



Bacterial communities from soil sediments of a mountain oasis in northern Oman

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ABSTRACT

Paleoecological records of a 20 meter deep profile near an oasis settlement in northern Oman have yielded a chronosequence providing insights into relationships between vegetation, the environment and development of human settlements in this area over a period of time spanning 19,000 years. In conjunction with analysis of the chemical and physical properties of this profile, we hypothesized that bacterial community structures associated with this chronosequence may also constitute a part of the biogeochemical record of the climate history that has been preserved at this site. To examine this hypothesis, we studied the composition of the community as revealed by profiling of 16S rRNA genes at 1 meter intervals along the entire profile. The results of our study show distinct changes in bacterial communities with increasing depth that correspond with differences in the climatic record as indicated by the occurrence of micro-charcoal particles. Sequencing of 16S rRNA genes proved the presence of *Acidobacteria*, *Actinobacteria*, *Proteobacteria*, *Gemmatimonadetes*, *Chloroflexi* and representatives from the candidate divisions SPAM, NC10, and OP10. Differences in the communities support the hypothesis that the bacterial species compositions in the sediment reflect properties of the organic matter and vegetation at the time they were deposited.

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1. Introduction

The relationship between climate and vegetation on bacterial community structures in soils has been well established (Martiny et al., 2006). Nonetheless, there has been little consideration of the possibility that today's bacterial distribution in soil chronosequences may continue to reflect aspects of prior vegetation and climatic history and thus comprise part of the biological record contained in soil profiles. During the last decade, many studies of palaeoclimatic records available from the Arabian Peninsula have contributed to a better understanding of the large fluctuations in the long-term climate history of this region. The geomorphology of dunes (Glennie and Singhvi, 2002; Preusser et al., 2002, 2005; Bray and Stokes, 2004), speleothems and cave fillings (Burns et al., 2002; Cremaschi and Negrino, 2005; Fleitmann et al., 2003, 2007) and, most importantly, from lake and ocean sediments (Gasse, 2000; Lézine et al., 2002, 2007; Gupta et al., 2003; Naidu and Niituma, 2003; Kröpelin and Soulié-Märsche, 1991; Radies et al., 2005) indicate that over the last 23,000 years numerous shifts between wet and dry periods have had a major impact on the landscape of the region. As such they have also caused large changes in its vegetation composition (such as

switches of dominance from C₃ to C₄ plants, Parker et al., 2006) and the occurrence of lakes in what today is the world's largest sandy desert (Radies et al., 2005; Lézine et al., 2007). Mainly as a consequence of a northwards movement of the IOM, periods wetter than today seem to have prevailed from 17,000 to 16,000 BP, from 15,000 to 14,500 (Gasse, 2000) and from 9000 to 7500 BP or even to 6000 BP (Overpeck et al., 1996; Naidu and Niituma, 2003; Lézine et al., 2007; Fleitmann et al., 2007). Latest by 4000 BP the climatic conditions on the Arabian Peninsula have become very arid leading to today's typical desert landscape.

Recently a sediment profile in a large depression near the mountain oasis of Maqta in northern Oman has been described of which luminescence dating made it one of the best documented long-term terrestrial soil chronosequence in the area (Fuchs and Buerkert, 2008; Urban and Buerkert, 2009). It includes pollen records as well as, charcoal and mollusc shells from which sedimentation rates and ages have been estimated (Fig. 1). In the present study, we carried out microbial community analyses of this unique undisturbed sediment profile using DNA based methods to characterize the community structures and their species composition at different depths reflecting distinct age ranges. In addition to comprising a potentially unique reflection of the chronosequence, the bacterial communities in these buried soils are also of interest for identifying the types of species that are able to tolerate the extreme nutrient and temporary water limitation that would occur in this arid environment (Balkwill et al., 1997; Kormas et al., 2003; Amend and Teske, 2005).

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