Chryseobacterium artocarpi sp. nov., isolated from the rhizosphere soil of Artocarpus integer

Chidambaram Kulandaisamy Venil,1 Nordiana Nordin,1 Zainul Akmar Zakaria2 and Wan Azlina Ahmad1

1Department of Chemistry, Faculty of Science, Universiti Teknologi Malaysia, 81310 UTM Johor Bahru, Johor, Malaysia
2Institute of Bioproduct Development, Universiti Teknologi Malaysia, 81310 UTM Johor Bahru, Johor, Malaysia

A bacterial strain, designated UTM-3T, isolated from the rhizosphere soil of Artocarpus integer (cempedak) in Malaysia was studied to determine its taxonomic position. Cells were Gram-stain-negative, non-spore-forming rods, devoid of flagella and gliding motility, that formed yellow-pigmented colonies on nutrient agar and contained MK-6 as the predominant menaquinone. Comparative analysis of the 16S rRNA gene sequence of strain UTM-3T with those of the most closely related species showed that the strain constituted a distinct phyletic line within the genus Chryseobacterium with the highest sequence similarities to Chryseobacterium lactis NCTC 11390T, Chryseobacterium vischeri 687B-08T, Chryseobacterium truciae 1084-08T, Chryseobacterium arthrosphaerae CC-VM-7T, Chryseobacterium oncorynchi 701B-08T, Chryseobacterium vietnamense GIMN1.005T, Chryseobacterium bernardetii NCTC 13530T, Chryseobacterium nakagawai NCTC 13529T, Chryseobacterium gallinarum LMG 27808T, Chryseobacterium culicis R4-1AT, Chryseobacterium flavum CW-E2T, Chryseobacterium aquiligrindense CW9T, Chryseobacterium ureilyticum CCUG 52546T, Chryseobacterium indologenes NBRC 14944T, Chryseobacterium gleum CCUG 14555T, Chryseobacterium jejuense JS17-8T, Chryseobacterium oranimense H8T and Chryseobacterium joostei LMG 18212T. The major whole-cell fatty acids were iso-C15:0 and iso-C17:1ω9c, followed by summed feature 4 (iso-C15:0 2-OH and/or C16:1ω7t) and iso-C17:0 3-OH, and the polar lipid profile consisted of phosphatidylethanolamine and several unknown lipids. The DNA G+C content strain UTM-3T was 34.8 mol%. On the basis of the phenotypic and phylogenetic evidence, it is concluded that the isolate represents a novel species of the genus Chryseobacterium, for which the name Chryseobacterium artocarpi sp. nov. is proposed. The type strain is UTM-3T (=CECT 8497T=KCTC 32509T).

The classification of members of the family Flavobacteriaceae is still in a state of development (Yoon et al., 2013), and in the course of subdividing the genus Flavobacterium, Vandamme et al. (1994) proposed the genus Chryseobacterium. At the time of writing, the genus Chryseobacterium contains around 80 species and represents one of the genera with the fastest growing number of species. Members of this genus are widely distributed in aquatic and soil environments and some species are pathogenic to humans and animals (Bernardet et al., 2006; Vanechoutte et al., 2007), indicating that the genus Chryseobacterium represents a group of organisms that are ubiquitous in nature. Many of the species have been found in association with plants considering their antagonistic potential against plant pathogens (Krause et al., 2001; Shin et al., 2007; Ramos Solano et al., 2008). Recent studies of the genus Chryseobacterium have documented the significance of its bioactive compounds as biocontrol agents, antioxidatants, prebiotics, sulfoabacin A and protease producers (Scheuplein et al., 2007; Wang et al., 2008, 2011; Chaudhari et al., 2009; Kim et al., 2012), which substantiate that it is a novel source of bioactive compounds. Members of the genus Chryseobacterium are Gram-negative, non-motive, psychrotolerant, halotolerant with a strict respiratory metabolism and contain MK-6 as the major respiratory quinone (Bernardet et al., 2006).

Strain UTM-3T was isolated from the rhizosphere soil of Artocarpus integer from an orchard located on the campus of Universiti Teknologi Malaysia (UTM), Malaysia in December 2012. Artocarpus integer, commonly known as
Chryseobacterium, is a species of tree in the family Moraceae native to South-East Asia. The soil sample (10 g) was placed in flasks containing 90 ml nutrient broth (Difco) and incubated at 30 °C under agitation (100 r.p.m.) for 48 h. An aliquot (0.1 ml) of the cell suspension was spread onto nutrient agar and incubated at 30 °C for 24 h. After primary isolation and purification, the strain was cultivated at 30 °C on the same medium and was preserved in nutrient broth containing 10% (v/v) glycerol at −80 °C. The strain was subsequently analysed for 16S rRNA gene sequence similarities, fatty acid composition, phenotypic characteristics and DNA–DNA relatedness to those species most closely related on the basis of 16S rRNA gene sequence similarities. Chryseobacterium lactis NCTC 11390T, Chryseobacterium viscerum CECT 7793T, Chryseobacterium tructae CECT 7798T, Chryseobacterium arthrophaeae CCUG 57618T, Chryseobacterium oncorhynchi CECT 7794T, Chryseobacterium vietnamense CCTCC M 209230T, Chryseobacterium bernardetii NCTC 13530T, Chryseobacterium nakagawai NCTC 13529T, Chryseobacterium gallinarum LMG 27808T, Chryseobacterium cunicis LMG 25442T, Chryseobacterium flavum KCTC 12877T, Chryseobacterium aquifrigidense KCTC 12894T, Chryseobacterium ureilyticum CCUG 52546T, Chryseobacterium indologenes LMG 8337T, Chryseobacterium gleum CCUG 14555T, Chryseobacterium jejuense JS17-8T, Chryseobacterium oranimense H8T and Chryseobacterium joostei LMG 18212T were used as reference strains for this study.

Cultural and morphological characteristics of the strains were observed on nutrient agar. The Gram reaction was performed by using the bioMérieux Gram stain kit according to the manufacturer’s instructions. Flagella and gliding motilities were determined using the hanging drop method and gliding motility was examined further using phase-contrast microscopy on 17 h-cultures on microscopic slides coated with marine agar (MA; Difco), according to Bowman (2000). Catalase activity was tested by using 10% (v/v) H2O2 and oxidase activity was tested in 1% N,N,N',N’-tetramethyl-p-phenylenediamine solution. The presence of flexirubin-type pigments was determined by flooding the cell mass with 20% (w/v) KOH (Bernardin et al., 2002). Growth was tested on nutrient agar, brain heart infusion agar, tryptic soy agar and MacConkey agar (Difco). Growth temperature (5, 10, 15, 20, 25, 30, 37 and 40 °C) and pH (pH 3–11, at 2 increments) were tested in tryptic soy broth. Salt tolerance was determined on nutrient agar containing varying concentrations of NaCl (2–10%, w/v, at 1% intervals) at 30 °C.

Physiological characterization was investigated as described by Kämper et al. (1991). Biochemical tests were performed for four strains using the API 20NE, API 20E and API ZYM identification systems (bioMérieux) according to the manufacturer’s instructions. Growth was checked under anaerobic and microaerobic conditions by using the GasPak™ (BD BBL™) at 30 °C for 15 days. For cellular fatty acid analysis, the seven strains were grown on

Table 1. Differential characteristics between strain UTM-3T and the type strains of closely related species of the genus Chryseobacterium

| Strains: 1, UTM-3T; 2, C. lactis NCTC 11390T; 3, C. viscerum CECT 7793T; 4, C. tructae CECT 7798T; 5, C. arthrophaeae CCUG 57618T; 6, C. oncorhynchi CECT 7794T; 7, C. vietnamense CCTCC M 209230T; 8, C. bernardetii NCTC 13530T; 9, C. nakagawai NCTC 13529T; 10, C. gallinarum LMG 27808T; 11, C. cunicis LMG 25442T; 12, C. flavum KCTC 12877T; 13, C. aquifrigidense KCTC 12894T; 14, C. ureilyticum CCUG 52546T; 15, C. indologenes LMG 8337T; 16, C. gleum CCUG 14555T; 17, C. jejuense JS17-8T; 18, C. oranimense H8T; 19, C. joostei LMG 18212T. All data are from this study. All strains produced acids from d-glucose and trehalose, hydrolysed starch, and grew with 3% NaCl and at 30 °C. None of the strains produced acid from l-arabinose, cellobiose, ethanol, lactose or d-xylose. +, Positive; (+), weakly positive; −, negative. |
| Characteristic | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |
| Production of: |   |   |   |   | − | − | − | + | + | + | + | + | + | + | + | + | + | + | + |
| Indole         | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| H2S            | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Nitrate reduction | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Acid production from: |   |   |   |   | − | − | − | + | + | + | + | + | + | + | + | + | + | + | + |
| d-Fructose     | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Glycerol      | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| d-Maltose     | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| d-Mannitol | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Raffinose | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Hydrolysis of: |   |   |   |   | − | − | − | + | + | + | + | + | + | + | + | + | + | + | + |
| Tyrosine    | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Urea         | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Growth at:    |   |   |   |   | − | − | − | + | + | + | + | + | + | + | + | + | + | + | + |
| 5 °C          | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
| 40 °C         | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + |
Table 2. Cellular fatty acid profiles of strain UTM-3<sup>T</sup> and related species of the genus *Chryseobacterium*

<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>
<th>12</th>
<th>13</th>
<th>14</th>
<th>15</th>
<th>16</th>
<th>17</th>
<th>18</th>
<th>19</th>
</tr>
</thead>
<tbody>
<tr>
<td>iso-C&lt;sub&gt;13:0&lt;/sub&gt;</td>
<td>1.4</td>
<td>1.2</td>
<td>1.3</td>
<td>1.6</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>1.1</td>
<td>TR</td>
<td>1.3</td>
<td>TR</td>
<td>TR</td>
<td>1.4</td>
<td>1.3</td>
<td>TR</td>
<td>TR</td>
<td>1.6</td>
<td>TR</td>
<td>TR</td>
</tr>
<tr>
<td>Unknown ECL 13.566</td>
<td>3.3</td>
<td>2.1</td>
<td>TR</td>
<td>3.1</td>
<td>2.2</td>
<td>5.4</td>
<td>2.3</td>
<td>3.2</td>
<td>7.4</td>
<td>3.6</td>
<td>8.7</td>
<td>1.9</td>
<td>1.2</td>
<td>TR</td>
<td>2.2</td>
<td>8.9</td>
<td>8.5</td>
<td>3.6</td>
<td>1.1</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>41.2</td>
<td>36.8</td>
<td>40.9</td>
<td>38.5</td>
<td>37.6</td>
<td>33.7</td>
<td>34.4</td>
<td>37.2</td>
<td>37.4</td>
<td>36.1</td>
<td>33.9</td>
<td>35.1</td>
<td>37.1</td>
<td>40.2</td>
<td>34.8</td>
<td>29.6</td>
<td>32.6</td>
<td>41.2</td>
<td>34.6</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;15:0&lt;/sub&gt; 3-OH</td>
<td>3.5</td>
<td>3.2</td>
<td>2.9</td>
<td>3.2</td>
<td>2.4</td>
<td>3.5</td>
<td>3.7</td>
<td>3.1</td>
<td>6.8</td>
<td>3.2</td>
<td>2.5</td>
<td>3.7</td>
<td>3.1</td>
<td>7.6</td>
<td>3.1</td>
<td>2.6</td>
<td>2.5</td>
<td>2.4</td>
<td>2.9</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;15:1&lt;/sub&gt;</td>
<td>TR</td>
<td>TR</td>
<td>1.1</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>1.1</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
</tr>
<tr>
<td>anteiso-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>TR</td>
<td>1</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt;</td>
<td>1.3</td>
<td>1.4</td>
<td>1.8</td>
<td>1.8</td>
<td>1.9</td>
<td>2.6</td>
<td>1.8</td>
<td>1.9</td>
<td>1.4</td>
<td>1.8</td>
<td>1.1</td>
<td>2.8</td>
<td>1.2</td>
<td>1.1</td>
<td>1.2</td>
<td>1.1</td>
<td>1.8</td>
<td>1.6</td>
<td>1.1</td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt; 3-OH</td>
<td>TR</td>
<td>1.6</td>
<td>TR</td>
<td>1.1</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>1.5</td>
<td>TR</td>
<td>1.3</td>
<td>2</td>
<td>2.2</td>
<td>1.8</td>
<td>1.6</td>
<td>1.2</td>
<td>2.2</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;16:0&lt;/sub&gt; 3-OH</td>
<td>1.4</td>
<td>1.6</td>
<td>1.9</td>
<td>1.8</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>1.1</td>
<td>1.6</td>
<td>1.7</td>
<td>1.2</td>
<td>1.6</td>
<td>1.2</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
<td>TR</td>
</tr>
<tr>
<td>Unknown ECL 16.580</td>
<td>1.7</td>
<td>2.1</td>
<td>1.1</td>
<td>1.4</td>
<td>1.5</td>
<td>1.1</td>
<td>1.4</td>
<td>1.7</td>
<td>2</td>
<td>3.1</td>
<td>1.3</td>
<td>1.5</td>
<td>-</td>
<td>TR</td>
<td>1.6</td>
<td>1.4</td>
<td>1.3</td>
<td>1.1</td>
<td>1.6</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;17:0&lt;/sub&gt;</td>
<td>3</td>
<td>2.6</td>
<td>2.5</td>
<td>3.8</td>
<td>14.1</td>
<td>1.2</td>
<td>3.2</td>
<td>2.8</td>
<td>1.8</td>
<td>2.2</td>
<td>1.4</td>
<td>TR</td>
<td>2.1</td>
<td>4.4</td>
<td>1.1</td>
<td>1.5</td>
<td>1.5</td>
<td>2.8</td>
<td>TR</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;17:0&lt;/sub&gt; 3-OH</td>
<td>10.3</td>
<td>22.4</td>
<td>14.7</td>
<td>14.7</td>
<td>24.1</td>
<td>21.6</td>
<td>25.7</td>
<td>23.6</td>
<td>20.8</td>
<td>16.4</td>
<td>15.5</td>
<td>18.5</td>
<td>17.3</td>
<td>14.7</td>
<td>20.5</td>
<td>18.4</td>
<td>15.4</td>
<td>22.4</td>
<td>20.2</td>
</tr>
<tr>
<td>iso-C&lt;sub&gt;17:1&lt;/sub&gt;9c</td>
<td>20.1</td>
<td>8.6</td>
<td>21.6</td>
<td>23.4</td>
<td>2.8</td>
<td>24.6</td>
<td>9.4</td>
<td>12.4</td>
<td>8.2</td>
<td>17.2</td>
<td>20.7</td>
<td>16.8</td>
<td>23.4</td>
<td>17.2</td>
<td>19.8</td>
<td>22.2</td>
<td>21.9</td>
<td>12.6</td>
<td>22.9</td>
</tr>
<tr>
<td>Summed feature*</td>
<td>4</td>
<td>12.1</td>
<td>14.8</td>
<td>8.2</td>
<td>4.8</td>
<td>12.8</td>
<td>11.2</td>
<td>15.3</td>
<td>8.4</td>
<td>10.4</td>
<td>12.1</td>
<td>11</td>
<td>13.3</td>
<td>3.8</td>
<td>8.4</td>
<td>11.6</td>
<td>11.3</td>
<td>11.0</td>
<td>8.6</td>
</tr>
<tr>
<td>5</td>
<td>ND</td>
<td>ND</td>
<td>1.1</td>
<td>ND</td>
<td>ND</td>
<td>1.2</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>2.4</td>
<td>1.2</td>
<td>TR</td>
<td>ND</td>
<td>ND</td>
<td>TR</td>
<td>ND</td>
<td>ND</td>
<td>1.1</td>
<td>TR</td>
</tr>
</tbody>
</table>

*Summed features represent groups or two or more fatty acids that cannot be separated by the Microbial Identification System. Summed feature 4 contains iso-C<sub>15:0</sub> 2-OH and/or C<sub>16:1</sub>ω7t; summed feature 5 contains iso-C<sub>17:1</sub> 1 and/or anteiso-C<sub>17:1</sub> B.
Columbia II agar (BBL) with 5% horse blood for 48 h at 30 °C using the standard protocol of the Sherlock Microbial Identification System (MIDI); the polar lipid profile was also detected (Ventosa et al., 1993). Extraction of genomic DNA, PCR amplification of 16S rRNA gene and sequencing of purified PCR products were carried out according to Miranda-Tello et al. (2004). First, DNA sequences (1381 bp) were aligned and trimmed using MEGA 6 software (Tamura et al., 2013) and an initial neighbour-joining tree using Kimura’s two-parameter method was generated. Next, a maximum-parsimony analysis using Tree-Bisection-Reconnection (TBR) with 10 initial trees was done with 1000 bootstrap replications. MODELTEST (Posada & Crandall, 1998) was then performed in TOPALi v2 (Milne et al., 2009) to calculate the most suitable substitution model for the maximum-likelihood analysis. Based on the MODELTEST scores, it was found that the General Time Reversible model together with Gamma distribution and Invariant sites (GTR + G + I) most fit the data. These parameters were used for the maximum-likelihood analysis in the MEGA 6 software package. Branch support for all phylogenetic trees were assessed via 1000 bootstrap replications.

The DNA base content (G + C) of strain UTM-3T was determined by HPLC as described by Tamaoka & Komagata (1984) using non-methylated i. DNA (Sigma) as a standard. DNA–DNA hybridization experiments were performed to confirm the taxonomic status of the novel strain. DNA–DNA hybridization experiments were performed between strain UTM-3T and the type strains of the most closely related species of the genus Chryseobacterium (C. lactis NCTC 11390T, C. viscosum 687B-08T, C. tructae 1084-08T, C. arthrophaeae CC-VM-7T, C. ornychonchi 701B-08T, C. vietnamense GIMNN1.005T, C. bernardetii NCTC 13530T, C. nakagawai NCTC 13529T, C. gallinarum LMG 27808T, C. culicis LMG 25442T, C. flavum KCTC 12877T, C. aquifrigidense KCTC 12894T, C. ureilyticum CCUG 52546T, C. indologenes LMG 8337T, C. gleum CCUG 14555T, C. jejuense JS17-8T, C. oraminense H8T and C. joostei LMG 18212T). DNA was isolated by chromatography on hydroxyapatite (Cashion et al., 1977), and hybridization was performed (De Ley et al., 1970) with the modifications of Escara & Hutton (1980) and Huss et al. (1983).

Strain UTM-3T was Gram-stain-negative, devoid of flagella and gliding motility, non-spore-forming and rod-shaped after 24 h at 30 °C. The colonies were yellowish, translucent and shiny with entire edges becoming mucoid after 72 h of incubation. No growth was observed at 5 °C and above 40 °C. Flexirubin-type pigment was produced on nutrient agar. Strain UTM-3T grew well on nutrient agar, tryptic soy agar and brain heart infusion agar, but was unable to grow on MacConkey agar. The physiological and other biochemical characteristics of strain UTM-3T are summarized in Table 1 and in the species description. The predominant respiratory quinone was menaquinoMK-6 with a minor amount of MK-5 present. The polar lipids were composed of phosphatidylethanolamine, an unknown aminolipid, an unknown phospholipid and several unknown lipids. Cellular fatty acid analysis showed that iso-C15:0 and iso-C17:0 3-OH were the most abundant fatty acids followed by summed feature 4 (iso-C15:0 2-OH and/or C16:1 9t) and iso-C17:0 3-OH. The complete fatty acid pattern of strain UTM-3T is shown in Table 2 in comparison to the most closely related species of the genus Chryseobacterium.

The 16S rRNA gene sequence of strain UTM-3T consisted of 1381 bp. Seventy bacterial strains were used to reconstruct the phylogenetic trees. MODELTEST results indicated that the General Time Reversible model together with Gamma distribution and Invariant sites (GTR + G + I) most fit the data and this substitution model was used to reconstruct the maximum-likelihood tree (Fig. 1). Sequence database searches revealed that the strain UTM-3T was most closely related to species of the genus Chryseobacterium. Phylogenetic analysis confirmed that strain UTM-3T associated with the genus Chryseobacterium, showing highest sequence similarities to C. lactis NCTC 11390T, C. viscosum 687B-08T, C. tructae 1084-08T, C. arthrophaeae CC-VM-7T, C. ornychonchi 701B-08T, C. vietnamense GIMNN1.005T, C. bernardetii NCTC 13530T, C. nakagawai NCTC 13529T, C. gallinarum LMG 27808T, C. culicis LMG 25442T, C. flavum KCTC 12877T, C. aquifrigidense KCTC 12894T, C. ureilyticum CCUG 52546T, C. indologenes LMG 8337T, C. gleum CCUG 14555T, C. jejuense JS17-8T, C. oraminense H8T and C. joostei LMG 18212T. DNA–DNA hybridization values of strain UTM-3T with C. lactis NCTC 11390T, C. viscosum CECT 7793T, C. tructae CECT 7793T, C. arthrophaeae CCUG 57518T, C. ornychonchi CECT 7794T, C. vietnamense CCTCC M 209230T, C. bernardetii NCTC 13530T, C. nakagawai NCTC 13529T, C. gallinarum LMG 27808T, C. culicis LMG 25442T, C. flavum KCTC 12877T, C. aquifrigidense KCTC 12894T, C. ureilyticum CCUG 52546T, C. indologenes LMG 8337T, C. gleum CCUG 14555T, C. jejuense JS17-8T, C. oraminense H8T and C. joostei LMG 18212T were 48.3%, 75.4%, 82.4%, 80.2%, 81.3%, 82.4%, 82.4%, 78.2%, 72.3%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%, 75.4%.
Description of Chryseobacterium articarpi sp. nov.

Chryseobacterium articarpi (ar.to.car’pi. N.L. gen. n. articarpi of the tree Artocarpus integer from whose rhizosphere soil the type strain was isolated).

Cells are Gram-stain-negative, non-spore-forming rods approximately 1.8 µm in length and 0.8 µm in diameter, and are devoid of flagella and gliding motility. Colonies are smooth, yellowish, translucent and shiny with entire edges. Colonies become mucoid and cannot be identified as a singly colony after prolonged incubation. Flexirubin-type pigments are produced. Growth is good at 20–30 °C (optimum, 30 °C); no growth at 5 or 40 °C. Growth occurs at pH 5–8 (optimum, pH 7) and in the presence of 0–6% (w/v) NaCl (optimum, 3%). Catalase- and oxidase-positive. In the API ZYM gallery, alkaline phosphatase, acid phosphatase, esterase (C4), lipase (C14), leucine arylamidase, valine arylamidase, trypsin and N-acetyl-β-glucoaminidase activities are present, but esterase lipase (C8), naphthol-AS-BI-phosphohydrolase, cystine arylamidase, x-chymotrypsin, x-galactosidase, β-galactosidase, β-glucoronidase, z-glucosidase, β-glucosidase and z-mannosidase activities are absent. With the API 20NE and API 20E kits, nitrate is reduced but nitrite is not reduced. Indole production, lysine decarboxylase, ornithine decarboxylase and tryptophan deaminase are negative. Aesculin, casein, gelatin, tyrosine and starch are hydrolysed, but Tweens 20 and tryptophan deaminase are negative. Aesculin, casein, D-glucose, D-fructose, glycerol, agar slants. No haemolysis occurs on 5% horse blood agar. Hydrogen sulphide is produced on Kligler’s iron agar, gelatin, tyrosine and starch are hydrolysed, but Tweens 20 and tryptophan deaminase are negative. Aesculin, casein, D-glucose, D-fructose, glycerol, agar slants. No haemolysis occurs on 5% horse blood agar. Hydrogen sulphide is produced on Kligler's iron agar slants. No haemolysis occurs on 5% horse blood agar. Hydrogen sulphide is produced on Kligler’s iron agar. Hydrogen sulphide is produced on Kligler’s iron agar. Hydrogen sulphide is produced on Kligler’s iron agar.

With the API 20NE and API 20E kits, nitrate is reduced but nitrite is not reduced. Indole production, lysine decarboxylase, ornithine decarboxylase and tryptophan deaminase are negative. Aesculin, casein, gelatin, tyrosine and starch are hydrolysed, but Tweens 20 and 80 and urea are not. No precipitation occurs on egg-yolk agar. Hydrogen sulphide is produced on Kligler’s iron agar slants. No haemolysis occurs on 5% horse blood agar. Acid is produced from D-glucose, D-fructose, glycerol, raffinose and trehalose, but not from L-arabinose, cellulbiose, ethanol, lactose, D-maltose, D-mannitol or D-xylene. Dextrin, D-glucose, glycogen, D-maltose, D-mannose, sucrose, Tween 40, acetate, propionate, methyl pyruvate, L-alanine, L-asparagine, L-aspartate, L-leucine, L-ornithine, L-phenylalanine, L-proline, L-serine, L-threonine and glyc erol are utilized as sole carbon sources. Cells contain MK-6 as the major respiratory quinone and phosphatidylethanolamine as the major polar lipid. The major whole-cell fatty acids are iso-C15:0, iso-C17:1ω9c followed by summed feature 4 (iso-C15:0 2-OH and/or C16:1ω7t) and iso-C17:0 3-OH.

The type strain, UTM-3T (=CECT 8497T=KCTC 32509T) was isolated from the rhizosphere soil of Artocarpus integer (cempedak) grown in an orchard located on the campus of Universiti Teknologi Malaysia, Malaysia. The DNA G+C content of the type strain is 34.8 mol%.

Acknowledgements

C. K. V. is grateful to the Universiti Teknologi Malaysia for the award of a post-doctoral fellowship. The authors would like to thank the Research University grants (QJ 130000.2526.02H84 and QJ 130000.2526.03H83) and the Ministry of Agriculture (MoA), Malaysia (for Techno fund grant TF0310F080), for financial support of research activities.

References


