Liberibacter crescens gen. nov., sp. nov., the first cultured member of the genus Liberibacter

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The Gram-stain-negative, rod-shaped bacterial isolate BT-1T is the closest relative to the genus ‘Candidatus Liberibacter’ cultured to date. BT-1T was recovered from the phloem sap of a defoliating mountain papaya in Puerto Rico. The BT-1T 16S rRNA gene sequence showed that strain BT-1T is most closely related to members of the genus ‘Ca. Liberibacter’ sharing 94.7 % 16S rRNA gene sequence similarity with ‘Ca. Liberibacter americanus’ and ‘Ca. Liberibacter asiaticus’. Additionally, average nucleotide identity, 16S rRNA gene sequences and conserved protein sequences supported inclusion of the previously described species of the genus ‘Ca. Liberibacter’ in a genus with BT-1T. The prominent fatty acids of isolate BT-1T were C18 : 1ω7C (77.2%), C18 : 0 OH (4.8%), C18 : 0 (4.4 %) and C16 : 0 (3.5 %). Both physiological and genomic characteristics support the creation of the genus Liberibacter, as well as the novel species Liberibacter crescens gen. nov., sp. nov. with type strain BT-1T (=ATCC BAA-2481T=DSM 26877T).

The candidate genus ‘Candidatus Liberibacter’ was first described as a member of the class Alphaproteobacteria (Jagoueix et al., 1994). The genus includes pathogens affecting economically important crops such as potato, tomato and citrus (Hansen et al., 2008; Jagoueix et al., 1994; Liefting et al., 2009; Teixeira et al., 2005). Ca. Liberibacter infection is confined to the phloem of the plant leading to symptoms indicative of a restricted nutrient supply, such as yellowing of the leaves and diminished fruit quality (Kapur et al., 1978). Previously described pathogens of the genus ‘Ca. Liberibacter’ are vectored by members of the Psyllidae family of insects and are introduced into the plant phloem during feeding (Capon et al., 1967; Pelz-Stelinski et al., 2010). All previously documented species of the genus ‘Ca. Liberibacter’ are fastidious and have yet to be cultured reproducibly in the laboratory. This has led to a dearth of physiological data and as such, each species of the genus ‘Ca. Liberibacter’ has been labelled ‘Candidatus’ (Murray & Stackebrandt, 1995).

A novel bacterium, BT-1T, was isolated from expressed sap of a Babaco papaya, Carica pentagona, family Caricaceae, during an investigation of Papaya Bunchytop Disease (Davis et al., 2008). Transmission electron microscopy imaging (Leonard et al., 2012) showed a rod-shaped bacterium of 0.5 x 1.75 µm. BT-1T exhibiting polar division consistent with that described in other members of the order Rhizobiales (Brown et al., 2012). Fimbriae were abundant, but no other outstanding surface features were observed.

To investigate further the phylogenetic placement of strain BT-1T, the genome of isolate BT-1T was sequenced (Leonard et al., 2012; NCBI Reference Sequence NC_019907.1). The 16S rRNA gene sequence derived from the completed genome was compared to those of species of the genus ‘Ca. Liberibacter’ as well as related members of the order Rhizobiales. The BT-1T 16S rRNA gene sequence was aligned against the NCBI non-redundant nucleotide database using Megablast. The alignment showed the 16S rRNA gene of BT-1T shares 94.7% sequence similarity with the 16S rRNA genes of ‘Ca. Liberibacter americanus’ and ‘Ca. Liberibacter asiaticus’, 94.0% similarity with ‘Ca. Liberibacter solanacearum’, and 93.4% similarity with ‘Ca. Liberibacter africanus’.

Phylogenetic placement of BT-1T was visualized with relatedness trees of both the 16S rRNA gene (Fig. 1a) and 118 conserved protein sequences (Fig. 1b). The 16S rRNA gene sequence tree (Fig. 1a) was reconstructed using DNA sequences from the BT-1T genome and close relatives. These sequences were aligned using MUSCLE (Edgar, 2004);
Fig. 1. Maximum-likelihood phylogenetic trees reconstructed using (a) 16S rRNA gene sequences and (b) concatenated amino acid sequences of 118 BT-1\textsuperscript{T} proteins and those of related members of the class Alphaproteobacteria. Bars, 0.03 substitutions per nucleotide position (a); 0.2 substitutions per amino acid position (b).
overhanging regions were manually removed; and the alignment was curated using Gblocks (Castresana, 2000). Phylogeny was determined with PhyML using the GTR substitution model with 100 bootstraps (Anisimova & Gascuel, 2002; Guindon & Gascuel, 2003). The resultant phylogenetic tree was generated with TreeDyn (Chevenet et al., 2006). These tools were accessed through phylogeny.fr (Dereeper et al., 2008). A second phylogenetic tree was reconstructed using the concatenated amino acid sequences of 118 shared proteins (Fig. 1b). Sequences were aligned by MUSCLE (Edgar, 2004), trimmed by Gblocks (Castresana, 2000), and the tree was reconstructed by RAxML (Stamatakis, 2006) using the WAG substitution model. Bootstrap values were based on 1000 iterations and were all reported at 100 %.

Average nucleotide identity (ANI) was determined across the BT-1T genome and those of two previously sequenced species of the genus ‘Ca. Liberibacter’ as well as close relatives from other genera. ANI was calculated in JSpecies (Edgar, 2004), trimmed by Gblocks (Castresana, 2000), and the alignment was curated using Gblocks (Castresana, 2000) based on 1000 iterations and were all reported at 100 %.

Table 1. Shared average nucleotide identity (ANI) across the genomes of BT-1T and close relatives including two species of the genus Bartonella

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<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
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<tr>
<td>1. Bartonella henselae</td>
<td>–</td>
<td>86.8</td>
<td>76.48</td>
<td>76.61</td>
<td>76.98</td>
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<tr>
<td>2. Bartonella quintana</td>
<td>86.81</td>
<td>–</td>
<td>76.63</td>
<td>76.63</td>
<td>77.13</td>
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<td>3. ‘Ca. Liberibacter solanacearum’</td>
<td>76.45</td>
<td>76.61</td>
<td>–</td>
<td>81.33</td>
<td>78.23</td>
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<tr>
<td>4. ‘Ca. Liberibacter asiaticus’</td>
<td>76.54</td>
<td>76.61</td>
<td>81.32</td>
<td>–</td>
<td>77.35</td>
</tr>
<tr>
<td>5. Liberibacter crescens sp. nov. BT-1T</td>
<td>77.01</td>
<td>77.12</td>
<td>78.19</td>
<td>77.37</td>
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BT-1T was challenged with the following laboratory antibiotics in liquid culture: ampicillin (25 \(\mu\)g ml\(^{-1}\)), kanamycin (50 \(\mu\)g ml\(^{-1}\)), nalidixic acid (10 \(\mu\)g ml\(^{-1}\)), rifampicin (2.5 \(\mu\)g ml\(^{-1}\)), chloramphenicol (30 \(\mu\)g ml\(^{-1}\)), streptomycin (50 \(\mu\)g ml\(^{-1}\)), spectinomycin (50 \(\mu\)g ml\(^{-1}\)), neomycin (50 \(\mu\)g ml\(^{-1}\)), tetracycline (15 \(\mu\)g ml\(^{-1}\)), vancomycin (40 \(\mu\)g ml\(^{-1}\)) and amikacin (100 \(\mu\)g ml\(^{-1}\)). Of these, BT-1T was resistant to nalidixic acid, vancomycin and amikacin. A more complete description of the BT-1T antibiotic profile is given in Table S2.

Although strain BT-1T was originally isolated from a diseased plant, it is not known whether it is a plant pathogen. All previously described species of the genus ‘Ca. Liberibacter’ are transmitted through an insect vector of the family Psyllidae (Capoor et al., 1967; Hansen et al., 2008; Raddadi et al., 2011). Whether BT-1T inhabits an insect host is unknown; however, the leafhopper Empoasca papayae is recommended for further study due to previous documentation of its association with phloem-limited bacteria in papaya (Perez et al., 2010).

Primers were designed for specific amplification of the chorismate synthase gene of BT-1T (LCF 9-CGCTCTCATGTGGGATTGGAA-3’ and LCR 9-GTGGGATTGGAA-3’). A recent comparative genomics study showed that this gene is absent in the uncultured species of the genus ‘Ca. Liberibacter’ whose complete genomes are available (Fagen et al., 2014). These primers amplify BT-1T sequences using the following thermal profile: 2 min at 94 °C; followed by 25 cycles of 94 °C for 20 s, 62 °C for 20 s, 72 °C for 30 s; and a final elongation at 72 °C for 5 min.

The 16S rRNA gene sequence similarities, conserved protein sequences and whole genome comparisons, as well as general attributes such as native ecology and reduced genome size (Table 2) show that isolate BT-1T is a novel member of the genus ‘Ca. Liberibacter’. Isolate BT-1T is divergent from the uncultured members of the genus, which cluster together in all comparisons presented in this work. This isolate is the first member of the genus to be maintained in culture and thereby allows for a complete description of the genus and removal of the Candidatus status. We propose that the name Liberibacter be retained for this genus and propose the name Liberibacter crescens sp. nov. to accommodate the BT-1T isolate.
Table 2. Distinguishing features of strain BT-1\textsuperscript{T} compared with close relatives

<table>
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<th>Characteristic</th>
<th>1</th>
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<th>6</th>
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<tr>
<td>Family</td>
<td>Rhizobiaceae</td>
<td>Rhizobiaceae</td>
<td>Rhizobiaceae</td>
<td>Bartonellaceae</td>
<td>Bartonellaceae</td>
<td>Rhizobiaceae</td>
<td>Rhizobiaceae</td>
<td>Anaplasmataceae</td>
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<tr>
<td>Lifestyle</td>
<td>Papaya phloem, commensal</td>
<td>Insect vectored, citrus pathogen</td>
<td>Insect vectored, potato/tomato pathogen</td>
<td>Insect vectored, human intracellular pathogen</td>
<td>Insect vectored, feline intracellular pathogen</td>
<td>Legume symbiont</td>
<td>Insect endosymbiont</td>
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<tr>
<td>Cell Shape</td>
<td>Rod</td>
<td>Elongated rod</td>
<td>Not observed</td>
<td>Not observed</td>
<td>Not observed</td>
<td>Rod</td>
<td>Rod</td>
<td>Rod</td>
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<tr>
<td>Flagellum</td>
<td>Not observed</td>
<td>Elongated rod</td>
<td>Not observed</td>
<td>Not observed</td>
<td>Not observed</td>
<td>Not observed</td>
<td>Summed feature 1*, C&lt;sub&gt;19&lt;/sub&gt;:0 cyclo, summed feature 2†</td>
<td>C&lt;sub&gt;19&lt;/sub&gt;:0 cyclo, C&lt;sub&gt;18&lt;/sub&gt;:0, C&lt;sub&gt;18&lt;/sub&gt;:1t</td>
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<td>Primary fatty acids</td>
<td>C&lt;sub&gt;16&lt;/sub&gt;:0, C&lt;sub&gt;18&lt;/sub&gt;:0</td>
<td>C&lt;sub&gt;18&lt;/sub&gt;:0, C&lt;sub&gt;18&lt;/sub&gt;:0, C&lt;sub&gt;18&lt;/sub&gt;:0</td>
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<td>Genome size</td>
<td>1.5 Mb</td>
<td>1.23 Mb</td>
<td>1.26 Mb</td>
<td>1.93 Mb</td>
<td>1.58 Mb</td>
<td>6.7 Mb</td>
<td>6.53 Mb</td>
<td>1.27 Mb</td>
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<td>DNA G+C content</td>
<td>35.3 mol%</td>
<td>36.5 mol%</td>
<td>35.2 mol%</td>
<td>38.2 mol%</td>
<td>39–40.0 mol%</td>
<td>62.0 mol%</td>
<td>60.5 mol%</td>
<td>34.0 mol%</td>
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*Summed feature 1 is composed of C<sub>18</sub>:0, C<sub>18</sub>:1t fatty acids.
†Summed feature 2 is composed of C<sub>12</sub>:0 aldehyde(?), iso-C<sub>16</sub>:1 t, C<sub>14</sub>:0 3-OH fatty acids and an unknown compound with an equivalent chain length (ECL) value of 10.928.
Description of Liberibacter gen. nov.

Liberibacter (L.i.be.ri.bac’ter. L. adj. liber free; N.L. n. bacter rod; N.L. masc. n. Liberibacter free rod).

Cells are Gram-stain-negative aerobic rods. Non-motile and restricted to the phloem of the host plant. Cells exhibit a reduced genome of approximately 1.5 Mb or less with a DNA G+C content of 31–37%, similar to many insect symbionts. The type species is Liberibacter crescens.

Description of Liberibacter crescens sp. nov.

Liberibacter crescens (cres’cens. L. part. adj. crescens growing, thriving).

Aerobic, Gram-stain-negative rods approximately 1.75 μm × 0.5 μm. Cream-coloured colonies with entire margins are visible 8–10 days after inoculation on solid medium. Negative for the presence of catalase, oxidase and urease, as well as for the production of indole from tryptophan.

The type strain is BT-1T ( = ATCC BAA-2481T = DSM 26877T), isolated from expressed sap of a Babaco papaya.

Acknowledgements

The authors thank Huiqin Chen and Maria Peacock for their diligent attention to maintaining cultivation of Liberibacter crescens and to Dr Victoria Pagan, Classics Professor of the University of Florida, for her assistance with Latin-naming. This work was funded by the Citrus Research and Development Foundation projects 336, 767 and 769.

References


