Chryseobacterium soldanellicola sp. nov. and *Chryseobacterium taeanense* sp. nov., isolated from roots of sand-dune plants

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Two Gram-negative, yellow-pigmented bacteria designated PSD1-4^T and PHA3-4^T, isolated from two sand-dune plant species inhabiting coastal areas in Tae-an, Korea, were subjected to taxonomic investigation. 16S rRNA gene sequence analysis indicated that both isolates should be placed in the genus *Chryseobacterium* of the family *Flavobacteriaceae*. The phenotypic properties of the strains were also consistent with their classification into this genus. The levels of 16S rRNA gene sequence similarity between strain PSD1-4^T and other *Chryseobacterium* species were 95.2–97.2%; those between PHA3-4^T and others were 93.7–97.8%. The DNA–DNA relatedness data indicated that strains PSD1-4^T and PHA3-4^T were clearly different from the nearest species, *Chryseobacterium indoltheticum* and *Chryseobacterium taichungense*. The major fatty acids were 13-methyltetradecanoic acid (iso-C15:0), 3-hydroxy-15-methylhexadecanoic acid (iso-C17:0 3-OH) and omega-9-*cis*-15-methylhexadecenoic acid (iso-C17:1 ω 9c) for both strains. On the basis of polyphasic taxonomic analysis results, it is evident that each of these strains represents a novel species of *Chryseobacterium*, for which the names *Chryseobacterium soldanellicola* sp. nov. (type strain PSD1-4^T = KCTC 12382^T = NBRC 100864^T) and *Chryseobacterium taeanense* sp. nov. (type strain PHA3-4^T = KCTC 12381^T = NBRC 100863^T) are proposed.

The genus *Chryseobacterium* currently includes the initially described species *Chryseobacterium balustinum*, *C. gleum*, *C. indologenes*, *C. indoltheticum* and *C. scopthalmum* (Vandamme *et al.*, 1994) and several more recently described species, *Chryseobacterium defluvii* (Kämpfer *et al.*, 2003), *C. joostei* (Hugo *et al.*, 2003), *C. daecheongense* (Kim *et al.*, 2005), *C. formosense* (Young *et al.*, 2005), *C. taichungense* (Shen *et al.*, 2005), *C. shigense* (Shimomura *et al.*, 2005) and *C. vrystaatense* (de Beer *et al.*, 2005). Two former *Chryseobacterium* species, *Chryseobacterium meningosepticum* (Vandamme *et al.*, 1994) and *Chryseobacterium miricola* (Li *et al.*, 2003), have been reclassified in a new genus *Elizabethkingia* (Kim *et al.*, 2005). Strains belonging to this genus have been found in a wide variety of environments such as soil, sewage, freshwater, marine sediment and clinical samples.

During a study of bacterial diversity associated with sand-dune plants using a culture-dependent approach, a number of bacterial strains were isolated from root samples of two sand-dune plant species (Park *et al.*, 2005). Two strains designated PSD1-4^T and PHA3-4^T, forming yellow colonies on R2A agar (Difco) at 30 °C, were isolated from the roots of *Calystegia soldanella* (beach morning glory) and *Elymus mollis* (wild rye), respectively, and subjected to further taxonomic investigation. Analysis of the 16S rRNA gene sequences showed that both of the isolates could be placed within the phylogenetic clade encompassed by the genus *Chryseobacterium* of the family *Flavobacteriaceae*. The strains were subcultured on tryptic soy agar (TSA; Difco) at 30 °C for 48 h and subsequently investigated for fatty acid methyl ester profiles, 16S rRNA gene sequences and phenotypic characteristics. The strains were also maintained as glycerol suspensions (20%, w/v) at –80 °C.

Cellular morphology was examined using a Nikon MICROPHOT-FAX phase-contrast microscope with cells grown for 3 days at 30 °C on TSA. Gram staining was carried out using the modification of Hucker's method as described

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by Gerhardt *et al.* (1994). Growth was investigated at different NaCl concentrations (0–7 %, w/v), at various temperatures (5–42 °C) and on MacConkey agar. Biochemical tests were performed using the API 20E, API 20NE, API CHB and API ZYM systems (bioMérieux). Oxidation of 95 selected carbon sources was tested using Biolog GN2 microplates according to the manufacturer's instructions. Antifungal activities were screened using four plant-pathogenic fungi, namely *Botrytis cinerea*, *Fusarium oxysporum*, *Rhizoctonia solani* and *Pythium ultimum* (cultures provided by the Korea Research Institute of Chemical Technology, Daejeon, Korea).

Strains PSD1-4^T and PHA3-4^T were Gram-negative and formed visible colonies (diameter of about 2 mm) on nutrient agar within 24 h at 30 °C. No growth was observed at temperatures above 42 °C within 14 days. At 5 °C, small colonies were seen on the agar plates. The colonies were yellowish, translucent and shiny with entire edges, becoming mucoid after prolonged incubation.

Strains PSD1-4^T and PHA3-4^T shared a number of phenotypic characteristics tested in common, with the following

differential characteristics: pH ranges for growth, tolerance to NaCl and degradation of Tween 80. Comparison of physiological and biochemical characteristics also enabled differentiation of each isolate from other representative species of the genus *Chryseobacterium* (Table 1). Strain PSD1-4^T was shown to inhibit growth of the plant pathogen *Fusarium oxysporum*, whereas strain PHA3-4^T exhibited no antifungal activity.

Fatty acid methyl esters were extracted and prepared by the standard protocol of the Sherlock Microbial Identification System (MIDI). The fatty acids analysed by a gas chromatograph (Hewlett Packard 6890) were identified by the Microbial Identification software package (Sasser, 1990). The fatty acid contents of PSD1-4^T and PHA3-4^T indicated that 13-methyltetradecanoic acid (iso-C15:0) was the most abundant fatty acid for both strains, which was followed by 3-hydroxy-15-methylhexadecanoic acid (iso-C17:0 3-OH) and omega-9-*cis*-15-methylhexadecenoic acid (iso-C17:1ω9c) (Table 2). These fatty acid profiles were similar to those of the type strains of other *Chryseobacterium* species. However, strains PSD1-4^T and PHA3-4^T differed from each

Table 1. Distinctive phenotypic characteristics of strains PSD1-4^T and PHA3-4^T and species of the genus *Chryseobacterium*

Species: 1, *C. soldanellicola* (strain PSD1-4^T); 2, *C. taeanense* (strain PHA3-4^T); 3, *C. taichungense* (n=1); 4, *C. balustinum* (n=1); 5, *C. daecheongense* (n=1); 6, *C. defluvii* (n=1); 7, *C. formosense* (n=1); 8, *C. gleum* (n=2); 9, *C. indologenes* (n=7); 10, *C. indoltheticum* (n=1); 11, *C. joostei* (n=11); 12, *C. scopthalmum* (n=2). Data for reference species were taken from Kämpfer *et al.* (2003), Li *et al.* (2003), Hugo *et al.* (2003), Kim *et al.* (2005), Shen *et al.* (2005) and Young *et al.* (2005). +, All strains positive; w, weakly positive; –, all strains negative; v, variable; D, delayed; NA, no data available. All species hydrolyse aesculin.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12
Growth on/at:												
MacConkey agar	–	–	–	+	–	–	–	+	+	+	+	–
5 °C	+	+	–	D	–	–	–	–	–	+	+	D
37 °C	+	+	+	+	+	+	–	+	–	+	–	–
42 °C	–	–	–	–	–	+	–	–	–	–	–	–
Enzyme activities												
DNase	–	–	NA	+	NA	NA	NA	+	+	+	+	+
Urease	–	–	–	–	–	–	–	–	–	–	v	+
Nitrate reduction	–	–	–	+	+	–	–	+	–	–	–	–
Nitrite reduction	–	–	NA	–	–	+	NA	+	–	–	–	–
Tween 80 hydrolysis	–	+	NA	+	–	NA	–	+	+	+	+	+
Production of:												
Hydrogen sulphide	–	–	–	–	–	–	–	–	–	+	–	–
Indole	–	–	w	+	–	+	+	+	+	+	+	–
Acid production from:												
L-Arabinose	–	–	–	–	–	–	–	+	–	–	–	–
Fructose	–	–	NA	+	+	+	NA	+	+	–	+	–
Glycerol	–	–	NA	–	+	+	NA	+	+	–	v	–
Lactose	–	–	–	–	–	–	NA	–	–	–	–	–
Maltose	–	–	+	–	–	+	–	+	+	+	+	–
Mannitol	–	–	–	–	–	–	–	–	–	–	v	–
Trehalose	–	–	+	–	+	+	+	+	+	–	+	+
D-Xylose	–	–	+	–	+	–	w	+	–	–	–	–
G + C content (mol%)	28.8	32.1	NA	33.1	36.6	38.8	NA	38.0	38.5	33.8	36.8	34.2

Table 2. Fatty acid content (%) of strains PSD1-4^T and PHA3-4^T and species of the genus *Chryseobacterium*

Species: 1, *C. soldanellicola* (strain PSD1-4^T); 2, *C. taeanense* (strain PHA3-4^T); 3, *C. taichungense* (*n*=1); 4, *C. balustinum* (*n*=1); 5, *C. daecheongense* (*n*=1); 6, *C. defluvii* (*n*=1); 7, *C. formosense* (*n*=1); 8, *C. gleum* (*n*=5); 9, *C. indologenes* (*n*=45); 10, *C. indoltheticum* (*n*=1); 11, *C. joostei* (*n*=11); 12, *C. scophthalmum* (*n*=7). Data for reference species were taken from Kämpfer *et al.* (2003), Li *et al.* (2003), Hugo *et al.* (2003), Kim *et al.* (2005), Shen *et al.* (2005) and Young *et al.* (2005). tr, Trace (less than 1.0% of the total); ND, not detected.

Fatty acid	1	2	3	4	5	6	7	8	9	10	11	12
iso-C13:0	tr	tr	tr	tr	1.6	2.8	3.6	tr	tr	ND	tr	tr
Unknown 13:566	2.3	3.1	6.7	1.6	1.5	tr	tr	1.2±0.4	2.1±0.7	tr	1.1±0.2	3.3±0.5
iso-C15:0	41.8	36.1	35.4	32.3	51.2	58.5	52.2	35.4±2.9	34.3±4.9	29.5	34.6±2.0	34.9±0.5
iso-C15:03-OH	2.7	3.1	4.3	2.7	2.0	2.6	1.8	2.5±0.1	2.6±0.2	2.2	2.9±0.3	2.9±0.1
anteiso-C15:0	1.9	1.1	tr	tr	1.0	3.2	2.1	tr	tr	4.9	tr	tr
C16:0	1.4	1.8	1.3	1.6	1.8	1.3	1.5	1.3±0.4	tr	tr	tr	1.1±0.1
C16:0 3-OH	1.3	tr	2.6	1.4	tr	tr	tr	1.1±0.1	1.0±0.2	tr	1.2±0.2	1.3±0.1
iso-C16:0 3-OH	tr	tr	1.4	tr	tr	tr	1.1	ND	ND	1.2	ND	tr
Unknown 16:580	1.5	1.4	1.7	1.3	1.0	tr	1.0	1.7±0.1	1.7±0.2	1.3	1.6±0.1	1.7±0.2
C17:0 2-OH	tr	tr	ND	tr	ND	tr	ND	ND	ND	2.7	ND	tr
iso-C17:0	tr	1.1	tr	1.0	3.0	2.0	2.3	1.6±0.6	tr	tr	tr	1.1±0.1
iso-C17:0 3-OH	17.7	18.8	22.4	16.8	15.7	14.1	10.9	21.8±0.3	19.2±1.8	15.4	20.1±1.2	17.1±0.2
iso-C17:1 ω 9 <i>c</i>	14.6	15.8	8.9	27.1	7.6	4.8	4.3	20.2±3.9	24.2±3.1	24.6	22.9±1.9	21.3±0.4
C18:1 ω 5 <i>c</i>	tr	tr	ND	tr	ND	ND	ND	tr	tr	tr	tr	tr
Summed feature 4*	9.7	11.2	13.8	9.2	10.3	8.4	6.5	11.8±0.8	11.1±1.3	12.0	12.1±1.3	11.8±0.6
Summed feature 5*	tr	tr	ND	tr	ND	ND	ND	tr	tr	ND	tr	ND

*Summed feature 4 contains iso-C15:0 2-OH and/or C16:1 ω 7*d**t*. Summed feature 5 contains iso-C17:0 I and/or anteiso-C17:1 B.

other and from other *Chryseobacterium* species in relative abundance of shared components (Table 2).

The 16S rRNA gene sequences of strains PSD1-4^T (1426 nucleotides) and PHA3-4^T (1425 nucleotides) were determined as described previously (Han *et al.*, 2003). The resultant sequences were aligned manually, based on 16S rRNA secondary structure, with representative sequences of *Chryseobacterium* species obtained from the GenBank database. The phylogenetic tree based on the 16S rRNA gene sequences was inferred using the neighbour-joining method (Saitou & Nei, 1987). Evolutionary distance matrices for the neighbour-joining method were generated according to Kimura's 2-parameter distance model (Kimura, 1980). The resultant neighbour-joining tree topology was evaluated by bootstrap analysis (Felsenstein, 1985) based on 1000 re-sampled datasets. Alignment with representative sequences of *Chryseobacterium* and subsequent phylogenetic analyses were carried out using the PHYDIT program (jPHYDIT is available at <http://chunlab.snu.ac.kr/jphydit/>) as described previously (Han *et al.*, 2003).

The final set of sequence data consisted of 1402 nucleotide positions. Strains PSD1-4^T and PHA3-4^T shared 96.2% 16S rRNA gene sequence similarity. Strain PSD1-4^T shared between 95.2 and 97.2% similarity with other established *Chryseobacterium* species, among which *C. indoltheticum* ATCC 27950^T was the closest neighbour. The similarity values between strain PHA3-4^T and other type strains of

Chryseobacterium species were in the range 93.7–97.8%, *C. taichungense* CC-TWGS1-8^T being the closest neighbour. The close relationship between the two organisms was reflected by the 100% bootstrap support and the recovery of the same topology using other algorithms (Fig. 1). However, the phylogenetic tree and DNA–DNA relatedness data clearly indicated that each of the two strains forms a distinct phyletic lineage. The level of DNA–DNA relatedness was determined according to the procedure described by Lim *et al.* (2003) and the resultant data supported the separation between PSD1-4^T and *C. indoltheticum* ATCC 27950^T (23%), and also between PHA3-4^T and *C. taichungense* CC-TWGS1-8^T (25%), as the relatedness levels were well below the suggested cut-off value of 70% for species differentiation.

On the basis of the results of the phenotypic and genotypic study, it is evident that PSD1-4^T and PHA3-4^T should be placed in the genus *Chryseobacterium* as the type strains of two novel species, for which the names *Chryseobacterium soldanellicola* sp. nov. and *Chryseobacterium taeanense* sp. nov. are proposed.

Strains of *Chryseobacterium* were found to form the second largest group after *Pseudomonas* among the culturable microbial populations retrieved from the root and rhizosphere of sand-dune plants (Park *et al.*, 2005). Since little information is available on the possible roles of bacteria belonging to *Chryseobacterium* associated with plants

Fig. 1. Neighbour-joining tree based on nearly complete 16S rRNA gene sequences showing relationships among strains PSD1-4^T and PHA3-4^T and other species of the genus *Chryseobacterium*. The values above each branch indicate the percentage levels of bootstrap support (>50%) for the branch point based on 1000 resamplings. The asterisks indicate branches that were also recovered in the maximum-likelihood and maximum-parsimony trees. Bar, 0.01 substitutions per nucleotide position.

(Bernardet *et al.*, 2001; McSpadden Gardener & Weller, 2001), it is not easy to speculate on their ecological significance to the sand dune vegetation. More detailed studies on these bacteria will be necessary to elucidate their significance in that specific ecosystem.

Description of *Chryseobacterium soldanellicola* sp. nov.

Chryseobacterium soldanellicola (sol.da.nel'li.co.la. N.L. n. *soldanella* the species epithet of a plant belonging to the genus *Calystegia*; L. suff. verbal n. *cola* dweller; N.L. masc. n. *soldanellicola* dweller of *Calystegia soldanella*).

Cells are non-spore-forming rods. Gram-negative. Good growth is observed on R2A agar, TSA and nutrient agar at 25–30 °C. Grows at 5 °C, but not at 42 °C. No growth is observed on MacConkey agar. Colonies are yellowish, circular and shiny. The pH range for growth is pH 5–7 and that for optimal growth is pH 5. Growth occurs aerobically, but not anaerobically. Growth occurs in the presence of 0–4% (w/v) NaCl within 14 days. The most abundant cellular fatty acids are iso-C15:0 and iso-C17:0 3-OH. Indole, H₂S and acetoin are not produced. Nitrate and nitrite are not reduced. Positive for cytochrome oxidase but negative for arginine dihydrolase, lysine decarboxylase,

citrate utilization, tryptophan deaminase and urease. Capable of hydrolysing aesculin and gelatin. Weakly assimilates glucose, arabinose, mannose and maltose. The following compounds are utilized as sole carbon sources: α -cyclodextrin, dextrin, glycogen, Tween 40, L-arabinose (weakly), D-fructose, gentiobiose, α -D-glucose, maltose, D-mannose, L-rhamnose, D-trehalose, turanose, mono-methyl succinate, acetic acid, D-galacturonic acid, α -ketobutyric acid, α -ketovaleric acid, propionic acid, L-alanine, L-alanyl glycine, L-asparagine, L-aspartic acid, L-glutamic acid, glycyl L-glutamic acid, L-phenylalanine, L-proline, L-serine, L-threonine, 2,3-butanediol (weakly) and glycerol (weakly). The following compounds are not utilized: Tween 80, *N*-acetyl-D-galactosamine, *N*-acetyl-D-glucosamine, adonitol, D-arabitol, cellobiose, i-erythritol, L-fucose, D-galactose, *myo*-inositol, α -L-lactose, lactulose, mannitol, D-melibiose, methyl β -D-glucoside, D-psicose, D-raffinose, D-sorbitol, sucrose, xylitol, methyl pyruvate, *cis*-aconitic acid, citric acid, formic acid, D-galactonic acid lactone, D-gluconic acid, D-glucosaminic acid, D-glucuronic acid, α -, β - and γ -hydroxybutyric acid, *p*-hydroxyphenylacetic acid, itaconic acid, α -ketoglutaric acid, DL-lactic acid, malonic acid, quinic acid, D-saccharic acid, sebacic acid, succinic acid, bromo-succinic acid, succinamic acid, glucuronamide, alaninamide, D-alanine, glycyl L-aspartic acid, L-histidine, hydroxy-L-proline, L-leucine, L-ornithine, L-pyroglytamic acid, D-serine, DL-carnitine, γ -aminobutyric acid, urocanic acid, inosine, uridine, thymidine, phenylethylamine, putrescine, 2-aminoethanol, DL- α -glycerol phosphate, glucose 1-phosphate and glucose 6-phosphate. Results from API ZYM tests are given in Table 3. The G+C content is 28.8 mol%.

The type strain is PSD1-4^T (=KCTC 12382^T=NBRC 100864^T), which was isolated from the roots of *Calystegia soldanella* growing on a coastal area in Tae-an, Korea. The type strain displays antifungal activity against *Fusarium oxysporum*.

Description of *Chryseobacterium taeanense* sp. nov.

Chryseobacterium taeanense (tae.an.en'se. N.L. neut. adj. *taeanense* of Tae-an, a geographical region in Chungnam, Korea, where the type strain was isolated).

Cells are non-spore-forming rods. Gram-negative. Good growth is observed on R2A agar, TSA and nutrient agar at 25–30 °C. Grows at 5 °C, but not at 42 °C. No growth is observed on MacConkey agar. Colonies are yellowish, circular and shiny. The pH range for growth is pH 5–9 and that for optimal growth is pH 5. Growth occurs aerobically, but not anaerobically. Growth occurs in 0–6% (w/v) NaCl within 14 days. The most abundant cellular fatty acids are iso-C15:0 and iso-C17:0 3-OH. Indole, H₂S and acetoin are not produced. Nitrate and nitrite are not reduced. Positive for cytochrome oxidase but negative for arginine dihydrolase, lysine decarboxylase, citrate utilization, tryptophan deaminase and urease. Capable of hydrolysing

Table 3. API ZYM profiles of strains PSD1-4^T and PHA3-4^T and other species of the genus *Chryseobacterium*

Species: 1, *C. soldanellicola* (strain PSD1-4^T); 2, *C. taeanense* (strain PHA3-4^T); 3, *C. taichungense*; 4, *C. balustinum*; 5, *C. daecheongense*; 6, *C. defluvi*; 7, *C. formosense*; 8, *C. gleum*; 9, *C. indologenes*; 10, *C. indoltheticum*; 11, *C. joostei*; 12, *C. scopthalmum*. All species showed positive reactions for 2-naphthyl phosphate, 2-naphthyl caprylate, L-leucyl 2-naphthylamide, L-valyl 2-naphthylamide, 2-naphthyl phosphate and naphthol-AS-BI-phosphate and showed negative reactions for 6-Br-2-naphthyl α -D-mannopyranoside. Data for strains PSD1-4^T and PHA3-4^T and *C. taichungense* were obtained in this study; those for other reference species were taken from Hugo *et al.* (2003), Kim *et al.* (2005) and Young *et al.* (2005). The intensity of the developed colour was measured on scale from 0 to 5 and interpreted as negative (–) when values ranged between 0 and 1 and positive (+) for values between 2 and 5 (Mudarris *et al.*, 1994).

Substrate	1	2	3	4	5	6	7	8	9	10	11	12
2-Naphthyl butyrate	+	+	+	–	–	–	+	–	–	–	–	+
2-Naphthyl myristate	–	–	+	–	–	–	–	–	–	–	–	–
L-Cystyl 2-naphthylamide	–	–	+	–	–	–	+	–	+	+	+	+
N-Benzoyl-DL-arginine 2-naphthylamide	–	–	+	–	–	–	+	–	–	–	+	+
N-Glutaryl-phenylalanine 2-naphthylamide	–	–	+	–	+	+	–	–	+	–	–	–
6-Br-2-Naphthyl α -D-galactopyranoside	–	–	–	–	–	–	–	–	–	–	–	–
2-Naphthyl β -D-galactopyranoside	–	–	w*	–	–	–	–	–	–	–	–	–
Naphthol-AS-BI β -D-glucuronide	–	–	+	–	–	–	–	–	–	–	–	–
2-Naphthyl α -D-glucopyranoside	+	+	+	+	–	+	–	+	+	+	+	+
6-Br-2-Naphthyl β -D-glucopyranoside	–	+	+	+	–	–	+	+	–	–	–	–
1-Naphthyl-N-acetyl β -D-glucosaminide	–	–	+	+	+	+	+	+	+	+	+	+
2-Naphthyl α -L-fucopyranoside	–	–	–	–	–	–	–	–	–	–	–	–

*Weakly positive.

ausculin and gelatin. Weakly assimilates glucose, arabinose, mannose and maltose. The following compounds are utilized as sole carbon sources: α -cyclodextrin, dextrin, glycogen, Tween 40, Tween 80, L-arabinose, cellobiose, D-fructose, L-fucose, D-galactose, gentiobiose, α -D-glucose, *myo*-inositol, α -D-lactose, lactulose, maltose, mannitol (weakly), D-mannose, methyl β -D-glucoside, D-psicose, D-raffinose, L-rhamnose, D-sorbitol, sucrose, D-trehalose, turanose, xylitol, methyl pyruvate, monomethyl succinate, *cis*-aconitic acid, citric acid, formic acid, D-galactonic acid lactone, D-galacturonic acid, D-gluconic acid, D-glucosaminic acid, D-glucuronic acid, α -hydroxybutyric acid, β -hydroxybutyric acid (weakly), itaconic acid, α -ketobutyric acid, α -ketoglutaric acid, α -ketovaleric acid, DL-lactic acid, malonic acid, propionic acid, quinic acid, D-saccharic acid, sebacic acid, succinamic acid, glucuronamide, alaninamide, L-alanine, L-alanyl glycine, L-asparagine, L-aspartic acid, L-glutamic acid, glycyl L-aspartic acid, glycyl L-glutamic acid, hydroxy-L-proline (weakly), L-leucine, L-ornithine, L-phenylalanine, L-proline, L-pyroglyutamic acid, L-serine, L-threonine, DL-carnitine, inosine (weakly) and uridine (weakly). The following compounds are not utilized; N-acetyl-D-galactosamine, N-acetyl-D-glucosamine, adonitol, D-arabitol, *i*-erythritol, D-melibiose, acetic acid, γ -hydroxybutyric acid, *p*-hydroxyphenylacetic acid, succinic acid, bromosuccinic acid, D-alanine, L-histidine, D-serine, γ -aminobutyric acid, urocanic acid, thymidine, phenylethylamine, putrescine, 2-aminoethanol, 2,3-butanediol, glycerol, DL- α -glycerol phosphate, glucose 1-phosphate and glucose 6-phosphate. Results from API ZYM tests are given in Table 3. The G + C content is 32.1 mol%.

The type strain is PHA3-4^T (=KCTC 12381^T=NBRC 100863^T), which was isolated from the roots of *Elymus mollis* growing on a coastal area in Tae-an, Korea.

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