Egibacter rhizosphaerae gen. nov., sp. nov., an obligately halophilic, facultatively alkaliphilic actinobacterium and proposal of Egibacteraceae fam. nov. and Egibacterales ord. nov.

Yong-Guang Zhang, Hong-Fei Wang, Ling-Ling Yang, Xing-Kui Zhou, Xiao-Yang Zhi, Yan-Qing Duan, Min Xiao, Yuan-Ming Zhang and Wen-Jun Li

Correspondence
Wen-Jun Li
liwenjun3@mail.sysu.edu.cn or liact@hotmail.com

1Key Laboratory of Biogeography and Bioresource in Arid Land, Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences, Urumqi 830011, PR China
2College of Life Science, Liaoning Normal University, Dalian, 116029, PR China
3Yunnan Institute of Microbiology, Yunnan University, Kunming, 650091, PR China
4China Tobacco Yunnan Industrial Co., Ltd, Kunming 650231, PR China
5State Key Laboratory of Biocontrol and Guangdong Provincial Key Laboratory of Plant Resources, College of Ecology and Evolution, Sun Yat-Sen University, Guangzhou, 510275, PR China

A novel obligately halophilic, facultatively alkaliphilic actinobacterium, designated EGI 80759T, was isolated from the rhizosphere of Tamarix hispida Willd, Karamay, Xinjiang province, north-west China. Cells of strain EGI 80759T were Gram-stain-positive, non-motile and non-endospore-forming rods. Strain EGI 80759T showed obligately halophilic growth with a tolerance to 8–25 % (w/v) NaCl (optimum growth at 10–12 %, w/v) and facultatively alkaliphilic growth within the pH range 7.0–11.0 (optimum growth at pH 9.0–10.0). Cell-wall hydrolysates of the isolate contained meso-diaminopimelic acid (peptidoglycan type A1-\(c\)), with glucose, glucosamine, ribose and mannose as the major sugars. The major fatty acids identified were 10-methyl-C\(17:0\), C\(17:1\)\(\text{v8c}\) and C\(17:0\). The predominant menaquinone was MK-9(H4). The G+C content of the genomic DNA was 72.1 mol%. Phylogenetic analysis, based on 16S rRNA gene sequences, revealed that strain EGI 80759T clustered with members of the class Nitriliruptoria and showed highest 16S rRNA gene sequence similarities with Euzebya tangerina F10T (90.3 %) and Nitriliruptor alkaliphilus ANL-iso2T (88.1 %). On the basis of the data obtained from phenotypic and chemotaxonomic studies and the phylogenetic analysis, the isolate is proposed to be a representative of a novel genus and a novel species, Egibacter rhizosphaerae gen. nov., sp. nov., of a proposed novel family, Egibacteraceae fam. nov., and order, Egibacterales ord. nov., within the class Nitriliruptoria. The type strain of the type species, Egibacter rhizosphaerae, is EGI 80759T (=CGMCC 1.14997T=KCTC 39588T).

The class Actinobacteria was first proposed by Stackebrandt et al. (1997), based on phylogenetic and signature nucleotide analysis of 16S rRNA gene sequences, and subsequently emended by Hugenholtz & Stackebrandt (2004), Zhi et al. (2009) and Kurahashi et al. (2010). With the aims of keeping consistency with the rank of other prokaryotes and developing a unified classification across all bacteria and archaea, the class Actinobacteria containing five subclasses (Goodfellow & Fiedler, 2010) was elevated to the rank of phylum Actinobacteria phyl. nov., which includes the classes Actinobacteria, Acidimicrobiia, Coriobacteria, Nitriliruptoria, Rubrobacteria and Thermoleophilia (Ludwig et al., 2012). At the time of writing, the class Nitriliruptoria comprises two orders, Euzebyales (Kurahashi et al., 2010) and Nitriliruptorales (Sorokin et al., 2009), and two species with validly published names, Nitriliruptor alkaliphilus (Sorokin et al., 2009) and Euzebya tangerina (Kurahashi et al., 2010). N. alkaliphilus was isolated from soda lake sediments of the Kulunda steppe (Sorokin et al., 2009), while E. tangerina was from the abdominal epidermis of a sea cucumber, Holothuria edulis (Kurahashi et al., 2010). The class Nitriliruptoria has a

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain EGI 80759T is KR605111.

One supplementary figure and two supplementary tables are available with the online Supplementary Material.
distinct phylectic lineage and signature nucleotides of 16S rRNA gene sequence, as well as other characteristics, such as Gram-staining-positive rods and the cell-wall peptidoglycan A1γ type (Sorokin et al., 2009; Kurahashi et al., 2010).

Actinobacteria are distributed ubiquitous in the biosphere, including in extreme environments, such as salt lakes, soda lakes and desert soil (Bull, 2011). These extreme environments are usually made up of more than one extreme condition. For example, salinized soil is commonly found in temperate deserts and is characterized by high levels of salt, solar radiation and/or pH. However, limited knowledge of the physiologies and the adaptive mechanisms to such conditions has resulted in the discovery of less extremophilic actinobacterial taxa compared to other bacteria. Recently, researchers have started formulating new culture methods to cultivate more novel taxa (Tang et al., 2008; Pham & Kim, 2012). Here, we report on the isolation of a novel halo-alkaliphilic actinobacterium, designated EGI 80759T, from a rhizospheric soil sample of *Tamarix hispida* Willd that formed a deep phylectic lineage within the class *Nitriliruptoria*. Based on the results of the polyphasic characterizations, strain EGI 80759T was characterized as a novel taxon within the class *Nitriliruptoria* of the phylum *Actinobacteria* for which the name *Egibacter rhizophaeae*, gen. nov., sp. nov. is proposed; there is also a proposal for a new family, *Egibacteraceae* fam. nov., and a new order, *Egibacterales* ord. nov.

The soil sample (pH 8.7; total salts, 5.3 %, g kg⁻¹) used in the current study was collected from the rhizosphere of *Tamarix hispida* Willd grown at Karamay, Xinjiang province, north-west China during July 2013, and stored aseptically in a refrigerator at 4 °C until processed for isolation. The soil sample was diluted to a concentration of 10⁻³ and 10⁻⁴ (w/v) with sterile distilled water, and 0.1 ml of each was spread onto modified R2A agar (Reasoner & Geldreich, 1985) plates supplemented with 10 % NaCl (w/v) and the pH was adjusted to 10.0. Colonies appearing after 28 days incubation at 30 °C were picked, purified, cultivated and maintained on the same medium. These strains were also preserved as 20 % (v/v) glycerol/10 % (w/v) NaCl suspensions at −80 °C. Among them, a pale yellow-pink, extremely halophilic and facultatively alkaliphilic strain, designated EGI 80759T, was selected for further characterization. Biomass for chemical and molecular studies was obtained by cultivating in modified R2A broth under shaking conditions (~150 r.p.m., 30 °C, 21 days) unless otherwise stated. All media used for biochemical and physiological studies were supplemented with 10 % NaCl (w/v) and pH was adjusted to 10 with NaOH, unless stated otherwise.

Gram staining was carried out using the standard Gram reaction (Gram, 1884). Colony characteristics were determined by growing the strain on the media described by Shirling & Gottlieb (1966) at 30 °C for 28 days. The colours of colonies were determined with ISCC–NBS colour charts (Kelly, 1964). Morphological characteristics of strain EGI 80759T were observed by light microscopy (Olympus; BH-2) and scanning electron microscopy (Quanta 200; FEI) after incubation on modified R2A agar at 30 °C for 14–28 days. Strain EGI 80759T grew well on potato-glucose agar (PDA) and R2A agar, moderately on oatmeal agar (ISP 3), glycerol-asparagine agar (ISP 5), Czapek’s agar and weakly on nutrient agar, but no growth was observed on yeast extract-malt extract agar (ISP 2), inorganic starch agar (ISP 4) or Gause No. 1. The strain formed pale yellow-pink colonies on R2A, but strong yellow-pink colonies on PDA plates. Colonies were opaque, wrinkled, unevenly sized (below 3 mm diameter), and had middle humps and irregular edges after 28 days incubation on R2A plates at 30 °C. No diffusible pigments were detected in tested media. Details are described in Table S1 (available in the online Supplementary Material). The strain was Gram-stain-positive, non-motile and non-endospore-forming rods (Fig. 1). Non-desalted cells of strain EGI 80759T were more elliptical and mature grape-shaped (Fig. 1a), while desalted cells were rod-shaped (Fig. 1b). The variation in cell morphology in the presence of extracellular salt may relate to the adaptive mechanism of strain EGI 80759T. Cell sizes ranged between 0.3–0.4 μm in diameter and 1.0–1.3 μm in length.

Growth at different temperatures (5–60 °C, at intervals of 5 °C) was examined by growing the strain on R2A agar modified by the addition of 10 % (w/v) NaCl and adjusting the pH to 10.0 with autoclaved 10M NaOH. Salt tolerance was determined on R2A agar modified with the addition of various concentrations of NaCl (0–20 %, at intervals of 1 %; 22, 24, 25, 26, 28, 30 %, w/v) and adjusting the pH to 10.0 with autoclaved 10M NaOH. The pH range for growth was tested between 4.0 and 12.0, at intervals of 1.0 pH unit, on R2A broth supplemented with 10 % (w/v) NaCl by using the buffer system described by Xu et al. (2005). Sole carbon and nitrogen-source utilization tests were performed by the methods described by Shirling & Gottlieb (1966) and Williams et al. (1983), respectively. Catalase activity was determined from the production of gas bubbles on the addition of a drop of 3 % (v/v) H₂O₂. Other physiological and biochemical characteristics were examined as described previously (Goodfellow, 1971; Williams et al., 1983). Strain EGI 80759T could grow at 25–50 °C, pH 7.0–11.0 and 8.0–25.0 % (w/v) NaCl. Optimal growth occurred at 30 °C, pH 9.0–10.0 and 10–12.0 % (w/v) NaCl. Other physiological characteristics of strain EGI 80759T are given in Table I and the species description below.

Diaminopimelic acid isomers in cell-wall hydrolysates were analysed by TLC as described by Staneck & Roberts (1974). A purified cell-wall preparation was obtained and hydrolysed as described by Schleifer & Kandler (1972) and analysed according to the method of Tang et al. (2009). Whole-cell sugars were detected according to the method used by Tang et al. (2009). Polar lipids were extracted and identified by two-dimensional TLC following the method of Minnikin et al. (1984). Menaquinones were extracted and purified according to Collins et al. (1977) and were analysed by HPLC (Groth et al., 1996). For fatty acid analysis, strain EGI 80759T was cultured on modified TSB medium (supplemented with 10 % (w/v) NaCl) at 30 °C and pH 10.0.
for 21 days. Cellular fatty acid analysis was performed as described by Sasser (1990) according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System. The genomic DNA of strain EGI 80759T was prepared according to Marmur (1961), and its G + C content was determined by HPLC according to Mesbah et al. (1989). The cell-wall peptidoglycan of strain EGI 80759T contained meso-diaminopimelic acid, alanine and glutamic acid as major amino acids, which indicated the presence of the A1c type peptidoglycan (Schleifer & Kandler, 1972; Sorokin et al., 2009; Kurahashi et al., 2010). Strain EGI 80759T contained glucose, glucosamine, ribose, mannose and one unknown sugar as the major cell-wall sugars. The predominant menaquinone detected was MK-9(H4), while the polar lipids were diphosphatidylglycerol, one unknown phosphoglycolipid, six unknown phospholipids, two unknown glycolipids and five unknown polar lipids (Fig. S1). Strain EGI 80759T had a cellular fatty acid profile containing major amounts of branched fatty acids, unsaturated straight-chain fatty acids and minor amounts of saturated straight-chain fatty acids: 10-methyl-C17:0 (32.0 %), C17:0ω8c (22.1 %), C17:0ω6c (11.1 %), C16:0 (7.9 %), summed feature 9 (iso-C17:0ω9c or 10-methyl-C16:0) (4.7 %), iso-C16:0 (4.2 %), C17:1ω6c (3.7 %), summed feature 3 (C16:1ω7c/C16:1ω6c, or C16:1ω6c/C16:1ω7c) (2.0 %), C15:1ω8c (1.7 %), C16:1ω9c (1.4 %), iso-C17:0.

### Table 1. Phenotypic and chemotypic features that distinguish strain EGI 80759T from its closest phylogenetic neighbours E. tangerina F10T and N. alkaliphilus ANL-iso2T

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1*</th>
<th>2†</th>
<th>3‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell size (μm)</td>
<td>0.3–0.4 × 1.0–1.3</td>
<td>0.6–0.8 × 1.5–6.0</td>
<td>0.4 × 1.5–3.0</td>
</tr>
<tr>
<td>Growth at pH range (optimum)</td>
<td>7–11 (9–10)</td>
<td>7–9 (ND)</td>
<td>8.2–10.6 (9.0–9.50)</td>
</tr>
<tr>
<td>NaCl concn range for growth (% w/v)</td>
<td>8–25 (10–12)</td>
<td>0.5–12 (ND)</td>
<td>0.1–11.6 (1.2–1.7)</td>
</tr>
<tr>
<td>Temperature range (°C) (optimum)</td>
<td>25–50 (30–35)</td>
<td>15–35 (20–28)</td>
<td>Mesophilic (32)</td>
</tr>
<tr>
<td>Cell-wall sugars</td>
<td>Glc, GlcN, Rib, Man, US</td>
<td>Rha, Gal</td>
<td>Glc, Gal</td>
</tr>
<tr>
<td>Major phospholipids</td>
<td>DPG, PGL, PL</td>
<td>PG</td>
<td>ND</td>
</tr>
<tr>
<td>G + C mol%</td>
<td>72.1</td>
<td>68.3</td>
<td>70.8</td>
</tr>
</tbody>
</table>

*Data from this study.
†Data from Kurahashi et al. (2010).
‡Data from Sorokin et al. (2009) and Kurahashi et al. (2010).
(1.4 %), C<sub>15</sub>:1ω6c (1.3 %), anteiso-C<sub>17</sub>:0 (1.2 %), 10-methyl-C<sub>18</sub>:0, TBSA (1.0 %), iso-C<sub>16</sub>:1 H (1.0 %), C<sub>18</sub>:0 (0.6 %), iso-C<sub>15</sub>:0 (0.5 %), C<sub>18</sub>:0ω9c (0.5 %), summed feature 8 (C<sub>18</sub>:0ω7c or C<sub>18</sub>:1ω6c) (0.6 %), C<sub>18</sub>:ω6c (6, 9, 12) (0.4 %), C<sub>14</sub>:0 (0.4 %), summed feature 5 (C<sub>18</sub>:ω6;9c/anteiso-C<sub>18</sub>:0 or anteiso-C<sub>18</sub>:1ω0c) (0.4 %) and anteiso-C<sub>15</sub>:0 (0.2 %). The genomic DNA G+C content of strain EGI 80759<sup>T</sup> was 72.1 mol%.

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene were carried out as described by Li et al. (2007). Multiple alignments with sequences of representative type species of the phylum Actinobacteria and calculations of levels of sequence similarity were carried out using the EzTaxon-e server (http://eztaxon-e.ezbiocloud.net/; Kim et al., 2012). Phylogenetic analysis was performed using three tree-making algorithms: the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods using MEGA 6 software (Tamura et al., 2013). The topologies of the resultant trees were evaluated by the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

An almost complete 16S rRNA gene sequence (1517 bp) was determined for strain EGI 80759<sup>T</sup>. Phylogenetic analysis, based on the 16S rRNA gene sequences, revealed that the strain clustered with members of the class Nitriliruptoria. The 16S rRNA gene sequence similarities between the novel isolate, EGI 80759<sup>T</sup>, and strains E. tangerina F10<sup>T</sup> and N. alkaliphilus ANL-iso2<sup>T</sup> were 90.3 % and 88.1 %, respectively. In the phylogenetic tree based on the neighbour-joining algorithm, strains EGI 80759<sup>T</sup> and E. tangerina F10<sup>T</sup> formed a single clade with a high bootstrap value (95 %), while N. alkaliphilus ANL-iso2<sup>T</sup> formed another clade (Fig. 2). The relationship was also supported by the other tree-making methods used in this study (Fig. 2).

The data above confirm that the novel isolate should be assigned to the class Nitriliruptoria. Although strain EGI 80759<sup>T</sup> exhibited similar characteristics to E. tangerina F10<sup>T</sup> and N. alkaliphilus ANL-iso2<sup>T</sup> in having rod-shaped morphology, a type (A<sub>1</sub>)<sub>c</sub> cell-wall peptidoglycan, MK-9(H<sub>4</sub>) as the major menaquinone, C<sub>17</sub>:1ω8c as one major fatty acid and a separate phylogenetic lineage, it had some features distinguishing it from E. tangerina and N. alkaliphilus. In phylogenetic analysis, the novel strain clustered with members of the class Nitriliruptoria based on the 16S rRNA gene sequences, revealed that the strain belongs to the order Nitriliruptoria.

Unlike E. tangerina, strain EGI 80759<sup>T</sup> is an obligate halophile that grows only at a higher concentration of NaCl. 10-Methyl-C<sub>17</sub>:0 is one of the major fatty acids of strain EGI 80759<sup>T</sup>, comprising 32.0 % of the total, but not of N. alkaliphilus ANL-iso2<sup>T</sup> (Kurahashi et al., 2010). The phylogenetic relationship of EGI 80759<sup>T</sup> and N. alkaliphilus ANL-iso2<sup>T</sup> (Sorokin et al., 2009) also differs greatly, thereby indicating that strain EGI 80759<sup>T</sup> does not fall into the order Nitriliruptoria. In conclusion, strain EGI 80759<sup>T</sup> does not belong to any order of the class Nitriliruptoria.

Higher hierarchical taxa in the class Actinobacteria should be based mainly on 16S rRNA gene signature nucleotide patterns and phylogenetic criteria (Stackebrandt et al., 1997; Zhi et al., 2009). Based on the phenotypic and phylogenetic data, we concluded that strain EGI 80759<sup>T</sup> represents a novel species in a novel genus, Egibacter rhizosphaerae, gen. nov., sp. nov. In addition, a new lineage, based on the distinct phylogenetic position of Egibacter rhizosphaerae gen. nov., sp. nov., with the novel order Egibacteriales ord. nov. and a novel family Egibacteraceae fam. nov. is proposed within the class Nitriliruptoria.

**Description of Egibacter gen. nov.**

*Egibacter* (Egi.bacter N.L. masc. n. bacter, rod; N.L. masc. n. Egibacter arbitrary name formed from the acronym of Institute of Ecology and Geography, EGI, where the first taxonomic studies of this taxon were performed).

Gram-stain-positive, non-mottile, non-endospore-forming rods. Aerobic and chemo-organotrophic. Catalase-positive. Obligately halophilic and facultatively alkaliphilic. The menaquinone pattern is MK-9(H<sub>4</sub>). Cell wall contains meso-diaminopimelic acid as the diagnostic diamino acid. The peptidoglycan type is A<sub>1</sub>γ. Glucose, glucosamine, ribose, mannose and one unknown sugar are detected as cell-wall sugars. The major fatty acids are 10-methyl-C<sub>17</sub>:0, C<sub>17</sub>:1ω8c and C<sub>17</sub>:0ω9c. Contains diphosphatidylglycerol, one unknown phospholipid and one phosphoglycolipid as major polar lipids. The type species is *Egibacter rhizosphaerae*.

**Description of Egibacter rhizosphaerae sp. nov.**

*Egibacter rhizosphaerae* (rhi.zo.sphae’rae. N.L. gen. n. rhizo-sphaerae of the rhizosphere).
In addition to the properties given for the genus, cells are approximately 0.3–0.4 × 1.0–1.3 μm. Colonies are pale yellow-pink, opaque and uneven in size, and have wrinkles, middle humps and irregular edges after 28 days incubation on R2A plates at 30 °C. Growth occurs at 25–50 °C, pH 7.0–11.0 and with 8–25.0 % (w/v) NaCl. Optimal growth occurs at 30–35 °C, pH 9.0–10.0 and with 10–12.0 % (w/v) NaCl. Grows well on R2A agar and PDA. Utilizes D-arabinose, L-arabinose, cellobiose, dulcitol, D-fructose, D-galactose, glycerol, myo-inositol, lactose, maltose, D-mannitol, D-mannose, L-rhamnose, D-ribose, D-sorbitol, sucrose, trehalose, D-xylene, D-xylitol, sodium acetate and sodium citrate as the sole carbon source for growth, but not D-glucose. Utilizes L-arginine, L-aspartic acid, L-histidine, L-leucine, L-isoleucine, L-phenylalanine, L-tryptophan, L-valine, L-serine and L-hyperxanthine as the sole nitrogen source for growth, but not L-alanine, L-cysteine, L-glutamic acid, L-glutamine, glycine, L-lysine, L-methionine, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 40 and 80, nitrate reduction, catalase, L-threonine, L-tyrosine or L-proline. Positive for the hydrolysis of Tweens 20 and 60, casein, cellulose, coagulation and peptonization of skimmed milk, while negative for the hydrolysis of Tweens 20 and 60, casein, cellulose, starch and tryptophan, and H2S production. The polar lipids are diphosphatidylglycerol, one unknown phosphoglycolipid, two unknown glycolipids, six unknown phospholipids and five unknown polar lipids. The major fatty acids are 10-methyl-C17:0, C17:0, C18:0 and C18:0. The type strain is EGI 80759T (DQ432396).
Xinjiang province, north-west China. The G + C content of the genomic DNA is of the type strain is 72.1 mol%.

**Description of Egibacteraceae fam. nov.**

*Egibacteraceae* (E.gi.bac.te.ra.ce’ae. N. L. masc. n. *Egibacter* type genus of the family; -aceae ending to denote a family; N.L. fem. pl. n. *Egibacteraceae* the family of the genus *Egibacter*).

The description is the same as that for the genus *Egibacter*. Segregation of these organisms into a novel family is justified by their distinct phyletic lineage based on the 16S rRNA gene sequence. The pattern of 16S rRNA gene sequence signature nucleotides of members of the family comprises 47 : 396 (C-G), 232 (C), 241 : 285 (C-G), 294 : 303 (C-G), 361 (G), 845 (A), 1038 (C), 1031 (U).

**Description of Egibacterales ord. nov.**

*Egibacterales* (E.gi.bac.te.ra’les. N.L. masc. n. *Egibacter* type genus of the family; -ales, ending to denote an order; N.L. fem. pl. n. *Egibacterales* the order of the genus *Egibacter*).

The description is the same as that for the genus *Egibacter*. Separation of these organisms into a novel order is justified by their distinct phyletic lineage based on the 16S rRNA gene sequence. The pattern of 16S rRNA gene sequence signature nucleotides of members of the order is as for the family *Egibacteraceae*. The order contains the family *Egibacteraceae*. *Egibacter rhizophorae* is the type genus.

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