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ORIGINAL PAPER

# *Kribbella sindirgiensis* sp. nov. isolated from soil

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**Abstract** A *Kribbella* strain FSN23$^T$ was isolated from soil sample which was collected from Caygoren Dam lakeside located in Sındırgı, Turkey. The isolate was investigated using a polyphasic approach consisting of numeric, chemotaxonomic and molecular analysis. The isolate indicated chemotaxonomic, morphological and phylogenetic properties associated with members of the genus *Kribbella*. Phylogenetic analysis based on the 16S rRNA sequence of the strain demonstrated that the strain forms a subclade with *K. aluminosa* HKI 0478$^T$ and *K. jejuensis* HD9$^T$. The organism formed an extensively branched substrate and aerial hyphae which generated spiral chains of spores with smooth surfaces. The cell wall contained LL-diaminopimelic acid, and the whole cell sugars were glucose and ribose along with trace amounts of mannose. The polar lipids were identified as phosphatidylglycerol, diphosphatidylglycerol, four unidentified lipids and five unidentified polar lipids. The predominant menaquinone was MK-9($H_4$). The major cellular fatty acids were anteiso-$C_{15:0}$ and iso-$C_{16:0}$. Polyphasic taxonomy properties confirm that strain FSN23$^T$ represents a novel *Kribbella* taxon distinguished from closely related type strains. Hence, strain FSN23$^T$ (=KCTC 29220$^T$ = DSM 27082$^T$) is proposed as the type strain of a novel species with the name *Kribbella sindirgiensis* sp. nov.

**Keywords** *Kribbella sindirgiensis* · *Nocardioidaceae* · Polyphasic taxonomy · 16S rRNA gene

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The Digital Protologue database Taxon Number for strain FSN23$^T$ is TA00120. The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA, *gyr*B, *rpo*B, *rec*A, *rel*A and *atp*D gene sequences of *Kribbella sindirgiensis* FSN23$^T$ (=KCTC 29220$^T$ = DSM 27082$^T$) are JN896614, KY581282, KY594014, KY594012, KY594013 and KY594011, respectively.

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## Introduction

The genus *Kribbella* is a member of the *Nocardioidaceae* family (Park et al. 1999) which was characterized by the presence of LL-diaminopimelic acid in the peptidoglycan (wall chemotype I sensu, Lechevalier and Lechevalier

1970). *Kribbella* genus comprises species mainly isolated from soil and different habitats from catacombs, medieval alum slate mine and plant rhizosphere. Members of the genus *Kribbella* contain Gram-type-positive or Gram-type-variable, non-motile, nocardioform actinomycetes that form an extensively branched vegetative mycelium and aerial hyphae fragmented into short elongated rod-like or coccoid elements. The members of the genus are designated by the presence of predominant fatty acids of anteiso-$C_{15:0}$, iso-$C_{16:0}$ and iso-$C_{14:0}$. MK-9($H_4$) is the main menaquinone and phosphatidylcholine is the indicative polar lipid (Park et al. 1999; Yoon and Park 2006). Lately, the genus *Kribbella* currently comprises 23 validly named species (Euzéby 2012).

In the present study, the polyphasic taxonomy of an aerobic actinomycete FSN23$^T$ strain isolated from soil was performed. The strain FSN23$^T$ is determined as a novel species of the genus *Kribbella*.

## Materials and methods

### Isolation of bacterial strain

Soil sample was collected from Caygoren Dam lakeside, Sındırgı (GPS coordinates for the sampling site are 39°14′49.40″N and 28°12′40.99″E), Turkey and air-dried at room temperature for 14 days and suspended in ¼ strength Ringer's solution (Oxoid) to prepare $10^{-1}$ dilution. The suspension was heated at 55 °C for 15 min and the prepared $10^{-1}$ dilutions were serially diluted down to $10^{-4}$. The diluted soil suspension (200 µl) was inoculated on tryptone–yeast extract–glucose agar (TYG) supplemented with filter-sterilized cycloheximide (50 µg ml$^{-1}$), nalidixic acid (10 µg ml$^{-1}$) and rifampicin (0.5 µg ml$^{-1}$), the medium was incubated at 28 °C for 21 days. After incubation, three colonies of the same kind belonging to strain FSN23$^T$ were picked randomly from the plates and then transferred and purified on yeast extract–malt extract agar [International Streptomyces Project medium 2 (ISP 2)] (Shirling and Gottlieb 1966) and held into glycerol suspensions (20%, v/v) at −80 °C.

### 16S rRNA, *gyr*B, *rpo*B, *rec*A, *rel*A and *atp*D gene sequence and phylogenetic analyses

Genomic DNA was extracted from biomass in tryptone–yeast extract–glucose broth via shaking incubator at 28 °C for 14 days. The details of the method were described elsewhere (Everest and Meyers 2008). The 16S rRNA gene amplification was carried out as described by Chun and Goodfellow (1995), the *gyr*B (Kirby et al. 2010) and the *atp*D, *rec*A, *rel*A and *rpo*B genes amplification were also obtained following standard method of Curtis and Meyers (2012). The almost complete gene sequence of 16S rRNA (1452 bp), *gyr*B gene sequence (1110 bp), *rpo*B gene sequence (951 bp), *rec*A gene sequence (532 bp), *rel*A gene sequence (1018 bp) and *atp*D gene sequence (601 bp) of strain FSN23$^T$ were determined using an ABI PRISM 3730 XL automatic sequencer. The identification of phylogenetic neighbours and calculation of pairwise 16S rRNA gene sequence similarities were obtained using the EzBioCloud Database (http://www.ezbiocloud.net/; Yoon et al. 2017). Multiple alignments with sequences from closely related strains were performed using the CLUSTAL W in MEGA version 6.0 software (Tamura et al. 2013). Phylogenetic trees were reconstructed with the neighbour-joining (Saitou and Nei 1987), maximum parsimony (Kluge and Farris 1969) and maximum-likelihood (Felsenstein 1981) algorithms in MEGA 6.0. Evolutionary distances were calculated using the model of Jukes and Cantor (1969). For maximum-parsimony analysis, the subtree-pruning–regrafting (SPR), and maximum likelihood analysis, the nearest-neighbor-interchange (NNI) heuristic algorithm was used for tree searching. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). Topologies of the resultant trees were evaluated by bootstrap analysis (Felsenstein 1985) based on 1000 resamplings.

Phylogenetic relationships between the strain FSN23$^T$ with type strains of *K. hippodromi* DSM 19227$^T$ (Everest and Meyers 2008), *K. shirazensis* DSM 45490$^T$ (Mohammadipanah et al. 2013), *K. aluminosa* DSM 18824$^T$ (Carlsohn et al. 2007), *K.karoonensis* DSM 17344$^T$ (Kirby et al. 2006), *K. soli* DSM 27132$^T$ (Özdemir-Koçak et al. 2017), *Kribbella jejuensis* DSM 17305$^T$ and *K. solani* DSM 17294$^T$ (Song et al. 2004) based on 16S rRNA gene sequence analysis were confirmed using multilocus sequence analysis (MLSA) for five individual housekeeping genes (*gyr*B, *rpo*B, *rec*A, *rel*A and *atp*D). The sequences of each locus were aligned using MEGA 6.0 software (Tamura et al. 2013) and trimmed manually at the same position before being used for further analysis and deposited in GenBank (http://www.ncbi.nlm.nih.gov/genbank). The data of the sequences were exported as a concatenated five-gene alignment for subsequent analysis using MEGA 6.0 with the model of Jukes and Cantor (1969), using neighbour-joining (Saitou and Nei 1987) algorithm based on 1000 bootstrap replication.

### DNA–DNA hybridization

DNA–DNA relatedness value was determined between strain FSN23$^T$ and its closely phylogenetic neighbours based on 16S rRNA gene sequence with *Kribbella* *hippodromi* DSM 19227$^T$ (DSM; Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH), *Kribbella shirazensis* DSM 45490$^T$, *Kribbella aluminosa* DSM 18824$^T$, *Kribbella karoonensis* DSM 17344$^T$ and *Kribbella soli* DSM 27132$^T$. Hybridization ratio was determined spectrophotometrically by DNA reassociation kinetics as described in the works of De Ley et al. (1970) and Huss et al. (1983) using a model Cary 100 Bio UV/Vis-spectrophotometer equipped with a Peltier-thermostatted 6 × 6 multicell changer and a temperature controller with in situ temperature probe (Varian). The experiments were conducted in duplicate in 2× SSC buffer and 10% formamide at 70 °C.

### Chemotaxonomic characterization

Biomass for chemotaxonomic studies was prepared by growing strain FSN23$^T$ in ISP 2 broth (Shirling and Gottlieb 1966) at 160 rpm for 10 days at 28 °C; cells were harvested by centrifugation, washed twice in distilled water, recentrifuged and freeze-dried. Whole-cell amino acids and sugars were prepared according to Lechevalier and Lechevalier (1970) and analysed by TLC (Staneck and Roberts 1974). Polar lipid and respiratory quinone analyses were carried out by the Identification Service of the DSMZ, Braunschweig, Germany. Respiratory quinones were extracted from 100 mg of freeze-dried cells based on the two-stage method described by Collins et al. (1977). They were separated into their different classes (menaquinones and ubiquinones) by a thin-layer chromatography on silica gel (Macherey–Nagel Art. No. 805 023), using hexane:tert-butylmethylether (9:1 v/v) as solvent. UV bands corresponding to menaquinones or ubiquinones were removed from the plate and further analysed by HPLC. This step was carried out on a LDC Analytical (Thermo Separation Products) HPLC fitted with a reverse-phase column (Macherey–Nagel, 2 mm × 125 mm, 3 µm, RP18) using methanol as the eluent. Respiratory lipoquinones were detected at 269 nm. Cellular fatty acids were extracted, methylated and separated by the Microbial Identification System (MIDI; MicrobialID, Inc.), utilizing an Agilent Technologies 6890 N gas chromatograph with a G2614A autosampler and a 6783 injector (Sasser 1990; Kämpfer and Kroppenstedt 1996). Fatty acid methyl ester peaks were analysed using the TSBA database, version 5.0. The DNA G + C content of strain FSN23$^T$ was determined following the procedure of Gonzalez and Saiz-Jimenez (2005).

### Morphological, cultural and physiological characterization

Cultural characteristics were determined on Czapek's agar (Waksman 1967), ISP media 2-7 (Shirling and Gottlieb 1966), modified Bennett's agar (MBA; Jones 1949), nutrient agar (Waksman 1961) and tryptic soy agar (TSA; Difco) after incubation at 28 for 14 days. The degree of growth, aerial mycelium and pigmentation were recorded. Colony colour of FSN23$^T$ strain was determined using the National Bureau of Standards (NBS) Colour Name Charts (Kelly 1964). Growth at different temperatures (4, 10, 20, 28, 37, 45, 50 and 55 °C) and pH (4–12) (at intervals of 1.0 pH unit), and in the presence of NaCl (0–10%; w/v) (at 1.0% intervals) was determined on ISP 2 after incubation for 14 days. Established methods were used to determine whether the strains degraded Tween 20, 40 and 80 (Nash and Krent 1991), the remaining degradation tests were conducted employing methods described by Williams et al. (1983). Carbon source utilization was tested using carbon source utilization (ISP 9) medium (Shirling and Gottlieb 1966) supplemented with a final concentration of 1% (w/v) of the tested carbon sources (0.1% for succinic acid). Nitrogen source utilization was determined using the method recommended by Williams et al. (1983). The medium was supplemented with a final concentration of 0.1% (w/v) of the tested nitrogen sources. The type strains of *K. hippodromi* DSM 19227$^T$, *K. shirazensis* DSM 45490$^T$, *K. aluminosa* DSM 18824$^T$, *K.karoonensis* DSM 17344$^T$, *K. soli* DSM 27132$^T$, *Kribbella jejuensis* DSM 17305$^T$ and *K. solani* DSM 17294$^T$ were included for comparison in all tests. Morphology properties of isolate FSN23$^T$ were observed by light microscopy and a JEOL JSM-6060 scanning electron microscope to examine gold-coated dehydrated specimens. The samples were prepared from the cultures grown for 21 days on ISP 2 medium at 28 °C.

## Results and discussion

### Molecular analysis

The 16S rRNA gene region (1452 bp) of isolate strain FSN23$^T$ was compared with corresponding sequences of phylogenetically related species which were published in the literature with a valid name. In the neighbour-joining tree, strain FSN23$^T$ formed a clade with *K. hippodromi* S1.4$^T$ (98.8%), *K. shirazensis* UTMC 693$^T$ (98.7%), *K. aluminosa* HKI 0478$^T$ (98.5%), *K. karoonensis* DSM 17344$^T$ (98.5%), *K. soli* FMN22$^T$ (98.3%), *K. jejuensis* HD9$^T$ (98.2%) and *K. solani* DSA1$^T$ (98.1%) (Fig. 1). This relationship was supported by all tree-making algorithms used in this study.

The housekeeping genes of five protein-coding loci, namely *gyr*B, *rpo*B, *rec*A, *rel*A and *atp*D, concatenated and aligned sequences contained 4250 bp for the strain FSN23$^T$. Sequence similarity of the five housekeeping genes together with 16S rRNA gene for the strain FSN23$^T$ is summarized


**Fig. 1** Phylogenetic tree of strain FSN23$^T$ and type strains of the genus *Kribbella* inferred from 16S rRNA gene based on 1496 bp of sequences under the neighbour-joining criterion. All positions containing gaps and missing data were eliminated. There were a total of 1336 positions in the final dataset. Bootstrap percentages based on 1000 replicates are shown; values ≥50% are shown. *Bar* 0.01 substitutions per nucleotide position. *Asterisks* clades that were conserved in the neighbour-joining, maximum-likelihood and maximum-parsimony trees. Accession numbers are indicated in *parentheses*. *Microlunatus phosphovorus* NM-1$^T$ was used as an outgroup

in Table S1. Accession numbers for the *Kribbella* used in generating the concatenated-sequence tree are given in Table S2. The neighbour-joining tree based on the five concatenated genes had a similar topology to the 16S rRNA gene tree with very high bootstrap value (99%) (Fig. 2), and this topology is supported by maximum-likelihood and maximum-parsimony algorithms (99% bootstrap values for each algorithm). Additionally, strain FSN23$^T$ forms a branch with *K. soli* FMN22$^T$ in clade with 100% bootstrap value (Fig. 2). These high bootstrap values are also supported by maximum-likelihood and maximum-parsimony algorithms (100% bootstrap values for each algorithm).

The *gyr*B genetic distance value of FSN23$^T$ strain was found in the range of 0.027–0.129 and the *gyr*B–*rpo*B–*rec*A–*rel*A–*atp*D-based genetic distance values that ranged 0.025–0.089 between FSN23$^T$ and all *Kribbella* type strains. As the genetic threshold to represent novel species for concatenated-gene sequence is 0.04 (Curtis and Meyers, 2012) and for *gyr*B gene sequences is 0.004 (Kirby et al., 2010), the low values indicate species status for the new isolate. The genetic distance values are shown in Table S3 between FSN23T and closely related type species.

Strain FSN23$^T$ showed DNA–DNA relatedness values of 48 ± 4.0% to *K. hippodromi* S1.4$^T$, 43.3 ± 4.0% to *K. shirazensis* UTMC 693$^T$, 43.7 ± 3.5% to *K. aluminosa* HKI 0478$^T$, 47.7 ± 4.0% to *K. karoonensis* DSM 17344$^T$, 53.6 ± 2.4% to *K. soli* DSM 27132$^T$ (based on a mean of duplicate determination in 2 × SSC and 10% formamide at 70 °C). These values were below the 70% threshold value

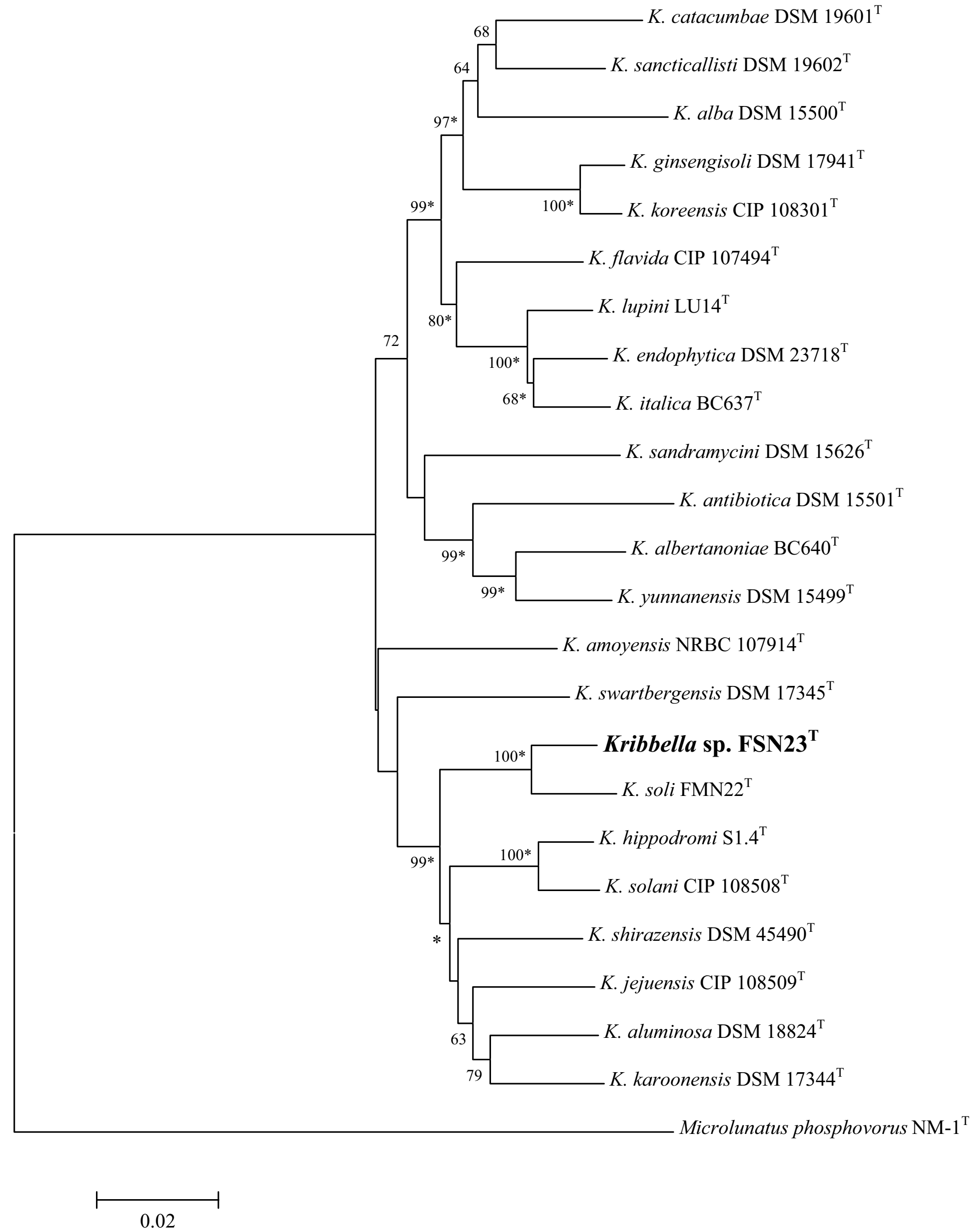


**Fig. 2** *gyr*B–*rpo*B–*rec*A–*rel*A–*atp*D phylogenetic tree showing the position of strain FSN23$^T$ within the genus *Kribbella*. The tree was reconstructed using the neighbour-joining method based on 3994 bp of sequence. Bootstrap percentages based on 1000 replicates are shown; values ≥50% are shown. *Bar* 0.02 substitutions per nucleotide position. *Asterisks* clades that were conserved in the neighbour-joining, maximum-likelihood and maximum-parsimony trees. Accession numbers of all the gene sequences used are listed in Table S2. *Microlunatus phosphovorus* NM-1$^T$ was used as an outgroup

for the definition of bacterial genomic species (Wayne et al. 1987; Stackebrandt and Goebel 1994).

## Chemotaxonomy

Strain FSN23$^T$ contained LL-diaminopimelic acid (cell wall type III; Lechevalier and Lechevalier 1970) as the cell wall diamino acid and the whole-cell sugars were glucose, ribose and trace of mannose. The polar lipids were phosphatidylglycerol, diphosphatidylglycerol, four unidentified lipids and five unidentified polar lipids (Fig. S1). The major menaquinone of strain FSN23$^T$ was MK-9($H_4$) and major cellular fatty acids were *anteiso*-$C_{15:0}$ and *iso*-$C_{16:0}$. The full fatty acid profile of strain FSN23$^T$ is shown in Table S4 and major fatty acid compositions obtained in same conditions, major menaquinones, polar lipid profiles and whole-cell sugars are comparatively shown in Table 1. The G + C content of the DNA was 68.28 mol %. FSN23$^T$ is generally compatible with the type strains of closely related *Kribbella* species in terms of fatty acids, major menaquinones and whole-cell sugars. However, strain FSN23$^T$, unlike the phylogenetic neighbours, was characterized by the absence of phosphatidylcholine in its polar lipid pattern.

## Phenotypic analyses

The results obtained so far indicated that the morphological properties of FSN23$^T$ strain were typical for the genus

**Table 1** Phenotypic and chemotaxonomic properties of strain FSN23$^T$ and the type strains of closely related species

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
|---|---|---|---|---|---|---|---|---|
| Biochemical tests | | | | | | | | |
| Allantoin hydrolysis | + | − | + | − | + | + | − | − |
| Nitrate reduction | + | − | + | + | + | + | + | + |
| Urea hydrolysis | + | + | + | + | + | + | − | − |
| pH tolerance | | | | | | | | |
| 5 | + | − | + | + | + | + | + | − |
| 9 | + | + | + | − | + | + | + | − |
| Temperature | | | | | | | | |
| 37 | + | + | + | + | + | − | + | − |
| NaCl (%, w/v) | | | | | | | | |
| 4.0 | − | − | + | − | + | − | + | + |
| 5.0 | − | − | − | − | − | − | + | + |
| Degradation of (%, w/v) | | | | | | | | |
| Adenine (0.5%) | + | − | + | + | + | + | + | − |
| Casein (1%) | − | − | − | + | + | − | + | − |
| Elastin (0.3%) | − | − | − | − | + | − | + | − |
| Hypoxanthine (0.4%) | + | − | + | + | + | + | + | − |
| Starch (1%) | + | − | + | + | + | + | + | − |
| Tween 20 (1%) | + | + | + | + | + | − | + | + |
| Tween 80 (1%) | + | − | + | + | − | − | + | + |
| Xanthine (0.4%) | + | − | + | + | + | − | − | + |
| Xylan (0.4%) | − | − | − | + | + | − | −− | − |
| Carbon source utilization (1.0%, w/v) | | | | | | | | |
| Adonitol | + | + | + | + | + | + | + | − |
| D-Galactose | + | + | − | + | + | + | + | − |
| D-Melibiose | + | + | + | + | − | + | + | + |
| Inulin | + | + | + | + | − | + | + | − |
| Mannitol | + | + | + | + | + | + | + | − |
| *Myo*-inositol | + | − | + | + | + | + | + | − |
| Succinic acid (0.1%) | + | − | + | − | + | + | − | − |
| Xylose | + | + | + | + | + | + | − | + |
| Nitrogen source utilization (0.1%, w/v) | | | | | | | | |
| DL-Phenylalanine | − | + | + | − | + | + | − | + |
| L-Alanine | + | + | − | + | + | + | + | + |
| L-Histidine | + | + | − | + | + | + | + | + |
| L-Isoleucine | + | + | + | + | + | + | − | + |
| L-Arginine | + | + | − | + | + | + | + | + |
| L-Cysteine | + | + | + | + | + | + | + | +- |

**Table 1** (continued)

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
|---|---|---|---|---|---|---|---|---|
| L-Lysine | + | − | − | + | + | + | + | − |
| L-Phenylalanine | − | + | + | − | + | + | − | − |
| L-Serine | + | + | − | + | + | + | + | + |
| L-Valine | + | − | + | + | + | + | − | − |
| L-Tyrosine | + | + | − | + | + | + | + | + |
| Major menaquinones (>10%) | MK-9($H_4$), MK-8($H_4$) | nr | MK-9($H_4$), MK-9($H_2$)[c] | MK-9($H_4$)[d] | nr | MK-9($H_4$)[a] | nr | nr |
| Polar lipid profile | PG, DPG | nr | DPG, PG, PC, PI[c] | PC, DPG, PG, PI[d] | nr | DPG, PG, PC, PI[a] | DPG, PC, PI[f] | DPG, PC, PI[f] |
| Major fatty acids (>10%) | anteiso C15:0, iso C16:0 | iso C16:0 10-methyl, anteiso C15:0, C15:0 3OH[a] | anteiso C15:0, iso C16:0[a] | anteiso C15:0, iso C16:0[a] | anteiso C15:0, iso C16:0, iso C16:0 10-methyl[a] | anteiso C15:0, iso C16:0[a] | anteiso C15:0, iso C16:0[a] | anteiso C15:0, iso C16:0[a] |
| Whole-cell sugars | Glu, Rib, Man | Glu, US1[b] | Glu, Rib[c] | Glu, Man, Rib[d] | Rib, Man[e] | Glu, Man, Rib[a] | Man, Glu, Gal, Rib[f] | Man, Glu, Gal, Rib[f] |

Strains: *1*, FSN23$^T$; *2*, *K. hippodromi* DSM 19227$^T$; *3*, *K. shirazensis* DSM 45490$^T$; *4*, *K. aluminosa* DSM 18824$^T$; *5*, *K. karoonensis* DSM 17344$^T$; *6*, *K. soli* DSM 27132$^T$; *7*, *K. jejuensis* DSM 17305$^T$; *8*, *K. solani* DSM 17294$^T$

*PL* unidentified phospholipid, *PG* phosphatidylglycerol, *DPG* diphosphatidylglycerol, *PE* phosphatidylethanolamine, *PI* phosphatidylinositol, *PIM* phosphatidylinositol mannoside, *PME* phosphatidylmethylethanolamine, *Gal* galactose, *Glu* glucose, *Man* mannose, *Rib* ribose, *US1* unidentified sugars, + positive, − negative, *nr* not reported

Data taken from [a] Özdemir-Koçak et al. (2017); [b] Everest and Meyers (2008); [c] Mohammadipanah et al. (2013); [d] Carlsohn et al. (2007); [e] Kirby et al. (2006); [f] Song et al. (2004)

*Kribbella*. FSN23$^T$ exhibited an extensively branched substrate mycelium and aerial mycelium. The aerial mycelium consisted of hyphae which fragmented into irregular rod-shaped elements (Fig. S2). While growth was good in other media, moderate growth was observed in ISP 3 and 6 media (Table S5). Diffusible or melanoid pigment was not detected on the tested media. Strain FSN23$^T$ was found to grow well between pH 5.0 and 9.0, between temperature 20 and 37 °C and between 0 and 3% (w/v) NaCl. Additional phenotypic properties are given in the species description and Table 1.

Based on polyphasic taxonomy, DNA–DNA hybridization data, MLSA, phenotypic and chemotaxonomic properties, strain FSN23$^T$ is considered to represent a novel species of the genus *Kribbella*, for which the name *Kribbella sindirgiensis* sp. nov. is proposed. The Digital Protologue database TaxonNumber for strain FSN23$^T$ is TA00120.

## Description of *Kribbella sindirgiensis* sp. nov

*Kribbella sindirgiensis* (sin.dir.gi.en'sis. N.L. fem. adj. *sindirgiensis* of or belonging to Sındırgı, Balıkesir, Turkey, the source of the type strain) is an aerobic, Gram-reaction positive, catalase-positive, oxidase-negative, non-motile actinobacterium which forms extensively branched, substrate mycelia. Vegetative mycelium appears to range from cream to orange yellow colour series. Aerial mycelium appears white on ISP 4. No diffusible pigment is observed on ISP 5. Good growth is observed on ISP 2, ISP 4, ISP 5, ISP 7, modified Bennett's, TSA, Czapek's and nutrient agar media, moderate growth is observed on ISP 3 and ISP 6 medium. Melanoid pigments are not produced on ISP 6 or ISP 7 agars. The pH range of growth was determined between 5.0 and 9.0 (optimum, pH 7.0), and the temperature range was 20–37 °C (optimum, 30 °C). Growth of the species was not observed at pH 4.0 and 10.0. The temperatures of 4, 10, 45 and 50 °C are also not suitable for species development. 0–3% (w/v) NaCl is convenient for species growth. The results of biochemical tests for arbutin, aesculin, allantoin, urea hydrolysis and nitrate reduction were positive. Tween 20, 40 and 80, adenine, xanthine, gelatin, hypoxanthine and starch are degraded, but not casein, guanine, xylan. The species can utilize adonitol, D-arabinose, D-cellobiose, D-fructose, dextrin, D-galactose, D-mannose, D-glucose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-trehalose, inulin, lactose, L-arabinose, L-rhamnose, maltose, D-mannitol, *myo*-inositol, succinic acid, sucrose and xylose as sole carbon sources, but not D-sorbitol, dextran and xylitol. Glycine, L-alanine, L-histidine, L-isoleucine, L-arginine, L-asparagine, L-cysteine, L-lysine, L-methionine, L-hydroxyproline, L-threonine, L-proline, L-serine, L-valine and L-tyrosine can be used as sole nitrogen sources, but not DL-phenylalanine and L-phenylalanine. The cell wall peptidoglycan contains LL-DAP. The characteristic whole cell sugars are glucose, ribose and trace of mannose. The major cellular fatty acids are anteiso-$C_{15:0}$ and iso-$C_{16:0}$. The polar lipid profile contains phosphatidylglycerol, diphosphatidylglycerol, four unidentified lipids and five unidentified phospholipids. The predominant menaquinones are MK-9($H_4$) (84.0%), MK-8($H_4$) (10.0%) and MK-9($H_6$) (4.0%). The G + C content of the DNA was 68.28 mol %.

The type strain, FSN23$^T$ (=DSM 27082$^T$ = KCTC 29220$^T$), was isolated from soil collected from Sındırgı, Balıkesir, Turkey.

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**Compliance with ethical standards**

**Conflict of interest** The authors declare that they have no conflict of interest.

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