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The taxonomic status of the families Actinosynnemataceae and Pseudonocardiaceae was assessed based on 16S rRNA gene sequence data available for the 151 taxa with validly published names, as well as chemotaxonomic and morphological properties available from the literature. 16S rRNA gene sequences for the type strains of all taxa within the suborder Pseudonocardineae were subjected to phylogenetic analyses using different algorithms in ARB and PHYLIP. The description of many new genera and species within the suborder Pseudonocardineae since the family Actinosynnemataceae was proposed in 2000 has resulted in a markedly different distribution of chemotaxonomic markers within the suborder from that observed at that time. For instance, it is noted that species of the genera Actinokineospora and Allokutzneria contain arabinose in whole-cell hydrolysates, which is not observed in the other genera within the Actinosynnemataceae, and that there are many genera within the family Pseudonocardiaceae as currently described that do not contain arabinose. Phylogenetic analyses of 16S rRNA gene sequences for all taxa within the suborder do not provide any statistical support for the family Actinosynnemataceae, nor are signature nucleotides found that support its continued differentiation from the family Pseudonocardiaceae. The description of the family Pseudonocardiaceae is therefore emended to include the genera previously classified within the family Actinosynnemataceae and the description of the suborder Pseudonocardineae is also emended to reflect this reclassification.

The suborder Pseudonocardineae as proposed by Stackebrandt et al. (1997) contained only a single family, the Pseudonocardineae Embley et al. 1989. Subsequently, Labeda & Kroppenstedt (2000) proposed that, on the basis of phylogenetic analysis of 16S rRNA gene sequences for a subset of all taxa within the family, the genera Actinosynnema, Actinokineospora, Lentzea and Saccharothrix should be placed in the new family Actinosynnemataceae. The description of the family Actinosynnemataceae was recently emended by Zhi et al. (2009) to include member genera described since 2000, namely Lechevalieria Labeda et al. 2001 and Umezawaea Labeda and Kroppenstedt 2007.

The taxonomic status of the families Actinosynnemataceae and Pseudonocardiaceae was assessed in the present study on the basis of phylogenetic analysis of 151 currently available 16S rRNA gene sequences and previously described chemotaxonomic and morphological properties of the member genera and species. It was observed that there is inadequate phylogenetic or chemotaxonomic support to maintain the family Actinosynnemataceae, as currently delineated, and it is proposed that the taxa within this family be transferred to the family Pseudonocardiaceae,
whose description is emended to accommodate these genera.

The 16S rRNA gene sequences for the type strains of all taxa within the suborder *Pseudonocardineae* were obtained from the SILVA database maintained at the Technical University of Munich (http://www.arb-silva.de/) or from locally maintained alignments, and subjected to phylogenetic analyses using ARB (Ludwig et al., 2004). The list of taxa, their strain numbers and the accession numbers of their 16S rRNA gene sequences in the public databases can be found in Supplementary Table S1, available in IJSEM Online. The alignment was trimmed at both ends to include only positions that contained data for all strains, totalling 1276 bases. The 16S rRNA gene sequence of *Micrococcus luteus* DSM 20030T was used as the outgroup for analyses. This dataset was subsequently evaluated using jPhydit (Jeon et al., 2005) to filter out the hypervariable loop regions from the analyses in order to determine the phylogenetic impact of these regions (not shown).

Phylogenetic analyses of 16S rRNA gene sequence data for all taxa currently described within the suborder *Pseudonocardineae* do not support the current description of the family *Actinosynemataceae*, as can be seen in Fig. 1. The species of the genus *Actinokineospora* are the most distant members of the clade that contains the other genera currently described within the family, namely *Actinosynema*, *Lechevalieria*, *Lentzea*, *Saccharothrix* and *Umezawaea*, but this clade also contains the genera *Actinnaulateichus*, *Alloactinosynema*, *Allokutzneria*, *Crossiella*, *Goodfellowiella*, *Kutzneria* and *Streptaonallateichus*. From a cursory examination of this phylogenetic tree, one can easily conclude that the suborder could be divided into three or more families rather than the current two, but these observations do not have statistical support in the present dataset, nor can signature nucleotide patterns be found that support any subdivision. Evaluation of the phylogeny of the 16S rRNA gene sequence alignment with all hypervariable loop regions removed (not shown) also did not demonstrate phylogenetic support for subdivision of the suborder into more than one family.

An evaluation of the previously reported chemotaxonomic properties of the genera within the suborder *Pseudonocardinae* (Table 1) demonstrates that certain properties, such as the presence of meso-diaminopimelic acid and galactose in whole-cell hydrolysates and, generally, the presence of tetrahydrogenated menaquinones with nine...
repeating units [i.e. MK-9(H4)], are common to all, but there is no observed segregation of properties that supports subdivision of the suborder into more than one family. For instance, the presence of arabinose in whole-cell hydrolysates is observed within genera scattered over the phylogenetic tree, such as Actinokineospora, Actinophytocola, Actinomycetospora, Allokutzneria, Amycolatopsis, Kibdelosporangium, Prauserella, Pseudonocardia, Saccharomonospora, Saccharopolyspora, Sciscionella, Thermocrispum and Yuhushiea, and therefore cannot be used to differentiate between members of the major clades within the suborder. Morphological properties, such as production of sporangia and motile spores, are also distributed throughout the taxa shown in Fig. 1, so they are of little differential use in grouping the genera into separate families.

In light of the lack of phylogenetic, chemotaxonomic and morphological support for differentiation of the genera within the family Actinosynnemataceae from those in the family Pseudonocardiaceae, as well as a lack of any strong support for any other subdivision of the suborder Pseudonocardinae at this time, it would appear that these genera should be transferred from the family Actinosynnemataceae into an emended family Pseudonocardinae. With the discovery, description and sequencing of many new taxa within the suborder Pseudonocardinae in the future, it might be possible to propose subdivision into additional families at a later date.

Formal emended descriptions of the family Pseudonocardiaceae and suborder Pseudonocardinae follow.


Pseudonocardiaceae (Pseu.do.no.car’di.a.cee.ae. N.L. fem. n. Pseudonocardia the type genus of the family; L. suff. -aceae ending to denote a family; N.L. fem. pl. n. Pseudonocardiaceae the Pseudonocardia family).


Aerobic, mesophilic or thermophilic, catalase-positive actinomycetes. Gram-positive. Not acid-fast. Morphologically heterogeneous; single or short chains of spores may be present on both aerial mycelium and substrate mycelium. Vegetative mycelium branches, diameter approximately 0.5–0.7 μm; aerial mycelium is produced and fragments in some genera into single smooth-surfaced, rod-shaped elements or chains of such elements. Some taxa may fail to produce aerial mycelium. Marked fragmentation of hyphae occurs in some taxa, but is absent in others. Other structures such as synnemata or dome-like bodies, sporangia or pseudosporangia may be produced in some genera. Motile spores may be produced in some genera. Most taxa are chemo-organotrophic, although some are autotrophic. A few taxa are halophilic. All genera contain meso-diaminopimelic acid as the diamino acid in their peptidoglycan and all except Haloechinothrix contain galactose as one of many diagnostic whole-cell sugars. Mycolic acids are not present in any of the genera. Tetrahydrogenated menaquinones of nine isoprene units are characteristic components, although menaquinones containing eight isoprene units predominate in the genus Pseudonocardia. The phospholipid profile generally includes phosphatidylethanolamine, sometimes containing hydroxylated fatty acids, as a major constituent, although representatives of one or more genera may also contain phosphatidylcholine. Resistant to lysozyme. The GC content of the DNA ranges from 66 to 74 mol%. The pattern of 16S rRNA signatures consists of nucleotides at positions 127:234 (G=C), 564 (U), 672:734 (U=G), 831:855 (U=G), 832:854 (G=Y), 833:853 (U=G), 952:1229 (U–A) and 986:1219 (U–A). Members of the family are found in a variety of environments, including soils, plant material, manure and clinical or veterinary samples. The type genus is Pseudonocardia Henssen 1957 (Approved Lists 1980) emend. Park et al. 2008.


Pseudonocardineae (Pseu.do.no.car’di.ne.aa.e. N.L. fem. n. Pseudonocardia the type genus of the suborder; N.L. suff. -ineae ending to denote a suborder; N.L. fem. pl. n. Pseudonocardineae the Pseudonocardia suborder).

Aerobic, mesophilic or thermophilic, catalase-positive actinomycetes comprising the family Pseudonocardiaceae, including the former members of the family Actinosynnemataceae. Morphology, chemotaxonomy, phylogeny and 16S rRNA signature nucleotides are those of the
Table 1. Comparison of chemotaxonomic profiles of genera within the order Pseudonocardineae

Data were obtained from the original and emended descriptions listed in the emended description of the family Pseudonocardiaceae.

<table>
<thead>
<tr>
<th>Genus</th>
<th>Sporangia produced</th>
<th>Motile spores</th>
<th>Whole-cell sugars*</th>
<th>Phospholipids†</th>
<th>Predominant menaquinone(s)</th>
<th>DNA G+C content (mol%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Actinoalloteichus</td>
<td>None</td>
<td>No</td>
<td>Glc, Gal, Man, Rib</td>
<td>PE, PIM, PI, PG, DPG, PME</td>
<td>9(H₄)</td>
<td>72–72.5</td>
</tr>
<tr>
<td>Actinokineospora</td>
<td>None</td>
<td>Variable</td>
<td>Gal, Ara, Rha, Man</td>
<td>PE, DPG, PI</td>
<td>9(H₄)</td>
<td>72.0</td>
</tr>
<tr>
<td>Actinomyctospora</td>
<td>None</td>
<td>No</td>
<td>Ara, Gal</td>
<td>PC, PI, PG</td>
<td>9(H₄)</td>
<td>69.0</td>
</tr>
<tr>
<td>Actinophytocola</td>
<td>None</td>
<td>No</td>
<td>Ara, Gal, Man, Rha, Rib</td>
<td>PE, OH-PE</td>
<td>9(H₄)</td>
<td>71.1</td>
</tr>
<tr>
<td>Actinosynnema</td>
<td>Synnemata</td>
<td>Yes</td>
<td>Gal, Man</td>
<td>PE, OH-PE, DPG</td>
<td>9(H₄), some 9(H₃)</td>
<td>73.0</td>
</tr>
<tr>
<td>Alloactinosynnema</td>
<td>Pseudosporangia</td>
<td>No</td>
<td>Gal, Rib</td>
<td>DPG, PG, PC</td>
<td>9(H₄)</td>
<td>68.2</td>
</tr>
<tr>
<td>Allokutzneria</td>
<td>Yes; no spores</td>
<td>No</td>
<td>Ara, Gal, Man</td>
<td>PE, PME, OH-PE, PI, lypo-PME, DPG, PG, lypo-PE</td>
<td>9(H₄)</td>
<td>71.6</td>
</tr>
<tr>
<td>Amycolatopsis</td>
<td>None</td>
<td>No</td>
<td>Ara, Gal</td>
<td>PE, DPG, PG, PI</td>
<td>9(H₄)</td>
<td>66.0–69.0</td>
</tr>
<tr>
<td>Crossiella</td>
<td>None</td>
<td>No</td>
<td>Gal, Man, Rha, Rib</td>
<td>PE, PME, PI, PIM</td>
<td>9(H₄)</td>
<td>74.1</td>
</tr>
<tr>
<td>Goodfellowiella</td>
<td>None</td>
<td>No</td>
<td>Gal, Rib</td>
<td>PE, DPG, OH-PE, PME</td>
<td>9(H₄), 10(H₄)</td>
<td>69.2</td>
</tr>
<tr>
<td>Haloechinothrix</td>
<td>None</td>
<td>No</td>
<td>Glc, Man, GlcN, NK</td>
<td>DPG, PG, PE, PI, PIM, PL</td>
<td>8(H₄)</td>
<td>68.1</td>
</tr>
<tr>
<td>Kibdelosporangium</td>
<td>Yes</td>
<td>No</td>
<td>Ara, Gal, Mad (v), Glc (v), Rha (v)</td>
<td>PE, PME, PI, PG, DPG, PIM</td>
<td>9(H₄), 9(H₄), 9(H₆)</td>
<td>66</td>
</tr>
<tr>
<td>Kutzneria</td>
<td>Yes</td>
<td>No</td>
<td>Gal, Rha</td>
<td>PE, PME, PI, PIM, PG, PIME</td>
<td>9(H₄)</td>
<td>70.3–70.7</td>
</tr>
<tr>
<td>Lechevalieria</td>
<td>None</td>
<td>No</td>
<td>Gal, Man, Rha (tr)</td>
<td>PE, DPG, PG, PI</td>
<td>9(H₄)</td>
<td>68.0–71.4</td>
</tr>
<tr>
<td>Lentzea</td>
<td>None</td>
<td>No</td>
<td>Gal, Man, Rib</td>
<td>PE, DPG, PI</td>
<td>9(H₄)</td>
<td>71.4</td>
</tr>
<tr>
<td>Prauserella</td>
<td>None</td>
<td>No</td>
<td>Ara, Gal</td>
<td>DPG, PE</td>
<td>9(H₂), 9(H₄)</td>
<td>67–68.9</td>
</tr>
<tr>
<td>Pseudonocardia</td>
<td>None</td>
<td>No</td>
<td>Ara, Gal</td>
<td>PC, PE, PME, PI, PIM, OH-PE</td>
<td>8(H₄)</td>
<td>68–69</td>
</tr>
<tr>
<td>Saccharomonospora</td>
<td>None</td>
<td>No</td>
<td>Ara, Gal</td>
<td>PE, DPG, PG, PI</td>
<td>9(H₄)</td>
<td>66.0–70.0</td>
</tr>
<tr>
<td>Saccharopolyspora</td>
<td>None</td>
<td>No</td>
<td>Ara, Gal</td>
<td>PC, PE, DPG, PG, PI</td>
<td>9(H₄)</td>
<td>66.0–74.0</td>
</tr>
<tr>
<td>Saccharothrix</td>
<td>None</td>
<td>No</td>
<td>Gal, Rha, Man (tr)</td>
<td>PE, OH-PE, DPG, PG, PI, PIME</td>
<td>9(H₄), 10(H₄)</td>
<td>71.4</td>
</tr>
<tr>
<td>Sciscionella</td>
<td>None</td>
<td>No</td>
<td>Ara, Gal, Glc</td>
<td>DPG, PC, PE, PI, PL, PIME</td>
<td>9(H₄)</td>
<td>69.0</td>
</tr>
<tr>
<td>Streptoalloteichus</td>
<td>Pseudosporangia</td>
<td>Variable</td>
<td>Gal, Man, Rha</td>
<td>PE, DPG, PI, PIM, PIME</td>
<td>9(H₄), 10(H₄)</td>
<td>71.6</td>
</tr>
<tr>
<td>Thermocrispum</td>
<td>Pseudosporangia</td>
<td>No</td>
<td>Ara, Man, Glc, Gal (tr)</td>
<td>PE, PI, OH-PE</td>
<td>9(H₄)</td>
<td>69.0–73.0</td>
</tr>
<tr>
<td>Umezawaeae</td>
<td>None</td>
<td>No</td>
<td>Gal, Man, Rib, Rha (tr)</td>
<td>PE, PI, OH-PE, lypo-PE</td>
<td>9(H₄), 10(H₄)</td>
<td>74.0</td>
</tr>
<tr>
<td>Yuhushiella</td>
<td>Pseudosporangia</td>
<td>No</td>
<td>Ara, Gal, Glc, Rib</td>
<td>PE, PIM, PIME, DPG, PL, GlcNu</td>
<td>9(H₄)</td>
<td>69.9</td>
</tr>
</tbody>
</table>

* Ara, Arabinose; Gal, galactose; Glc, glucose; GlcN, glucosamine; Mad, madurose; Man, mannose; Rha, rhamnose; Rib, ribose; NK, unknown sugar; tr, trace; v, sugar is variably present in whole-cell hydrolysates.
† DPG, Diphosphatidylglycerol; GlcNu, phospholipids of unknown structure containing glucosamine; OH-PE, phosphatidylethanolamine with hydroxy fatty acids; lypo-PE, phosphatidylyethanolamine where one fatty acid chain is missing from the glycerol backbone; lypo-PME, phosphatidylmethylethanolamine where one fatty acid chain is missing from the glycerol backbone; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PIM, phosphatidylinositol mannosides; PL, unknown phospholipids; PME, phosphatidymethylethanolamine.
family Pseudonocardiaceae. The type genus is Pseudo-
Park et al. 2008.

Acknowledgements

Names are necessary to report factually on available data; however,
the USDA neither guarantees nor warrants the standard of the
product, and the use of the name by USDA implies no approval of the
product to the exclusion of others that may also be suitable.

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