Description of *Lysinibacillus sinduriensis* sp. nov., and transfer of *Bacillus massiliensis* and *Bacillus odysseyi* to the genus *Lysinibacillus* as *Lysinibacillus massiliensis* comb. nov. and *Lysinibacillus odysseyi* comb. nov. with emended description of the genus *Lysinibacillus*

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A Gram-positive, rod-shaped, endospore-forming bacterium, designated strain BLB-1T, was isolated from samples of tidal flat sediment from the Yellow Sea. 16S rRNA gene sequence analysis demonstrated that the isolate belonged to the *Bacillus* rRNA group 2 and was closely related to *Bacillus massiliensis* CIP 108446T (97.4 %), *Bacillus odysseyi* ATCC PTA-4993T (96.7 %), *Lysinibacillus fusiformis* DSM 2898T (96.2 %) and *Lysinibacillus boronitolerans* DSM 17140T (95.9 %). Sequence similarities with related species in other genera, including *Caryophanon*, *Sporosarcina* and *Solibacillus*, were <96.1 %. Chemotaxonomic data supported the affiliation of strain BLB-1T with the genus *Lysinibacillus*. The major menaquinone was MK-7, the cell-wall sugars were glucose and xylose, the cell-wall peptidoglycan type was A4\(\text{a}\) (L-Lys–D-Asp), the major polar lipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine and several unknown phospholipids, and the major fatty acids were anteiso-C\(15:0\) (35.6 %), iso-C\(15:0\) (25.6 %) and anteiso-C\(17:0\) (16.5 %). The most closely related species, *Bacillus massiliensis* and *Bacillus odysseyi*, were also assigned to this genus based on phylogenetic analysis and phenotypic data. The results of DNA–DNA hybridizations and phenotypic tests supported the differentiation of all three taxa from species of the genus *Lysinibacillus* with validly published names. Thus, strain BLB-1T (≡KCTC 13296T =JCM 15800T) represents a novel species, for which the name *Lysinibacillus sinduriensis* sp. nov. is proposed. It is also proposed that *Bacillus massiliensis* CIP 108446T (≡4400831T) would be transferred to the genus *Lysinibacillus* as *Lysinibacillus massiliensis* comb. nov.

**Abbreviations:** AL, aminolipid; APL, aminophospholipid; DPG, diphosphatidylglycerol; GBG, gentiobiosydiaacylglycerol; GL, glycolipid; L1, unknown lipid; NPG, ninhydrin-positive phosphoglycolipid; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PL, phospholipid; PS, phosphatidylserine.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *Lysinibacillus sinduriensis* BLB-1T is FJ169465.

A supplementary figure is available with the online version of this paper.
Species of the genus *Bacillus* have been isolated from diverse habitats (Nakamura et al., 2002; La Duc et al., 2004; Heyrman et al., 2005; Glazunova et al., 2006). Based on genotypic analysis and chemotaxonomic data, several spore-forming species in the *Bacillus* rRNA group 2 (Ash et al., 1991) were reclassified into the following novel taxa: *Sporosarcina globispora*, *Sporosarcina psychrophila* and *Sporosarcina pasteurii* (Yoon et al., 2001); *Lysinibacillus fusiformis* and *Lysinibacillus sphaericus* (Ahmed et al., 2007); *Viridibacillus arvi*, *Viridibacillus arenosi* and *Viridibacillus neidei* (Albert et al., 2007); *Solibacillus silvestris* (Krishnamurthi et al., 2009); *Rummeliibacillus pycnus* (Vaishampayan et al., 2009); and *Psychrobacillus insolitus*, *Psychrobacillus psychrotolerans* and *Psychrobacillus psychrodurans* (Krishnamurthi et al., 2010). Several investigators have suggested that some species placed within the *Bacillus* rRNA group 2 do not belong to the genus *Bacillus* and that they should be reclassified as novel genera or transferred to existing genera within the group (Farrow et al., 1994; Yoon et al., 2001; Ahmed et al., 2007; Albert et al., 2007; Krishnamurthi et al., 2009). Based on polyphasic taxonomic data, a new genus, *Lysinibacillus*, was recently proposed for the reclassification of two species assigned to the genus *Bacillus* and a newly described species (Ahmed et al., 2007). At the time of publication, the genus *Lysinibacillus* contained six species with validly published names: *Lysinibacillus boronitolerans*, *Lysinibacillus fusiformis*, *Lysinibacillus sphaericus* (Ahmed et al., 2007), *Lysinibacillus parviboronicapiens* (Miwa et al., 2009), *Lysinibacillus xylanilyticus* (Lee et al., 2010) and *Lysinibacillus macroides* (Coorevits et al., 2012). The taxonomic positions of *Bacillus massiliensis* and *Bacillus odysseyi* indicate that these species are phylogenetically distantly related to *Rummeliibacillus pycnus* or *Solibacillus silvestris*. This issue has been discussed previously (Ahmed et al., 2007; Krishnamurthi et al., 2009) but no proposal has yet been made for transferring these species into new or existing genera. In the present study, we used a polyphasic taxonomic approach to re-evaluate the taxonomic position of *B. massiliensis* and *B. odysseyi*, as well as characterize a strain isolated from tidal flat sediments during this study, identifying it as a novel species.

A novel strain, designated BLB-1T, was isolated from 50 g samples of tidal flat sediment collected at a depth of 20 cm from the Shinduri sand dunes (35° 50’ 09.22” N 126° 12’ 11.90” E) at Tae-An on the Yellow Sea coast, Republic of Korea. Samples were individually placed into 50 ml sterile tubes (Corning) and pooled into an anaerobic pouch (GasPak, Becton Dickinson) in an icebox, before transporting them to the laboratory for immediate processing. Each sample was serially diluted in saline solution (0.85 %, w/v, NaCl), spread onto tryptic soy broth medium (TSB; pH 7.3; Difco) solidified with 15.0 g l$^{-1}$ agar (TSBA) and incubated at 30 °C for 48 h. The strain was subcultured several times to obtain a purified culture, before further characterization. Reference strains used in this study included *B. massiliensis* KCTC 13178$^T$, *B. odysseyi* KCTC 3961$^T$, *L. boronitolerans* KCTC 13709$^T$, *L. fusiformis* KCTC 3454$^T$ and *L. sphaericus* KCTC 3346$^T$. Strains were cultured routinely on TSBA medium under the same conditions before storage at −80 °C as skimmed milk (Difco) suspensions (10 %, w/v).

To determine the differential phenotypic properties of the novel isolate, strain BLB-1T and several reference strains were subjected to morphological, physiological and biochemical analyses (Chang et al., 2002, 2008). All tests were performed using fresh cultures of purified strains grown under the same conditions. Cell morphology was examined by bright-field microscopy (Nikon Optiphot-2), phase-contrast microscopy (Nikon 80i) and electron microscopy (S4300N, Hitachi). For the electron microscopic analysis, cells were fixed in a 2.5 % (v/v) paraformaldehyde/glutaraldehyde mixture, sputter-coated with gold (SC502, Polaron) and observed using a scanning electron microscope (S4300N, Hitachi). Cells were negatively stained with 1 % (w/v) uranyl acetate and the flagella type was observed using a model CM-20 transmission electron microscope (Philips) (Chang et al., 2002). Growth at 10–60 °C and 0–7 % (w/v) NaCl (0.5 % increments) was determined over a period of 3–7 days in TSB medium. Growth was assessed by monitoring OD$\text{600}$ using a spectrophotometer (Bio-Rad). The pH range for growth was determined in buffered TSB medium at 30 °C using a 500 ml flask (Corning) containing 250 ml medium at pH 4–9 (increments of 0.5 pH units). The medium was buffered using one of three different solutions: 50 mM succinic acid/NaOH (pH 4–6), 100 mM NaH$_2$PO$_4$/Na$_2$HPO$_4$ (pH 6–8) or 50 mM 2-amino-2-methyl-1,3-propanediol/HCl (pH 8–9). Motility was tested in TSB medium containing 0.4 % agar. Gram reaction, enzyme activity, carbohydrate utilization and hydrolysis reactions were conducted using standard methods (Smibert & Krieg, 1994; Chang et al., 2002). The catalase and oxidase activity, indole production, nitrate reduction, KOH test and endospore staining were conducted as previously described (Smibert & Krieg, 1994). Hydrolysis of casein and starch were tested on skimmed milk agar and starch agar, respectively. Gelatin liquefaction was determined by inoculation on 12 % gelatin followed by incubation for 7 days. Arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and urease, utilization...
of citrate and amino acids activities, the Voges–Proskauer test and utilization of various carbohydrates were determined as previously described (Smibert & Krieg, 1994; Chang et al., 2002). A variety of tests to determine biochemical characteristics were also performed using API 20 E, API ZYM, and API 50 CH B/E strips (bioMérieux), and the Biolog GP2 MicroPlate system (Biolog).

Strain BLB-1T was catalase-positive and oxidase-negative. Catalase activity was also present in B. massiliensis and B. odysseyi, whereas oxidase activity was not detected in strain B. odysseyi (La Duc et al., 2004; Glazunova et al., 2006). At the time of publication, L. parviboronicapiens was the only oxidase-negative species out of all the species in the genus Lysinibacillus (Miwa et al., 2009). No sugars were fermented in the API 50 CH strips with strain BLB-1T or B. odysseyi, which matched the results of tests performed with B. massiliensis (Glazunova et al., 2006). Strain BLB-1T and B. massiliensis cells produced spherical endospores whereas B. odysseyi produced round endospores in the terminal position. Detailed phenotypic characteristics of strain BLB-1T are presented in Table 1 and the species description.

A nearly complete 16S rRNA gene sequence (1413 bp) for strain BLB-1T was obtained using the method of Chang et al. (2008). Preliminary sequence comparison was conducted against 16S rRNA gene sequences of species with validly published names retrieved from the EzTaxon and GenBank databases of prokaryotic type strains. The nearly complete 16S rRNA gene sequences of the strains were aligned manually against those of closely related representatives from other genera based on the bacterial 16S rRNA secondary structure model (Woese et al., 1980). The regions available for all sequences (conserved and variable regions) showed unambiguous alignment and they were used to reconstruct phylogenetic trees. Sequences were aligned and neighbour-joining (Saitou & Nei, 1987) analysis was performed using the PHYLIP (Felsenstein, 1993) and jPHYDIT (Jeon et al., 2005) programs. Phylogenetic trees were also reconstructed using the maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods. An evolutionary distance matrix for the neighbour-joining tree was generated according to the model of Jukes & Cantor (1969). The reliability of each tree was evaluated by bootstrap analysis (Felsenstein, 1985) based on 1000 resamplings.

### Table 1. Differential characteristics of the strain BLB-1T and closely related species

<table>
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<tr>
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<td>6.0–10.0</td>
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<td>–</td>
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<tr>
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<tr>
<td>Dextrin</td>
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<td>+</td>
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</table>
Phylogenetic analysis demonstrated that the isolate belonged to the Bacillus rRNA group 2, members of which are closely related to B. massiliensis CIP 108446\(^T\) and B. odysseyi NBRC 100172\(^T\). However, strain BLB-1\(^T\) could be clearly distinguished from all species with validly published names in the genus Bacillus. Strain BLB-1\(^T\), B. massiliensis and B. odysseyi were closely related and were grouped in a single clade in the neighbour-joining tree containing type strains of species belonging to this group (Fig. 1). Furthermore, all three taxa and species of the genus Lysinibacillus were separated into a different clade from members of the genera Solibacillus, Rummeliibacillus and Viridibacillus. The distinct branch formed by the radiation of this group did not depend on the tree-making algorithm used and was supported by a 96 % bootstrap value (Fig. S1, available in IJSEM Online). The phylogenetic analysis strongly indicated that the three taxa represent novel species belonging to the genus Lysinibacillus.

The closest phylogenetic relatives to strain BLB-1\(^T\) were B. massiliensis CIP 108446\(^T\) (97.4 % 16S rRNA gene sequence similarity) followed by B. odysseyi NBRC 100172\(^T\) (96.7 %), L. fusiformis DSM 2898\(^T\) (96.2 %), L. sphaericus DSM 28\(^T\) (96.1 %) and L. boronitolerans DSM 17140\(^T\) (95.9 %). The recently described species L. parviboronicapicans (95.7 %), L. xylanilyticus (97.2 %; Lee et al., 2010) and L. macroides (96.2 %; Coorevits et al., 2012) appeared to be distant phylogenetic relatives of strain BLB-1\(^T\). Sequence similarity values between strain BLB-1\(^T\) and other species in the genera Solibacillus, Sporosarcina, Solibacillus, Rummeliibacillus and Viridibacillus were <96.1 %. Therefore, additional DNA–DNA hybridization was performed to more accurately differentiate these closely related species (Tindall et al., 2010).

DNA–DNA hybridization was performed as previously described (Ezaki et al., 1989) using photobiotin-labelled probes at 45 °C with a Fluoroskan Ascent Fluorescent plate reader (Thermo Life Sciences). Three replicates of each sample were tested. The DNA–DNA hybridization values between strain BLB-1\(^T\) and B. massiliensis KCTC 13178\(^T\), L. sphaericus KCTC 3346\(^T\), B. odysseyi KCTC 3961\(^T\), L. fusiformis KCTC 3454\(^T\) and L. boronitolerans KCTC 13709\(^T\) were 24.9, 24.1, 21.0, 20.5 and 18.3 %, respectively. These values are much lower than the suggested threshold value for species delineation (Wayne et al., 1987) and indicate that the isolate represents a novel species that is distinct from closely related species.

To determine the DNA G+C content, DNA was analysed by real-time PCR (Thermocycler, Bio-Rad) with SYBR Green I, according to a previously described fluorometric method (Gonzalez & Saiz-Jimenez, 2002). The relative values were calculated based on E. coli KCTC 2441\(^T\) DNA (50.8 mol%, \(T_m\)) as a standard. The mean DNA G+C contents of strains BLB-1\(^T\), B. massiliensis KCTC 13178\(^T\) and B. odysseyi KCTC 3961\(^T\) were 35.9, 36.3 and 35.6 mol%, respectively. These data corresponded more closely with the typical ranges of members of the genera Lysinibacillus (35–38 mol%; Ahmed et al., 2007), Kurthia (36–38 mol%; Keddie & Jones, 1992), Viridibacillus (35–40.4 mol%; Albert

![Fig. 1. Phylogenetic tree inferred by neighbour-joining method based on 16S rRNA gene sequences (1413 bp). The tree shows the relationship between strain BLB-1\(^T\) and closely related taxa. Bootstrap values >50% (based on 1000 replications) are shown at branch points. Filled circles indicate the corresponding nodes were also recovered in the tree generated with the maximum-parsimony algorithm. Bar, 0.01 substitutions per nucleotide position.](https://example.com/fig1.png)
et al., 2007) and Bacillus (32–69 mol%; Heyrman et al., 2005) rather than the genera Sporosarcina (40–42 mol%; Yoon et al., 2001) or Caryophanon (44–46 mol%; Claus et al., 1992).

The cellular fatty acid profiles of strain BLB-1T and closely related strains grown on TSBA medium at 28 °C for 48 h were determined according to the Sherlock Microbial Identification System (MIDI). The fatty acids were separated using an automated GC system (model 6890N and 7683 Autosampler; Agilent) and identified with the associated software package version 4.0 (Library TSBA 40, MIDI). The fatty acid profile of strain BLB-1T (Table 2) was characterized by high proportions of saturated branched fatty acids, such as anteiso-C15:0 (35.6 %), iso-C15:0 (25.6 %) and anteiso-C17:0 (16.5 %). Significant differences in the relative amounts of iso-C15:0 and anteiso-C17:0 were found between strain BLB-1T and its closest relatives and these characteristics could be used to differentiate the novel isolate from related species (Kämpfer et al., 1994; Ahmed et al., 2007). The major fatty acids detected in strain BLB-1T, iso- and anteiso-C15:0, have also been detected as major components in B. subtilis and members of the genera Lysinibacillus, Viridibacillus, Rummeliibacillus and Kurthia (Shaw & Keddie, 1983; Kämpfer et al., 2006; Ahmed et al., 2007; Albert et al., 2007). In contrast, iso-C15:0 and iso-C16:1 were detected as the major fatty acids in members of the genus Solibacillus (Krishnamurthi et al., 2009).

Respiratory quinones were determined as described previously (Komagata & Suzuki, 1987) using TLC and HPLC. Respiratory quinones were determined as described previously (Schleifer & Kandler, 1972) using TLC with cellulose plates (Merck). Glucose and xylose were the predominant cell-wall sugars in strain BLB-1T. The closest relative, B. massiliensis KCTC 13178T, produced similar results to strain BLB-1T, whereas B. odysseyi KCTC 3961T was different, with only xylose as the predominant cell-wall sugar.

Peptidoglycan structure was determined as described previously (Schleifer & Kandler, 1972; Schleifer, 1985) with modification of the TLC using cellulose plates rather than paper chromatography. Quantitative analysis of amino acids in the peptidoglycan was performed by GC according to the method of MacKenzie (1987). Strain BLB-1T contained peptidoglycan with alanine, glutamic acid, lysine and aspartic acid as diagnostic amino acids in a molar ratio of 1.3:1.0:0.9:1.0, respectively. The close relatives B. massiliensis KCTC 13178T and B. odysseyi KCTC 3961T had similar amino acid molar ratios. The peptidoglycan type A4α-L-Lys-d-Asp (A11.31; DSMZ, 2001) was very similar to that found in species of the genera Lysinibacillus, Kurthia and Viridibacillus (Shaw & Keddie, 1983; Ahmed et al., 2007; Krishnamurthi et al., 2009). By contrast, the type species of the genus Bacillus, B subtilis, is known to possess meso-diaminopimelic acid in the cell-wall peptidoglycan (Schleifer & Kandler, 1972). These data strongly indicate that B. massiliensis KCTC 13178T and B. odysseyi KCTC 3961T do not belong to the genus Bacillus and instead they should be reclassified into new or existing genera. We propose that these species be transferred to the genus Lysinibacillus.

Polar lipids were extracted from 100 mg freeze-dried cell material and separated using a two-stage method as described previously (Tindall, 1990). Polar lipid analysis was conducted by the DSMZ Identification Service and Dr Brian Tindall (DSMZ Braunschweig, Germany). TLC plates were stained with 5 % molybdophosphoric acid to detect all the lipids. The major polar lipids in strain BLB-1T and B. odysseyi KCTC 3961T were diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), and phosphatidylethanolamine (PE). Moderate amounts of phospholipid (PL2) and minor amounts of two phospholipids (PL1, PL4) and an unknown lipid (L1) were also detected. B. odysseyi KCTC 3961T also contained PL5, L3 and L4 (Fig. 2). By contrast, B. massiliensis KCTC 13178T showed a significantly different profile with major components of DPG and PG, moderate amounts of two glycolipids (GL1, 2) and minor amounts of PL1, 2, 3 and 4 and L1, but no PE was detected. Glycolipids

### Table 2. Cellular fatty acid compositions of strain BLB-1T and closely related species

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<th>Fatty acid</th>
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<td>anteiso-C17:010c</td>
<td>16.5</td>
<td>3.2</td>
<td>1.9</td>
<td>t</td>
<td>2.6</td>
<td>1.2</td>
</tr>
<tr>
<td>Summed feature 4*</td>
<td>3.4</td>
<td>–</td>
<td>1.2</td>
<td>1.2</td>
<td>1.2</td>
<td>1.8</td>
</tr>
</tbody>
</table>

*Summed features represent groups of two or three fatty acids that could not be separated by GC using the Microbial Identification System. Summed feature 4 comprises iso-C17:1 I and/or anteiso-C17:1 B.
have also been reported in members of the genera *Bacillus*, *Paenibacillus* and *Cohnella* (Kämpfer et al., 2006), where the absence of PE is used to differentiate species. The profiles of three strains were compared with *B. subtilis* (Kämpfer et al., 2006) and significant differences were observed, i.e. the presence of gentiobiosyldiacylglycerol (GBG) and amino-phospholipids (APL) in *B. subtilis*. The phylogenetic relative, *Solibacillus silvestris* (Krishnamurthi et al., 2009) differed from the three strains in terms of the presence of phosphatidylserine (PS). In addition, the presence of aminolipids (AL) was reported in the genus *Viridibacillus* (Albert et al., 2007), whereas AL and APL are also found in the genus *Rummeliibacillus* (Vaishampayan et al., 2009). The closest phylogenetic relatives, species of the genus *Lysinibacillus*, matched the lipid profiles of strains BLB-1T, *B. odysseyi* KCTC 3961T and *B. massiliensis* KCTC 13178T because they shared DPG and PG as major components (Ahmed et al., 2007). However, the ninhydrin-positive phosphoglycolipids (NPG) that are typical of members of the genus *Lysinibacillus* were not detected in the strains investigated in this study.

This investigation had to be expanded to include more detailed polar lipid profiles for the type species of the genus *Lysinibacillus*. Thus, comparative analyses of *L. boronitolerans* KCTC 13709T (=DSM 17140T), *L. fusiformis* KCTC 3454T (=DSM 2898T) and *L. sphaericus* KCTC 3346T (=DSM 28T) were performed to better understand their lipid profiles. The major profiles of these three species contained DPG, PG and PE, as well as minor amounts of PL2, PL3 and L1 (Fig. 2). *L. sphaericus* KCTC 3346T also possessed PL4. NPG was not detected in these three species, which was in agreement with the lipid profile of BLB-1T determined in the current study. No spots had the same Rf value as the major component NPG reported by Ahmed et al. (2007). *L. xylanilyticus* and *L. macroides* also lacked the previously reported NPG (Lee et al., 2010; Coorevits et al., 2012). Thus, the affiliation of these species differs from the description of the genus *Lysinibacillus* in terms of their polar lipid profiles (Ahmed et al., 2007), which suggests that the original description of the genus needs to be amended based on the current analysis. The profiles of strains BLB-1T, *B. odysseyi* KCTC 3961T and *B. massiliensis* KCTC 13178T were far more complex than those of previously reported species of the genus *Lysinibacillus* (Ahmed et al., 2007; Miwa et al., 2009; Lee et al., 2010). Furthermore, the presence of GL and the lack of PE in *B. massiliensis* KCTC 13178T showed that it had a significantly different profile from its closest relative strain, as well as from BLB-1T and species of the genus *Lysinibacillus*. This difference could be used to differentiate the species from closely related taxa but was insufficient to exclude it from the genus *Lysinibacillus*. In conclusion, the polar lipid profiles indicate that the genus *Lysinibacillus* is as heterogeneous as the genera *Bacillus* and *Paenibacillus* (Kämpfer et al., 2006).

In conclusion, the novel isolate BLB-1T, *B. massiliensis* KCTC 13178T, and *B. odysseyi* KCTC 3961T all possess
peptidoglycan type A4\(\alpha\) (L-Lys–D-Asp) and they share this characteristic with members of the genus *Lysinibacillus* (Ahmed *et al.*, 2007). The phylogenetic analysis (Fig. 1) also showed that all three taxa, along with species of the genus *Lysinibacillus*, belong to the same clade within the *Bacillus* rRNA group 2. Based on these data, it is reasonable to assign the three taxa to the genus *Lysinibacillus*. The data presented in this study also show that the isolated strain BLB-1\(^T\) can be differentiated from other members of the genus *Lysinibacillus* and represents a novel species, for which the name *Lysinibacillus sinduriensis* sp. nov. is proposed. The chemotaxonomic and phylogenetic analyses also demonstrated that *B. massiliensis* and *B. odysseyi* should be transferred to the genus *Lysinibacillus* with the names *Lysinibacillus massiliensis* comb. nov. and *Lysinibacillus odysseyi* comb. nov., respectively.

**Emended description of the genus *Lysinibacillus* Ahmed *et al.* 2007**

The description is as given previously (Ahmed *et al.*, 2007) with the following amendments. Oxidase activity is variable. Major cellular fatty acids iso-C\(_{15:0}\) or anteiso-C\(_{15:0}\) are present. The polar lipid profiles contain DPG, PG and PE as predominant lipids, with varying numbers of unidentified polar lipids and amino-group-containing lipids. Some species do not contain PE and instead contain unidentified glycolipids as major components.

**Description of *Lysinibacillus sinduriensis* sp. nov.**

*Lysinibacillus sinduriensis* (sin.du.ri.en’sis. N.L. masc. adj. *sinduriensis* pertaining to the Sinduri, Republic of Korea, geographical origin of the type strain of the species).

Cells are Gram-positive, strictly aerobic, terminal spherical spore-forming, straight and club-shaped rods (0.5–1.2 × 0.7–3.5 μm) with swollen sporangium and are motile by peritrichous flagella. Colonies grown on TSBA medium are circular, convex, undulate, greyish white and 3 mm in diameter. Cells grow at 15–45°C (optimum 30°C), at pH 5–9 (optimum pH 7) and in 0–5 % (w/v) NaCl but not in 6 % (w/v) NaCl. Negative for nitrate reduction, oxidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, urease and tryptophan deaminase activities; positive for esterase, esterase lipase, leucine arylamidase and \(\alpha\)-chymotrypsin activities. Oxidizes \(\alpha\)-ketovaleric acid, pyruvic acid methyl ester and dextrin. Negative for oxidase, citrate utilization, urease and tryptophan deaminase activity, hydrolysis of casein and starch and indole production and positive for Voges–Proskauer test and acetoin production. No sugar is fermented in API 50 CH strips using CHB/E suspension medium. The cell-wall peptidoglycan contains L-Lys–D-Asp (type A4\(\alpha\)). The major cell-wall sugar is xylose. The major menaquinone is MK-7. The type strain, 34hs-1\(^T\) (=KCTC 13296\(^T\) =JCM 15800\(^T\)), was isolated from tidal flat sediment in the Shinduri sand dunes of the Yellow Sea, Republic of Korea. The DNA G+C content of the type strain is 35.9 mol%.

**Description of *Lysinibacillus odysseyi* comb. nov.**

*Lysinibacillus odysseyi* (o.dys.se’yi. L. n. Odyssey the Odyssey; N.L. gen. n. odysseyi pertaining to the Mars Odyssey spacecraft, from which the organism was isolated).

Basonym: *Bacillus odysseyi* La Duc *et al.* (2004).

In addition to the description of the type strain given by La Duc *et al.* (2004), cells are negative for alkaline phosphatase, valine arylamidase, cystine arylamidase, \(\alpha\)- and \(\beta\)-galactosidase, \(\alpha\)- and \(\beta\)-glucosidase, N-acetyl-\(\beta\)-glucosaminidase, \(\alpha\)-mannosidase, \(\alpha\)-fucosidase, trypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase activities; positive for esterase, esterase lipase, leucine arylamidase and \(\alpha\)-chymotrypsin activities. Oxidizes \(\alpha\)-ketovaleric acid, pyruvic acid methyl ester and dextrin. Negative for oxidase, citrate utilization, urease and tryptophan deaminase activity, hydrolysis of casein and starch and indole production and positive for Voges–Proskauer test and acetoin production. No sugar is fermented in API 50 CH strips using CHB/E suspension medium. The cell-wall peptidoglycan contains L-Lys–D-Asp (type A4\(\alpha\)). The major polar lipids are DPG, PG, PE and three unknown phospholipids, PL1, PL2 and PL3. The predominant fatty acids are anteiso-C\(_{15:0}\) (35.6 %), iso-C\(_{15:0}\) (25.6 %) and anteiso-C\(_{17:0}\) (16.5 %). The major cell-wall sugars are glucose and xylose. The cell-wall peptidoglycan contains L-Lys–D-Asp (type A4\(\alpha\)). The major menaquinone is MK-7.

The type strain, BLB-1\(^T\) (=KCTC 13296\(^T\) =JCM 15800\(^T\)), was isolated from tidal flat sediment in the Shinduri sand dunes of the Yellow Sea, Republic of Korea. The DNA G+C content of the type strain is 35.9 mol%.

**Description of *Lysinibacillus massiliensis* comb. nov.**

*Lysinibacillus massiliensis* (mas.si.li.en’sis. L. masc. adj. massiliensis of Massilia, the ancient Greek and Roman name for Marseille, France, where the type strain was isolated).

Basonym: *Bacillus massiliensis* Glazunova *et al.* 2006.

In addition to the description of the type strain given by Glazunova *et al.* (2006), cells are negative for trypsin, \(\alpha\)-chymotrypsin, acid phosphatase, lipase, valine arylamidase,
cystine arylamidase, \( \alpha \)- and \( \beta \)-galactosidase, \( \beta \)-glucuronidase, \( \beta \)-glucosidase, \( N \)-acetyl-\( \beta \)-glucosaminidase, \( x \)-mannosidase, and \( x \)-fucosidase activities; positive for alkaline phosphatase, esterase, esterase lipase, leucine arylamidase, acetoxy production, \( x \)-glucosidase, and naphthol-AS-BI-phosphohydrolase activities. Negative for nitrate reduction, and hydrolysis of casein and starch. Oxidizes \( x \)-ketoleric acid, pyruvic acid methyl ester and dextrin. The cell-wall peptidoglycan contains L-Lys–D-Asp (type A4\(_d\)). The major polar lipids are DPG, PG, three unknown phospholipids, PL1, PL2 and PL3, and two unknown glycolipids, GL1 and GL2. The major cell-wall sugars are glucose and xylose. The major menaquinone is MK-7.

The type strain, 4400831\(^T\) (= CIP 108446\(^T\) = CCUG 49529\(^T\) = KCTC 13178\(^T\)), was isolated from human cerebrospinal fluid. The DNA G+C content of the type strain is 36.3 mol%.

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