The family Intrasporangiaceae was proposed as a family of the suborder Micrococccinae by Stackebrandt et al. (1997) on the basis of 16S rRNA gene sequence analysis and the family currently consists of 11 genera. The family Intrasporangiaceae is a phenotypically heterogeneous taxon which can be divided into three groups on the basis of the diagnostic diamino acid in the cell-wall peptidoglycan. The genera Intrasporangium (Kalakoutskii et al., 1967), Terrabacter (Collins et al., 1989), Terracoccus (Prauser et al., 1997) and Arsenicicoccus (Collins et al., 2004) contain L-diaminopimelic acid, the genera Janibacter (Martin et al., 1997), Tetrasphaera (Maszenan et al., 2000), Knoellia (Groth et al., 2002) and Oryzihumus (Kageyama et al., 2005) contain meso-diaminopimelic acid and the genera Ornithinimicroccus (Groth et al., 1999), Ornithinimicrobium (Groth et al., 2001) and Serinicoccus (Yi et al., 2004) contain L-ornithine. In this study, we describe two meso-diaminopimelic acid-containing bacterial strains, N113T and R33, which are phenotypically related to the family Intrasporangiaceae. The aim of the present study was to determine the exact taxonomic position of strains N113T and R33 using a polyphasic approach that included analysis of phenotypic properties, detailed phylogenetic analysis based on 16S rRNA gene sequences and genetic relatedness.

Tidal flat sediment collected from Kwangyang, Korea, was used as the source for the isolation of diesel oil-degrading bacteria. Strains N113T and R33 were isolated from an enrichment culture with diesel oil-degradation activity by dilution plating on 10× diluted nutrient agar (Difco) and R2A agar (Difco), respectively. To investigate their morphological, physiological and biochemical characteristics, strains N113T and R33 were routinely cultivated at 30°C on trypticase soy agar (TSA; Difco). Growth at various temperatures from 4 to 50°C was measured on TSA. The pH range for growth was determined in nutrient broth (NB; Difco) that was adjusted to various pH values (initial pH 4.5–11.5) at intervals of 0.5 pH units. Growth under anaerobic conditions was determined after incubation in an anaerobic chamber on TSA and on TSA supplemented with nitrate, both of which had been prepared anaerobically using nitrogen. Cell morphology and presence of flagella were examined by light microscopy (E600; Nikon) and transmission electron microscopy by using cells grown on TSA. Gram reaction was determined by using the bioMérieux Gram stain kit according to the manufacturer’s instructions. Catalase and oxidase activities and hydrolysis of casein, hypoxanthine, tyrosine, xanthine, starch and

Abbreviation: FAME, fatty acid methyl ester.

The GenBank/EMBL/DDJB accession numbers for the 16S rRNA gene sequences of strains N113T and R33 are DQ372707 and DQ062659, respectively.

A supplementary table detailing the cellular fatty acid contents of Kribbia dieselivorans sp. nov. strains N113T and R33 is available in USEM Online.

Kribbia dieselivorans gen. nov., sp. nov., a novel member of the family Intrasporangiaceae

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Two Gram-positive, catalase-positive, irregular short rod- or coccolid-shaped bacterial strains, N113T and R33, were isolated from an enrichment culture with diesel oil-degradation activity and their taxonomic positions were investigated using a polyphasic approach. Phenotypic, phylogenetic and genetic similarities indicated that strains N113T and R33 were representatives of the same species. Phylogenetic analysis based on 16S rRNA gene sequences showed that strains N113T and R33 form a lineage independent from those of members of the family Intrasporangiaceae. The novel isolates had cell-wall peptidoglycan based on meso-diaminopimelic acid, MK-8(H4) as the predominant menaquinone and 10-methyl-C18:0, iso-C16:0, C18:1ω9c, C16:0 and C18:0 as the major cellular fatty acids. The DNA G+C contents were 69.6–69.9 mol%. These chemotaxonomic properties, together with phylogenetic distinctiveness, distinguish the two novel strains from recognized members of the family Intrasporangiaceae. On the basis of phenotypic, phylogenetic and genetic data, strains N113T (=KCTC 19143T =JCM 13585T) and R33 are classified as representatives of a novel genus and species, Kribbia dieselivorans gen. nov., sp. nov., within the family Intrasporangiaceae.
Tweens 20, 40, 60 and 80 were determined as described by Cowan & Steel (1965). Hydrolysis of aesculin, gelatin and urea and nitrate reduction were studied as described previously (Lanyi, 1987). Acid production from carbohydrates was determined according to Leifson (1963). Utilization of various substrates for growth was tested as described by Yurkov et al. (1994). The API ZYM system (bioMérieux) was used to determine enzyme activity. Other physiological and biochemical tests were performed with the API 20E and API 20NE systems (bioMérieux). Antibiotic sensitivity was tested by spreading bacterial suspension on TSA and applying discs impregnated with the following antibiotics (concentration per disc): ampicillin (10 μg), carbenicillin (100 μg), cephalothin (30 μg), chloramphenicol (100 μg), gentamicin (30 μg), lincomycin (15 μg), kanamycin (30 μg), neomycin (30 μg), novobiocin (5 μg), oleandomycin (15 μg), penicillin G (20 U), polymyxin B (100 U), streptomycin (50 μg) and tetracycline (30 μg).

Strains N113T and R33 were cultivated for 3 days in trypticase soy broth (Difco) at 30°C to obtain the cell mass required for isoprenoid quinone and cell wall analyses and DNA extraction. Isoprenoid quinones were analysed as described previously (Komagata & Suzuki, 1987) using reverse-phase HPLC. The isomer type of the cell-wall diamino acid was analysed according to the method of Komagata & Suzuki (1987). For fatty acid methyl ester (FAME) analysis, cell mass of strains N113T and R33 was harvested from TSA plates after cultivation for 3 days at 30°C. FAMEs were extracted and prepared according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). Chromosomal DNA was extracted and purified by the procedure described previously (Yoon et al., 1996). The DNA G + C content was determined by the method of Tamaoka & Komagata (1984) with a modification that DNA was hydrolysed and the resultant nucleotides were analysed by reverse-phase HPLC.

The 16S rRNA gene amplification was performed according to the method of Yoon et al. (1998) using two universal primers. Sequencing of the amplified 16S rRNA gene was performed as described by Yoon et al. (2003). Alignment of sequences was carried out with CLUSTAL W (Thompson et al., 1994) and gaps at the 5' and 3' ends of the alignment were omitted from further analysis. The evolutionary distances were calculated using the Kimura two-parameter correction with the CLUSTAL W package (Thompson et al., 1994). A phylogenetic tree was constructed by using the neighbour-joining method (Saitou & Nei, 1987) on the basis of distance matrix data. The reliability of the grouping was assessed by 1000 bootstrap resamplings of the neighbour-joining dataset by using the CLUSTAL W package. DNA–DNA hybridization was determined by the microplate hybridization method (Ezaki et al., 1989) using photobiotin-labelled DNA probes.

Morphological, cultural, physiological and biochemical characteristics of strains N113T and R33 are given in the genus and species descriptions (see below) or shown in Table 1. Strains N113T and R33 had meso-diaminopimelic acid as the diagnostic diamino acid in the cell-wall peptidoglycan. They contained MK-8(H4) as the predominant menaquinone. Strains N113T and R33 had cellular fatty acid profiles that contained large amounts of straight-chain, branched, unsaturated and 10-methyl fatty acids. The major components (> 10% of total fatty acids) were 10-methyl-C18:0 (iso-C16:0; C18:1ω9c, C16:0 and C18:0 (see Supplementary Table S1 in IJSEM Online). The DNA G + C contents of strains N113T and R33 were 69.9 and 69.6 mol%, respectively. The 16S rRNA gene sequences of strains N113T and R33 determined in this study each comprised 1476 nucleotides and were 99.9% similar (one nucleotide difference). Comparative 16S rRNA gene sequence analyses revealed that strains N113T and R33 were phylogenetically most closely related to the family Intrasporangiaceae. In a phylogenetic tree based on the neighbouring-joining algorithm, strains N113T and R33 formed a distinct phylogenetic lineage within the family Intrasporangiaceae (Fig. 1). 16S rRNA gene sequence similarity values between strains N113T and R33 and genera within the family Intrasporangiaceae were as follows: Janibacter (95.3–96.0%), Intrasporangium (95.6%), Terracoccus (95.6%), Terrabacter (95.7–95.9%), Arsenicoccus (95.5%), Knoellia (94.8–95.0%), Ornithinicoccus (94.8%), Ornthininimicrobium (94.8%), Orzyihumus (94.2%), Serincoccus (94.2%) and Tetrasphaera (93.8–94.5%). Strains N113T and R33 exhibited a mean DNA–DNA relatedness value of 90% when their DNAs were used individually as labelled DNA probes for cross-hybridization, indicating that the two strains are members of the same genomic species (Wayne et al., 1987). In view of their phenotypic, phylogenetic and genetic similarities, strains N113T and R33 are representatives of the same species.

Strains N113T and R33 could be clearly distinguished from recognized members of the family Intrasporangiaceae by differences in chemotaxonomic properties, particularly by the diamino acid type in position 3 of the peptidoglycan and by fatty acid profiles (Table 1). Strains N113T and R33 are distinguishable from the genera which contain LL-diaminopimelic acid or L-ornithine as the diagnostic diamino acid in the cell-wall peptidoglycan. They contained MK-8(H4) as the predominant menaquinone. Strains N113T and R33, but they were absent or present as minor components in other genera of the family Intrasporangiaceae. On the basis of the phylogenetic data and differential chemotaxonomic properties reported here, it is suggested that strains N113T and R33 represent a new genus...
Table 1. Differential characteristics of *Kribbia dieselivorans* gen. nov., sp. nov. and genera of the family *Intrasporangiaceae*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>12</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell morphology</td>
<td>Irregular short rods or cocci</td>
<td>Cocci</td>
<td>Irregular rods and cocci</td>
<td>Cocci</td>
<td>Cocci to rod-shaped meso-A2pm</td>
<td>Irregular rods and cocci</td>
<td>Cocci or short rods meso-A2pm</td>
<td>Cocci</td>
<td>Irregular rods</td>
<td>Hyphae</td>
<td>Cocci</td>
<td>Irregular rods</td>
</tr>
<tr>
<td>Cell wall diamino acid</td>
<td>meso-A2pm</td>
<td>L-A2pm</td>
<td>L-Orn</td>
<td>meso-A2pm</td>
<td>L-Orn</td>
<td>meso-A2pm</td>
<td>L-Orn</td>
<td>meso-A2pm</td>
<td>L-Orn</td>
<td>meso-A2pm</td>
<td>L-Orn</td>
<td>meso-A2pm</td>
</tr>
<tr>
<td>Major menaquinone</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
<td>MK-8(H4)</td>
</tr>
<tr>
<td>Major fatty acid (&gt;10% of total fatty acids)</td>
<td>10-methyl-C18:0, iso-C16:0, C18:1ω9c, anteiso-C15:0</td>
<td>C16:0, ω7c, iso-C16:0, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td>iso-C16:0, ω7c, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td>iso-C16:0, ω7c, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td>iso-C16:0, ω7c, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td>(anteiso-C15:0, iso-C13:0), or (iso-C16:0, anteiso-C17:0, iso-C15:0)† or (iso-C15:0, anteiso-C15:0, anteiso-C17:0, ω9c)† or (anteiso-C15:0, iso-C15:0, anteiso-C17:0, ω9c)†</td>
<td>iso-C16:0, ω7c, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td>iso-C16:0, ω7c, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td>iso-C16:0, ω7c, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td>iso-C16:0, ω7c, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td>iso-C16:0, ω7c, iso-C15:0, C18:1ω9c, anteiso-C15:0</td>
<td></td>
</tr>
<tr>
<td>DNA G+C (mol%)</td>
<td>69–70</td>
<td>72±2</td>
<td>70</td>
<td>69–73</td>
<td>68–69</td>
<td>68–71</td>
<td>72</td>
<td>72–73</td>
<td>68–2</td>
<td>73</td>
<td>69–72–74</td>
<td></td>
</tr>
</tbody>
</table>

Data for *Tetrasphaera elongata*, †*Tetrasphaera australiensis*, §*Tetrasphaera japonica*, ¶*Terrabacter terrae* and ||*Terrabacter tumescens*.
and novel species within the family Intrasporangiaceae, for which the name Kribbia dieselivorans gen. nov., sp. nov. is proposed.

Description of Kribbia gen. nov.

Kribbia (Kribbi.a. N.L. fem. n. Kribbia arbitrary name formed from the acronym of the Korea Research Institute of Bioscience and Biotechnology, KRIBB, where taxonomic studies of this taxon were performed).

Cells are Gram-positive, non-flagellated, irregular short rods or cocci. The cell-wall peptidoglycan contains meso-diaminopimelic acid. The predominant menaquinone is MK-8(H4). Major cellular fatty acids (>10% of total fatty acids) are 10-methyl-C18:0, iso-C16:0, C18:1ω9c, C16:0 and C18:0. The DNA G+C content is 69–70 mol%. Phylogenetically, the genus is a member of the family Intrasporangiaceae within the suborder Micrococcineae of the order Actinomycetales. The type species is Kribbia dieselivorans.

Description of Kribbia dieselivorans sp. nov.

Kribbia dieselivorans (die.se.lli.vo’rans. N.L. n. dieselum diesel; L. v. vorare to devour; N.L. part. adj. dieselivorans diesel oil-devouring).

Exhibits the following properties in addition to those given in the genus description. Cells are 0.4–0.6 × 1.0–1.5 μm. Catalase-positive, oxidase-negative and urease-negative. Growth occurs between 8 and 42°C with an optimum temperature of 30°C. Optimal pH for growth is 6.5–7.5. Anaerobic growth occurs on TSA and on TSA with nitrate.

Casein, gelatin, aesculin and Tweens 20, 40, 60 and 80 are hydrolysed, but starch, hypoxanthine, xanthine and tyrosine are not. Arginine dihydrolase, lysine decarboxylase and ornithine decarboxylase are absent. H2S and indole are not produced. Nitrate is reduced to nitrite. Acetate, benzoate, D-cellobiose and pyruvate are utilized as sole carbon and energy sources; D-glucose, D-trehalose, sucrose and maltose are weakly utilized. D-Fructose, D-galactose, D-mannose, D-xylene, L-arabinose, citrate, formate, salicin, succinate, L-glutamate and L-malate are not utilized. Acid is produced from D-glucose, D-cellobiose, sucrose, maltose and D-trehalose, but not from D-sorbitol, N-acetylglucosaminidase, a-glucosaminidase, b-glucuronidase, N-acetyl-b-glucosaminidase, a-mannosidase and a-fucosidase. The major cellular fatty acids (>10% of total fatty acids) are 10-methyl-C18:0, iso-C16:0, C18:1ω9c, C16:0 and C18:0. The DNA G+C content is 69–69.9 mol%.

The type strain, N113T (= KCTC 19143T = JCM 13585T), was isolated from tidal flat sediment from Kwangyang, Korea.

Fig. 1. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic positions of Kribbia dieselivorans gen. nov., sp. nov. and some other related taxa. Bar, 0.01 substitutions per nucleotide position.
Note added in proof

Another new genus has been described in the Intrasporangiaceae with the same diagnostic diamino acid, Phycicoccus jeuensis (see Lee, 2006, this issue IJSEM, pp. 2369–2373).

Acknowledgements

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