Ribosome analysis reveals prominent activity of an uncultured member of the class Actinobacteria in grassland soils

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A 16S rRNA-based molecular ecological study was performed to search for dominant bacterial sequences in Drentse A grassland soils (The Netherlands). In the first step, a library of 165 clones was generated from PCR-amplified 16S rDNA. By sequence comparison, clone DA079 and two other identical clones could be affiliated to a group of recently described uncultured Actinobacteria. This group contained 16S rDNA clone sequences obtained from different environments across the world. To determine whether such uncultured organisms were part of the physiologically active population in the soil, ribosomes were isolated from the environment and 16S rRNA was partially amplified via RT-PCR using conserved primers for members of the domain Bacteria. Subsequent sequence-specific separation by temperature-gradient gel electrophoresis (TGGE) generated fingerprints of the amplicons. Such community fingerprints were compared with the TGGE pattern of PCR-amplified rDNA of clone DA079 which was generated with the same set of primers. One of the dominant fingerprint bands matched with the band obtained from the actinobacterial clone. Southern blot hybridization with a probe made from clone DA079 confirmed sequence identity of clone and fingerprint band. This is the first report that a member of the novel actinobacterial group may play a physiologically active role in a native microbial community.

Keywords: 16S rDNA library, Actinobacteria, temperature-gradient gel electrophoresis (TGGE), ribosome extraction from soil, V6 probe

INTRODUCTION

Over the last few years, molecular ecological studies on mainly terrestrial environments (Liesack & Stackebrandt, 1992a, b; Stackebrandt et al., 1993; Rheims et al., 1996a, b) have indicated the existence of two monophyletic groups of uncultured bacteria from the class Actinobacteria (Stackebrandt et al., 1997). As judged from the analysis of PCR-amplified 16S rDNA these sequences showed only rather remote similarities to sequences of cultured actinobacteria. The relevant clones were obtained from an Australian forested soil taken from the Mount Coot-tha region in Brisbane, Queensland (Liesack & Stackebrandt, 1992a, b; Stackebrandt et al., 1993), a peat bog sample from Germany (Rheims et al., 1996a, b), geothermally heated soil from New Zealand (Rainey et al., 1993) and a soil sample from Finland (Saano et al., 1995). Also, short 16S rDNA clone sequences from a paddy field (Maidak et al., 1994), a soybean field (Ueda et al., 1995) and a marine environment (Fuhrman et al., 1993) were demonstrated to cluster with these actinobacterial sequences. Thus it has been concluded that this group of uncultured organisms might contribute to ecologically important processes (Rheims et al., 1996b).

The presence of rDNA sequences in a clone library proves neither activity nor abundance of the microorganism from which the DNA is represented in the library. Previous investigations already indicated that a large fraction of environmental microbial communities
is in a stage of low activity or resting (Bakken & Olsen, 1987; Roszak et al., 1993), or even from free DNA. Adsorption of DNA at mineral surfaces, especially in soils, could harbour more or less intact nucleic acids a long time after lysis of the source organism (Lorenz & Wackernagel, 1987). Our strategy to obtain information about the presence of metabolically active bacteria in the environment focuses on the analysis of 16S rRNA from isolated ribosomes. As the ribosome per cell ratio is roughly proportional to growth rate of bacteria (Wagner, 1994), rRNA is regarded as an indicator of total bacterial activity.

Here we report on the finding of a novel sequence of one of the actinobacterial lineages from the Drentse A rDNA clone library (A. Felske, A. Wolterink, R. van Lis & A. D. L. Akkermans, unpublished results). The cloned sequence DA079 was investigated for its significance in the environmental 16S rDNA population and 16S rRNA fractions of ribosomes that were isolated from the same site (Drentse A agricultural test area, The Netherlands). After direct ribosome isolation from soil samples (Felske et al., 1996), rRNA was purified and used for RT-PCR with bacteria-specific primers. This partial 16S rRNA amplicon, representing the complex sequence population of the soil, was sequence-specifically separated by temperature-gradient gel electrophoresis (TGGE; Rosnebaum & Riesner, 1987). The resulting fingerprint was screened for the cloned sequence DA079 by amplifying the plasmid DNA with the same primers as those used for soil rRNA. Running this product next to the rRNA fingerprint indicated possible matches. Subsequent electrophoretic Southern blotting and hybridization with a clone-specific probe was applied to confirm the match.

METHODS

Collection of soil samples. Peaty, acid grasslands of the Drentse A agricultural research fields next to the Anloër Diepje River, the Netherlands (06° 41’ E, 53° 03’ N), were the sites of sample collection. A total of 120 surface samples (< 10 cm depth) were taken on three different testfields during March 1996. Another 240 surface samples were taken on the same and additional three testfields in October 1996. Six different testfields (A, B, C, F, K and 0) along the Anloër Diepje River were investigated. Distances between the relevant testfields were several hundred metres, with a maximum of 1.5 km between testfields F and K. On each testfield, 40 soil cores of about 50 g were taken with a drill (0-10 cm depth) and transferred into sterile sample bags. The 40 samples of each testfield were pooled to four samples by sieving and mixing 10 single samples (5 g input each). Details of the soil properties were published by Stienstra et al. (1994).

Isolation, amplification, cloning and sequencing of 16S rDNA sequences. Total DNA was isolated from Drentse A soil samples by a parallel pathway during ribosome isolation (Felske et al., 1996). Amplification of 16S rDNA sequences was performed with a GeneAmp PCR System 2400 thermocycler (Perkin Elmer Cetus). Reverse transcription reactions (10 μl) contained 10 mM Tris/Cl (pH 8.3), 90 mM KCl, 1 mM MnCl₂, 200 μM each of dATP, dCTP, dGTP and dTTP, 750 nM primer L1401 (as below), 2.5 U Taq DNA polymerase and 1 μl template RNA. After incubation for 15 min at 68 °C (reverse transcription), 40 μl PCR additive containing 10 mM Tris/Cl (pH 8.3), 100 mM KCl, 0.75 mM EGTA, 0.05% (v/v) Tween 20, 375 mM MgCl₂, 50 μM each of dATP, dCTP, dGTP, and dTTP, 190 nM primer U968/GC (as below) were added. Amplification was performed in a GeneAmp PCR System 2400 thermocycler, using 35 cycles of 94 °C for 10 s, 56 °C for 40 s and 68 °C for 40 s. The correct size of amplification products was checked by electrophoresis on a 1.4% agarose gel.

Partial 16S rDNA amplification of clone DA079 for TGGE. A single DA079 clone colony (identified by sequence analysis) was taken up with a sterile toothpick and transferred to a 1.5 ml microcentrifuge tube containing 50 μl TE buffer. The tube was heated for 15 min at 95 °C and then chilled on ice. A TGGE-suitable 16S rDNA amplicon was generated with a GeneAmp PCR System 2400 thermocycler, using 25 cycles of 94 °C for 10 s, 56 °C for 40 s and 68 °C for 40 s. The PCR reaction (20 μl) contained 10 mM Tris/Cl (pH 8.3), 50 mM KCl, 3 mM MgCl₂, 50 μM each of dATP, dCTP, dGTP, and dTTP, 100 pmol primers U968/GC and L1401 (as below), 0.5 U Taq DNA polymerase and 1 μl DA079 cell lysate. The PCR reaction (20 μl) contained 10 mM Tris/Cl (pH 8.3), 50 mM KCl, 3 mM MgCl₂, 50 μM each of dATP, dCTP, dGTP, and dTTP, 100 pmol primers U968/GC and L1401 (as below), 0.5 U Taq DNA polymerase and 1 μl DA079 cell lysate. The PCR products were purified and concentrated by ethanol precipitation. The precipitated DNA was resuspended in 50 μl nanopure water and then 5'-labelled using phage T4 polynucleotide kinase (Promega) and 97 Bq of [γ-32P]ATP (370 MBq ml⁻¹; Amersham Buchler) in a 30 min reaction at 37 °C.

TGGE, electrophoretic Southern blot and hybridization. The Diagen TGGE system was used for sequence-specific separation of PCR products. The temperature gradient was optimized to 9 °C difference for improved resolution. Electro-
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Detection of clone DA079 rDNA and related environmental sequences in soils

Clone DA079 originates from a Drentse A 16S rDNA clone library, comprising 165 positive clones (A. Felske, A. Wolterink, R. van Lies & A. D. L. Akkermans, unpublished results). Two other clones were identical in sequence, so finally three of 165 clones represented this DA079 sequence. Some closely related German peat clones (designated TM clones) were previously found to have relatives in geographically widely separated soil environments, i.e. Australia, Finland, Japan, New Zealand, and in the Atlantic and Pacific oceans (summarized by Rheims et al., 1996b). With the detection of the uncultured organism DA079 in Drentse A grassland soils another example for the wide distribution of this novel group of uncultured actinobacteria in different soil types is given.

In detail, clone DA079 is a member of peat clone group II (as defined by Rheims et al., 1996b), showing a similarity of 95·3% to clone TM208 (Fig. 1). No close relationship exists between the peat clone group II (including clone DA079) and the nearest cultured relative, Acidimicrobium ferroxidans (Clark & Norris, 1996). According to the current taxonomic structure of the class Actinobacteria (Stackebrandt et al., 1997), even a relationship at family level seems unlikely.

Quantification of sequences in clone libraries

To draw a conclusion on the importance of these organisms, as detected by analysis of amplification products, the following factors should be considered. Deduction of the number of organisms characterized by a unique 16S rDNA sequence in the community from the number of sequences in a 16S rDNA library is difficult. As most 16S rDNA sequences appear only once during sequence analysis of clones (Weller et al., 1991; Borne- man et al., 1996), the question is raised whether this reflects the real abundance or whether these unique sequences were randomly recovered from a low-abundance background?

One may imagine a model in which 50% of all the 16S rDNA within a native bacterial community originates from a few dozen dominant species. The other 50% consists of thousands of rare sequences occurring with
a very low mean abundance each. This model is not unreasonable as the presence of thousands of different bacterial species can be expected to occur in a single soil sample (Torsvik et al., 1990). Extraction of DNA and subsequent PCR amplification with universal bacterial primers yields a 16S rDNA amplicon of a very complex sequence composition, optimally reflecting the native composition. In the subsequent steps of ligation and transformation, the selection of sequences is random. Hence rare sequences have a realistic chance of appearing in a successfully cloned insert. In our model, one-half of all clones will represent the few dominant species, while the other half is composed of randomly selected members of a low-abundance background. The higher the microbial diversity, the more likely is the appearance of such randomly selected rare sequences. Thus the normally limited size of environmental clone libraries (a few hundred clones) has the danger of overestimating unique clones. Multiple detection of identical clone sequences within one clone library, on the other hand, might indeed indicate abundance in the original population. In this study three identical 16S rDNA sequences of the type DA079 were identified within the Drentse A library of 165 clones.

In contrast to the uncertain meaning of sequence quantities in clone libraries, the semi-quantitative assessment of PCR amplicons in TGGE fingerprints is only based on staining intensity. A silver-stained TGGE gel would show a background of thousands of different sequences as a faint background smear, somewhere between invisibility and extremely faint bands. Hence estimation of sequence abundance in genetic material isolated from the environment is more likely to be representative by application of the TGGE approach.

**Detection of sequence DA079 by TGGE in total rRNA and rDNA from soil**

Direct ribosome isolation yielded purified rRNA \( [1.5 \pm 0.6 \, \mu g \, (g \, soil)^{-1}] \) which could be used for RT-PCR with bacteria-specific primers. Ribosome isolation and subsequent RT-PCR were reproducible as demonstrated by TGGE. Partial sequences of the 16S rRNA were reversibly transcribed into cDNA, amplified by PCR and the products separated by high-resolution TGGE. The TGGE fingerprint (Fig. 2) reflects the diversity of dominant rRNA sequences of pooled soils from different sampling sites. Fingerprints from the same testfield were highly reproducible. Pooled samples from the same testfield, as presented in this study, appeared to be identical (Fig. 2). This indicates a high spatial constancy of the dominant bacteria in these grassland soils.

To determine whether one of the major bands could be affiliated to 16S rDNA of clone DA079, its plasmid insert was amplified with TGGE primers U968/GC and L1401. The migration distance of the fragment obtained from

**Fig. 2.** Amplicon fingerprints on silver-stained TGGE gels. RT-PCR products from ribosomes and a partial 16S rDNA PCR product from genomic DNA from the same probing site, obtained with the corresponding set of primers, each show bands of equal position, matching with the DA079 signal as indicated. Fingerprints represent two of four pooled samples each from Drentse A sites A, F and K. ‘SS’ indicates the position and size of the single-stranded cDNA/rDNA fraction.
the DA079 clone was identical to one of the strongest bands obtained from amplified cDNA. Here the definition of total activity allows two scenarios for abundance and state of the bacterial cells: this species counts for high total activity within the community by only low activity per cell, but extraordinarily high cell number; or this species could show an extraordinarily high activity per cell, but only low cell number within the community. The TGGE fingerprints obtained from amplified genomic rDNA from soil (Fig. 2) point more to the first scenario. They indicate that sequence DA079 is not only one of the most abundant 16S rRNA but also 16S rDNA sequences. The relative abundance of DA079 in the rDNA fingerprints appears comparable to the 16S rRNA in the ribosomal RT-PCR fingerprints. Thus it seems likely that the prominent ribosome number from this species is caused more by the high number of active cells rather than by extraordinarily high activity per cell. The high reproducibility of the TGGE fingerprints further indicates a homogeneous distribution of this activity.

Confirmation of sequence DA079 by V6 probing

As even the high resolution of TGGE does not absolutely exclude the possibility that two different 16S cDNA sequences might migrate to exactly the same position in the gel, the authenticity of the two corresponding bands needed to be verified. A TGGE gel was symmetrically loaded, each half containing cDNA samples prepared from ribosomes of different sampling sites and dilutions of the PCR products obtained from 16S rDNA of clone DA079. One-half of the gel was stained with silver, while the material of the second half was blotted onto a membrane and hybridized with a DA079-specific, radioactively labelled probe (Fig. 3). Comparison of the signals of both approaches allows the conclusion that 97±5% of the silver-stained fingerprint band was indeed composed of the DA079 16S rDNA fragment (Table 1).

The 95 nt probe used in Southern hybridization was derived from the 16S rDNA insert of clone DA079. Comparison of the probe sequence with the homologous region of clone sequences from highly related actinobacteria detected in a peat bog (Rheims et al., 1996b) gave highest similarity values above 98% (data not shown). The question is raised whether the hybridization results indicate the presence of sequence DA079 in the ribosome fraction and rDNA clone library to the exclusion of other highly related actinobacterial sequences, as found in the peat bog clone library. Most likely, such sequences would migrate to different positions in the TGGE gel. It must be assumed that sequence DA079 is the only prominent member of this group in the ribosome fraction. Other highly related actinobacterial sequences might also be present in the minority population, but they are not detectable in the TGGE fingerprints.

Conclusions

This study suggests that the cloned sequence DA079 originated from one of the most active bacterial species in Drentse A grassland soils. The strength of the DA079 band in the TGGE fingerprints and the hybridization signal demonstrated a prominent abundance of this sequence within the ribosomal 16S rRNA and genomic 16S rDNA fractions from soil. Hence, it can be concluded that the as-yet-uncultured actinobacteria are a potentially important part of the native bacterial community in Drentse A grassland soil. This leads to the speculation that their role is similar in the other environments where their presence had been described previously. The 16S rDNA clone libraries generated in the past provided first indications of the enormous degree of prokaryotic diversity by revealing hitherto unknown sequences of unidentified organisms. After analysis of the cloned sequences we can now turn back to the environment to reveal the ecologically relevant
organisms. Application of ribosome isolation, subsequent RT-PCR and separation of amplicons by TGGE, in combination with taxon-specific probing, leads to the identification of the metabolically dominant portion of the community. This allows us to more specifically discuss the composition of environmental microbial communities.

ACKNOWLEDGEMENTS

This work was supported by a grant from the European Community project ‘High Resolution Automated Microbial Identification’ (EC-HRAMI project BIO2-CT94-3098). H.R. was supported by a grant from the German research council (DFG-Sta184/13-1). We want to thank the Dutch State Forestry Commission, who allowed us access to the nature reserve.

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Received 13 March 1997; revised 27 May 1997; accepted 3 June 1997.