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Kitasatospora putterlickiae sp. nov., isolated from rhizosphere soil, transfer of *Streptomyces kifunensis* to the genus *Kitasatospora* as *Kitasatospora kifunensis* comb. nov., and emended description of *Streptomyces aureofaciens* Duggar 1948

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A polyphasic study was undertaken to establish the taxonomic position of a rhizosphere isolate that had been assigned provisionally to the genus *Kitasatospora*. The organism, isolate F18-98^T, was found to have chemical and morphological properties that were consistent with its classification as a *Kitasatospora* strain. Direct 16S rDNA sequence data confirmed the taxonomic position of the strain, following the generation of phylogenetic trees by using three treeing algorithms. The organism formed a 16S rDNA subclade with *Kitasatospora azatica* and *Streptomyces kifunensis*, but was distinguished readily from the latter by using a combination of biochemical and physiological properties. Genotypic and phenotypic data show that strain F18-98^T should be classified in the genus *Kitasatospora* as a novel species, for which the name *Kitasatospora putterlickiae* sp. nov. is proposed; the type strain has been deposited in culture collections as strain F18-98^T (=DSM 44665^T=NCIMB 13932^T). It is also proposed that *Streptomyces kifunensis* should be transferred to the genus *Kitasatospora* as *Kitasatospora kifunensis* comb. nov. An emended description of *Streptomyces aureofaciens* Duggar 1948 is also given.

INTRODUCTION

The genus *Kitasatospora* (formerly *Kitasatosporia*) has had a short but turbulent taxonomic history. The taxon was proposed by Ōmura *et al.* (1982), subsequently subsumed within the genus *Streptomyces* (Wellington *et al.*, 1992; Ochi & Hiranuma, 1994), re-established by Zhang *et al.* (1997) and thereafter recognized in subsequent studies (Chung *et al.*, 1999; Tajima *et al.*, 2001). The genus belongs to the family *Streptomycetaceae*, together with the genera *Streptacidiphilus* and *Streptomyces* (Kim *et al.*, 2003). Kitasatosporae are aerobic, Gram-positive, chemo-organotrophic actinomycetes that form an extensively branched substrate mycelium and aerial hyphae that differentiate into long chains of spores and typically produce whole-organism hydrolysates that are rich in galactose and LL- and *meso*-diaminopimelic acid (A_2pm). Aerial spores on solid culture and submerged spores in liquid culture contain LL-A_2pm, whereas mycelium grown under both culture conditions mainly contains *meso*-A_2pm (Ōmura *et al.*, 1981, 1982; Takahashi *et al.*, 1984).

The eleven species of *Kitasatospora* that have validly published names at the time of writing are *Kitasatospora azatica* (Nakagaito *et al.* 1993) Zhang *et al.* 1997, *Kitasatospora cheerisanensis* Chung *et al.* 1999, *Kitasatospora cineracea* Tajima *et al.* 2001, *Kitasatospora cochleata* (Nakagaito *et al.* 1993) Zhang *et al.* 1997, *Kitasatospora cystarginea* Kusakabe and Isono 1992, *Kitasatospora griseola* Takahashi *et al.* 1985, *Kitasatospora mediocidica* Labeda 1988, *Kitasatospora niigatensis* Tajima *et al.* 2001, *Kitasatospora paracochleata* (Nakagaito *et al.* 1993) Zhang *et al.* 1997, *Kitasatospora*

Abbreviations: A_2pm, diaminopimelic acid; ISP, International *Streptomyces* Project.

The GenBank/EMBL/DDBJ accession numbers for the 16S rDNA sequences of *Kitasatospora putterlickiae* F18-98^T and *Streptomyces aureofaciens* IMET 43577^T are AY189976 and AY289116, respectively. The accession number for the 16S–23S rDNA spacer region of *Kitasatospora putterlickiae* is AY189977.

phosalacinea Takahashi *et al.* 1985 and *Kitasatospora setae* Ōmura *et al.* 1983 [species name corrected by Ōmura *et al.* (1985)], which is the type species of the genus. The taxonomic integrity of these species, which form a distinct phyletic branch in the 16S rDNA tree, is supported by a wealth of genotypic and phenotypic data. The current classification of the genus provides a sound framework for the description of additional *Kitasatospora* species, some of which can be expected to include strains of industrial significance.

The taxonomic position of *Streptomyces aureofaciens* Duggar 1948 needs to be clarified. The organism was included in the International *Streptomyces* Project (ISP) (Shirling & Gottlieb, 1968) as a *bone fide* member of the genus *Streptomyces* and was considered subsequently to be an agent of potato scab (Goyer *et al.*, 1996; Kreuze *et al.*, 1999; Bouchek-Mechiche *et al.*, 2000). However, Kreuze *et al.* (1999) suggested that *S. aureofaciens* NRRL 2209^T was misclassified in the genus *Streptomyces* and probably belonged to the genus *Kitasatospora*, a view that was based mainly on 16S rDNA sequence data. However, in a numerical taxonomic survey based on the simple matching coefficient and the UPGMA algorithm, strain NRRL 2209^T was recovered in an aggregate cluster equated with the genus *Streptomyces* (Williams *et al.*, 1983).

The primary aim of the present investigation was to determine the taxonomic position of an organism presumptively assigned to the genus *Kitasatospora*, strain F18-98^T, which had been isolated from the rhizosphere of a *Putterlickia verrucosa* plant in South Africa during an investigation of endophytic actinomycetes associated with the plant family *Celastraceae* (Pullen *et al.*, 2002, 2003). Data from polyphasic taxonomic study of the organism showed that it should be recognized as a novel species of *Kitasatospora*, for which the name *Kitasatospora putterlickiae* sp. nov. is proposed. Studies were also carried out to clarify the taxonomic positions of the type strains of *S. aureofaciens* and *Streptomyces kifunensis*.

METHODS

Bacterial strains and culture conditions. Strain F18-98^T was isolated from the rhizosphere of plant 'F', a *Putterlickia verrucosa* (E. Meyer *ex* Sonder) Szyszyl plant that grows in South Africa; the location and biotope of this plant were described by Pullen *et al.* (2003). The organism was isolated following a procedure modified slightly from that described by Hunter-Cevera *et al.* (1986): an air-dried soil sample (1 g) that contained hairy roots of the plant was pre-treated at 95 °C in a dry oven for 1 h, suspended in sterile water (2 ml) and a 0·1 ml aliquot was spread over a yeast extract/malt agar plate (ISP medium 2; Shirling & Gottlieb, 1966) supplemented with propiconazol (10 p.p.m.). The inoculated plate was incubated at 28 °C for 3–4 days, while representative actinomycete colonies were grown under the same conditions on ISP 2 agar that lacked propiconazol. Stock cultures of the selected isolate (strain F18-98^T) in liquid organic medium 79 (Prauser *et al.*, 1987) supplemented with 5 % DMSO were maintained in either the vapour phase of liquid nitrogen or at −80 °C by adding glycerol medium (1 : 1) that consisted of: K_2HPO_4, 1·26 %; KH_2PO_4, 0·36 %; $MgSO_4$, 0·01 %; sodium citrate, 0·09 %; $(NH_4)_2SO_4$, 0·18 %; and glycerol, 8·8 %.

Bacterial growth for chemotaxonomic and morphological studies on all three strains was prepared by cultivating them in liquid organic medium 79 (Prauser *et al.*, 1987), Bacto tryptic soy broth (Sigma-Aldrich) and on ISP media 2, 3, 4 and 5 (Difco; Shirling & Gottlieb, 1966) at 28 °C for 10–15 days. Physiological tests were carried out on carbon utilization agar (ISP medium 9) or on ISP medium 2. Susceptibility to polyvalent *Streptomyces* phages was tested by dropping high-titre suspensions of phage S7 (DSM 49153) onto agar plates seeded with spores of strain F18-98^T held in a soft agar layer. Phage S7 was propagated in host strain *Streptomyces olivaceus* DSM 41536 by growing the latter in liquid organic medium 79 for 24 h at 28 °C. *K. azatica* DSM 41650^T was included in these studies for comparative purposes.

Morphological and physiological characteristics. Morphological characteristics were observed by light and electron microscopy. Dimensions of spores were measured by using an Axioskop 2 microscope equipped with image analysing AxioVision 2.05 software (both from Zeiss). Samples for electron microscopy were prepared following Shirling & Gottlieb (1966) and observed by using a CEM 902A electron microscope (Zeiss) at an acceleration voltage of 80 kV. Culture characteristics, production of melanoid pigments and utilization of carbon sources were determined according to methods described by Shirling & Gottlieb (1966). pH range for growth was established by using liquid ISP medium 2, adjusted to pH values between 4 and 10 with either 1 M HCl or 20 % (w/v) Na_2CO_3 solution and incubated at 28 °C for up to 10 days. Temperature growth range and tolerance to NaCl were recorded on ISP 2 agar plates that were incubated at 28 °C for up to 21 days. Liquefaction of gelatin, hydrogen sulfide production and nitrate reduction were examined as described by Lányi (1987). Casein degradation, hydrolysis of potato starch and peptonization of milk were determined according to Cowan & Steel (1965). Enzymic activities of 48-h-old cultures grown in liquid organic medium 79 were examined by using API ZYM galleries (bioMérieux), following the manufacturer's instructions. Susceptibility to antibiotics was tested by placing antibiotic discs (Difco) on organic medium 79 agar plates that were seeded with suspensions of the tested strains that had been grown in a soft agar layer for 1–2 days at 28 °C. Additionally, nalidixic acid and novobiocin were added at different concentrations to ISP 2 agar plates, which were then inoculated with spores of the tested strains.

Chemotaxonomic characteristics. Isomers of A_2pm in whole-organism hydrolysates were analysed according to the method of Hasegawa *et al.* (1983) by using the solvent system of Rhuland *et al.* (1955) and paper chromatography. Whole-organism sugars were determined by the method of Becker *et al.* (1965) and by GC according to Saddler *et al.* (1991). The colorimetric method of Uchida & Aida (1984) was used to determine muramic acid type. Menaquinones were extracted as described by Collins *et al.* (1977) and analysed by using an HPLC instrument (Shimadzu), which consisted of a model LC-9A solvent delivery module, an on-line degasser (Knauer), a model CTO-6A column oven, a model SIL-9A automatic sample injector and a model SPD-6AV UV-VIS spectrophotometric detector and was fitted with an EC 250/4 Nucleosil 120-5 C18 column (Macherey–Nagel). Fatty acid profiles were analysed by using the MIDI system (Agilent) and cultures grown in Bacto tryptic soy broth for 48 h at 28 °C; mycolic acids were sought by using the TLC procedure described by Minnikin *et al.* (1975). Polar lipids, extracted by the method of Minnikin *et al.* (1979), were identified by two-dimensional TLC and spraying with specific reagents (Collins & Jones, 1980).

Small-subunit rDNA sequencing. 16S rDNA amplification and sequencing of strain F18-98^T were carried out as described by Edwards *et al.* (1989). The resultant sequence was aligned manually with corresponding almost-complete sequences of representatives of most actinomycete genera and then with almost-complete sequences

of the type strains of *Kitasatospora*, *Streptacidiphilus* and representative *Streptomyces* species; in each case, reference sequences were retrieved from DDBJ/EMBL/GenBank. Evolutionary trees were inferred by using the least-squares (Fitch & Margoliash, 1967), maximum-likelihood (Felsenstein, 1981) and neighbour-joining (Saitou & Nei, 1987) algorithms, which form part of the PHYLIP 3.5c package (Felsenstein, 1993); evolutionary distance matrices for the neighbour-joining method were generated as described by Jukes & Cantor (1969). The resultant unrooted tree topologies were evaluated by carrying out bootstrap analyses (Felsenstein, 1985) of the neighbour-joining data, based on 1000 resamplings, by using the SEQBOOT and CONSENSE programs from PHYLIP 3.5c (Felsenstein, 1993).

Similarly, 16S rDNA amplification and sequencing of *S. aureofaciens* IMET 43577^{T} was carried out as described by Kim *et al.* (1998). The resultant sequence was aligned manually with corresponding almost-complete sequences of available type strains of *Streptomyces* species that were retrieved from DDBJ/EMBL/GenBank by using the AL16S program (Chun, 1995). Evolutionary trees were inferred by using the neighbour-joining algorithm (Saitou & Nei, 1987). Robustness of the tree was evaluated by performing bootstrap analysis, as described above. A partial 16S rDNA nucleotide sequence (120 nt) of the tested strain, based on the variable γ-region, was compared with the corresponding nucleotide sequences of *Streptomyces* strains retrieved from GenBank. A phylogenetic tree based on these sequences was generated by using the neighbour-joining algorithm (Saitou & Nei, 1987).

Cloning and sequencing of the 16S–23S rDNA spacer region. Cloning and sequencing of PCR-amplified spacer fragments of the three strains were carried out as described by Wang *et al.* (1996a, b).

RESULTS AND DISCUSSION

Phenotypic and phylogenetic characteristics of strain F18-98^{T} and *S. kifunensis* DSM 41654^{T} are consistent with their classification in the genus *Kitasatospora* (Ōmura *et al.*, 1982; Zhang *et al.*, 1997).

An almost-complete 16S rDNA sequence (1553 nt) was determined for strain F18-98^{T}. Preliminary phylogenetic analysis placed the strain within the evolutionary radiation encompassed by the genus *Kitasatospora* (data not shown). When the sequence of strain F18-98^{T} was compared with corresponding 16S rDNA sequences of the type strains of *Kitasatospora* and *Streptacidiphilus* species and representatives of the genus *Streptomyces*, the organism formed a monophyletic clade with *K. azatica* NBRC 13803^{T} and *S. kifunensis* NBRC 15206^{T} (Fig. 1). This relationship was evident in evolutionary trees based on three different treeing algorithms and was supported by a bootstrap value of 84 %. Nucleotide sequence similarity values between the isolate and the kitasatosporae ranged from 96·4 % (with *K. niigatensis*) to 98·6 % (with *S. kifunensis*), values that correspond to 51 and 20 nucleotide differences in 1430 nucleotide positions, respectively. The 16S–23S rDNA spacer sequence data showed that the tested strain contained the nine nucleotide sequence characteristics of the genus *Kitasatospora* (Zhang *et al.*, 1997).

Strain F18-98^{T} formed an extensively branched, non-fragmenting substrate mycelium that was seen to carry aerial hyphae and spores within 3 days. Smooth-surfaced, cylindrical spores were borne in long, straight to flexuous spore-chains. Culture characteristics of the strain are shown in Table 1. It was evident that aerial spore-mass colour changed from pale brown to grey as colonies aged. In liquid culture, spores germinated to form long, sparsely branched hyphae that fragmented subsequently into irregular segments and spore-like bodies.

Whole-organism hydrolysates of strain F18-98^{T} contained predominant amounts of LL-A_2pm and relatively small amounts of the corresponding *meso*-isomer. The organism was also characterized by the presence of *N*-acetylated muramic acid, the sugars galactose, mannose and rhamnose,

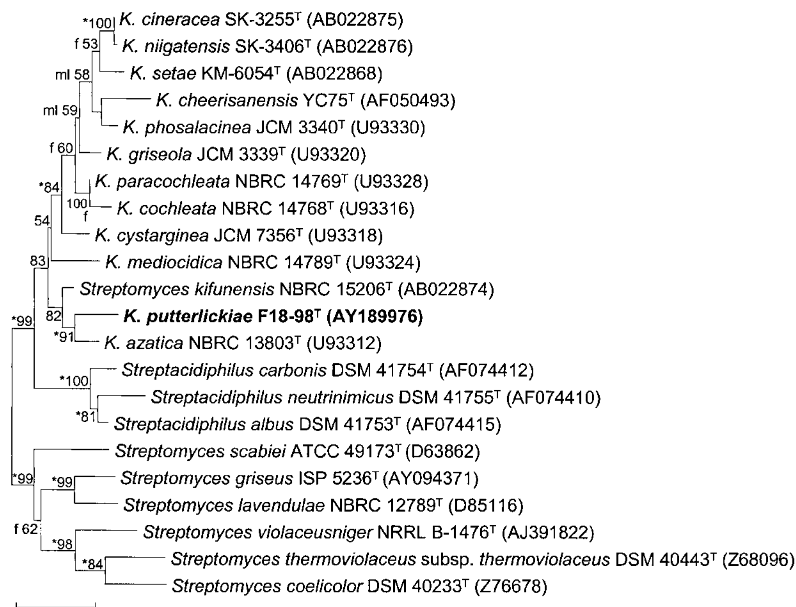

Fig. 1. Unrooted neighbour-joining tree (Saitou & Nei, 1987) based on nearly complete 16S rDNA sequences, showing the position of strain F18-98^{T} in the *Kitasatospora* tree. Asterisks indicate branches that were also recovered by using both the least-squares (Fitch & Margoliash, 1967) and maximum-likelihood (Felsenstein, 1981) algorithms; f and ml indicate branches formed by using the least-squares or maximum-likelihood treeing methods, respectively. Numbers at nodes are bootstrap values (%) based on 1000 resampled datasets; only values >50 % are given. Bar, 0·1 nucleotide substitutions per nucleotide position.

Table 1. Culture characteristics of strain F18-98^T

Medium*	Colour of aerial spore-mass	Reverse colour	Soluble pigment
Yeast extract/malt extract agar (ISP 2)	Dark grey	Dark brown	Dark brown
Oatmeal agar (ISP 3)	Grey	Yellowish brown	Brown
Inorganic salts/starch agar (ISP 4)	Dark grey	Beige, pale grey	None
Glycerol/asparagine agar (ISP 5)	Dark grey	Dark brown	None

*Good growth occurred on all media.

major amounts of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, phosphatidylinositol and phosphatidylinositol mannosides [phospholipid type 2 *sensu* Lechevalier *et al.* (1977)] and a menaquinone profile that consisted of di-, tetra- and hexahydrogenated components with nine isoprene units and tetrahydrogenated components with 10 and 11 isoprene units (peak area ratios: 14, 23, 24, 14 and 10, respectively). The cellular fatty acid profile was characterized by major proportions of 14-methylpentadecanoic acid (iso-$C_{16:0}$, 36·5 %), hexadecanoic acid ($C_{16:0}$, 9·2 %), hexadecenoic acid ($C_{16:1}$, 8·9 %) and 13-methyltetradecanoic acid (iso-$C_{15:0}$, 8·6 %); mycolic acids were not detected.

Chemotaxonomic and morphological data, together with the results of molecular systematic studies, show that strain F18-98^T is a *bona fide* member of the genus *Kitasatospora*. It is also interesting that the strain is resistant to polyvalent *Streptomyces* phage S7, which is known to lyse 121 of 151 *Streptomyces* strains that represent 90 species (H. Prauser, personal communication). It is clear from Table 2 that strain F18-98^T can be distinguished readily from its two closest phylogenetic neighbours by using a combination of biochemical and physiological tests. All three of these strains were sensitive to low concentrations of novobiocin (5 μg ml^{-1}) and hence cannot be expected to grow on the novobiocin-containing agar medium used by Tajima *et al.* (2001) to isolate strains of *K. cineracea* and *K. niigatensis*.

It can be concluded from the genotypic and phenotypic data that strain F18-98^T forms a novel *Kitasatospora* species. It is, therefore, proposed that this organism should be classified as *Kitasatospora putterlickiae* sp. nov.

'*Kitasatospora kifunense*' was proposed by Iwami *et al.* (1987) and later transferred to the genus *Streptomyces* as *S. kifunensis* Nakagaito *et al.* 1993 with NBRC 15206^T as the type strain. The results of the present investigation are in line with those from previous studies (Nakagaito *et al.*, 1992a, b; Zhang *et al.*, 1997) in showing that the type strain of *S. kifunensis* belongs to the genus *Kitasatospora*. In the present study, *S. kifunensis* DSM 41654^T was shown to contain LL- and *meso*-A_2pm in whole-organism hydrolysates, *N*-acetylated muramic acid, major amounts of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, phosphatidylinositol and phosphatidylinositol mannosides, hexahydrogenated menaquinone with

Table 2. Phenotypic properties that separate strain F18-98^T from related *Kitasatospora* species

Taxa: 1, strain F18-98^T; 2, *K. azatica* DSM 41650^T; 3, *K. kifunensis* DSM 41654^T. +, Positive; $+^d$, delayed positive; −, negative; W, weakly expressed.

Characteristic	1	2	3
Formation of melanoid pigments	+	−	+
Biochemical tests:			
Gelatin liquefaction	+	$+^d$	−
Hydrolysis of potato starch	−	+	+
Nitrate reduction	+	+	−
Enzyme assay (API ZYM):			
α-Glucosidase	−	W	+
β-Glucosidase	+	−	−
Naphthol-AS-BI-phosphohydrolase	−	+	+
Growth on sole carbon sources:			
L(+)-Arabinose	−	+	+
D(+)-Fructose	W	+	−
D(+)-Mannitol	−	−	+
D(−)-Sucrose	W	+	+
D(+)-Xylose	−	+	+
Growth in the presence of NaCl (%):			
2	+	−	+
2·5	+	−	+
3	+	−	−
pH for growth:			
9	+	−	+*
9·5	+	−	−
Growth at 35 °C	+	W	−
Resistance to antibiotics:			
Penicillin G (10 IU)	−	−	+
Polymyxin B (300 IU)	W	−	+
Sulfonamide (200 μg)	+	−	−

*Growth after 6 days.

nine isoprene units as the predominant isoprenologue, galactose, glucose, mannose and ribose as whole-organism sugars and fatty acids rich in iso- and anteiso-branched components. In addition, the 16S–23S rDNA spacer region contained the nine nucleotide sequence characteristics of the genus *Kitasatospora* (Zhang *et al.*, 1997). The organism was also resistant to polyvalent *Streptomyces* phage S7. It is

evident from Fig. 1 that the organism forms a 16S rDNA subclade with the type strains of *K. azatica* and *K. putterlickiae*, but can be distinguished readily from the latter by using a combination of phenotypic properties (Table 2). It is therefore clear that *S. kifunensis* Nakagaito *et al.* 1993 should be transferred to the genus *Kitasatospora* as *Kitasatospora kifunensis* comb. nov.

The chemical and morphological properties of *S. aureofaciens* IMET 43577^T recorded in the present study are consistent with its classification in the genus *Streptomyces* (Williams *et al.*, 1989; Manfio *et al.*, 1995). The organism forms an extensively branched substrate mycelium and aerial hyphae that differentiate into chains of spores and contains LL-A_2pm in the cell-wall peptidoglycan, *N*-acetylated muramic acid, complex mixtures of iso- and anteiso-branched fatty acids and tetra-, hexa- and octa-hydrogenated menaquinones as the predominant isoprenologues. The strain was also sensitive to polyvalent *Streptomyces* phage S7 and has a 16S–23S rDNA spacer region sequence that lacks the nucleotide signature of *Kitasatospora* strains (Zhang *et al.*, 1997). Retention of the organism in the genus *Streptomyces* is also supported by the present 16S rDNA nucleotide sequence data.

Comparison of the almost-complete 16S rDNA nucleotide sequence of *S. aureofaciens* IMET 43577^T with corresponding sequences of marker strains of the genera *Kitasatospora*, *Streptacidiphilus* and *Streptomyces* clearly show that it forms a distinct phyletic line within the evolutionary radiation occupied by the genus *Streptomyces* (data not shown). The organism was related most closely to the type strains of *Streptomyces ambofaciens*, *Streptomyces paradoxus* and *Streptomyces tendae*, although these relationships were not supported by high bootstrap values. Strain IMET 43577^T shared 16S rDNA nucleotide similarities with the three type strains of 98·9, 98·9 and 98·8 %, respectively; values that corresponded to 16, 15 and 17 nucleotide differences at 1448 sites. 16S rDNA similarity values much higher than these figures have been recorded between type strains of several *Streptomyces* species that are known to have relatively low DNA–DNA relatedness values (Sembiring *et al.*, 2000; Kim & Goodfellow, 2002), i.e. below the 80 % cut-off point recommended for the recognition of genomic species of *Streptomyces* (Labeda & Lyons, 1992; Labeda, 1993, 1998). The clear separation of *S. aureofaciens* IMET 43577^T from representatives of *Streptomyces* species with validly published names is underpinned by the results from the 120 nt 16S rDNA sequence analysis (data not shown). The present 16S rDNA nucleotide sequence of the type strain of *S. aureofaciens* differed from the earlier one that was deposited in GenBank under accession no. Y15504 by 89 nucleotide differences at 1438 sites.

Description of *Kitasatospora putterlickiae* sp. nov.

Kitasatospora putterlickiae (put.ter.lic′ki.ae. N.L. gen. n. *putterlickiae* of the plant genus *Putterlickia*).

Aerobic, Gram-positive, non-acid-fast actinomycete that produces a dark-brown substrate mycelium and a dark-grey aerial spore-mass on glycerol/asparagine and yeast extract/malt extract agars. Brown soluble pigments are formed on oatmeal and yeast extract/malt extract agars and melanoid pigments are formed on peptone/yeast extract/iron and tyrosine agars. Spore-chains are straight to flexuous (*rectiflexibiles*), with 20 or more cylindrical, smooth-surfaced spores ($1{\cdot}6–2{\cdot}5 \times 1{\cdot}0–1{\cdot}5$ μm) per chain. Submerged spores are formed in liquid culture. Temperature range for growth is 10–37 °C (optimum is between 28 and 32 °C); growth does not occur at either 6 or 40 °C. Good growth occurs at pH 5–9; growth does not occur at pH 4·5 or above pH 9·5. Nitrate is reduced to nitrite, gelatin is liquefied, milk is peptonized, casein is degraded and H_2S is weakly produced. Starch is not hydrolysed. Alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, acid phosphatase, *β*-galactosidase and *β*-glucosidase are produced, but *N*-acetyl-*β*-glucosamidase, α-chymotrypsin, cystine arylamidase, α-fucosidase, α-galactosidase, α-glucosidase, *β*-glucuronidase, lipase (C14), α-mannosidase, naphthol-AS-BI-phosphohydrolase, trypsin and valine arylamidase are not. D(+)-Fructose (weak), D(+)-glucose and D(−)-sucrose (weak) are used as sole sources of carbon for energy and growth, but L(+)-arabinose, cellulose, *i*-inositol, D(−)-mannitol, D(+)-raffinose, L(+)-rhamnose and D(+)-xylose are not. Growth is inhibited by ampicillin (10 μg ml^{-1}), chloramphenicol (30 μg ml^{-1}), ciprofloxacin (5 μg ml^{-1}), imipenem (10 μg ml^{-1}), kanamycin sulfate (30 μg ml^{-1}), methicillin (5 μg ml^{-1}, weak), novobiocin (2·5 μg ml^{-1}), oxytetracycline hydrochloride (30 μg ml^{-1}), penicillin G (10 IU), polymyxin B (300 IU, weak), rifampicin (30 μg ml^{-1}), streptomycin sulfate (10 μg ml^{-1}), vancomycin hydrochloride (30 μg ml^{-1}) and nalidixic acid (50 μg ml^{-1}), but not by lincomycin hydrochloride (2 μg ml^{-1}), norfloxacin (10 μg ml^{-1}) or sulfonamide (200 μg ml^{-1}). NaCl is tolerated up to a concentration of 3·5 % (w/v). Resistance is shown to polyvalent *Streptomyces* phage S7. Whole-cell chemistry reveals the presence of both *meso*- and LL-A_2pm; the muramic acid moiety is *N*-acetylated. Whole-organism hydrolysates contain galactose, madurose, mannose and rhamnose and the major polar lipids are diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, phosphatidylinositol and phosphatidylinositol mannosides. Predominant fatty acids are $C_{16:0}$, $C_{16:0}$ and iso-$C_{15:0}$; mycolic acids are absent. Major menaquinones are tetra- and hexahydrogenated with nine isoprene units.

The type strain is F18-98^T (=DSM 44665^T=NCIMB 13932^T). The organism was isolated from the rhizosphere of *Putterlickia verrucosa*.

Description of *Kitasatospora kifunensis* Nakagaito, Shimazu, Yokota and Hasegawa comb. nov.

Kitasatospora kifunensis (ki.fu.nen′sis. N.L. adj. *kifunensis* named for Mt Kifune, Kyoto Prefecture, Japan, source of the soil from which the organism was isolated).

In addition to the properties given in earlier descriptions of this organism (Iwami *et al.*, 1987; Nakagaito *et al.*, 1992a), this species is also characterized by properties acquired in the present study. Aerobic, Gram-positive, non-acid-fast actinomycete that produces melanoid pigments on tyrosine agar, but not on peptone/yeast extract/iron agar or in tryptone/yeast extract broth. Spore-chains are straight, hooked to spiral (*rectiflexibiles* to *spirales*). Spores are short, cylindrical and smooth-surfaced ($1{\cdot}2$–$1{\cdot}3 \times 0{\cdot}6$–$0{\cdot}7$ μm). Submerged spores are formed sparsely in liquid culture. Temperature range for growth is 10–32 °C; the organism does not grow below 10 °C or above 32 °C. pH range for growth is 5–9; growth does not occur at pH 4·5 or 9·5. Nitrate is not reduced to nitrite. Gelatin is not liquefied and milk is not peptonized. Casein is degraded. H_2S is produced. Starch is hydrolysed. Alkaline phosphatase, esterase (C4), esterase lipase (C8), β-galactosidase, α-glucosidase, leucine arylamidase, naphthol-AS-BI-phosphohydrolase, α-mannosidase (weak) and acid phosphatase are produced, but *N*-acetyl-β-glucosamidase, α-chymotrypsin, cystine arylamidase, α-fucosidase, α-galactosidase, β-glucosidase, β-glucuronidase, lipase (C14), trypsin and valine arylamidase are not. L(+)-Arabinose, D(+)-galactose, D(+)-glucose, glycerol, D(+)-maltose, D(−)-mannitol, D(+)-mannose, D(−)-sucrose, D(+)-trehalose and D(+)-xylose are used as sole sources of carbon for energy and growth, but cellulose, chitin, D(−)-fructose, *i*-inositol, inulin, D(+)-lactose, D(+)-raffinose, L(+)-rhamnose and salicin are not. Growth is inhibited by ampicillin (10 μg ml^{-1}, weak), chloramphenicol (30 μg ml^{-1}), ciprofloxacin (5 μg ml^{-1}), imipenem (10 μg ml^{-1}), kanamycin sulfate (30 μg ml^{-1}), methicillin (5 μg ml^{-1}, weak), nalidixic acid (50 μg ml^{-1}), novobiocin (2·5 μg ml^{-1}), oxytetracycline hydrochloride (30 μg ml^{-1}), rifampicin (30 μg ml^{-1}), streptomycin sulfate (10 μg ml^{-1}), sulfonamide (200 μg ml^{-1}, weak) and vancomycin hydrochloride (30 μg ml^{-1}), but not by lincomycin hydrochloride (2 μg ml^{-1}), norfloxacin (10 μg ml^{-1}), penicillin G (10 IU) or polymyxin B (300 IU). The strain tolerates 2·5 %, but not 3·5 %, NaCl (w/v). Resistance is shown to the polyvalent *Streptomyces* phage S7. Whole-cell chemistry reveals the presence of both *meso*- and LL-A_2pm; the muramic acid moiety is *N*-acetylated. Whole-organism hydrolysates contain galactose, mannose, glucose and ribose and the major polar lipids are phosphatidylethanolamine, diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and phosphatidylinositol mannosides. Predominant fatty acids are $C_{16:0}$, anteiso-$C_{15:0}$ and iso-$C_{15:0}$; mycolic acids are absent. Major menaquinone is hexahydrogenated with nine isoprene units.

The type strain is NBRC 15206^T (=DSM 41654^T). The organism was isolated from a soil sample obtained at Mt Kifune, Kyoto Prefecture, Japan.

Emended description of *Streptomyces aureofaciens* Duggar 1948

Streptomyces aureofaciens (au.re.o.fa′ci.ens. L. adj. *aureus* golden; L. part. adj. *faciens* producing; N.L. part. adj. *aureofaciens* golden-producing, referring to the pigment produced).

In addition to the properties given in descriptions from earlier studies (Duggar, 1948; Shirling & Gottlieb, 1968; Williams *et al.*, 1983), this species is also characterized by features acquired in the present study. Aerobic, Gram-positive, non-acid-fast actinomycete that produces a yellow-brown substrate mycelium and a reddish to grey aerial spore-mass. Does not produce diffusible or melanoid pigments. Spore-chains are flexuous (*rectiflexibiles*), open loops, hooks or extended spirals (*retinaculiaperti*) with 10–50 or more cylindrical, smooth-surfaced spores ($1{\cdot}2$–$2{\cdot}3 \times 1{\cdot}0$–$1{\cdot}5$ μm) per chain. Temperature range for growth is 10–45 °C (optimum, 28 °C). pH range for growth is 6–9·5; growth does not occur at pH 5 or 10. Nitrate is not reduced to nitrite. Gelatin is liquefied and milk is peptonized. Casein is degraded and H_2S is produced. Starch is hydrolysed. Adenine, elastin, guanine, hypoxanthine, testosterone, Tween 80, L-tyrosine and xanthine are degraded. Aesculin and urea are hydrolysed, but allantoin is not. *N*-Acetyl-β-glucosamidase, acid phosphatase, alkaline phosphatase, α-chymotrypsin, esterase (C4), esterase lipase (C8), α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, leucine arylamidase, α-mannosidase, naphthol-AS-BI-phosphohydrolase, trypsin and valine arylamidase are produced, but cystine arylamidase, α-fucosidase, β-glucuronidase and lipase (C14) are not. Adonitol (weak), L(+)-arabinose, D(+)-cellobiose, dextran (weak), D(−)-fructose (weak), D(+)-galactose, D(+)-glucose, inulin (weak), *i*-inositol, D(+)-lactose, D(+)-mannose (weak), D(−)-mannitol, D(+)-melibiose, D(+)-melezitose, D(+)-raffinose (weak), L(+)-rhamnose, salicin, D(−)-sucrose, D(+)-trehalose and D(+)-xylose are used as sole sources of carbon for energy and growth, but cellulose, L-histidine and L-phenylalanine are not. Growth is inhibited by chloramphenicol (30 μg ml^{-1}), ciprofloxacin (5 μg ml^{-1}), imipenem (10 μg ml^{-1}), kanamycin sulfate (30 μg ml^{-1}), oxytetracycline hydrochloride (30 μg ml^{-1}), polymyxin B (300 IU), rifampicin (30 μg ml^{-1}), streptomycin sulfate (10 μg ml^{-1}), sulfonamide (200 μg ml^{-1}) and vancomycin hydrochloride (30 μg ml^{-1}), but not by ampicillin (10 μg ml^{-1}), lincomycin hydrochloride (2 μg ml^{-1}), methicillin (5 μg ml^{-1}), norfloxacin (10 μg ml^{-1}) or penicillin G (10 IU). NaCl is tolerated up to a concentration of 8 % (w/v). Sensitive to the polyvalent *Streptomyces* phage S7. Cell wall contains LL-A_2pm; the muramic acid moiety is *N*-acetylated. Whole-organism hydrolysates contain ribose, glucose and mannose and major polar lipids are diphosphatidylglycerol, phosphatidylethanolamine and phosphatidylinositol. Predominant fatty acids are anteiso-$C_{15:0}$, $C_{16:0}$, iso-$C_{15:0}$ and anteiso-$C_{17:0}$; mycolic acids are absent. The major menaquinones are tetra-, hexa- and octahydrogenated with nine isoprene units.

The type strain is NRRL 2209^T (=DSM 40127^T). The strain was isolated from timothy field soil, Missouri, USA.

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