

## **RECIPE: Hyytiälä meeting, 4<sup>th</sup> - 5<sup>th</sup> June, 2004**

### **Minutes of “Microbial ecology group” sessions**

(Participants: A. Chatzinotas, M. Schloter, A. Siegenthaler, R. Artz, F. Laggoun-Defarge; D. Gilbert)

1. Biomass discussions: It is a big advantage of RECIPE that two independent biomass parameters are included in the project. Both parameters should be compared in the near future by Andreas Gattinger and Daniel Gilbert
2. All data should be statistically evaluated using cluster analysis – to give everybody the change to compare results easily, without using multivariate statistics. Processed data should be sent before the autumn meeting to Rebekka, who will mail things around.
3. Discussion about the use of the different fixatives for FISH and DAPI staining as Andy would like to look at the microbes involved in methane cycling in more detail. The present procedures should be adhered to for the time being.
4. Activity vs. presence of microbial indicators. Analyses currently are based on DNA. Some of the data generated thus far show some unusual results, e.g. highly diverse fungal presence throughout the cores. It is possible that this may be due to undecomposed fungal hyphae or spores present in the samples. The PLFA analyses should at least give an idea of fungal activity by their specific marker lipids. It was agreed to use RNA in the future if possible. The samples generated for WP1 were in general frozen slowly (i.e. in -20 or -80°C freezers) and are thus unsuitable for RNA analysis. To enable RNA extraction from WP2 samples, these need to be quick frozen by immersion in liquid nitrogen immediately after slicing of the cores. A corresponding experiment should be planned for 2005 based on the DNA and PLFA results obtained.