especially of acetic acid bacteria].

Gram-negative rods and non-motile, measuring  $0.5\text{--}0.8 \times 1.0\text{--}3.0 \mu\text{m}$ . Colonies are white-creamy and smooth with entire margin or rough. Oxidizes acetate and lactate to carbon dioxide and water. Produces acetic acid from ethanol. Growth is positive in the presence of 0.35% acetic acid v/v. In general, grows on glutamate agar and mannitol agar. Does not produce a water-soluble brown pigment on glucose/yeast extract/calcium carbonate medium. In some strains, cellulosic materials are produced. In some strains, acetic acid is required for growth. Ammoniac nitrogen is generally assimilated on D-mannitol. Production of dihydroxyacetone from glycerol is generally positive. Produces 2-keto-D-gluconate and/or 5-keto-D-gluconate from D-glucose, but 2,5-diketo-D-gluconate is not produced.  $\gamma$ -Pyrone compounds are not produced. In some strains, ketogluconates are not produced. Acid is produced from D-glucose, D-galactose, D-xylose, L-arabinose or ethanol, but not from D-fructose, L-sor-

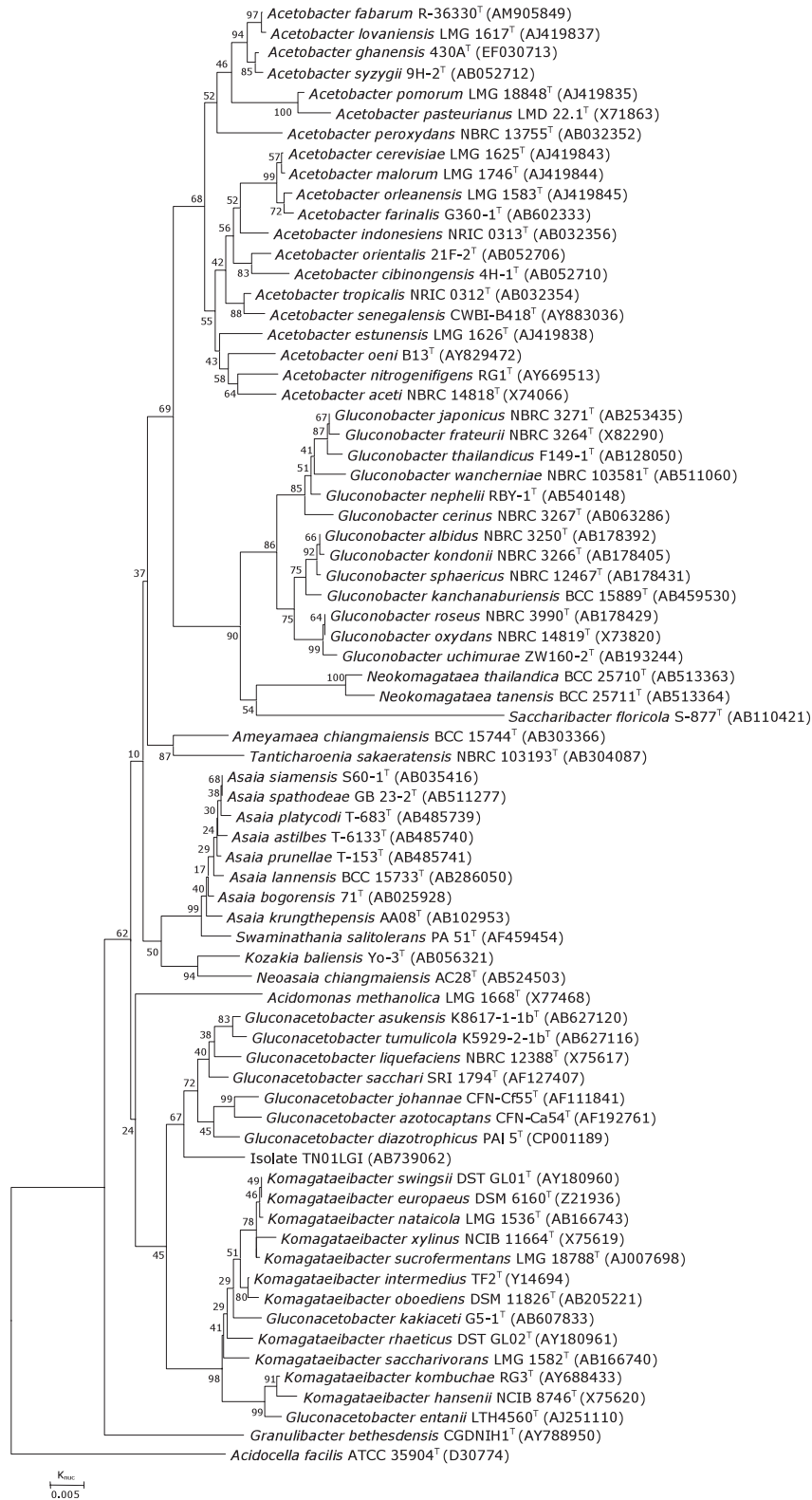


Fig. 1. A phylogenetic tree based on 16S rRNA gene sequences for acetic acid bacteria. The phylogenetic tree derived from the neighbor-joining method was newly constructed (Yamada et al., 2012). The type strain of *Acidocella facilis* was used as an outgroup. The numerals at the respective branching points indicate bootstrap values (%) based on 1,000 replications.

Table 1. Differential characteristics of the genera *Gluconacetobacter* and *Komagataeibacter*.

Characteristics	<i>Gluconacetobacter</i>					<i>Komagataeibacter</i>										
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Flagellation	per	per	per	per	per	no	no	no	no	no	no	no	no	no	no <sup>c</sup>	no
Oxidation of Acetate	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Lactate	+	+	+	+	+	+	+	+	nd	nd	nd	nd	+	+	+	+
Growth without acetic acid	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+
Growth on <sup>a,b</sup>																
Glutamate agar	+	+	+	nd	nd	+	+	+	nd	+	nd	nd	+	+	nd	+
Mannitol agar	+	+	+	nd	nd	+	+	+	nd	+	nd	nd	+	+	nd	+
Production of acetic acid from ethanol	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Production of a water-soluble brown pigment	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-
Production of dihydroxyacetone from glycerol	+	+	-	nd	nd	+	+	nd	+	nd	nd	nd	+	+	nd	+
Cellulose production	-	-	-	-	-	+	-	-	-	-	+	+	-	+	+	+
Production of $\gamma$ -pyrone compounds	+	+ <sup>c</sup>	+ <sup>c</sup>	+ <sup>c</sup>	+ <sup>c</sup>	-	-	-	-	-	-	-	-	-	-	-
Assimilation of ammoniac nitrogen on <sup>b</sup>																
Mannitol	+	+	+	-	-	nd	+	nd	nd	nd	nd	nd	+	+	nd	nd
Ethanol	- <sup>c,d</sup>	+	+	+	+	nd	-	nd	nd	nd	nd	nd	-	-	nd	nd
Production of																
2-Keto-D-gluconate	+	+	+	- <sup>f</sup>	- <sup>f</sup>	+	+	+	+	-	+	+	+	+	-	+
5-Keto-D-gluconate	+	-	+	- <sup>f</sup>	- <sup>f</sup>	+	+	+	-	-	+	+	-	+	+	-
2,5-Diketo-D-gluconate	+	+	+	+ <sup>f</sup>	+ <sup>f</sup>	-	-	-	-	-	-	-	-	-	-	-
DNA G+C content (mol%)	64.5 <sup>e</sup>	61	65	58.0	64.0	62.5	59.0	56.2-57.3	59.9	61.6	61.7	63.4	61	62	55.8 <sup>g</sup>	62.3

The table was cited from Yamada et al. (2012) with slight modifications.

per, peritrichous; no, none; +, positive; -, negative; nd, not determined. A major ubiquinone was Q-10 in all the strains tested.

1, *Gluconacetobacter liquefaciens* NBRC 12388<sup>T</sup> (Navarro and Komagata, 1999); 2, *G. diazotrophicus* LMG 7603<sup>T</sup> (Gillis et al., 1989); 3, *G. sacchari* strain SRI 1794<sup>T</sup> (Franke et al., 1999) 4, *G. johannae* strain CFN-Cf55<sup>T</sup> (Fuentes-Ramirez et al., 2001); 5, *G. azotocaptans* strain CFN-Ca54<sup>T</sup> (Fuentes-Ramirez et al., 2001); 6, *Komagataeibacter xylinus* JCM 7644<sup>T</sup> (Navarro and Komagata, 1999); 7, *K. hansenii* NBRC 14820<sup>T</sup> (Lisdilyanti et al., 2006); 8, *K. europaeus* strain DES 11<sup>T</sup> (Sievers et al., 1992); 9, *K. oboediens* LTH 2460<sup>T</sup> (Sokollek et al., 1998); 10, *K. intermedium* strain TF2<sup>T</sup> (Boesch et al., 1998); 11, *K. swingsii* strain DST GL01<sup>T</sup> (Dellaglio et al., 2005); 12, *K. rhaeticus* strain DST GL02<sup>T</sup> (Dellaglio et al., 2005); 13, *K. saccharivorans* LMG 1582<sup>T</sup> (Lisdilyanti et al., 2006); 14, *K. nataicola* LMG 1536<sup>T</sup> (Lisdilyanti et al., 2006); 15, *K. kombuchae* strain RG3<sup>T</sup> (Dutta and Gachhui, 2007) 16, *K. sucrofermentans* strain BPR 2001<sup>T</sup> (Cleenwerck et al., 2010; Toyosaki et al., 1995).

<sup>a</sup>Navarro and Komagata (1999); <sup>b</sup>Lisdilyanti et al. (2006); <sup>c</sup>Yamada et al. (2012); <sup>d</sup>Lisdilyanti et al. (2000); <sup>e</sup>Yamada et al. (1981); <sup>f</sup>Tazato et al. (2012); <sup>g</sup>According to Cleenwerck et al. (2009), the DNA G+C content is 59.5 mol%.

bose, D-mannitol, D-sorbitol, maltose or lactose. Grows on D-glucose, D-fructose or D-mannitol, but not on lactose. A major isoprenoid quinone is Q-10. DNA base composition is 55.8–63.4 mol% G+C with a range of 7.6 mol%. The type species is *Komagataeibacter xylinus* (Brown 1886) comb. nov.

Description of *Komagataeibacter xylinus* (Brown 1886) comb. nov.

*Komagataeibacter xylinus* (xyli'nus. L. adj. *xylinus* of cotton).

Characteristics are the same as those described in the genus and those given by Yamada (1983) and Navarro and Komagata (1999). Strains classified in the species do not require acetic acid for growth. Some strains including the type strain produce cellulosic materials (Yamada et al., 1976). DNA base composition is 59.4–63.2 mol% G+C with a range of 3.8 mol% (Navarro and Komagata, 1999). The type strain is NCIMB 11664<sup>T</sup> (=NBRC 15237<sup>T</sup>=JCM 7644<sup>T</sup>=BCC 49175<sup>T</sup>=DSM 6513<sup>T</sup>=LMG 1515<sup>T</sup>).

Synonym: *Gluconacetobacter xylinus* (Brown 1886) Yamada, Hoshino and Ishikawa, Biosci. Biotechnol. Biochem. 61: 1250, 1997 (Validation list no. 64, Int. J. Syst. Bacteriol. 48: 327, 1998); *Acetobacter xylinus* (Brown 1886) Yamada, J. Gen. Appl. Microbiol. 29: 419, 1983 (Validation list no. 14, Int. J. Syst. Bacteriol. 34: 270, 1984).

Basonym: *Acetobacter acetii* (Beijerinck 1898) subsp. *xylinus* (Brown 1886) corrig. De Ley and Frateur 1974 (Approved lists, Int. J. Syst. Bacteriol. 30: 239, 1980).

The following *Gluconacetobacter* species were transferred to the genus *Komagataeibacter*.

*Komagataeibacter hansenii* (Gosselé, Swings, Kersters, Pauwels and De Ley 1983) comb. nov.

The description of the species is identical with that given for the new genus and that given by Gosselé et al. (1983) and Lisdiyanti et al. (2006).

The type strain is NCIMB 8746<sup>T</sup> (=NBRC 14820<sup>T</sup>=JCM 7643<sup>T</sup>=BCC 6318<sup>T</sup>=DSM 5602<sup>T</sup>=LMG 1527<sup>T</sup>).

Synonym: *Gluconacetobacter hansenii* (Gosselé, Swings, Kersters, Pauwels and De Ley 1983) Yamada, Hoshino and Ishikawa, Biosci. Biotechnol. Biochem. 61: 1250, 1997 (Validation list no. 64, Int. J. Syst. Bacteriol. 48: 327, 1998).

Basonym: *Acetobacter hansenii* Gosselé, Swings,

Kersters, Pauwels and De Ley, Syst. Appl. Microbiol. 4: 366, 1983 (Validation list no. 12, Int. J. Syst. Bacteriol. 33: 896, 1983).

*Komagataeibacter europaeus* (Sievers, Sellmer and Teuber 1992) comb. nov.

The description of the species is identical with that given for the new genus and that given by Sievers et al. (1992).

The type strain is DSM 6160<sup>T</sup> (=JCM 16935<sup>T</sup>=BCC 36446<sup>T</sup>).

Synonym: *Gluconacetobacter europaeus* (Sievers, Sellmer and Teuber 1992) Yamada, Hoshino and Ishikawa, Biosci. Biotechnol. Biochem. 61: 1250, 1997 (Validation list no. 64, Int. J. Syst. Bacteriol. 48: 327, 1998).

Basonym: *Acetobacter europaeus* Sievers, Sellmer and Teuber, Syst. Appl. Microbiol. 15: 391, 1992 (Validation list no. 43, Int. J. Syst. Bacteriol. 42: 656, 1992).

*Komagataeibacter oboediens* (Sokollek, Hertel and Hammes 1998) comb. nov.

The description of the species is identical with that given for the new genus and that given by Sokollek et al. (1998).

The type strain is DSM 11826<sup>T</sup> (=JCM 16937<sup>T</sup>=BCC 36445<sup>T</sup>=LMG 18849<sup>T</sup>).

Synonym: *Gluconacetobacter oboediens* (Sokollek, Hertel and Hammes 1998) Yamada, Int. J. Syst. Evol. Microbiol. 50: 226, 2000.

Basonym: *Acetobacter oboediens* Sokollek, Hertel and Hammes, Int. J. Syst. Bacteriol. 48: 939, 1998.

*Komagataeibacter intermedius* (Boesch, Trček, Sievers and Teuber 1998) comb. nov.

The description of the species is identical with that given for the new genus and that given by Boesch et al. (1998).

The type strain is DSM 11804<sup>T</sup> (=JCM 16936<sup>T</sup>=BCC 36447<sup>T</sup>=LMG 18909<sup>T</sup>).

Synonym: *Gluconacetobacter intermedius* (Boesch, Trček, Sievers and Teuber 1998) Yamada, Int. J. Syst. Evol. Microbiol. 50: 226, 2000.

Basonym: *Acetobacter intermedius* Boesch, Trček, Sievers and Teuber, Syst. Appl. Microbiol. 21: 228, 1998 (Validation list no. 67, Int. J. Syst. Bacteriol. 48: 1083, 1998).

According to Lisdiyanti et al. (2006), this species is a

later heterotypic synonym of *Gluconacetobacter oboediens*.

*Komagataeibacter swingsii* (Dellaglio, Cleenwerck, Felis, Engelbeen, Janssens and Marzotto 2005) comb. nov.

The description of the species is identical with that given for the new genus and that given by Dellaglio et al. (2005).

The type strain is LMG 22125<sup>T</sup> (=JCM 17123<sup>T</sup>=BCC 36451<sup>T</sup>=DSM 16373<sup>T</sup>).

Basonym: *Gluconacetobacter swingsii* Dellaglio, Cleenwerck, Felis, Engelbeen, Janssens and Marzotto, Int. J. Syst. Evol. Microbiol. 55: 2368, 2005.

*Komagataeibacter rhaeticus* (Dellaglio, Cleenwerck, Felis, Engelbeen, Janssens and Marzotto 2005) comb. nov.

The description of the species is identical with that given for the new genus and that given by Dellaglio et al. (2005).

The type strain is LMG 22126<sup>T</sup> (=JCM 17122<sup>T</sup>=BCC 36452<sup>T</sup>=DSM 16663<sup>T</sup>).

Basonym: *Gluconacetobacter rhaeticus* Dellaglio, Cleenwerck, Felis, Engelbeen, Janssens and Marzotto, Int. J. Syst. Evol. Microbiol. 55: 2369, 2005.

*Komagataeibacter saccharivorans* (Lisdiyanti, Navarro, Uchimura and Komagata 2006) comb. nov.

The description of the species is identical with that given for the new genus and that given by Lisdiyanti et al. (2006).

The type strain is LMG 1582<sup>T</sup> (=JCM 25121<sup>T</sup>=NRIC 0614<sup>T</sup>=BCC 36444<sup>T</sup>).

Basonym: *Gluconacetobacter saccharivorans* Lisdiyanti, Navarro, Uchimura and Komagata, Int. J. Syst. Evol. Microbiol. 56: 2108, 2006.

*Komagataeibacter nataicola* (Lisdiyanti, Navarro, Uchimura and Komagata 2006) comb. nov.

The description of the species is identical with that given for the new genus and that given by Lisdiyanti et al. (2006).

The type strain is LMG 1536<sup>T</sup> (=JCM 25120<sup>T</sup>=NRIC 0616<sup>T</sup>=BCC 36443<sup>T</sup>).

Basonym: *Gluconacetobacter nataicola* Lisdiyanti, Navarro, Uchimura and Komagata, Int. J. Syst. Evol. Microbiol. 56: 2109, 2006.

*Komagataeibacter kombuchae* (Dutta and Gachhui 2007) comb. nov.

The description of the species is identical with that given for the new genus and that given by Dutta and Gachhui (2007).

The type strain is LMG 23726<sup>T</sup> (=NBRC 14820<sup>T</sup>=MTCC 6913<sup>T</sup>).

Basonym: *Gluconacetobacter kombuchae* Dutta and Gachhui, Int. J. Syst. Evol. Microbiol. 57: 356, 2007.

According to Cleenwerck et al. (2009), this species is a later heterotypic synonym of *Gluconacetobacter hansenii*.

*Komagataeibacter sucrofermentans* (Toyosaki, Kojima, Tsuchida, Hoshino, Yamada and Yoshinaga 1996) comb. nov.

The description of the species is identical with that given for the new genus and that given by Toyosaki et al. (1995) and Cleenwerck et al. (2010).

The type strain is LMG 18788<sup>T</sup> (=JCM 9730<sup>T</sup>=BCC 7227<sup>T</sup>=DSM 15973<sup>T</sup>).

Synonym: *Gluconacetobacter sucrofermentans* (Toyosaki, Kojima, Tsuchida, Hoshino, Yamada and Yoshinaga 1996) Cleenwerck, De Vos and Vuyst, Int. J. Syst. Evol. Microbiol. 60: 2282, 2010.

Basonym: *Acetobacter xylinus* (Brown 1886) (*xylinum* [sic]) Yamada 1984 subsp. *sucrofermentans* Toyosaki, Kojima, Tsuchida, Hoshino, Yamada and Yoshinaga, J. Gen. Appl. Microbiol. 41:312, 1995 (Validation list no. 58, Int. J. Syst. Bacteriol. 46: 836, 1996).

Since the type strain of *Gluconacetobacter entanii* Schüller Hertel and Hammes 2000 is not available in any culture collection including DSM (Schüller et al., 2000), the species cannot be listed as a new combination, according to Rule 27 of the Bacteriological Code (Tindall et al., 2006).

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