A yellow-pigmented strain (JM-1081\textsuperscript{T}) isolated from healthy stem tissue of Zea mays was taxonomically characterized. Cells of the strain were rod-shaped and Gram-stain-negative. Comparative 16S rRNA gene sequence analysis revealed closest relationship to the type strains of Sphingobacterium multitum (98.1\% similarity), Sphingobacterium mucilaginosus (97.9\%) and Sphingobacterium siyangense (97.8\%). 16S rRNA gene sequence similarities to the type strains of all other Sphingobacterium species were below 97.8\%. Fatty acid analysis of whole-cell hydrolysates of the strain resulted in a pattern typical of the genus Sphingobacterium with iso-C\textsubscript{15:0} 2-OH and/or C\textsubscript{16:1}ω7c, iso-C\textsubscript{15:0}, iso-C\textsubscript{17:0} 3-OH and C\textsubscript{16:0} as the most prevalent compounds. Characteristic chemotaxonomic markers are the high content of sphingophospholipids among cellular lipids and menaquinone 7 (MK-7) as the predominant respiratory quinone (Yabuuchi et al., 1983). At the time of writing, the genus comprised 32 species with validly published names, including four species that were isolated from plant material, Sphingobacterium canadense isolated from corn root (Mehnaz et al., 2007), Sphingobacterium nematocida, a tobacco endophyte (Liu et al., 2012), Sphingobacterium yanglingense isolated from the nodule surface of soybean (Peng et al., 2014) and Sphingobacterium pakistanense, a plant-growth-promoting rhizobacterium isolated from the rhizosphere of Vigna mungo (Ahmed et al., 2014).

Here we describe strain JM-1081\textsuperscript{T}, which was isolated as an endophyte from the healthy internal stem tissue of mature maize (Zea mays, cultivar ‘Sweet Belle’). The strain was isolated and grown on tryptic soy agar (TSA; Oxoid) at 30°C and also further maintained and subcultivated on this agar at 30°C for 48 h.

The cultural and morphological characteristics were taken from observation with cultures grown on TSA. Gram staining was done according to Gerhardt et al. (1994) and a motility test was done under a light microscope with cells grown for 3 days in tryptic soy broth (TSB; Oxoid) at 30°C. Temperature-dependent growth was tested at 4, 10, 15, 25, 28, 30, 36, 42, 45 and 50°C on nutrient agar. NaCl tolerance was investigated at different concentrations of NaCl [1.0–8.0 \% (w/v); in 1 \% increments] in TSB. pH-dependent growth was tested using TSB adjusted to pH values of pH

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The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain JM-1081\textsuperscript{T} is KU201960.
4.5–10.5 (in 1.0 pH units intervals). The pH values were adjusted using 1 M HCl and 1 M KOH and stabilized by the addition of 5 mM phosphate buffer adjusted to the same pH values.

Strain JM-1081<sup>T</sup> showed a Gram-negative staining behaviour and produced visible (diameter about 2 mm) yellow colonies within 48 h at 30 °C. The isolate did not grow below 4 °C or above 45 °C. The strain grew very slowly at 45 °C and at NaCl concentrations of 1–4 % (w/v), but not at 5 % (w/v) and above. In addition, the strain grew at pH values of 5.5–9.0 under the conditions described above, but not at pH values below 5.5 or above 9.0.

Colonies revealed a translucent glistening appearance with entire edges. The yellow pigment was shown to be of the flexirubin type (KOH method according to Reichenbach, 1989). Oxidase activity was positive with oxidase reagent (bioMérieux). Cells of the strain were non-motile rods (approx. 1 µm wide and 2 µm long). Spores could not be detected. The strain grew well on complex agar media, such as nutrient agar, brain heart infusion agar, R2A agar and TSA, but not on MacConkey agar (Oxoid).

For phylogenetic identification, the nearly full-length 16S rRNA gene of strain JM-1081<sup>T</sup> was PCR-amplified with primers 8F (5′-AGAGTTTGATCCTGCGTGAGC-3′) and 1492R (5′-ACGCTACCTTGTTACGACTT-3′, Lane, 1991) and sequenced by the dideoxy sequencing method with primers 8F and E786F (5′-GATTAGATACCCTGCTAGTAG-3′). The manually corrected 16S rRNA gene sequence represented a continuous stretch of 1436 nt spanning gene positions 20–1477 (according to the Escherichia coli numbering published by Brosius et al., 1978). A BLAST analysis in the EzTaxon type strain 16S rRNA gene sequence database (Kim et al., 2012) showed that strain JM-1081<sup>T</sup> shared highest 16S rRNA gene sequence similarity with the type strains of Sphingobacterium multivorum (98.1 %), Sphingobacterium mucilaginosum (97.9 %) and Sphingobacterium siyangense (97.8 %). All other Sphingobacterium type strains showed a gene sequence similarity to strain JM-1081<sup>T</sup> that was below 97.8 %. The next closest related plant-derived species, S. canadense, showed a 16S rRNA gene sequence similarity to strain JM-1081<sup>T</sup> of 97.7 %. Sequence similarities to the type strains of all described species was below the proposed 16S rRNA gene sequence cut-off value of 98.65 % for species delineation (Kim et al., 2014). The phylogenetic relationship between strain JM-1081<sup>T</sup> and all Sphingobacterium type strains was investigated in more detail using DNA–DNA hybridization experiments performed with strain JM-1081<sup>T</sup> and the type strains of two of the most closely related Sphingobacterium species, S. siyangense SY1<sup>T</sup> and S. multivorum NCTC 11343<sup>T</sup>, and the closest related plant-derived species, S. canadense LMG 23727<sup>T</sup>. Hybridization was done according to the method of Ziemke et al. (1998) (except that for nick translation 2 µg DNA was labelled during 3 h of incubation at 15 °C) using DNA extracted according to the method of Pitcher & Saunders (1989). Strain JM-1081<sup>T</sup> showed low levels of DNA–DNA relatedness to all three reference strains, S. multivorum NCTC 11343<sup>T</sup> (29 %, reciprocal 29 %), S. siyangense SY1<sup>T</sup> (47 %, reciprocal 20 %) and S. canadense LMG 23727<sup>T</sup> (56 %, reciprocal 37 %).

Strain JM-1081<sup>T</sup> was physiologically/biochemically studied by using the methods described by Kämper et al. (1991) and by additional biochemical tests, among them the production of hydrogen sulphide using the lead acetate paper and triple-sugar-iron methods, indole reaction with Ehrlich’s and Kovacs’ reagents, activity of arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, DNase (Oxoid CM321; supplemented with 0.01 % toluidine blue), β-galactosidase (ONPG) and urease on Christensen’s urea agar (Kämper, 1990); and hydrolysis of casein, gelatin (plate method), starch and tyrosine (Smith & Krieg, 1994). The biochemical/physiological data are given in Table 1 and in the species description.

Analysis of the cellular fatty acid profiles from whole-cell hydrolysates was performed as described previously (Kämper & Kropf, 1996) by using an HP 6890 gas chromatograph with Sherlock MIDI software version 2.11 and a TSBA peak naming table version 4.1. Prior to fatty acid extraction the strain was cultured on TSA at 28 °C for 48 h. The results are shown in Table 2 in comparison with...
the most closely related type strains (including S. multivor-
rum JCM 21156\(^\text{1} \), S. siyangense SC-1\(^\text{1} \) and S. canadense
CR11\(^\text{1} \)) and revealed a profile typical for the genus Sphingo-
bacterium, with the following most abundant fatty acids:
iso-C\(_{15:0}\) 2-OH and/or C\(_{16:1}\) \(\omega 7\) detected as summed feature
3, but as shown in previous studies could be
clearly identified as iso-C\(_{15:0}\) 2-OH (Montero-Calasanz
et al., 2013), iso-C\(_{15:0}\) iso-C\(_{17:0}\) 3-OH and C\(_{16:1}\) \(\omega 7\). Only
minor differences were found in comparison with the
profiles of the type strains of the most closely related Sphingo-
bacterium species.

Polyamines, quinones, sphingolipids, polar lipids and
meso-diaminopimelic acid were extracted from biomass
grown in PYE broth [0.3 % (w/v) peptone from casein,
0.3 % (w/v) yeast extract, pH 7.2]. Polyamines were
extracted according to Busse & Auling (1988) and analysed
according to Kato et al., (1995). The presence of a sphingolipid
was unambiguously demonstrated by a single spot which
stained positive for an amino group and a phosphate
group. The polyamine pattern consisted of sym-homospem-
midine [36.7 µmol (g dry weight)\(^{-1}\)], spermidine [4.1 µmol
(g dry weight)\(^{-1}\)], spermine [1.6 µmol (g dry weight)\(^{-1}\)],

Fig. 1. Maximum-parsimony tree based on nearly full-length 16S rRNA gene sequences showing the phylogenetic affiliation of
strain JM-1081\(^\text{1} \) among the type strains of all Sphingobacterium species. The tree was calculated in arbor and based on 16S
rRNA gene sequences between termini 59 and 1440 (according to the E. coli numbering; Brosius et al., 1978). Numbers
at nodes represent bootstrap values \(\geq 70\% \) (100 replications). Nodes marked with filled circles were also present in the
respective maximum-likelihood and neighbour-joining trees. Larger circles mark nodes with \(\geq 70\% \) bootstrap support in the
other treeing methods, small circles \(<70\% \). Mucllaginibacter gracilis TPT18\(^\text{1} \) and Mucllaginibacter paludis TPT56\(^\text{1} \) were
used as the outgroup. Bar, 0.1 substitutions per nucleotide position.
and traces of putrescine and cadaverine (each 0.1 µmol (g dry weight)) and the quinone system consisted of menaquinone MK-7 (99 %) and MK-6 (1 %). Both polyamine pattern (Hamana & Matsuzaki, 1991; Albert et al., 2013) and quinone system were in accordance with the characteristics of other species of the genus Sphingobacterium. In the polar lipid profile (Fig. 2) phosphatidylethanolamine, phosphatidylserine, one phospholipid and four polar lipids.

### Table 1. Differential characteristics between strain JM-1081<sup>+</sup> and related Sphingobacterium species

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
</tr>
</thead>
<tbody>
<tr>
<td>Growth at:</td>
<td>(+)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>4 °C (5 °C)</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Starch</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Aesculin</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<td>+</td>
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<td>Urea</td>
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<td>+</td>
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<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Utilization of:</td>
<td>t-Rhamnose</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>t-Arabinose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Gluconate</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Acid production from:</td>
<td>t-Glucose</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
</tbody>
</table>

### Table 2. Fatty acid contents (%) of strain JM-1081<sup>+</sup> and related Sphingobacterium species

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
</tr>
</thead>
<tbody>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt;</td>
<td>1.8</td>
<td>2.7</td>
<td>3.9</td>
<td>1.0 (1.4)</td>
<td>2.8</td>
<td>3.2</td>
<td>TR</td>
<td>TR</td>
<td>–</td>
<td>1.0</td>
<td>–</td>
</tr>
<tr>
<td>anteiso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>–</td>
<td>–</td>
<td>2.7</td>
<td>1.8 (0.3)</td>
<td>–</td>
<td>–</td>
<td>TR</td>
<td>TR</td>
<td>2.6</td>
<td>TR</td>
<td>–</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>26.9</td>
<td>22.2</td>
<td>32.9</td>
<td>30.9 (22.0)</td>
<td>23.0</td>
<td>17.7</td>
<td>24.6</td>
<td>30.0</td>
<td>45.6</td>
<td>30.1</td>
<td>29.5</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt; 3-OH</td>
<td>3.2</td>
<td>3.2</td>
<td>3.0</td>
<td>2.3 (2.8)</td>
<td>4.7</td>
<td>4.3</td>
<td>3.7</td>
<td>3.0</td>
<td>1.5</td>
<td>2.2</td>
<td>2.3</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt; 2-OH</td>
<td>8.3</td>
<td>7.8</td>
<td>10.9</td>
<td>3.5 (8.7)</td>
<td>10.8</td>
<td>6.0</td>
<td>4.5</td>
<td>TR</td>
<td>3.4</td>
<td>3.5</td>
<td>2.2</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt; 3-OH</td>
<td>–</td>
<td>TR</td>
<td>TR</td>
<td>TR (0.4)</td>
<td>–</td>
<td>3.2</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt; 10-methyl</td>
<td>2.9</td>
<td>5.3</td>
<td>6.4</td>
<td>2.2 (3.2)</td>
<td>3.1</td>
<td>6.3</td>
<td>2.1</td>
<td>TR</td>
<td>–</td>
<td>2.7</td>
<td>1.2</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:1&lt;/sub&gt; p&lt;sub&gt;5c&lt;/sub&gt;</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<td>–</td>
<td>–</td>
<td>1.4</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;17:0&lt;/sub&gt; 3-OH</td>
<td>9.8</td>
<td>7.1</td>
<td>5.9</td>
<td>8.3 (9.8)</td>
<td>5.9</td>
<td>10.0</td>
<td>10.0</td>
<td>22.1</td>
<td>16.6</td>
<td>12.5</td>
<td>19.7</td>
</tr>
<tr>
<td>C&lt;sub&gt;17:0&lt;/sub&gt; 9c</td>
<td>–</td>
<td>TR</td>
<td>1.1</td>
<td>–</td>
<td>1.2</td>
<td>–</td>
<td>–</td>
<td>3.7</td>
<td>2.9</td>
<td>1.7</td>
<td>2.9</td>
</tr>
<tr>
<td>C&lt;sub&gt;18:0&lt;/sub&gt;</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>1.6</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>C&lt;sub&gt;18:1&lt;/sub&gt; iso7c</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>TR (1.0)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Summed feature 3*</td>
<td>45.1</td>
<td>49.0</td>
<td>24.1</td>
<td>42.6 (45.9)</td>
<td>37.8</td>
<td>47.8</td>
<td>48.1</td>
<td>35.1</td>
<td>23.8</td>
<td>42.7</td>
<td>37.5</td>
</tr>
<tr>
<td>ECL 13,566</td>
<td>1.9</td>
<td>–</td>
<td>TR</td>
<td>1.8 (–)</td>
<td>1.4</td>
<td>TR</td>
<td>1.3</td>
<td>TR</td>
<td>1.0</td>
<td>TR</td>
<td>–</td>
</tr>
</tbody>
</table>

*Summed feature 3 contains iso-C<sub>15:0</sub> 2-OH and/or C<sub>16:1</sub> 7c.
Cells grow in the presence of 1.0 % ethanol and produce a yellow colour and appear circular, translucent and glistening with entire edges. The yellow pigment of the flexirubin type is non-diffusible and non-fluorescent. Acid is produced from D-glucose, lactose, sucrose, salicin, L-arabinose, raffinose, L-rhamnose, maltose, trehalose, cellobiose and methyl α-D-glucoside. No acid is produced from adonitol, D-arabitol, dulcitol, erythritol, i-inositol, D-mannitol, melibiose, D-sorbitol or D-xylose. Positive for aesculin, β-galactosidase, and hydrolysis of casein, gelatin and starch, but negative for urease activity, indole production, hydrogen sulphide production, and activity of arginine dihydrolase, lysolecithin deacylase and ornithine decarboxylase. The following compounds are weakly utilized as a sole source of carbon: D-glucose, maltose, D-mannose, L-arabinose, acetate, N-acetylglucosamine, cellobiose, D-galactose, gluconate, salicin, D-fructose, maltitol, α-melibiose, L-rhamnose, D-ribose and sucrose. The following compounds are not utilized as a sole source of carbon: N-acetylgalactosamine, D-mannitol, D-xylene, adonitol, i-inositol, D-sorbitol, putrescine, cis-aconitate, trans-aconitate, 4-amino- butyrate, adipate, azelate, fumarate, glutarate, DL-3-hydroxybutyrate, itaconate, DL-lactate, 2-oxoglutarate, pyruvate, suberate, citrate, mesaconate, L-alanine, β-alanine, L-ornithine, L-phenylalanine, L-serine, L-aspartate, L-histidine, L-leucine, L-proline, L-tryptophan, 3-hydroxybenzoate, 4-hydroxybenzoate and phenylacetate. The chromogenic substrates p-nitrophenyl-α-D-glucopyranoside, p-nitrophenyl-β-D-glucopyranoside (weak), p-nitrophenyl-β-D-galactopyranoside, p-nitrophenyl-β-D-xylopyranoside, bis-p-nitrophenyl-phosphate, bis-p-nitrophenyl-phenyl-phosphonate, bis-p-nitrophenyl-phosphoryl-choline, 2-deoxyxy- midine-2′-p-nitrophenyl-phosphate, L-alanine-p-nitroanilide, γ-L-glutamate-p-nitroanilide and L-proline-p-nitroanilide are hydrolysed. p-Nitrophenyl-β-D-glucuronide is not hydrolysed. The major cellular fatty acids are iso-C₁₅:₀, C₁₆:₁, iso-C₁₅:₁, C₁₆:₀ and iso-C₁₇:₀. The diamino acid of the peptidoglycan is meso-diaminopimelic acid. The polyamine pattern is characterized by the major compound sym-homospermidine and a moderate amount of spermidine. The quinone system contains predominantly menaquinone MK-7. Phosphatidylethanolamine, phosphatidylserine, one phospholipid and four polar lipids are the major lipids. Moderate to minor amounts of two unidentified aminolipids, two unidentified phospholipids, one unidentified aminophospholipid, one unidentified glycolipid and four unidentified polar lipids are detectable. A sphingoglycolipid is also present.

On the basis of the results of this polyphasic study, it is clear that strain JM-1081ᵀ represents a novel species, for which the name Sphingobacterium zeae sp. nov. is proposed.

**Description of Sphingobacterium zeae sp. nov.**

*Sphingobacterium zeae* (zeˈae. L. gen. n. zeae of spelt, of Zea mays).

Cells are Gram-stain-negative. They are non-motile, and appear as non-spore-forming rods, approx. 1 μm in width and 2 μm in length. Aerobic, oxidase-positive and catalase-positive. Good growth is observed after 48 h growth on nutrient agar, brain heart infusion agar, TSA and R2A agar (all Oxoid) at 10–30 °C. No growth occurs on MacConkey agar (Oxoid) at 28 °C. Unable to grow below 4 °C and above 45 °C. Cells grow in the presence of 1.0–4.0 % (w/v) NaCl as an additional ingredient of nutrient agar. Grows at pH values of 5.5–9.0 under the conditions described above, but not at pH values below 5.5 or above 9.0. Colonies on nutrient agar produce a yellow colour and appear circular, translucent and glistening with entire edges. The yellow pigment of the flexirubin type is non-diffusible and non-fluorescent. Acid is produced from D-glucose, lactose, sucrose, salicin, L-arabinose, raffinose, L-rhamnose, maltose, trehalose, cellobiose and methyl α-D-glucoside. No acid is produced from adonitol, D-arabitol, dulcitol, erythritol, i-inositol, D-mannitol, melibiose, D-sorbitol or D-xylose. Positive for aesculin, β-galactosidase, and hydrolysis of casein, gelatin and starch, but negative for urease activity, indole production, hydrogen sulphide production, and activity of arginine dihydrolase, lysolecithin deacylase and ornithine decarboxylase. The following compounds are weakly utilized as a sole source of carbon: D-glucose, maltose, D-mannose, L-arabinose, acetate, N-acetylglucosamine, cellobiose, D-galactose, gluconate, salicin, D-fructose, maltitol, α-melibiose, L-rhamnose, D-ribose and sucrose. The following compounds are not utilized as a sole source of carbon: N-acetylgalactosamine, D-mannitol, D-xylene, adonitol, i-inositol, D-sorbitol, putrescine, cis-aconitate, trans-aconitate, 4-amino- butyrate, adipate, azelate, fumarate, glutarate, DL-3-hydroxybutyrate, itaconate, DL-lactate, 2-oxoglutarate, pyruvate, suberate, citrate, mesaconate, L-alanine, β-alanine, L-ornithine, L-phenylalanine, L-serine, L-aspartate, L-histidine, L-leucine, L-proline, L-tryptophan, 3-hydroxybenzoate, 4-hydroxybenzoate and phenylacetate. The chromogenic substrates p-nitrophenyl-α-D-glucopyranoside, p-nitrophenyl-β-D-glucopyranoside (weak), p-nitrophenyl-β-D-galactopyranoside, p-nitrophenyl-β-D-xylopyranoside, bis-p-nitrophenyl-phosphate, bis-p-nitrophenyl-phenyl-phosphonate, bis-p-nitrophenyl-phosphoryl-choline, 2-deoxyxymidine-2′-p-nitrophenyl-phosphate, L-alanine-p-nitroanilide, γ-L-glutamate-p-nitroanilide and L-proline-p-nitroanilide are hydrolysed. p-Nitrophenyl-β-D-glucuronide is not hydrolysed. The major cellular fatty acids are iso-C₁₅:₀, C₁₆:₁, iso-C₁₅:₁, C₁₆:₀, iso-C₁₇:₀. The diamino acid of the peptidoglycan is meso-diaminopimelic acid. The polyamine pattern is characterized by the major compound sym-homospermidine and a moderate amount of spermidine. The quinone system contains predominantly menaquinone MK-7. Phosphatidylethanolamine, phosphatidylserine, one phospholipid and four polar lipids are the major lipids. Moderate to minor amounts of two unidentified aminolipids, two unidentified phospholipids, one unidentified aminophospholipid, one unidentified glycolipid and four unidentified polar lipids are detectable. A sphingoglycolipid is also present.

The type strain is JM-1081ᵀ (=LMG 29191ᵀ=CCM 8652ᵀ), which was isolated in 1990 as an endophyte from the healthy internal stem tissue of maize (*Zea mays,* cultivar 'Sweet Belle') at the time of harvest. The field plot was located at the E.V. Smith Research Center in Tallassee (Elmore county), AL, USA.
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References


