A New Genus of the Order *Actinomycetales*, *Spirilliplanes* gen. nov., with Description of *Spirilliplanes yamanashiensis* sp. nov.

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Actinomycete strain YU127-1^T (T = type strain), which produces zoospores, was isolated from a soil sample. The aerial mycelium of this organism at maturity forms short chains of spores. The hyphae form coils, and sporangia are not observed. Strain YU127-1^T contains glutamic acid, glucosamine, glycine, alanine, and meso-diaminopimelic acid in its cell wall (wall chemotype II), 3-O-methylmannose, mannose, xylose, and glucose as whole-cell sugars, menaquinone 10(H₄), and glycolyl cell wall polysaccharides and has a guanine-plus-cytosine content of 69.0 mol%. Mycolic acids are absent. Phosphatidylinositol and phosphatidylethanolamine are diagnostic phospholipids. The chemotaxonomic data, except for the lack of arabinose in the whole-cell sugars, indicate that this strain belongs to the family *Micromonosporaceae*. The morphological and physiological characteristics and chemotaxonomic and phylogenetic data for this strain differ from those of the previously described actinomycetes. We therefore propose a new genus, *Spirilliplanes*, for this organism; the type species of the genus is *Spirilliplanes yamanashiensis* sp. nov., and the type strain of *S. yamanashiensis* is strain YU127-1 (= IFO 15828).

The family *Micromonosporaceae* was emended by Goodfellow et al. (5) to include the chemotaxonomically defined actinomycete group whose members are cell wall chemotype II and whole-cell sugar pattern D organisms (14). At that time, this family included the genera *Micromonospora*, *Actinoplanes*, *Dactylosporangium*, and *Pilimelia*. The genera *Catellatospora* (2) and *Glycomyces* (12) also have these properties. Furthermore, it was suggested that the genera *Catenuloplanes* and *Couchioplanes*, which are cell wall type VI and whole-cell sugar pattern D taxa or have xylose as the sole diagnostic sugar (25, 28), should be included in this family based on a phylogenetic study in which 16S rRNA sequences were used (25).

During our taxonomic studies of motile actinomycetes, we isolated strain YU127-1^T (T = type strain) from a soil sample from Yamanashi Prefecture, Japan. This organism produces zoospores and has meso-diaminopimelic acid and glycine in its cell wall (chemotype II). Among the actinomycete genera with chemotype II walls, the genera *Micromonospora*, *Catellatospora*, and *Glycomyces* do not produce zoospores, and the genera *Actinoplanes*, *Dactylosporangium*, and *Pilimelia* are known to form motile sporangiospores. The following five genera that form zoospores in chains have been described previously: *Sporichthya* (15), *Actinosynnema* (7), *Actinokineospira* (6), *Catenuloplanes*, and *Couchioplanes*. However, the genus *Sporichthya* is a wall chemotype I taxon, the genus *Actinosynnema* is a wall chemotype III taxon, the genus *Actinokineospira* is a wall chemotype IV taxon, and the genera *Catenuloplanes* and *Couchioplanes* are wall chemotype VI taxa. Therefore, strain YU127-1^T differs from the previously described members of chemotype II genera and the actinomycete genera which produce zoospores in chains.

In this paper we describe the characterization and classification of strain YU127-1^T, and we propose that this organism should be included in a new genus, the genus *Spirilliplanes*, and a new species, *Spirilliplanes yamanashiensis*.

MATERIALS AND METHODS

Microorganisms and culture conditions. Strain YU127-1^T was isolated from a soil sample that was collected at Kofu in Yamanashi Prefecture, Japan, treated by dry heating (120°C, 1 h) (18), suspended in sterile water, and spread onto humic acid-vitamin (HV) agar (8). *Mycobacterium smegmatis* was used for a comparison of cell wall sugar compositions. To obtain freeze-dried cells for chemotaxonomic analyses, a culture was grown in yeast extract-glucose broth (containing 10 g of yeast extract and 10 g of D-glucose in 1,000 ml of distilled water; pH 7.0) on a rotary shaker at 28°C. Strain YU127-1^T has been deposited in the Institute for Fermentation, Osaka culture collection as strain IFO 15828^T.

Cultural characteristics were determined after 14 days of incubation at 28°C by International *Streptomyces* Project (ISP) methods (24). Colors are described below in common terms, but exact colors were determined by comparison with color chips in *A Mycological Colour Chart* (20).

Morphological and physiological characterization. Morphological features were observed on HV agar, and physiological features were observed on media commonly used for characterization of *Streptomyces* species (24). Motility was studied with a light microscope by using spores grown on HV agar for 7 to 10 days at 28°C and then incubated at 28°C for 1 h in distilled water or 0.01 M phosphate buffer (pH 7.0) containing 10% soil extract. Colonies grown on HV agar for 14 days at 28°C were investigated with a scanning electron microscope (model JSM-5400; JEOL, Ltd., Tokyo, Japan). Samples for scanning electron microscopy were prepared by cutting a block from an agar plate, fixing it in 2% osmium tetroxide vapor at room temperature for 4 h, dehydrating it through a graded ethanol series, substituting isoamyl acetate for ethanol, critical point drying (model HCP-2 apparatus; Hitachi Koki Co., Ltd., Tokyo, Japan), and then sputter coating with palladium under a vacuum.

Analyses of chemotaxonomic characteristics. The glycolate test and analyses of whole-cell sugars, polar lipids, cellular fatty acids, mycolic acids, isoprenoid quinones, peptidoglycan, and DNA base composition were performed as described previously (25).

To identify an unknown sugar in the whole cells of strain YU127-1^T, a sample was prepared as follows. Dried whole cells were hydrolyzed with 2 N HCl as previously described (25). The hydrolysate was reduced with sodium borohydride in D₂O to make the ³H-labeled alditols, which were acetylated by the method of Albersheim et al. (1). The products were analyzed with a model GC-17A gas chromatograph (Shimadzu, Kyoto, Japan) equipped with a type Rtx-2330 column (30 m by 0.25 mm; Restek Co., Bellefonte, Pa.) and a Shimadzu model QP-5000 mass spectrofluorometer.

PCR and sequencing of the products. 16S rRNA was amplified by PCR (21) by using TaKaRa *Taq* (Takara Shuzo, Kyoto, Japan) and primers 9F (5'-GAGTTTGATCTGGCTCAG) and 1541R (5'-AAGGAGGTGATCCAACC). The conditions used for thermal cycling were as follows: denaturation of the target DNA at 95°C for 1 min, followed by 30 cycles consisting of denaturation at 95°C for 1 min, primer annealing at 50°C for 1 min, and primer extension at 72°C for 1.5 min. At the end of the cycle, the reaction mixture was kept at 72°C for 5 min and then cooled to 4°C. The 1.5-kb amplified 16S ribosomal DNA (rDNA) fragment was separated by agarose gel electrophoresis and purified by using a Prep-A-Gene DNA purification kit (Bio-Rad Laboratories, Hercules, Calif.).

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TABLE 1. Strains investigated in this study and 16S rDNA accession numbers

Taxon	Strain	Accession no.
<i>Spirilliplanes yamanashiensis</i>	YU127-1 ^T (= IFO 15828 ^T)	D63912
<i>Actinobispora yunnanensis</i>	IFO 15681	D85472
<i>Actinocorallia herbida</i>	IFO 15485	D85473
<i>Actinomadura madurae</i>	IFO 14623	D85468
<i>Actinomadura viridis</i>	IFO 15238	D85467 ^a
<i>Actinoplanes philippinensis</i>	IFO 13878	D85474 ^a
<i>Actinosynnema mirum</i>	IFO 14064	D85475
<i>Amycolatopsis orientalis</i> subsp. <i>orientalis</i>	IFO 12806	D86935
<i>Catellatospora citrea</i> subsp. <i>citrea</i>	IFO 14495	D85477
<i>Catenuloplanes japonicus</i>	IFO 14176	D85476
<i>Couchioplanes caeruleus</i> subsp. <i>azureus</i>	IFO 13993	D85478
<i>Couchioplanes caeruleus</i> subsp. <i>caeruleus</i>	IFO 13939	D85479
<i>Dactylosporangium aurantiacum</i>	IFO 12592	D85480 ^a
<i>Dactylosporangium fulvum</i>	IFO 14381	D86942 ^a
<i>Dactylosporangium matsuzakiense</i>	IFO 14259	D86940 ^a
<i>Dactylosporangium roseum</i>	IFO 14352	D86941 ^a
<i>Dactylosporangium salmonium</i>	IFO 14103	D86938 ^a
<i>Dactylosporangium thailandense</i>	IFO 12593	D85481 ^a
<i>Dactylosporangium vinaceum</i>	IFO 14181	D86939 ^a
<i>Excellispora viridilutea</i>	IFO 14480	D86943 ^a
<i>Glycomyces harbinensis</i>	IFO 14487	D85483 ^a
<i>Glycomyces rutgersensis</i>	IFO 14488	D85484 ^a
<i>Glycomyces tenuis</i>	IFO 15904	D85482 ^a
<i>Herbidospora cretacea</i>	IFO 15474	D85485
<i>Intrasporangium calvum</i>	IFO 12989	D85486
<i>Luteococcus japonicus</i>	IFO 12422	D85487
<i>Microbispora rosea</i> subsp. <i>rosea</i>	IFO 14044	D86936 ^a
<i>Micromonospora chalcone</i>	IFO 12135	D85489
<i>Microtetraspora glauca</i>	IFO 14761	D85490 ^a
<i>Microtetraspora pusilla</i>	IFO 14684	D85491 ^a
<i>Nocardiosis dassonvillei</i>	IFO 14626	D85492 ^a
<i>Pilimelia terevasa</i>	IFO 15964	D86946 ^a
<i>Planobispora longispora</i>	IFO 13918	D85494 ^a
<i>Planomonospora parantospora</i>	IFO 13880	D85495 ^a
<i>Planotetraspora mira</i>	IFO 15435	D85496
<i>Spirillospora alba</i>	IFO 12248	D85498
<i>Streptoalloteichus hindustanus</i>	IFO 15115	D85497
<i>Streptosporangium album</i>	IFO 13900	D85469
<i>Thermomonospora curvata</i>	IFO 15933	D86945

^a Data from direct sequencing.

The purified fragment was blunt ended with T4 DNA polymerase by using a DNA blunting kit (Takara Shuzo), and the 5' end of the amplified DNA was phosphorylated with T4 polynucleotide kinase (Takara Shuzo) according to the manufacturer's instructions. The DNA was ligated into the dephosphorylated *HincII* site of phagemid vector pUC118 (Takara Shuzo). The phagemid was introduced into *Escherichia coli* JM109 (27). Single-stranded DNA for use as a sequencing template was obtained after infection with bacteriophage M13KO7 (26). Plasmids were prepared by the Miniprep protocol (16).

The single-stranded DNA and plasmid-cloned material were sequenced by using an AutoRead sequencing kit (Pharmacia, Uppsala, Sweden) and were analyzed with a Pharmacia model A.L.F. DNA Sequencer II apparatus. The 5'-fluorescein-labeled oligonucleotide primers used were M13 Universal and Reverse primer (Pharmacia) and primer 1111R (5'-TTGCGCTCGTGTGCGG ACT).

Phylogenetic analysis. The 16S rRNA sequences of the strains examined (Table 1) and the sequences of reference organisms obtained from databases were aligned with the sequence of *Streptomyces ambifaciens* (19). Evolutionary distances were represented by the K_{nuc} value of Kimura (9), and a phylogenetic tree was constructed by the neighbor-joining method (22) from K_{nuc} values. The topology of the phylogenetic tree was evaluated by the bootstrap resampling method of Felsenstein (4) with 1,000 replicates.

Nucleotide sequence accession numbers. The nucleotide sequence data reported in this paper have been deposited in the DDBJ, EMBL, and GenBank nucleotide sequence databases, under the accession numbers shown in Table 1.

RESULTS

Morphological observations. Morphological observation of a 14-day-old culture of strain YU127-1^T grown on HV agar revealed the presence of short hyphae arranged in spirals, which could arise from the substrate mycelia. The aerial mycelium at maturity formed short chains of spores (Fig. 1B through D). Although the sporogenous hyphae aggregated into clusters resembling sporangia (Fig. 1A), no true sporangia were observed, because the hyphae were not covered with a sheath (Fig. 1B through D). Several spores per sporogenous hypha were observed, and the spores were ovals to short rods (0.5 to 0.7 by 0.7 to 1.0 μm) with smooth surfaces (Fig. 1).

After incubation at 28°C for 1 h in both water and 0.01 M phosphate buffer (pH 7.0) containing 10% soil extract, spores showed active motility. More zoospores were observed when phosphate buffer was used than when water was used.

Growth characteristics. As shown in Table 2, strain YU127-1^T developed yellow to orange colonies on most media tested. It showed good growth on oatmeal agar (ISP medium 3), inorganic salts-starch agar (ISP medium 4), and peptone-yeast extract-iron agar (ISP medium 6), and it produced a brown soluble pigment on tyrosine agar (ISP medium 7). It developed aerial hyphae on most media tested, especially inorganic salts-starch agar (ISP medium 4) and HV agar (Fig. 1).

Physiological and biochemical characteristics. The biochemical properties of strain YU127-1^T are shown in Table 3. The strain utilized glucose, rhamnose, and mannitol. It was positive for gelatin liquefaction and hydrolysis of starch and negative for decomposition of calcium malate, reduction of nitrate, and peptonization of milk.

Chemotaxonomic characteristics. The menaquinone composition, cell wall amino acid composition, whole-cell sugar pattern, phospholipid type, and DNA guanine-plus-cytosine (G+C) content of strain YU127-1^T are shown in Table 4. The major menaquinone was MK-10(H₄), and small amounts of MK-10(H₆) and MK-10(H₈) were also present. The cell walls contained *meso*-diaminopimelic acid, glucosamine, glycine, glutamic acid, and alanine, indicating that the strain is a wall chemotype II strain according to the scheme of Lechevalier and Lechevalier (14), and the peptidoglycan type was type A1 γ according to the classification of Schleifer and Kandler (23). Whole cells of strain YU127-1^T contained large amounts of mannose, glucose, and an unknown sugar and small amounts of galactose and xylose. Arabinose and rhamnose were not detected. The unknown sugar was identified as 3-O-methylmannose by an analysis of the fragment pattern after a gas chromatography-mass spectrometry analysis and comparison of the retention time with the retention time of *Mycobacterium smegmatis* (17) during high-performance liquid chromatography. Phosphatidylethanolamine and phosphatidylinositol were diagnostic phospholipids, and phosphatidylglycerol, phosphatidylcholine, and an unidentified phospholipid including glucosamine were not detected. This pattern corresponds to phospholipid type II (13). The G+C content of DNA was 69.0 mol%. The fatty acids are shown in Table 5. The major cellular fatty acids detected were C_{17:1}, C_{17:0}, anteiso-C_{15:0}, iso-C_{15:0}, and iso-C_{16:0}, which corresponds to fatty acid type 2d (11). The acyl type of the cell wall polysaccharides was glycolyl. Mycolic acid was absent.

Phylogenetic position. The sequencing strategy generated a continuous sequence ranging from position 10 to position 1541 (*E. coli* numbering system [3]). The total number of nucleotides compared was 1,173 after elimination of all sites whose nucleotides were not determined in any sequence. The phylogenetic tree obtained by applying the neighbor-joining method

FIG. 1. Light micrograph (A) and scanning electron micrographs (B through D) of *S. yamanashiensis* YU127-1^T grown on HV agar for 14 days at 28°C.

to K_{nuc} values is shown in Fig. 2. 16S rDNA analysis revealed that YU127-1^T is phylogenetically related to members of the genera *Micromonospora*, *Actinoplanes*, *Dactylosporangium*, *Pilimelia*, *Catellatospora*, *Catenuloplanes*, and *Couchioplanes* (similarity levels, 95.9 to 97.6%). These strains phylogenetically form a cluster, and this cluster is distinct from other groups, such as the families *Streptosporangiaceae*, *Pseudonocardaceae*, etc. The bootstrap analysis gave a relatively high level (99%) for the separation of this cluster from other groups, so the branching order in this region is definite. The genus *Glycomyces* is phylogenetically independent; it is clearly less closely related to members of the family *Micromonosporaceae*

(similarity levels, 87.4 to 89.8%) and other actinomycetes (similarity levels, 87.4 to 85.5%).

DISCUSSION

Strain YU127-1^T is a wall chemotype II organism. The chains of very narrow and coiled sporogenous hyphae with zoospores often appear to be sporangium-like structures under a light microscope. Under a scanning electron microscope, however, these structures are found to be aggregated hyphae, not true sporangia.

The genera *Micromonospora*, *Actinoplanes*, *Dactylospor-*

TABLE 2. Cultural characteristics of strain YU127-1^T

Medium	Growth	Sporulation	Diffusible pigment ^a	Color of colony ^a
Yeast extract-malt extract agar (ISP medium 2)	Moderate	Moderate	Absent	Strong orange (7)
Oatmeal agar (ISP medium 3)	Good	Moderate	Absent	Light to moderate orange-yellow (10)
Inorganic salts-starch agar (ISP medium 4)	Good	Good	Absent	Light to moderate orange-yellow (10) to strong orange (7)
Glycerol-asparagine agar (ISP medium 5)	Moderate	Poor	Absent	Light to moderate orange-yellow (10)
Peptone-yeast extract-iron agar (ISP medium 6)	Good	Poor	Absent	Moderate orange-yellow (44) to vivid yellow (12)
Tyrosine agar (ISP medium 7)	Moderate	Poor to moderate	Moderate brown (63)	Moderate reddish brown (60) to moderate orange (62)
Nutrient agar	Moderate	Absent	Absent	Moderate orange (42)

^a The color codes in parentheses correspond to the color codes in *A Mycological Colour Chart* (20).

TABLE 3. Phenotypic characteristics of strain YU127-1^T

Characteristic	Strain YU127-1 ^T reaction
Utilization of:	
Glucose	++ ^a
D-Xylose	+
Inositol	-
Saccharose	+
Raffinose	+
Rhamnose	++
D-Mannitol	++
D-Fructose	-
L-Arabinose	±
Pigmentation in:	
ISP medium 1	None
ISP medium 6	None
ISP medium 7	Brown
Gelatin liquefaction	P
Peptonization of milk	N
Starch hydrolysis	P
Calcium malate hydrolysis	N
Nitrite produced from nitrate	N
Cellulose decomposition	N

^a ++, good; +, moderate; ±, poor; -, none; P, positive; N, negative.

gium, *Pilimelia*, *Glycomyces*, and *Catellatospora* are wall chemotype II taxa. Among the wall chemotype II genera, the genera *Actinoplanes*, *Dactylosporangium*, and *Pilimelia* have motile elements. However, YU127-1^T is distinguishable from these genera in that its spores are not enclosed in a sporangial wall and arabinose is not a whole-cell sugar. Strain YU127-1^T can also be distinguished from the genera *Dactylosporangium* and *Pilimelia* by its menaquinone pattern. We previously reported that the genera *Catenuloplanes* and *Couchioplanes* phylogenetically belong to the family *Micromonosporaceae* (25). YU127-1^T resembles these genera in that all of these taxa have sporogenous hyphae with zoospores. However, it differs from them in wall chemotype and in menaquinone and cellular fatty acid contents (Table 6).

On the basis of morphological, physiological, chemotaxonomic, and phylogenetic criteria, strain YU127-1^T is readily distinguishable from the motile actinomycetes mentioned above and warrants a new taxon. Therefore, we propose that strain YU127-1^T (= IFO 15828^T) be classified in a new genus, the genus *Spirilliplanes*, whose the type species is *Spirilliplanes yamanashiensis* sp. nov.

The genus *Spirilliplanes* should be considered a member of the family *Micromonosporaceae* Krassilnikov 1938 emend. Goodfellow et al. 1990 (5) on the basis of the results of the comparative analysis of 16S rRNA sequences described here. Furthermore, the genus *Catellatospora*, which is a wall chemotype II taxon, should also be placed in this family on the basis of the results of the comparative analysis of 16S rRNA sequences described here. Goodfellow et al. (5) described the criteria for members of the family *Micromonosporaceae* as follows. The wall peptidoglycan of members of the family *Micromonosporaceae* contains *meso*- and/or 3-hydroxy-diaminopimelic acid and is a type A1γ, peptidoglycan, and whole-cell hydrolysates are rich in arabinose and xylose and contain variable amounts of other sugars (5). However, the genus *Spirilliplanes* contains no detectable arabinose in its whole-cell sugars, and the genus *Catenuloplanes* contains small amounts of arabinose or no arabinose (28). Furthermore, the genus *Spirilliplanes* contains 3-*O*-methyl-mannose as a characteristic sugar. The genera *Catenuloplanes* and *Couchioplanes*, while phyloge-

TABLE 4. Chemotaxonomic characteristics of strain YU127-1^T

Characteristic	Strain YU127-1 ^T
Major menaquinones ^a	
MK-10(H ₄)	++
MK-10(H ₆)	+
MK-10(H ₈)	+
Amino acid composition of peptidoglycan (molar ratio) ^b	
Glutamic acid	1.00
Muramic acid	0.43
Glucosamine	0.84
Glycine	1.43
Alanine	0.79
<i>meso</i> -Diaminopimelic acid	1.05
Sugar composition of whole cells ^c	
3- <i>O</i> -Methylmannose	+
Mannose	+
Arabinose	-
Galactose	+
Rhamnose	-
Xylose	+
Glucose	+
Phospholipid composition ^c	
Phosphatidylinositol	+
Phosphatidylethanolamine	+
Phosphatidylcholine	-
Phosphatidylglycerol	-
Unidentified phospholipid including glucosamine	-
Glycolyl test	Glycolyl type
G+C content of DNA (mol%)	69.0

^a ++, >20%; +, 10 to 20%.

^b Calculated by defining the amount of glutamic acid as 1.00.

^c +, present; -, absent.

netically belonging to the family *Micromonosporaceae*, have L-lysine instead of *meso*-diaminopimelic acid in their wall peptidoglycan and their peptidoglycan type is type A3γ (25, 28). Thus, the diamino acid in the cell wall and the presence of arabinose in the whole-cell sugars are not important criteria for membership in the family *Micromonosporaceae*. It is thought that the criteria for membership in the family *Micro-*

TABLE 5. Cellular fatty acid composition of strain YU127-1^T

Fatty acid	% in strain YU127-1 ^T
anteiso-branched fatty acids	
C _{15:0}	14.6
C _{17:0}	5.3
iso-branched fatty acids	
C _{14:0}	2.7
C _{15:0}	12.9
C _{16:0}	12.9
C _{17:0}	1.2
Saturated fatty acids	
C _{15:0}	4.8
C _{16:0}	2.6
C _{17:0}	15.0
C _{18:0}	3.3
C _{19:0}	2.0
Unsaturated fatty acids	
C _{16:1}	1.5
C _{17:1}	17.5
C _{18:1}	2.2
Unidentified fatty acid	1.5

FIG. 2. Phylogenetic tree derived from 16S rRNA sequences of actinomycetes. *E. coli* was used as the root organism. Scale bar = 0.01 K_{nuc} in nucleotide sequences. The numbers on the branches are confidence limits (expressed as percentages) estimated from a bootstrap analysis with 1,000 replicates.

monosporaceae include the presence of *meso*- and/or 3-hydroxy-diaminopimelic acid or L-lysine in the wall peptidoglycan and the presence of xylose in whole cells, while the presence of arabinose in the whole cells is variable (sugar pattern D or xylose is the sole diagnostic sugar) (14).

The genus *Glycomyces*, a wall chemotype II taxon, should not be placed in this family on the basis of the comparative analysis of 16S rRNA sequences described here. Further study will be necessary to determine the position of the genus *Glycomyces*.

The family *Micromonosporaceae* was recently emended by Koch et al. (10), and thus we could not address that issue.

Description of *Spirilliplanes* gen. nov. *Spirilliplanes* (Spi.ril.li.plan'es. Gr. n. *speira*, coil; Gr. n. *planes*, a wanderer; M.L. fem.n. *Spirilliplanes*, an organism with wandering cells, in spirals). Gram-positive, non-acid-fast, aerobic organisms with branching hyphae. Nonfragmenting substrate mycelia are present. The aerial hyphae aggregate into clusters resembling coils, but true sporangia are not observed; 14-day-old cultures grown on inorganic salts-starch agar have hyphae arranged in spirals of 5 to 10 turns with several spores per spore chain. Spores are

ovals or short rods (0.5 to 0.7 by 0.7 to 1.0 μ m) with smooth surfaces and are motile when they are suspended in 0.01 M phosphate buffer (pH 7.0) containing 10% soil extract or distilled water.

Strictly aerobic. Good growth occurs at temperatures between 25 and 30°C. The organism shows good growth on oatmeal agar, inorganic salts-starch agar, and peptone-yeast extract-iron agar. In general, the vegetative mycelia of the strain are yellow to orange, and aerial hyphae are white.

Cell walls contain glutamic acid, glucosamine, glycine, alanine, and *meso*-diaminopimelic acid. The wall chemotype is type II according to the scheme of Lechevalier and Lechevalier (14), and the peptidoglycan type is presumed to be type A1 γ according to the classification of Schleifer and Kandler (23). Mannose, 3-*O*-methylmannose, glucose, xylose, and galactose are detected in the whole-cell sugars. C_{17:1}, C_{17:0}, anteiso-C_{15:0}, iso-C_{15:0}, and iso-C_{16:0} are present as major cellular fatty acids. The G+C content of the DNA is 69 mol%. The major menaquinone is MK-10(H₄), and small amounts of MK-10(H₆) and MK-10(H₈) are also present. Phosphatidylethanolamine and phosphatidylinositol are diagnostic phospholipids (phospho-

TABLE 6. Differential characteristics of the genus *Spirilliplanes* and related genera^a

Genus	G+C content of DNA (mol%)	Motility of spores	Sporangium formation	Glycolyl test	Fatty acid type ^b	Cell wall type ^c	Major menaquinone(s)	Phospholipid type ^d	Characteristic sugar(s) in whole cells ^e
<i>Spirilliplanes</i>	69	+	—	Glycolyl	2d	II	MK-10(H ₄)	PII	Xyl, Gal
<i>Actinoplanes</i>	72–73	+	+	Glycolyl	2d	II	MK-9(H ₄), MK-10(H ₄)	PII	Ara, Xyl
<i>Dactylosporangium</i>	72–73	+	+	Glycolyl	3b	II	MK-9(H ₄ , H ₆ , H ₈)	PII	Ara, Xyl
<i>Pilimelia</i>	ND	+	+	Glycolyl	2d	II	MK-9(H ₂ , H ₄)	PII	Ara, Xyl
<i>Micromonospora</i>	71–73	—	—	Glycolyl	3b	II	MK-10(H ₄ , H ₆), MK-9(H ₄ , H ₆)	PII	Ara, Xyl
<i>Catenuloplanes</i>	71–73	+	—	Glycolyl	2c	VI	MK-9(H ₈), MK-10(H ₈)	PIII	Xyl
<i>Couchioplanes</i>	70–72	+	—	Glycolyl	2c	VI	MK-9(H ₄)	PII	Xyl, Ara, Gal
<i>Catellatospora</i>	71–72	—	—	Glycolyl	ND	II	MK-10(H ₈ , H ₆), MK-9(H ₄ , H ₆)	PII	Ara, Xyl
<i>Glycomyces</i>	71–73	—	—	Glycolyl	2c	II	MK-9(H ₄), MK-10(H ₂ , H ₄)	PI	Ara, Xyl

^a +, present; —, absent; ND, not determined.^b According to the classification of Kroppenstedt (11).^c According to the classification of Lechevalier and Lechevalier (14).^d According to the classification of Lechevalier et al. (13).^e Xyl, xylose; Gal, galactose; Ara, arabinose.

lipid pattern type PII). The acyl type of the cell wall polysaccharides is glycolyl. Habitat: soil.

The type species is *Spirilliplanes yamanashiensis*.

Description of *Spirilliplanes yamanashiensis* sp. nov. *Spirilliplanes yamanashiensis* (ya.ma.na.shi.en'sis. M.L. adj. *yamanashiensis*, pertaining to Yamanashi Prefecture, Japan, the source of soil from which the organism was isolated.) The morphological, chemotaxonomic, and general characteristics are the same as those given above for the genus. Brownish soluble pigment is produced on tyrosine agar (ISP medium 7). Gelatin liquefaction positive. Hydrolyzes starch. Does not decompose calcium malate. Does not coagulate milk. Xylose, glucose, inositol, raffinose, rhamnose, mannitol, and sucrose are utilized, but fructose and inositol are not. The G+C content of the DNA is 69 mol%. The type strain is strain IFO 15828.

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