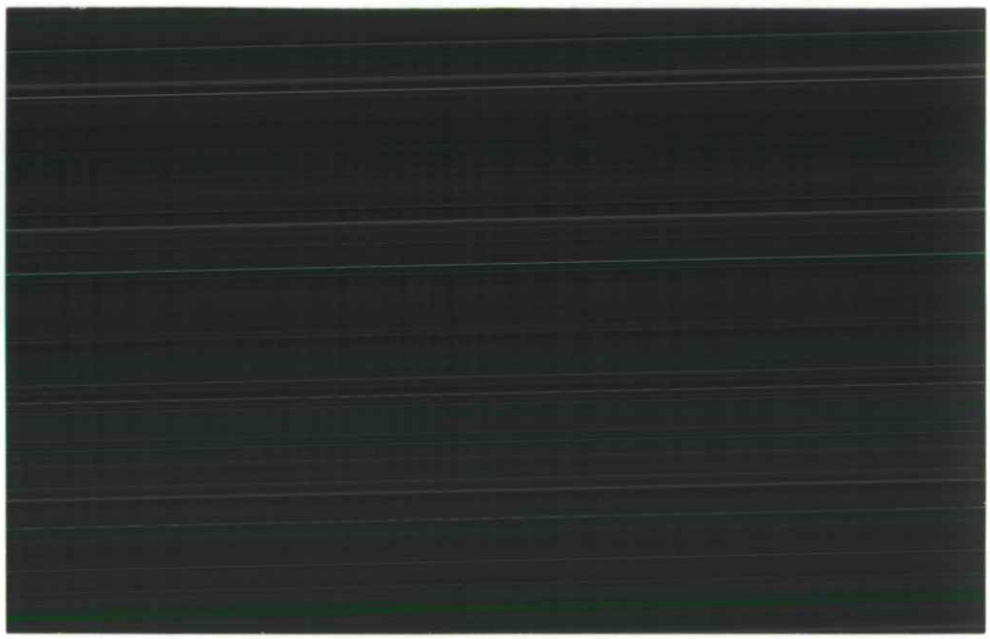
Centre for Ecology & Hydrology



Natural Environment Research Council

Centre for Ecology & Hydrology

Institute of Freshwater Ecology
Institute of Hydrology
Institute of Terrestrial Ecology
Institute of Virology & Environmental Microbiology

Natural Environment Research Council

Microbial Diversity and Ecosystem Function

CEH Integrating Fund

Project T10062R6

Second progress report to the Director, Centre for Ecology and Hydrology

Reporting period: Nov 1996 - Sept 1997

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Summary

1. Staff from IFE, IVEM and ITE have discovered that in a small lake, the nature and scale of ecosystem functions such as carbon-fixation and nutrient cycling appear to be governed by reciprocal interactions involving physical, chemical and microbiological factors. These interactions continuously create new microbial niches that are quickly filled from the resident pool of ubiquitous microbial species. One important implication is that **microbial diversity in an ecosystem is never so impoverished that the microbial community can not play its full part in biogeochemical cycling**, so there are probably no conservation issues associated with biodiversity at the microbial level.

2. We have collected additional evidence for this theory. Microbial niches, especially those connected with the methane cycle are, indeed, quickly filled; and this may be true also for theoretical niches (e.g. anoxic ammonia oxidation) for which there is no known organism.

3. However, we still have only a crude idea of what constitutes a natural microbial community. We are attempting (a) to develop rapid and reliable methods of characterising the complete microbial community, and the relative abundances of component 'species', and (b) to improve understanding of some functional groups, such as the viruses that infect other micro-organisms.

4. Fatty acid methyl ester (FAME) analysis is being used to identify bacteria collected from the lake, to distinguish algae from blue-green bacteria, and to compare the 'species' compositions of the different microbial communities in the lake. In the past year, we have begun to investigate the occurrence of cryptic (lysogenic) viruses in our collection of around 800 bacterial isolates from the lake. Preliminary analysis of the first 73 isolates indicates that eleven are lysogenic.

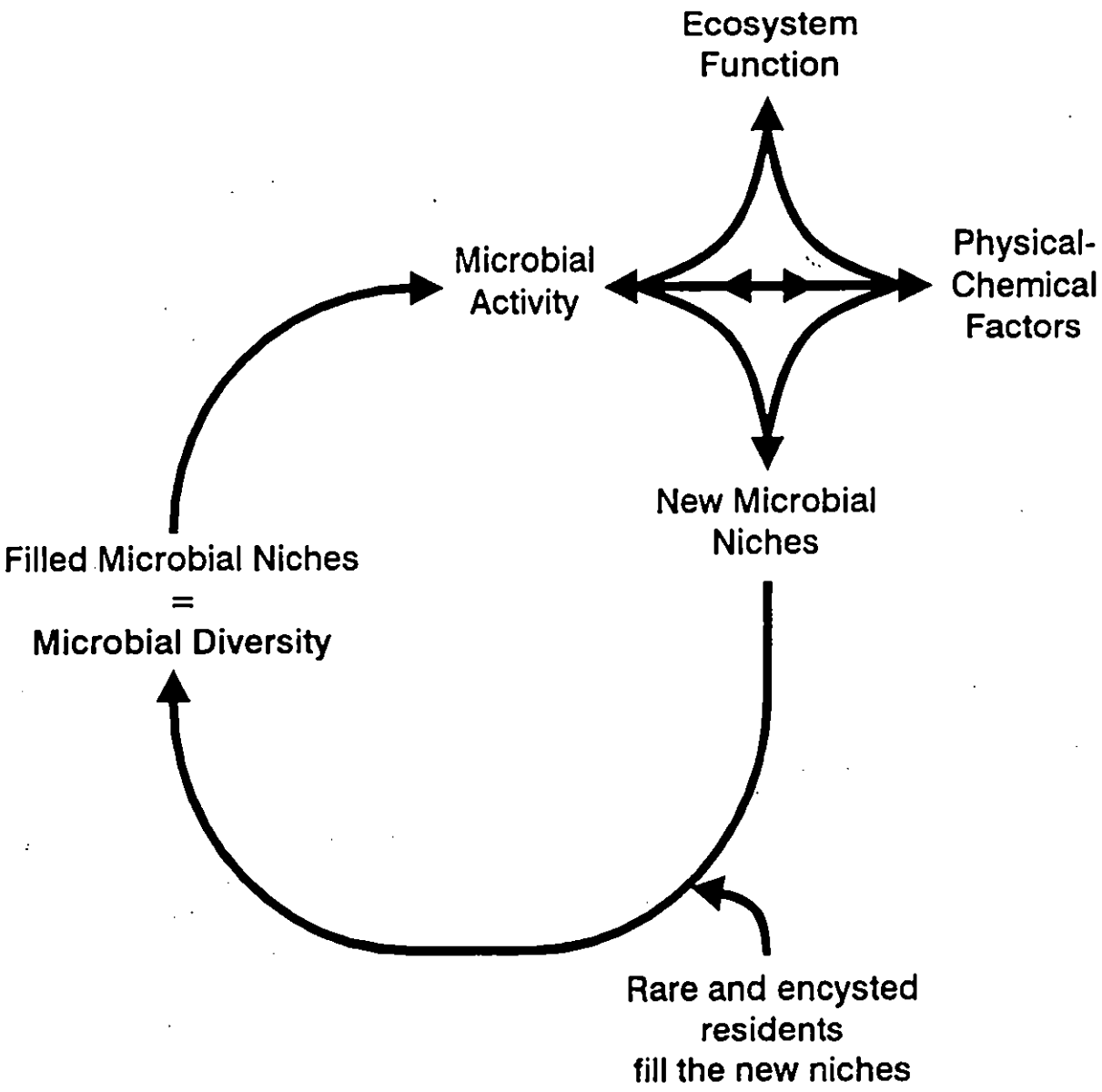
5. One major benefit of this intensive study of the diversity of microbial activities in a discrete ecosystem is that we gain a much better understanding of ecosystem function, and greater confidence in measurements of whole ecosystem fluxes, e.g. of methane and carbon dioxide. This work will be developed within a major proposal to Framework V (cycling of greenhouse gases in wetland and aquatic ecosystems).

Background

- 'Priest Pot' is a one hectare, biologically productive, freshwater pond
- Ecosystem functions in the pond (e.g. carbon flow, nutrient cycling) are dominated by microbial activity

Principal discoveries 1995-96

- Ecosystem functions are the result of reciprocal interactions between physical, chemical and microbiological factors
- These interactions continuously create new microbial niches
- Niches are quickly filled from the pool of ubiquitous microbial species
- Microbial activity and diversity are both a part of ecosystem function.



Gathering support for the theory

If microbes are ubiquitous:

- local species richness must be a substantial proportion of global species richness
- all microbial niches will always be quickly filled

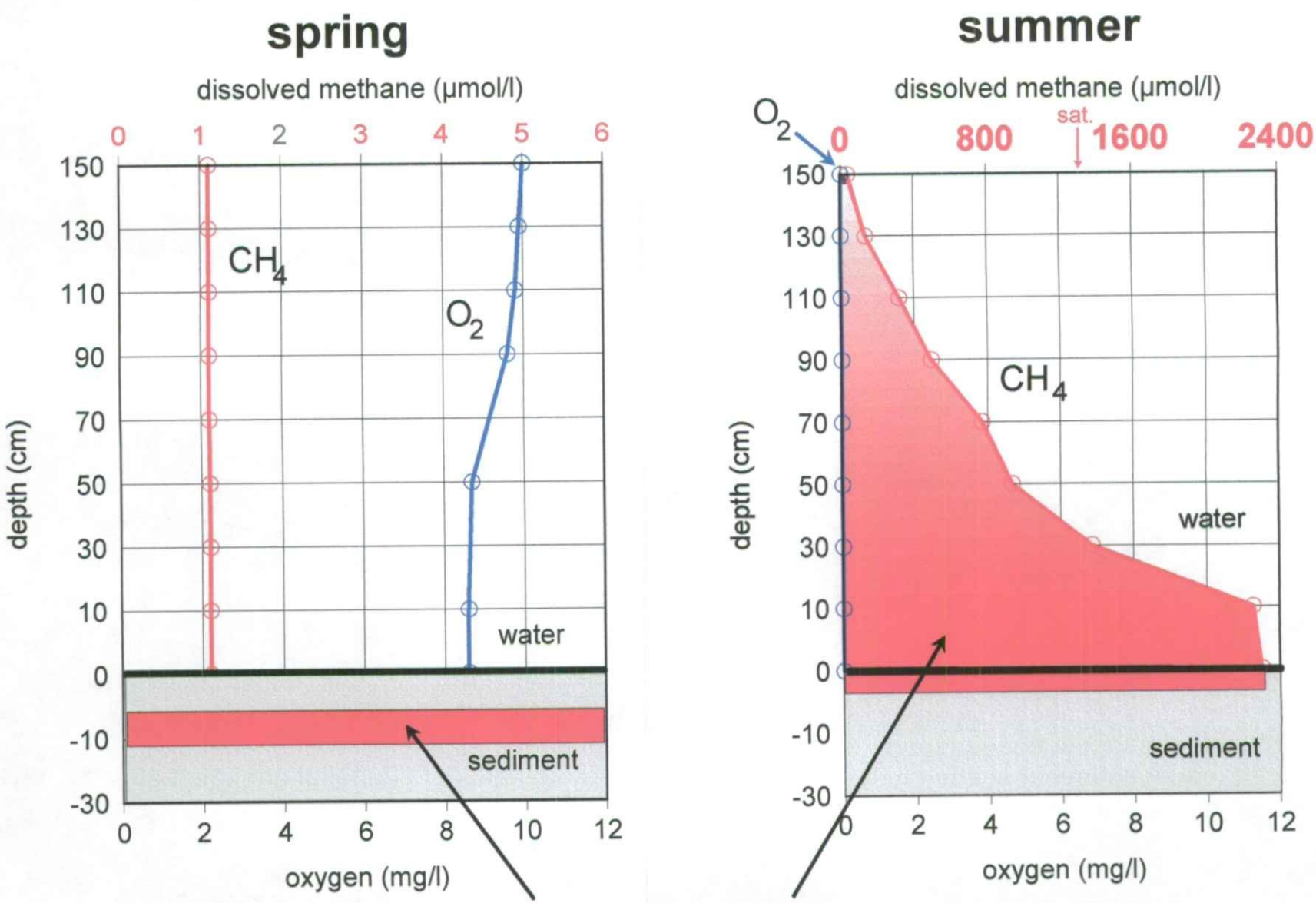
Local versus global species richness

	Species in Priest Pot	% of global total
Ciliates	>240	> **24**
Paraphysomonas spp.	> 27	> **54**

All microbial niches will always be quickly filled

e.g.:

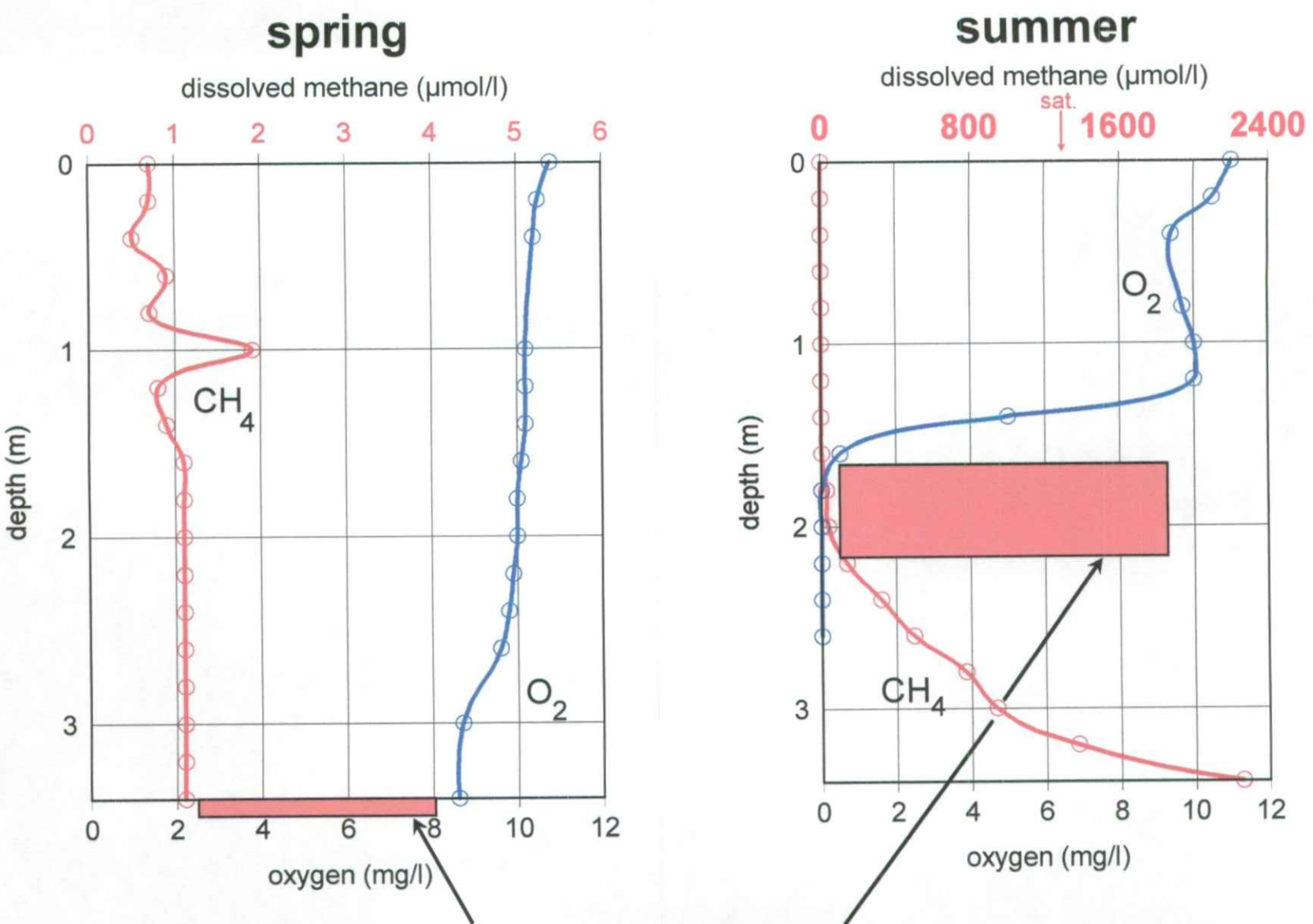
- methane oxidation and methanogenesis in the water column
- anoxic photosynthetic NH_3 oxidation
- intracellular niches (e.g. viruses and lysogeny)



spatial niches for methanogens

sediments
water
CH_4
depth (cm)

depth (cm)



spatial niches for methane oxidizers

qebɟɹ (ɯ)

qebɟɹ (ɯ)

BUT:

- We still have a very simplistic idea of what constitutes a natural microbial community. We need rapid and reliable methods of characterising the complete microbial community, and the relative abundances of component 'species'.
- Very little is known about some functional groups e.g. we need to develop new assay systems to detect and identify viruses and non-apparent infection (lysogeny)

FAME

We are using FAME to :

- identify the bacteria that will grow on a defined medium
- distinguish algae from blue-green bacteria
- compare natural microbial communities living at different depths on the same sampling occasion

BACTERIA

- We have isolated bacteria from Priest Pot at different times and from different depths, enumerated colonies, and begun FAME identification/characterisation

ALGAE/BLUE-GREEN BACTERIA

- We have compared FAME profiles of axenic cultures of algae/blue-green bacteria from the CCAP Culture Collection and from Priest Pot, to show the potential of the method for identifying species. The database is being enlarged from its very small current number of profiles (largely comprising clusters of pseudomonads)

WHOLE MICROBIAL COMMUNITIES

- We are beginning to investigate FAME analysis for the comparison of whole microbial communities collected from different depths in the water column of Priest Pot. We have reached a turning point in the investigation, having for the first time described a community - and having identified at least three new fatty acids in water samples at 1.5 - 1.75m deep that do not occur in samples taken above or below that depth.

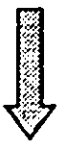
VIRUSES

- We are using mitomycin c induction to investigate the incidence of lysogeny in bacteria isolated in pure culture from Priest Pot water.

- Virus-like agents (morphological entities of unproven pathogenicity) have been triggered by the treatment (particularly in pseudomonads). In 50 cultures tested to date, we have not found any that are sensitive to the virus-like particles.

- Improved holistic picture (*see 1996 Report*)

- Better understanding of how the more important microbial groups contribute to ecosystem function



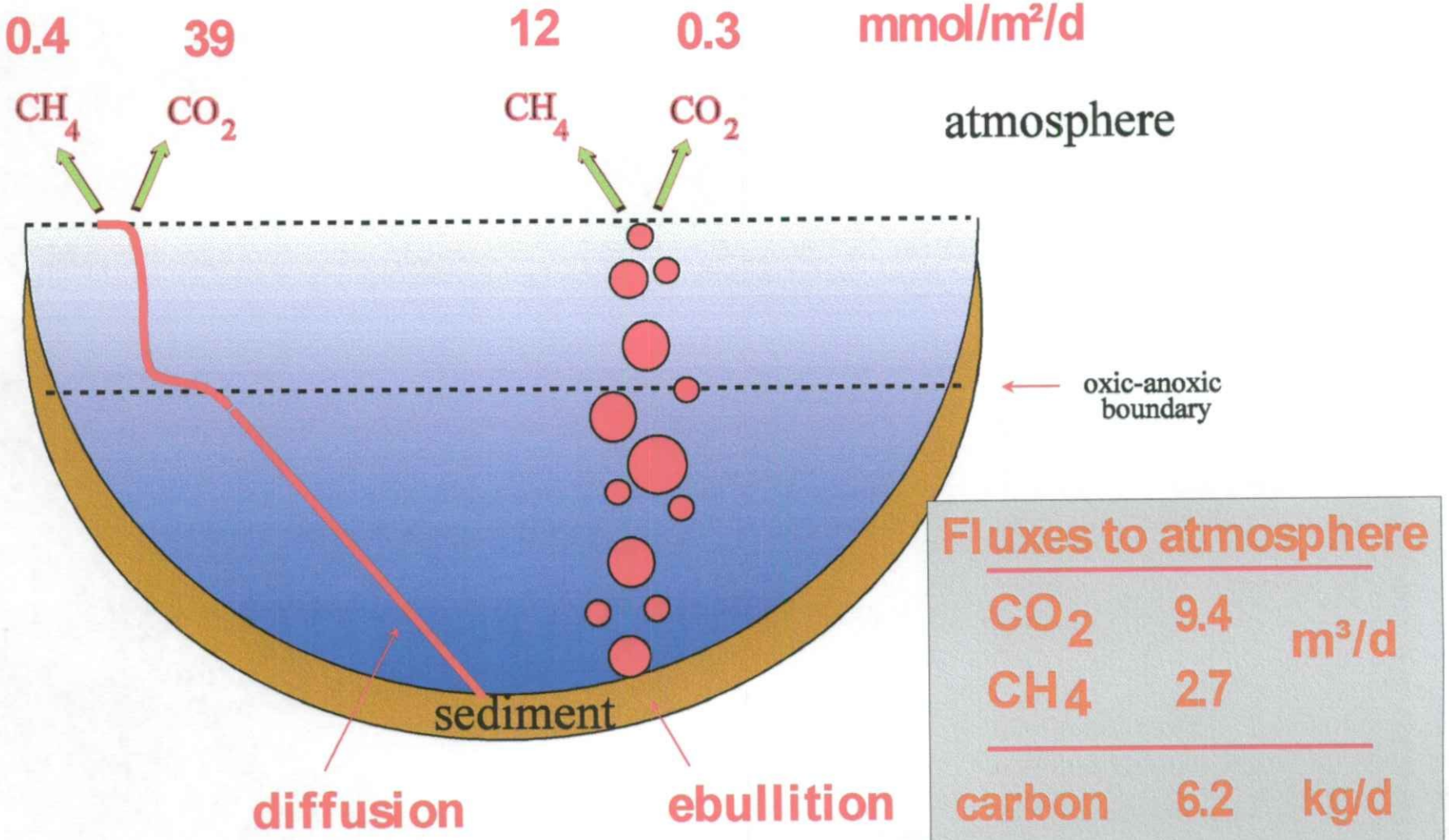
- Greater confidence in measurements of 'whole ecosystem' fluxes e.g. of 'greenhouse' gases

Our general conclusions are still well-supported:

1. Most species of free-living micro-organisms are probably ubiquitous

2. Empty microbial niches are quickly filled

3. Microbial diversity in an ecosystem is never so impoverished that the microbial community cannot play its full part in biogeochemical cycling.


0.4
39
12
0.3
mmol/m²/d
CH4
CO2
CH4
CO2
atmosphere
oxic-anoxic boundary
sediment
diffusion
ebullition
Fluxes to atmosphere
CO2 9.4 m³/d
CH4 27
carbon 6.2 kg/d