Longispora urticae sp. nov., isolated from rhizosphere soil of Urtica urens L., and emended descriptions of the species Longispora albida and Longispora fulva

Chenyu Piao,‡ Liying Jin,‡ Junwei Zhao,‡ Chongxi Liu,‡ Yue Zhao,‡ Xiangjing Wang‡,* and Wensheng Xiang‡,2,*

Abstract

Two Gram-stain-positive, aerobic actinomycete strains, designated NEAU-PCY-3ª and NEAU-PCY-4, were isolated from rhizosphere soil of Urtica urens L. collected from Anshan, Liaoning Province, northeast PR China. The 16S rRNA gene sequence analysis showed that the two strains exhibited 99.9% 16S rRNA gene sequence similarity with each other and that they were most closely to Longispora fulva DSM 45356ª (98.7, 98.9%) and Longispora albida DSM 11711ª (97.1, 97.2%). Phylogenetic analysis based on the 16S rRNA gene sequences indicated that the two strains were located in the same lineage and formed a cluster with the genus Longispora. Both strains were observed to contain MK-10(H4) and MK-10(H6) as the predominant menaquinoles. The cell wall peptidoglycan was found to contain meso-diaminopimelic acid, d-glutamic acid, glycine and L-alanine. Whole-cell hydrolysates mainly contained galactose, ribose and xylose. The phospholipid profile contained diphostatidylglycerol, phosphatidyethanolamine, phosphatidylinositol, several glycolipids and several unknown lipids. The major cellular fatty acids for strain NEAU-PCY-3ª were iso-C16:0, iso-C17:0, anteiso-C17:0 and C18:1ω5c. The DNA–DNA hybridization value between strains NEAU-PCY-3ª and NEAU-PCY-4 was 83.6±0.4%, and the values between the two strains and their closest phylogenetic relatives, belonging to the genus Longispora, were well below 70%, supporting that they represented a distinct genomic species. An array of phenotypic characteristics also differentiated the strains from their closely related species, the only two validly published Longispora species. On the basis of the genetic, chemotaxonomic and phenotypic properties, strains NEAU-PCY-3ª and NEAU-PCY-4 were classified as representatives of a novel species of the genus Longispora, for which the name Longispora urticae sp. nov. is proposed. The type strain is NEAU-PCY-3ª (=DSM 105119ª=CCTCC AA 2017017ª).

The genus Longispora, within the family Micromonosporaceae, was first proposed by Matsumoto et al. [1]. At the time of writing, two species of Longispora have been described, comprising Longispora albida K97-0003ª, which can produce a novel anti-HIV protein (actinohivin) [2, 3], and Longispora fulva KZ0017ª, with the ability of inhibiting growth of Bacillus subtilis when cultured under a high (5%) CO2 atmosphere [4, 5]. Urtica urens L. is widely distributed in various parts of the world and traditionally used as a herbal medicine for a wide variety of purposes. Under the long-term influence of the secretion of plant roots, the proportion of antibiotic product of rhizosphere microorganisms is significantly higher than that of non-rhizosphere soil microorganisms [6]. As a part of a programme to research the diversity of actinomycetes from rhizosphere soil of Urtica urens L. collected from Anshan, Liaoning Province, strains NEAU-PCY-3ª and NEAU-PCY-4 were isolated. In this study, we performed polyphasic taxonomy on these two strains and propose that they represent a novel species of the genus Longispora, which is named Longispora urticae sp. nov.

Strains NEAU-PCY-3ª and NEAU-PCY-4 were isolated from rhizosphere soil of Urtica urens L. collected from Anshan, Liaoning Province (40°27’N, 122°10’E). The soil sample (5 g) was suspended in distilled water (2 ml) followed by an ultrasonic treatment (160 W) for 3 min. After the addition of distilled water (43 ml), the soil suspension was incubated at 28°C and 250 r.p.m. on a rotary shaker for 30 min. Subsequently, a 200 μl suspension sample was spread on a plate of sodium succinate–asparagine agar medium (asparagine, 0.2 g; sodium succinate, 1 g; CaCl2

Author affiliations: †Key Laboratory of Agriculture Biological Functional Gene of Heilongjiang Provincial Education Committee, Northeast Agricultural University, 59 Mucai Street, Xiangfang District, Harbin 150030, PR China; 2State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, PR China.

*Correspondence: Xiangjing Wang, wangneau2013@163.com; Wensheng Xiang, xiangwensheng@neau.edu.cn

Keywords: Longispora urticae sp. nov.; polyphasic taxonomy; 16S rRNA gene.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains NEAU-PCY-3ª and NEAU-PCY-4 are KY788225 and KY788227, respectively.

Two supplementary tables and five supplementary figures are available with the online Supplementary Material.
-2H₂O, 0.2 g; FeSO₄·7H₂O, 1 mg; KCl, 0.3 g; KH₂PO₄, 0.9 g; K₂HPO₄·3H₂O, 0.6 g; agar, 20 g; distilled water, 1 l; pH, 7.2) supplemented with cycloheximide (50 mg l⁻¹) and nalidixic acid (20 mg l⁻¹). After 20 days of aerobic incubation at 28 °C, colonies were transferred and purified on International Streptomyces Project (ISP) 3 medium [7], incubated at 28 °C for 14–21 days and maintained as glycerol suspensions (20 %, v/v) at −80 °C. The type strains of L. fulva and L. albida were purchased from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) and the Japan Collection of Microorganisms (JCM), respectively, and cultured under the same conditions for comparative analysis.

Morphological characteristics were observed by light microscopy (Nikon ECLIPSE E200) and scanning electron microscopy (Hitachi SU8010) using cultures grown on ISP 3 medium at 28 °C for 4 weeks. Spore motility was assessed by light microscopy (Nikon ECLIPSE E200) observation of cells suspended in phosphate buffer (pH 7.0, 1 mM). Cultural characteristics were determined after 2 weeks at 28 °C using ISP 1–7, nutrient agar (NA), modified Bennett’s agar (MBA), Czapek’s agar (CA) [7–10], water–proline agar (1 % proline; tap water), sucrose–nitrate agar (sucrose, 30 g; NaNO₃, 2 g; K₂HPO₄, 1 g; KCl, 0.5 g; MgSO₄·7H₂O, 0.5 g; FeSO₄·7H₂O, 0.01 g; agar, 15 g; distilled water, 1 l; pH 7.0–7.3), glucose–nitrate agar (glucose, 30 g; NaNO₃, 2 g; K₂HPO₄, 1 g; KCl, 0.5 g; MgSO₄·7H₂O, 0.5 g; FeSO₄·7H₂O, 0.01 g; agar, 15 g; distilled water, 1 l; pH 7.0–7.3) and humic acid–vitamin (HV) agar media [11]. Colour determination was done with colour chips from the ISCC-NBS colour charts [12]. Hydrolysis of Tweens (20, 40 and 80) and production of catalase and urease were tested as described by Smibert and Krieg [13]. The utilization of sole carbon and nitrogen sources, decomposition of cellulose, hydrolysis of starch, aesculin, xylan and chitin, reduction of nitrate, peptonization of milk, liquefaction of gelatin and production of H₂S were examined as described previously [14–17]. Growth at different temperatures (5, 10, 12, 15, 20, 25, 28, 30, 33, 37 and 40 °C) was determined in glucose–yeast extract (GY) broth [18] after incubation for 14 days. The pH range for growth (pH 4–12, at intervals of 1 pH unit) was tested in GY broth using the buffer system described by Xie et al. [19], and NaCl tolerance was determined in GY broth supplemented with 1–10 % (w/v) NaCl (with an interval of 1 % w/v) at 28 °C for 14 days on a rotary shaker.

Biomass for chemotaxonomical characteristics was prepared by growing strains NEAU-PCY-3³ and NEAU-PCY-4 in GY broth in shake flasks at 28 °C for 7 days. The isomers of diaminopimelic acid in the cell wall were derivatized according to McKerrow et al. [20] and analysed by an HPLC method using an Agilent TC-C18 column (250 × 4.6 mm, internal diameter 5 μm). The whole-cell sugars were analysed according to the procedures developed by Lechevalier and Lechevalier [21]. Phospholipids were examined by two-dimensional TLC and identified using the method of Minnikin et al. [22]. Menaquinones were extracted from freeze-dried biomass and purified according to Collins [23] and analysed by an HPLC-UV method as described previously [24]. To determine cellular fatty acid compositions, strains NEAU-PCY-3³ and NEAU-PCY-4 were cultivated in GY broth for 7 days in shake flasks at 28 °C. A similar fatty acid profile was determined for L. fulva DSM 45356T and L. albida JCM 11711T in this study. Fatty acid methyl esters were extracted from the biomass as described by Gao et al. [25] and analysed by GC-MS using the method of Xiang et al. [26]. Acid-fastness was checked by the Ziehl–Neelsen staining method as described previously [4].

Extraction of chromosomal DNA and PCR amplification of the 16S rRNA gene sequence were carried out using a standard procedure [27, 28]. The PCR product was purified and cloned into the vector pMD19-T (TaKaRa) and sequenced using an Applied Biosystems DNA sequencer (model 3730XL). The almost full-length 16S rRNA gene sequences of strains NEAU-PCY-3³ and NEAU-PCY-4 were aligned with multiple sequences obtained from the GenBank/EMBL/DDBJ databases using CLUSTAL X 1.83 software. Phylogenetic trees were generated with the neighbour-joining [29], maximum-likelihood [30] and maximum-parsimony [31] algorithms using molecular evolutionary genetics analysis (MEGA) software version 6.06 [32]. The stability of the topology of the phylogenetic tree was assessed using the bootstrap method with 1000 replicates [33]. A distance matrix was generated using Kimura’s two-parameter model [34]. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). Pairwise alignment analysis of 16S rRNA gene sequence similarities between strains was conducted on the EzBioCloud [35].

The G+C contents of strains NEAU-PCY-3³ and NEAU-PCY-4 were determined by using the thermal denaturation (Tm) method [36] with Escherichia coli JM109 DNA as the control. DNA–DNA hybridization was carried out between the two isolates and related type strains belonging to the genus Longispora according to De Ley et al. [37], using a Cary model 100 Bio UV-VIS spectrophotometer equipped with a Peltier-thermostatted 6×6 multiecell changer and a temperature controller with in situ temperature probe (Varian) under modified conditions as described by Huss et al. [38]. The DNA samples used for hybridization were diluted to 1.0 using 0.1×SSC (saline sodium citrate buffer) with OD₂₆₀ around 1.0, then sheared using a JY92-II ultrasonic cell disruptor (ultrasonic time 3 s, interval time 4 s, 90 times). The DNA renaturation rates were determined in triplicate in 2×SSC at 70 °C with three replications and the DNA–DNA relatedness value was expressed as a mean value.

Spore chains were straight, and branched from the substrate mycelia of strains NEAU-PCY-3³ and NEAU-PCY-4 on ISP 3 media, but no aerial mycelia were detected. Spores were cylindrical (0.50–0.60×0.8–1.2 μm) and non-motile with rough surfaces (Fig. 1). Both strains showed good growth on ISP 1, ISP 2, ISP 3, ISP 5, ISP 6, sucrose–nitrate, glucose–nitrate, water–proline, NA and MBA media, moderate growth on ISP 4, ISP 7 and CA media and poor
HV medium. The colour of the colonies was yellow, which were also detected in CA media, light yellow green on ISP 2 medium and light greenish yellow on MBA medium. The colours of colonies of the two isolates were nearly the same, and are summarized in Table S1 (available in the online Supplementary Material). No diffusible pigments were observed on any of the media tested. The two strains were observed to grow well between 10 and 37 °C, with an optimum temperature at 28 °C. The pH range for growth of the two strains was pH 6.0–9.0, with an optimum pH at 7.0, and growth of both strains was observed in the presence of 0–1.0 % NaCl (w/v). Detailed physiological characteristics are presented in the species description.

The two organisms contained meso-diaminopimelic acid, d-glutamic acid, glycine and L-alanine as the cell-wall diamino acids. Whole-cell sugars included galactose, rhamnose and xylose, which were also detected in L. fulva, but rhamnose was not observed as a major constituent in L. albida [4]. The phospholipid profiles of both strains were found to consist of diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), phosphatidylinositol (PI), three unknown glycolipids (GLs) and three unknown lipids (Ls), which were also found in L. fulva in our study, while in L. albida only one unknown glycolipid was found; other polar lipids were the same with the above two strains (Fig. S2). The menaquinones of strains NEAU-PCY-3T/NEAU-PCY-4 were identified as MK-10(H4) (75.1/73.9 %) and MK-10(H6) (24.9/26.1 %), which were also the predominant components of L. fulva and L. albida; however, MK-10(H8), a minor component found in L. fulva and L. albida, was not found in our study. The major cellular fatty acids (>10 %) for strain NEAU-PCY-3T were iso-C16:0 (30.1 %), C18:1ω7c (14.1 %), anteiso-C17:0 (12.8 %) and iso-C17:0 (11.5 %). Strain NEAU-PCY-3T could be differentiated from L. fulva by the absence of C14:0, C17:0, C16:1ω7c, 10-methyl C17:0 and C17:0 cyclo, and the presence of C18:1ω5c and C19:ω9c. The absence of C19:0, C17:1ω9c and iso-C18:0, and the presence of C15:0, C18:0, C18:1ω7c, C19:1ω9c and C19:0 cyclo could distinguish strain NEAU-PCY-3T from L. albida (Table S2).

Comparative 16S rRNA gene sequence analysis by using the EzBioCloud server showed that the two strains were phylogenetically related to members of the genus Longispora. Strains NEAU-PCY-3T and NEAU-PCY-4 shared 99.9 % similarity, and showed the highest similarities to L. fulva DSM 45356T (98.7, 98.9 %) and L. albida JCM 11711T (97.1, 97.2 %). 16S rRNA gene sequence similarities between strains NEAU-PCY-3T/NEAU-PCY-4 and related species other than the two validly Longispora species were lower than 98 %. Phylogenetic analysis based on the 16S rRNA gene sequences indicated that the two strains formed a stable cluster with L. fulva DSM 45356T and L. albida JCM 11711T (Fig. 2), which was also supported by the maximum-likelihood and maximum-parsimony algorithm (Figs S3 and S4). The DNA G+C contents of the DNA of strains NEAU-PCY-3T and NEAU-PCY-4 were 70.3±0.4 and 70.3±0.2 mol %, respectively. The DNA–DNA relatedness between strains NEAU-PCY-3T and NEAU-PCY-4 was 83.6±0.4 %, and they showed DNA–DNA relatedness of 54.6±0.5/46.9±0.7 % with L. fulva DSM 45356T and 48.9±0.7/36.5±0.6 % with L. albida JCM 11711T. The DNA–DNA relatedness values between the isolates and the two valid type species are below the threshold value of 70 % recommended by Wayne et al. [39] for assigning strains to the same species.

The data from morphology, physiology and biochemistry examinations showed that strains NEAU-PCY-3T and NEAU-PCY-4 had typical characteristics of the genus Longispora, such as: Gram-positive; straight spore chains; non-motile spores with rough surfaces (Figs 1 and S5); MK-10 (H4) and MK-10(H6) as predominant menaquinones; iso-C16:0 as the largest fatty acid component; diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, unknown glycolipids and unknown polar lipids as polar lipid profile. Moreover, phylogenetic analysis based on 16S rRNA gene sequences indicated that the two isolates fell within the clade of the genus Longispora (Figs 2, S3 and S4). These results indicated that strains NEAU-PCY-3T and NEAU-PCY-4 should be affiliated to the genus Longispora. Comparison of phenotypic characteristics between strains NEAU-PCY-3T/NEAU-PCY-4 and the closely related type strains, L. fulva DSM 45356T and L. albida JCM 11711T, was performed to differentiate between the strains (Table 1 and Fig. S1). Differential cultural characteristics included: the colony colour on MBA (Fig. S1), ISP 1, ISP 6, water–proline and glucose–nitrate media; NaCl tolerance; hydrolysis of aesculin, starch and Tween 80; peptonization of milk; production of H2S; liquefaction of gelatin; reduction of nitrate; and patterns of carbon and nitrogen utilization (Table 1).
The phenotypic, chemotaxonomic and genotypic data were sufficient to differentiate novel strains NEAU-PCY-3$^\dagger$ and NEAU-PCY-4 from recognized species of the genus *Longispora*. The high similarities of 16S rRNA gene sequences, the phenotypic properties and the >80% DNA–DNA relatedness value between the two strains indicated that they should belong to one species of the genus *Longispora*, for which the name *Longispora urticae* sp. nov. is proposed.

**DESCRIPTION OF LONGISpora URTICAE SP. NOV.**

*Longispora urticae* (ur’ti.cae. L. gen. n. urticae of the stinging nettle, of the genus *Urtica*, the type strain was isolated from the rhizosphere soil of *Urtica urens* L.).

Aerobic, Gram-stain-positive, non-acid-fast actinomycete that forms abundant substrate mycelia on ISP 3 medium, but no aerial mycelia are detected. Spores are cylindrical and non-motile with rough surfaces. Good growth on ISP 1, ISP 2, ISP 3, ISP 6, sucrose–nitrate, glucose–nitrate, water–proline, NA and MBA media, moderate growth on ISP 4, ISP 7 and CA media and poor growth on HV medium. No diffusible pigments are observed on these media. Tolerates 1% NaCl and grows at temperatures of between 10 and 37°C, with an optimum temperature of 28°C. Growth occurs at pH values between 6 and 9, the optimum being pH 7–8. Positive for hydrolysis of aesculin and urea, liquefaction of gelatin, production of catalase and H$_2$S, and degradation of Tween.

---

Fig. 2. Neighbour-joining tree showing the phylogenetic position of strains NEAU-PCY-3$^\dagger$, NEAU-PCY-4 and related species based on 16S rRNA (1508 nt) gene sequences. Asterisks indicate branches that were also recovered using the maximum-likelihood method. Bootstrap values >50% (based on 1000 replications) are shown at branch points. Bar, 0.01 substitution per nucleotide position.
Table 1. Differential phenotypic characteristics of strains NEAU-PCY-3\textsuperscript{T}/NEAU-PCY-4 and their closely related species in the genus *Longispora*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain 1</th>
<th>Strain 2</th>
<th>Strain 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colony colour</td>
<td>Yellowish white</td>
<td>Greyish olive</td>
<td>Pinkish white</td>
</tr>
<tr>
<td>ISP 1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ISP 6</td>
<td>Yellowish white</td>
<td>Olive grey</td>
<td>White</td>
</tr>
<tr>
<td>MBA</td>
<td>Brilliant greenish yellow</td>
<td>Dark yellowish brown</td>
<td>Yellowish white</td>
</tr>
<tr>
<td>HV</td>
<td>White</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Water-proline</td>
<td>Yellowish white</td>
<td>Pale yellow</td>
<td>White</td>
</tr>
<tr>
<td>Glucose-nitrate</td>
<td>White</td>
<td>Yellowish grey</td>
<td>Pale yellow</td>
</tr>
<tr>
<td>Soluble pigment on ISP 6</td>
<td>None</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Hydrolysis of</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aesculin</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Starch</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Tween 80</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Liquefaction of gelatin</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Peptonization of milk</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Production of H\textsubscript{2}S</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Reduction of nitrate</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Use as sole nitrogen source:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Creatine</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>
| D-
|Glutamine                      | +        | –        | –        |
| L-
|Proline                        | +        | –        | +        |
| L-
|Serine                         | –        | +        | +        |
| L-
|Threonine                      | –        | –        | +        |
| Use as sole carbon source:     |          |          |          |
| Sucrose                        | +        | –        | –        |
| D-
|Galactose                      | –        | +        | +        |
| Inositol                       | +        | –        | –        |
| L-
|Asparagine                     | –        | +        | +        |
| Growth in/at                   |          |          |          |
| NaCl concentration (\%, w/v)   | 1        | 1.2\‡    | <2\§    |
| Temperature (\°C)              | 10–37    | 10–33\‡  | 12–37\§ |
| Range of pH                    | 6–9      | 6–8.5\‡  | 6–9\§   |
| Phospholipids\*                | DPG, PE, PI, GLs, Ls | DPG, PE, PI, GLs, Ls | DPG, PE, PI, GL, Ls |
| Major whole-cell sugars†       | Gal, Rha, Xyl | Gal, Rha, Xyl\‡ | Gal, Xyl\‡ |

\*DPG, Diphosphatidylglycerol; PE, phosphatidylethanolamine; PI, phosphatidylinositol; GL, glycolipid; L, unknown lipid.
†Gal, Galactose; Rha, rhamnose; Xyl, xylose.
‡Data from Shiratori-Takano et al. [4].
§Data from Matsumoto et al. [1].

40. Negative for hydrolysis of cellulose, xylan, chitin and starch, degradation of Tween 20 and 80, reduction of nitrate and peptonization of milk. D-Glucose, inositol, maltose, D-mannose, D-raffinose and sucrose are utilized as sole carbon sources, but not L-arabinose, D-fructose, D-galactose, lactose, D-mannitol, L-rhamnose, D-ribose, D-sorbitol or D-xylene. L-Alanine, L-arginine, L-asparagine, L-aspartic acid, creatine, L-glutamic acid, L-glutamine, glycine, L-proline, L-threonine and L-tyrosine are utilized as sole nitrogen sources but not L-serine. The diagnostic diamino acids of the peptidoglycan are meso-diaminopimelic acid, D-glutamic acid, glycine and L-alanine. Whole-cell sugars comprise galactose, rhamnose and xylose. The major menaquinones are MK-10(H\textsubscript{4}) and MK-10(H\textsubscript{6}). The phospholipid profile consists of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, several glycolipids and several unknown lipids. The major fatty acids (>10\%) are iso-C\textsubscript{16:0}, iso-C\textsubscript{17:0}, anteiso-C\textsubscript{17:0} and C\textsubscript{18:1}ω5c.

The type strain is NEAU-PCY-3\textsuperscript{T} (=DSM 105119\textsuperscript{T}=CCTCC AA 2017017\textsuperscript{T}), isolated from rhizosphere soil of *Urtica urens* L. collected from Anshan, Liaoning Province (PR China). The G+C content of the DNA of the type strain is 70.3 mol\%. 
EMENDED DESCRIPTION OF THE SPECIES
LONGISPOR A L B I D A M ATSUMOTO ET AL. 2003

The species is as described by Matsumoto et al. [1], with the following emendation. Spores are non-motile and cylindrical with rough surfaces (Fig. S5). The phospholipid profile consists of diposphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, an unknown glycolipid and several unknown lipids, while hydroxyphosphatidylethanolamine is absent.

EMENDED DESCRIPTION OF THE SPECIES
LONGISPOR A F U L V A SHIRATORI-TAKANO ET AL. 2011

The species is as described by Shiratori-Takano et al. [4], with the following emendations. Spores are non-motile and cylindrical with rough surfaces (Fig. S5). The phospholipid profile consists of diposphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, several unknown glycolipids and several unknown lipids, while hydroxyphosphatidylethanolamine is absent.

Funding information
This work was supported in part by grants from the National Natural Science Foundation of China (No. 31572070), Chang Jiang Scholar Candidates Program for Provincial Universities in Heilongjiang (CSCP).

Conflicts of interest
The authors declare that there are no conflicts of interest.

Acknowledgements
We are grateful to Professor Aharon Oren for helpful advice on the specific epithet.

References


Five reasons to publish your next article with a Microbiology Society journal

1. The Microbiology Society is a not-for-profit organization.
2. We offer fast and rigorous peer review – average time to first decision is 4–6 weeks.
3. Our journals have a global readership with subscriptions held in research institutions around the world.
4. 80% of our authors rate our submission process as ‘excellent’ or ‘very good’.
5. Your article will be published on an interactive journal platform with advanced metrics.

Find out more and submit your article at microbiologyresearch.org.