EVIDENCE OF PHYLOGENETIC HETEROGENEITY WITHIN THE GENUS *RHODOCOCCUS*: REVIVAL OF THE GENUS *GORDONA* (TSUKAMURA)

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Reverse transcriptase sequencing of 16S ribosomal ribonucleic acids of some representatives of the genus *Rhodococcus* were performed in an attempt to clarify their intra- and inter-generic relationships. The results indicate that the genus *Rhodococcus* as presently constituted is phylogenetically heterogeneous. On the basis of the 16S ribosomal-RNA sequence and earlier chemical data it is proposed that the genus *Gordona* (Tsukamura) be revived to accommodate those rhodococcal species containing relatively long-chain mycolic acids (48 to 66 carbon atoms) and MK-9(H₂) as the predominant menaquinone type.

The genus “*Gordona*” was proposed by TSUKAMURA in 1971 for some slightly acid-fast organisms originally isolated from the sputa of patients with pulmonary disease and from soil (1). Three species, “*Gordona bronchialis*,” “*G. rubra*” and “*G. terrae*” were originally described (1). GOODFELLOW and ALDERSON in 1977 resurrected the genus *Rhodococcus* for the group of bacteria collectively known as “*Mycobacterium rhodochrous*” and the “rhodochrous” complex (2). Strains of the genus “*Gordona*” were also reclassified in the genus *Rhodococcus* (2). Over the past decade it has become evident that the genus *Rhodococcus* as defined by GOODFELLOW and ALDERSON (2) is heterogeneous. Rhodococcal species can be divided into two distinct groups on the basis of chemical criteria. All of the species originally assigned to the genus “*Gordona*” (1) (i.e. *R. bronchialis*, *R. rubroperitinctus*, and *R. terrae*) have mycolic acids with 48 to 66 carbon atoms and major amounts of dihydrogenated menaquinones with nine isoprene units, whereas the other species

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contain shorter mycolic acids (approximately 34 to 52 carbon atoms) and predominantly dihydrogenated menaquinones with eight isoprene units (3–5).

Ribosomal-RNA (rRNA) analysis is currently the most powerful method for establishing the phylogenetic relationships of microorganisms (6–8). Chemo-taxonomic methods have been responsible for many of the recent improvements in the systematics of actinomycete and coryneform bacteria. To date there is excellent correlation between the groupings obtained using chemical criteria and those derived from 16S rRNA analysis (9). Therefore in the present study we have compared long stretches of the 16S rRNA primary structures of representatives of the two rhodococcal groups in an attempt to ascertain whether or not these warrant separate taxa.

MATERIALS AND METHODS

Organisms and growth conditions. *Rhodococcus erythropolis* DSM 43188, *R. fascians* DSM 20131, *R. bronchialis* DSM 43247, and *R. terrae* DSM 43249 were grown in shake flasks (malt extract 10 g, yeast extract 4 g, glucose 4 g, H₂O 1 l, pH 7.2) to the late exponential phase at 30°C.

Isolation of RNA and reverse transcriptase sequencing. Crude RNA was isolated as described previously (10). Reverse transcriptase sequencing (11) was done as described by LANE and associates (12). The sequence of oligonucleotide primers, their target sites and electrophoretic separation conditions of cDNA were as described previously (10). Selected stretches were aligned to the homologous region of more than 25 actinomycetes representing 17 genera. Computation of homologies (13), evolutionary distance values (Knuc) (14) and the construction of an unrooted tree (15) followed published procedures.

RESULTS AND DISCUSSION

The reverse transcriptase sequences of partial 16S rRNAs of *R. erythropolis* (DSM 43188), *R. fascians* (DM 20131), and *R. terrae* (DSM 43249) are shown aligned in Scheme 1. The above sequences were compared with those of 25 reference actinomycetes (10, 16, 17, unpublished data). Homology and derived Knuc values were based on 480 nucleotides involving only variable positions between points 200 and 1,435 (*E. coli* numbering system). The unrooted phylogenetic tree derived from the latter values are depicted in Fig. 1. A large fragment of the 16S rRNA from *R. bronchialis* (DSM 43247) (positions 100–900) was also analyzed and revealed high sequence homology to the corresponding region of *R. terrae* (97.7%). Lower values, between 89.2 and 93.6%, were found between *R. bronchialis* and *R. erythropolis*, *R. fascians* and representatives of *Nocardia* and *Mycobacterium*. The branching pattern of the tree derived from this long uninterrupted stretch was so similar to that based on the variable positions that the results of both analyses are merged in Fig. 1. The rhodococcal strains formed two groups on the basis of sequence

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rt  GAACGGGUGAGUAACACGUGGGUUAUCUACGnnGACUCUGGGUAAGCCUGGGAAACUGGGUCUAUUAACGGGAUUAUGACCAACUGGCGCAnnnUnnUGG
rb  GAACGGGUGAGUAACACGUGGGUUAUCUACGnnGACUCUGGGUAAGCCUGGGAAACUGGGUCUAUUAACGGGAUUAUGACCAACUGGCGCAnnnUnnUGG
rf  .....AUCUGCCCGCUCACUCUGGGUUAAGCCUGGGAAACUGGGUCUAUUAACGGGAUUAUGACCAACUGGCGCAnnnUnnUGG
re  GAACGGGUGAGUAACACGUGGGUUAUCUACGnnGACUCUGGGUAAGCCUGGGAAACUGGGUCUAUUAACGGGAUUAUGACCAACUGGCGCAnnnUnnUGG
na  GAACGGGUGAGUAACACGUGGGUUAUCUACGnnGACUCUGGGUAAGCCUGGGAAACUGGGUCUAUUAACGGGAUUAUGACCAACUGGCGCAnnnUnnUGG

rt  GUGGAAGCUUnnUGGGUnnUGGAGU  GcnnCGGGCUUAUCAGCUUUGUGGGGGUnnUGGCCUACCAAGGGCAGCAGGGUAGCGCAGCUGAGAGGGU
rb  GUGGAAGCUUUGUGGGUUGGGGAGU  GCCCGCGGGCUUAUCAGCUUUGUGGGGGUUAUGGCCUACCAAGGGCAGCAGGGUAGCGCAGCUGAGAGGGU
rf  GUGGAAGCUUUAUCGGUnnCGGAGU  GCCCGCGGGCUUAUCAGCUUUGUGGGGGUUAUGGCCUACCAAGGGCAGCAGGGUAGCGCAGCUGAGAGGGU
re  GUGGAAGCUUUAUCGGUGCGAGGUG  GCCCGCGGGCUUAUCAGCUUUGUGGGGGUUAUGGCCUACCAAGGGCAGCAGGGUAGCGCAGCUGAGAGGGU
na  GUnGAAGAUUUAUCGGUGCGAGGUG  GCCCGCGGGCUUAUCAGCUUUGUGGGGGUUAUGGCCUACCAAGGGCAGCAGGGUAGCGCAGCUGAGAGGGU

rt  GAUCGGCCACACUGGGACUGAGACACGGCCGAGACUCCUACGGGAGGCAGCAGUGGGGAAUUAUGCACAAGGGGCGCAAGCCUUAUGCAGCAGCAGCGCGG
rb  GAUCGGCCACACUGGGACUGAGACACGGCCGAGACUCCUACGGGAGGCAGCAGUGGGGSSUAUUGCACAAGGGGCGCAAGCCUUAUGCAGCAGCAGCGCGG
rf  GACCGGCCACACUGGGACUGAGACACGGCCGAGACUCCUACGGGAGGCAGCAGUGGGGAAUUAUGCACAAGGGGCGCAAGCCUUAUGCAGCAGCAGCGCGG
re  GACCGGCCACACUGGGACUGAGACACGGCCGAGACUCCUACGGGAGGCAGCAGUGGGGAAUUAUGCACAAGGGGCGCAAGCCUUAUGCAGCAGCAGCGCGG
na  GACCGGCCACACUGGGACUGAGACACGGCCGAGACUCCUACGGGAGGCAGCAGUGGGGAAUUAUGCACAAGGGGCGCAAGCCUUAUGCAGCAGCAGCGCGG

rt  UGAGGGUAUGACGGCCUUCGGGUGUUAACCUUnnUUACACAGGGAGCAAGCGUGAGUGACGGUACCUUnnGAGAAGAGCAGCGGCAACUACUGGCGCAGCAG
rb  UGAGGGUAUGACGGCCUUCGGGUGUUAACCUUnnUUACACAGGGAGCAAGCGUGAGUGACGGUACCUUnnGAGAAGAGCAGCGGCAACUACUGGCGCAGCAG
rf  UGAGGGUAUGACGGCCUUCGGGUGUUAACCUUnnUUACACAGGGAGCAAGCGUGAGUGACGGUACCUUnnGAGAAGAGCAGCGGCAACUACUGGCGCAGCAG
re  UGAGGGUAUGACGGCCUUCGGGUGUUAACCUUnnUUACACAGGGAGCAAGCGUGAGUGACGGUACCUUnnGAGAAGAGCAGCGGCAACUACUGGCGCAGCAG
na  UGAGGGUAUGACGGCCUUCGGGUGUUAACCUUnnUUACACAGGGAGCAAGCGUGAGUGACGGUACCUUnnGAGAAGAGCAGCGGCAACUACUGGCGCAGCAG

rt  CCGCGGUAAUACUGAGGGUGCGAGCGUUGUCGGAAUUAUCUGGGCGUAAAGAGCUCUGAGGCGUUGUGUGCGGUGCUGUGUAAAUGUGCAACUCAAUU
rb  CCGCGGUAAUACUGAGGGUGCGAGCGUUGUCGGAAUUAUCUGGGCGUAAAGAGCUCUGAGGCGUUGUGUGCGGUGCUGUGUAAAUGUGCAACUCAAUU
rf  CCGCGGUAAUACUGAGGGUGCGAGCGUUGUCGGAAUUAUCUGGGCGUAAAGAGUUCUGAGGCGGUGUGUGCGGUGCUGUGUAAAUGUGCAACUCAAUU
re  CCGCGGUAAUACUGAGGGUGCGAGCGUUGUCGGAAUUAUCUGGGCGUAAAGAGUUCUGAGGCGGUGUGUGCGGUGCUGUGUAAAUGUGCAACUCAAUU
na  CCGCGGUAAUACUGAGGGUGCGAGCGUUGUCGGAAUUAUCUGGGCGUAAAGAGCUGGUGGCGGUGUGUGCGGUGCUGUGUAAAUGUGGCGUAAAC

rt  GCAGGGCUGCAGGGCAUAACGGCGAGACUGAGUACUACAGGGGAGACUGGAUUAUCUGGUGUAGCGGUGUAAUUGCGCAGAUUAUCAGGAGGAACACCGGUG
rb  UAGGGCUGCAGGGCAUAACGGCGAGACUGAGUACUACAGGGGAGACUGGAUUAUCUGGUGUAGCGGUGUAAUUGCGCAGAUUAUCAGGAGGAACACCGGUG
rf  UCGGGCUGCAGGGCAUAACGGCGAGACUGAGUAGUUGUUCAGGGGAGACUGGAUUAUCUGGUGUAGCGGUGUAAUUGCGCAGAUUAUCAGGAGGAACACCGGUG
re  nCUUGUGUGCAGGGCAUAACGGCGAGACUGAGUACUACAGGGGAGACUGGAUUAUCUGGUGUAGCGGUGUAAUUGCGCAGAUUAUCAGGAGGAACACCGGUG
na  CCAAGCUGUGCGGUGGAUAACGGCGAGGUGAGUACUUCGGGGGnGGCUGGAUUAUCUGGUGUAGCGGUGUAAUUGCGCAGAUUAUCAGGAGGAACACCGGUG

rt  GCGAAGCGGGGnUCUGGGUAGUUAACUGACCGUGAGGAGCGAAGCGUGGGUAGCGAAGCAGGAUUAAGUUAACCGUGUAGUCCAGCGGUAACCGGUGGGU
rb  GCGAAGCGGGGnUCUGGGUAGUUAACUGACCGUGAGGAGCGAAGCGUGGGUAGCGAAGCAGGAUUAAGUUAACCGUGUAGUCCAGCGGUAACCGGUGGGU
rf  GCGAAGCGGGGnUCUGGGUAGUUAACUGACCGUGAGGAGCGAAGCGUGGGUAGCGAAGCAGGAUUAAGUUAACCGUGUAGUCCAGCGGUAACCGGUGGGU
re  nCGAAGCGGGGnUCUGGGUAGUUAACUGACCGUGAGGAGCGAAGCGUGGGUAGCGAAGCAGGAUUAAGUUAACCGUGUAGUCCAGCGGUAACCGGUGGGU
na  GCGAAGCGGGGnUCUGGGUAGUUAACUGACCGUGAGGAGCGAAGCGUGGGUAGCGAAGCAGGAUUAAGUUAACCGUGUAGUCCAGCGGUAACCGGUGGGU

rt  ACUAGGUGUGGGUUCUUUAUCAGGGAUUCUGGCGUAGCUAACCGCAUUAAGUUnCCnGCGUGGGGAGUAACGGCGCGCAAGGCUAAACUCAAAGGAUUUG
rb  ACUAGGUGUGGG  CUUUUAUCAGGGAUUCUGGCGUAGCUAACCGCAUUAAGUUnCCnGCGUGGGGAGUAACGGCGCGCAAGGCUAAACUCAAAGGAUUUG
rf  GCUAGGUGUGGG  UUCUUUAUCAGGGAUUCUGGCGUAGCUAACCGCAUUAAGGCGCnGCGUUnGGGnUACGGCGCGCAAGGCUAAACUCAAAGGAUUUG
re  GCUAGGUGUGGG  UUCUUUAUCAGGGAUUCUGGCGUAGCUAACCGCAUUAAGGCGCnGCGUGGGGAGUAACGGCGCGCAAGGCUAAACUCAAAGGAUUUG
na  nCUAGGUGUGGGUUAUCAGGGAUUCUGGCGUAGCUAACCGCAUUAAGUUnCCnGCGUGGGGAGUAACGGCGCGCAAGGCUAAACUCAAAGGAUUUG

rt  ACGGGGGCGnGCACAAGCGCGGAGCAUGUGGAUUAUUGCAUGnAACGCGAAGAACCUUACCGGGGnUGACAUAACACGAGCGGGGUGAGCAUAGUC
rb  ACGGGGGCGnGCACAAGCGCGGAGCAUGUGGAUUAUUGCAUGnAACGCGAAGAACCUUACCGGGGnUGACAUAACACGAGCGGGGUGAGCAUAGUC
re  ACGGGGGCGnGCACAAGCGCGGAGCAUGUGGAUUAUUGCAUGnAACGCGAAGAACCUUACCGGGGnUGACAUAACACGAGCGGGGUGAGCAUAGUC
na  ACGGGGGCGnGCACAAGCGCGGAGCAUGUGGAUUAUUGCAUGnAACGCGAAGAACCUUACCGGGGnUGACAUAACACGAGCGGGGUGAGCAUAGUC

rt  UUGCCAGCGGGUUAUGCCGGGGACUnGAGGAGACUGCCGGGGUnAACUGGAGGAAGGUGGGGUAUGCGUAAUGUUAUGCCCUUUAUGUCCAGGGG
rb  UUGCCAGCGGGUUAUGCCGGGGACUnGAGGAGACUGCCGGGGUnAACUGGAGGAAGGUGGGGUAUGCGUAAUGUUAUGCCCUUUAUGUCCAGGGG
rf  UUGCCAGCGGGUUAUGCCGGGGACUnGAGGAGACUGCCGGGGUnAACUGGAGGAAGGUGGGGUAUGCGUAAUGUUAUGCCCUUUAUGUCCAGGGG
re  UUGCCAGCGGGUUAUGCCGGGGACUnGAGGAGACUGCCGGGGUnAACUGGAGGAAGGUGGGGUAUGCGUAAUGUUAUGCCCUUUAUGUCCAGGGG
na  UUGCCAGCGGGUUAUGCCGGGGACUnGAGGAGACUGCCGGGGUnAACUGGAGGAAGGUGGGGUAUGCGUAAUGUUAUGCCCUUUAUGUCCAGGGG

rt  UUCACACAUUGCUAAUGGUGGUAACAGAGGGGUGCGAUACCGUAGGUnGAGCGAAUCCCUUAAAGCnGnUUCAGUUCGGAUUGGGGUGUGCAACUnG
rb  UUCACACAUUGCUAAUGGUGGUAACAGAGGGGUGCGAUACCGUAGGUnGAGCGAAUCCCUUAAAGCnGnUUCAGUUCGGAUUGGGGUGUGCAACUnG
rf  UUCACACAUUGCUAAUGGUGGUAACAGAGGGGUGCGAUACCGUAGGUnGAGCGAAUCCCUUAAAGCnGnUUCAGUUCGGAUUGGGGUGUGCAACUnG
re  UUCACACAUUGCUAAUGGUGGUAACAGAGGGGUGCGAUACCGUAGGUnGAGCGAAUCCCUUAAAGCnGnUUCAGUUCGGAUUGGGGUGUGCAACUnG
na  UUCACACAUUGCUAAUGGUGGUAACAGAGGGGUGCGAUACCGUAGGUnGAGCGAAUCCCUUAAAGCnGnUUCAGUUCGGAUUGGGGUGUGCAACUnG

rt  ACCCCAUGAAGUGCGAGUGCGUAGUAUUCGAGAUACGCAACCGUGCGGUAUUAUGUCCCGGGCGUGUACACACCGCGGUUACGnCAUGAAGUGCG
rb  ACCCCAUGAAGUGCGAGUGCGUAGUAUUCGAGAUACGCAACCGUGCGGUAUUAUGUCCCGGGCGUGUACACACCGCGGUUACGnCAUGAAGUGCG
rf  ACCnGUGAAGUGCGAGUGCGUAGUAUUCGAGAUACGCAACCGUGCGGUAUUAUGUCCCGGGCGUGUACACACCGCGGUUACGnCAUGAAGUGCG
re  ACCnGUGAAGUGCGAGUGCGUAGUAUUCGAGAUACGCAACCGUGCGGUAUUAUGUCCCGGGCGUGUACACACCGCGGUUACGnCAUGAAGUGCG
na  ACCnGUGAAGUGCGAGUGCGUAGUAUUCGAGAUACGCAACCGUGCGGUAUUAUGUCCCGGGCGUGUACACACCGCGGUUACGnCAUGAAGUGCG

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Scheme 1. Partial sequence of 16S rRNAs of *R. bronchialis* (rb), *R. erythropolis* (re), *R. fascians* (rf), *R. terrae* (rt), and *N. asteroides* (na). n, undetermined nucleotide; dots, undetermined sequences; gap, alignment gap. The first nucleotide at the 5' terminus corresponds to position 107 and the last nucleotide at the 3' terminus corresponds to position 1497 of the *E. coli* sequence.

analysis. *R. erythropolis* and *R. fascians* had relatively high sequence homology and belong to a single group. *R. erythropolis* and *R. fascians* exhibited a closer relationship to *N. asteroides* than to the *R. terrae*/*R. bronchialis* pair of organisms.

Table 1. 16S rRNA sequence homologies (lower left triangle) between *Rhodococcus* species and some reference actinomycetes.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1 <i>Rhodococcus erythropolis</i>	—																	
2 <i>Rhodococcus fascians</i>	90.1	—																
3 <i>Rhodococcus terrae</i>	85.8	81.2	—															
4 <i>Corynebacterium bovis</i>	79.8	77.0	78.2	—														
5 <i>Corynebacterium glutamicum</i>	78.7	79.0	79.4	86.4	—													
6 <i>Corynebacterium variabilis</i>	79.4	78.9	80.8	90.2	89.2	—												
7 <i>Mycobacterium phlei</i>	85.3	81.3	84.8	79.4	77.1	77.2	—											
8 <i>Mycobacterium tuberculosis</i>	82.3	79.4	83.3	78.3	77.6	78.3	89.9	—										
9 <i>Nocardia asteroides</i>	88.0	83.5	82.2	77.4	75.8	75.8	82.3	81.6	—									
10 <i>Tsukamurella paurometabolum</i>	87.7	84.8	84.6	78.3	81.1	80.8	86.2	83.5	84.0	—								
11 <i>Dactylosporangium aurantiacum</i>	79.3	75.1	77.2	73.3	73.6	73.2	76.7	73.3	78.5	75.7	—							
12 <i>Frankia</i> species	78.3	75.0	74.6	69.6	67.6	67.7	75.1	73.6	76.9	77.0	75.3	—						
13 <i>Actinopolyspora halophila</i>	71.6	68.6	72.8	67.0	66.2	68.0	69.1	72.2	66.1	67.2	69.9	63.2	—					
14 <i>Bifidobacterium bifidum</i>	63.9	60.9	62.3	65.3	63.4	63.6	64.6	62.2	62.3	63.5	63.2	59.0	55.7	—				
15 <i>Propionibacterium freudenreichii</i>	76.3	71.3	76.0	71.9	70.4	71.7	75.4	75.8	73.5	76.7	71.9	70.7	65.0	63.1	—			
16 <i>Actinomyces bovis</i>	72.3	68.0	73.9	73.9	69.5	72.3	72.3	72.4	70.1	73.8	75.0	69.0	66.0	67.7	69.0	—		
17 <i>Nocardiotides albus</i>	78.7	76.5	76.2	73.3	73.4	74.8	74.4	74.2	76.2	75.5	74.4	74.2	69.4	63.8	73.5	68.2	—	
18 <i>Streptovorticillum baldacii</i>	76.2	71.0	73.6	69.7	69.7	70.5	71.7	71.4	75.0	75.4	72.9	74.3	62.5	63.0	71.3	69.7	74.5	—

16S rRNA sequences of reference strains are given in references (10), (16), (17) and unpublished.

Fig. 1. Unrooted phylogenetic tree displaying the relationship of rhodococcal species to other reference actinomycetes. The position of *R. bronchialis* is interpolated from a reduced data set (see text).

The latter species occupied an isolated position in the tree approximately equidistant to representatives of *Mycobacterium*, *Nocardia*, *Tsukamurella*, and *R. erythropolis*/*R. fascians*.

In view of the distinct phylogenetic position of *R. terrae* and *R. bronchialis* we consider these organisms and chemically related species should be reclassified in a separate genus. It is therefore formally proposed that the genus *Gordona* (Tsukamura) (1) be revived to accommodate the long-chain mycolic acid/MK-9(H₂) group of rhodococcal species (namely *R. bronchialis*, *R. rubroperitinctus*, *R. sputi*, and *R. terrae*). Furthermore, the removal of these species from the genus *Rhodococcus* makes the latter chemically more homogeneous. The description of the genus *Rhodococcus* (2) is therefore emended accordingly.

Description of *Gordona* (Tsukamura) Stackebrandt, Smida and Collins nom.rev., gen.nov.

Gram-positive, slightly acid-fast short rods or coccoid forms. Rod-coccus life cycle. Mycelium are not formed. Non-motile and neither conidia nor endospores are produced. Growth occurs at 28 and 37°C but not at 45°C. Obligately aerobic chemoorganotrophic with an oxidative type metabolism. Acid is produced from glucose and some other sugars. A wide range of organic compounds are utilized as sole sources of carbon for energy and growth. Catalase positive. Oxidase negative. Nitrate is reduced to nitrite. Urease positive. Casein, cellulose, chitin, elastin and xylan are not degraded. Arylsulphatase negative. Cell wall peptidoglycan is based upon *meso*-diaminopimelic acid (variation Al γ). Glycan moiety of peptidoglycan contains N-glycolylmuramic acid. Wall sugars are arabinose and galactose. Mycolic acids are present with a range of ca. 48 to 66 carbon atoms. Long-chain fatty acids

Table 2. Differential characteristics of the genus *Gordona*

Characteristics	Mycolic acids		
	Overall size (No. of carbons)	Number of double bonds	Ester released on pyrolysis
<i>Caseobacter</i>	30–36	0–2	14–18
<i>Corynebacterium</i>	22–36	0–2	8–18 ^a
<i>Gordona</i>	48–66	1–4	16–18
<i>Mycobacterium</i>	60–90	1–2	20–26
<i>Nocardia</i>	44–60	0–3	12–18
<i>Rhodococcus</i>	34–52	0–2	12–16
<i>Tsukamurella</i>	64–78	1–6	20–22

^a Most corynebacteria release esters of 14–18 carbons except *C. bovis* which releases esters of 8–10 carbons.

^b Present in *C. bovis*, *C. minutissimum*, and *C. variabilis*.

are predominantly of the straight-chain saturated, monounsaturated, and 10-methyl branched types. MK-9(H₂) is the predominant menaquinone; a few strains may have comparable amounts of MK-8(H₂). The major phospholipids are diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol, and phosphatidylinositol dimannosides. The G + C content of DNA is 63 to 69 mol%. Isolated from sputa of patients with pulmonary disease and from soil. The type species of *Gordona* is *Gordona bronchialis* Tsukamura 1971.

Description of *Gordona bronchialis* (Tsukamura) nom. rev.

Full specific details may be found in references 1) and 2). Type strain is ATCC 25592.

Description of *Gordona rubropertinctus* (Hefferan) comb. nov.

Full specific details may be found in references 2) and 18). Type strain is ATCC 14352.

Description of *Gordona sputi* (Tsukamura) comb. nov.

Full specific details may be found in references 19) and 20). Type strain is ATCC 29627.

Description of *Gordona terrae* (Tsukamura) nom. rev.

Full specific details may be found in references 1), 2), and 18). Type strain is ATCC 25594.

Emendation of *Rhodococcus* (Zopf).

The description of GOODFELLOW and ALDERSON (2) should be emended to include the following: Mycolic acids are present with a range of ca. 34 to 52 carbon

and other wall chemotype IV taxa containing mycolic acids.

Tuberculo- stearic acid	Phosphatidyl- ethanolamine	Menaquinone	N-glycolyl in glycan moiety of wall	Mol% G+C of DNA
+	ND	MK-8(H ₂), MK-9(H ₂)	—	65–67
— ^b	—	MK-8(H ₂), MK-9(H ₂)	—	51–67
+	+	MK-9(H ₂)	+	63–69
+	+	MK-9(H ₂)	+	62–70
+	+	MK-8(H ₄ , ω -cycl) ^c	+	64–72
+	+	MK-8(H ₂)	+	63–73
+	+	MK-9	+	67–68

^c Members of the genus *Nocardia* were originally reported to have MK-8(H₄). Recent studies however demonstrate the major quinone is a "pseudo-MK-8(H₆)" in which the end of the multiprenyl side-chain is cyclized (21).

atoms. MK-8(H₂) is the predominant menaquinone.

The genus *Gordona* is most easily confused with members of the genus *Mycobacterium*. *Gordonae* however may be distinguished from the latter in producing significantly shorter mycolic acids (48–66 carbons compared with 60 to 90 carbons for mycobacteria). The esters released on pyrolysis of mycolic acid methyl esters of *gordonae* and mycobacteria are also quite different (16 to 18 carbons and 20 to 26 carbons respectively). The genus *Gordona* may be distinguished from rhodococci and other mycolic acid-containing taxa by the criteria shown in Table 2.

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