

The untapped microbial diversity and its implications

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Current estimates of prokaryotic diversity on the planet amount to values between 10^6 to 10^{17} different species. Whatever the species number might be, it has major implications for (1) the cultivation and collection, (2) the delineation of the evolving units and (3) the biotechnological potential and exploitation of the microbial diversity.

Microbial ecology studies revealed that microbes dominating natural communities often exhibit previously unknown physiological properties, as exemplified by the extremely low maintenance energy requirements of bacteria in the deep biosphere, or the high substrate affinities of soil methanotrophs. In fact, entire phyla within the bacterial radiation that have been defined based on their 16S rRNA gene sequences have so far largely escaped cultivation. Collecting and archiving such microbes represent major future tasks of BRCs which, however, can only be accomplished by establishing improved and high throughput cultivation methods. Ultimately, the extent of microbial diversity and the mechanisms maintaining it can only be fully appreciated if the evolving units within the prokaryotic radiation can be delineated. Systematic comparisons of closely related bacterial genomes provide the means to gain a principle understanding of the relevance of homologous recombination, lateral gene transfer and the niche-specific genes for genome evolution. Yet, understanding the ecophysiology of the corresponding bacterial lineages is indispensable to reliably identify evolving units and their selection. In combination, these approaches will help to refine the prokaryotic species concept but also are the preconditions for an improved bioeconomical exploitation of microbial diversity.