



Non-extremophilic ‘extremophiles’ – Archaeal dominance in the subsurface and their implication for life

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Archaea – besides bacteria and eukaryota constituting the third big domain of life – were so far regarded as typical inhabitants of extreme environments, as indicated by the name (Archaeon, Greek: ‘original’, ‘primal’). Previous research and cultivation successes were basically carried out in habitats characterized by extreme temperature, pH and salinity regimes. Such extreme conditions, as expected at the beginning of the Earth’s evolution, are occasionally also prevalent on extraterrestrial planets and moons and make the Archaeal domain a key group to be studied concerning life’s evolution and the most likely pioneer organisms to colonize environments that are regarded as hostile. However, in recent years it became obvious that Archaea, in particular non-extremophilic species, can be found almost ubiquitously in marine, freshwater, terrestrial and also subsurface habitats and occasionally outnumber other microbial domains and hold key positions in globally relevant energy and nutrient cycles. Besides extreme environments – the big question remains how to define a parameter as extreme – subsurface and cave environments present a window to the past, where adaptations to early life’s conditions can be studied and how microbiomes may be structured in a habitat that represents a refugium on extraterrestrial celestial bodies, were surface conditions might be at first sight too extreme for life.

The lower part of the alpine Hundsalm cave in Tyrol (Austria) offered a unique opportunity to study an almost pristine cave habitat, which is separated from the touristic part of the ice cave. The main focus of our research was laid on the microbial communities that were supposed to be in connection with secondary carbonate precipitations (‘moonmilk’). For the ascertainment of these so far poorly evaluated structures a multiple approach assessment was chosen to generate a virtually complete picture of these subsurface microbiomes. Thereby, a combination of different cultivation strategies was applied as well as physiological analyses, comprising HPLC and GC analyses, and molecular approaches, covering end-point and quantitative PCRs, DGGE, cloning, and sequencing analyses. Outstanding in the course of this research was that assumed non-extremophilic Archaea clearly outnumbered bacteria within the different moonmilk deposits, while fungi were only of minor importance. Moreover, the Archaeal species formed a constant element within the investigated samples, while bacteria and fungi showed a much more diverse and inhomogeneous community pattern. This indicates that the Archaea might constitute the central element within the microbial communities, holding key positions in nutrient and energy-cycles. Furthermore, it was possible to cultivate the Archaeal community over a certain time period, demonstrating that so far uncultured or as ‘not cultivable’ regarded organisms are accessible with certain cultivation strategies. On the other hand the vast majority of bacterial and fungal representatives are in close relation to species, which are valuable concerning biotechnological or medical applications.

Summing up, further research on cave microbiomes, especially Archaea, might be reasonable with regards to life’s evolution, global nutrient cycles, requirements for possible refuges of extraterrestrial life forms and also concerning new technological applications.