PS.09.063 METAGENOMIC ANALYSIS OF AMMONIA OXIDIZING ARCHAEA FROM AN AUSTRIAN THERMAL SPRING

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Even though ammonia-oxidizing archaea have been detected only recently, they are now considered to comprise a significant component of many microbial communities. Initial genome analyses of the first representatives of this group indicate that they do not belong to *Crenarchaeota* as suggested by 16S rRNA phylogenies but rather form a distinct phylum, the *Thaumarchaeota* (Brochier-Armanet *et al.,* 2008, Spang *et al.,* submitted). As only few ammonia-oxidizing archaea have been successfully enriched and sequenced, we took a metagenomic approach in order to extend our knowledge on the genomic diversity of uncultivated Thaumarchaeota. For this purpose, a fosmid library was generated from biofilm samples taken in a radioactive thermal cave (45°C) in the Austrian Central Alps in which ammonia-oxidizing archaea were found to form a major part of the microbial community and in which we have measured considerable gross nitrification rates using a pool dilution technique. The library contained 18 fosmids with either an *amoA* or 16S rRNA gene affiliating with ammonia-oxidizing archaea. Five of those fosmids were chosen for sequencing and further analysis. Four of the fosmids appear to be affiliated with the soil group I.1b of Archaea. The fifth fosmid in contrast probably derived from an archaeon belonging to the marine group I.1a including *Cenarchaeum symbiosum* and *Nitrosopumilus maritimus*. Informational processing genes present on the different fosmids were analysed phylogenetically providing further support for the distinctiveness of the phylum *Thaumarchaeota*. Additionally, several putative genes that do not have homologues in the current databases indicate that ammonia oxidizing archaea of the soil group contain a specific gene set different from their marine counterparts. Thus, this study provides further support for the distinctiveness of *Thaumarchaeota* but also points to genetic diversity within the different lineages of this phylum that awaits further characterization.

Abstract Category
09 Evolutionary Ecology of Microbial Communities

PS.09.064 INFLUENCE OF FEEDLOT MANURE APPLICATIONS ON SOIL MICROBIAL COMMUNITIES ASSOCIATED WITH SHORT GRASS PRAIRIE AND CONSERVATION RESERVE PROGRAM GRASSLAND

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Available beef cattle manure exceeds the assimilative capacity of farm land in many areas of the High Plains. About half of the agricultural land base of the fed cattle producing region of the southern High Plains is grassland. This study documents the effect of annual (both fall and spring) applications of three rates of N (50, 125, and 200 kg/ha) in the form of feedyard cattle manure on grassland ecosystems and on soil microbial composition. Replicate treatments (n=4) of feedyard cattle manure N applications plus controls were made to native short grass prairie and old world bluestem grass ecosystems starting in the spring of 2000 and continued until the fall of 2006. A significant increase in biomass in response to N application was first observed in 2004 and continued through the last biomass sampling in 2007. Soil samples for microbial community composition at three depth ranges (0-2.5, 5.0-7.5, and 30.0 to 32.5 cm) were obtained in November of 2008. Microbial composition was investigated via DGGE-PCR methods using both general (V3 region) and improve-group specific 16S-PCR primers (Muhling et al., 2008) targeted at the following groups: *Alpha-, Beta-* and *Gamma-Proteobacteria, Bacteriodetes*, and *Firmicutes*. DNA sequence analysis of 16S rDNA gene libraries was also employed. DGGE-PCR data were analyzed by hierarchal clustering, group separation evaluation, and principal components analysis. Microbial community composition was most strongly influenced in order of importance by: 1) soil depth, 2) seasonal applications of manure over rate of N, and 3) lastly by grassland composition. Manure applications also resulted in significant differences between 16S gene libraries as did soil depth. The influence of grassland type was subtle and complex. However, soil depth and manure application treatments provided a strong influence on overall microbial community composition and tended to obscure or suppress grassland influences on microbial community composition.

isme13

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