Isolation of *Jeotgalibacillus malaysiensis* sp. nov. from a sandy beach, and emended description of the genus *Jeotgalibacillus*

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A Gram-stain-positive, endospore-forming, rod-shaped bacterial strain, designated D5T, was isolated from seawater collected from a sandy beach in a southern state of Malaysia and subjected to a polyphasic taxonomic study. Sequence analysis of the 16S rRNA gene demonstrated that this isolate belongs to the genus *Jeotgalibacillus*, with 99.87% similarity to *Jeotgalibacillus alimentarius* JCM 10872T. DNA–DNA hybridization of strain D5T with *J. alimentarius* JCM 10872T demonstrated 26.3% relatedness. The peptidoglycan type was A1α linked directly to L-lysine as the diamino acid. The predominant quinones identified in strain D5T were menaquinones MK-7 and MK-8. The major fatty acids were iso-C15:0 and anteiso-C15:0. The G+C content of its DNA was 43.0 mol%. The major polar lipids were diphosphatidylglycerol, phosphatidylglycerol and sulfoquinovosyl diacylglycerol, as well as two unknown phospholipids and three unknown lipids. The phenotypic, chemotaxonomic and genotypic data indicated that strain D5T represents a novel species of the genus *Jeotgalibacillus*, for which the name *Jeotgalibacillus malaysiensis* sp. nov. is proposed (type strain D5T = DSM 28777T = KCTC33550T). An emended description of the genus *Jeotgalibacillus* is also provided.

The genus *Jeotgalibacillus* is a member of the phylum *Firmicutes*. The genus was first proposed by Yoon et al. (2001). At the time of writing, the genus *Jeotgalibacillus* comprised five recognized species. The cell-wall peptidoglycan of *Jeotgalibacillus alimentarius* is constituted by L-lysine as the diamino acid, while the predominant quinones are menaquinones MK-7 and MK-8 and the predominant fatty acid is iso-C15:0. Because species of the genus *Marinibacillus* produce MK-7 and MK-8, anteiso-C15:0 and similar peptidoglycans to those in the genus *Jeotgalibacillus*, two *Marinibacillus* species were later renamed as *Jeotgalibacillus campisalis* and *Jeotgalibacillus marinus* (Yoon et al., 2010). The genus *Jeotgalibacillus* thus comprises *J. alimentarius* (Yoon et al., 2001), *Jeotgalibacillus soli* (Cunha et al., 2012), *Jeotgalibacillus salarius* (Yoon et al., 2010), *J. marinus* (Rüger, 1983; Rüger & Richter, 1979) and *J. campisalis* (Yoon et al., 2004). Except for *J. soli*, which was isolated from alkaline sandy soil, the other species originated from salty environments, i.e. marine saltern, sea sediments and salted fermented food. The aim of the present study was to determine the taxonomic position of strain D5T, which was isolated from a sandy beach in Johor state, Malaysia. Here we describe the morphological, phenotypic, chemotaxonomic and phylogenetic properties of this strain. The results of this polyphasic analysis indicate that strain D5T should be positioned taxonomically in the genus *Jeotgalibacillus* as representing a novel species.

Pure colonies of strain D5T were obtained by growing cells on marine agar 2216 (MA; Difco). The reference strains *J. alimentarius* JCM 10872T, *J. salarius* DSM 23492T, *J. campisalis* DSM 18983T and *J. soli* DSM 23228T were obtained from the DSMZ (Braunschweig, Germany) and cultured for 48 h at 30°C on MA (pH 7.5), unless otherwise specified. Gram staining was performed using a standard procedure and confirmed using the KOH lysis method (Cerny, 1978). Endospore formation was detected on MA supplemented with 5 mg MnSO4 l−1 after 5 days of growth.
incubation, as described by Schaeffer & Fulton (1933). The cell morphology of strain D5\textsuperscript{T} was examined directly using a Leica DM300 light microscope for Gram staining and endospore detection. Field emission scanning electron microscopy was used to determine cell shapes and sizes. Flagella of strain D5\textsuperscript{T} were visualized by transmission electron microscopy, using a Philips CM-12 microscope. Cells from exponentially growing cultures were negatively stained with 1% (w/v) phosphotungstic acid and air-dried before making observations.

The pH range supporting bacterial growth was determined using marine broth 2216 (MB; Difco), adjusted in intervals of 0.5 pH units over a pH range of 3.0–12.0. Media with high pH were buffered with Na\textsubscript{2}CO\textsubscript{3}/NaHCO\textsubscript{3}. Cell growth at various temperatures, ranging from 4 to 50°C (4, 10, 15, 20, 25, 30, 35, 37, 40, 45 and 50°C), was investigated on MA with 48 or 72 h growth periods. The salt tolerance of cells was determined in two media: (1) trypsinase soy broth medium containing 0, 0.5, 1.0, 2.0 or 3.0% (w/v) NaCl, supplemented with 0.06% (w/v) KCl, and (2) MB medium containing 2–30% (w/v) NaCl, at increments of 1.0% (w/v).

Catalase activity, oxidase activity and the hydrolysis of casein, starch, hypoxanthine, tyrosine, xanthine, and Tween 20, 40, 60 and 80 were determined as described by Cowan & Steel (1965). Carbohydrate utilization was measured using API 50CH/B/E test strips, while the API 20E and API 20NE basic biochemical test strips (bioMérieux) were used to test for nitrate reduction, indole production, motility, the presence of \beta-galactosidase and urease and the hydrolysis of gelatin and aesculin. Selective enzyme activities were identified using API ZYM test strips. Susceptibility to antibiotics was investigated on MA plates using antibiotic discs containing kanamycin (30 μg), penicillin G (10 μg), chloramphenicol (50 μg), ampicillin (10 μg), cephalothin (30 μg), gentamicin (30 μg), novobiocin (5 μg), tetracycline (30 μg), carbencillin (100 μg), rifampicin (5 μg), ciprofloxacin (5 μg), vancomycin (30 μg), erythromycin (30 μg), colistin (10 μg), bacitracin (10 μg), nalidixic acid (100 μg), sulfa-methoxazole (30 μg) and tetracycline (30 μg).

Genomic DNA was extracted using a DNeasy Tissue kit (Qiagen), according to the manufacturer’s instructions. The 16S rRNA gene of strain D5\textsuperscript{T} was amplified by PCR using a forward primer (27F: 5’-AGAGTTTTGATCCTGGCTCAG-3’) and a reverse primer (1525R: 5’-AAGAGGTTGATCCAGGCC-3’), as described by Lane (1991). The purified PCR product was ligated into the pGEM-T vector (Yeastern Biotech) and transformed into Escherichia coli DH5\textalpha (Yeastern Biotech). Gene sequencing was performed by Malaysian First Base Sdn. Bhd. The complete 16S rRNA gene sequence (1546 bp) of strain D5\textsuperscript{T} was compared with those of other Jeotgalibacillus strains and taxa from the family Planococcaceae. Phylogenetic analysis was performed using MEGA 6 software (Tamura et al., 2013), and bootstrap analysis was performed to evaluate tree topologies using the neighbour-joining method (Saitou & Nei, 1987) and the maximum-likelihood method (Felsenstein, 1981), with 1000 resamplings. Pairwise sequence similarities were calculated using the EzTaxon server (Kim et al., 2012). Extraction of whole-cell proteins from growing cells of strain D5\textsuperscript{T}, J. alimentarius JCM 10872\textsuperscript{T}, J. salarius DSM 23492\textsuperscript{T}, J. campisalis DSM 18983\textsuperscript{T} and J. soli DSM 23228\textsuperscript{T} and SDS-PAGE analyses were performed as described by Berber et al. (2003). Sample identification by matrix-assisted laser-desorption/ionization time-of-flight (MALDI-TOF) MS was performed using a Microflex MALDI-TOF bench-top mass spectrometer (Bruker Daltonik) and Bruker FlexControl 3.3 software (Build 108), (Lim et al., 2014). Briefly, cell extracts were prepared from fresh colonies using the ethanol/formic acid extraction procedure as recommended by the manufacturer (Bruker Daltonik) and as described previously (Mellmann et al., 2008). Extracts were pipetted onto a clean, polished steel target plate and, after air-drying, were overlaid with a saturated solution of \alpha-cyano-4-hydroxy-cinnamic acid. The air-dried sample plate was loaded into the mass spectrometer and the mass of ions in the range 2–20 kDa was recorded following bombardment with a 337 nm nitrogen laser. A mass/charge range of 2000–20 000 m/z was used for analysis and comparison purposes.

The following analyses were performed by the DSMZ Identification Service. The methods used for preparing cell walls and determining peptidoglycan structures were based on protocols described by Schumann (2011). Isoprenoid quinones were analysed as described by Tindall (1990). Polar lipids were extracted following the methods of Tindall et al. (2007) and analysed by two-dimensional silica gel TLC. Analyses of total lipids and functional groups were conducted based on the method described by Tindall et al. (2007). To analyse bacterial cellular fatty acid methyl ester contents, cells of strain D5\textsuperscript{T}, J. alimentarius JCM 10872\textsuperscript{T}, J. salarius DSM 23492\textsuperscript{T}, J. campisalis DSM 18983\textsuperscript{T} and J. soli DSM 23228\textsuperscript{T} were harvested from MB during exponential growth, and fatty acids were extracted and fatty acid methyl esters were prepared according to the standard protocol of the Microbial Identification System (Sasser, 1990). The DNA G+C content of strain D5\textsuperscript{T} was determined as described by Tamaoka & Komagata (1984), with the modification that the DNA was hydrolysed with nuclease P1 (Sigma) (Mesbah et al., 1989) and the resultant nucleotides were analysed by reversed-phase HPLC. DNA–DNA hybridization was performed as described by De Ley et al. (1970) with the modification described by Huss et al. (1983), using a Cary 100 Bio UV/ VIS-spectrophotometer equipped with a Peltier-thermostatted 6 × 6 multitier changer and a temperature controller with an in-situ temperature probe (Varian). Genome comparison between strain D5\textsuperscript{T} and J. alimentarius JCM 10872\textsuperscript{T} was performed by determining the average nucleotide identity (Goris et al., 2007; Kim et al., 2014).
Strain D5\textsuperscript{T} formed slightly raised colonies on MA, with yellowish orange pigmentation. Cells were Gram-stain-positive, rod-shaped and slightly swollen by central ellipsoidal spores. Scanning electron microscopy observations revealed that the cells were rod-shaped, with mean dimensions of 0.5–0.7 × 0.6–1.2 μm at 50 000 × magnification (Fig. S1, available in the online Supplementary Material). The presence of flagella was observed with transmission electron microscopy (Fig. S2).

Growth of strain D5\textsuperscript{T} was observed at pH 6.0–11.0 and 4–50°C. Strain D5\textsuperscript{T} grew slowly in buffered MB at pH 11.0 (Fig. S3). The optimum growth conditions were pH 7.0–8.0 and 37°C. Results from salt tolerance studies indicated that growth occurred at NaCl concentrations of 0–30% (w/v), with optimal growth at 10% (w/v) NaCl. Strain D5\textsuperscript{T} showed a higher salt tolerance range and optimum temperature than the reference type strains. The organism was aerobic, catalase- and oxidase-positive and showed properties similar to those for the genus *Jeotgalibacillus*, as described by Yoon et al. (2001). Strain D5\textsuperscript{T} was resistant to ampicillin, penicillin G, carbencillin, rifampicin, ciprofloxacin, vancomycin, erythromycin and sulfamethoxazole. This antibiotic resistance profile matched those of other species of the genus *Jeotgalibacillus* (Yoon et al., 2010). Results from additional tests for antibiotic resistance, carbohydrate utilization and enzyme activities, as well as a more detailed description of the physiological characteristics of strain D5\textsuperscript{T}, are given in Table 1 and in the species description.

The 16S rRNA gene sequence of strain D5\textsuperscript{T} was 1546 bp in length based on strain D5\textsuperscript{T} genome sequencing data and confirmed by amplicon sequencing of the 16S rRNA gene. The complete genome was sequenced using a Pacific Biosciences RS II sequencer (CP009416). Comparing its sequence with those of representatives of the main lines of descent within the domain *Bacteria* indicated that strain D5\textsuperscript{T} is a member of the family *Planococcaceae* (Fig. 1; see also Fig. S4). Strain D5\textsuperscript{T} formed a coherent cluster, with a bootstrap resampling value of 100% with *J. alimentarius* JCM 10872\textsuperscript{T} (99.87% 16S rRNA gene sequence similarity). Strain D5\textsuperscript{T} shared lower 16S rRNA gene sequence similarity values of 97.25, 95.83, 95.73 and 94.78% with the type strains of *J. salarius*, *J. soli*, *J. marinus* and *J. campisalis*, respectively. The SDS-PAGE electrophoretic patterns of the whole-cell proteins and the MALDI-TOF mass spectra showed differences between strain D5\textsuperscript{T} and the patterns observed with *J. alimentarius* JCM 10872\textsuperscript{T}, *J. salarius* DSM 23492\textsuperscript{T}, *J. campisalis* DSM 18983\textsuperscript{T} and *J. soli* DSM 23228\textsuperscript{T} (Figs S5 and S6).

Several characteristics of strain D5\textsuperscript{T} match those of the type strains of other species in the genus *Jeotgalibacillus*, particularly peptidoglycan of the A1\textsubscript{z} type linked directly to l-lysine (Fig. S7) and MK-7 (86%) and MK-8 (10%) as major menaquinones. These similarities reinforce the phylogenetic assignment of strain D5\textsuperscript{T} to this genus. The major polar lipids observed in strain D5\textsuperscript{T} were diphosphatidylglycerol, phosphatidyglycerol, sulfoquinovosyl diacylglycerol, two unknown phospholipids and three unknown lipids (Fig. S8). The spot for sulfoquinovosyl diacylglycerol observed by TLC was phosphate-negative, thus confirming it as a glycolipid. In addition, the RE value and staining behaviour of this spot were consistent with the properties of sulfoquinovosyl diacylglycerol rather than a phospholipid. In addition, the fatty acid content was characterized by large amounts of branched components and a predominance of iso-C\textsubscript{15:0} and anteiso-C\textsubscript{15:0}. Nevertheless, differences in the proportions of some fatty acids, particularly in the levels of iso-C\textsubscript{13:0}, iso-C\textsubscript{15:0} and anteiso-C\textsubscript{15:0}, iso-C\textsubscript{16:0}, iso-C\textsubscript{17:0} and C\textsubscript{16:1}ω7c alcohol (Table 2), were found between the novel isolate and *J. alimentarius* JCM 10872\textsuperscript{T}. The G + C content of strain D5\textsuperscript{T} was determined by HPLC and genome sequencing to be 43 and 42.71 mol%, respectively, values that are similar to those observed for other species of the genus *Jeotgalibacillus* (Cunha et al., 2012; Yoon et al., 2010).

The DNA–DNA hybridization value between strain D5\textsuperscript{T} and *J. alimentarius* JCM 10872\textsuperscript{T} was 26.3%, which is significantly below the threshold value of 70% for species delineation (Huss et al., 1983). The average nucleotide identity value of strain D5\textsuperscript{T} relative to *J. alimentarius* was 80%, again significantly lower than the 95% cut-off value for species delineation (Goris et al., 2007). Differences in phenotypic and genotypic characteristics such as colony morphology, endospore position and shape, acid production from carbohydrates, maximum growth temperature, tolerance to NaCl and fatty acid composition, as well as the genomic DNA G + C content and DNA–DNA relatedness values, distinguish D5\textsuperscript{T} from the closely related *J. alimentarius* JCM 10872\textsuperscript{T}. On the basis of its phenotypic, chemotaxonomic and genotypic properties, strain D5\textsuperscript{T} represents a novel species of the genus *Jeotgalibacillus*, for which the name *Jeotgalibacillus malaysiensis* sp. nov. is proposed.

**Description of *Jeotgalibacillus malaysiensis* sp. nov.**

*Jeotgalibacillus malaysiensis* (ma.lay.si.en’sis. L. masc. adj. *malaysiensis* belonging or pertaining to Malaysia, the source of the seawater from which the type strain was isolated).

Cells are Gram-stain-positive rods (0.5–0.7 × 0.6–1.2 μm) that are motile by means of a single polar/subpolar flagella. Colonies grown on MA appear circular to irregular, raised, glistening, smooth, yellowish orange and 2.0–3.0 mm in diameter after 2 days of incubation at 37°C. Endospores, located in the central position of cells, are slightly swollen and form in growth media supplemented with 5 mg MnSO\textsubscript{4} 1\textsuperscript{-1}. The optimal growth temperature is 37°C; growth occurs between 4 and 50°C, but not at 55°C. The optimal pH for growth is between pH 7.0 and 8.0, but growth also occurs between pH 6.0 and 11.0. Optimal growth occurs in the presence of 10% (w/v) NaCl, but growth is still observed at 0–30% (w/v) NaCl. The peptidoglycan type is A1\textsubscript{z}.
Table 1. Differential phenotypic characteristics between strain D5T and the type strains of species of the genus *Jeotgalibacillus*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
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<tr>
<td><strong>Spore shape</strong></td>
<td>Round</td>
<td>Central</td>
<td>Round</td>
<td>Terminal or subterminal</td>
<td>Ellipsoidal</td>
</tr>
<tr>
<td><strong>Spore position</strong></td>
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<td></td>
<td>Ellipsoidal</td>
<td>Subterminal</td>
<td>Terminal or subterminal</td>
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<tr>
<td><strong>Swollen sporangia</strong></td>
<td>Slight</td>
<td>Single subpolar</td>
<td>+</td>
<td>Peritrichous</td>
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<td><strong>Flagella type</strong></td>
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<td>+</td>
<td>v</td>
<td>v</td>
<td>+ or v</td>
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<td>+</td>
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<td>+</td>
<td>−</td>
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<tr>
<td><strong>Oxidase</strong></td>
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<td>+</td>
<td>+</td>
<td>−</td>
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<td><strong>Hydrolysis of:</strong></td>
<td></td>
<td></td>
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<tr>
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<td>+</td>
<td>+</td>
<td>+</td>
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<td>+</td>
<td>−</td>
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<tr>
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<td>w</td>
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<tr>
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<td>Urea</td>
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<td>Nitrate reduction</td>
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<td>H₂S production</td>
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<td>+</td>
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<td>0–18</td>
<td>0–15</td>
<td>0–9</td>
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<td>0–1</td>
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<td>4–45</td>
<td>4–39</td>
<td>15–40</td>
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<tr>
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<td>30–35</td>
<td>30</td>
<td>30–35</td>
<td>30–37</td>
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<td><strong>pH range</strong></td>
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<td>6.5–10.0</td>
<td>6.0–10.5</td>
<td>6–10.5</td>
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<tr>
<td><strong>pH optimum</strong></td>
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<td>7.0–8.0</td>
<td>7.0–8.0</td>
<td>7.0–8.0</td>
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<tr>
<td>Cellobiose</td>
<td>w</td>
<td>−</td>
<td>w</td>
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<tr>
<td>D-Galactose</td>
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<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
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<tr>
<td>Maltose</td>
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<td>+</td>
<td>+</td>
<td>−</td>
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<td>D-Ribose</td>
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<td>+</td>
<td>+</td>
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<tr>
<td>Melezitose</td>
<td>w</td>
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<td>w</td>
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<tr>
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<tr>
<td>Raffinose</td>
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<td><strong>Enzyme activity (API ZYM)</strong></td>
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<td>Esterase (C4)</td>
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<td>Cystine arylamidase</td>
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<td>Trypsin</td>
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<tr>
<td>Naphthol-AS-BI-phosphohydrolase</td>
<td>+</td>
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<tr>
<td>β-Galactosidase</td>
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<td><strong>Susceptibility to antibiotics</strong></td>
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<tr>
<td>Erythromycin</td>
<td>−</td>
<td>+</td>
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<td>Sulfamethoxazole</td>
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<tr>
<td>Predominant menaquinone(s)</td>
<td>MK-7, MK-8</td>
<td>MK-7, MK-8</td>
<td>MK-7, MK-8</td>
<td>MK-7, MK-8</td>
<td>MK-7, MK-8</td>
</tr>
<tr>
<td>Predominant fatty acid</td>
<td>iso-C₁₅ : ⁰</td>
<td>iso-C₁₅ : ⁰</td>
<td>anteiso-C₁₅ : ⁰</td>
<td>anteiso-C₁₅ : ⁰</td>
<td>anteiso-C₁₅ : ⁰</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>43</td>
<td>44</td>
<td>42.9</td>
<td>41.8</td>
<td>39.4</td>
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</table>

*Data for the type strains of reference species were from this study.*
(L-Lys direct). The predominant menaquinone is MK-7 (86%), while the minor menaquinones are MK-8 (10%) and MK-6 (4%). The major fatty acids are iso-C₁₅:0 and anteiso-C₁₅:0. Nitrate is reduced; starch, urea, aesculin and casein are hydrolysed. Gelatin is partially hydrolysed, but xanthine, hypoxanthine, tyrosine, and Tweens 20, 40, 60 and 80 are not hydrolysed. In API 50CHB/E tests, acid is produced from glycerol, L-arabinose, D-ribose, D-galactose, D-glucose, D-fructose, D-mannitol, methyl α-D-glucopyranoside, ascin, cellobiose, sucrose, raffinose, melezitose, starch, glycogen, potassium gluconate, turanose and inulin, but not from melibiose, cellobiose, D-xylene, L-xylene, D-mannose, L-rhamnose, D-arabitol, L-arabitol, erythritol, D-adenitol, methyl β-D-xylpyranoside, D-arabinose, L-sorbose, sorbitol, inositol, D-sorbitol, methyl α-D-mannopyranoside, N-acetylglycosamine, maltose, trehalose, amygdalin, arbutin, salicin, lactose, xyitol, gentiobiase, L-lyxose, D-tagatose, D-fucose, L-fucose, potassium 2-ketogluconate or potassium 5-ketogluconate. Esterase (C4), esterase lipase (C8), trypsin, α-chymotrypsin, naphthol-AS-BI-phosphohydrolase and N-acetyl-β-glucosaminidase are present, but activities for alkaline phosphatase, lipase (C14), leucine arylamidase, valine arylamidase, cysteine arylamidase, acid phosphatase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, α-mannosidase and β-fucosidase are

**Fig. 1.** Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the positions of strain D5ᵀ and other related taxa. The sequence of *Escherichia coli* K-12ᵀ was used as an outgroup. Bootstrap values are expressed as percentages of 1000 replications. Bar, 0.02 substitutions per nucleotide position.

http://ijs.sgmjournals.org 2219
Table 2. Comparison of the cellular fatty acids of strain D5\textsuperscript{T} and the type strains of other species of the genus Jeotgalibacillus

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
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<tr>
<td>Straight chain</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>C\textsubscript{14:0}</td>
<td>0.2</td>
<td>0.3</td>
<td>0.3</td>
<td>0.3</td>
<td>1.25</td>
</tr>
<tr>
<td>C\textsubscript{15:0}</td>
<td>0.3</td>
<td>0.2</td>
<td>1.1</td>
<td>0.7</td>
<td>0.3</td>
</tr>
<tr>
<td>C\textsubscript{16:0}</td>
<td>0.2</td>
<td>0.2</td>
<td>0.2</td>
<td>0.3</td>
<td>1.5</td>
</tr>
<tr>
<td>Branched</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>iso-C\textsubscript{13:0}</td>
<td>0.3</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>iso-C\textsubscript{15:0}</td>
<td>57.1</td>
<td>46.6</td>
<td>9.1</td>
<td>4.6</td>
<td>26.3</td>
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<tr>
<td>anteiso-C\textsubscript{15:0}</td>
<td>18.3</td>
<td>21.7</td>
<td>44.4</td>
<td>44.9</td>
<td>44.6</td>
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<tr>
<td>iso-C\textsubscript{16:0}</td>
<td>0.6</td>
<td>1.0</td>
<td>4.0</td>
<td>4.5</td>
<td>0.9</td>
</tr>
<tr>
<td>iso-C\textsubscript{17:0}</td>
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<td>6.6</td>
<td>1.7</td>
<td>0.7</td>
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<tr>
<td>anteiso-C\textsubscript{17:0}</td>
<td>2.6</td>
<td>5.4</td>
<td>12.1</td>
<td>9.8</td>
<td>7.5</td>
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<tr>
<td>iso-C\textsubscript{17:1\alpha\textsuperscript{10}c}</td>
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<td>4.8</td>
<td>0.4</td>
<td>0.3</td>
<td>2.5</td>
</tr>
<tr>
<td>Unsaturated</td>
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<tr>
<td>C\textsubscript{16:0\textsuperscript{7}c} alcohol</td>
<td>3.6</td>
<td>5.5</td>
<td>13.8</td>
<td>16.0</td>
<td>2.0</td>
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<tr>
<td>C\textsubscript{16:1\textsuperscript{11}c}</td>
<td>0.9</td>
<td>1.0</td>
<td>1.2</td>
<td>4.5</td>
<td>4.8</td>
</tr>
<tr>
<td>Summed feature 4*</td>
<td>4.3</td>
<td>4.8</td>
<td>1.9</td>
<td>6.8</td>
<td>4.0</td>
</tr>
</tbody>
</table>

*Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system. Summed feature 4* contained iso-C\textsubscript{17:1} I and/or anteiso-C\textsubscript{17:1} B.

not detected. Cells are susceptible to gentamicin, kanamycin, chloramphenicol, colistin, bacitracin, nalidixic acid and tetracycline, but not to ampicillin, penicillin G, carbenicillin, rifampicin, ciprofloxacin, vancomycin, erythromycin or sulfamethoxazole.

The type strain, D5\textsuperscript{T} (=DSM 28777\textsuperscript{T}=KCTC33550\textsuperscript{T}), was isolated from a sandy beach located in Johor state, Malaysia. The DNA G+C content of the type strain is 43.0 mol%, as determined by HPLC.

Emended description of the genus Jeotgalibacillus

The description of the genus Jeotgalibacillus is as described by Yoon et al. (2001), with the following amendments. Cell size is 0.4–1.2 × 0.6–8.5 μm. Cells are round, with ellipsoidal endospores in swollen or non-swollen sporangia, with single polar, subpolar or peritrichous flagella. Growth occurs at 1–50°C, at pH 5.5–11.0 and with 0–30% (w/v) NaCl. Cells are Gram-stain-positive, as confirmed by KOH testing. Hydrolyses gelatin weakly and is positive or negative for acid production from ascin and cascin. The major fatty acids are iso-C\textsubscript{15:0} and/or anteiso-C\textsubscript{15:0}. The genomic DNA G+C content is 39–44 mol%.

Acknowledgements

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References


