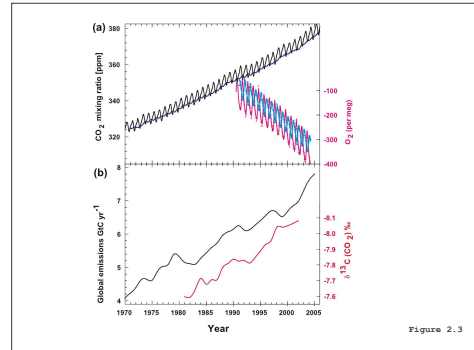
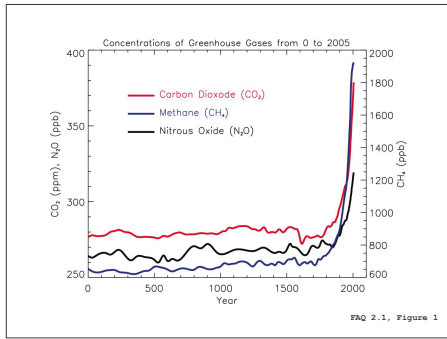


Climate and Microbiology

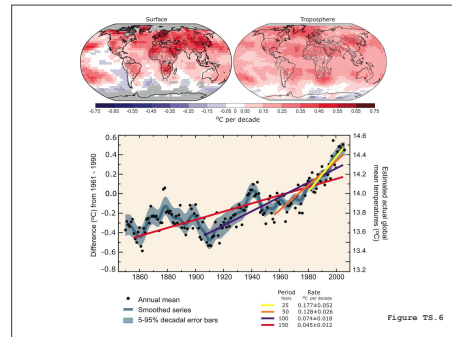
ESM 219



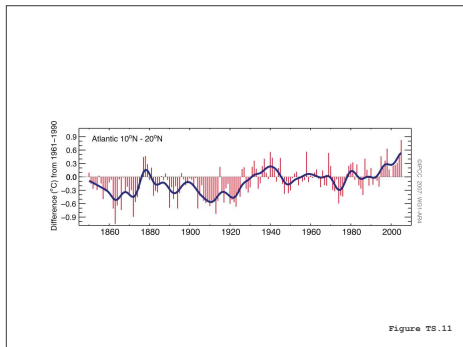
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<http://www.ipcc.ch/graphics/gr-ar4-wg1.htm>



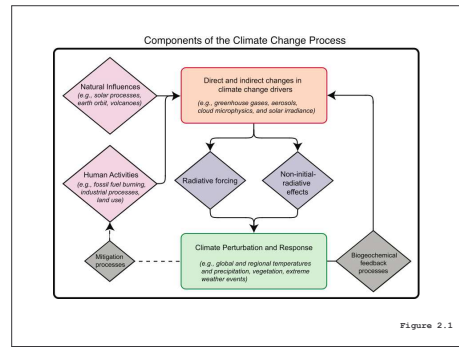
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IPCC Working Group 1, Technical Summary, 2007
<http://www.ipcc.ch/graphics/gr-ar4-wg1.htm>



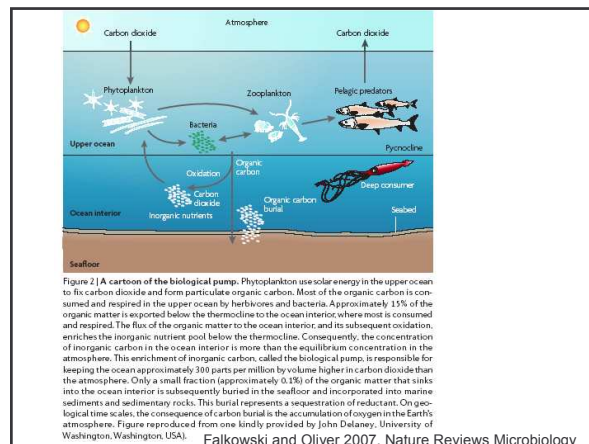
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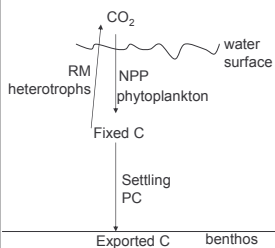
IPCC Working Group 1, Chapter 2, 2007
<http://www.ipcc.ch/graphics/gr-ar4-wg1.htm>

Some Microbial Issues in a Changing Global Climate

- Responses to T (growth rate, catalysis)
- Responses to C (storage in/out of cells)
- Responses to water (desiccation stress; anaerobiosis)
- Community structure and function changes that may drive changes in
 - Decomposition of organic matter
 - Nutrient cycling (e.g. N)
 - Feedbacks to greenhouse gases



Climate and the ocean: what might occur?



- Mixing changes (turbulence in ocean)
- Higher fixed C leading to higher exports
 - Tied to bacterial growth rates

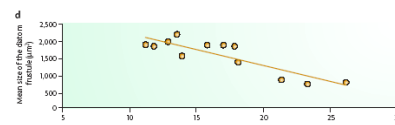


Figure 5 | Changes in ocean thermal structure and the size of diatoms in the Cenozoic period. Changes in temperature (a), the average size of marine diatom shells (frustules) (b) and the species richness of marine diatoms (c) over the past 65 million years. Correlation between temperature and the average size of marine diatoms over the past 65 million years (d). Pleistocene.

climate → thermal gradients → turbulent mixing → nutrient fluxes → cell sizes

Falkowski and Oliver 2007. Nature Reviews Microbiology

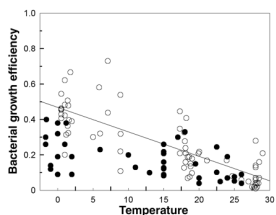


Figure 1. Scatter plot of bacterial growth efficiency as a function of temperature for bacterioplankton from polar, temperate, and tropical oceans. Bacterial growth efficiency was determined from concurrent measurements of bacterial production and DOC uptake (open symbols) or of bacterial production and size-fractionated O₂ uptake (filled symbols). The ordinary least squares regression (regression line shown) between temperature (T) and bacterial growth efficiency (BGE) is: $BGE = 0.374 \pm 0.04 - 0.0104 \pm 0.002 T$. ($r^2 = 0.54$, $n = 107$, $F = 84.27$, $P < 0.001$). Values in brackets are the 95% confidence intervals of the regression parameters. (Rivkin and Legendre, Science 2001)

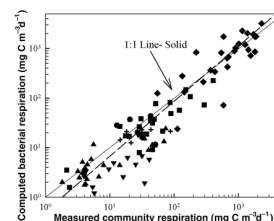
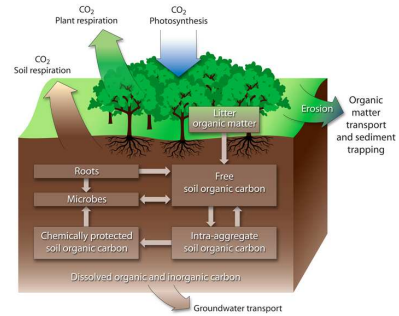


Figure 2. Scatter plot of field-measured community respiration versus computed bacterial respiration for the Antarctic (+), Arctic (•), Arabian Sea (◊), Gulf of Mexico (◻), North Atlantic (◊), and South Atlantic Bight (◊). The solid 1:1 line is shown for visual reference. Using the database described in (34), bacterial respiration was computed from the reported bacterial production and ambient temperature using Eq. 4. The data were log-transformed to normalize variances. The structural (reduced major axis) regression (dashed line) between field-measured community respiration (CR) and computed bacterial respiration (C-BR) is: $\text{Log C-BR} = -0.36 \pm 0.13 + 1.10 \pm 0.08 \text{ Log CR}$. ($r^2 = 0.88$, $n = 100$, $F = 738.8$, $P < 0.0001$). Values in brackets are the 95% confidence intervals of the regression parameters. The slope (1.14), r^2 (0.81), and significance ($F = 404.8$, $P < 0.0001$) of the structural relationship between measured community respiration versus computed bacterial respiration for the raw (i.e., nontransformed) data were similar to those for the log-transformed data. (Rivkin and Legendre, Science 2001)

Feedbacks

- Temperature increases, then growth efficiency decreases and CO₂ export to atmosphere increases, and T increases....
- Monitoring C export can be by RS of chlorophyll *a* and Temperature because they determine Bacterial production, and bacterial efficiency is related to temp, and respiration and production determine efficiency.

(Rivkin and Legendre, Science 2001)



Genomics:GTL Roadmap, U.S. Department of Energy Office of Science, August 2005, <http://genomicsgtl.energy.gov/roadmap/>

Carbon: Montealegre et al

- FACE experiment (free air carbon dioxide enrichment)
- 2 plant communities, soil
- Rhizosphere effects versus bulk
- PLFA for community, direct counts of respiring bacteria for abundance

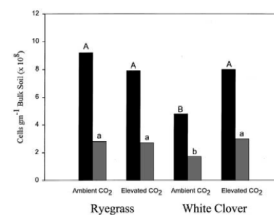


Figure 1. Bacterial populations per gram bulk soil for perennial ryegrass and white clover grown under ambient (350 ppm) and elevated (600 ppm) atmospheric CO₂. Bars followed by different letters indicate significant differences in total (upper case) or respiring (lower case) bacterial numbers, respectively ($P < 0.05$). Legend: ■ total bacteria, ■ respiring bacteria.

(Montealegre et al. Plant and Soil 2002)

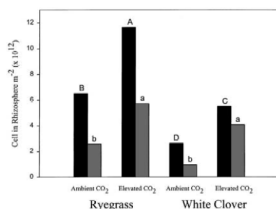


Figure 2. Bacterial numbers expressed on a per unit land area basis (m²) in rhizosphere soil under perennial ryegrass and white clover grown under ambient (350 ppm) and elevated (600 ppm) atmospheric CO₂. Bars followed by different letters indicate significant differences in total (upper case) or respiring (lower case) bacterial numbers, respectively ($P < 0.05$). Legend: ■ total bacteria, ■ respiring bacteria.

(Montealegre et al. Plant and Soil 2002)

Table 1. Community structure analysis based on phospholipid fatty acids (PLFA) for rhizosphere and bulk soil of white clover grown under two CO₂ levels

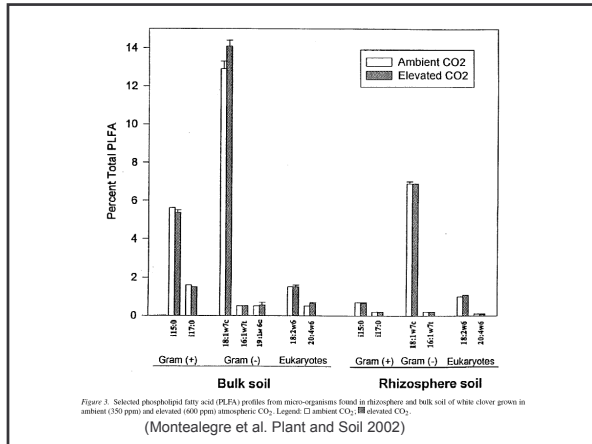
PFLA Profiles	Percentage of Total PFLA ^a			
	Rhizosphere Soil		Bulk Soil	
	Ambient CO ₂	Elevated CO ₂	Ambient CO ₂	Elevated CO ₂
Monoenics	76.2 ± 0.8	75.8 ± 0.7	45.4 ± 0.1**	46.5 ± 0.1**
Normal saturates	11.9 ± 0.8	11.9 ± 0.6	11.5 ± 0.2	11.5 ± 0.2
Terminally branched saturates	4.0 ± 0.0	4.0 ± 0.1	18.4 ± 0.1	18.3 ± 0.1
Mid-chain branched saturates	0.6 ± 0.0	0.7 ± 0.0	13.0 ± 0.5	12.2 ± 0.4
Branched monoenics	0.5 ± 0.1	0.5 ± 0.1	6.8 ± 0.2	6.6 ± 0.1
Other Fatty Acids	0	0	0.2 ± 0.1	0.2 ± 0.1
Eukaryotes	6.8 ± 0.1*	7.2 ± 0.1*	4.8 ± 0.1	4.8 ± 0.1

^aValues are means of two replications ± standard errors on mean.

*Denotes significant CO₂ effect at $P < 0.1$.

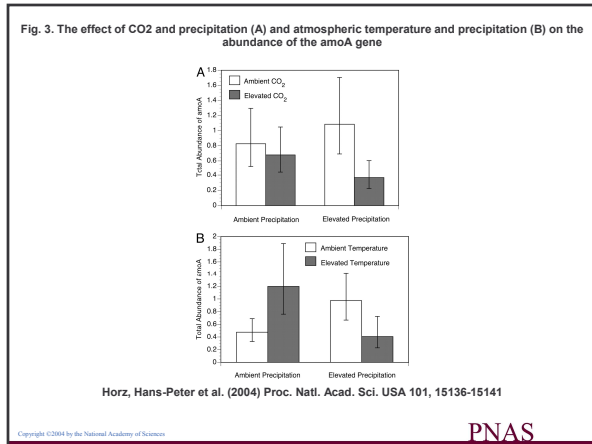
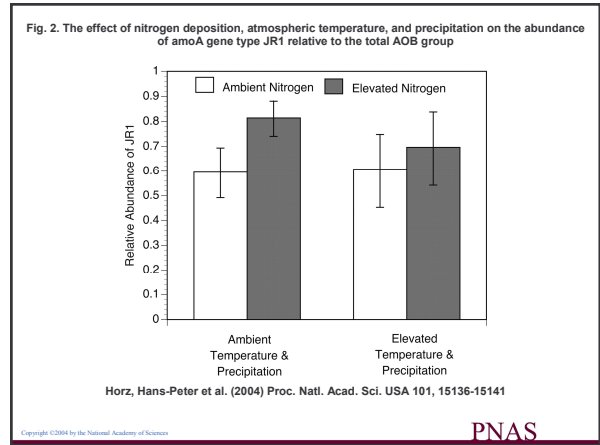
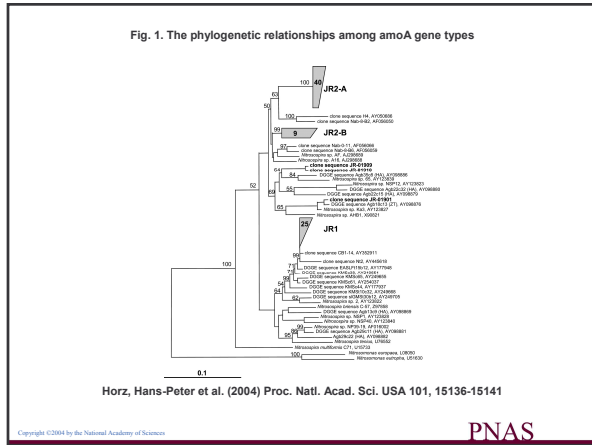
**Denotes significant CO₂ effect at $P < 0.05$.

(Montealegre et al. Plant and Soil 2002)



Horz, 2004

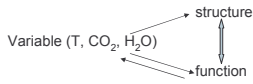
- FACE experiment again
- T, CO₂ and precipitation changing together—what are the effects on ammonia oxidizers?
 - 1st step in nitrification
 - Specialists involved
 - chemoautotrophic process



Community Structure & Function




- What are the links?
 - Does microbial community composition effect microbial community function?
 - What are the relationships between other (e.g. plant) communities and microbial communities?
- What are the feedbacks and interactions?
 - e.g. Structure changing function changing structure
 - e.g. Changes due to C then changing water relations

Structure : Function



- Climatic variable can affect community composition (structure) and /or observed function
- Feed backs between structure and function can shape the outcome to both.
- There may also be feed backs to the “variable”.

Studying Microbial Communities & Ecosystem Function

- Environmental treatment 
- Common garden 
- Reciprocal Transplant 

Reed and Martiny, 2007

Soil Water: issues?

- Changes in precipitation causing changes in frequency / duration of anaerobiosis?
- Desiccation in previously wet environments?
- Plant-propagated C into soils—directly or indirectly creating a water “sponge”?
 - Feedbacks between moisture and C to, in turn, change moisture characteristics

Some Microbial Issues in a Changing Global Climate

- Shifts in disease
 - Wider geographical ranges for pathogens
 - Variations in virulence factor production

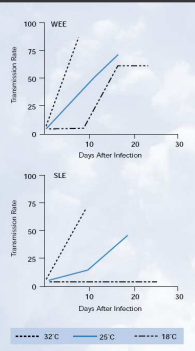


Figure 1. Effect of temperature on transmission rates (the percentage of bites that result in transmission) of Western equine encephalitis (WEE) and St. Louis encephalitis (SLE) viruses by the mosquito, *Culex tarsalis*. Reeves W.C., Hardy J.L., Ritten W.K., Milby M.M. "The Potential Effect of Global Warming on Mosquito-Borne Arboviruses." *Journal of Medical Entomology*. 31(3): 323-332.

Colwell and Patz, 1998, American Academy of Microbiology

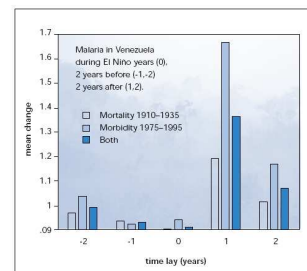


Figure 2. Malaria in Venezuela During El Niño. Bouma, M.J. & Dye C.: 1997. "Cycles of Malaria Associated with El Niño in Venezuela." *Journal of the American Medical Association*. 278: 1772-74. Copyright: 1997 American Medical Association

Colwell and Patz, 1998, American Academy of Microbiology

