

## Gerhard Herndl

### Integrating prokaryotic microdiversity into ecosystems function theory

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Sufficient information on the phylogenetic diversity of marine prokaryotes have been collected over the past 15 years to allow assessment whether ecological theories on diversity and ecosystem functioning largely established on findings in plant communities also hold for marine prokaryotic communities. From the plethora of ecosystem functions of prokaryotes, examples are given in this presentation from two main functions, the remineralization of dissolved organic carbon to CO<sub>2</sub> and the production of methane by anaerobic bacteria. Both functions have been measured over a wide range of different marine subsystems. The responsible bacterial consortia are well defined in terms of electron acceptors and donors used and moreover, exhibit considerable richness. Thus, these two major prokaryotic consortia are ideal to exemplify and discuss functional versus phylogenetic variability in marine bacterial communities. As evident from these two examples, there is substantial complementarity among prokaryotic species, i.e., species with overlapping ecological niches. Species-rich communities are therefore more productive because more of the overall resource is used. Species-rich communities are also functionally more stable since niche overlap leads to parallel processing of a given substrate and synergistic effects within a network of species. Thus, this 'complementary mechanism' seems to be more important than the 'selection mechanism', i.e., species-rich communities are more productive because they are more likely to contain individual species with a large effect on ecosystem functioning. The recently emerging view that there is substantial microdiversity beyond the 97% sequence similarity level in marine prokaryotes has not been incorporated into general ecosystems theory yet. In this presentation an attempt is made to highlight some approaches to accomplish this. Based on recent major advances using a novel pyro-sequencing approach it becomes obvious that 1) the 'rare but closely related genotypes' are never attaining substantial abundance. Thus, Beijerinck's 'everything is everywhere' postulate probably does not hold for this rare biosphere. 2) Next to the few highly abundant genotypes present in all the water masses, several very closely related genotypes are present, decreasing in abundance with decreasing sequence similarity, leading to a bell-shaped distribution pattern of genotypes around the dominant one. 3) The rare genotypes all exhibit a certain level of sequence dissimilarity to the abundant genotypes, however, the sheer richness of the rare genotypes is enormous. This 'rare but closely related genotypes' are probably originating from divergence from the relatively few but abundant genotypes present. The genotypes most closely related to the parent genotype reach abundances almost as high as their parent genotype. Therefore, they likely contribute to parallel substrate processing and hence, to the complementarity network of prokaryotic activity and therefore, add to stability in ecosystem function of prokaryotic plankton.