

**Cultivation and characterization of the gut symbionts of honey bees and bumble bees: *Snodgrassella alvi* gen. nov., sp. nov., a member of the *Neisseriaceae* family of the *Betaproteobacteria*; and *Gilliamella apicola* gen. nov., sp. nov., a member of the *Orbaceae* fam. nov., *Orbales* ord. nov., a sister taxon to the *Enterobacteriales* order of the *Gammaproteobacteria*.**

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**Running title:** Cultivation of the gut symbionts of bees

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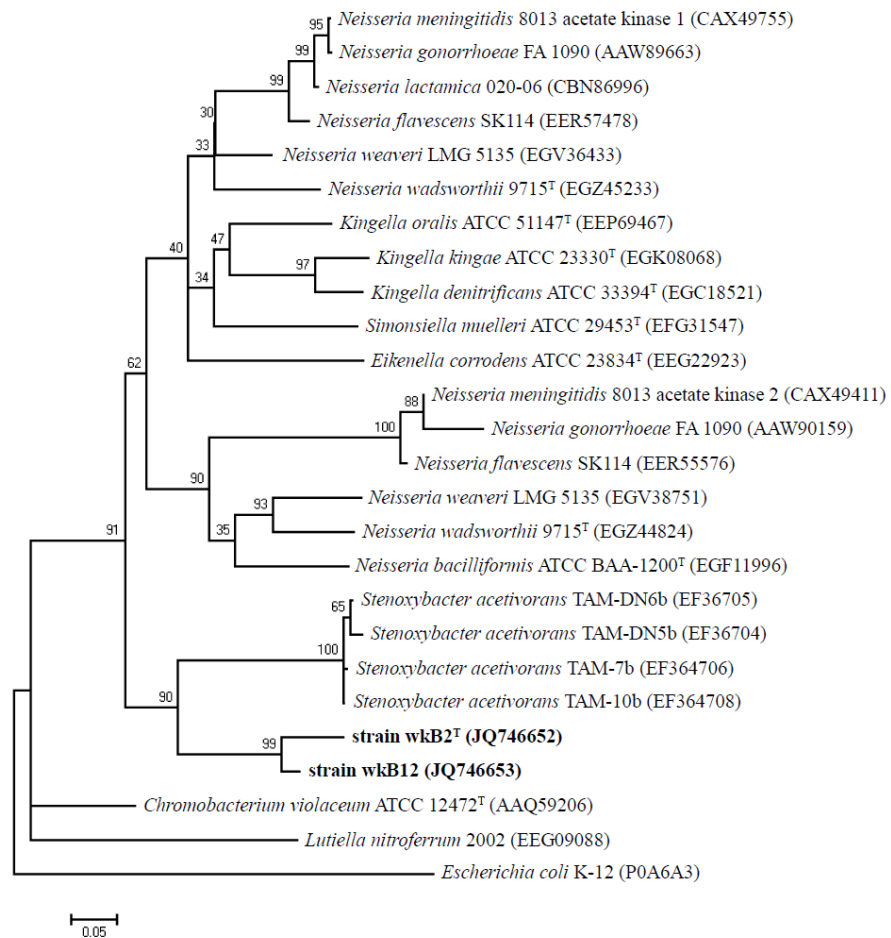
**Category:** New Taxa (Proteobacteria)

**Sequence deposited:**

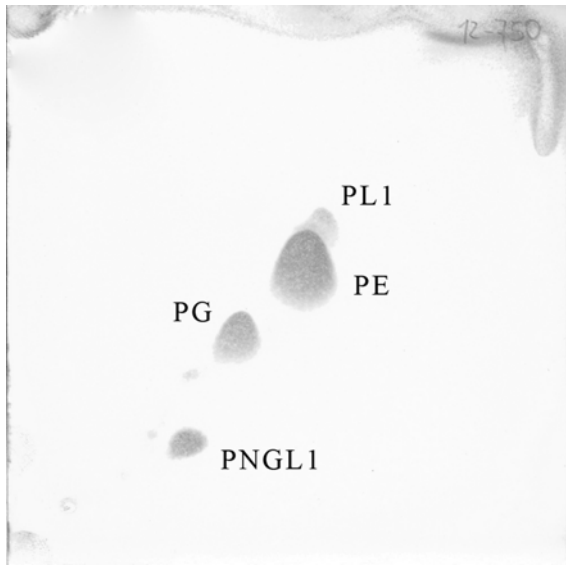
The 16S rRNA gene sequences of strains wkB2<sup>T</sup>, wkB12, and wkB29 are deposited in GenBank with accession numbers JQ746645 through JQ746651, while those of strains wkB1<sup>T</sup>, wkB11, and wkB30 are JQ936674 through JQ936676. Accession numbers for the *ack* gene of strains wkB2<sup>T</sup> and wkB12 are JQ746652 and JQ746653 respectively. Protein-coding genes of strains wkB1<sup>T</sup>, wkB11, and wkB30 used in this study are deposited under JQ894901 through JQ894930.

**Table S1.** GenBank accession numbers of sequences used to produce Fig. 5

| <b>Gene</b> | <b>Strain</b>     | <b>Accession no.</b> | <b>Length (aa)</b> |
|-------------|-------------------|----------------------|--------------------|
| <i>dnaE</i> | wkB1 <sup>T</sup> | JQ894928             | 1021               |
| <i>dnaE</i> | wkB11             | JQ894929             | 1021               |
| <i>dnaE</i> | wkB29             | JQ894930             | 1021               |
| <i>ftsH</i> | wkB1 <sup>T</sup> | JQ894925             | 599                |
| <i>ftsH</i> | wkB11             | JQ894926             | 598                |
| <i>ftsH</i> | wkB29             | JQ894927             | 598                |
| <i>glyS</i> | wkB1 <sup>T</sup> | JQ894922             | 685                |
| <i>glyS</i> | wkB11             | JQ894923             | 685                |
| <i>glyS</i> | wkB29             | JQ894924             | 685                |
| <i>mutS</i> | wkB1 <sup>T</sup> | JQ894919             | 859                |
| <i>mutS</i> | wkB11             | JQ894920             | 859                |
| <i>mutS</i> | wkB29             | JQ894921             | 859                |
| <i>parC</i> | wkB1 <sup>T</sup> | JQ894916             | 730                |
| <i>parC</i> | wkB11             | JQ894917             | 730                |
| <i>parC</i> | wkB29             | JQ894918             | 730                |
| <i>recA</i> | wkB1 <sup>T</sup> | JQ894913             | 315                |
| <i>recA</i> | wkB11             | JQ894914             | 315                |
| <i>recA</i> | wkB29             | JQ894915             | 315                |
| <i>rpoB</i> | wkB1 <sup>T</sup> | JQ894910             | 1341               |
| <i>rpoB</i> | wkB11             | JQ894911             | 1341               |
| <i>rpoB</i> | wkB29             | JQ894912             | 1341               |
| <i>secA</i> | wkB1 <sup>T</sup> | JQ894907             | 906                |
| <i>secA</i> | wkB11             | JQ894908             | 904                |
| <i>secA</i> | wkB29             | JQ894909             | 906                |
| <i>serS</i> | wkB1 <sup>T</sup> | JQ894904             | 429                |
| <i>serS</i> | wkB11             | JQ894905             | 429                |
| <i>serS</i> | wkB29             | JQ894906             | 429                |
| <i>uvrA</i> | wkB1 <sup>T</sup> | JQ894901             | 932                |
| <i>uvrA</i> | wkB11             | JQ894902             | 932                |
| <i>uvrA</i> | wkB29             | JQ894903             | 932                |



**Figure S1.** Maximum-likelihood phylogeny of *Snodgrassella alvi* strains and other *Neisseriaceae* based on partial acetate kinase (*ack*) amino acid sequence. A length of 202 residues, corresponding to the region available in *Stenoxybacter* (EF364702), was aligned by ClustalW. Strain wkB2<sup>T</sup> and wkB12 *ack* sequences were retrieved from whole genome sequencing data. The tree was reconstructed using the JTT substitution model and bootstrapped 500 times. *E. coli* K12 *ackA* is the outgroup.



**Figure S2.** Polar lipid composition of strain wkb1<sup>T</sup>, from two dimensional silica gel thin layer chromatography (DSMZ, Braunschweig, Germany). PE = phosphatidylethanolamine, PG = phosphatidylglycerol, PNGL1 = phosphoaminoglycolipid, PL1 = phospholipid.