Taxonomic description

***Kibdelosporangium persicum* sp. nov., a new member of the Actinomycetes from a hot desert in Iran**

Nasim Safaei^a, Imen Nouioui^b, Yvonne Mast^{b,c}, Nestor Zaburannyi^{d,e}, Manfred Rohde^f, Peter Schumann^b, Rolf Müller^{d,e}, Joachim Wink^{a,e*}

^aMicrobial Strain Collection, Helmholtz Centre for Infection Research, Inhoffenstrasse 7, D-38124 Braunschweig, Germany

^bLeibniz Institute DSMZ, Braunschweig, Inhoffenstrasse 7B, D-38124 Braunschweig, Germany

^cGerman Center for Infection Research (DZIF), Partner Site Tübingen, Germany

^dDepartment of Microbial Natural Products, Helmholtz Institute for Pharmaceutical Research Saarland, Helmholtz Centre for Infection Research and Department of Pharmacy at Saarland University, D-66041 Saarbrücken, Germany

^eGerman Center for Infection Research (DZIF), Partner Site Hannover-Braunschweig, Braunschweig, Germany

^fCentral Facility for Microscopy, Helmholtz Centre for Infection Research, Inhoffenstrasse 7, D-38124 Braunschweig, Germany

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* Corresponding author. Tel.: +49-531-6181-4223; fax: +49-531-6181-9499; e-mail: joachim.wink@helmholtz-hzi.de

*Corresponding author.

Mailing Address: Helmholtz Centre for Infection Research, Inhoffenstrasse 7, 38124
Braunschweig, Germany

Phone: +4953161814223

E-mail address Joachim.Wink@helmholtz-hzi.de

The GenBank/EMBL/DDBJ accession number of the 16S rRNA gene sequence of strain NCCB 100701 = CIP 111705 = DSM 110728 is MN947980. The Whole Genome Shotgun project has been deposited at GenBank/ENA/DDBJ under the accession JAAATY000000000 and BioSample SAMN13056085. The version described in this paper is version JAAATY010000000.

ABSTRACT

Isolate 4NS15^T was isolated from a neglected arid habitat of Kerman, Iran. The strain showed 16S rRNA gene sequence similarity values of 98.9% with the type strains of *Kibdelosporangium aridum* subsp. *aridum*, *Kibdelosporangium phytohabitans*, *Kibdelosporangium philippinense* and 98.6% with the type strain *K. aridum* subsp. *largum*, respectively. Genome-based phylogenetic analysis revealed that isolate 4NS15^T is closely related to *Kibdelosporangium aridum* subsp. *aridum* DSM 43828^T. The digital DNA-DNA hybridization (dDDH) value among the genome sequences of 4NS15^T and strain DSM 43828^T is 29.8%. Strain 4NS15^T produces long chains of spores without sporangium-like structure which can be distinguished from other *Kibdelosporangium* species. Isolate 4NS15^T has a genome size of 10.35 Mbp with a G+C content of 68.1 mol %. Whole cell hydrolysates of isolate 4NS15^T are rich in meso-diaminopimelic acid and cell wall sugars such as arabinose, galactose,

glucose and ribose. Major fatty acids (>10%) are C_{16:0}, *iso*-C_{16:0} and *iso*-C_{15:0}. The phospholipid profile contains diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylhydroxyethanolamine, aminolipid, glycoaminolipid and the predominant menaquinone is MK-9(H₄). Based on the phenotypic and genotypic characteristics, isolate 4NS15^T (NCCB 100701 = CIP 111705 = DSM 110728) merits the recognition as a novel species of the genus *Kibdelosporangium*, for which the name *Kibdelosporangium persicum* sp. nov. is proposed.

Dramatic reduction in discovery of new anti-microbial compounds has led researchers to search for rare antibiotic-producing species from unexplored habitats like deserts [1]. Deserts are neglected ecosystems that await further investigation especially regarding the isolation of rare actinomycetes [2]. Rare actinomycetes are referred to as strains that have a less isolation rate due to different isolation methods and difficult conditions in terms of cultivation and maintenance [3]. The genus *Kibdelosporangium*, belonging to the family *Pseudonocardiaceae* and the order *Pseudonocardiales* [11], is considered as a rare genus as reported by Jose and Jebakumar [4]. This taxon encompasses nine validly published species with *Kibdelosporangium aridum* subsp. *aridum* DSM 43828^T as the type species [11]. The only species isolated from arid habitats are *K. aridum* subsp. *aridum* DSM 43828^T and *K. aridum* subsp. *largum* DSM 44150^T, others have mostly been isolated from rhizosphere of plants [5].

Members of the genus *Kibdelosporangium* grow aerobically and are catalase-positive and oxidase-negative. The cell-wall peptidoglycan contains *meso*-diaminopimelic acid, whereas mycolic acids are not present. Whole-cell sugar pattern consists of arabinose and D-galactose, with traces of madurose [6]. The phospholipid profile contains diphosphatidylglycerol, phosphatidylethanolamine,

phosphatidylinositol, phosphatidylinositol mannosides, and phosphatidylmethylethanolamine [6]. A typical characteristic of this genus is that the aerial mycelium forms long spore chains and sporangium-like structures (pseudosporangia) [6], which are also found in other actinobacteria, such as *Amycolatopsis* and *Actinoplanes* [7]. Members of the genus *Kibdelosporangium*, like *Kibdelosporangium aridum* subsp. *largum* and *Kibdelosporangium philippinense*, were found to produce antibiotics such as aridicins A [8], B, and C [9] and kibdelins A, B [10], C, and D [11], respectively.

A polyphasic taxonomic study was performed with strain 4NS15^T, which was isolated from a desert soil sample of Kerman, Iran. In this paper we describe strain 4NS15^T, which based on its phenotypic and genotypic characteristics, is a novel species with the proposed name *Kibdelosporangium persicum* sp. nov.

Isolation and maintenance

Strain 4NS15^T was recovered from a soil sample collected in the path to the shahdad desert in Kerman, which is located in the Southeast of Iran (1759 m above sea level). 4NS15^T was isolated using the dilution plate technique [12] after 15 days of incubation at 30 °C. The medium used for isolation was 5336 agar (10 % soluble starch, 1 % casein, 0.5 % K₂HPO₄, 5 % MgSO₄·7H₂O) supplemented with 1 % cycloheximide [13]. The selected colonies were transferred to glucose-yeast-malt extract medium (GYM; DSMZ medium 65). Pure isolates were maintained as bacterial suspension in 50 % glycerol (v/v) at -80 °C for long-term storage.

Strain 4NS15^T together with its closest relatives, *Kibdelosporangium philippinense* DSM 44226^T, *Kibdelosporangium phytohabitans* DSM 104448^T and *Kibdelosporangium aridum* subsp. *aridum* DSM 43828^T were subject of phenotypic

and chemotaxonomic analyses. The selection of the reference strains was based on the high 16S rRNA gene sequence similarity value of 98.9% between the studied isolate and the strains cited above. The three type strains were obtained from the German collection of microorganisms and cell cultures (DSMZ).

Phylogeny

Genomic DNA was obtained from strain 4NS15^T for phylogenetic analysis. For this purpose, 4NS15^T was grown in liquid GYM medium for 5 days at 30 °C. Genomic DNA was isolated with the Invisorb Spin Plant Mini Kit (250) (Stratec Molecular, Germany) following the protocol provided by the manufacturer.

For 16S rRNA sequence analysis, amplification of the 16S rRNA gene was performed by PCR using genomic DNA of 4NS15^T as a template together with the primers 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and 1492R (5'-GGTTACCTTGTTACGACTT-3'). Primers used for sequencing were F1100 (5'-CAACGAGCGCAACCC-3'), R1100 (5'-GGGTTGCGCTCGTTG-3') and R518 (5'-CGTATTACCGCGGCTGCTGG-3') and verified amplification of almost a full-length 16S rRNA product (1459 bp). The acquired sequences were assembled using the program Bioedit (version 7.2.6) [14]. The 16S rRNA gene sequence was compared with the EzTaxon database (www.ezbiocloud.net/) [15]. Strain 4NS15^T showed 16S rRNA gene sequence similarity of 98.9% to the type strains of *K. aridum* subsp. *aridum*, *K. phytohabitans*, *K. philippinense* and 98.6% to *K. aridum* subsp. *largum*. Pairwise 16S rRNA gene sequence similarities as well as the maximum-likelihood (ML) and maximum-parsimony (MP) trees were carried out using the DSMZ phylogenomic pipeline of the Genome to Genome distance calculator server [16] available at <http://ggdc.dsmz.de/>. Muscle [17], RAxML [18] and TNT [19] were used

for multiple sequence alignment, ML and MP phylogenies, respectively. Rapid bootstrapping and AutoMRE bootstrapping criterion [20] were used for ML tree while tree-bisection-and-reconnection branch swapping and ten random sequence addition replicates were used for MP analysis. The X2 test implemented in PAUP was used for the compositional bias sequence check (Fig. 1) [21]. Phylogenomic analysis was performed using the TYGS server (<https://tygs.dsmz.de/>) [22].

Based on 16S rRNA gene phylogenetic tree, strain 4NS15^T appears in a poorly supported distinct branch closely related to the sub-clade housing *K. metalli* KC226^T and *K. philippinense* DSM 44226^T and distant from *K. aridum* subsp. *aridum* DSM 43828^T, *K. aridum* subsp. *largum* DSM 44150^T and *K. phytohabitans* KLBMP jh1111^T (Fig. 1). These results are not in line with the pairwise 16S rRNA gene sequence similarity. For this reason, whole-genome-based-phylogeny was constructed and in which the studied strain forms a well-supported sub-clade with *K. aridum* subsp. *aridum* DSM 43828^T, which locates next to the branch of the *K. phytohabitans* DSM 104448^T species (Fig. 2).

Genome Features

Genomic DNA for whole genome sequencing was extracted following the protocol described by Jin *et al.*, [23] and sequenced using the Illumina MiSeq platform in paired-end 300 bp mode generating 3.988.152 quality filtered reads. Assembly of reads was performed with the abyss-pe 2.0.2 software [21] yielding 89 contigs above cut-off value of 1000 bp with a total sequence length of 10.35 Mbp. Sequence annotation was carried out with ProSnap (<https://prosnap.helmholtz-hzi.de>) 8679 putative coding sequences, 4 x 16S-23S-5S rRNA gene clusters, 62 tRNA genes and a single tmRNA gene have been identified. In order to estimate the biosynthetic potential of 4NS15^T, the genome sequence was submitted for

analysis by antiSMASH 5.0 [24]. A total of 46 biosynthetic gene clusters (BGCs) were found. With the exception of a terpene-class BGC and an ectoine-class BGC both with highly similar hits to known BGCs, most of remaining 44 biosynthetic gene clusters had none-to-modest similarity to BGCs producing known compounds (Table S1), hinting at an interesting biosynthetic potential of 4NS15^T. It has been proposed indeed that isolates from dry or similar habitats are more likely to deliver interesting and novel biosynthetic scaffolds [25, 26]. However, great care should be taken while evaluating these preliminary results from a draft genome of 4NS15^T, as the majority of BGCs were found at contig edges (Table S1, rows marked in dark grey) and are likely to be merged or otherwise rearranged upon genome completion.

The digital DNA-DNA hybridization (dDDH) values between the genome sequences of strain 4NS15^T and its close phylogenetic neighbours *K. aridum* subsp. *aridum* DSM 43828^T (FWXV000000000) and *K. phytohabitans* KLBMP 1111^T (NZ_CP012752.1) were calculated using the Genome-to-Genome Distance Calculator GGDC 2.1 (<http://ggdc.dsmz.de>) [27] and the recommended formula 2. The dDDH values between strain 4NS15^T and strains DSM 43828^T and KLBMP 1111^T were 29.8% and 27.6%, respectively; values well below the threshold of 70% (dDDH) commonly used for species delineation [28]. The genome sequence of the type strain of *K. philippinense* is not publicly available but its absence does not affect the assignment of the studied strain to a new species. The type strain of *K. philippinense* and isolate 4NS15^T showed 16S rRNA gene sequence similarity value below the Actinobacteria-specific threshold of 99.0 % suggested as cut-off value for which DNA–DNA hybridization experiments were not required [27].

Strain 4NS15^T and its closest phylogenetic relative *K. aridum* subsp. *aridum* have a genome size of 10.35 Mbp and 12.28 Mbp with a G+C content of 68.1 and 66.2, respectively. The calculated difference of the *in silico* G+C content between the two studied genomes was 2.0%, which is above the 1.0% of variation in the G+C content within bacterial species [29].

Physiology and Chemotaxonomy

Morphological and physiological characteristics of 4NS15^T and *K. philippinense* DSM 44226^T, *K. phytohabitans* DSM 104448^T and *K. aridum* subsp. *aridum* DSM 43828^T were determined after 14 days of incubation at 30 °C on International *Streptomyces* Project (ISP) media [30]. Different solid media were used for cell growth, which were yeast extract–malt extract agar (ISP2), oatmeal agar (ISP3), inorganic salt starch agar (ISP4), glycerol–asparagine agar (ISP5), peptone–yeast extract iron agar (ISP6) and tyrosine agar (ISP7). The colour of the culture was determined by comparison with (RAL colour code 1005; Deutsches Institut für Gütesicherung und Kennzeichnung e. V. – Reichs-Ausschuss für Lieferbedingungen). Good growth was observed on GYM, ISP2 and ISP7 media for the four strains mentioned above. Substrate mycelium of isolate 4NS15^T was black red (RAL3007) and others were pale yellow. All had moderate growth on ISP4 media except *K. aridum* subsp. *aridum* DSM 43828^T. 4NS15^T grew poorly on ISP3 and ISP5 agar with brown beige colonies (RAL 1011), whereas other type strains showed moderate growth on ISP3 and ISP5 agar. Except *K. aridum* subsp. *aridum*, other type strains produced aerial mycelia on ISP2 and ISP7 agar (Fig. S1).

For scanning electron microscopic analysis, a section of the ISP2 plate containing a bacterial lawn after 14 days of incubation at 30°C was fixed in 5 % aqueous

glutaraldehyde. After two times washing with TE buffer (10 mM TRIS, 1 mM EDTA, pH 6.9), it was dehydrated with a graded series of acetone (10, 30, 50, 70, 90, 100 %). Each step for 15 min on ice. After drying samples with liquid CO₂ (Bal-Tec CPD 030, Liechtenstein), the samples were sputter-coated with gold/palladium (Bal-Tec SCD 500) and subsequently examined in a Zeiss Merlin field emission scanning electron microscope at an acceleration voltage of 5 kV applying the HE-SE-detector and the inlens-SE-detector in a 75:25 ratio. Images were recorded with SmartSEM software version 6.06. Long chains of spores were found under the scanning electron microscope but no sporangium-like structures were detected (Fig. 3).

The pH range of 5.0 to 10.0 (intervals of 1 pH unit) and four temperatures of 20, 30, 35 and 40 °C were determined on GYM agar by incubation at 30 °C for 1 week. Optimum growth was observed on GYM with pH 7.5 and at 35 °C. Salt tolerance of 0, 2.5, 5, 7 and 10 % was tested after 7 days of incubation at 30 °C. 4NS15^T, *K. philippinense* and *K. aridum* subsp. *aridum* tolerated 2.5 % and *K. phytohabitans* 5% of NaCl concentration. The enzyme activities and utilization of carbohydrates were determined and compared under identical test conditions with API-ZYM and API-Coryne test strips (bioMerieux). Differences in the phenotypic features and enzyme activities of analysed strains are shown in Table 1. 4NS15^T differed from *K. aridum* subsp. *aridum*, *K. philippinense* and *K. phytohabitans* in N-acetyl-β-glucosaminidase, α-mannosidase and urease activities. Urease activity, esculin and nitrate reduction for strain 4NS15^T were negative. Gelatin liquefaction and melanin production were positive. *K. aridum* subsp. *aridum* and 4NS15^T were able to utilize different carbon sources in comparison to *K. philippinense* and *K. phytohabitans*. D-arabinose, xylose, rhamnose and mannose were utilized as sole carbon sources for strain 4NS15^T, whereas D-raffinose and cellulose were not used as a carbon source. The

differences were the ability of *K. aridum* subsp. *aridum* in cellulose and D-raffinose utilization (Table 1).

MALDI-TOF/MS analyses were performed with 4NS15^T, *K. philippinense* DSM 44226^T, *K. phytohabitans* DSM 104448^T and *K. aridum* subsp. *aridum* DSM 43828^T applying the following processing steps. The sample preparation was done by ethanol/formic acid extraction as described in Protocol 3 of Schumann & Maier (2014) [31]: About 10 mg of biomass from a liquid culture (cultivated in the complex medium GYM at 30 °C for 7 days) was suspended in 300 µl H₂O and homogenised carefully. 900 µl ethanol were added to the resulting suspension. The cells were collected after a centrifugation step and re-suspended in 50 µl of 70 % formic acid. After the addition of 50 µl of acetonitrile, the suspension was mixed and centrifuged. The supernatant was removed and aliquots of 1.5 µl were placed on each spot of a stainless-steel target plate. After air drying 1.5 µl of matrix solution (saturated solution of α-cyano-hydroxy-cinnaminic acid in 50 % aqueous acetonitrile containing 2.5 % trifluoro acetic acid) was added to each spot. Mass spectrometric analysis was conducted using a MALDI Biotyper smart System GP (Bruker Daltonics) with a N2 laser unit. The spectra were recorded in linear positive mode and the acceleration voltage was 20 kV. In sum a spectrum was collected out of 240 shots across a spot. To analyse the data, a mass range of 2000-20000 m/z was observed. For internal calibration the Bacterial Test Standard #255343 (Bruker Daltonics) was used. Using the Flex Analysis software (version 3.4, Bruker Daltonics), the MALDI-TOF MS spectra were smoothed, baseline corrected and re-calibrated. A score-orientated dendrogram was calculated by using the BioTyper Compass Explorer software (version 4.1, Bruker Daltonics). The MALDI-TOF MS analyses yielded a dendrogram with three different clusters from which strain 4NS15^T represents its own branch that

is closely related to the type strain of *K. aridum* DSM 43828^T (threshold 800) (Fig. S2).

Freeze dried cells for chemotaxonomic analyses of polar lipids, fatty acid, cell-wall quinones, sugars and amino acids were obtained from biomass. The biomass was obtained from cells that were cultivated at 30° C in GYM liquid culture after 7 days. The culture was centrifuged (9000 r.p.m., 5min) and harvested cells were washed three times with sterile distilled water before lyophilization.

The polar lipids were extracted applying the method of Minnikin *et al.*, [32] and were identified by two-dimensional thin-layer chromatography (2D-TLC). The quinone system determined by extraction according to the method described from Collins *et al.*, [33] and analysed by HPLC [34]. Cell-wall amino acids and sugars analysis was carried out following the method of Hasegawa *et al.*, [35]. The polar lipid profile of 4NS15^T is composed of diphosphatidylglycerol (DPG), phosphatidylethanolamine (PE), phosphatidylhydroxyethanolamine (PE-OH), followed by aminolipid (AL), glycoaminolipid (GAL) and glycolipid (GL) (Fig. S3) while its close neighbour *K. aridum* SK&F-AAD-216^T has phosphatidylinositol (PI), phosphatidylinositol mannosides (PIM) together with PE, PME and DPG [8]. The polar lipids patterns of *K. phytohabitans* KLBMP 1111^T and *K. philippinense* A80407^T are phospholipids type PII with minor variation with the studied strain as shown in Table 1. The quinone system of strain 4NS15^T consists of MK-9(H₄) (75%) and MK-9(H₂) (25%). The cell-wall peptidoglycan contained *meso*-diaminopimelic acid and the whole-cell sugars comprised arabinose, D-galactose, glucose and ribose. However, strain SK&F-AAD-216^T has arabinose, D-galactose and traces of madurose [8]. The whole cell sugars profiles of strain KLBMP 1111^T consisted of arabinose and galactose while strain A80407^T had in addition glucose, mannose and ribose (Table 1).

The cellular fatty acids were extracted, methylated and analysed by gas chromatography according to standard protocol (method RTSBA6) from Sherlock microbial identification software system version 6.2B [36]. The major fatty acids (>10%) of strain 4NS15^T and three tested type strains *K. philippinense* DSM 44226^T, *K. phytohabitans* DSM 104448^T and *K. aridum* subsp. *aridum* DSM 43828^T were similar in possessing *iso*-C_{15:0} and *iso*-C_{16:0}, whereas 4NS15^T differentiated from others by containing C_{16:0} (25.6 %) as major cellular fatty acid (Table S2).

The results of the phenotypic, chemotaxonomic and phylogenetic analyses indicate that strain 4NS15^T belongs to the genus *Kibdelosporangium*. 16S rRNA gene analysis showed similarity value of 98.9% to the three type strains of *K. aridum* subsp. *aridum*, *K. phytohabitans*, *K. philippinense*, but phylogenetic relationships based on whole genome sequence data and dDDH indicated that the most closely related type strain to isolate 4NS15^T is *K. aridum* subsp. *aridum* DSM 43823^T. The calculated digital DNA-DNA hybridization (dDDH) value between the two strains 4NS15^T and DSM 43828^T is 29.8% which is below the threshold of 70% used for species delineation. MALDI-TOF results confirmed *K. aridum* as most closely related species. Furthermore, 4NS15^T and strain *K. aridum* DSM 43823^T differed in their major fatty acid composition, carbohydrate utilization and physiological characteristics. This is the first report of new species of *Kibdelosporangium* without sporangium-like structure. Based on these results, strain 4NS15^T represents a new species and the name *Kibdelosporangium persicum* sp. nov. is proposed.

Description of *Kibdelosporangium persicum* sp. nov.

Kibdelosporangium persicum (per'si.cum. L. neut. n. *persicum* from Persia, classical name of Iran, where the organism was isolated).

Aerobic, Gram-stain-positive, non-motile, forming branched substrate mycelium, without sporangium-like (pseudosporangia) structures. The black red substrate mycelium and oxide red diffusible pigments are produced on GYM, ISP2 and ISP7. Optimal growth was observed on GYM at temperature 35 °C, pH 7.5 and in presence of NaCl concentration up to 2.5 % (w/v). Urease activity, esculin and nitrate reduction are negative. Gelatin liquefaction and melanin production are positive. D-arabinose, xylose, rhamnose and mannose are utilized as sole carbon sources, whereas D-raffinose and cellulose are not used as a carbon source. The cell wall contains *meso*-diaminopimelic acid and the whole-cell sugars are arabinose, galactose, glucose and ribose. The quinone pattern consists of major MK-9(H₄) (75%) and minor amounts of MK-9(H₂) (25%). The present phospholipids are diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylhydroxyethanolamine, aminolipid, glycoaminolipid and glycolipid. Major cellular fatty acids pattern (>10%) are C_{16:0}, *iso*-C_{16:0} and *iso*-C_{15:0}.

The type strain 4NS15^T (NCCB 100701 = CIP 111705 = DSM 110728), was isolated from a desert soil sample in Kerman, Iran. The whole genome shotgun sequence of the type strain has a size of 10.35 Mbp with DNA G+C content of 68.1 mol % and has been deposited at DDBJ/ENA/GenBank under the accession JAAATY000000000. The GenBank accession number for the 16S rRNA gene sequences of strain 4NS15^T is MN947980.

The type strain is 4NS15^T (NCCB 100701 = CIP 111705 = DSM 110728).

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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Fig. 1. Maximum-likelihood phylogenetic tree based on nearly complete 16S rRNA gene sequence of 4NS15^T and most related species using the GTR+GAMMA model. The numbers above the branches are bootstrap support values greater than 60% for maximum-likelihood (left) and maximum-parsimony (right). Bar, 0.01

Fig. 2. Whole-genome sequence tree generated with the TYGS web server for strain 4NS15^T and closely related species. Tree inferred with FastME from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d_5 . The numbers above branches are GBDP pseudo-bootstrap support values >60% from 100 replications, with an average branch support of 84.4%. The tree was rooted at the midpoint.

Fig. 3. Scanning electron micrographs of 4NS15^T. Cultivation was carried out on ISP2 medium at 30°C for 14 days. a) scale 10 μm, b) scale 2 μm.

Table 1. Physiological properties of isolate 4NS15^T; *K. aridum* subsp. *aridum* DSM 43828^T; *K. philippinense* DSM 44226^T; *K. phytohabitans* DSM 104448^T.

Characteristic	4NS15 ^T	DSM 43828 ^T <i>K. aridum</i>	DSM 44226 ^T <i>K. philippinense</i>	DSM 104448 ^T <i>K. phytohabitans</i>
Diffusible pigment on GYM	+	-	-	-
Formation of aerial mycelia on ISP 2	+	-	+	(+)
NaCl tolerance	2.50%	2.50%	2.50%	5%
Enzymatic activities:				
Naphthol-AS-BI-phosphohydrolase	+	-	+	+
β-Galactosidase	+	+	+	-
α-Glucosidase	+	-	+	+
N-acetyl-β-Glucosaminidase	-	+	+	+
α-Mannosidase	-	+	+	+
Pyrrolidonyl arylamidase	+	+	+	-
Urease	-	+	+	+
Utilization of carbon source:				
D-Arabinose	+	+	-	-
Xylose	+	+	-	+
Cellulose	-	+	-	-
Mannose	+	+	+	-
D-Rhamnose	+	+	-	+
D-Raffinose	-	+	-	-
GC content %	68.1	66.2	-	68.4
Fatty acid profile	C16:0, <i>iso</i> -C16:0, <i>iso</i> -C15:0	<i>iso</i> -C16:0	<i>iso</i> -C16:0, <i>iso</i> -C15:0, c/t C16:1ω7	<i>iso</i> -C16:0
Phospholipid profile	PE, PE-OH, DPG,	PE, PME, DPG, PI,	PE, PI, DPG, PIM ^[37, 38]	PE, PME, PG, PI, PL ^[39]

	AL, GAL, L	PIM ^[8]		
Menaquinone patterns	MK-9(H ₄) and MK- 9(H ₂)	-	-	MK-9(H ₄)
Cell wall sugars	arabinose, D- galactose, glucose and ribose	arabinose, D-galactose and traces of madurose	galactose, glucose, mannose, arabinose, and ribose	arabinose, galactose

Note: + Positive or present; (+) weakly positive; - negative or absent. All the data were obtained from this study under identical growth conditions