NOTE

Description of *Bogoriellaceae* fam. nov., *Dermacoccaceae* fam. nov., *Rarobacteraceae* fam. nov. and *Sanguibacteraceae* fam. nov. and emendation of some families of the suborder *Micrococcineae*

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The hierarchic taxonomic framework described recently for the phylogenetic structure of the suborder *Micrococcineae*, class *Actinobacteria*, on the basis of 16S rDNA sequences and signature nucleotides was modified and extended. With the recent addition of novel taxa into the suborder, the phylogenetic coherence of some families was disrupted, leading to the emergence of novel lineages that, as judged by the depth of their branching points, were equivalent to those of described families. *Bogoriellaceae* fam. nov., *Dermacoccaceae* fam. nov., *Rarobacteraceae* fam. nov. and *Sanguibacteraceae* fam. nov. are proposed for these lineages. As a consequence of the restructuring process, some families have had to be emended, i.e. *Dermatophilaceae*, *Cellulomonadaceae* and *Intrasporangiaceae*.

Keywords: *Bogoriellaceae*, *Dermacoccaceae*, *Sanguibacteraceae*, *Rarobacteraceae*, *Micrococcineae*

The establishment of a classification system is a dynamic process. Novel organisms with novel properties or characteristics that have been either overlooked or not hitherto considered to be of taxonomic significance in the past will extend the range of properties to be used in classification. On the other hand, novel species considered to be members of a genus may lack characteristics that have been used in the process of delineation of this genus. Both the presence of new properties and the absence of properties hitherto used in the description of this taxon make it necessary either to emend the descriptions of the taxon or to dissect current taxa. In this respect, 16S rDNA signature nucleotide data, used as the basis of the recently proposed higher classification system of the *Actinobacteria* (Stackebrandt *et al.*, 1997), are not different from morphological, chemotaxonomic and physiological data, which have been used traditionally in the delineation of actinobacterial families and higher taxa. Today, actinomycete genera are characterized by a rich spectrum of mainly chemotaxonomic properties,

such as profiles of fatty acids, polar lipids, amino acids of peptidoglycan, isoprenoid quinones and, less frequently, polyamines (Busse & Schumann, 1999; Gvozdiak *et al.*, 1998; Altenburger *et al.*, 1997). Attempts often fail to link phylogenetically neighbouring genera into a higher taxon on the basis either of these patterns (Table 1) or of morphological and physiological traits, as no common non-molecular denominator can be identified that would circumscribe this taxon. More detailed analysis of the chemical composition of strains will show whether some of these characteristics will support the 16S rDNA-based classification of higher taxa. As demonstrated already by Busse & Schumann (1999), differences in the polyamine composition between members of the *Intrasporangiaceae* point towards the chemical uniqueness of *Sanguibacter* species.

Several novel species and genera have been described recently to be placed within the suborder *Micrococcineae*, some of which constitute monospecific lineages while others fall within the radiation of described higher taxa. The widely used algorithms that transform pairwise 16S rDNA similarity values into dissimilarity values, including the compensation for multiple substitutions that may occur at the same site

The GenBank/EMBL accession numbers for the 16S rDNA sequences of *Dermatophilus congolensis* DSM 44180^T and *Dermatophilus chelonae* DSM 44178^T are AJ243918 and AJ243919.

Table 1. Examples of chemotaxonomic diversity of genera of the phylogenetically defined families *Intrasporangiaceae* and *Micrococcaceae* of the suborder *Micrococcineae*

Data for the *Intrasporangiaceae* from Schleifer & Kandler (1972), Kalakoutskii (1989), Collins *et al.* (1989), Martin *et al.* (1997), Prauser *et al.* (1997), Schumann *et al.* (1997) and Busse & Schumann (1999). Data for the *Micrococcaceae* from Schleifer & Kandler (1972), Collins (1982), Embley *et al.* (1983), Jones & Collins (1986), Gerencser & Bowden (1986), Stackebrandt *et al.* (1983), Schleifer (1986), Fiedler & Draxl (1986), Stackebrandt *et al.* (1995) and Gvozdiak *et al.* (1998). Abbreviations: A₂pm, diaminopimelic acid; MCA_{var}, variable monocarboxylic amino acid in the interpeptide bridge; DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PI, phosphatidylinositol; PE, phosphatidylethanolamine; PIM, phosphatidylinositol mannosides; DMDG, dimannosyldiacylglycerol; PL, unidentified phospholipid; GL, unidentified glycolipid; PUT, putrescine; SPD, spermidine; CAD, cadaverine; SPM, spermine. Abbreviations for menaquinones exemplified by MK-8(H₂), partially saturated menaquinone with one of eight isoprene units hydrogenated. Abbreviations for fatty acids exemplified by ai-C_{15:0}, 12-methyltetradecanoic acid; i-C_{15:0}, 13-methyltetradecanoic acid; C_{16:0}, hexadecanoic acid. ND, Not determined.

Taxon	Diamino acid	Interpeptide bridge	Major menaquinone(s)	Polar lipids	Predominant fatty acids	Polyamines	G + C content (mol %)
<i>Intrasporangiaceae</i>							
<i>Intrasporangium</i>	LL-A ₂ pm	Gly ₃ *	MK-8	PI, PIM, PG, DPG	i-C _{15:0} , ai-C _{15:0} , i-C _{16:0}	PUT, SPD	68
<i>Janibacter</i>	meso-A ₂ pm	None	MK-8(H ₂)	PI, PG, DPG	C _{17:1} , C _{17:0} , i-C _{16:0}	PUT, CAD, (SPD)	70
<i>Terrabacter</i>	LL-A ₂ pm	Gly ₃ *	MK-8(H ₂)	PE, PI, DPG, PL	i-C _{15:0} , i-C _{14:0} , i-C _{16:0}	PUT	70–73
<i>Terracoccus</i>	LL-A ₂ pm	Gly ₃ *	MK-8(H ₂)	PE, PI, PG, DPG	i-C _{15:0} , ai-C _{15:0} , C _{16:0}	PUT, SPD, SPM	73
<i>Micrococcaceae</i>							
<i>Micrococcus</i>	L-Lys	Peptide subunit or D-Asp	MK-8, MK-8(H ₂)	DPG, PI, PG, PL, GL	i-C _{15:0} , ai-C _{15:0}	SPD, SPM, CAD	69–76
<i>Arthrobacter</i> †	L-Lys	MCA _{var}	MK-9(H ₂)	DPG, PG, PI, DMDG	i-C _{15:0} , ai-C _{15:0} , i-C _{16:0}	SPM, SPD	61–66
<i>Kocuria</i>	L-Lys	L-Ala ₃₋₄	MK-7(H ₂), MK-8(H ₂)	DPG, PG, (PI, PL, GL)	ai-C _{15:0} , ai-C _{17:0} , i-C _{16:0}	SPM, SPD	66–75
<i>Nesterenkonia</i>	L-Lys	Gly-L-Glu	MK-8, MK-9	DPG, PG, PI, PL, GL	ai-C _{15:0} , ai-C _{17:0} , i-C _{16:0}	CAD, SPD, SPM	70–72
<i>Renibacterium</i>	L-Lys	L-Ala-Gly‡	MK-9, MK-10	DPG, GL	ai-C _{15:0} , ai-C _{17:0}	ND	52–54
<i>Rothia</i>	L-Lys	L-Ala ₃	MK-7	DPG, PG	ai-C _{15:0} , ai-C _{17:0} , C _{16:0}	ND	49–53
<i>Stomatococcus</i>	L-Lys	L-Ala, L-Ser or Gly	MK-7	DPG, PG	ai-C _{15:0} , i-C _{16:0} , C _{16:0}	SPD, SPM	56–60

* Glycine bound to D-glutamic acid at position 2 of the peptide subunit.

† *Arthrobacter globiformis* group; polyamine data are from *Arthrobacter agilis* DSM 20550^T.

‡ D-Alanine amide bound to D-glutamic acid at position 2 of the peptide subunit.

(Jukes & Cantor, 1969), have been described by De Soete (1983) and Felsenstein (1993). These dissimilarity values are then transformed into phylogenetic distances to allow the graphic visualization of relationships. Any new sequence or region of the sequence included in the phylogenetic analysis is likely to change the similarity values and hence the topology of a dendrogram in which individual or groups of lines of descent may change the branching order.

Most main actinobacterial lines of descent described as orders, suborders and families are not well separated and the statistical significance of branching points is low. Because of the lack of common properties of phylogenetic significance shared by most taxa of a higher taxon, their delineation from each other is somewhat arbitrary and artificial. However, revision of an established system appears justified when the addition of novel entries into the 16S rDNA database leads to the dissection of described higher taxa. The sequence of a newly affiliated species allows a more precise judgement of the significance of 16S rDNA signature nucleotides, used in the past to circumscribe higher taxa of the class *Actinobacteria*, and may lead to the redefinition of a set of signatures for a given taxon.

Signature oligonucleotides are defined as present in the vast majority (>90%) of representatives of a taxon for which the signature has been described, the

structure of which is visible from the topology of the 16S rDNA dendrogram. It has been mentioned before that the pattern of signature nucleotides, but not necessarily the individual nucleotide, is indicative of a taxon being a member of a higher taxon (Stackebrandt *et al.*, 1997). Both a separate phylogenetic position and the emergence of novel signature patterns are indicative of a novel higher taxon; and the justification of the dissection of existing taxa is even more convincing if accompanied by the emergence of distinct phenotypic traits.

The 16S rDNA sequences of species either forming individual phylogenetic lineages or known to disrupt the coherence of higher taxa within the suborder *Micrococcineae* (Fig. 1) have been checked for the occurrence of described 16S rDNA signature nucleotides and the occurrence of novel sets of signatures in sequences described recently. These sequences are from *Dermatophilus congolensis* DSM 44180^T (accession number AJ243918), *Dermatophilus chelonae* DSM 44178^T (AJ243919) (these two strains were sequenced in this study using the methods of Rainey *et al.*, 1996), *Bogoriella caseilytia* DSM 11294^T (Y09911), *Demetria terragena* DSM 11295^T (Y14152), *Janibacter limosus* DSM 11140^T (Y08539) and DSM 11141 (Y08540), *Ornithinococcus hortensis* DSM 12335^T (Y17869), *Rarobacter faecitabidus* DSM 4813^T (Y17870), *Sanguibacter keddiei* NCFB 3025^T (X79450), *Sanguibacter*

Fig. 1. Phylogenetic relatedness among genera of the suborder *Micrococcineae*, order *Actinomycetales*, class *Actinobacteria*, based on 16S rDNA sequence comparison. Numbers within the dendrogram indicate the percentages of occurrence of the branching order in 500 bootstrapped trees (only values of 70% and above are shown). Regions of the tree in which the branching order of lineages was prone to the results of the treeing algorithm used are indicated as dashed lines. Sequences of species of other actinobacterial suborders served as a root. The scale bar represents 5 nucleotide substitutions per 100 nucleotides. The genus *Ornithinococcus*, for which no family has yet been described, is indicated by an asterisk.

suarezii NCFB 3023^T (X79452) and *Terracoccus luteus* DSM 44267^T (Y11928), as well as other published sequences (Fig. 1) that were included as references for taxa described to constitute families (Stackebrandt *et al.*, 1997).

An alignment of 16S rDNA sequences of type species currently available for members of the *Micrococcineae* was created using the ae2 editor (Maidak *et al.*, 1997). The sequences included in this alignment were obtained from the Ribosomal Database Project (Maidak *et al.*, 1997) and the ARB package (<http://www.mikro.biologie.tu-muenchen.de/pub/ARB>) as well as our own entries. The 16S rDNA sequences were aligned manually to provide a secondary structure-based optimal alignment. The data set used for the analyses described in this study contained information on more than 1400 unambiguous nucleotide positions present in all sequences between positions 40 and 1480 (*Escherichia coli* numbering; Brosius *et al.*, 1978). For the reconstruction of the phylogenetic dendrograms, evolutionary distances were calculated by the method of Jukes & Cantor (1969). Phylogenetic dendrograms were reconstructed using treeing algorithms contained in the PHYLIP package (Felsenstein, 1993) (neighbour-joining and maximum-likelihood) and the ae2 editor (Maidak *et al.*, 1997). The robustness of tree topologies

was evaluated by bootstrap analyses (Felsenstein, 1993) of the dendrogram generated on the basis of the algorithm of De Soete (1983) by performing 500 resamplings.

Compared with the 16S rDNA tree of the *Micrococcineae* presented by Stackebrandt *et al.* (1997) (not shown), the new sequence entries led to changes in the topology at which certain families branched from each other. The branching also changed depending on the algorithm used for the calculation of dendrograms. The edges that connect branching points with low bootstrap values (i.e. those that are not indicated by numbers in Fig. 1) are indicated by dashed lines. In most cases, the intrafamily composition remained stable, but in certain cases, the composition of genera within families changed. This is seen for *Sanguibacter* (affiliated to the *Intraspangiaceae*), *Rarobacter* (affiliated to the *Cellulomonadaceae*) and the genera *Dermacoccus* and *Kytococcus* (affiliated to the *Dermatophilaceae*). The newly described genus *Demetria* (Groth *et al.*, 1997b) clusters with the latter two genera, while *Bogoriella* (Groth *et al.*, 1997a) constitutes an individual line of descent within the suborder. Phylogenetic analysis of *Dermatophilus chelonae* DSM 44178^T indicates that the degree of relatedness to the type species *Dermatophilus congolensis* DSM 44180^T is

Table 2. Patterns of selected 16S rDNA signature nucleotides that define families of the suborder *Micrococcineae*

Patterns are indicated for the families *Dermacoccaceae* (1), *Rarobacteraceae* (2), *Sanguibacteraceae* (3), *Bogoriellaceae* (4), *Dermatophilaceae* (based on the sequence of *Dermatophilus congolensis* DSM 44180^T) (5), *Cellulomonadaceae* (6), *Intrasporangiaceae* (7), *Dermabacteraceae* (8), *Jonesiaceae* (9), *Micrococcaceae* (10), *Microbacteriaceae* (11), *Brevibacteriaceae* (12) and *Promicromonosporaceae* (13). R, Purine; Y, pyrimidine; VAR, variable. Residues in small capitals are present in some but not all strains.

Position	1	2	3	4	5	6	7	8	9	10	11	12	13
41–401	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	U–A	G–C
45–396	U–G	U–G	U–G	U–G	U–G	U–G	U–G	U–G	U–G	U–G	U–A	U–G	U–G
69–99	R–U	A–U	G–U	A–U	A–U	G–U	G–U	A–U	A–U	A–U	R–U	C–U	G–U
144–178	C–G	U–G	C–G	U–G	U–A	C–G	C–G	U–G	U–G	C–G	C–G	U–G	U–G
140–223	C–G, g–c*	C–G	G–C	G–U	C–G	C–G	G–Y	C–G	U–U	R–U	G–Y	G–C	C–G
142–221	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	U–A	U–A	C–G
248–276	C–G	C–G	C–G	C–G	C–G	C–G	C–G	U–G	C–G	C–G	C–G	C–C	C–G
258–268	G–C	G–C	A–U	G–C	A–U	G–C	A–U	A–U	G–C	A–U	A–U	G–C	G–C
293–304	G–Y	G–C	G–C	G–U	G–U	G–C	G–C	G–C	G–C	G–U	G–U	G–C	G–C
379–384	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	G–U	C–G	C–G	G–C	C–G
407–435	A–U, g–c*	A–U	A–U	A–U	A–U	c–G	A–U	G–Y	G–C	A–U	A–U	C–G	A–U
502–543	A–U	G–C	G–C	G–C	A–U†	G–c	A–U	R–Y	G–C	R–Y	R–Y	A–U	G–C
586–755	C–G	U–G	C–G	C–G	C–G	C–G	Y–R	U–A	C–G	C–G	C–G	U–A	C–G
589–650	U–A	U–A	U–A	C–G	U–G	U–A	U–A	U–G	U–G	C–G	U–A	U–A	U–A
591–648	U–A	U–A	U–A	U–A	U–A	U–A	U–A	U–A	U–A	U–A	U–A	G–U	U–A
610	R	A	U	A	A	A	A	A	U	G	VAR	A	U
602–636	C–G	G–U	G–U	C–G	C–G	C–G	C–G	C–G	U–G	C–G	C–G	C–G	G–U
612–628	Y–G	U–A	U–A	C–G	C–G	C–G	C–G	Y–G	C–G	C–G	C–G	G–C	C–G
615–625	G–C	C–G	A–U	G–C	G–C	A–U	R–Y	A–U	A–U	G–C	A–U	A–U	U–A
616–624	G–Y	G–C	G–C	G–C	G–C	G–C	G–C	G–C	U–G	G–Y	G–C	C–G	G–U
660–745	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	VAR	G–C	A–U	U–A
668–738	A–U	A–U	U–A	A–U	A–U	U–A	A–U	A–U	U–A	A–U	A–U	A–U	A–U
670–736	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	U–A	A–U
839–847	U–A	U–A	U–A	C–G	C–G	C–G	U–A	R–U	U–A	A–U	G–U	A–U	C–G
863	U	A	U	U	U	A	U	U	U	U	U	U	U
1133–1141	A–U	G–C	A–U	A–U	A–U	G–C	A–U	A–U	A–U	A–U	A–U	A–U	G–C
1134–1140	C–G	G–C	C–G	C–G	C–G	G–C	C–G	C–G	C–G	C–G	C–G	C–G	G–C
1244–1293	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	C–G	U–A	C–G
1254–1283	G–C	G–C	G–C	G–C	U–A	G–C	G–C	G–C	G–C	G–C	G–C	A–C	G–C
1263–1272	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	A–U	C–G	A–U
1310–1327	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	G–C	R–Y	A–U	U–A	G–C
1414–1486	C–G	C–G	C–G	C–G	C–G	U–G	C–G	C–G	C–G	C–G	U–A	C–G	C–G

* Composition of *Demetria terrigena* DSM 11295^T.

† The nucleotide pair G–C was erroneously indicated at positions 502–543 by Stackebrandt *et al.* (1997).

lower (94.4% 16S rDNA similarity) than to *Dermacoccus nishinomiyaensis* DSM 20448^T (96.2% similarity) and certain members of the *Intrasporangiaceae* (95.5% similarity). The assignment of *Dermatophilus chelonae* to the genus *Dermatophilus* was based mainly on morphological evidence (Masters *et al.*, 1995). Currently, analysis is in progress to characterize strain DSM 44178^T chemotaxonomically.

The signature nucleotides of 16S rDNA that define the currently established and proposed families of the suborder *Micrococcineae* are listed in Table 2. Most of the 32 positions are involved in base pairing in the secondary structure as proposed for the *E. coli* 16S rDNA sequence (Woese *et al.*, 1983). Some of the

positions are specific for members of a single family (e.g. *Brevibacteriaceae*, positions 41–401, 69–99 and 591–648), while other positions show two or more different nucleotide compositions (e.g. positions 586–755, 589–650 and 602–636). The numbers of differences in signature nucleotide pairs determined for members of the *Dermacoccaceae*, *Bogoriellaceae*, *Rarobacteraceae* and *Sanguibacteraceae* among themselves and for members of some neighbouring families vary from two to 15 (Table 3). The number of common signature nucleotides thus does not have to match pairwise 16S rDNA similarity values.

Bogoriella caseilytica was described for a single alkaliphilic actinomycete strain isolated from soda soil (pH

Table 3. Numbers of common signature nucleotides and pairs of signature nucleotides of 16S rDNA defined for some families of the suborder *Micrococcineae*

Family	1	2	3	4	5	6*	7	8	9
1. <i>Dermacoccaceae</i>	–	7	5	9	8	5	2	9	9
2. <i>Dermabacteraceae</i>	–	8	13	11	10	6	13	12	
3. <i>Bogoriellaceae</i>	–	11	12	6	7	11	10		
4. <i>Rarobacteraceae</i>	–	10	13	11	11	13			
5. <i>Sanguibacteraceae</i>	–	13	5	11	10				
6. <i>Dermatophilaceae</i>	–	7	15	13					
7. <i>Intrasporangiaceae</i>	–	9	11						
8. <i>Cellulomonadaceae</i>	–	13							

* Based on the sequence of *Dermatophilus congolensis* DSM 44180^T.

10) near Lake Bogoria in the Kenyan–Tanzanian Rift Valley in Africa (Groth *et al.*, 1997a). Chemotaxonomically, this species is distinct from other actinomycete taxa. 16S rDNA sequence comparison revealed that *Bogoriella caseilytica* represents a distinct lineage within the suborder *Micrococcineae*, exhibiting less than 94% similarity to the neighbouring phylogenetic taxa. As this lineage branches among other lineages described as individual families, the family *Bogoriellaceae* fam. nov. is proposed to accommodate the monospecific genus *Bogoriella*.

On the basis of 16S rDNA sequence data and the presence of specific signature nucleotides, the family *Dermatophilaceae* (Austwick, 1958) was emended (Stackebrandt *et al.*, 1997) to contain the type genus *Dermatophilus* (Van Saceghem, 1915; Gordon, 1964), as well as the genera *Dermacoccus* (Stackebrandt *et al.*, 1995) and *Kytococcus* (Stackebrandt *et al.*, 1995). When new 16S rDNA sequences were added to the database of actinomycetes, the incoherence of the family *Dermatophilaceae* became obvious, in that the type genus *Dermatophilus* clustered separately from the other two genera of the family. Consequently, the family has to be split into the *Dermatophilaceae* and a new family, *Dermacoccaceae* fam. nov., the latter family embracing the genera *Dermacoccus*, *Kytococcus* and *Demetria*. The relationship among the latter three genera has already been noticed in the original description of *Demetria terrigena* (Groth *et al.*, 1997b).

The genera *Terracoccus* (Prauser *et al.*, 1997) and *Janibacter* (Martin *et al.*, 1997) are included in the *Intrasporangiaceae* because of their phylogenetic position and correspondence in the signature nucleotides. *Ornithinococcus hortensis* (Groth *et al.*, 1999) appears to be the closest related taxon to this family, although its 16S rDNA nucleotides show significant deviations from the set of signature nucleotides of the *Intrasporangiaceae*. This genus is therefore not included in the *Intrasporangiaceae* and the affiliation of *Ornithinococcus* to a novel family should await the description of more representatives of this lineage. The addition of

new taxa within and close to the family *Intrasporangiaceae* leads to the exclusion of the genus *Sanguibacter*, which formed a deep branching lineage within the *Intrasporangiaceae* (see e.g. Martin *et al.*, 1997) as defined previously.

Description of *Bogoriellaceae* fam. nov. Schumann and Stackebrandt

Bogoriellaceae (Bo.go.ri.el.la'ce.ae. M.L. fem. n. *Bogoriella* type genus of the family; -aceae ending to denote a family; M.L. fem. pl. n. *Bogoriellaceae* the *Bogoriella* family).

The pattern of 16S rDNA signatures consists of nucleotides at positions 69–99 (A–U), 140–223 (G–U), 144–178 (U–G), 248–276 (C–G), 258–268 (G–C), 379–384 (C–G), 407–435 (A–U), 502–543 (G–C), 586–755 (C–G), 589–650 (C–G), 602–636 (C–G), 610 (A), 612–628 (C–G), 615–625 (G–C), 616–624 (G–C), 630 (C), 668–738 (A–U), 839–847 (C–G), 863 (U), 1133–1141 (A–U) and 1134–1140 (C–G). The family contains the type genus *Bogoriella* (Groth *et al.*, 1997a).

Description of *Dermacoccaceae* fam. nov. Schumann and Stackebrandt

Dermacoccaceae (Der.ma.coc.ca'ce.ae. M.L. masc. n. *Dermacoccus* type genus of the family; -aceae ending to denote a family; M.L. fem. pl. n. *Dermacoccaceae* the *Dermacoccus* family).

The pattern of 16S rDNA signatures consists of nucleotides at positions 139–224 (Y–R), 140–223 (C–G, g–c), 144–178 (C–G), 183'–193' (G–U), 248–276 (C–G), 258–268 (G–C), 379–384 (C–G), 407–435 (A–U, g–c), 502–543 (A–U), 586–755 (C–G), 589–650 (U–A), 602–636 (C–G), 610 (R), 612–628 (Y–G), 615–625 (G–C), 616–624 (G–Y), 630 (Y), 668–738 (A–U), 839–847 (U–A), 863 (U), 1133–1141 (A–U) and 1134–1140 (C–G). The family contains the type genus *Dermacoccus* (Stackebrandt *et al.*, 1995) as well as the genera *Kytococcus* (Stackebrandt *et al.*, 1995) and *Demetria* (Groth *et al.*, 1997b).

As a result of this dissection of the family *Dermatophilaceae*, the description of the original family must be emended.

Emended description of *Dermatophilaceae* Austwick 1958, emend. Stackebrandt, Rainey and Ward-Rainey 1997, emend. Stackebrandt and Schumann

The pattern of 16S rDNA/rRNA signatures consists of nucleotides at positions 140–223 (C–G), 144–178 (U–A), 248–276 (C–G), 258–268 (A–U), 293–304 (G–U), 379–384 (C–G), 407–435 (A–U), 502–543 (A–U), 586–755 (C–G), 589–650 (U–G), 602–636 (C–G), 610 (A), 612–628 (C–G), 615–625 (G–C), 616–624 (G–C), 630 (C), 668–738 (A–U), 839–847 (C–G), 863 (A), 1133–1141 (A–U), 1134–1140 (C–G) and 1254–1283 (U–A). The family contains the type

genus *Dermatophilus* (Austwick, 1958; Stackebrandt *et al.*, 1997).

Description of *Rarobacteraceae* fam. nov. Stackebrandt and Schumann

Rarobacteraceae (Ra.ro.bac.te.ra'ce.ae. M.L. masc. n. *Rarobacter* type genus of the family; -aceae ending to denote a family; M.L. fem. pl. n. *Rarobacteraceae* the *Rarobacter* family).

The pattern of 16S rDNA signatures consists of nucleotides at positions 69–99 (G–U), 140–223 (C–G), 144–178 (U–G), 248–276 (C–G), 258–268 (G–C), 379–384 (C–G), 407–435 (A–U), 502–543 (G–C), 586–755 (U–G), 589–650 (U–A), 602–636 (G–U), 610 (A), 612–628 (U–A), 615–625 (C–G), 616–624 (G–C), 630 (C), 668–738 (A–U), 839–847 (U–A), 863 (A), 1133–1141 (G–C) and 1134–1140 (G–C). The family contains the type genus *Rarobacter* (Yamamoto *et al.*, 1988).

With the exclusion of *Rarobacter*, the description of the family *Cellulomonadaceae* must be emended.

Emended description of *Cellulomonadaceae* Stackebrandt and Prauser 1991, emend. Stackebrandt, Rainey and Ward-Rainey 1997, emend. Stackebrandt and Schumann

The pattern of 16S rDNA/rRNA signatures consists of nucleotides at positions 69–99 (G–U), 140–223 (C–G), 144–178 (C–G), 248–276 (C–G), 258–268 (G–C), 379–384 (C–G), 407–435 (C–G), 502–543 (G–C), 586–755 (C–G), 589–650 (U–A), 602–636 (C–G), 610 (A), 612–628 (C–G), 615–625 (A–U), 616–624 (G–C), 630 (C), 668–738 (U–A), 839–847 (C–G), 863 (A), 1133–1141 (G–C), 1134–1140 (G–C) and 1414–1486 (U–G). The family contains the type genus *Cellulomonas* (Bergey *et al.*, 1923; emended by Clark, 1952; Stackebrandt *et al.*, 1982) as well as the genus *Oerskovia* (Prauser *et al.*, 1970; emended by Lechevalier, 1972).

Description of *Sanguibacteraceae* fam. nov. Stackebrandt and Schumann

Sanguibacteraceae (San.gui.bac.te.ra'ce.ae. M.L. masc. n. *Sanguibacter* type genus of the family; -aceae ending to denote a family; M.L. fem. pl. n. *Sanguibacteraceae* the *Sanguibacter* family).

The pattern of 16S rDNA signatures consists of nucleotides at position 69–99 (G–U), 140–223 (G–C), 144–178 (C–G), 248–276 (C–G), 258–268 (A–U), 379–384 (C–G), 407–435 (A–U), 502–543 (G–C), 586–755 (C–G), 589–650 (U–A), 602–636 (G–U), 610 (U), 612–628 (U–A), 615–625 (A–U), 616–624 (G–C), 630 (C), 668–738 (U–A), 839–847 (U–A), 863 (U), 1133–1141 (A–U) and 1134–1140 (C–G). The family contains the type genus *Sanguibacter* (Fernández-Garayzábal *et al.*, 1995).

With the exclusion of *Sanguibacter* from the *Intrasporangiaceae*, the specific set of signature nucleotides needs to be redefined for an emended family *Intrasporangiaceae*.

Emended description of *Intrasporangiaceae* Rainey, Ward-Rainey and Stackebrandt 1997, emend. Stackebrandt and Schumann

The pattern of the most discriminating 16S rDNA signatures (Table 1) consists of nucleotides at positions 69–99 (G–U), 139–224 (A–U), 140–223 (G–Y), 144–178 (C–G), 183–193 (C–G), 248–276 (C–G), 258–268 (A–U), 379–384 (C–G), 407–435 (A–U), 502–543 (A–U), 589–650 (U–A), 602–636 (C–G), 610 (A), 612–628 (C–G), 616–624 (G–C), 630 (C), 668–738 (A–U), 839–847 (U–A), 863 (U), 1133–1141 (A–U) and 1134–1140 (C–G). The family contains the type genus *Intrasporangium* (Kalakoutskii *et al.*, 1967) as well as the genera *Terrabacter* (Collins *et al.*, 1989), *Terracoccus* (Prauser *et al.*, 1997) and *Janibacter* (Martin *et al.*, 1997).

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