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Diversity and Distribution of Freshwater Bacteria; Insights from the 16S rRNA gene and ITS Perspective

G. Zwart, M.P. Kamst-van Agterveld, S. van Oosterzee, F. Hagen, I. van der Werff-Staverman

Netherlands Institute of Ecology, Centre for Limnology, Nieuwersluis, The Netherlands (g.zwart@nioo.knaw.nl)

The assessment of microbial diversity is very much dependent on the level of resolution used by the observer. We and others have shown that particular groups of bacteria are frequently encountered in freshwater habitats. These groups were defined on the basis of 16S rRNA similarities of greater than 95%. The high abundances frequently seen and high encounter probability of these groups indicate that the bacterial diversity in freshwater is relatively low at this level of resolution. In addition, evidence is accumulating that the identified groups have worldwide distribution. Gradually we are obtaining insight into the diversity within these groups. We will show an example of a shallow lake in which multiple 'variants' (with small differences at 16S or ITS level) of one such narrow group coexist. Clearly, the metabolic potential or physiological capacity to utilize available resources is an important factor in driving diversity, however, predation and parasitism may be even more important for within group diversification. Another issue concerning the within group diversity is endemism versus global distribution. For the LD12 group (freshwater SAR11), the worldwide recovered sequences are unusually similar, even at the ITS level. This suggests that this is not a group, but a single species with worldwide distribution.