Adhaeribacter aerophilus sp. nov., *Adhaeribacter aerolatus* sp. nov. and *Segetibacter aerophilus* sp. nov., isolated from air samples

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Three bacterial isolates from air samples in Korea, designated strains 6424S-25^T, 6515J-31^T and 6424S-61^T, were characterized using a polyphasic approach. The cells were strictly aerobic, Gram-stain-negative, non-motile, non-spore-forming and rod-shaped. Phylogenetic analysis of their 16S rRNA gene sequences revealed a clear affiliation with the phylum *Bacteroidetes*. Strains 6424S-25^T and 6515J-31^T showed 16S rRNA gene sequence similarities of 92.7–94.8% to type strains of recognized species of the genus *Adhaeribacter* and strain 6424S-61^T was closely related to *Segetibacter koreensis* Gsoil 664^T (93.9% similarity). The G + C contents of the DNA of strains 6424S-25^T, 6515J-31^T and 6424S-61^T were 44.5, 43.9 and 38.4 mol%, respectively. Major fatty acids of strains 6424S-25^T and 6515J-31^T were summed feature 4 (iso-C_{17:1} I and/or anteiso-C_{17:1} B), iso-C_{15:0} and C_{16:1}ω5c. The fatty acid content of strain 6424S-61^T mainly comprised iso-C_{15:1} G and iso-C_{15:0}. Comparative analysis of phenotypic and phylogenetic traits indicated that strains 6424S-25^T and 6515J-31^T represented two novel species of the genus *Adhaeribacter* and that strain 6424S-61^T should be considered as a novel species of the genus *Segetibacter*. The names *Adhaeribacter aerophilus* sp. nov. (type strain 6424S-25^T = KACC 14118^T = NBRC 106134^T), *Adhaeribacter aerolatus* sp. nov. (type strain 6515J-31^T = KACC 14117^T = NBRC 106133^T) and *Segetibacter aerophilus* sp. nov. (type strain 6424S-61^T = KACC 14119^T = NBRC 106135^T) are proposed for these organisms.

The genus *Adhaeribacter* was proposed for a Gram-negative, obligately aerobic, non-motile, chemo-organotrophic bacterium isolated from a potable water biofilm (Rickard *et al.*, 2005). More recently, a novel species from forest soil, *Adhaeribacter terreus*, was described by Zhang *et al.* (2009). At the time of writing, the genus comprised two species, including *Adhaeribacter aquaticus* as the type species. Phylogenetically, these micro-organisms are related to the genera *Hymenobacter* and *Pontibacter* within the family 'Flexibacteraceae' of the phylum *Bacteroidetes*. The genus *Segetibacter* was proposed by An *et al.* (2007) for an isolate from soil of a ginseng field; the type species

Segetibacter koreensis is at present the only described species. Phylogenetically, *Segetibacter* belongs to the family 'Chitinophagaceae' and is related to the genera *Flavisolibacter*, *Niabella*, *Niastella* and *Terrimonas* in the phylum *Bacteroidetes* (Ludwig *et al.*, 2008).

When violent sandstorms happen in northern China or Mongolia, they produce lots of fine particles that float at a high altitude. These fine particles drift to the Korean peninsula in the spring. This is referred to as the Asian dust ('Hwangsae' in Korean) phenomenon, and usually happens between March and May. To compare the airborne bacteria in Asian dust with those present normally, air samples were collected in Suwon (37° 16' 46" N 126° 59' 10" E), Taean (36° 38' 36" N 126° 18' 13" E) and Jeju (33° 28' 08" N 126° 31' 05" E) regions of the Republic of Korea, with an MAS-100 air sampler (single-stage multiple-hole impactor, Merck) containing Petri dishes with R2A agar (Difco) amended with 200 µg cycloheximide ml⁻¹ (Sigma). After sampling, the plates were incubated in the dark at 28 °C for

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains 6424S-25^T, 6515J-31^T and 6424S-61^T are GQ421850, GQ421846 and GQ421847, respectively.

Cellular fatty acid compositions of strains 6424S-25^T, 6515J-31^T and 6424S-61^T and the type strains of related species, and a table showing differential carbon source utilization between strains 6424S-25^T and 6515J-31^T are available with the online version of this paper.

5 days. During this process, we isolated two pink-coloured bacteria (designated strains 6424S-25^T and 6515J-31^T) and one yellow-coloured bacterium (designated strain 6424S-61^T). Routine cultivation was conducted at 28 °C with R2A agar.

Phenotypic characteristics, including Gram-staining, catalase activity, oxidase activity and hydrolysis of CM-cellulose, casein, chitin, hypoxanthine, tyrosine, Tween 40, Tween 80, starch and xanthine, were performed by using the methods of Smibert & Krieg (1994). The pH range (pH 4.0–10.0 at intervals of 0.5 pH units) for growth was determined in R2A broth that was buffered with citrate/phosphate buffer or Tris/hydrochloride buffer (Breznak & Costilow, 1994). Growth at 0.5, 1.0, 1.5, 2.0, 3.0 and 5.0 % NaCl (w/v), and at various temperatures (5–50 °C at intervals of 5 °C) was investigated in R2A agar. Tests using the commercial systems API 20NE, API ID 32GN and API ZYM (bioMérieux) were performed according to the manufacturer's instructions. The API ZYM test strip was read after 4 h incubation at 37 °C, whilst the other API strips were examined after 4 days at 30 °C. Carbon-source utilization tests were performed with microtitre plates as described by Ten *et al.* (2006). Growth was examined visually after incubation at 28 °C for 14 days. Cell morphology was observed by transmission electron microscopy (912AB; LEO) and phase-contrast microscopy (AXIO; Zeiss) by using cells grown on R2A agar.

The cells of strains 6424S-25^T, 6515J-31^T and 6424S-61^T were strictly aerobic, Gram-stain-negative, non-spore-forming, non-motile and rod-shaped. Strain 6424S-25^T grew well on Luria–Bertani (LB; Difco) and CM3 nutrient agar (Oxoid), weakly on water agar (WA) and did not grow on trypticase soy agar (TSA; Difco), nutrient agar (NA; Difco) or MacConkey agar (Difco). Strain 6515J-31^T grew well on CM3 nutrient agar and NA, and weakly on WA, but did not grow on TSA, LB or MacConkey agar. Strain 6424S-61^T grew well on R2A agar and NA, very weakly on one-tenth strength TSA, but did not grow on TSA, LB or MacConkey agar. According to the API 20NE and ID32GN strips, strains 6424S-25^T, 6515J-31^T and 6424S-61^T did not assimilate any of the available substrates (up to 14 days of incubation). The phenotypic characteristics of the strains are summarized and compared with those of type strains of closely related taxa in Tables 1 and 2.

Fatty acid methyl esters were extracted and prepared by using the standard protocol of the Microbial Identification system (MIDI, 1999) after cells were grown on R2A agar for 3 days (6424S-25^T and 6515J-31^T) or 4 days (6424S-61^T) at 30 °C. Isoprenoid quinones were analysed by HPLC as described by Groth *et al.* (1996). The DNA G+C content was determined by HPLC analysis of deoxyribonucleosides as described by Mesbah *et al.* (1989) using a reversed-phase column (Supelcosil LC-18 S; Supelco).

Strain 6424S-25^T contained summed feature 4 (comprising iso-C_{17:1} I and/or anteiso-C_{17:1} B, 33.1 %), iso-C_{15:0} (19.1 %) and C_{16:1}ω5c (11.3 %), and strain 6515J-31^T

contained summed feature 4 (comprising iso-C_{17:1} I and/or anteiso-C_{17:1} B, 29.9 %), C_{16:1}ω5c (17.4 %) and iso-C_{15:0} (15.0 %) as the major fatty acids (see Supplementary Table S1 available in IJSEM Online). The DNA G+C contents of strains 6424S-25^T and 6515J-31^T were 44.5 and 43.9 mol%, respectively, lying within the range (40.4–48.1 mol%) for the genus *Adhaeribacter*. The fatty acid content of strain 6424S-61^T mainly comprised iso-C_{15:1} G (26.4 %) and iso-C_{15:0} (16.9 %) (see Supplementary Table S2). The DNA G+C content of strain 6424S-61^T was 38.4 mol%. MK-7 was the predominant menaquinone in the three strains.

16S rRNA gene sequences were determined by PCR amplification (Kwon *et al.*, 2003) and direct sequencing (Hiraishi, 1992). Almost-complete 16S rRNA gene sequences were determined for strains 6424S-25^T (1410 bp), 6515J-31^T (1486 bp) and 6424S-61^T (1422 bp). Identification of phylogenetic neighbours and calculation of pairwise 16S rRNA gene sequence similarities were achieved by using the EzTaxon server (<http://www.eztaxon.org/>; Chun *et al.*, 2007). CLUSTAL W version 1.8 (Thompson *et al.*, 1994) was used to align the sequences of strains 6424S-25^T, 6515J-31^T and 6424S-61^T with corresponding sequences from related taxa retrieved from public databases. Phylogenetic analysis was performed by using the software package MEGA version 3.1 (Kumar *et al.*, 2004), using the neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods with bootstrap (Felsenstein, 1985) values based on 1000 replications.

Similarity analyses indicated that strain 6424S-25^T was most similar to *Adhaeribacter aquaticus* MBRG1.5^T (93.0 %) and *Adhaeribacter terreus* DNG6^T (94.1 %). Strain 6515J-31^T had 92.7 and 94.8 % sequence similarities with respect to *Adhaeribacter aquaticus* MBRG1.5^T and *Adhaeribacter terreus* DNG6^T, respectively. The 16S rRNA gene sequence similarity between strains 6424S-25^T and 6515J-31^T was 96.6 %. Strain 6424S-61^T showed the highest 16S rRNA gene sequence similarity (93.9 %) with respect to *Segetibacter koreensis* Gsoil 664^T. As the 16S rRNA gene sequence divergence of the three isolated strains from their closest phylogenetically related species was >3 %, this supports the proposal that they may represent novel species (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994).

In the neighbour-joining tree, strains 6424S-25^T and 6515J-31^T formed a cluster with 100 % bootstrap support and this cluster grouped with the two type strains of the genus *Adhaeribacter* (99 % bootstrap value). The phylogenetic tree also showed that strain 6424S-61^T was grouped with *Segetibacter koreensis* Gsoil 664^T with 99 % bootstrap support (Fig. 1). The tree reconstructed using maximum-parsimony also supported the affiliation of these three strains with the genera *Adhaeribacter* and *Segetibacter*.

Phenotypically, strains 6424S-25^T and 6515J-31^T differed from each other in properties such as growth media, pH, NaCl and temperature ranges for growth, activity of valine arylamidase (API ZYM) and carbon source assimilation

Table 1. Differential phenotypic characteristics of strains 6424S-25^T and 6515J-31^T and type strains of species of the genus *Adhaeribacter*

Strains: 1, *Adhaeribacter aerophilus* sp. nov. 6424S-25^T; 2, *Adhaeribacter aerolatus* sp. nov. 6515J-31^T; 3, *Adhaeribacter aquaticus* MBRG1.5^T (Zhang *et al.*, 2009 and this study); 4, *Adhaeribacter terreus* DNG6^T (Zhang *et al.*, 2009). All strains are positive for oxidase, aesculin hydrolysis, enzyme activities of alkaline phosphatase, leucine arylamidase, acid phosphatase and naphthol-AS-BI-phosphohydrolase (API ZYM), but are negative for nitrate reduction, indole production, glucose fermentation, and enzyme activities of cystine arylamidase, trypsin, α -chymotrypsin, β -glucuronidase and α -fucosidase (API ZYM). +, Positive; w, weakly positive; –, negative.

Characteristics	1	2	3	4
Isolation source	Air	Air	Biofilm	Forest soil
Media supporting growth	R2A, LB, CM3-NA, WA	R2A, CM3-NA, NA, WA	R2A, MA, WA	R2A, 0.5–1 strength TSB, 0.1–1 strength LB
Media not supporting growth	TSA, NA, MacConkey	TSA, LB, MacConkey	CM3-NA	0.05–0.2 strength TSB
Cell size	0.9–1.1 $\times$ 2.0–4.3	1.0–1.2 $\times$ 1.8–2.8	0.9–1.7 $\times$ 2.8–4.1	0.3–0.5 $\times$ 1.0–2.0
pH range for growth	6.5–8.5	6.5–9.0	5.5–8.5*	6.0–9.0
Temperature range for growth (°C)	10–37	10–35	4–37	16–33
Highest NaCl concn (% w/v) tolerated	1.0	1.5	4	1
Hydrolysis of:				
Starch	+	+	–	–
Gelatin	+	+	–	+
Casein	–	–	–*	+
Urea	–	–	–	+
Catalase	w	w	w	–
Arginine dihydrolase	–	–	+	–
Enzyme activities (API ZYM)				
Esterase (C4)	+	+	–	–
Esterase lipase (C8)	+	+	–	w
Valine arylamidase	+	–	+	+
α -Galactosidase	+	+	+	–
β -Galactosidase	–	–	w	–
α -Glucosidase	–	–	+	–
β -Glucosidase	–	–	+	–
N-Acetyl- β -glucosaminidase	+	+	+	–
α -Mannosidase	+	+	–	–
DNA G + C content (%)	44.5	43.9	40.4	48.1

*Data taken from this study.

(Table 1 and Supplementary Table S3), and fatty acid profile (Supplementary Table S1). In addition, the two novel strains could be differentiated from other members of the genus *Adhaeribacter* on the basis of phenotypic characteristics, fatty acid composition and DNA G + C contents (Table 1 and Supplementary Table S1).

Strain 6424S-61^T exhibited a number of phenotypic similarities with respect to *Segetibacter koreensis* Gsoil 664^T, including cell morphology, yellow-coloured pigments, strictly aerobic growth, the hydrolysis of CM-cellulose and aesculin, MK-7 as the major quinone and similar DNA G + C content. However, strain 6424S-61^T can be clearly differentiated from *Segetibacter koreensis* on the basis of the novel strain's ability to hydrolyse starch and gelatin, negative reactions for catalase, oxidase, arginine dihydrolase and urease, and some API ZYM enzyme profiles (Table 2). Also,

the novel strain had lower amounts of anteiso-C_{17:0} and anteiso-C_{17:1} A, and higher amounts of iso-C_{13:0}, iso-C_{13:0} 3-OH and summed feature 3 than *Segetibacter koreensis* (Supplementary Table S2).

On the basis of the data presented here, we propose that strains 6424S-25^T, 6515J-31^T and 6424S-61^T represent three novel species. We propose to name them *Adhaeribacter aerophilus* sp. nov., *Adhaeribacter aerolatus* sp. nov. and *Segetibacter aerophilus* sp. nov., respectively.

Description of *Adhaeribacter aerophilus* sp. nov.

Adhaeribacter aerophilus (ae.ro.phi'lus. Gr. n. *aer* air; Gr. adj. *philos* loving; N.L. masc. adj. *aerophilus* air-loving).

Cells are strictly aerobic, Gram-stain-negative, non-motile, non-spore-forming rods that are 0.9–1.1 μ m in diameter

Table 2. Phenotypic characteristics that differentiate strain 6424S-61^T from *Segetibacter koreensis* Gsoil 664^T

Data for *Segetibacter koreensis* Gsoil 664^T were taken from An *et al.* (2007). Both strains are positive for hydrolysis of CM-cellulose and aesculin, enzyme activities of alkaline phosphatase, leucine arylamidase, acid phosphatase, α -galactosidase and *N*-acetyl- β -glucosaminidase (API ZYM), but are negative for hydrolysis of casein, chitin and tyrosine, anaerobic test, nitrate reduction, indole production and glucose fermentation, and enzyme activities of lipase (C14), trypsin, α -chymotrypsin and β -glucuronidase (API ZYM). +, Positive; w, weakly positive; –, negative.

Characteristics	strain 6424S-61 ^T	<i>S. koreensis</i> Gsoil 664 ^T
Isolation source	Air	Soil
Media supporting growth	R2A, NA, 0.1 strength TSA	R2A, 0.1 strength TSA
Media not supporting growth	LB, TSA, MacConkey	NA, TSA, MacConkey
Cell size	0.9–1.1 $\times$ 3.0–6.3	1.0–1.3 $\times$ 1.6–2.0
Highest NaCl concn (% w/v) tolerated	1.0	3.0
Hydrolysis of:		
Gelatin	+	–
Starch	+	–
Urea	–	+
Catalase	–	+
Oxidase	–	+
Arginine dihydrolase	–	+
Enzyme activities (API ZYM)		
Cystine arylamidase	+	–
Esterase (C4)	+	–
Esterase lipase (C8)	+	–
α -Fucosidase	–	w
β -Galactosidase	+	–
α -Glucosidase	+	w
β -Glucosidase	+	w
α -Mannosidase	+	–
Naphthol-AS-BI-phosphohydrolase	+	–
Valine arylamidase	+	–
DNA G + C content (%)	38.4	40.4

and 2.0–4.3 μ m in length. Colonies are smooth, circular, convex and pink after 3 days at 30 °C on R2A agar. Grows on LB, CM3-nutrient agar and WA (very weakly), but not on

NA, TSA or MacConkey agar. Growth occurs at 10–37 °C, at pH 6.5–8.5 and with 0–1% NaCl. Catalase is weakly positive. Oxidase positive. Hydrolyses starch. Does not

Fig. 1. Neighbour-joining phylogenetic tree reconstructed from a comparative analysis of 16S rRNA gene sequences showing the relationships between strains 6424S-25^T, 6515J-31^T and 6424S-61^T and related species. Bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at branch points. Dots indicate that the corresponding branches were also recovered in the maximum-parsimony tree. *Flavobacterium aquatile* ATCC 11947^T (M62797) was used as an outgroup. Bar, 2 substitutions per 100 nt positions.

hydrolyse casein, chitin, hypoxanthine, tyrosine or xanthine. Positive (in API 20NE and API ZYM strips) for hydrolysis of aesculin and gelatin, alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α -galactosidase, *N*-acetyl- β -glucosaminidase and α -mannosidase, and negative for nitrate reduction, indole production, acid production from glucose, arginine dihydrolase, urease, β -galactosidase (substrate *p*-nitrophenyl β -D-galactopyranoside), lipase (C14), cystine arylamidase, trypsin, α -chymotrypsin, β -galactosidase, β -glucuronidase, α -glucosidase, β -glucosidase and α -fucosidase. Does not assimilate any of the carbohydrates tested (API 20NE and API ID 32GN). Positive for assimilation of the following substrates: amygdalin, D-arabinose, L-arabinose, cellobiose, D-galactose, gentiobiose, D-glucose, glutaric acid, glycogen, itaconate, lactose, malonate, maltose, D-mannose, melezitose, melibiose, methyl α -D-glucoside, methyl α -D-mannoside, methyl β -D-xyloside, *N*-acetylglucosamine, oxalic acid, raffinose, L-rhamnose, salicin, sucrose, trehalose, turanose and D-xylose. Negative for assimilation of the following substrates: acetate, adipate, D-adonitol, D-arabitol, L-arabitol, arbutin, citrate, dextran, dulcitol, erythritol, formate, D-fructose, D-fucose, L-fucose, gluconate, L-glutamic acid, glycerol, histidine, inositol, inulin, lactate, D-lyxose, malate, maleic acid, D-mannitol, phenylacetate, L-proline, propionate, pyruvic acid, D-ribose, D-sorbitol, L-sorbose, succinic acid, D-tagatose, tartaric acid, xylitol and L-xylose. The predominant isoprenoid quinone is MK-7. The major fatty acids are summed feature 4 (comprising iso-C_{17:1} I and/or anteiso-C_{17:1} B), iso-C_{15:0} and C_{16:1}ω5c. The DNA G + C content of the type strain is 44.5 mol%.

The type strain, 6424S-25^T (=KACC 14118^T =NBRC 106134^T), was isolated from an air sample from Suwon, Republic of Korea.

Description of *Adhaeribacter aerolatus* sp. nov.

Adhaeribacter aerolatus (ae.ro.la'tus. Gr. n. *aer* air; L. part. adj. *latus* carried; N.L. masc. part. adj. *aerolatus* airborne).

Cells are strictly aerobic, Gram-stain-negative, non-motile, non-spore-forming rods that are 1.0–1.2 µm in diameter and 1.8–2.8 µm in length. Colonies are smooth, circular, convex and pink after 3 days at 30 °C on R2A agar. Grows on NA and WA (very weakly) but not on LB, TSA and MacConkey agar. Growth occurs at 10–35 °C, at pH 6.5–9.0 and with 0–1.5 % NaCl. Catalase is weakly positive. Oxidase positive. Hydrolyses starch. Does not hydrolyse casein, chitin, hypoxanthine, tyrosine or xanthine. Positive (in API 20NE and API ZYM strips) for hydrolysis of aesculin and gelatin, alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α -galactosidase, *N*-acetyl- β -glucosaminidase and α -mannosidase, and negative for nitrate reduction, indole production, acid production from glucose, arginine dihydrolase, urease, β -galactosidase (substrate *p*-nitrophenyl β -D-galactopyranoside), lipase

(C14), valine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin, β -galactosidase, β -glucuronidase, α -glucosidase, β -glucosidase and α -fucosidase. Does not assimilate any of the carbohydrates tested (API 20NE and API ID 32GN). Positive for assimilation of the following substrates: amygdalin, D-arabinose, L-arabinose, arbutin, cellobiose, D-fructose, D-galactose, gentiobiose, D-glucose, inulin, lactate, lactose, maltose, D-mannose, melezitose, melibiose, methyl α -D-glucoside, methyl α -D-mannoside, methyl β -D-xyloside, *N*-acetylglucosamine, raffinose, L-rhamnose, D-ribose, salicin, sucrose, trehalose, turanose and D-xylose. Negative for assimilation of the following substrates: acetate, adipate, D-adonitol, D-arabitol, L-arabitol, citrate, dextran, dulcitol, erythritol, formate, D-fucose, L-fucose, gluconate, L-glutamic acid, glutaric acid, glycerol, glycogen, histidine, inositol, itaconate, D-lyxose, malate, maleic acid, malonate, D-mannitol, oxalic acid, phenylacetate, L-proline, propionate, pyruvic acid, D-sorbitol, L-sorbose, succinic acid, D-tagatose, tartaric acid, xylitol and L-xylose. The predominant isoprenoid quinone is MK-7. The major fatty acids are summed feature 4 (comprising iso-C_{17:1} I and/or anteiso-C_{17:1} B), C_{16:1}ω5c and iso-C_{15:0}. The DNA G + C content of the type strain is 43.9 mol%.

The type strain, 6515J-31^T (=KACC 14117^T =NBRC 106133^T), was isolated from an air sample from Jeju, Republic of Korea.

Description of *Segetibacter aerophilus* sp. nov.

Segetibacter aerophilus (ae.ro.phi'lus. Gr. n. *aer* air; Gr. adj. *philos* loving; N.L. masc. adj. *aerophilus* air-loving).

Cells are strictly aerobic, Gram-stain-negative, non-motile, non-spore-forming rods that are 0.9–1.1 µm in diameter and 3.0–6.3 µm in length. Colonies are smooth, circular, convex and yellowish after 4 days at 30 °C on R2A agar. Good growth occurs on R2A agar and nutrient agar. Growth occurs at 15–30 °C and with 0–1 % NaCl. Catalase and oxidase negative. Hydrolyses CM-cellulose and starch. Does not hydrolyse casein, chitin, hypoxanthine, Tween 40, Tween 80, tyrosine or xanthine. Positive (in API 20NE and API ZYM strips) for hydrolysis of aesculin and gelatin, β -galactosidase (substrate *p*-nitrophenyl β -D-galactopyranoside), alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α -galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, *N*-acetyl- β -glucosaminidase and α -mannosidase, and negative for glucose fermentation, arginine dihydrolase, urease, nitrate reduction, indole production, lipase (C14), trypsin, α -chymotrypsin, β -glucuronidase and α -fucosidase. Does not assimilate any of the carbohydrates tested (API 20NE and API ID 32GN). The predominant isoprenoid quinone is MK-7. The major fatty acids are iso-C_{15:1} G and iso-C_{15:0}. The DNA G + C content of the type strain is 38.4 mol%.

The type strain, 6424S-61^T (=KACC 14119^T =NBRC 106135^T), was isolated from an air sample from Suwon, Republic of Korea.

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References

- An, D.-S., Lee, H.-G., Im, W.-T., Liu, Q.-M. & Lee, S.-T. (2007). *Segetibacter koreensis* gen. nov., sp. nov., a novel member of the phylum *Bacteroidetes*, isolated from the soil of a ginseng field in South Korea. *Int J Syst Evol Microbiol* **57**, 1828–1833.
- Breznak, J. A. & Costilow, R. N. (1994). Physicochemical factors in growth. In *Methods for General and Molecular Bacteriology*, pp. 137–154. Edited by P. Gerhardt, R. G. E. Murray, W. A. Wood & N. R. Krieg. Washington, DC: American Society for Microbiology.
- Chun, J., Lee, J.-H., Jung, Y., Kim, M., Kim, S., Kim, B. K. & Lim, Y.-W. (2007). EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. *Int J Syst Evol Microbiol* **57**, 2259–2261.
- Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* **39**, 783–791.
- Fitch, W. M. (1971). Toward defining the course of evolution: minimum change for a specific tree topology. *Syst Zool* **20**, 406–416.
- Groth, I., Schumann, P., Weiss, N., Martin, K. & Rainey, F. A. (1996). *Agrococcus jenensis* gen. nov., sp. nov., a new genus of actinomycetes with diaminobutyric acid in the cell wall. *Int J Syst Bacteriol* **46**, 234–239.
- Hiraishi, A. (1992). Direct automated sequencing of 16S rDNA amplified by polymerase chain reaction from bacterial cultures without DNA purification. *Lett Appl Microbiol* **15**, 210–213.
- Kumar, S., Tamura, K. & Nei, M. (2004). MEGA3: integrated software for molecular evolutionary genetics analysis and sequence alignment. *Brief Bioinform* **5**, 150–163.
- Kwon, S. W., Kim, J. S., Park, I. C., Yoon, S. H., Park, D. H., Lim, C. K. & Go, S. J. (2003). *Pseudomonas koreensis* sp. nov., *Pseudomonas umsongensis* sp. nov. and *Pseudomonas jinjuensis* sp. nov., novel species from farm soils in Korea. *Int J Syst Evol Microbiol* **53**, 21–27.
- Ludwig, W., Euzéby, J. & Whitman, W. B. (2008). Draft taxonomic outline of the *Bacteroidetes*, *Planctomycetes*, *Chlamydiae*, *Spirochaetes*, *Fibrobacteres*, *Fusobacteria*, *Acidobacteria*, *Verrucomicrobia*, *Dictyoglomi*, and *Gemmatimonadetes*. http://www.bergeys.org/outlines/Bergeys_Vol_4_Outline.pdf
- Mesbah, M., Premachandran, U. & Whitman, W. B. (1989). Precise measurement of the G + C content of deoxyribonucleic acid by high-performance liquid chromatography. *Int J Syst Bacteriol* **39**, 159–167.
- MIDI (1999). *Sherlock Microbial Identification System Operating Manual*, version 3.0. Newark, DE: MIDI, Inc.
- Rickard, A. H., Stead, A. T., O'May, G. A., Lindsay, S., Banner, M., Handley, P. S. & Gilbert, P. (2005). *Adhaeribacter aquaticus* gen. nov., sp. nov., a Gram-negative isolate from a potable water biofilm. *Int J Syst Evol Microbiol* **55**, 821–829.
- Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* **4**, 406–425.
- Smibert, R. M. & Krieg, N. R. (1994). Phenotypic characterization. In *Methods for General and Molecular Bacteriology*, pp. 607–654. Edited by P. Gerhardt, R. G. E. Murray, W. A. Wood & N. R. Krieg. Washington, DC: American Society for Microbiology.
- Stackebrandt, E. & Goebel, B. M. (1994). Taxonomic note: a place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int J Syst Bacteriol* **44**, 846–849.
- Ten, L. N., Baek, S.-H., Im, W.-T., Liu, Q.-M., Aslam, Z. & Lee, S.-T. (2006). *Bacillus panaciterrae* sp. nov., isolated from soil of a ginseng field. *Int J Syst Evol Microbiol* **56**, 2861–2866.
- Thompson, J. D., Higgins, D. G. & Gibson, T. J. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* **22**, 4673–4680.
- Wayne, L. G., Brenner, D. J., Colwell, R. R., Grimont, P. A. D., Kandler, O., Krichevsky, M. I., Moore, L. H., Moore, W. E. C., Murray, R. G. E. & other authors (1987). International Committee on Systematic Bacteriology. Report of the ad hoc committee on reconciliation of approaches to bacterial systematics. *Int J Syst Bacteriol* **37**, 463–464.
- Zhang, J.-Y., Liu, X.-Y. & Liu, S.-J. (2009). *Adhaeribacter terreus* sp. nov., isolated from forest soil. *Int J Syst Evol Microbiol* **59**, 1595–1598.