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Accessibility
Family- and Genus-Level 16S rRNA-Targeted Oligonucleotide Probes for Ecological Studies of Methanotrophic Bacteria

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Methanotrophic bacteria play a major role in the global carbon cycle, degrade xenobiotic pollutants, and have the potential for a variety of biotechnological applications. To facilitate ecological studies of these important organisms, we developed a suite of oligonucleotide probes for quantitative analysis of methanotroph-specific 16S rRNA from environmental samples. Two probes target methanotrophs in the family Methylococccaceae (type II methanotrophs) as a group. No oligonucleotide signatures that distinguish between the two genera in this family, Methylocystis and Methylosinus, were identified. Two other probes target, as a single group, a majority of the known methanotrophs belonging to the family Methylococccaeceae (type I/X methanotrophs). The remaining probes target members of individual genera of the Methylococccaceae, including Methylobacter, Methylocystis, Methylococcum, Methylococcus, and Methylocaldum. One of the family-level probes also covers all methanotrophic endosymbionts of marine mollusks for which 16S rRNA sequences have been published. The two known species of the newly described genus Methylosarcina gen. nov. are covered by a probe that otherwise targets only members of the closely related genus Methylococcaceae. None of the probes covers strains of the newly proposed genera Methylocaldum and “Methylothermus,” which are polyphyletic with respect to the recognized methanotrophic families. Empirically determined midpoint dissociation temperatures were 49 to 57°C for all probes. In dot blot screening against RNA from positive- and negative-control strains, the probes were specific to their intended targets. The broad coverage and high degree of specificity of this new suite of probes will provide more detailed, quantitative information about the community structure of methanotrophs in environmental samples than was previously available.

MATERIALS AND METHODS

Bacterial cultures. The reference cultures used in this study were obtained from various sources, as indicated, and are available from either the National Collection of Industrial and Marine Bacteria (NCIMB, Aberdeen, United Kingdom) or the American Type Culture Collection (ATCC, Manassas, Va.). Ref-
ference strains include Methylosinus trichosporium OB3b (NCIMB 11131) and Methylococcus capsulatus Bath (NCIMB 11132) (both provided by J. C. Murrel), Methylobacter luteus (NCIMB 11194; provided by R. Knowles), Methylobacter marinus A45 (nonex tant culture; genomic DNA provided by A. A. DiSpirito), Methylocricetus holophagus DSM 11132 (both provided by J. D. Semrau), Methylococcus gramineus (NCIMB 11912; purchased from NCIMB), Cibicidoides wuusti CB15A (ATCC 19089; provided by J. S. Pinder), Escherichia coli K11 (K11):H7 (ATCC 11775; from laboratory stock culture).

All methanotrophs were grown at 30°C except Methylococcus capsulatus Bath and Methylocaldum graminis, which were grown at 45°C, in nitrate mineral salts medium with CH₄ and CO₂ at an initial headspace mixing ratio of 45:5:50 (CH₄, to CO₂; to air) (35). E. coli was grown in Luria-Bertani broth under standard conditions (53), and C. crescentus CB15A was grown in PYCM medium (27) at room temperature.

Sequencing of 16S rRNA genes. Because ambiguous and missing bases in several of the sequences available from GenBank hindered sequence comparisons, we resequenced the 16S rRNA genes of Methylosinus rubra NCIMB 11913, Methylococcus luteus NCIMB 11194, Methylosphaera methanica S1 NCIMB 11130, and Methylobacter marinus strain A45. Nearly complete (1,450-bp) sequences were obtained for both the sense and antisense strands of the 16S rRNA gene using 5% Long Ranger gel and an ABI PRISM DNA sequence (41).

Selection of reference sequences. Probes were designed based on reference 16S rRNA sequences available from GenBank (6) and the Ribosomal Database Project (RDP-II) (42), as well as resequencing of key laboratory strains (see Table 1 and Fig. 3). BLAST (GenBank) and Probe Match (RDP-II) database searches were used to assess the potential breadth and specificity of the probe sequences. The reference sequences were aligned with the probe sequences to determine the apparent range of coverage of the candidate probes relative to the abundance and diversity of known methanotrophs. The 16S rRNA sequences specified by accession numbers in Fig. 2 and 3 represent all those available in the databases for confirmed methanotrophic isolates at the time of analysis. With the exception of the methanotrophic endosymbionts of marine mollusks (see below), we did not include sequences obtained from cultures that had not been characterized phenotypically or that were obtained by PCR amplification of environmental DNA.

Only cultured isolates with published, genus-level phylogenetic data were assigned genus designations in Fig. 2 and 3. Three general groups of confirmed methanotrophs were placed under “other α-methanotrophs” (Fig. 2) or “other γ-methanotrophs” (Fig. 3): (i) strains clearly belonging to the α- or γ-methanotrophs, but lacking or having dubious generic affiliations because of insufficient phylogenetic and taxonomic information (for example, “Methylosomas methanicus” strain S1Z is clearly a γ-methanotroph [57] but has not been characterized at the genus level); (ii) isolates validly assigned to the genera Methylocella, Methylophaga, and Methylocarcina, for which we did not design genus-level probes because there were only one or two known representatives of each genus; and (iii) the methanotrophic endosymbionts of marine mollusks, which lack generic description but are distinguished from the free-living α-methanotrophs included because they are of active interest to microbial ecologists and evolutionary biologists and because there is strong phenotypic and phylogenetic evidence that they are γ-methanotrophs (19, 20, 25, 28).

All available methanotroph 16S rRNA sequences that met the criteria given above were included in our analysis, regardless of sequence quality. However, a number of sequences appeared to be affected by common sequencing errors, including transposition of bases and duplicated or omitted bases. Some errors could be confirmed because they violated the integrity of the secondary structure of the 16S rRNA molecule, but others could not because they occurred in unpaired loop positions. Because sequence errors make designing group-level probes very difficult, we developed specific criteria for disregarding unexpected mismatches between a probe and a target sequence. We deemed destabilization of secondary structure sufficient grounds for disregarding mismatches. Additionally, we considered any two of the following criteria sufficient: (i) the mismatch occurs in a low-quality sequence as indicated by ambiguous bases in >0.5% of the positions in the entire sequence; (ii) the mismatch results from an ambiguous or missing base in the probe target region; (iii) multiple sequences for the same strain disagree in the mismatch position, and the higher-quality sequence, as indicated by percent ambiguity, matches the probe; (iv) a multiple alignment of all the target sequences representing the target genus shows that the mismatch is not representative of the target group; (v) the mismatch occurs in a highly conserved position of the 16S rRNA molecule; (vi) the mismatch is consistent with a common sequencing error, such as the transposition of two bases or the repetition of the same base, that disagrees with several other related sequences.

Oligonucleotide probe design. The oligonucleotide probes developed and/or optimized in this study are listed in Table 4. The number in the probe designation represents the forward position of the homologous base in the E. coli 16S rRNA gene. By use of the SEQLAB sequence editor in the Wisconsin Package (Genetics Computer Group, Madison, Wis.), 16S rRNA sequences (>1,300 bp) were aligned initially using thePILEUP function within the editor and then adjusted manually with secondary-structure considerations as described previously (2). With the help of computer-generated consensus sequences, the alignments were scanned visually for signature sequences of 18 to 30 nucleotides that distinguished methanotrophs at the family or genus level. Candidate oligonucleotide sequences were then examined for specificity using the basic BLAST search and Probe Match functions of GenBank and the RDP-II, respectively (5, 42). Except as described below, only sequences exhibiting high specificity for methanotrophs and retrieving a majority of the sequences in their target groups were pursued further.

Tₚ determination and specificity testing. Oligodeoxynucleotides were synthesized commercially (DNAgency, Malvern, Pa.). Each probe was characterized by empirical determination of its midpoint dissociation temperature (Tₛ) using a serial washing procedure with progressively higher temperatures in a PCR thermal cycler as described by Gulledge and Cavanaugh (32). All Tₛ curves were determined using triplicate blots for both positive and negative controls (see Fig. 1). The ability of each probe to distinguish between positive and negative controls was screened in Northern dot blot hybridization assays, as described below, using total RNA from reference cultures representing target strains as positive controls and total RNA from reference cultures representing nontarget strains with 1- or 2-base mismatches as negative controls. In all but two cases, a strain with a single-base mismatch with the probe was used as a negative control (Table 1).

Because no nontarget organisms that had fewer than two mismatches with probe Am445 were identified, an organism with two mismatches was used as a negative control. Also, because no potential control organisms with fewer than four mismatches to probe Med77 were identified, we designed a probe with a single mismatch at position 15 to serve as a negative control (Table 1).

RNA extraction from bacterial cultures. Pure cultures were grown to late-log phase in 40 ml of liquid growth medium and centrifuged at 5,000 g for 10 min at 4°C. Total RNA was extracted selectively from cell pellets using the FastPrep bead beater system with the FastRNA Blue kit according to the manufacturer’s protocol (Bio 101, La Jolla, Calif.). Cells were beaten in the FP120 bead beater for 25 to 40 s at a speed of 6 m/s. After extraction and centrifugation, the RNA pellets were air dried, resuspended in diethyl pyrocarbonate-treated H₂O, and stored at −80°C.

RNA dot blotting and hybridization. Northern dot blots were prepared from RNA extracts as described previously (48) using a Minifold I Microsample Filtration Manifold (Schleicher & Schuell, Keene, N.H.). Blots were prepared with 100 ng of 16S rRNA per dot to be blotted, assuming that 16S rRNA represented 27% of total RNA (47), as described previously (49).

Oligonucleotide probes were labeled enzymatically with ³²P (49), and hybridization assays were carried out as described previously (48). Labeled oligonucleotides were hybridized to the dot blots overnight at 30°C, finishing with a 20-30 min rinse at the appropriate Tₛ for each probe (Table 1). Oligonucleotide labeling of the dot blots was analyzed by radiodensitometry using a BAS-MS 2025 imaging plate and a Fuji 2000 PhosphorImager, with MacBAS, version 2.5, image analysis software (Fuji Medical Systems, Stamford, Conn.).

Nucleotide sequence accession numbers. The new sequences of the 16S rRNA genes of Methylosomas rubra NCIMB 11913, Methylococcus luteus NCIMB 11194, Methylosphaera methanica S1 NCIMB 11130, and Methylobacter marinus strain A45 have been deposited in GenBank (accession numbers AF304194 to AF304197).

RESULTS AND DISCUSSION

Overview. In recent years, interest in the physiology, ecology, and evolution of methanotrophs has intensified, and there is high demand for tools to facilitate quantitative studies of in situ methanotroph community structure (21, 34, 46, 50). Our objectives were to develop phylogenetic oligonucleotide probes for analysis of methanotrophs at the family and genus levels and to optimize the probes for use in quantitative hybridization through empirical determination of their Tₛ under standard hybridization conditions.

Visual comparison of aligned 16S rRNA reference sequences initially revealed 36 potential probe sequences for fur-
TABLE 1. Oligonucleotide probes targeting methanotrophic bacteria

<table>
<thead>
<tr>
<th>Target group(s)</th>
<th>Probe sequence (5'→3')</th>
<th>Positive control(s)</th>
<th>Negative control(s)</th>
</tr>
</thead>
</table>
| Am445           | TCC                   | M. trichosporium    | Gm or Mtr, Am, Mlm, Mlb, Mmb, Mlc |}

**Probe coverage for omega-methanotrophs.** Two family-level probes, Am445 and Am976, perfectly match the 16S rRNA sequences of nearly all known omega-methanotrophs (Fig. 2), including some novel strains recently isolated from landfill soils (59) and lake sediments (22). *Methylocella palustris* strain K7, a novel acidophilic methanotroph isolated recently from a northern peat bog and the only cultured representative of its genus (24), was the only omega-methanotroph whose 16S rRNA sequence was not covered by either probe. Because these probes do not distinguish between the *Methylosinus* and *Methylocystis* genera, they can detect omega-methanotrophs only as a group. No oligonucleotide signatures that distinguish between these two genera were identified.

**Probe coverage for gamma-methanotrophs.** For gamma-methanotrophs we identified both family- and genus-level probes. Together,
FIG. 2. Range of strain coverage for oligonucleotide probes targeting \(\alpha\)-methanotrophs (Am). % Ambiguity, percentage of positions within the entire sequence that indicate ambiguous bases, shown as an index of overall sequence quality. Under “Probes,” solid fill indicates identity between the probe and a target sequence; cross-hatching indicates identity between the probe and a nonmethanotroph; numbers are mismatches between the probe sequence and the corresponding 16S rRNA sequence. Where a number is shown in white on a solid background, the apparent mismatches were disregarded based on criteria outlined in Materials and Methods. An open diamond denotes the occurrence of one or more ambiguous bases in the probe target region that are consistent with the probe sequence. For example, if the probe has an A corresponding to a Y (International Union of Pure and Applied Chemistry [IUPAC] ambiguity code for C or T), then the possible T is consistent with the probe sequence. No sequence available in probe target region.

Two family-level probes (Gm633 and Gm705) covered 82% of the available \(\gamma\)-methanotroph 16S rRNA sequences (Fig. 3). Gm633 had the broadest coverage, including representatives of six \(\gamma\)-methanotroph genera and the methanotrophic endosymbionts of marine mollusks. Gm705 was more limited, but it covered all of the recognized \(\gamma\)-methanotroph isolates. Representatives of this genus fell into two groups that differ by an A versus a C at position 746 (E. coli numbering). We designed two probes (Mlm732a and Mlm732b) to distinguish between the two subgenus groups. Mlm482 provided the broadest coverage of Methylosarcina spp., but all representatives of the genus were covered only when the three Mlm probes were combined.

Three probes covered all representatives of the two recognized thermophilic genera, Methylococcus and Methylocaldum. Mlc123 and Mlc1436 each matched all Methylococcus sequences available. PCR primers corresponding to these two probes might be ideal for specific amplification of nearly complete (~1,300-bp) 16S rRNA genes from Methylococcus strains in environmental samples. Probe Mcd77 covered the three recognized strains of the recently described genus Methylocaldum. The target region was unique, and a Probe Match analysis retrieved no sequences with fewer than four mismatches from non-Methylocaldum species.

The complete suite of \(\gamma\)-methanotroph probes covered 97% of the strains listed in Fig. 3; only two sequences were not covered. One is that of Methylosarcina strain 81Z, cultures of which are no longer extant and whose affiliation with the genus Methylosarcina was never verified (J. P. Bowman and P. N. Green, personal communication). Because this sequence is of low overall quality (3.3% ambiguity), one or more of the indicated mismatches could be incorrect. The other organism not covered by the probes is a novel thermophilic methanotroph, “Methylothermus sp.” strain HB. Because it is the only known \(\gamma\)-methanotroph that is phylophyletic with respect to the family Methylloccaceae (8), this result was expected.

**Probe specificity and optimization for quantitative hybridization.** The probes described here are intended to quantify 16S rRNA from specific microbial populations against a background of many unknown populations in environmental samples. The probes must discriminate against unknown, nontarget 16S rRNA that may have a difference of only 1 base from the intended target. The primary factor for achieving stringent specificity and quantitative hybridization of 16S rRNA from environmental samples is accurate determination of the melting characteristics of the probe-target duplex. Hence, empirical determination of the \(T_m\) is essential (32, 54). We have optimized the probes presented here for stringent discrimination against nontarget RNA and also for quantitative hybridization by empirically determining the \(T_m\) for each probe.

The \(T_m\)'s of the probes ranged from 49 to 57°C (Table 1). When Northern blots were hybridized overnight and then washed at the appropriate \(T_m\), target and nontarget rRNAs were visually distinguishable on blots and yielded quantitatively distinct results when analyzed using a scintillation counter (Fig. 1) or a phosphorimager (data not shown). These results verify that the use of known concentrations of reference rRNA as standards will permit quantitative analysis of environmental rRNA possessing the target sequence, as demonstrated previously (49, 54).
Probes Am445, Mmb1007, Mlm482, Mlm732b, Mlc123, and Mcd77 each exhibited at least two base mismatches against any nonmethanotroph sequence, whereas probes Gm633, Gm705, Mlb482, Mmb482, Mlm732a, and Mlc1436 each exhibited at least one base mismatch with any nonmethanotroph sequence. Probes Mlb662, Mmb482, and Mmb1007 matched sequences from one to four /I9253/-methanotrophs outside their respective target genera (Fig. 3). Although we consider this problem to be minor, these probes could yield ambiguous results for fine-scale descriptions of /I9253/-methanotroph communities. All other genus-level probes were specific to their intended target genera. The a- and y-methanotroph probes had no cross-family hybridization potential.

FIG. 3. Range of strain coverage for oligonucleotide probes targeting y-methanotrophs (Gm). Mic, Methylococcus; Mcd, Methylocaldum. % Ambiguity, percentage of positions within the entire sequence that indicate ambiguous bases, shown as an index of overall sequence quality. The unpublished 16S rRNA sequence for Methylomonas methanica strain S1 (marked with a star in the “GenBank accession number” column) is available as RDP sequence Mlm.metha1 (C. R. Woese, 1991). Under “Probes,” solid fill indicates identity between the probe and a target sequence; diagonal hatching indicates identity between the probe and a nontarget /I9253/-methanotroph strain; cross-hatching indicates identity between the probe and a nonmethanotroph; numbers are numbers of mismatches between the probe sequence and the corresponding 16S rRNA sequence. Where a number is shown in white on a solid background, the apparent mismatches were disregarded based on criteria outlined in Materials and Methods. An open diamond denotes the occurrence of one or more ambiguous bases in the probe target region that are consistent with the probe sequence. For example, if the probe has an A corresponding to a Y (IUPAC ambiguity code for C or T), then the possible T is consistent with the probe sequence. ns, no sequence available in probe target region.
mental approaches, such as monitoring of CH₄ enrichment cultures, use as PCR primers in cases where amplification approaches, such as monitoring of CH₄ enrichment

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and Mlc1436 retrieved a number of sequences representing

or in publications cited therein.

searches were performed on 6 March 2001.

All nonmethanotroph sequences represent Cycloclasticus strains.

Searches were performed on 6 March 2001.

As PCR primers in cases where amplification approaches, such as monitoring of CH₄ enrichment

identified as methanotrophs (Table 2). Probes Am976, Mlb662, and Mlc1436 retrieved a number of sequences representing a narrow range of nonmethanotrophic taxa. The first two of these probes matched environmentally restricted taxa, such as obligate pathogens (Afipia spp.) and obligate marine bacteria (Cycloclasticus spp.). If used strategically, these probes are likely to be useful for studying methanotroph communities. From the data in Table 2, it would be premature to conclude that Mlc1436 is nonspecific. All but one of the nonmethanotroph sequences retrieved by this probe were nearly identical clones of putative β-Proteobacteria from an activated sludge reactor. However, no cultured organisms belonging to the β-Proteobacteria were retrieved, and no published data were cited in the accession records to confirm the phylogenetic position of these environmental clones. Overall, the data in Table 2 suggest that at least 11 and possibly 12 of the probes presented here are highly specific to methanotrophic bacteria and that the two clearly nonspecific probes should hybridize to a phylogenetically limited range of nonmethanotrophs with restricted environmental distributions.

Summary and conclusions. The breadth and specificity of the probes reported here are unprecedented, providing 97% coverage of the 87 methanotroph 16S rRNA sequences examined (Fig. 2 and 3). Several new methanotroph genera that have been proposed recently following the isolation of novel strains are covered. Of the three strains apparently not covered by the probes, one is no longer extant and the available 16S rRNA sequence is of low overall quality, bringing into question whether the indicated probe mismatches are correct. The other two strains (Methyllocella palustris sp. strain K and Methylolithemus sp. strain HB) that did not match any probe are polyphyletic with respect to the Methylocystaceae and Methylococcaceae, thus reflecting the high specificity of the probes to the phylogenetic clades they were designed to target. Initial results from studies with several soils indicate that the probes are effective for studying methanotroph communities in soil (unpublished data), perhaps the most difficult substrate on which to perform quantitative hybridization assays (4). Hence, all of the methanotroph taxa that have become well known through years of laboratory studies, as well as several recently described taxa, can now be studied at both the family and genus levels in environmental samples by using the probes reported here.

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