Phylogenetic Relationships and Uncertain Taxonomy of Pedobacterium Species

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The phylogenetic relationships among the species of the genus Pedobacterium were studied by comparing their 16S rRNA sequences. The Pedobacterium species form a coherent phylogenetic cluster within the genera of the hyphal budding bacteria in the α-Proteobacteria. The sequences of two strains of Pedobacterium australicum were obtained from DNAs extracted from nonviable freeze-dried cells, which are the only source of material available, and were found to be almost identical (level of similarity, 99.9%). Overall, the Pedobacterium species are closely related, with sequence similarities ranging from 96.2 to 99.9%. Pedobacterium manganicum is phylogenetically the most distantly related species and exhibits the lowest similarity (96.2%) with Pedobacterium americanum. Australian isolate Pedobacterium sp. strain ACM 3067, P. americanum, and P. australicum are all very highly related, with similarities greater than 99%. Pedobacterium sp. strain ACM 3067 is most closely related to P. australicum (level of similarity, 99.6%) and P. americanum (99.4%). These manganese-oxidizing species are more closely related to the iron-oxidizing species Pedobacterium ferrugineum than to the other manganese-oxidizing species, P. manganicum. Taxonomic uncertainties resulting from the loss of the type culture of P. australicum are discussed.

In 1988, Sly et al. reported on the characteristics of strains of Pedobacterium manganicum isolated from manganese-depositing biofilms in drinking water distribution systems in Australia (28). At that time, there were only two valid species of the genus Pedobacterium, Pedobacterium ferrugineum and P. manganicum (20, 27). Later, Gebers and Beese (7) described two new species, Pedobacterium americanum and Pedobacterium australicum. Unfortunately, the type strain and a second isolate of P. australicum were lost before they could be accessioned for comparison (13, 14, 32), and we were unable to compare these strains with our isolates, which appeared to be more closely related phenotypically to P. australicum and P. americanum than to P. manganicum.

The absence of a viable type strain of P. australicum is contributing to taxonomic uncertainty in the genus Pedobacterium. The availability of PCR techniques provided an opportunity to amplify 16S rRNA genes from nonviable freeze-dried amorphous and to determine the 16S rRNA sequences of P. australicum for comparison with the sequences of the other Pedobacterium species and our local isolates. Although Gebers and Beese (7) showed that P. australicum and P. americanum exhibited only 25 to 28% DNA homology and were separate species as determined by currently accepted standards for DNA-DNA homology levels (31, 35), there were no reliable phenotypic characteristics to differentiate the two species. If sufficient differences in the sequences of the 16S rRNAs of P. australicum and P. americanum can be found, then it may be possible to determine species-specific RNA sequence signatures for designating a neotype strain of P. australicum for further study.

MATERIALS AND METHODS

Microorganisms. Most of the strains used in the study were obtained from the Australian Collection of Microorganisms, Department of Microbiology, University of Queensland, Brisbane, Australia; the only exceptions were P. australicum IFAM ST-1067 (T = type strain) and IFAM WD-1355, which were obtained from nonviable freeze-dried material from Peter Hirsch at the Institut fur Allgemeine Mikrobiologie in Kiel, Germany. Details of the strains are shown in Table 1. All viable strains were maintained on PSM agar plates (6) and were incubated at 28°C. Manganese oxidation was verified by growing on manganese-impregnated plates.

Extraction and purification of genomic DNA. Bacterial growth from PSM agar plates or freeze-dried material of those strains which were nonviable was collected and pelleted by centrifugation in a microcentrifuge at 3,000 rpm, and the genomic DNA was isolated by the method of Bollet et al. (2). DNA was released from cells in 1.5-m I microcentrifuge tubes (Treff Laboratories, Degerstein, Switzerland) by heating the tubes in a 650-W microwave oven for three 1-min intervals. The concentration of DNA in a sample was estimated by electrophoresing 5 μl of purified DNA with 3 μl of loading buffer (0.25% bromophenol blue and 30% glycerol in water) and a 1-kb DNA ladder (Gibco, Gaithersburg, Md.) on a 1% agarose gel containing 5 μl of a 10-mg/ml ethidium bromide solution per 100 ml.

PCR amplification of 16S ribosomal DNA (rDNA). A 1- to 3-μl portion of bacterial genomic DNA was used in each PCR mixture, as described by Bond et al. (3). The first denaturation step consisted of incubation at 98°C for 2 min. The thermal profile of the PCR apparatus (Perkin-Elmer Cetus, Norwalk, Conn.) included repeated cycles of primer annealing at 48°C for 1 min, extension at 72°C for 2 min, and denaturation at 93°C for 1 min. After 28 cycles, primer annealing was repeated, and this was followed by a final extension step at 72°C for 5 min. The primers used for amplification were primers 27f and 1520r (18). The PCR products were purified by using Wizard Mini Prep for DNA purification (Promega, Madison, Wis.) as recommended by the supplier. The concentrations of purified PCR products were estimated by electrophoresing 2 μl of each PCR product on a 1% agarose gel as described above for genomic DNA.

Sequencing of 16S rDNA. Sequencing reactions were carried out by using a PRISM Ready Reaction DyeDeoxy terminator cycle sequencing kit (Perkin-Elmer/Applied Biosystems Div., Foster City, Calif.). A 1- to 3-μl portion of purified PCR product was used per reaction mixture (total volume, 20 μl) containing 5 μl of loading buffer (0.25% bromophenol blue and 30% glycerol in water) and a 1-kb DNA ladder (Gibco, Gaithersburg, Md.) on a 1% agarose gel containing 5 μl of a 10-mg/ml ethidium bromide solution per 100 ml. Sequencing products were purified, and sequences were determined by automated DNA sequencing with an Applied Biosystems model 373A instrument as recommended by the manufacturer.

Phylogenetic analysis. The full-length 16S rRNA sequences of P. ferrugineum ACM 3086T, P. manganicum ACM 3035T, P. americanum ACM 3067T, P. australicum IFAM ST-1067T and IFAM WD-1355, and Pedobacterium sp. strain ACM 3067 were manually aligned with sequences of eight other members of the Proteobacteria, including the nearest known relative, Hyphomicrobium vulgaris (30), by using the ClustalW version 1.8 software as the reference sequence. The sequences of the following strains were obtained from the Ribosomal Database Project, Urbana, Ill. (19): Hyphomicrobium vulgaris ATCC 27508 (accession no. X53182), Hyphomicrobium inanischaena ATCC 33883 (accession no. M33860), Hirchellia bifida ATCC 49814T (accession no. X52909), Rhodobacterium vannieli ATCC 51194 (accession no. M34127), E. coli (accession no. J01695), Neisseria gonorrhoeae ATCC 19424 (accession no. X07714), Desulfovibrio desulfuricans ATCC 27774 (accession no. X53143), and Campylobacter jejuni ATCC 43431 (accession no. Z29326).
The outgroup chosen for each analysis was the organism most distantly related to the genus Pedomicrobium on the prokaryotic phylogenetic tree (23) in each data set. Unsequenced regions and regions of alignment uncertainty due to length variations were omitted from the analyses. Levels of similarity were calculated for each pair of sequences by using the se2 editor program (19) and a Sun workstation.

Three different methods available in the PHYLIP version 3.52 phylogeny inference package (4) were employed to infer the phylogenetic relationships. Pairwise evolutionary distances were computed with DNADIST by using the correction of Jukes and Cantor (16). Phylogenetic trees were constructed by using the neighbor-joining method of Saitou and Nei (26) in the program NEIGHBOR (4). Parsimony and maximum-likelihood analyses were carried out by using DNAPARS and DNAML (4), respectively. Bootstrap analyses that generated 100 data sets also were performed on the phylogeny derived from the neighbor-joining analysis by using the programs SEQBOOT, DNADIST, CONSENSE (4) to determine the statistical level of confidence for the branch points.

Nucleotide sequence accession numbers. The sequences determined in this study for P. australicum IFAM ST-13067 (accession no. X97693), P. australicum IFAM WD-1355 (accession no. X97694), P. americanum ACM 3090T (accession no. X97692), P. ferruginium ACM 3037T (accession no. X97690), P. manganicum ACM 3038T (accession no. X97691), and Pedomicrobium sp. strain ACM 3067 (accession no. X97695) have been deposited in the EMBL database, Cambridge, United Kingdom.

RESULTS AND DISCUSSION

As the type culture of P. australicum had been lost since its description by Gebers and Beece (7), a complete analysis of the phylogenetic relationships among the species of the genus Pedomicrobium depended on the ability to extract DNA from nonviable freeze-dried material. Cells of two strains of P. australicum that had been freeze-dried in skim milk during the period from 1984 to 1991 were kindly provided by Peter Hirsch. Preliminary experiments (data not shown) performed with cells of Pedomicrobium sp. strain ACM 3067 showed that the presence of 20% skim milk in the reaction mixtures did not adversely affect extraction of DNA from the cells or interfere with subsequent PCR amplification of the 16S rDNA in the extracted DNA. Extraction of DNA from Pedomicrobium species has been reported to be difficult (12). However, the microwave method of Boltel et al. (2) was found to release sufficient DNA for PCR amplification.

Full 16S rDNA sequences were obtained for the type cultures of the validly published Pedomicrobium species (20, 27), as well as for P. australicum IFAM WD-1355 and Pedomicrobium sp. strain ACM 3067. The sequences of the Pedomicrobium strains were found to contain 27 of the 29 16S rRNA signature sequences for the α-Proteobacteria (36), which confirmed the membership of the genus Pedomicrobium in the α subdivision (30).

A phylogenetic tree based on Jukes-Cantor evolutionary distances was constructed by using the neighbor-joining method for 1,201 nucleotide positions of the sequences of six Pedomicrobium strains and eight reference species, including four representatives of the hyphal budding bacteria in the α-Proteobacteria for which sequences are available for the type strains and four representatives of the β-, γ-, and ε-Proteobacteria. C. jejuni was used as the outgroup. Bootstrap values from 100 analyses are shown at the branch points. Scale bar = 10 nucleotide substitutions per 100 nucleotides of 16S rRNA sequence.

![FIG. 1. Neighbor-joining tree showing the relationships among six Pedomicrobium strains, four other hyphal budding bacteria, and representatives of the α-, β-, γ-, and ε-Proteobacteria. C. jejuni was used as the outgroup. Bootstrap values from 100 analyses are shown at the branch points. Scale bar = 10 nucleotide substitutions per 100 nucleotides of 16S rRNA sequence.](image-url)
bium sp. strain ACM 3067 is most similar to *P. australicum* (level of similarity, 99.6%) and *P. americanum* (99.4%). The latter manganese-oxidizing species are more closely related to the iron-oxidizing species *P. ferrugineum* (levels of similarity, 98.8 to 99%) than to the other manganese-oxidizing species, *P. manganicum* (levels of similarity, 96.2 to 96.5%).

Stackebrandt et al. (30) found in a catalog analysis of 16S rRNA oligonucleotides that the genus *Pedomicrobium* fell within the *Hyphomonas* cluster and questioned the validity of the genus *Pedomicrobium*. However, there was considerable diversity in the *Hyphomonas* strains studied, which may have been representatives of more than one genus. This view is supported by the RNA cistron similarity data of Roggentin and Hirsch (24), which showed the phylogenetic heterogeneity of strains currently assigned to the genus *Hyphomonas*. Likewise, the genomic DNA base compositions (9) of the *Hyphomonas* strains that have been studied are very different, and two of the strains, T-854 and SW-808, are considered only *Hyphomonas*-like (12). This demonstrates the difficulties faced in accurately positioning these organisms, which are closely related phylogenetically and have few differential phenotypic characteristics to accurately define the genus. It is encouraging for the validity of the genus *Pedomicrobium* that all of its species grouped together to the exclusion of the other genera of hyphal budding bacteria on the basis of their 16S rRNA sequences determined in the present study. However, there is only one sequence of a *Hyphomonas* species available for comparison, so these results are not conclusive. A complete data set of the sequences of members of the genus *Hyphomonas* and other genera of the hyphal budding bacteria will be needed to clarify the validity of the genus *Pedomicrobium*, which has been questioned on the basis of morphology (1, 33) and phylogeny (30) and has been supported on the basis of DNA composition (8, 12), genome size (17), and DNA homology (10, 11).

Because of the high levels of 16S rRNA sequence similarity among the species of the genus *Pedomicrobium*, it is not possible to use this criterion to accurately assign the local isolate *Pedomicrobium* sp. strain ACM 3067 to one of the existing *Pedomicrobium* species. However, the 16S rRNA similarity between this isolate and *P. manganicum* is less than 97%, and it is therefore unlikely that strain ACM 3067 belongs to *P. manganicum*, as originally thought (28, 31). Because strain ACM 3067 exhibits 98.8 to 99.6% sequence similarity with *P. australicum*, *P. americanum*, and *P. ferrugineum*, determination of its species status will depend on supporting DNA-DNA homology data or similar evidence obtained by using techniques such as cellular protein polyacrylamide gel electrophoresis patterns. This will not be possible for *P. australicum*, whose type strain is unavailable.

The taxonomic position of *P. australicum* is problematic and uncertain. Gebers and Beeze (7) showed that *P. australicum* was a distinct species on the basis of its DNA-DNA homology values of less than 28% with all other *Pedomicrobium* species. However, circumscription of a species also requires phylogenetic characteristics to adequately differentiate the organism from other species (21, 35), and there are insufficient phylogenetic characteristics to differentiate *P. australicum* from *P. americanum* (7). A similar situation exists in the genus *Bacillus*, in which Fox et al. (5) reported that strains which exhibited more than 99.5% 16S rRNA sequence similarity and had phylogenetic similarities were convincingly established as separate species on the basis of previous DNA-DNA hybridization studies (5, 22, 25). Thus, Fox et al. (5) concluded that some species may not be recognizable from their 16S rRNA gene sequences, even though sequences can be used to distinguish relationships between genera and some well-resolved species.

The taxonomic uncertainty of *P. australicum* is exacerbated by the additional loss of the only other strain studied by Gebers and Beeze (7), strain IFAM WD-1355, so the prospect of designating a neotype strain for the species is remote in the absence of suitable differentiating phenotypic characteristics and their close phylogenetic relationships. The objective of finding a neotype strain for *P. australicum* will have to remain unresolved because it is not possible at this time to extract a sufficient quantity of DNA from the freeze-dried ampoules to carry out DNA-DNA hybridization studies.

In view of the absence of a type strain, insufficient phenotypic characteristics to differentiate isolates of closely related species, and the absence of phylogenetic 16S rRNA signature sequences, the species *P. australicum* should not be retained. The present research has demonstrated the value of using nonviable preserved specimens to investigate taxonomic issues by molecular methods, as foreshadowed by Sneath (29).

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**REFERENCES**


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