A novel Gram-positive, rod-shaped actinobacterium, designated strain YIM 90718\textsuperscript{T}, was isolated from a saline soil in Xinjiang province, north-west China, and subjected to polyphasic taxonomy. The peptidoglycan type was A\textsubscript{1γ} and the cell-wall sugars contained galactose. Phospholipids were phosphatidylglycerol and diphosphatidylglycerol. The predominant menaquinone was MK-8(H\textsubscript{2}). The major fatty acids were anteiso-C\textsubscript{15:0}, anteiso-C\textsubscript{17:0} and iso-C\textsubscript{15:0}. All of these chemotaxonomic data assigned the new isolate YIM 90718\textsuperscript{T} consistently to the genus \textit{Brevibacterium}. Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain YIM 90718\textsuperscript{T} formed a distinct phylogenetic lineage in the genus \textit{Brevibacterium} and showed the highest sequence similarity (96.2\%) to \textit{Brevibacterium samyangense} SST-\textsuperscript{8T} \textsuperscript{T} and low similarity (<95.5\%) to other species of the genus \textit{Brevibacterium}. On the basis of the polyphasic evidence, \textit{Brevibacterium album} sp. nov., is proposed, with the type strain YIM 90718\textsuperscript{T} (=DSM 18261\textsuperscript{T} = KCTC 19173\textsuperscript{T} = CCTCC AB 206112\textsuperscript{T}).
growth was investigated between pH 4.0 and 10.0 at intervals of 1 pH unit using the following buffer systems: pH 4.0–5.0, 0.1 M citric acid/0.1 M sodium citrate; pH 6.0–8.0, 0.1 M KH₂PO₄/0.1 M NaOH; pH 9.0–10.0, 0.1 M NaHCO₃/0.1 M Na₂CO₃. Catalase activity was determined by production of bubbles after the addition of a drop of 3 % H₂O₂. Oxidase activity was observed by oxidation of tetramethyl-p-phenylenediamine. Carbon source utilization tests were carried out using GP2 microplates of the Microlog system (Biolog; 95 substrates). Some physiological properties were tested by using the API CORYNE and API ZYM strips (bioMérieux) according to the manufacturer’s instructions. The morphological, cultural and physiological properties of strain YIM 90718ᵀ are given in Table 1 and in the species description.

Peptidoglycan was purified and the cell-wall amino acids and peptides in cell-wall hydrolysates were analysed by two-dimensional ascending TLC on cellulose plates using the solvent system of Schleifer & Kandler (1972). The cell-wall sugars were analysed according to the procedures developed by Hasegawa et al. (1983). Polar lipids were extracted, examined by two-dimensional TLC and identified using procedures described previously (Minnikin et al., 1984). Menaquinones were isolated according to Minnikin et al. (1984) and separated by HPLC (Kroppenstedt, 1982). Cellular fatty acid analysis was performed as described by Sasser (1990) using the Microbial Identification System (MIDI). The peptidoglycan type of YIM 90718ᵀ was A₁,γ-saccharate was the cell-wall sugar. Phospholipids contained phosphatidylglycerol and diphosphatidylglycerol. The predominant menaquinone was MK-8(H₂). The major fatty acids were anteiso-C₁₅ : 0, anteiso-C₁₇ : 0 and iso-C₁₅ : 0. All of these features are consistent with the chemotaxonomic description of the genus Brevibacterium (Collins et al., 1980). Details of the phospholipids and menaquinones and the cellular fatty acid profile are reported in the species description.

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene were done as described by Li et al. (2007). Multiple alignments with sequences of the most closely related members of Brevibacterium and calculations of levels of sequence similarity were carried out using CLUSTAL_X (Thompson et al., 1997). Phylogenetic analyses were performed using three tree-making algorithms: the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971) methods. A phylogenetic tree was constructed using the neighbour-joining method from Kₘₑᵤ values (Kimura, 1980) using MEGA version 2.1 (Kumar et al., 2001). The topology of the phylogenetic tree was evaluated by the bootstrap resampling method of Felsenstein (1985) with 1000 replicates. Genomic DNA of strain YIM 90718ᵀ for the determination of G+C content was prepared according to the method of Marmur (1961). The G+C content of the DNA was determined by reversed-phase HPLC of nucleosides according to Mesbah et al. (1989).

A neighbour-joining phylogenetic tree (Fig. 1) based on 16S rRNA gene sequence comparison clearly showed that strain YIM 90718ᵀ belongs to the genus of Brevibacterium and forms a distinct subclade with B. samyangense. The 16S rRNA gene sequence similarity between strain YIM 90718ᵀ and its nearest neighbour, B. samyangense SST-8ᵀ, was 96.2 %, and low 16S rRNA gene sequence similarity (<95.5 %) was revealed with other species of the genus.
Brevibacterium. The G+C content of the DNA was 70.0 mol%.

On the basis of the phenotypic, chemotaxonomic and phylogenetic data, strain YIM 90718ᵀ merits recognition within a novel species of the genus Brevibacterium, for which we propose the name Brevibacterium album sp. nov.

**Description of Brevibacterium album sp. nov.**

Brevibacterium album (alˈbəm. L. neut. adj. album white).

Cells are aerobic, Gram-positive, motile, catalase-positive, oxidase-negative, non-spore-forming rods, 1.8 × 4.0–5.0 μm. Colonies are smooth, circular, opaque and approximately 1–2 mm in diameter after 48 h incubation at 37 °C on ISP medium 5 containing 5 % (w/v) NaCl. Growth occurs in the temperature, pH and salt ranges of 28–45 °C, pH 6–8, 0–10 % NaCl (w/v), 0–20 % KCl (w/v) and 0–30 % MgCl₂·6H₂O (w/v). Good growth occurs at 37 °C, pH 7.5, 0–5 % (w/v) NaCl, 0–10 % KCl (w/v) and 0–15 % MgCl₂·6H₂O (w/v). The following substrates are utilized as sole carbon sources for growth in Biolog GP2 microplates: β-cyclodextrin, Tween 80, N-acetyl-D-glucosamine, L-fucose, D-glucuronic acid, myo-inositol, lactulose, D-mannitol, methyl β-D-galactoside, methyl α-D-glucoside, palatinose, L-mannose, salicin, trehalose, turanose, D-malic acid, succinic acid, D-alanine, L-alanyl glycine, putrescine, 1,2-3-butane-diol, glycerol, adenosine, 2′-deoxyadenosine, inosine, thymidine, uridine, adenosine 5′-monophosphate and fructose 6-phosphate. The following substrates are not utilized in the Biolog GP2 system: α-cyclodextrin, dextrin, glycogen, inulin, mannan, Tween 40, N-acetyl-β-D-mannosamine, amygdalin, L-arabinose, D-arabitol, arbutin, cellulbiose, D-fructose, D-galactose, D-galacturonic acid, gentiobiose, D-glucose, D-lactose, maltose, maltotriose, D-mannose, melezitose, melibiose, methyl α-D-galactoside, D-methyl glycoside, methyl β-D-glucoside, methyl α-D-mannoside, D-psicose, raffinose, D-ribose, sedoheptulose, D-sorbitol, stachyose, sucrose, D-tagatose, xylitol, D-xyllose, acetic acid, α-, β- and γ-hydroxybutyric acid, p-hydroxyphenylacetic acid, α-ketoglutaric acid, α-ketovaleric acid, lactamide, D-lactate acid methyl ester, L-lactic acid, L-malic acid, methyl pyruvate, monomethyl succinate, propionic acid, pyruvic acid, succinamic acid, N-acetyl-L-glutamic acid, D-alanine, L-alanine, L-asparagine, L-glutamic acid, glycyl L-glutamic acid, L-pyroglutamic acid, L-serine, 2,3-butane-diol, glycerol, adenosine, 2′-deoxyadenosine, inosine, thymidine, uridine, adenosine 5′-monophosphate, thymidine 5′-monophosphate, glucose 1-phosphate, glucose 6-phosphate and Dl-α-glycerol phosphate. In the API CORYNE system, tests for pyrazinamidase, pyrrolidonyl arylamidase, alkaline phosphatase, gelatin hydrolysis and acid production from D-ribose are positive. Tests for nitrate reduction, β-glucuronidase, β-galactosidase, α-glucosidase, N-acetyl-β-glucosaminidase, β-glucosidase (aesculin hydrolysis), urease and acid production from D-glucose, D-xyllose, D-mannitol, maltose, D-lactose, sucrose and glycogen are negative. Using the API ZYM system, acid and alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, z-chymotrypsin and naphthol-AS-BI-phosphohydrolase tests are positive. Lipase (C14), α-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, β-glucosidase, N-acetyl-β-β-glucosaminidase, α-mannosidase and α-fucosidase tests are negative. The peptidoglycan is A1γ, meso-diaminopimelic acid directly cross-linked. Cell-wall sugar contains galactose. The phospholipids are phosphatidylglycerol and diphosphatidylglycerol. The menaquinones are MK-8(H2), MK-7(H2), MK-6(H2), MK-8, MK-6 and MK-9(H2) (ratio of peak areas, 76 : 10 : 5 : 3 : 2 : 1). The fatty acid profile contains anteisolic-C₁₅:₀ (58.71 %), anteiso-C₁₇:₀ (19.0 %), iso-C₁₅:₀ (12.29 %) and iso-C₁₆:₀ (7.24 %). The G+C content of the DNA of the type strain is 70.0 mol%.

The type strain is YIM 90718ᵀ (DSM 18261ᵀ =KCTC 19173ᵀ =CCTCC AB 206112ᵀ), isolated from a saline soil in the north-west of China.

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