

Phylogenetic analysis of methanogens from the bovine rumen

ABSTRACT

The current set of 16S rRNA hybridization probes targeting methanogenic Archaea does not cover the phylogenetic diversity present in the rumen and possibly other gastro-intestinal tract environments. New probes and quantitative PCR assays are needed to determine the distribution of the newly identified methanogen clusters in rumen microbial communities.

INTRODUCTION

Background Methanogens are members of the domain Archaea, and fall within the kingdom Euryarchaeota. They are obligate anaerobes and can be unambiguously differentiated from other organisms since they all produce methane as a major catabolic product. Interest in methanogens from ruminants has resulted from the role of methane in global warming and from the fact that cattle typically lose 6 % of ingested energy as methane. Several species of methanogens have been isolated from ruminants, but few have been consistently found in high numbers and it is likely that major species of rumen methanogens are yet to be identified. The most common species of methanogens isolated from the rumen are strains of *Methanobrevibacter*, *Methanomicrobium*, *Methanobacterium*, and *Methanosarcina*. The taxonomic status of isolated rumen methanogens has not been adequately resolved and will require analysis at the molecular level for clarification. Methanogens are frequently found in association with protozoa. A recent study using 16S rRNA probes directed against different families of methanogens indicated that some methanogens have a preferred association with protists while others are primarily free living. We have undertaken this study to examine the free living community of methanogens within bovine rumen fluid using comparative sequence analysis of cloned 16S rRNA genes (rDNA) amplified from total DNA extracted from clarified rumen fluid.

CONCLUSION

Conclusions This study has revealed the phylogenetic diversity of methanogens found in the rumen fluid of dairy cattle. One of the methanogen groups is highly similar to the type strain of *M. ruminantium*, but other groups represent methanogens not previously recovered from the rumen or not yet represented in culture collections. Based on sequence analysis it was found that the set of probes for specific groups of methanogens developed by Raskin et al. would not hybridize to a potentially important group of rumen methanogen sequences identified in this study. Additional studies need to be conducted to determine the quantitative significance of the newly identified groups, as well as how the diversity of rumen methanogens varies with animal diet.