Description of *Salilacibacter albus* gen. nov., sp. nov., isolated from a dried salt lake, and reclassification of *Paraglycomyces xinjiangensis* Luo *et al.* 2015 as a later heterotypic synonym of *Salininema proteolyticum* Nikou *et al.* 2015 with emended descriptions of the genus *Salininema* and *Salininema proteolyticum*

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A novel halophilic actinomycete, designated strain J11Y309³, was isolated from a soil sample collected from a dried salt lake in China. This isolate grew optimally at 28–37 °C, with 3–5% (w/v) NaCl and at pH 7.0–7.5. It contained meso-diaminopimelic acid as the diagnostic diamino acid and glucose, ribose and xylose were present in the whole-cell hydrolysates. MK-10(H₄) was detected as the predominant menaquinone. The major fatty acids were anteiso-C₁₇:0, iso-C₁₆:0, iso-C₁₇:0 and iso-C₁₅:0. Polar lipids were phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylinositol, phosphatidylinositol mannoside, phosphoglycolipids, glycolipids, an unidentified phospholipid and additional unidentified lipids. The G+C content of the genomic DNA was 63.0 mol%. The novel strain shared highest 16S rRNA gene sequence similarity with *Salininema proteolyticum* Miq-4³ (95.80%), *Paraglycomyces xinjiangensis* TRM 49201³ (95.77%) and *Haloglycomyces albus* YIM 92370³ (94.84%). Phylogenetic trees showed that it could not be clearly assigned to any known genus within the family *Glycomycetaceae* and formed a distinct phylogenetic line in the clade comprising members of the genera *Salininema*, *Paraglycomyces* and *Haloglycomyces*. Based on data from the present polyphasic taxonomic study, strain J11Y309³ represents a novel species of a new genus in the family *Glycomycetaceae*, for which the name *Salilacibacter albus* gen. nov., sp. nov. is proposed with *Salilacibacter albus* sp. nov. as the type species. The type strain of *Salilacibacter albus* is J11Y309³ (=DSM 46875³ =CGMCC 4.7242³ =LMG 29297³). Reclassification of *Paraglycomyces xinjiangensis* Luo *et al.* 2015 as a later heterotypic synonym of *Salininema proteolyticum* Nikou *et al.* 2015 is also discussed in this study.

Abbreviation: DAP, diaminopimelic acid.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain J11Y309 T is KR149811.

Three supplementary figures are available in the online Supplementary Material.

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During a previous investigation of the diversity of cultivable actinobacteria in salt lakes, a novel halophilic strain, designated J11Y309\textsuperscript{T}, was isolated from a soil sample collected in Jiuliancheng Nur (41° 33' 43.05" N 115° 01' 52.01" E), a dried salt lake located in Hebei Province, China. The results of phylogenetic analyses based on 16S rRNA gene sequences indicated that strain J11Y309\textsuperscript{T} may represent a novel member affiliated with the family Glycomycetaceae.

The family Glycomycetaceae, affiliated with the order Glycomycetales (Labeda, 2012), was proposed by Rainey et al. (in Stackebrandt et al., 1997) and the description was successively emended by Labeda & Kroppenstedt (2005), Zhi et al. (2009) and Nikou et al. (2015). Before 2015, only three validly described genera were included in the family Glycomycetaceae, namely Glycosmyces (Labeda et al., 1985; Labeda & Kroppenstedt, 2004), Stackebrandttia (Labeda & Kroppenstedt, 2005) and Haloglycosmyces (Guan et al., 2009). In 2015, two new genera affiliated with the family Glycomycetaceae were proposed almost simultaneously. The genus Salinemana was proposed with Salinemana proteolyticum as the type and only species in October 2015, a novel halophilic actinobacterium isolated from soil around Meighan wetland in the centre of Iran, and a month later, the genus Paraglycosmyces was proposed with Paraglycosmyces xinjiangensis as the type and only species, a novel halophilic actinobacterium isolated from hypersaline soil in Xinjiang Province, north-west China. Comparative analyses of the 16S rRNA gene sequences revealed that P. xinjiangensis TRM 49201\textsuperscript{T} was closely related to S. proteolyticum Miq-4\textsuperscript{T}, sharing 99.5\% similarity. However, this close taxonomic relationship between the two genera was not noticed until recently. In this paper, the taxonomic relationship between P. xinjiangensis and S. proteolyticum is discussed. Meanwhile, the taxonomic characterization of a new isolate (J11Y309\textsuperscript{T}) is described and a novel genus and species are proposed.

Strain J11Y309\textsuperscript{T} was isolated by using the dilution plating technique on modified glycerol agar plates (containing, per litre: 2.0 g arginine, 12.5 g glycerol, 50.0 g NaCl, 2.0 g K\textsubscript{2}HPO\textsubscript{4}, 3H\textsubscript{2}O, 0.01 g FeSO\textsubscript{4}.7H\textsubscript{2}O, 0.05 g MgSO\textsubscript{4}.7H\textsubscript{2}O, 0.001 g CuSO\textsubscript{4}.5H\textsubscript{2}O, 0.001 g ZnSO\textsubscript{4}.7H\textsubscript{2}O, 0.001 g MnSO\textsubscript{4}.2H\textsubscript{2}O, 18.0 g agar, pH 7.2–7.4) supplemented with cycloheximide (45 mg l\textsuperscript{-1}), nalidixic acid (25 mg l\textsuperscript{-1}) and potassium dichromate (45 mg l\textsuperscript{-1}). Colonies of strain J11Y309\textsuperscript{T} appeared on the agar plate after incubation for 3 weeks at 28 °C and were transferred onto International Streptomycetes Project 2 (ISP 2, yeast extract-malt extract agar, Shirling & Gottlieb, 1966) plates supplemented with 5 % (w/v) NaCl using the serial streaking technique until pure isolates were obtained. The purified isolates were maintained on ISP 2 slants supplemented with 5 % (w/v) NaCl at 4 °C and stored as aqueous glycerol suspensions (20 %, v/v) at −80 °C.

A Gram-stain test was performed as described by Magee et al. (1975). Culture characteristics were observed on the following media supplemented with 5 % (w/v) NaCl: ISP 2, oatmeal agar (ISP 3), inorganic salts-starch agar (ISP 4), glycerol-asparagine agar (ISP 5) (Shirling & Gottlieb, 1966), nutrient agar (NA; BD), tryptic soy agar (TSA; BD), Czapek’s agar and potato dextrose agar (PDA) (Atlas, 1993) at 32 °C for 7–28 days. The colony colour and diffusible pigments were determined by comparison with chips from the ISCC-NBS colour charts (Kelly, 1964). Morphological properties were observed on Czapek’s agar by light microscopy (BH2; Olympus) and scanning electron microscopy (Quanta 200; FEI) after incubation at 32 °C for 7, 14, 21 and 28 days. Growth at different temperatures (4, 10, 15, 20, 28, 32, 37, 42 and 45 °C) and NaCl concentrations (w/v) (0, 1, 3, 5, 7, 8, 10, 12, 15, 18 %) were determined on ISP 2 for 2 weeks. The pH range for growth was tested in ISP 2 broth between pH 4.0 and 11.0 at intervals of 0.5 pH units using the buffer system described by Xu et al. (2005). Carbon source utilization and acid production were determined using Biolog GENIII Microplates (BIOLOG) and the API 50 CH system (bioMérieux, respectively). Enzyme activities were examined using API ZYM strips (bioMérieux) following the manufacturer’s instructions. Catalase activity was determined by bubble production in a 3 % (v/v) hydrogen peroxide solution, and oxidase activity was tested by using a 1 % (w/v) solution of tetramethyl-p-phenylenediamine. Other physiological tests, including those for hydrolysis or degradation of tyrosine, casein, urea, starch, Tween 20, Tween 40 and Tween 80, milk coagulation and peptonization, gelatin liquefaction and nitrate reduction, were determined as described by Williams et al. (1983).

Cells of strain J11Y309\textsuperscript{T} were Gram-stain-positive. We observed good growth on Czapek’s agar, ISP 2, ISP 4 and TSA, moderate growth on ISP 3, ISP 5 and NA, and no growth on PDA. No diffusible pigments were produced on any media tested. Substrate mycelium was light olive grey on ISP 4, light grey on ISP 2, light greyish olive on TSA and moderate yellowish green on other media tested. Raised and plicated growth was observed on all the media tested except PDA. White aerial mycelia formed on Czapek’s agar, ISP 4, ISP 2, TSA and NA after incubation for 3 weeks. Substrate mycelium showed extensive branching and was non-fragmenting; filamentous and slightly twisted aerial mycelia.
Table 1. Menaquinone profiles of strain J11Y309T and the type strains of related genera in the family Glycomycetaceae

Strains: 1, J11Y309T; 2, S. proteolyticum IBRC-M 10908T; 3, P. xinjiangensis CCTCC AA 2013002T; 4, H. albus DSM 45210T. Data for all the strains were obtained in this study. Values are percentages of total menaquinones. –, Not detected or not reported; TR, trace amount.

Table 2. Comparison of the fatty acid profiles of strain J11Y309T and the type strains of species of related genera in the family Glycomycetaceae

Strains: 1, J11Y309T; 2, S. proteolyticum IBRC-M 10908T; 3, P. xinjiangensis CCTCC AA 2013002T; 4, H. albus DSM 45210T. Data for all the strains were obtained in this study. Values are percentages of total fatty acids. –, Not detected.
fatty acid content. Detailed polar lipid chromatograms and cellular fatty acid profiles of strain J11Y309<sup>T</sup> and the reference type strains are given in Fig. S1 and Table 2.

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene from strain J11Y309<sup>T</sup> were performed according to Li et al. (2007). The PCR product was cloned into a pEASY-T1 cloning vector (TransGen Biotech) according to the manufacturer's instructions and sequenced using an ABI PRISM 3730XL DNA analyser. Levels of 16S rRNA gene sequence similarity were determined via the EzTaxon-e server (http://eztaxon-e.ezbiocloud.net/; Kim et al., 2012), and the BLAST search program (Altschul et al., 1997). The 16S rRNA gene sequences of corresponding species were obtained from the GenBank/EMBL/DDJB databases, and the multiple alignments were performed using BioEdit (version 7.0.9.0) (Hall, 1999). Phylogenetic trees were reconstructed with the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods by using the software package MEGA version 5.0 (Tamura et al., 2011). Evolutionary distance matrices were calculated according to Kimura's two-parameter model (Kimura, 1980, 1983) for the neighbour-joining and maximum-likelihood algorithms, and close-neighbour interchange (search level=2, random addition=100) was applied in the maximum-parsimony algorithm. The robustness of the tree topology was evaluated by bootstrap analysis (Felsenstein, 1985) with 1000 replications.

For the determination of G+C content and levels of DNA–DNA relatedness, the genomic DNA of strain J11Y309<sup>T</sup> and reference type strains was prepared according to the method described by Marmur (1961). The G+C content of the genomic DNA of strain J11Y309<sup>T</sup> was determined by HPLC (Mesbah et al., 1989). DNA–DNA hybridizations between strain J11Y309<sup>T</sup> and <i>S. proteolyticum</i> LMG 28391<sup>T</sup> (BCCM/ LMG Bacteria Collection) were carried out by the BCCM/ LMG Identification Service. Hybridizations were performed in the presence of 50 % formamide at 52.8 °C according to a modification (Goris et al., 1998; Cleenwerck et al., 2002) of the method described by Ezaki et al. (1989), and reciprocal reactions were performed in quadruplicate. DNA–DNA hybridizations between strain J11Y309<sup>T</sup> and <i>P. xinjiangensis</i> CCTCC AA 2013002<sup>T</sup>, and between <i>P. xinjiangensis</i> CCTCC AA 2013002<sup>T</sup> and <i>S. proteolyticum</i> IBRC-M 10908<sup>T</sup> were performed by the thermal denaturation and renaturation method of De Ley et al. (1970) using a PharmaSpec UV/VIS spectrophotometer (UV-2550; Shimadzu) equipped with a Peltier-thermostated multichannel changer and a temperature controller (S-1700; Shimadzu) with <i>in situ</i> temperature probe. The DNA–DNA hybridizations were conducted three times in each case with three replicates.

A nearly full-length 16S rRNA gene sequence (1494 bp) of strain J11Y309<sup>T</sup> was obtained. Comparative analyses of the 16S rRNA gene sequence revealed that strain J11Y309<sup>T</sup> was related most closely to <i>S. proteolyticum</i> Miq-4<sup>T</sup> (95.80 %), <i>P. xinjiangensis</i> TRM 49201<sup>T</sup> (95.77 %) and <i>H. albus</i> YIM 92370<sup>T</sup> (94.84 %), whereas it shared lower levels of 16S rRNA gene sequence similarity (90.31–93.42 %) with all the other recognized species of the family Glycomycetaceae. Phylogenetic trees reconstructed with all three treeing methods showed that strain J11Y309<sup>T</sup> was clustered with <i>S. proteolyticum</i> Miq-4<sup>T</sup>, <i>P. xinjiangensis</i> TRM 49201<sup>T</sup> and <i>H. albus</i> YIM 92370<sup>T</sup> in the family Glycomycetaceae (Figs 2, S2 and S3), but it formed an independent phylogenetic line in the clade. Analysis of 16S rRNA signature nucleotides showed that strain J11Y309<sup>T</sup> shared the signature pattern defined for the family Glycomycetaceae (Nikou et al., 2015). The G+C content of the genomic DNA of strain J11Y309<sup>T</sup> was 63.0 mol%. Levels of DNA–DNA relatedness between strain J11Y309<sup>T</sup> and the two most closely related type strains, <i>S. proteolyticum</i> LMG 28391<sup>T</sup> and <i>P. xinjiangensis</i> CCTCC AA 2013002<sup>T</sup>, were 12.0 % (reciprocal, 13.0 %) and 19.2±3.0 % (mean±SD), respectively.

Phylogenetic analyses based on 16S rRNA gene sequences revealed that strain J11Y309<sup>T</sup> may represent a novel member belonging to the family Glycomycetaceae. Meanwhile, the chemotaxonomic data stated above also showed that strain J11Y309<sup>T</sup> exhibited the typical characteristics of the family Glycomycetaceae, with <i>meso</i>-DAP as the diamino acid, ribose as the whole-cell diagnostic sugar, iso- and anteiso-branched fatty acids as major fatty acids and phosphatidylglycerol and diphosphatidylglycerol in the phospholipid profile (Labeda, 2012; Stackebrandt, 2014). The phylogenetic position of strain J11Y309<sup>T</sup> in three phylogenetic trees (Figs 2, S2 and S3) showed that it could not be clearly assigned to any known genus within the family Glycomycetaceae, although it was related most closely to the genera <i>Sabininema</i>, <i>Paraglycomyces</i> and <i>Haloglycomyces</i>, which indicates that strain J11Y309<sup>T</sup> may represent a novel species of a new genus within the family Glycomycetaceae. Relatively low levels of DNA–DNA relatedness with its two most closely related type strains, <i>S. proteolyticum</i> IBRC-M 10908<sup>T</sup> (12 %, reciprocal, 13.0 %) and <i>P. xinjiangensis</i> CCTCC AA 2013002<sup>T</sup> (19.2±3.0 %), also supported this conclusion. Analysis of 16S rRNA signature nucleotides also showed that the 16S rRNA gene sequence of strain J11Y309<sup>T</sup> contained several exclusive signature nucleotides, which clearly distinguished it from all available members of the three phylogenetic neighbours, namely the genera <i>Sabininema</i>, <i>Paraglycomyces</i> and <i>Haloglycomyces</i> (Table 3). Moreover, strain J11Y309<sup>T</sup> could be differentiated from members of these three genera based on some chemotaxonomic properties. For polar lipids, two unknown lipids (L2 and L4) detected in strain J11Y309<sup>T</sup> were not found in the type strains of the three related genera, while an aminolipid (AL) typical of <i>Sabininema</i> species and a phospholipid (PL2) typical of <i>Haloglycomyces</i> species were absent in the polar lipid profile of strain J11Y309<sup>T</sup> (Fig. S1). The major menaquinones of strain J11Y309<sup>T</sup> were MK-10(H<sub>4</sub>) and MK-9(H<sub>4</sub>), which differentiated it from <i>S. proteolyticum</i> IBRC-M 10908<sup>T</sup> and <i>P. xinjiangensis</i> CCTCC AA 2013002<sup>T</sup> with MK-10(H<sub>4</sub>), MK-10(H<sub>2</sub>) and MK-9(H<sub>4</sub>) as major

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Fig. 2. Neighbour-joining tree showing the phylogenetic relationships between strain J11Y309\(^{\dagger}\) and species of related genera in the family *Glycomycetaceae* based on 16S rRNA gene sequences (1408 bp). The sequence of *Krasilnikovia cinnamomea* 3-54/41\(^{\dagger}\) was used as the outgroup. Filled circles at nodes indicate corresponding branches that were also recovered by using the maximum-likelihood and maximum-parsimony algorithms. Numbers at branch nodes refer to bootstrap values of 1000 replications; only values >50% are shown. Bar, 0.01 nucleotide substitutions per site.

Table 3. 16S rRNA signature nucleotides distinguishing the genus *Salilacibacter* gen. nov. from members of the closest genera of the family *Glycomycetaceae*

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<tr>
<td>Position</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
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<tr>
<td>76–93</td>
<td>U—</td>
<td>C—</td>
<td>C—</td>
<td>C—</td>
</tr>
<tr>
<td>184–193</td>
<td>C-C</td>
<td>A-C</td>
<td>A-C</td>
<td>A-C</td>
</tr>
<tr>
<td>185–192</td>
<td>C-G</td>
<td>U-G</td>
<td>U-G</td>
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<tr>
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<td>A-C</td>
<td>C-C</td>
<td>C-C</td>
<td>G-C</td>
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<tr>
<td>204</td>
<td>G</td>
<td>U</td>
<td>U</td>
<td>U</td>
</tr>
<tr>
<td>278</td>
<td>U</td>
<td>G</td>
<td>G</td>
<td>G</td>
</tr>
<tr>
<td>458–474</td>
<td>A-A</td>
<td>G-G</td>
<td>G-G</td>
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<tr>
<td>459–473</td>
<td>G-C</td>
<td>G-U</td>
<td>G-U</td>
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<tr>
<td>601–637</td>
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<td>G-U</td>
<td>G-U</td>
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<tr>
<td>1005</td>
<td>A</td>
<td>C</td>
<td>C</td>
<td>C</td>
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<tr>
<td>1006–1023</td>
<td>A-G</td>
<td>G-G</td>
<td>G-G</td>
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<td>G-U</td>
<td>G-U</td>
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<td>U-A</td>
<td>U-A</td>
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<tr>
<td>1026–1035</td>
<td>C—</td>
<td>U—</td>
<td>U—</td>
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<td>1164–1172</td>
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<td>1165–1171</td>
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<td>U-A</td>
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<tr>
<td>1257</td>
<td>U</td>
<td>A</td>
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menaquinones, as shown in Table 1. The fatty acids anteiso-C\(_{17:0}\) and anteiso-C\(_{15:0}\) accounted for almost half of the total in strain J11Y309\(^{\dagger}\), and was in agreement with the three reference type strains, as shown in Table 2. The fatty acid profile of strain J11Y309\(^{\dagger}\) was similar to that of *H. albus* DSM 45210\(^{\dagger}\), while it was different from those of *S. proteolyticum* IBRC-M 10908\(^{\dagger}\) and *P. xinjiangensis* CCTCC AA 2013002\(^{\dagger}\) in the proportions of iso-C\(_{17:0}\) and anteiso-C\(_{15:0}\). Resistance to salt concentration also differentiated strain J11Y309\(^{\dagger}\) from members of the genera *Salininema*, *Paraglycomyces* and *Haloglycomyces*. Differential characteristics between strain J11Y309\(^{\dagger}\) and its phylogenetic neighbours in the family *Glycomycetaceae* are summarized in Table 4.

In conclusion, on the basis of phylogenetic analysis, physiological characteristics and chemotaxonomic data, strain J11Y309\(^{\dagger}\) represents a novel species of a new genus within the family *Glycomycetaceae*, for which the name *Salilacibacter albus* gen. nov., sp. nov. is proposed.

To determine the taxonomic relationship between *P. xinjiangensis* TRM 49201\(^{\dagger}\) and *S. proteolyticum* Miq-4\(^{\dagger}\), a polyphasic approach was employed. 16S rRNA gene sequences of *P. xinjiangensis* CCTCC AA 2013002\(^{\dagger}\) and *S. proteolyticum* IBRC-M 10908\(^{\dagger}\) were obtained in this study, which were identical to those of *P. xinjiangensis* TRM 49201\(^{\dagger}\) (GenBank accession no. AB857719) reported by Luo et al.
Table 4. Differential characteristics between strain J11Y309T, its closest phylogenetic neighbours and other genera of the family *Glycomycetaceae*

<table>
<thead>
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<th>Characteristic</th>
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<th>4</th>
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<th>6</th>
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<tbody>
<tr>
<td>Isolation source</td>
<td>Dried salt lake soil</td>
<td>Wetland soil</td>
<td>Salt lake soil</td>
<td>Hypersaline soil</td>
<td>Soil</td>
<td>Road side soil</td>
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<tr>
<td>NaCl concentration (%, w/v)</td>
<td>0–8</td>
<td>3–15</td>
<td>3–15</td>
<td>3–18</td>
<td>5</td>
<td>4–9</td>
</tr>
<tr>
<td>Whole-cell sugars</td>
<td>Glucose, ribose, xylose</td>
<td>Glucose, ribose, xylose</td>
<td>Glucose, ribose, xylose</td>
<td>Ribose, xylose, glucose</td>
<td>Xylose, arabinose</td>
<td>Ribose, inositol, arabinose, mannose</td>
</tr>
<tr>
<td>Major menaquinones</td>
<td>MK-10(H4), MK-9(H4)</td>
<td>PE, PG, DPG, PI, PIM, PGL, PL, GL, L, ai-C17:0, i-C16:0, i-C15:0, 63.0</td>
<td>PE, PG, DPG, PI, PIM, PGL, PL, GL, L, ai-C17:0, i-C16:0, i-C15:0, 68.2</td>
<td>AL, L, i-C17:0, i-C15:0, 60.8</td>
<td>GL, PIM, PGL, PL, GL, L, ai-C17:0, i-C16:0, 71.0</td>
<td></td>
</tr>
<tr>
<td>Polar lipids</td>
<td>PE, PG, DPG, PI, PIM, PGL, PL, GL, L, ai-C17:0, i-C16:0, i-C15:0, 63.0</td>
<td>PE, PG, DPG, PI, PIM, PGL, PL, GL, L, ai-C17:0, i-C16:0, i-C15:0, 63.0</td>
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<tr>
<td>Major fatty acids</td>
<td>PE, PG, DPG, PI, PIM, PGL, PL, GL, L, ai-C17:0, i-C16:0, i-C15:0, 63.0</td>
<td>PE, PG, DPG, PI, PIM, PGL, PL, GL, L, ai-C17:0, i-C16:0, i-C15:0, 63.0</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>63.0</td>
<td>68.2</td>
<td>70.0*</td>
<td>60.8</td>
<td>69.0</td>
<td>69.4–72.4</td>
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</tbody>
</table>

*DNA G+C contents of the three reference type strains were from Nikou et al. (2015), Luo, et al. (2015) and Guan et al. (2009), respectively.*

(2015) and *S. proteolyticum* Miq-4T (KP162267) reported by Nikou et al. (2015), respectively. Phylogenetic analysis based on the 16S rRNA gene sequences revealed that *P. xinjiangensis* TRM 49201T is closely related to *S. proteolyticum* Miq-4T, sharing 99.5% 16S rRNA gene sequence similarity, and the two type strains formed a well-supported cluster (Figs 2, S2 and S3). The level of DNA–DNA relatedness between *P. xinjiangensis* CCTCC AA 2013002T and *S. proteolyticum* IBRC-M 10908T was 75.5 ± 4.0%, above the 70% cut-off value considered to be the threshold for the definition of genomic species (Wayne et al., 1987), and the result indicated that they belonged to the same species. Both strains contained meso-DAP as the diagnostic diamino acid in whole-cell hydrolysates in our study, which does not support the type III cell-wall composition for *S. proteolyticum* IBRC-M 10908T as reported by Nikou et al. (2015). Both strains contained glucose, ribose and xylose as whole-cell sugars. Major menaquinones, fatty acid profiles and polar lipid patterns were also similar between *P. xinjiangensis* CCTCC AA 2013002T and *S. proteolyticum* IBRC-M 10908T, as shown in Table 1, Table 2 and Fig. S1. Results of carbon source utilization (Biolog GEN III Microplates), acid production (API 50 CH strips), enzyme activities (API ZYM strips) and other physiological tests also showed that phenotypic characteristics were mostly identical between *P. xinjiangensis* CCTCC AA 2013002T and *S. proteolyticum* IBRC-M 10908T.

Based on the combined data from the present polyphasic taxonomic study, we propose to unite the species *P. xinjiangensis* Luo et al., 2015 and *S. proteolyticum* Nikou et al., 2015. According to Rule 42 of the International Code of Nomenclature of Bacteria (Lapage et al., 1992) the name *Salininema proteolyticum* has priority and hence should be used for the unified taxon, with *Paraglycomyces xinjiangensis* as a later heterotypic synonym.

**Emeded description of the genus**

**Salininema Nikou et al., 2015**

The genus description is as given by Nikou et al. (2015) with the following amendments. Contains meso-DAP as the diagnostic diamino acid. The major menaquinones are MK-10(H4), MK-10(H2) and MK-9(H4).

**Emeded description of Salininema proteolyticum Nikou et al., 2015**

The characteristics of the species are as described by Nikou et al. (2015) with the above modifications and the following amendments. Acids can be produced from L-arabinose, D-glucose, N-acetylglucosamine, arbutin, aesculin ferric citrate, salicin, D-lactose, sucrose, starch and glycogen. Acid production from D-maltose is strain-dependent. The genomic DNA G+C content is 68.2–70.0 mol%.

**Description of Salilacibacter gen. nov.**

*Salilacibacter* (Sa.li.lac.ibacter. L. n. *sal* salt; L. gen. n. *lacus* a lake; N.L. masc. n. *bacter* a staff or rod; N.L. masc. n. *Salilacibacter* a rod isolated from a salt lake).
Aerobic, Gram-stain-positive and halophilic actinomycetes. Substrate mycelium is branched and non-fragmenting. Filamentous and slightly twisted aerial mycelia and square-ended conidia are produced on some media. Contain meso-DAP as the diagnostic diamino acid. The whole-cell sugars are glucose, ribose and xylose. The phospholipid profile contains phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, phosphatidyl-inositol mannnoside, two unidentified phosphoglycolipids and one unidentified phospholipid. The predominant menaquinone is MK-10(H4) and one unidentified phospholipid. The predominant lino- side mannoside, two unidentified phosphoglycolipids contains phosphatidylethanolamine, phosphatidylglycerol, DAP as the diagnostic diamino acid. The whole-cell sugars are glucose, ribose and xylose. Acetic acid, acetoacetic acid, glycogen. Aerator, T. A. (1999). Evaluation of a microplate DNA–DNA hybridization method compared with the initial renaturation method. Can J Microbiol 44, 1148–1153. Guan, T. W., Tang, S. K., Wu, J. Y., Zhi, X. Y., Xu, L. H., Zhang, L. L. & Li, W. J. (2009). Phylogenetic analysis of the type strain is 63.0 mol%.

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References


Description of Salilacibacter albus sp. nov.

Salilacibacter albus (al’bus. L. masc. adj. albus white, referring to the white aerial mycelium).

General morphological and chemotaxonomic characteristics are as given in the genus description. Raised and plicated growth is observed on all media tested except PDA. Substrate mycelium ranges from light olive grey to moderate yellowish green depending on the media and white aerial mycelia are produced on some media. No diffusible pigments are produced. Growth occurs at 15–42 °C (optimum 28–37 °C), at pH 5.5–9.5 (optimum 7.0–7.5) and in the presence of 0–8 % (w/v) NaCl (optimum 3–5 %). Positive for hydrolysis of starch, casein, cellulose, Tween 20, Tween 40 and Tween 80. Catalase, milk coagulation and peptonization, gelatin liquefaction and nitrate reduction are positive. Oxidase activity, urease and H2S production are negative. Acid phosphatase, esterase (C4), esterase lipase (C8), α-glucosi- dase, β-glucosidase, leucine arylamidase, naphthol-AS-BI phosphohydrolase, valine arylamidase and trypsin are positive. Alkaline phosphatase, N-acetyl-β-glucosaminidase, α-chymotrypsin, cystine arylamidase, α-fucosidase, α-galac- tosidase, β-galactosidase, lipase (C14) and α-mannosidase are negative. Acetic acid, acetoacetic acid, N-acetyl-D-glucosamine, N-acetyl-β-D-mannosamine, D-cellobiose, L-fucose, D-fucose, D-fructose, galacturonic acid, gentiobiose, α-D-glucos- cose, D-glucose 6-phosphate, glucuronamide, D-glucuronic acid, α-ketobutyric acid, D-maltose, D-mannitol, D-mannose, salicin, D-sorbitol, sucrose and turanose can be utilized as carbon sources; and glycerol and l-malic acid can be weakly utilized; but citric acid, dextrin, formic acid, D-galactose, inosine, myo-inositol, α-D-lactose, D-melibiose, propionic acid, D-raf- finose, L-rhamnose and stachyose cannot be utilized. Acids are produced from D- cellobiose, aesculin ferric citrate, D-fructose, D-glucose, D-maltose, starch, sucrose and glycogen.

The type strain, J11Y309T (=DSM 48765T=CGMCC 47242T=LMG 29297T), was isolated from a soil sample collected in Jiuliancheng Nur, a dried salt lake, located in Hebei Province, China. The genomic DNA G+C content of the type strain is 63.0 mol%.


