

Microbe, April 2006

Microbial Ecology: Searching for Principles

The extraordinary diversity of microbial ecosystems complicates efforts to develop principles encompassing microbial ecology

Allan Konopka

Population vs. community ecology

It's the microenvironment!

Community redundancy and population versatility

Ecotype – how can we recognize it?

Genetic “microdiversity”

Population ecology

The study of the processes that affect the distribution and abundance of populations (set of individuals of one ecotype).

Community ecology

The study of the organization and functioning of assemblages of interacting populations in a habitat.

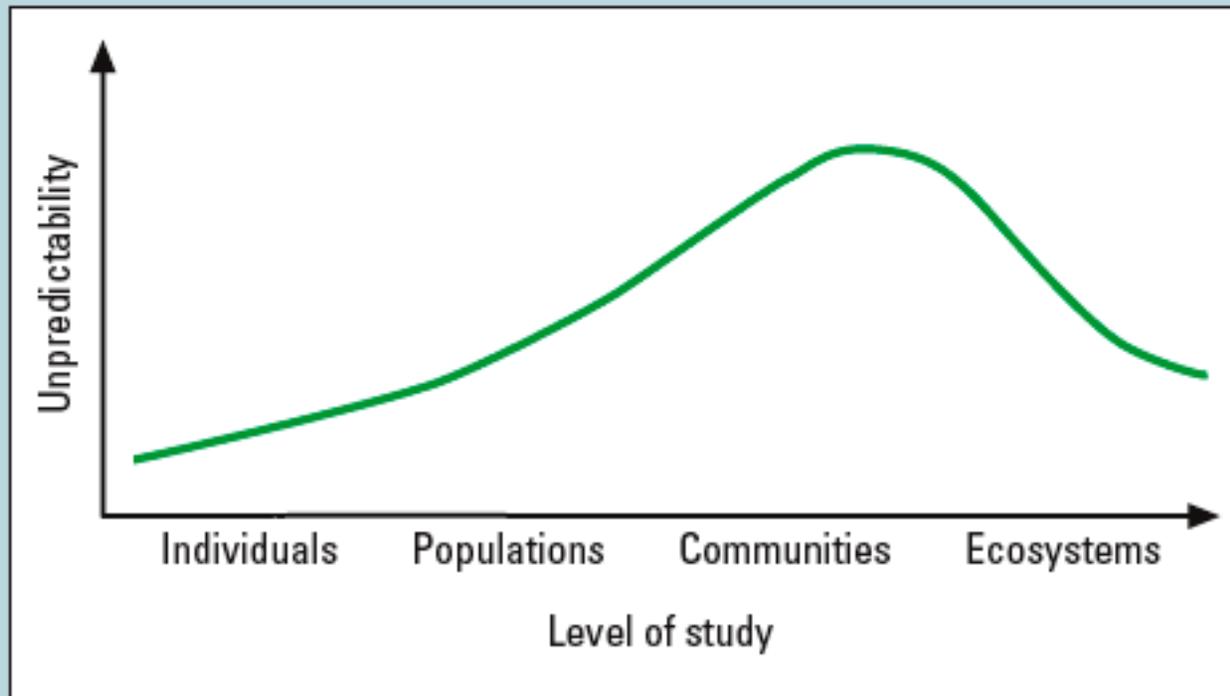
Van Straalen N

Ecotoxicology becomes stress ecology

ENVIRONMENTAL SCIENCE & TECHNOLOGY 37: 324A-330A (2003)

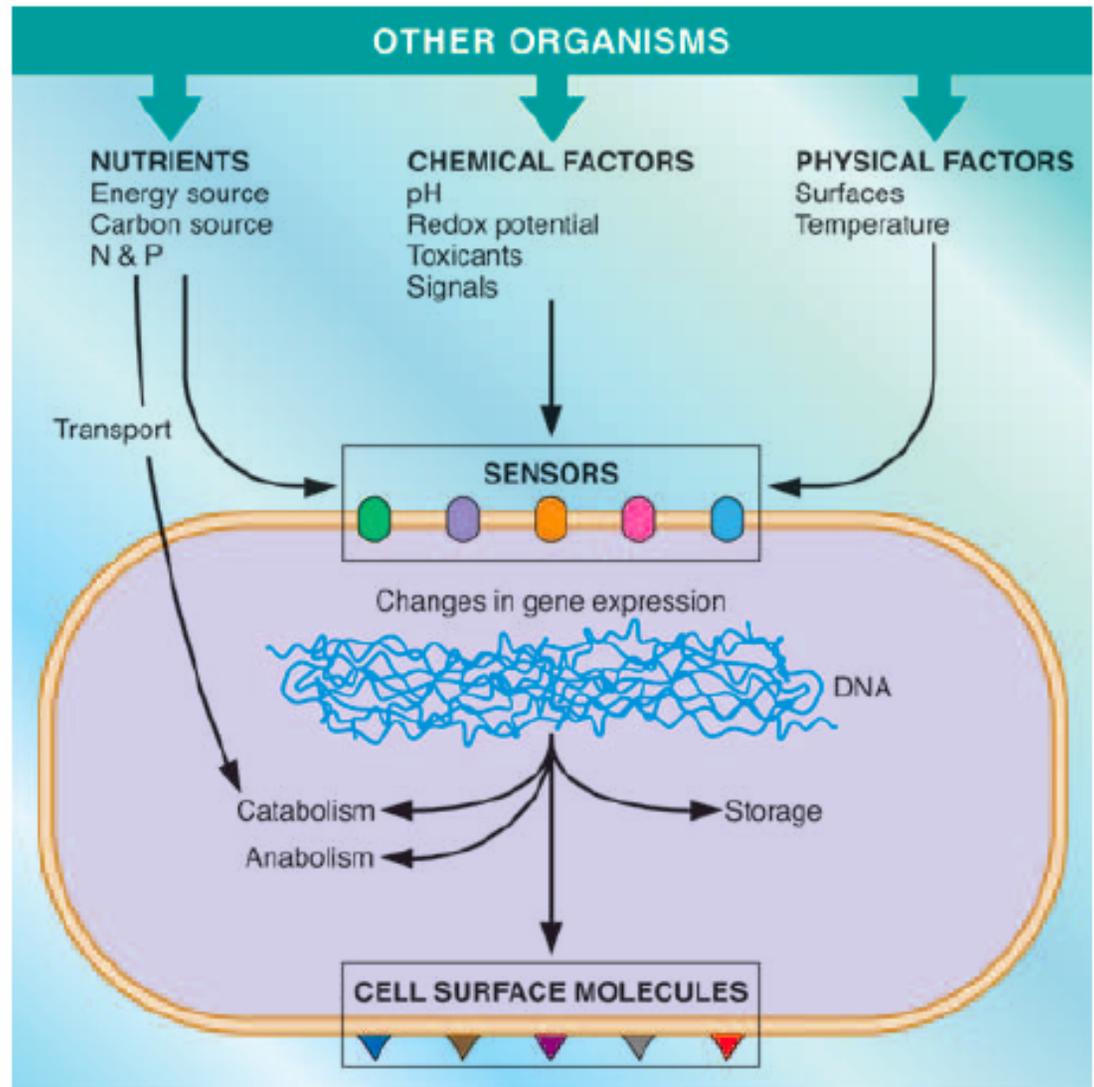
Ecosystems are unpredictable

The qualitative graph demonstrates changes in unpredictability—defined as the absence of laws or the degree of contingency on initial conditions—in ecological systems as a function of hierarchical level of study (32).



The Microenvironment

FIGURE 1



Processes at the microenvironment scale.

Towards an evolutionary ecology of life in soil

Crawford JW, Harris JA, Ritz K, Young IM

TRENDS IN ECOLOGY & EVOLUTION 20: 81-87 (2005)

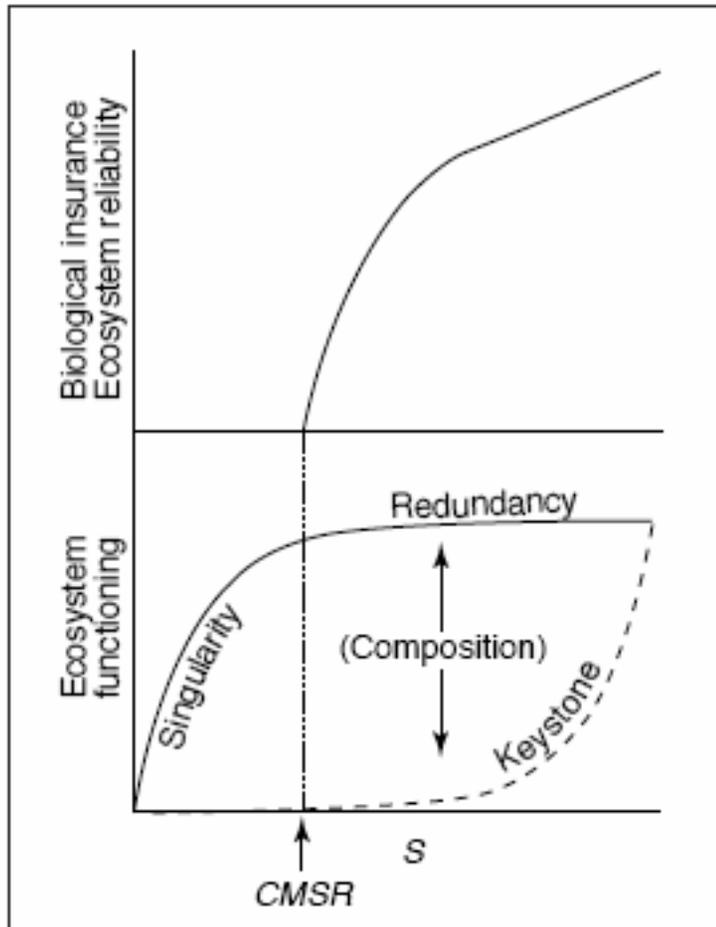


Figure 1. An X-ray CT image of soil obtained using the Advanced Photon Source, University of Chicago (http://www.aps.anl.gov/aps/frame_home.html). The resolution is $4\ \mu\text{m}$, and the size of the sample is $0.8\ \text{mm}$. Green denotes pore space and red denotes the solid matrix. The image illustrates the complex geometric features of soil including a tortuous pore space and a broad range in size of pore volume elements.

Community redundancy

Naeem et al. TREE vol. 13, no. 4 April 1998

Transcending boundaries in biodiversity research



The relationship between ecosystem properties, and biodiversity (number of species (S)).

Singularity:

rapid rise in functioning as unique species are added.

CMSR:

critical minimum species richness for maximal functionality.

Upper plot:

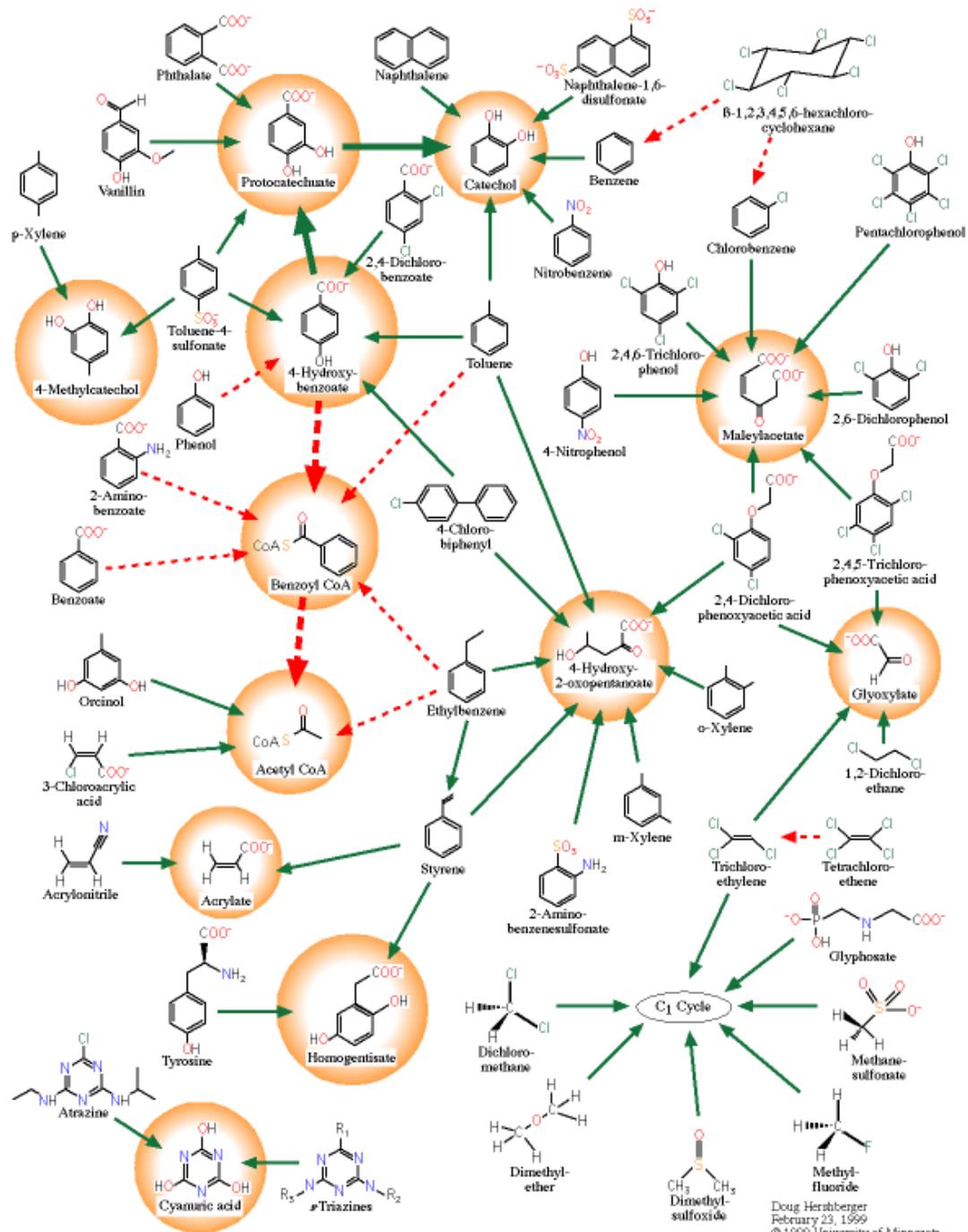
Biological insurance and ecosystem reliability is lowest below CMSR, but rises quickly with small amounts of redundancy.

“Keystone” species can cause dramatic declines in functioning if they suffer extinction.

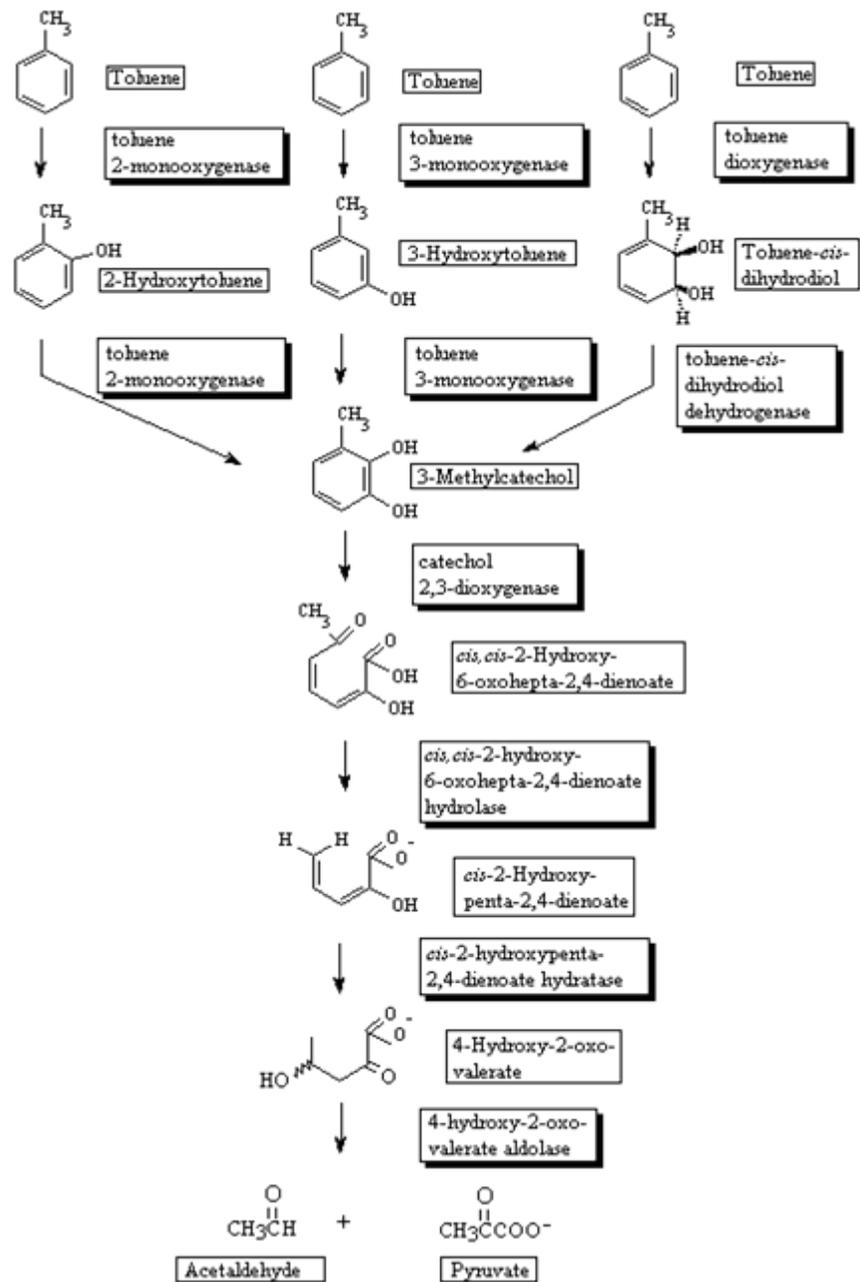
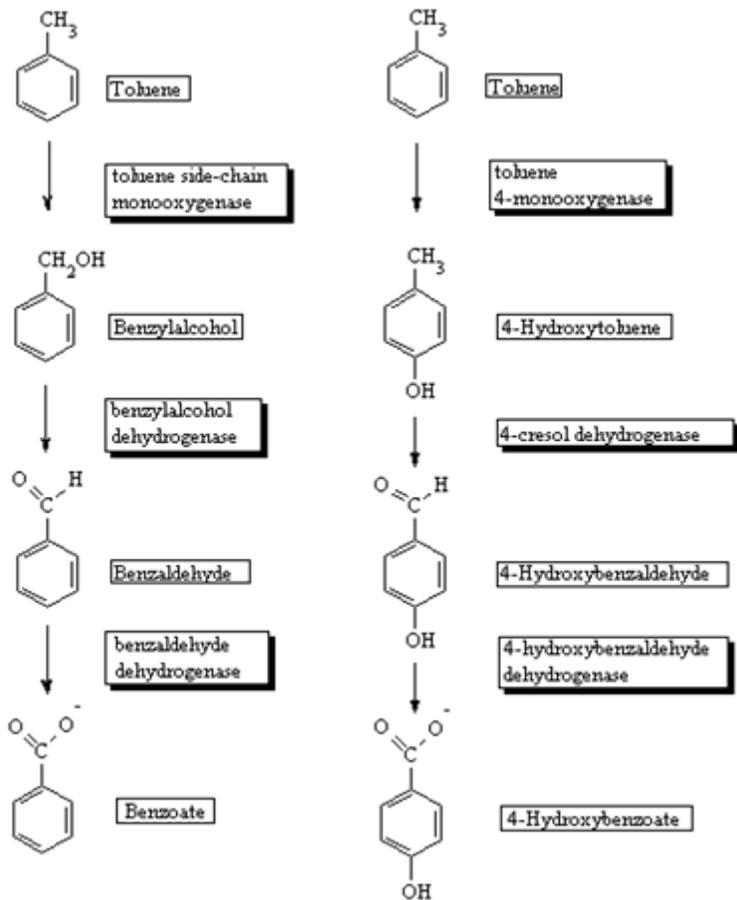
Thus, a range of possible relationships between biodiversity and ecosystem properties can occur, bounded by redundancy and keystone models.

Microbial versatility and the evolution of metabolic pathways:

Funnel to “nodes”:
Diverse aromatic substrates are converted to a few key intermediates (di-OH aromatics)



**Aerobic Toluene catabolism:
5 different pathways found in
various bacteria**



In a world filled with genome sequences ...

| | Complete | Incomplete | Totals |
|----------|------------|------------|------------|
| Bacteria | 259 | 9 | <u>268</u> |
| Archaea | 23 | 0 | <u>23</u> |
| Viruses | 3 | 0 | <u>3</u> |
| Totals | <u>285</u> | <u>9</u> | <u>294</u> |

How do we define ecologically-significant differences?

Ecotype

The smallest taxonomic subdivision of an eco-species, consisting of populations adapted to a particular set of environmental conditions.

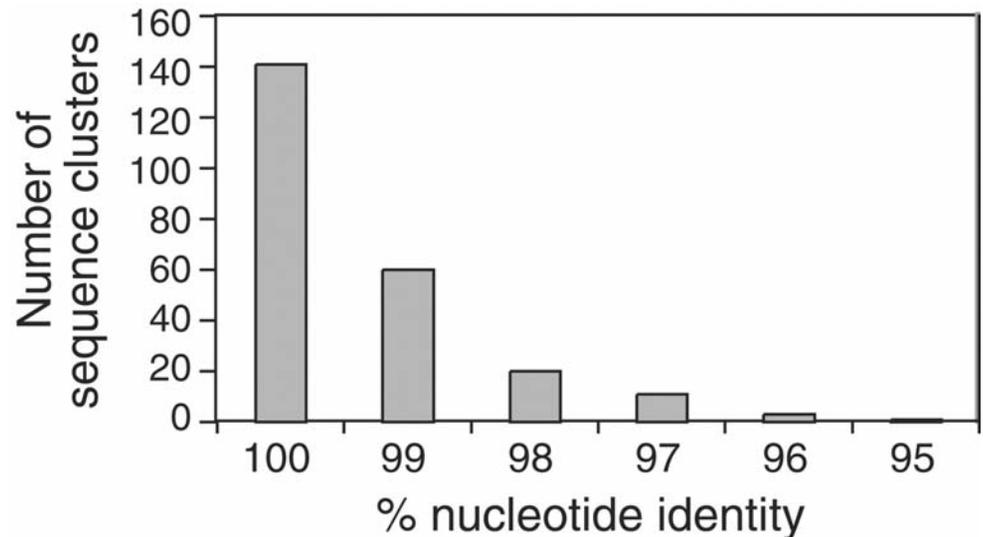
There may be a lot of genetic micro-diversity out there

Genotypic Diversity Within a Natural Coastal Bacterioplankton Population

Janelle R. Thompson, Sarah Pacocha, Chanathip Pharino, Vanja Klepac-Ceraj, Dana E. Hunt, Jennifer Benoit, Ramahi Sarma-Rupavtarm, Daniel L. Distel, and Martin F. Polz

Science 307: 1311-1313, 25 February 2005

Number of distinct *Hsp60* clusters among *V. splendidus* isolates observed as cluster cutoff values are decreased from 100 to 95%. [



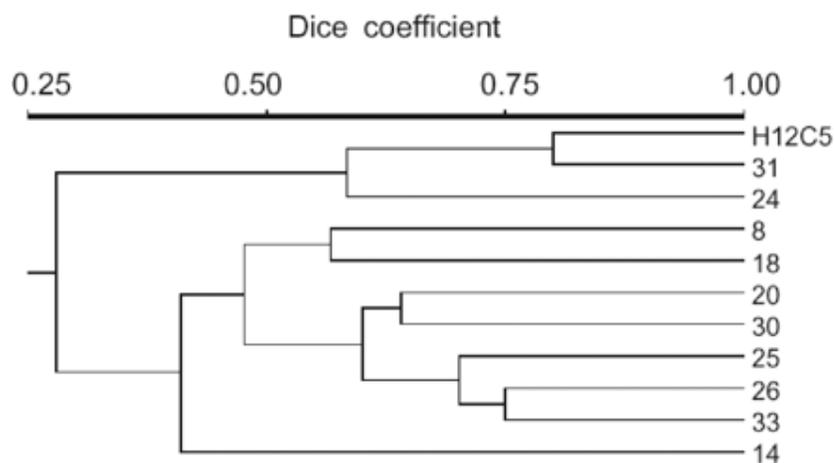
Pulsed Field Gel Electrophoresis detected 180 different genome patterns among 206 strains.

The Chao-1 algorithm estimates ca. 1300 *Vibrio splendidus* genotypes in the samples,

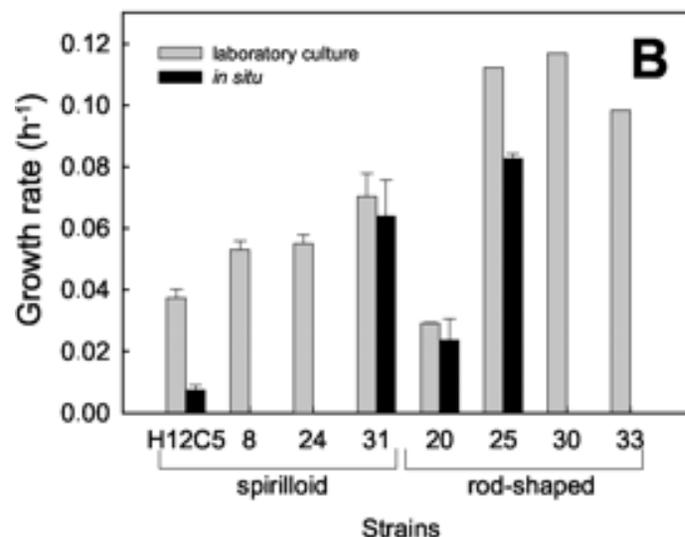
Ecological Significance of Microdiversity: Identical 16S rRNA Gene Sequences Can Be Found in Bacteria with Highly Divergent Genomes and Ecophysologies.

Elke Jaspers and Jörg Overmanⁿ

A set of 11 strains of *Brevundimonas alba* were isolated from a bacterial freshwater community. These strains had identical 16S rRNA gene sequences



Physiological similarity of the 11 *Brevundimonas* strains as assessed by cluster analysis based on the substrate utilization patterns.



Growth rates of the 11 *B. alba* strains in pure laboratory cultures growing in artificial freshwater medium with YPG as the substrate and growing in dialysis bags in situ in Zwischenahner Meer.

