Genomic and phylogenomic insights into the family *Streptomycesaceae* leads to proposal of six novel genera

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**ABSTRACT**

The family *Streptomycesaceae* is a large and diverse family within the phylum *Actinobacteria*. The members of the family are known for their ability to produce medically important secondary metabolites, notably antibiotics. In this study, strains showing low 16S rRNA gene similarity (<97.3%) to other members of the family *Streptomycesaceae* were identified and their high genetic diversity was reflected in a phylogenomic analysis using genome wide conserved proteins. This analysis resulted in the identification of six distinct genus level clades, with two separated from the genus *Streptacidiphilus* and four separated from the genus *Streptomyces*. Compared to members of *Streptacidiphilus* and *Streptomyces*, average amino acid identity (AAI) analysis of the new genera identified gave values within the range of 60 – 80%, as has been previously observed for comparisons of related but distinct bacterial genera. The whole genome phylogeny was reconstructed based on genome wise optimized and conserved proteins and AAI analyses indicated that these phylogenetically distinct taxa may be assigned to six novel genera, namely *Actinacidiphila*.
gen. nov., Phaeacidiphilus gen. nov., Mangrovactinospora gen. nov., and Peterkaempfera gen. nov. and Streptantibioticus gen. nov. and Wenjunlia gen. nov.

Keywords Actinobacteria · genome-based phylogeny · genome metrics · genome-based taxonomy · Streptomyctales

Abbreviations AAI – Average Amino acid Identity · dDDH – Digital DNA-DNA hybridization · ANI – Average Nucleotide Identity · POCP – Percentage of conserved proteins

Introduction

The family Streptomycetaceae Waksman and Henrici 1943 (Approved Lists 1980) emend. Nououi et al. 2018 [1, 2] currently contains six genera, which themselves contain more than 700 species with a validly published and correct name (https://lpsn.dsmz.de/family/streptomycetaceae). The family was first described by Waksman and Henrici (1943) [1] and has recently been placed within the sub-order Streptomycineae (Stackebrandt et al. 1997) emend. Zhi et al. 2009 [3, 4] of the class Actinomycetia (Salam et al. 2020) [5]. Members of the family Streptomycetaceae are Gram-positive, aerobic organisms lacking mycolic acids and form extensively branched substrate mycelium, with generally non-septate hyphae that rarely fragment into conidia (Kämpfer 2015; Waksman and Henrici 1943) [1, 6]. In 1982, Kitasatospora was added to the family Streptomycetaceae (with Kitasatospora setae as the type species) but members of the genus were later reclassified into Streptomyces (Ōmura et al. 1982; Wellington et al. 1992) [7, 8]. However, Kitasatospora was reestablished based on the exclusive presence of galactose and differences in the diamino acids of the cell walls of members of the genus compared to Streptomyces (Zhang et al. 1997) [9]. Subsequently the genera Streptacidiphilus and Allostreptomyces were added to the family Streptomycetaceae (Kim et al. 2003; Huang et al. 2017) [10, 11]. Recently, a genome-based approach has further clarified the taxonomy within the family, allowing the demarcation of two novel genera, Embleya and Yinghuangia (Nouioui et al. 2018) [2]. Thus, the family Streptomycetaceae currently contains six genera, i.e., Allostreptomyces, Embleya, Kitasatospora, Streptacidiphilus, Streptomyces and Yinghuangia (Waksman and Henrici 1943; Ōmura et al. 1982; Kim et al. 2003; Huang et al. 2017; Nouioui et al. 2018; Li et al. 2021) [1, 2, 7, 10, 11, 12], although Salam et al (2020) [5] have proposed placement of Allostreptomyces in Allostreptomyctaceae fam. nov.

Initially, the taxonomy of Streptomycetaceae was mainly based on the morphological characteristics (Waksman and Henrici 1943) [1]. However, later ‘polyphasic’ studies based on phenotypic and single gene phylogenetic analyses have been unable to provide a well-resolved phylogeny within this family (Kämpfer
2006; Glaeser and Kämpfer 2016) [13, 14]. Labeda et al. (2012) [15] showed 16S rRNA gene sequences could be used to demonstrate the species diversity within the family *Streptomyces*, defining 130 statistically supported clades, several unsupported clusters and additional single species lineages. The phylogenetic resolution within the family was significantly improved by the development of a multi-locus sequence analysis (MLSA) scheme using the *atpD, gyrB, rpoB, recA*, and *trpB* housekeeping genes (Labeda et al. 2017) [16]. This analysis supported the phylogenetic distinctiveness of the closely related genera *Kitasatospora* and *Streptacidiphilus*, and the transfer of nine *Streptomyces* species into the genus *Kitasatospora*. Further clarification was achieved by the presentation of an emended description of the genus *Kitasatospora* and the reclassification of *Streptomyces indigoferus* and *Streptomyces xanthocidicus* into the genus (Nouioui et al. 2018) [2].

Taxonomic studies based on genomic metrics have gained momentum as a promising approach for delineation of genera and species related to and within *Streptomyces* (Glaeser and Kämpfer 2016; Nouioui et al. 2018; Komaki and Tamura 2020; Madhaiyan et al. 2020; Volpiano et al. 2021; Li et al. 2021) [4, 12, 14, 17, 18, 19]. Genome sequence-derived parameters such as dDDH (digital DNA-DNA hybridization), ANI (Average Nucleotide Identity), AAI (Average Amino acid Identity) are now routinely used for taxonomic delineation especially at the species and genus levels (Chun et al. 2018, Barco et al. 2020) [20, 21]. Furthermore, genome wise optimized and conserved proteins based phylogenomic trees surpassing an MLSA performed with a few housekeeping genes for higher taxonomic placements. Hence, the present study was designed to elucidate the evolutionary relationships of taxa belonging to the family *Streptomyces* using genome sequence data and to assign the appropriate taxonomic rank to taxa identified as needing reclassification.

**Materials and methods**

**16S rRNA and conserved protein based phylogenetic analysis**

To understand the evolutionary relationships between the members of *Streptomyces*, a phylogenetic tree was reconstructed using the 16S rRNA gene sequences from 456 type strains belonging to *Streptomyces* (Table S1) and *Acidothermus cellulolyticus* ATCC 43068 as an outgroup, using to the sequence accessions provided by the List of Prokaryotic names with Standing in Nomenclature [https://lpsn.dsmz.de/family/streptomycetaceae; Parte et al. 2020] [22]. The sequences were aligned using SINA 1.2.11 (Pruesse et al., 2012) [23] and positions containing gaps were then removed. The 'phangorn' ([Schliep 2011] [24] v. 2.6.3 R package was used to construct a neighbor-joining (NJ) tree. The ModelTest function was used to select the GTR+G+I as the best-fitted model according to the Akaike information...
Results and discussion

PhyloPhlAn automatically identifies species-specific core proteins using UniRef90 gene families and calculates a maximum-likelihood tree from an alignment of selected high-scoring phylogenetically relevant positions (Segata at al., 2013; Asnicar et al., 2020 [29, 30]).

Analyses of genomic metrics

Genome distances in the form of dDDH values were calculated by the Genome-to-Genome Distance Calculator version 2.1 (Meier-Kolthoff et al. 2013) [31]. The ANI was calculated based on the BLASTn method for close relatives using EDGAR v2.3 [Blom et al. 2016] [32]. The pairwise average AAI was calculated using the AAI workflow with default settings in CompareM package v0.0.23 (https://github.com/dparks1134/CompareM) for selected representatives from each clade.

The percentage of conserved protein (POCP) in each pair of genomes was derived using the formula [(C1+C2)/(T1+T2)]×100%, where C1 and C2 denote the numbers of conserved proteins of T1 and T2, representing the total numbers of predicted proteins respectively in the pair of genomes in comparison. Conserved proteins were identified using BLASTp match with an e-value of less than 1e-5, sequence identity of more than 40% and an alignable region of the query protein sequence of more than 50%, as previously recommended (Qin et al., 2014) [33].
To study the taxonomic relationships within the family Streptomycetaceae, we first reconstructed a 16S rRNA gene phylogeny with most of the Allostreptomyces, Embleya, Kitasatospora, Streptacidiphilus and Streptomyces type strains described so far ([Fig. S1](#fig-s1)–c). The 16S rRNA gene sequence alignment using SINA produced 1,144 nt with no gaps. Of these, 331 (28.9%) sites were variable. The bootstrap support values for the 16S rRNA trees reconstructed was low in many branches, which is expected for phylogenies based on a single phylogenetic marker and for strains that share highly similar 16S rRNA sequences, such as members of Streptomyces ([Guo et al., 2008](#guo2008)) [34]. In these analyses Allostreptomyces and Embleya were resolved from Streptomyces, whereas Kitasatospora and Streptacidiphilus were recovered within Streptomyces. Whilst Kitasatospora species were recovered in a single cluster, the analyses showed both Streptomyces and Streptacidiphilus to be polyphyletic.

In order to provide further taxonomic resolution for the family Streptomycetaceae, a phylogenomic analysis based on universally conserved and genome wise optimized proteins within the Streptomycetaceae was carried out. This resolved members of the genera Streptacidiphilus and Streptomyces into several well supported lineages ([Fig. 1](#fig-1)). Three lineages were identified within the genus Streptacidiphilus. Seven species ([Streptacidiphilus anmyonensis, Streptacidiphilus carbonis, Streptacidiphilus jiangxienensis, Streptacidiphilus melanogenes, Streptacidiphilus neuraminicus, Streptacidiphilus pinicola and Streptacidiphilus rugosus] clustered with the type species, Streptacidiphilus albus i.e., form Streptacidiphilus sensu stricto [s.s.]). The second lineage, which formed a sister clade to Kitasatospora, consisted of Streptacidiphilus griseoplanus, a recently reclassified Streptomyces that produces grey mycelium, and Streptacidiphilus bronchialis, a ciprofloxacin resistant bacterium producing aerial mycelium of different colours depending on the growth medium ([Nououi et al., 2019](#nououi2019)) [35]. Their 16S rRNA gene sequences exhibit 98.8% similarity and on phylogenetic analysis formed a cluster with high bootstrap support. The earlier MLSA analysis of Labeda et al. ([2017](#labeda2017)) [16] also placed *S. griseoplanus* outside of *Streptacidiphilus* s.s. and suggested that this species might belong to a novel genus, whilst [Nououi et al. (2019)](#nououi2019) [35] discussed characteristics of *S. bronchialis* indicative of a ‘fuzzy’ species with a hybrid of genomic and chemotaxonomic features from *Streptacidiphilus* and *Streptomyces*. The conserved protein-based phylogeny presented here ([Fig. 1](#fig-1)) clearly shows that these taxa are phylogenetically more closely related to *Kitasatospora* than *Streptacidiphilus* s.s. These phylogenetic groupings were also highly consistent with the *PhyloPhlAn* analysis ([Fig. 1](#fig-1)). *PhyloPhlAn* constructs highly robust phylogenetic trees from a protein sequence alignment generated by concatenating computationally selected subset of amino acid sequences from 400 most conserved universal proteins ([Segata et al., 2013; Asnicar et al., 2020](#segata2013)) [29, 30]. The coherent grouping of these two species is also evident through visualization of the AAI data ([Fig. 2](#fig-2)). Furthermore, both these type strains share 81.3% AAI with one another but share 67.8–70.0% (mean: 70.0) % AAI with one another but share 67.8–70.0% (mean: 70.0)
AAI with other Streptacidiphilus species (Table 1, Fig. 2 and Table S2) i.e., below the ~70-74% AAI threshold for comparisons of different genera (Luo et al. 2014; Nicholson et al. 2020) [36, 37]. When the AAI values for the type strains of these two species were determined in comparison with the members of Kitasatospora (Table 1, Fig. 2 and Table S2), a slightly higher mean value of 70.7% (range 69.2 – 72.8%) was obtained, supporting the suggestion that these two species may be a sister clade of Kitasatospora, but should not be placed within Kitasatospora. POCP values for these two species compared to each other were found to be 56.4% and 45.2 – 46.9% to other Streptacidiphilus species (Fig. 3), consistent with both belonging to a genus distinct from Streptacidiphilus. Notably, these two species were not recovered within Streptacidiphilus s.s. in the TYGS-generated phylogenomic analysis of Malik et al. (2020) [38] and have also been placed within a novel genus in the Genome Taxonomy Database (GTDB, release 06-RS202; Parks et al. 2020) [39], which classifies them as ‘g. Streptomyces_D’ within the family Streptomycetaceae (https://gtdb.ecogenomic.org/tree?ref__Streptomycetaceae). The phylogenomic analysis of Li et al. (2021) [12] also noted that the S. bronchialis type strain is more closely related to Kitasatospora than Streptacidiphilus and may belong to a novel genus. Cumulatively, these data support the reclassification of these two species into a novel genus within the family Streptomycetaceae, for which the name Peterkaempfera gen. nov. is proposed, with Peterkaempfera griseoplanus as type species. Phenotypically, members of this genus possessed galactose, ribose and traces of mannose in the whole cell hydrolysates, with MK9 (H6) as a menaquinone (Table 2).

The third cluster distinguished within Streptacidiphilus contains the type strain of Streptacidiphilus oryzae, an acidophilic actinomycete (which grows between pH 3.0 to 6.5), strains of which were originally recovered from the acidic soil of a rice paddy in Thailand (Wang et al. 2006) [40]. When its 16S rRNA gene was analyzed, the phylogenetically closest member was found to be S. griseoplanus with 97.4% similarity and these two taxa were originally grouped in ‘Cluster S4’ in the comprehensive 16S rRNA phylogenetic analysis of Labeda et al. (2012) [15]. However, S. oryzae was recovered with Streptacidiphilus species in the subsequent MLSA analysis (Labeda et al. 2017) [16]. The distinctness of this cluster is reflected in the conserved protein based phylogenomic analysis (Fig. 1). The AAI analysis showed that S. oryzae shares 67.3 – 68.6% (mean: 67.8%) with other Streptacidiphilus s.s. species (Table 1; Table S2 and Fig. 2), again below the AAI threshold of ~70-74% that can be used to delineate genera. When this strain was compared with members of Kitasatospora (Table S2 and Fig. 2), the mean AAI was 66.2% (range 65.7-66.7%). POCP values for this species compared to other Streptacidiphilus species were 46.4 – 51.2% (Fig. 3, mean 48.8%) consistent with the type strain belonging to a genus distinct from Streptacidiphilus. Moreover, this species was not recovered within Streptacidiphilus s.s. in the analyses of Nouioui et al. (2018) and Malik et al. (2020) [2, 38], and the species has also been placed within a novel genus in the
GTDB classification, which classifies it as genus ‘g_Streptacidiphilus_A’ within the family Streptomyctetaeae. Distinguishing phenotypic properties detected are that the diagnostic sugars in the whole cell hydrolysates include galactose, glucose, mannose, and ribose, and that the cell wall contains LL- & meso-A:pm as diamino acid (Table 2). Therefore these polyphasic data support the proposal of a novel genus, Phaeacidiphilus gen. nov., to accommodate Streptacidiphilus oryzae as the type species.

The core genome analysis also identified unique lineages at the periphery of the genus Streptomyces (Fig. 1). One early branch, supported by 100% bootstrap support, contains “Streptomyces cattleya”, a single species lineage, separated (with 81% bootstrap support) from a group of eleven species. “S. cattleya” has received study as a source of secondary metabolites, notably including the antibiotic thienamycin and fluorinated compounds (Noble et al. 1978; Kahan et al. 1979; Barbe et al. 2011; Zhao et al. 2012) [41-44]) but has not been formally described as a species (Labeda et al. 2017) [16]. “S. cattleya” is recognized as phylogenetically divergent from Streptomyces (Hsiao and Kirby, 2008; Labeda et al. 2017) [16, 45] and has been placed in a novel genus by the GTDB (g_Streptomyces_C). The mean AAI between the type strain of this species and reference Streptomyces spp. was 70.0% (Table 1; range 69.0-71.1, Table S2 and Fig. 2) and the POCP value with the type strain of the genus, Streptomyces albus subsp. albus, is 52.7% (Fig. 3).

Although this value is slightly greater than the originally proposed 50% POCP threshold for delineating genera (Qin et al. 2014) [33], numerous studies have suggested this threshold is too stringent (Wirth and Whitman 2018; Sangal et al 2018 and Zhu et al 2021) [46-48]. These values are both consistent with the classification of “S. cattleya” in a separate genus. Based on these phylogenomic data we propose that “S. cattleya” is classified as the type species of Streptantibioticus gen. nov. However, in order to correct the malformed species epithet in “S. cattleya” we here name the type species Streptantibioticus cattleyicolor. The MLSA study of Labeda et al. (2017) [16] also suggests that Streptomyces ferralitis (Saintpierre-Bonaccio et al. 2004) [49] may be a member of this genus and a 16S rRNA gene phylogeny analysis indicated Streptomyces rubrisoli, a neutrotolerant, acidophilic bacteria recovered from red soil (Guo et al 2015) [50] was also present within this clade, but this needs to be confirmed by further analysis.

A closely related group of eleven species are the type strains of Streptomyces acididurans, Streptomyces alni, Streptomyces bryophytorum, Streptomyces glau ciniger, Streptomyces guanduensis, Streptomyces oryziradicis, Streptomyces paucisporeus, Streptomyces rubidas, “Streptomyces soli” Streptomyces yanglinensis and Streptomyces yeochonensis. The members of this clade showed low 16S rRNA gene similarity range (96.3- 97.4 %) to “S. cattleya” and to Streptomyces s.s. species (ranging between 96.1- 97.3 %). When the genomes of these eleven species were subjected to AAI analysis, the organisms within this clade share 70.6–87.2 % (mean: 74.9 %) AAI with one another, but only share 67.2– 71.3 % (mean: 69.0 %) AAI with the reference Streptomyces species, which is reflected in the AAI data visualized as a heat map (Fig. 2 and Table S2). These AAI values are thus consistent with the ~70-74%
AAI threshold for comparisons of different genera (Luo et al. 2014; Nicholson et al. 2020) [36, 37]. POCP values among this group of 11 type strains were 41.8–71.2% (mean: 54.2%) whereas values compared to the Streptomyces reference strains were 38.9-62.7% (mean: 47.3%. Table 1, Fig 3 and Table S3). Seven among these 11 taxa have been placed in a novel genus by the GTDB (g_Streptomyces_B), whilst S. glauciniger, S. rubidus, S. yanglinensis and S. yeochonensis were well separated from Streptomyces s.s. in the phylogenomic analysis by Malik et al. (2020) [38] and the nine of these species included in the phylogenomic analysis of Chantavorakit et al. (2021) [51] formed a coherent grouping separated from the Streptomyces reference strains. Likewise, the recently described Streptomyces epipremni also clusters with members of this group in phylogenomic analyses [52] (Duangupama et al. 2022; data not shown).

Cumulatively, these data support the conclusion that these 12 species should be classified in a separate genus, for which we propose the name Actinacidiphila gen. nov., with Actinacidiphila yeochonensis comb. nov. as the type species. The MLSA analysis of Labeda et al. (2017) [16] suggests that Streptomyces cockleensis may also be a member of this genus but this needs to be confirmed by further analysis.

A single lineage containing the type strain of “Streptomyces gilvigriseus” (Ser et al. 2015) [53] showed low 16S rRNA gene sequence similarity of 96.2 % with its apparent nearest relative, Streptomyces qinglanensis (with which it shares ANI, dDDH and AAI values of 74.8, 20.8, and 64.1 %, respectively).

This lineage branched formed a sister clade to Embleya, branching before Streptomyces in the conserved protein phylogeny (Fig. 1). The AAI analysis shows that “S. gilvigriseus” shares 63.9 − 64.9% (mean: 64.5 %, Table 1) AAI with the reference Streptomyces species (Fig. 3 and Table S2) i.e., below the AAI threshold of >70-74% than can be used to delineate genera. Likewise, POCP data show <55.5% values (average 44.0%) to all Streptomyces species included (Fig. 3), again suggesting this species belongs to a separate genus. This species has also been placed in a novel genus (g_Streptomyces_G) by the GTDB classification. The phylogenetic analyses, combined with the low AAI values, support the proposal of novel genus Mangrovactinospora to accommodate “S. gilvigriseus”.

Similarly, to “S. gilvigriseus”, an early branch distinct from Streptomyces within the conserved protein-based tree (Fig. 1) was recovered containing the type strain of Streptomyces vitaminophilus (Shomura et al. 1983) Goodfellow et al. 1986 [54, 55]. This species was also found to form a clade in the 16S rRNA gene tree with Streptomyces tyrosinilyticus (Fig S1a-c) a similar position of S. tyrosinilyticus in the phylogenetic tree was reported by Zhao et al. 2015 [56]. In addition, the mean AAI values of S. vitaminophilus and S. tyrosinilyticus and the phylogenetically closely related taxa in the core genome tree i.e. “S. cattleya” and “S. gilvigriseus” are 69.6 and 65.0%, respectively (Fig. 2 and Table S2) i.e. below the ~70-74% threshold for delineating genera (Luo et al. 2014; Nicholson et al. 2020) [36, 38]. Both S. vitaminophilus and S. tyrosinilyticus have been placed in a novel genus (g_Streptomyces_A) by the GTDB.
classification, and they share 73.6% AAI (Fig 2 and Table S2) i.e. on the boundary used here for genus
delineation. Although a POCP value of 49.5% was calculated between S. vitaminophilus and S.
tyrosinilyticus (Fig. 3), for now it seems prudent to classify them in the same genus based on the AAI and
GTDB data. S. vitaminophilus was originally named Actinosporangium vitaminophilum (Shomura et al.
1983) [54] before transfer to the genus Streptomyces based on physiological properties and certain
chemotaxonomic characteristics (cell wall type, type-II phospholipid pattern, presence of hexa- and octa-
hydrogenated menaquinones (Goodfellow et al. 1986) [55]. The name Actinosporangium, with the type
species of Actinosporangium violaceum corrig. Krassilnikov and Yuan 1961 (Approved Lists 1980) [57],
remains validly published even though the type species is currently classified in the genus Streptomyces
(Goodfellow et al. 1986) [55]. Therefore, it is necessary to propose a new genus to accommodate these two
species, for which we propose the name Wenjunlia, with Wenjunlia vitaminophilum comb. nov. as the type
species. No genome is available for Streptomyces capparidis but 16S rRNA analysis is not ed to suggest a
close relationship with S. vitaminophilus (Wang et al. 2017) [58] and thus the taxonomic placement of this
species needs further investigation.

Conclusion

In conclusion, from phylogenomic and AAI analyses, combined with 16S rRNA analysis and a synthesis
of data from other studies (notably GTDB), it is clearly evident that several taxa within the family
Streptomycetaceae require reclassification at the genus level. Cumulatively, the data support the proposal
of two novel genera containing species previously classified within Streptacidiphilus and four genera
containing species previously classified in Streptomyces. The descriptions of these genera are provided
herewith.

Taxonomic consequences:

Description of Actinacidiphila gen. nov.

Actinacidiphila (Ac.ti.na.c.i.di′phi.la. Gr. fem. n. actis, actinos, a ray; N.L. neut. n. acidum, acid; Gr. masc.
adj. philos, loving; N.L. fem. adj. Actinacidiphila, an acid-loving actinomycete).

Aerobic, Gram-positive, non-motile, acidophilic to neutrotolerant, sporulating streptomycetes that form
branched substrate and aerial hyphae. Mesophilic. The cell wall contains LL-diaminopimelic acid. Contains
diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol and phosphatidylinositol
mannosides as major polar lipids. Hexa- and octa-hydrogenated menaquinones with nine isoprene units
[MK-9 (H6, H8)] are the predominant menaquinones. The genomic DNA G+C content ranges from 72-
74 mol%. The genus can be separated from *Streptomyces* based on phylogenomic analyses. The type species is *Actinacidiphila yeochonensis*.

**Description of Actinacidiphila acididurans comb. nov.**


Basonym: *Streptomyces acididurans* Chantavorakit et al. 2021

The description is the same as that given for *Streptomyces acididurans* (Chantavorakit et al. 2021) [51]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.3 % and its approximate genome size is 9.68 Mbp (GenBank accession number GCA_016918855.1). The type strain is KK5PA1T (= NBRC 114802T = TBRC 13094T).

**Description of Actinacidiphila alni comb. nov.**

*Actinacidiphila alni* (a.l.ni. L. gen. fem. n. *alni*, of the alder, referring to the isolation of the type strain from *Alnus nepalensis*).


The description is the same as that given for *Streptomyces alni* (Liu et al. 2009) [59]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.1 % and its approximate genome size is 8.27 Mbp (GenBank accession number GCA_900112845.1). The type strain is D65T (= CGMCC 4.3510T = DSM 42036T = JCM 16122T = NRRL B-24611T).

**Description of Actinacidiphila bryophytorum comb. nov.**

*Actinacidiphila bryophytorum* (bry.o.phy.to.rum. N.L. gen. neut. pl. n. *bryophytorum*, of Bryophyta, referring to the isolation of the type strain from a member of the phylum Bryophyta)

Basonym: *Streptomyces bryophytorum* Li et al. 2016

The description is the same as that given for *Streptomyces bryophytorum* (Li et al. 2016) [60]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is
72.5 % and its approximate genome size is 8.05 Mbp (GenBank accession number GCA_016916835.1). The type strain is NEAU-HZ10\textsuperscript{T} (= CGMCC 4.7151\textsuperscript{T} = DSM 42138\textsuperscript{T}).

**Description of Actinacidiphila epipremni** comb. nov.

*Actinacidiphila epipremni* (e.pi.prem′ni. N.L. gen. n. epipremni, of Epipremnum, referring to the generic name of *Epipremnum aureum* from which the strain is isolated).

Basonym: *Streptomyces epipremni* Duangupama et al. 2022

The description is same as that given for *Streptomyces epipremni* (Duangupama et al. 2022) [52]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.6 % and its approximate genome size is 8.2 Mbp (GenBank accession number JAATEJ000000000). The type strain is PRB2-1\textsuperscript{T} (= NBRC 113169\textsuperscript{T} = TBRC 7642\textsuperscript{T}).

**Description of Actinacidiphila glaucinigra** comb. nov.

*Actinacidiphila glaucinigra* (glau.ci.ni′gra L. masc. adj. glaucus, greenish grey; L. masc. adj. niger, black; N.L. fem. adj. glaucinigra, greenish black, referring to the color of the colony reverse on modified Bennett’s agar).


The description is same as that given for *Streptomyces glauciniger* (Huang et al. 2004) [61]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.3 % and its approximate genome size is 9.81 Mbp (GenBank accession number GCA_900188405.1). The type strain is FXJ14\textsuperscript{T} (= AS 4.1858\textsuperscript{T} = DSM 41867\textsuperscript{T} = JCM 12278\textsuperscript{T} = LMG 22082\textsuperscript{T} = NBRC 100913\textsuperscript{T}).

**Description of Actinacidiphila guanduensis** comb. nov.

*Actinacidiphila guanduensis* (gu.an.du.en′sis. N.L. fem. adj. guanduensis, of or belonging to Guandu, the source of the soil from which the type strain was isolated).

Basonym: *Streptomyces guanduensis* Xu et al. 2006.

The description is the same as that given for *Streptomyces guanduensis* (Xu et al. 2006) [62]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is
73.1 % and its approximate genome size is 8.22 Mbp (GenBank accession number GCA_900103985.1). The type strain is 701\(^T\) (= CGMCC 4.2022\(^T\) = DSM 41944\(^T\) = JCM 13274\(^T\) = NBRC 102070\(^T\)).

**Description of Actinacidiphila oryzaeaeis comb. nov.**

*Actinacidiphila oryzaeaeis* (o.ly.za.ei.\(\prime\)di.eis. L. fem. n. oryza, rice; L. fem. n. radix (gen. radicis), root; N.L. gen. fem. n. oryzaeaeis, of the rice root)

Basonym: *Streptomyces oryzaeaeis* Li et al. 2020

The description is the same as that given for *Streptomyces oryzaeaeis* (Li et al. 2020) [64]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 69.5 % and its approximate genome size is 11.5 Mbp (GenBank accession number GCA_005047355.1). The type strain is NEAU-C40\(^T\) (= DSM 107943\(^T\) = CCTCC AA 2018038\(^T\)).

**Description of Actinacidiphila paucisporea comb. nov.**

*Actinacidiphila paucisporea* (pau.ci.spo\(\prime\)re.a. L. masc. adj. paucus, few; N.L. masc. adj. sporeus, spored; N.L. fem. adj. paucisporea, few spored, forming few spores).


The description is the same as that given for *Streptomyces paucisporea* (Xu et al. 2006) [62]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.2 % and its approximate genome size is 8.16 Mbp (GenBank accession number GCA_900142575.1). The type strain is 1413\(^T\) (= DSM 107943\(^T\) = CCTCC AA 2018038\(^T\)).

**Description of Actinacidiphila rubida comb. nov.**


The description is the same as that given for *Streptomyces rubidas* (Xu et al. 2006) [62]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.9 % and its approximate genome size is 9.01 Mbp (GenBank accession number GCA_900110255.1). The type strain is 13c15\(^T\) (= CGMCC 4.2025\(^T\) = DSM 41946\(^T\) = JCM 13276\(^T\) = NBRC 102072\(^T\)).
Description of Actinacidiphila soli sp. nov.

Actinacidiphila soli (sol'i. L. gen. n. soli of soil).

The description is the same as that given for “Streptomyces soli” (Xing et al. 2020) [63]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 69.95 % and its approximate genome size is 9.40 Mbp (GenBank accession number GCA_003999195.1). The type strain is LAM7114^T (= CGMCC 4.7581T = JCM 32822^T).

Description of Actinacidiphila yanglinensis comb. nov.

Actinacidiphila yanglinensis (yang.lin.en'sis. N.L. fem. adj. yanglinensis, of or belonging to Yanglin, the source of the soil from which the type strain was isolated).


The description is the same as that given for Streptomyces yanglinensis (Xu et al. 2006) [62]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.6 % and its approximate genome size is 9.59 Mbp (GenBank accession is GCA_900107965.1). The type strain is 1307^T (= CGMCC 4.2023T = DSM 41945^T = JCM 13275^T = NBRC 102071^T).

Description of Actinacidiphila yeochonensis comb. nov.

Actinacidiphila yeochonensis (ye.o.chon.en'sis. N.L. fem. adj. yeochonensis, of Yeochon, a province in Korea, referring to the place where the organism was first isolated).


The description is the same as that given for Streptomyces yeochonensis (Kim et al. 2004) [65]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 73.6 % and its approximate genome size is 7.82 Mbp (GenBank accession number GCA_000745345.1). The type strain is CN 732^T (= DSM 41868^T = IMSNU 50114^T = JCM 12366^T = KCTC 9926^T = NBRC 100782^T = NRRL B-24245^T).

Description of Mangrovactinospora gen. nov.
Mangrovactinospora (Man.grov.ac.ti.no.spo'ra. N.L. neut. n. mangrovum, a mangrove; Gr. fem. n. actis, actinos, a ray; Gr. fem. n. spora, a seed and, in biology, a spore; N.L. fem. n. Mangrovactinospora, a mangrove actinomycete with spiny spores).

Gram-stain positive mesophilic actinomycete. Forms substrate and aerial mycelium. The cell wall peptidoglycan contains LL-diaminopimelic acid. The major polar lipids include diphosphatidylglycerol, phosphatidylethanolamine, hydroxyphosphatidylethanolamine, phosphatidylmethylethanolamine and hydroxyphosphatidylethanolamine, and the major fatty acids are anteiso-C_{15:0}, iso-C_{16:0}, iso-C_{15:0} and anteiso-C_{17:0}. The menaquinones are MK-9 (H_8) and MK-9(H_6). The cell wall sugars include galactose, glucose, mannose, ribose and rhamnose. The genomic DNA G+C content is around 73%. The genus can be distinguished from Streptomyces based on phylogenomic analyses. The type species is Mangrovactinospora gilvigrisea.

Description of Mangrovactinospora gilvigrisea sp. nov.

Mangrovactinospora gilvigrisea (gil.vi.gri'se.a. L. masc. adj. gilvus, yellow; L. masc. adj. griseus, grey; N.L. fem. adj. gilvigrisea, yellow-grey, referring to the colour of the mycelium).

The description is the same as that given for Streptomyces gilvigriseus (Ser et al. 2015) [53]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 73% and its approximate genome size is 5.21 Mbp (GenBank accession number GCA_001879105.1). The type strain is MUSC 26^T (=DSM 42173^T = MCCC 1K00504^T = NBRC 110931^T).

Description of Peterkaempfera gen. nov.

Peterkaempfera (Pe.ter.kae.mp'fe.ra. N.L. fem. gen. n. Peterkaempfera, named in recognition of the contribution of Peter Kämpfer to the systematics of actinomycetes).

Aerobic, mesophilic Gram-stain positive, non-acid-fast, non-motile, streptomycetes producing branched mycelium and aerial hyphae. The cell wall peptidoglycan contains LL-diaminopimelic acid as the diagnostic diamino acid and glucose, mannose and ribose are present in whole cell hydrolysates; the major menaquinones are MK9 (H_8) or MK9 (H_6). The polar lipid profile contains diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, and other lipids; the major fatty acids are anteiso-C_{15:0} and iso-C_{16:0}. The genomic DNA G+C content is around 72 mol%. The genus can be separated from Streptacidiphilus based on phylogenomic analyses. The type species is Peterkaempfera griseoplanus.
**Description of Peterkaempfera bronchialis comb. nov.**

*Peterkaempfera bronchialis* (bron.chi.a′lis. L. pl. n. bronchia the bronchial tubes; L. fem. suff. -alis suffix used with the sense of pertaining to; N.L. fem. adj. bronchialis, pertaining to the bronchial tubes).


The description is the same as that given for *Streptacidiphilus bronchialis* (Nouioui et al. 2019) [35]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.6 % and its approximate genome size is 7.01 Mbp (GenBank accession number GCA_003258605.2). The type strain is 15-057A\(^\text{T}\) (=DSM 106435\(^\text{T}\) = ATCC BAA-2934\(^\text{T}\)).

**Description of Peterkaempfera griseopla\(\text{\textsuperscript{a}}\)na comb. nov.**

*Peterkaempfera griseopla\(\text{\textsuperscript{a}}\)na* (gri.se.o.pla′na. L. masc. adj. griseus, grey; L. masc. adj. planus, flat, level; N.L. fem. adj. griseopla\(\text{\textsuperscript{a}}\)na flat, grey, referring to the restricted, flat, planar growth and greyish spore color in masse of the organism).


The description is the same as that given for *Streptacidiphilus griseoplanus* (Backus et al. 1957; Kämpfer 2012; Nouioui et al., 2019) [35, 66, 67]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72.5 % and its approximate genome size is 8.25 Mbp (GenBank accession number GCA_001418575.1). The type strain is DSM 40009\(^\text{T}\) (=NBRC 12779\(^\text{T}\) = ISP 5009\(^\text{T}\) = CBS 505.68\(^\text{T}\) = IFO 12779\(^\text{T}\) = ATCC 19766\(^\text{T}\) = AS 4.1868\(^\text{T}\)).

**Description of Phaeacidiphilus gen. nov.**

*Phaeacidiphilus* (Phae.a.ci.di′phi.lus. Gr. masc. adj. phaeos, grey, brown; L. neut. n. acidum, acid; Gr. masc. adj. philos, loving; N.L. masc. adj. Phaeacidiphilus, brown colored substrate mycelium producing, acid-loving).

Aerobic, mesophilic and acidophilic Gram-stain positive, non-acid alcohol fast staining actinomycetes. Spores are born on aerial hyphae. The diamino acid of the cell wall peptidoglycan is LL-diaminopimelic acid, although minor amounts of the meso-isomer may be present. Whole cell hydrolysates contain galactose, glucose, mannose and ribose. Contains hexa- and octa-hydrogenated menaquinones with nine isoprene units. The major polar lipids are diphosphatidylglycerol, phosphatidylethanolamine,
phosphatidylinositol and phosphatidylinositol mannosides. The genus can be distinguished from the genus *Streptacidiphilus* based on phylogenomic analyses. The type species is *Phaeacidiphilus oryzae*.

**Description of Phaeacidiphilus oryzae comb. nov.**

*Phaeacidiphilus oryzae* (o.ry'zae. L. gen. fem. n. oryzae, of rice, denoting the isolation of the strains from a rice field).


The description is the same as that given for *Streptacidiphilus oryzae* (Wang et al. 2006) [40]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 73.4 % and its approximate genome size is 7.81 Mbp (GenBank accession number GCA_000744815.1).

The type strain is TH49\(^\text{T}\) (=CGMCC 4.2012\(^\text{T}\) = DSM 45098\(^\text{T}\) = JCM 13271\(^\text{T}\)).

**Description of Streptantibioticus gen. nov.**

*Streptantibioticus* (Strept.an.ti.bi.o'ti.cus. Gr. masc. adj. streptos, pliant, twisted; N.L. masc. adj. antibioticus, against life, antibiotic; N.L. masc. n. *Streptantibioticus*, a streptomycete that produces antibiotics).

Aerobic, mesophilic Gram-stain positive non-acid fast staining sporulating actinomycetes. Sporophores are produced on the aerial mycelium. The genomic DNA G+C content is around 73 %. The genus can be distinguished from *Streptomyces* based on phylogenomic analyses. The type species is *Streptantibioticus cattleyicolor*.

**Description of Streptantibioticus cattleyicolor sp. nov.**

*Streptantibioticus cattleyicolor* (catt.ley.i'co.lor. N.L. fem. n. Cattleya, an orchid genus; L. masc. n. color, colour; N.L. masc. adj. cattleyicolor, Cattleya-coloured, orchid white).

The description is the same as that given for "*Streptomyces cattleya*" (Noble et al. 1978; Kahan et al. 1979) [41, 42]. The species epithet reflects the original intention of Kahan et al. (1979) that "*S. cattleya*" should be named in recognition of its distinctive orchid-white colored aerial mycelium but corrects the Latinisation of the name. Further characteristics are given in the genome description (Barbe et al. 2011). The species is assigned to the genus based on phylogenomic analysis. The type strain is notable for the production of the antibiotic thienamycin and the fluorinated antibiotic 4-fluorothreonine when cultivated in the presence of...
fluorine. The G+C content of the type strain genome is 73 % and its approximate genome size is 8.10 Mbp including one linear plasmid (GenBank accession number GCA_000240165.1). The type strain is MA4297\(^T\) (=ATCC 35852\(^T\) = DSM 46488\(^T\) = NCIMB 11928\(^T\) = NBRC 14057\(^T\) = NRRL 8057\(^T\)).

**Description of Wenjunlia gen. nov.**


Cells are Gram-stain positive, aerobic, mesophilic and can form non-motile spores. Spores are formed on the aerial mycelium. The major menaquinones are MK-9(H\(_6\)) and MK-9(H\(_8\)). LL-diaminopimelic acid is present in the cell wall. The major phospholipids include diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol and phosphatidylinositol mannosides. The genomic DNA G+C content is around 72 %. The genus can be distinguished from *Streptomyces* based on phylogenomic analyses. The type species is *Wenjunlia vitaminophilus*.

**Description of Wenjunlia vitaminophila comb. nov.**


The description is the same as that given for *Streptomyces vitaminophilus* (Goodfellow et al. 1986; Shomura et al. 1983; Nouioui et al. 2018) [2, 54, 55]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 72 % and its approximate genome size is 6.55 Mbp (GenBank accession number GCA_001445835.1). The type strain is SF 2080\(^T\) (=ATCC 31673\(^T\) = DSM 41686\(^T\) = IFO 14294\(^T\) = JCM 6054\(^T\) = NBRC 14294\(^T\) = NRRL B-16933\(^T\)).

**Description of Wenjunlia tyrosinilytica comb nov.**


Basonym: *Streptomyces tyrosinilyticus* Zhao et al. 2015
The description is the same as that given for *Streptomyces tyrosiniylicus* (Zhao *et al.* 2015) [56]. The species is assigned to the genus based on phylogenomic analysis. The G+C content of the type strain genome is 71 % and its approximate genome size is 8.49 Mbp (GenBank accession number GCA_014646055.1). The type strain is NEAU-Jh3-20^T (= CGMCC4.7201^T = DS42170^T).

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Table 1. Mean POCP and AAI values between *Streptomyces* and other validly described genera; and newly proposed genera (bold) derived from *Streptomyces* and *Streptacidiphilus*.

| Sl.No | Taxa                              | 1   | 2   | 3   | 4   | 5   | 6   | 7   | 8   | 9   | 10  | 11  |
|-------|-----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1     | *Allostreptomyces*                | 100 | 50.19 | 45.79 | 42.99 | 44.89 | 40.42 | 42.10 | 36.45 | 35.98 | 45.80 | 47.51 |
| 2     | *Streptomyces*                    | 71.63 | 100 | 47.30 | 43.93 | 46.20 | 41.17 | 45.02 | 37.37 | 43.98 | 47.45 | 52.00 |
| 3     | *Actinacidiphila gen. nov.*       | 69.20 | 100 | 68.99 | 100 | 44.13 | 47.47 | 44.04 | 45.98 | 36.57 | 42.51 | 46.64 |
| 4     | *Kitasatospora*                   | 64.73 | 100 | 65.25 | 100 | 48.68 | 47.03 | 44.31 | 38.69 | 36.74 | 42.77 | 45.71 |
| 5     | *Peterkaempfera gen. nov.*       | 66.60 | 100 | 67.51 | 100 | 46.26 | 48.40 | 37.22 | 39.29 | 46.25 | 47.33 |
| 6     | *Streptacidiphilus*               | 64.66 | 100 | 67.07 | 100 | 48.78 | 36.34 | 35.98 | 40.82 | 44.34 |
| 7     | *Phaeacidiphilus gen. nov.*      | 65.39 | 100 | 66.15 | 100 | 48.78 | 36.34 | 35.98 | 40.82 | 44.34 |
| 8     | *Embleya*                         | 62.00 | 100 | 61.91 | 100 | 46.26 | 48.40 | 37.22 | 39.29 | 46.25 | 47.33 |
| 9     | *Mangrovactinospora gen. nov*    | 64.10 | 100 | 65.32 | 100 | 48.78 | 36.34 | 35.98 | 40.82 | 44.34 |
| 10    | *Wenjunlia gen. nov.*            | 68.44 | 100 | 67.84 | 100 | 48.78 | 36.34 | 35.98 | 40.82 | 44.34 |
| 11    | *Streptantibioticus* gen. nov.*  | 69.84 | 100 | 70.77 | 100 | 48.78 | 36.34 | 35.98 | 40.82 | 44.34 |


1. POCP - Percentage of Conserved Protein
2. AAI – Average Amino-acid Identity
<table>
<thead>
<tr>
<th>Genera / Characteristic</th>
<th>Long chains of spores formed on aerial hyphae</th>
<th>pH range for growth (Optimal range)</th>
<th>Temperature range (optimum)</th>
<th>Diagnostic sugars in whole organism hydrolysates</th>
<th>Isomer(s) of diaminopimelic acids in whole-organism hydrolysates</th>
<th>Fatty acid pattern</th>
<th>Predominant phospholipids</th>
<th>Major menaquinones</th>
<th>G + C content of DNA (mol%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Newly proposed genera</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Actinosalicophyllum gen. nov.</td>
<td>+</td>
<td>4.5–7.3 (5.0–5.5)</td>
<td>20–37°C</td>
<td>nd</td>
<td>LL-Apm</td>
<td>Type 2c</td>
<td>DPG, PE, PIME, PME</td>
<td>MK-9(Hl, H)</td>
<td>72.1 to 73.6</td>
</tr>
<tr>
<td>Phaeacidiphilus gen. nov.</td>
<td>+</td>
<td>3.0–6.5 (4.5)</td>
<td>28–37°C</td>
<td>Gal, Glic, Man, Rib</td>
<td>LL &amp; meso-Apm</td>
<td>Type 2, iso-C9, anteiso-C9, iso-C10, anteiso-C10, iso-C15, anteiso-C15</td>
<td>DPG, PI, PE, PME</td>
<td>MK-9(Hl, H)</td>
<td>73.4</td>
</tr>
<tr>
<td>Mangrovactinospora gen. nov.</td>
<td>–</td>
<td>5.0–8.0</td>
<td>Optimum pH 6.0–7.0</td>
<td>Gal, Glic, Man, Rib and Hlu.</td>
<td>LL-Apm</td>
<td>Type 2c</td>
<td>PE, PI, DPG, GPL, AGL &amp; unknown L</td>
<td>MK-9(Hl, H)</td>
<td>72.5</td>
</tr>
<tr>
<td>Prevotiaclavus gen. nov.</td>
<td>+</td>
<td>5.7 (5.6)</td>
<td>20–40°C</td>
<td>Glic, Man (trace), Rib</td>
<td>LL-Apm</td>
<td>Type 2c</td>
<td>PE, PI, PME</td>
<td>MK-9(Hl, H)</td>
<td>71.5–71.8</td>
</tr>
<tr>
<td>Wenjunlia gen. nov.</td>
<td>–</td>
<td>6 to 8</td>
<td>15–45°C (25–34°C)</td>
<td>Fic, Man, Rib, Glic</td>
<td>LL-Apm</td>
<td>Type 2c</td>
<td>PE, PI, PIME</td>
<td>MK-9(Hl, H, Hc)</td>
<td>72</td>
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<tr>
<td>Previously described genera</td>
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<tr>
<td>Allostreptomyces</td>
<td>+</td>
<td>5.6–11.0 (7.0)</td>
<td>10–30°C (28–10°C)</td>
<td>Gal, Man</td>
<td>LL-Apm</td>
<td>Type 2c</td>
<td>DPG, PIME</td>
<td>MK-9(Hl, H)</td>
<td>75.3</td>
</tr>
<tr>
<td>Embliosa</td>
<td>–</td>
<td>6–11 (6–9)</td>
<td>10–28°C (25–28°C)</td>
<td>Arb</td>
<td>LL-A2pm</td>
<td></td>
<td>MK-9(Hl, H)</td>
<td>70.9 to 71.6</td>
<td></td>
</tr>
<tr>
<td>Kusumautoporus</td>
<td>+</td>
<td>6.5–9.0</td>
<td>10–37°C</td>
<td>Gal or Rib, Glic and Man</td>
<td>LL &amp; meso-Apm</td>
<td>Type 2c</td>
<td>PE, PIME, PME</td>
<td>MK-9(Hl, Hc or Hl)</td>
<td>65–80</td>
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<tr>
<td>Salsolactobacillus</td>
<td>+</td>
<td>5.5–6.0 (6.5–5.5)</td>
<td>20–40°C</td>
<td>Gal, aux</td>
<td>LL-Apm</td>
<td>Type 2c</td>
<td>PE, PI, PME</td>
<td>MK-9(Hl, H)</td>
<td>71.5–71.8</td>
</tr>
<tr>
<td>Yinghuangia</td>
<td>+</td>
<td>5.6–11.5 (5.5–8.0)</td>
<td>28–37°C</td>
<td>Gal</td>
<td>LL &amp; meso-Apm</td>
<td>Type 2c</td>
<td>PE, PI, PME</td>
<td>MK-9(Hl, H)</td>
<td>66–75</td>
</tr>
<tr>
<td>-</td>
<td>–</td>
<td>5–7 (6–7)</td>
<td>15–37°C</td>
<td>Arb, Glic, Rib, Hlu or Rib and Man and Gal</td>
<td>LL-Apm</td>
<td>Type 2c</td>
<td>PE, DPG and P</td>
<td>MK-9(Hl, H)</td>
<td>70–75</td>
</tr>
</tbody>
</table>

*Data obtained from Kim et al. 1997 [68]; Shirling and Gottlieb 1977 [69]; Ómura et al. 1989 [70]; Lonsdale, 1985 [71]; Williams et al. 1989 [72]; Nakagaito et al. 1992 [73]; Antony-Babu and Goodfellow 2008 [74]; Noutsou et al. 2019 [35]; Komaki et al. 2020 [75]; Komaki and Tamura, 2019 [76]; Rob et al. 2018 [77]; Ser et al. 2015 [53]; Huang et al. 2017 [11]; Ping et al. 2004 [78]; Nagai et al. 2011 [79]; *Alkalophilic strains, which grow between pH 5.0 and 11.0, have an optimum at pH 9 to 9.5 (Mikami et al. 1982); Antony-Babu and Goodfellow 2008 [80, 81]; *Cell wall sugars: Arb, arabinose; Frc, fructose; Gal, galactose; Glc, glucose; Man, mannose; Rha, rhamnose, Rib, ribose; *Aerial and submerged spores contain LL-A2pm (LL-diaminopimelic acid) and vegetative mycelia meso-A2pm or DL-A2pm (Meso-diaminopimelic acid); *Fatty acid pattern: 2c, iso- and anteiso-branched and saturated fatty acids (Kroppenstedt, 1985) [81]; *DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PI, phosphatidylinositol; PIMs, phosphatidylinositol mannosides; OH-PE, hydroxy phosphatidylethanolamine; OH-PME, hydroxy Phosphatidymethylethanolamine; GPL, glycopholipid; AGL, aminoglycopholipid; *MK-9(Hl, Hc, Hc, Hc), dl-tetra-hexa, octa- and deca-hydrogenated menaquinones with nine isoprene units; nd, not determined. Allostreptomyces and Yinghuangia - genome data not available at the time of analysis.
Fig. 1. Midpoint rooted maximum likelihood phylogeny of *Streptomycetaceae* members. The tree was constructed using PhyloPhlAn 3.0. The scale bar indicates normalized fraction of total branch length as explained by Segata et al. (2013). Strain information and accession numbers can be found in Table S1.

Fig. 2. AAI from pairwise whole-genome comparisons within the family *Streptomycetaceae*. The heat map shows AAI values between genomes, along with the tree cladogram to show relationships. In the genus *Streptomyces*, only selected members from each clade were used for analysis. Boxed regions indicate inferred genus clusters with at least two members based on AAI comparisons, as well as monophyly in the genome-based phylogeny. Strain information and accession numbers can be found in Table S1.

Fig. 3. POCP from pairwise whole-genome comparisons within the family *Streptomycetaceae*. The heat map shows AAI and POCP values between genomes, along with the tree cladogram to show relationships. Boxed regions indicate inferred genus clusters with at least two members based on POCP comparisons, as well as monophyly in the genome-based phylogeny. Strain information and accession numbers can be found in Table S1.