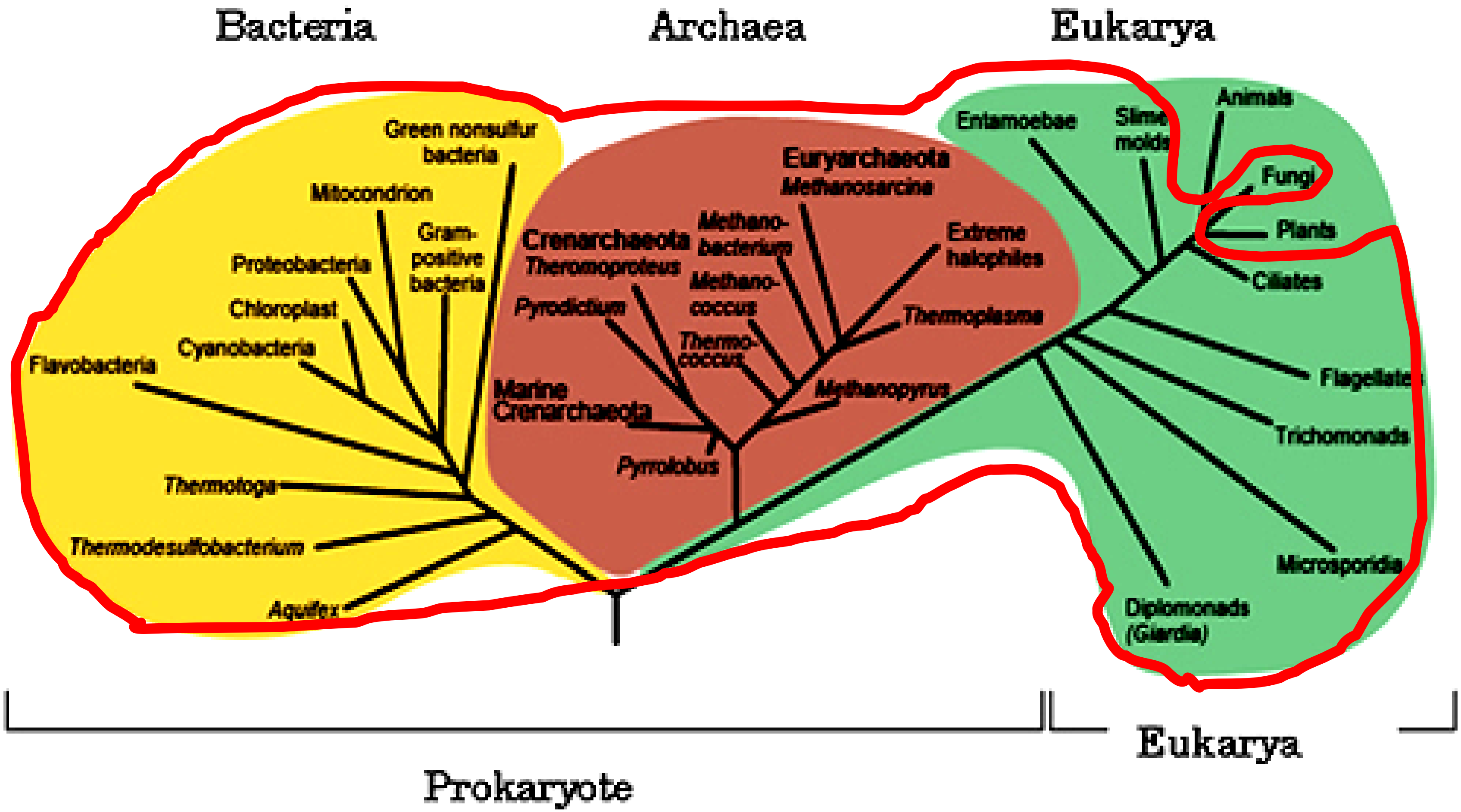
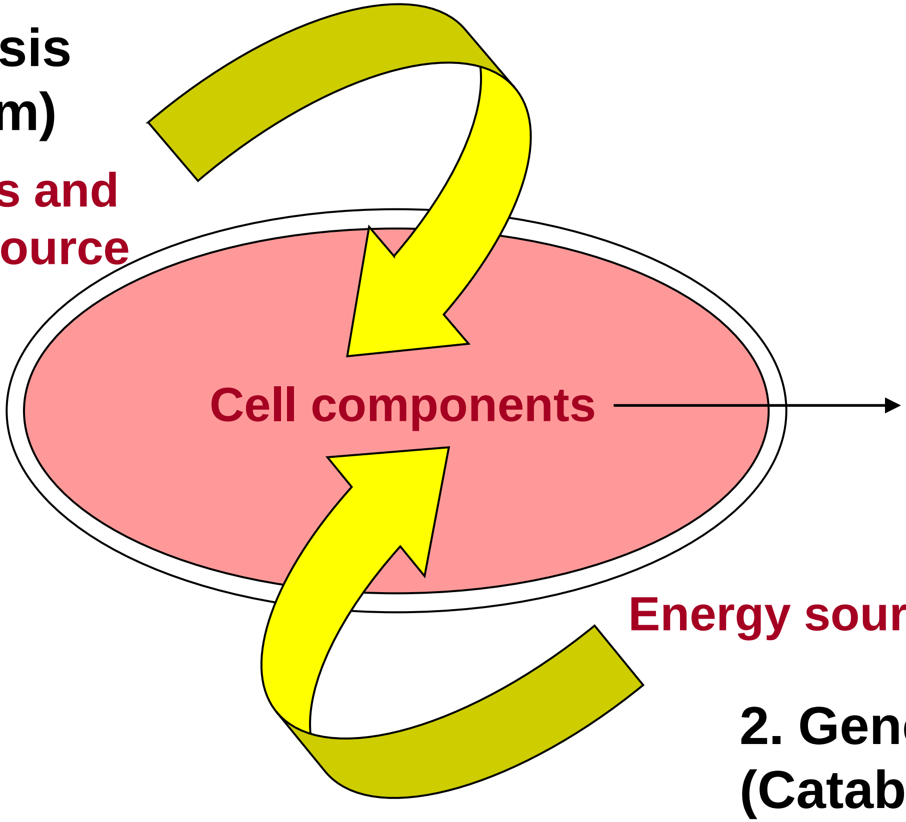
Bacteria in the Environment

Is there anything but microbes ….

Tree of Life





1. Synthesis
(Anabolism)

Nutrients and carbon source

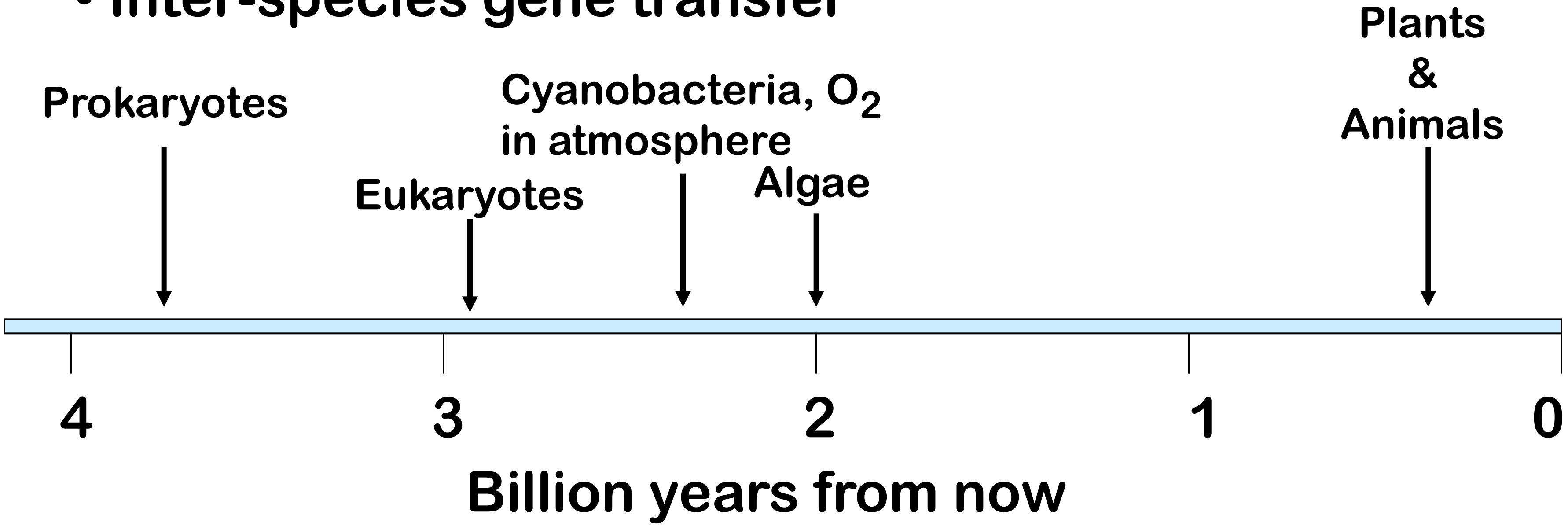
Cell components → **Growth**

Energy source

2. Generate energy
(Catabolism)

Origins of microbial diversity

- **Mo's have much longer evolutionary history**
- **Initially access to all habitats on Earth**
- **Survived the largets span of conditions**
- **Short generation times**
- **Inter-species gene transfer**



Prokaryotes

Eukaryotes

Cyanobacteria, O_2 in atmosphere

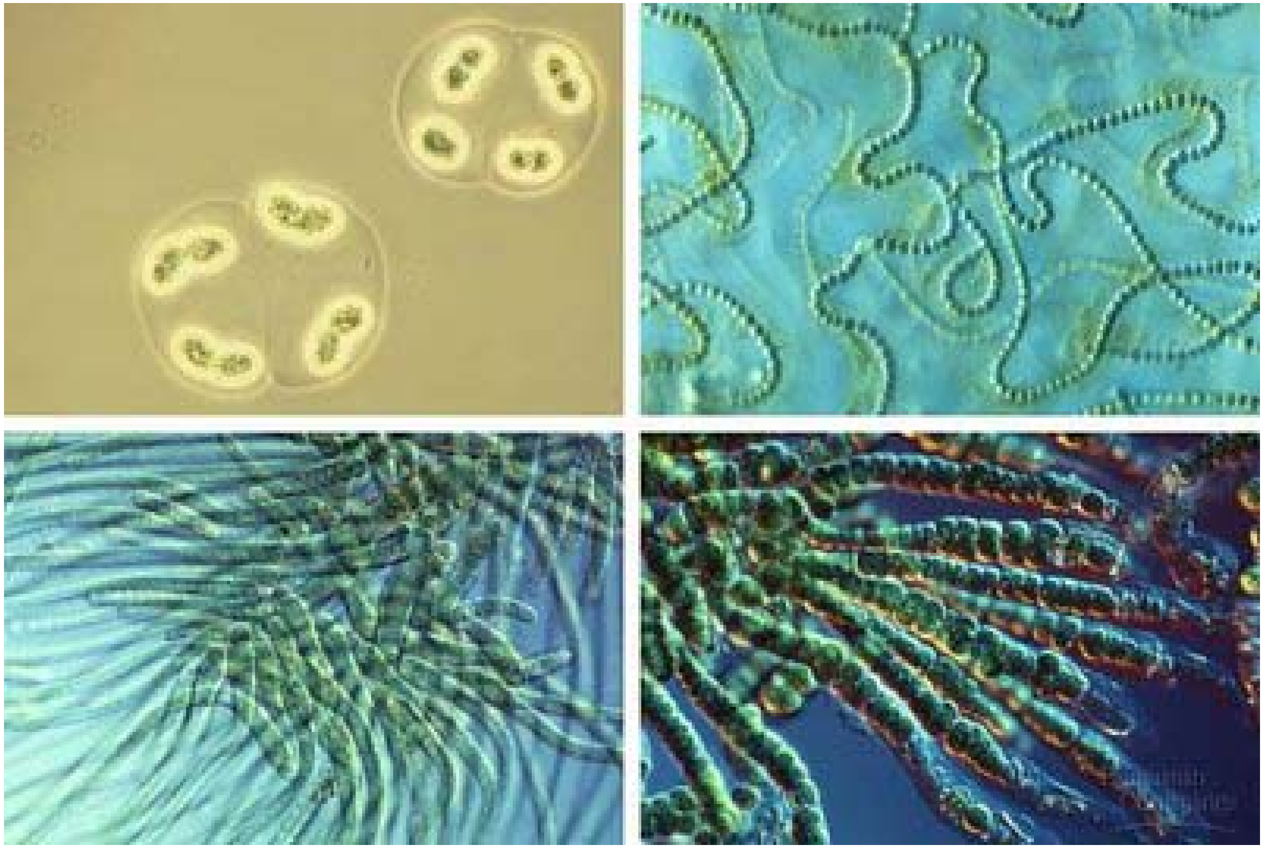
Algae

Plants & Animals

4 3 2 1 0

Billion years from now

Cyanobacteria

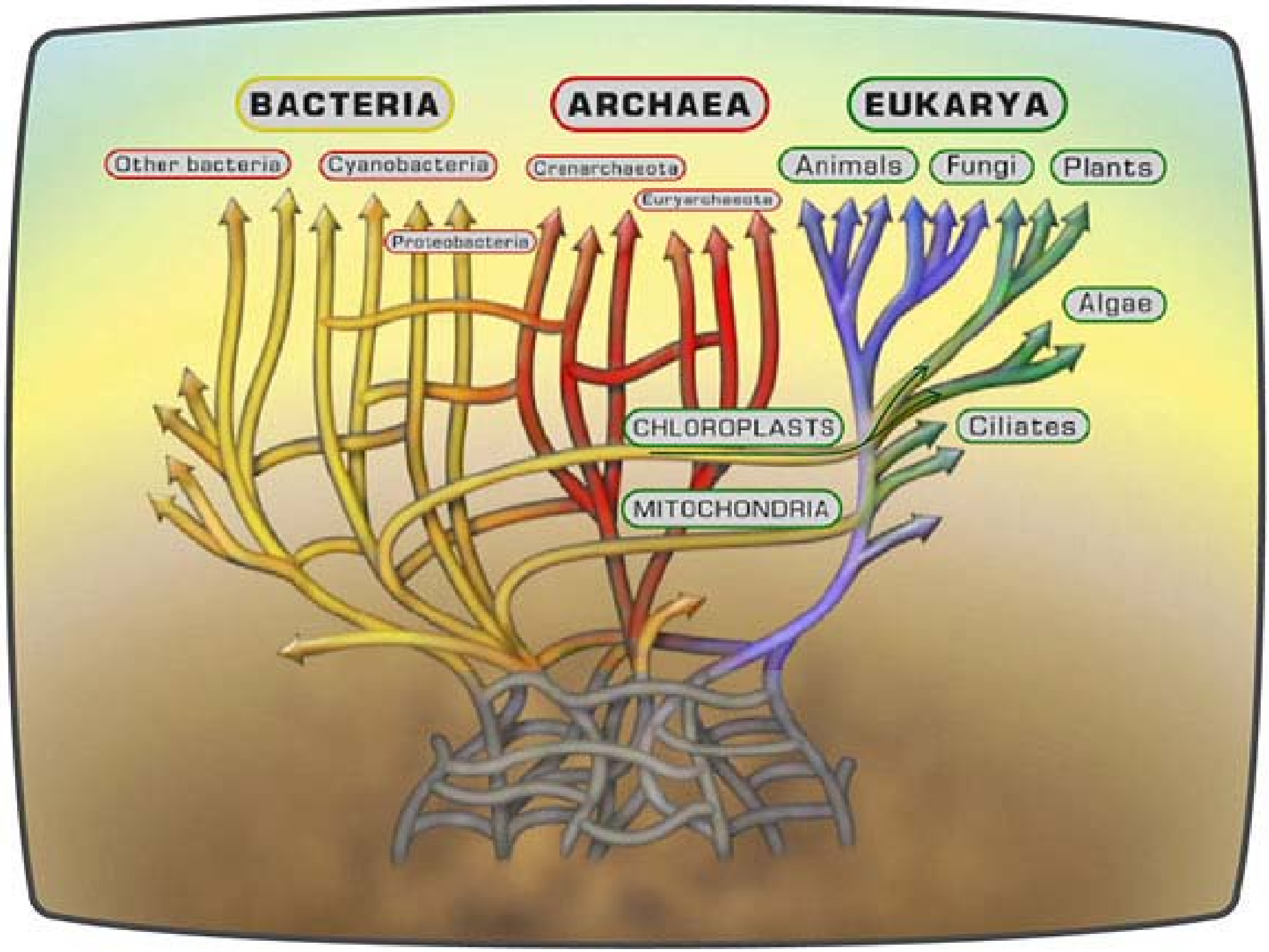


Origins of microbial diversity

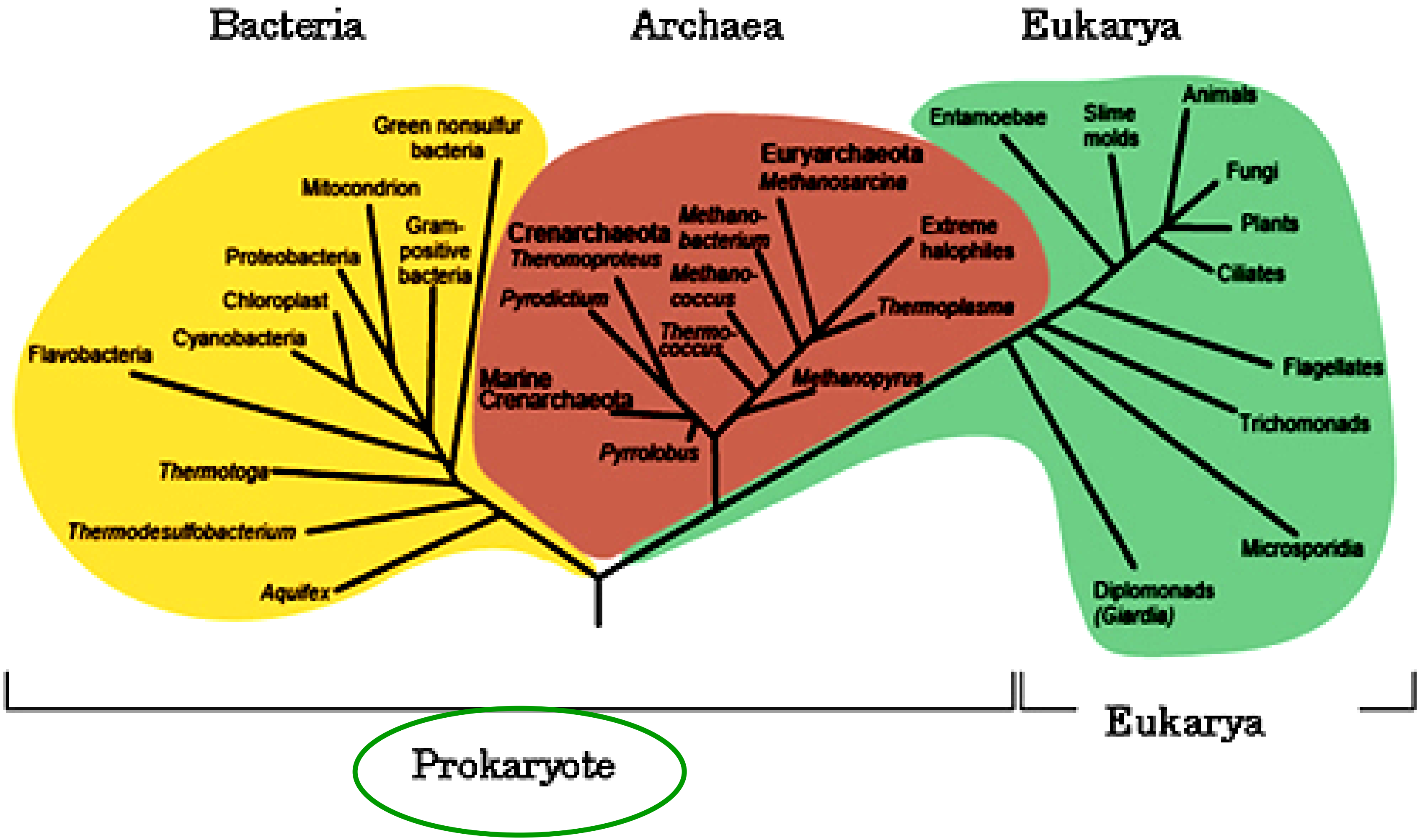
- Introduction of O_2 – major revolution:
  - more oxidized forms
  - formation of ozone layer → terrestrial habitats!
- Mo's altered Earth

- More niches were created → increased diversity

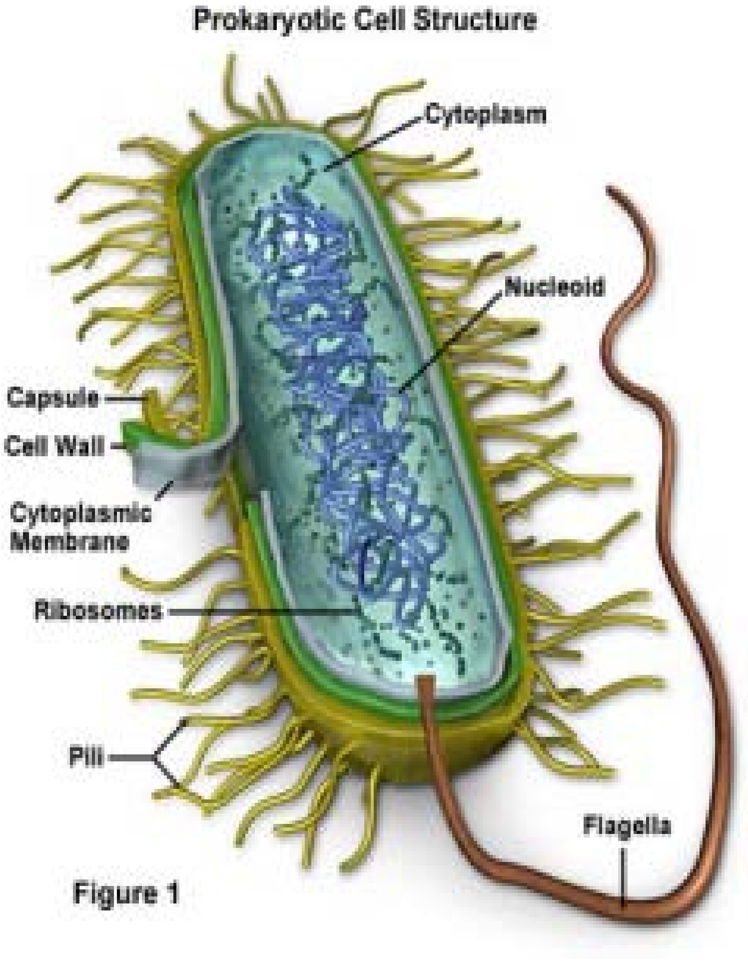
Web of life


BACTERIA
ARCHAEA
EUKARYA
Other bacteria
Cyanobacteria
Crenarchaeota
Euryarchaeota
Animals
Fungi
Plants
Proteobacteria
Algae
CHLOROPLASTS
Ciliates
MITOCHONDRIA

Tree of Life


Bacteria
Archaea
Eukarya
Green nonsulfur bacteria
Mitocondrion
Gram-positive bacteria
Proteobacteria
Chloroplast
Cyanobacteria
Flavobacteria
Thermotoga
Thermodesulfobacterium
Aquifex
Euryarchaeota
Methanosarcina
Crenarchaeota
Theromoproteus
Methano-bacterium
Methano-coccus
Extreme halophiles
Pyrodictium
Thermoplasma
Thermo-coccus
Methanopyrus
Marine Crenarchaeota
Pyrrolobus
Entamoebae
Slime molds
Animals
Fungi
Plants
Ciliates
Flagellates
Trichomonads
Microsporidia
Diplomonads (Giardia)
Prokaryote
Eukarya

Prokaryotes



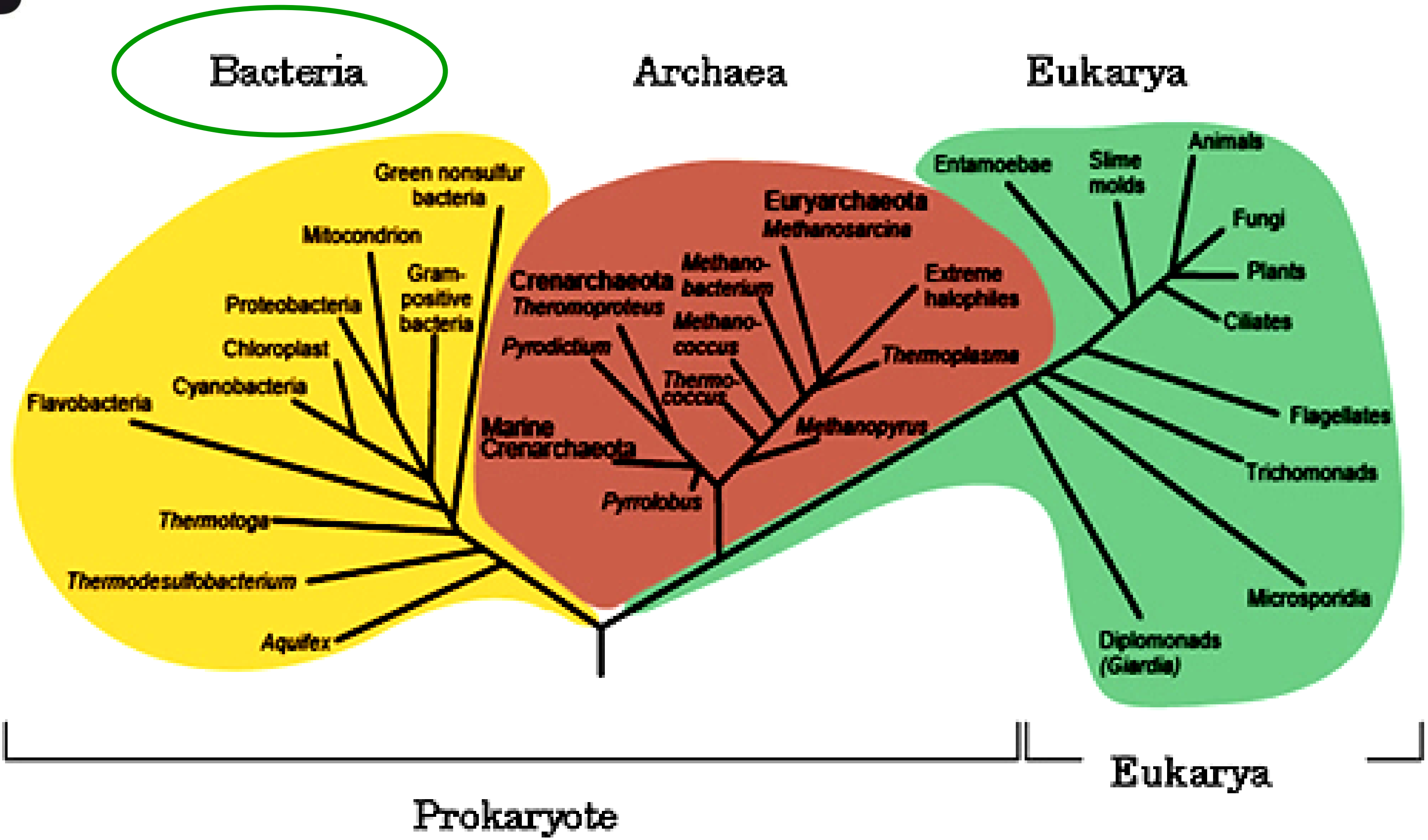
Prokaryotes are single celled organisms that do not have a nucleus, mitochondria or any other membrane bound organelles.

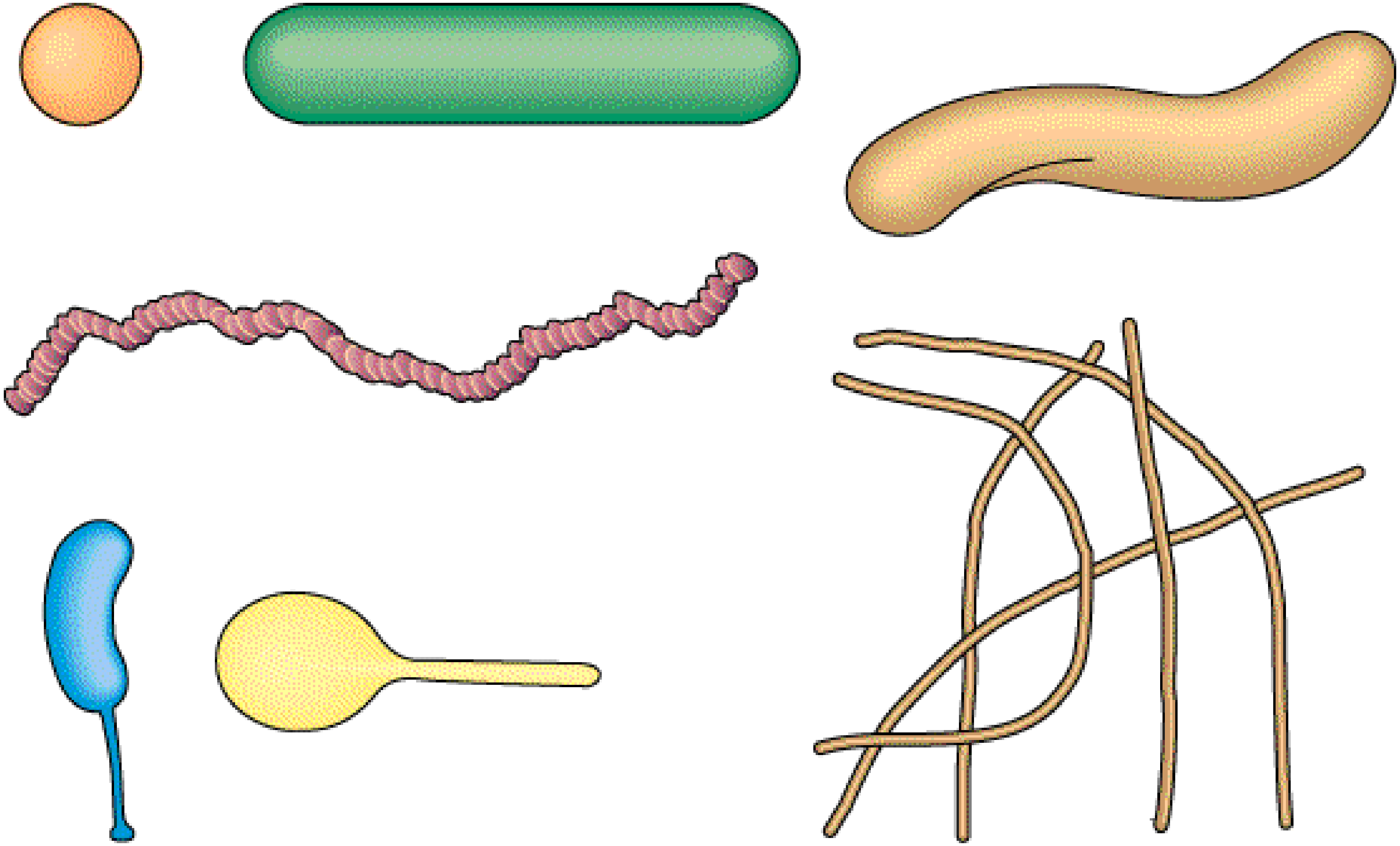
Instead everything is openly accessible within the cell, some free floating, some bound to the walls of the cell membrane,

Prokaryotes come in two sorts, *Archaea* and *Bacteria*.

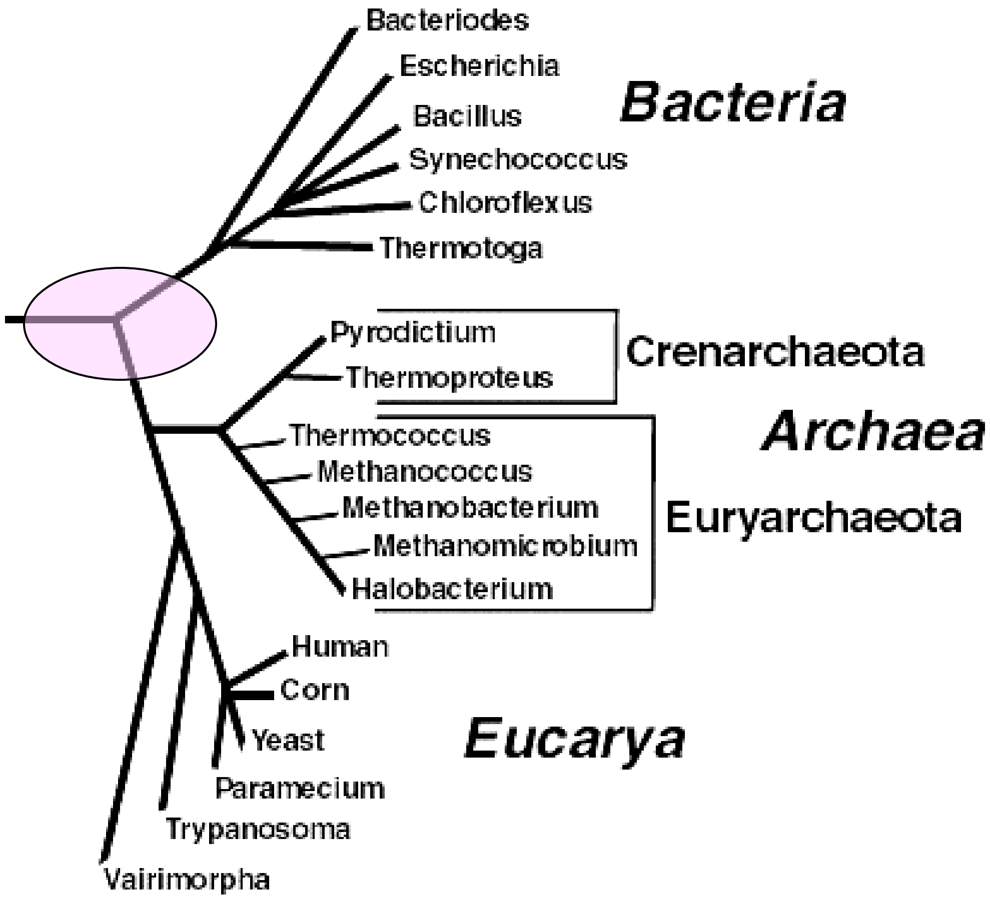
As different, if not more different, from each other, than they are from protozoans, fungi, plants and us.

Tree of Life


Bacteria
Archaea
Eukarya
Green nonsulfur bacteria
Mitocondrion
Gram-positive bacteria
Proteobacteria
Chloroplast
Cyanobacteria
Flavobacteria
Thermotoga
Thermodesulfobacterium
Aquifex
Crenarchaeota
Theromoproteus
Pyrodictium
Marine Crenarchaeota
Pyrolobus
Euryarchaeota
Methanosarcina
Methanobacterium
Methanococcus
Thermococcus
Methanopyrus
Extreme halophiles
Thermoplasma
Entamoebae
Slime molds
Animals
Fungi
Plants
Ciliates
Flagellates
Trichomonads
Microsporidia
Diplomonads (Giardia)
Prokaryote
Eukarya



Systematics



Domain
↓
Class
↓
Order
↓
Family
↓
Genera
↓
Species

What is a species?

”A collection of strains that all share the same major properties but differ in one or more significant properties from other collections of strains”

Old species differentiation relied on phenotype.

The species concept: >70% homology in genome
>97% or 99% homology in entire16S rRNA gene

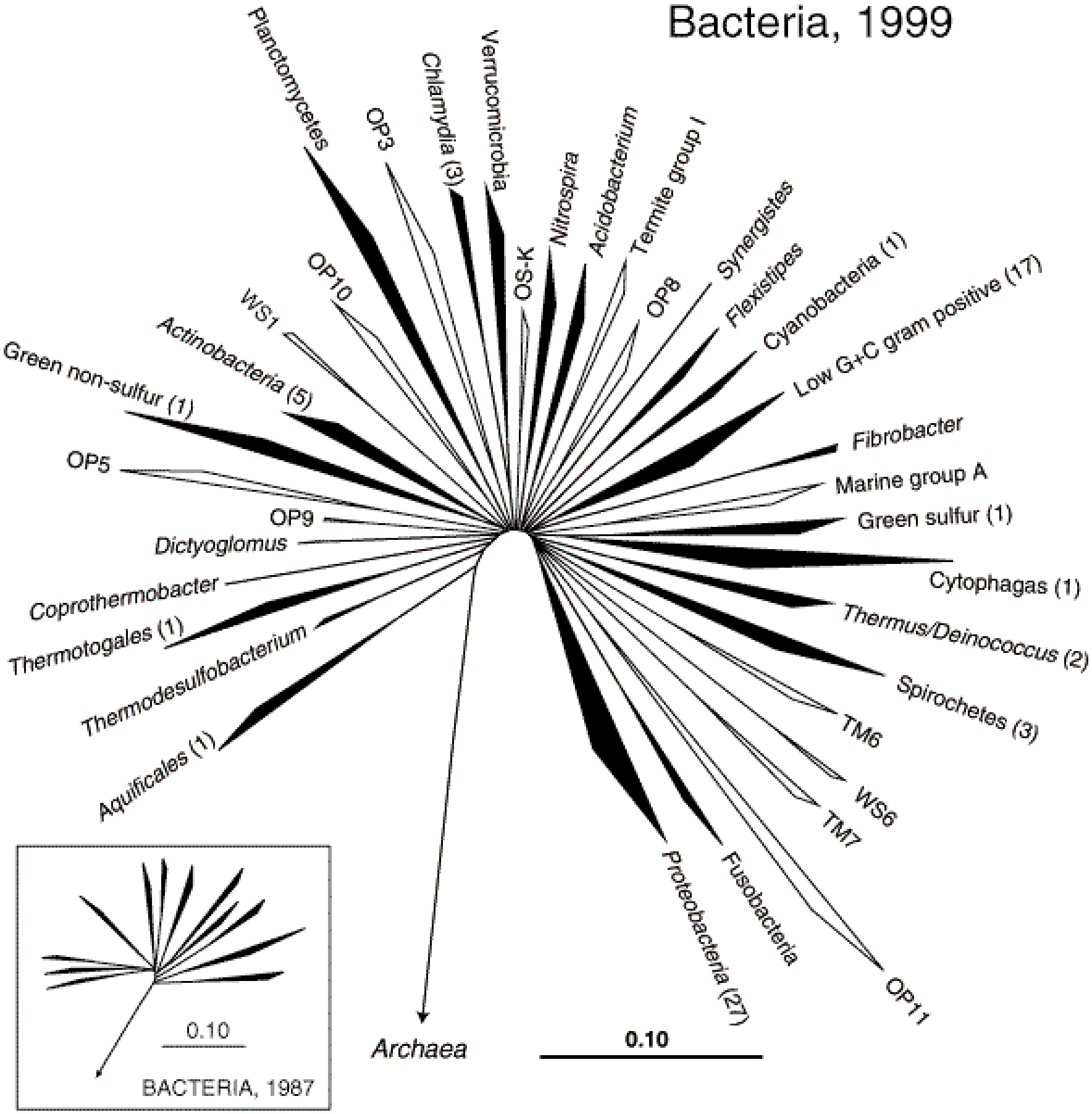
The term genome often used instead of species.

BACTERIA

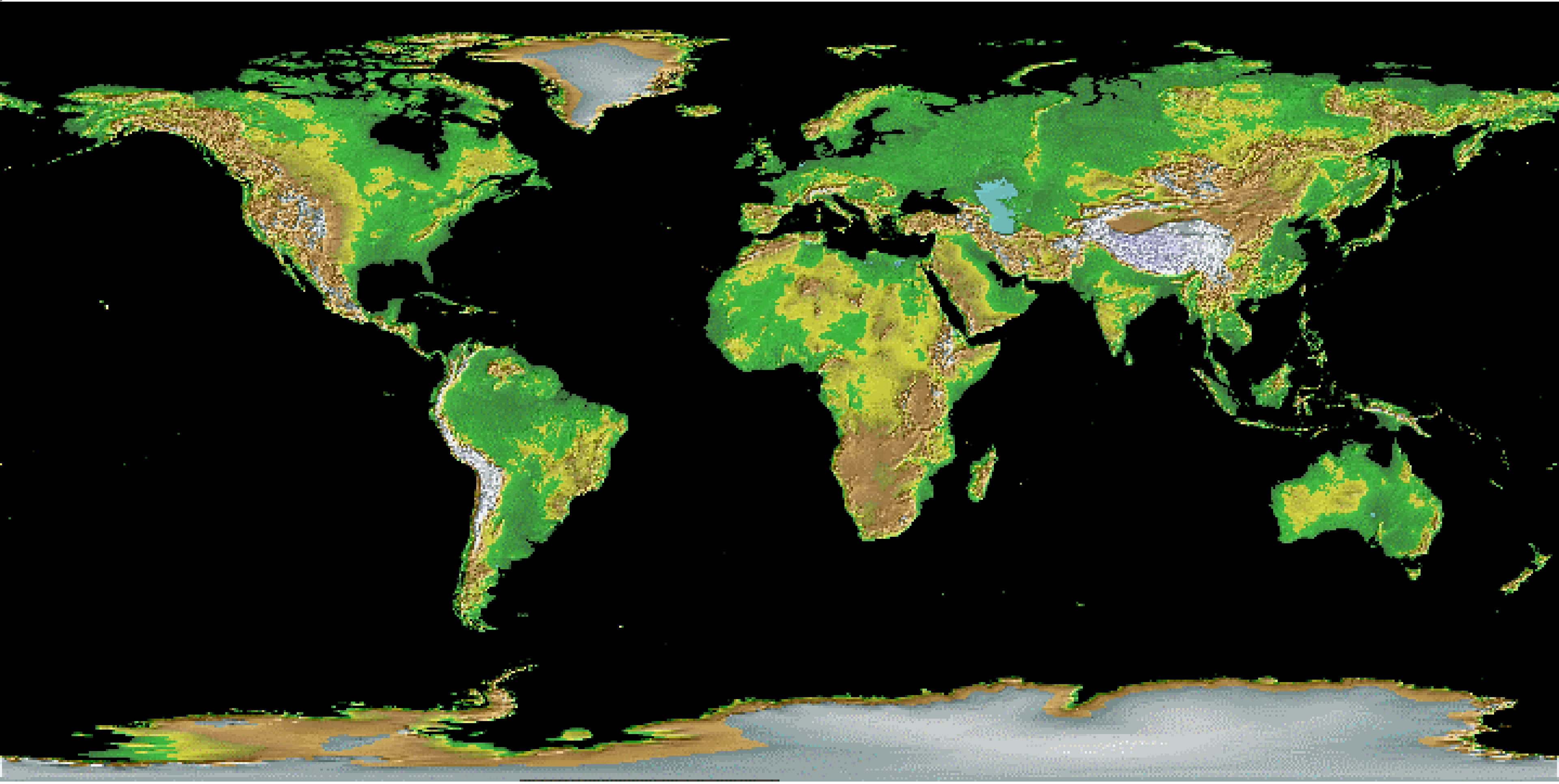
1987: 12 phyla

1999: 36 phyla

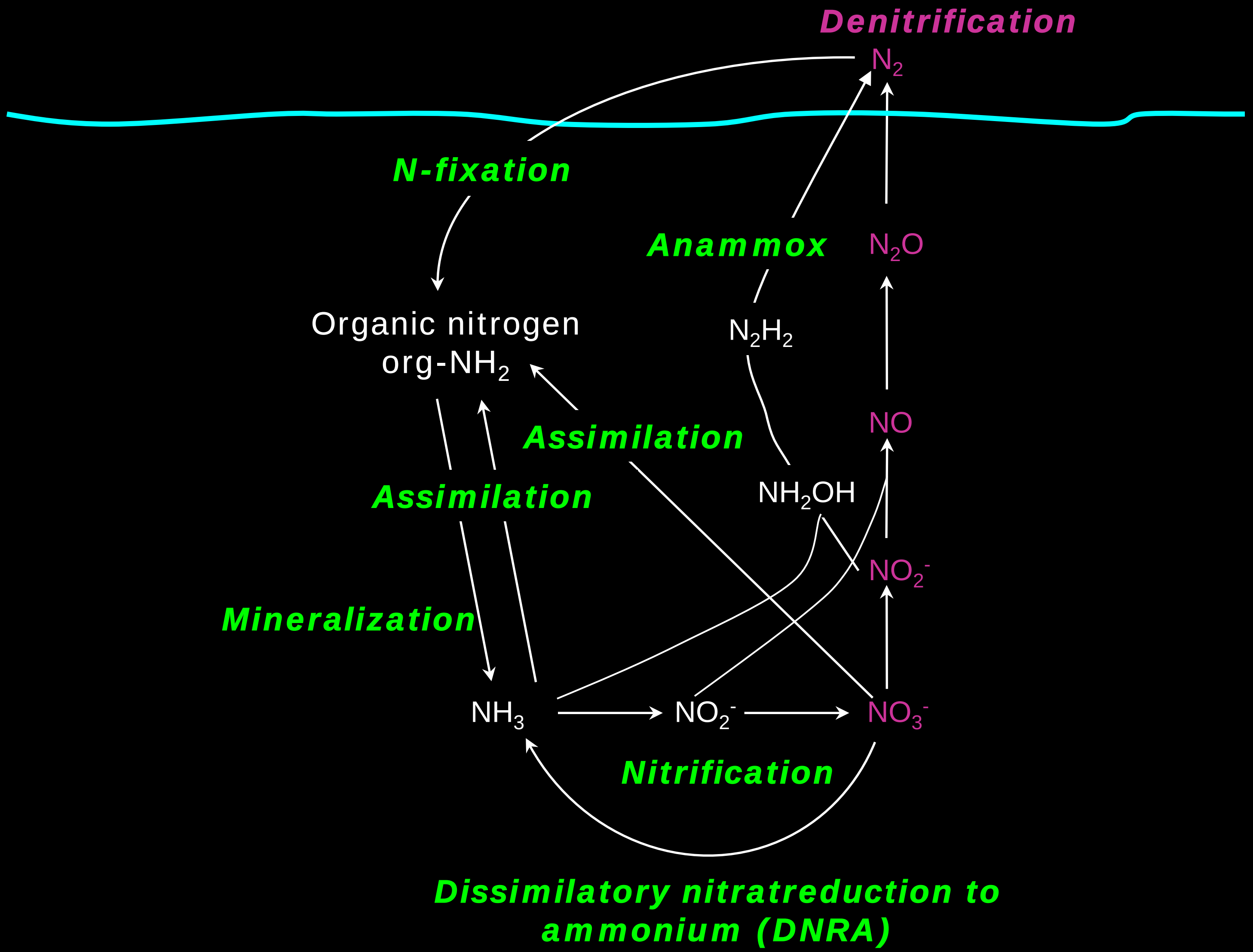
2008 40 phyla



Global patterns



Example from the N-cycle



Denitrification

N_2

N-fixation

Anammox

N_2O

Organic nitrogen
org-NH_2

N_2H_2

Assimilation

NO

Assimilation

NH_2OH

NO_2^-

Mineralization

NH_3

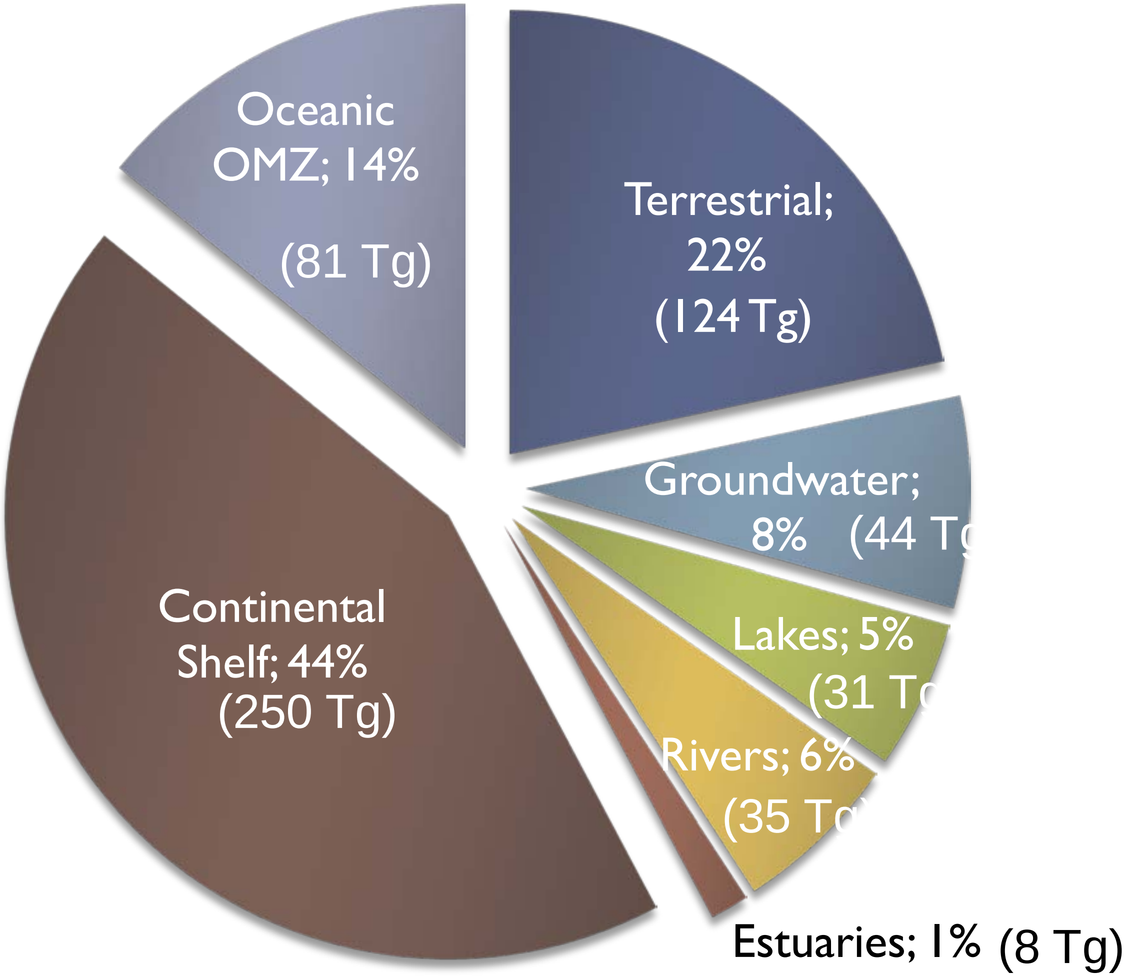
NO_2^-

NO_3^-

Nitrification

Dissimilatory nitratreduction to ammonium (DNRA)

Denitrification in ecosystems

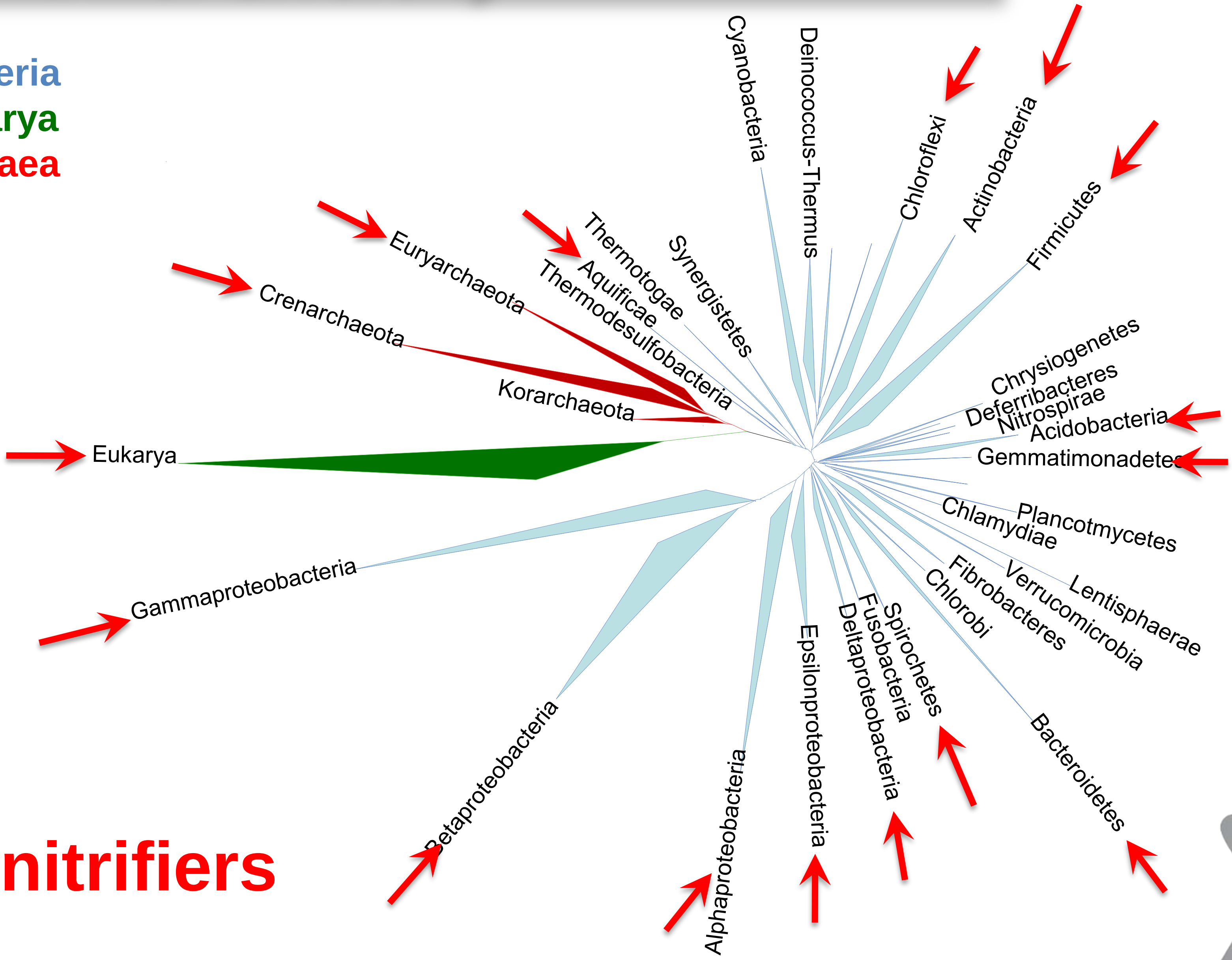


Annual N exported to atmosphere via denitrification

(Seitzinge

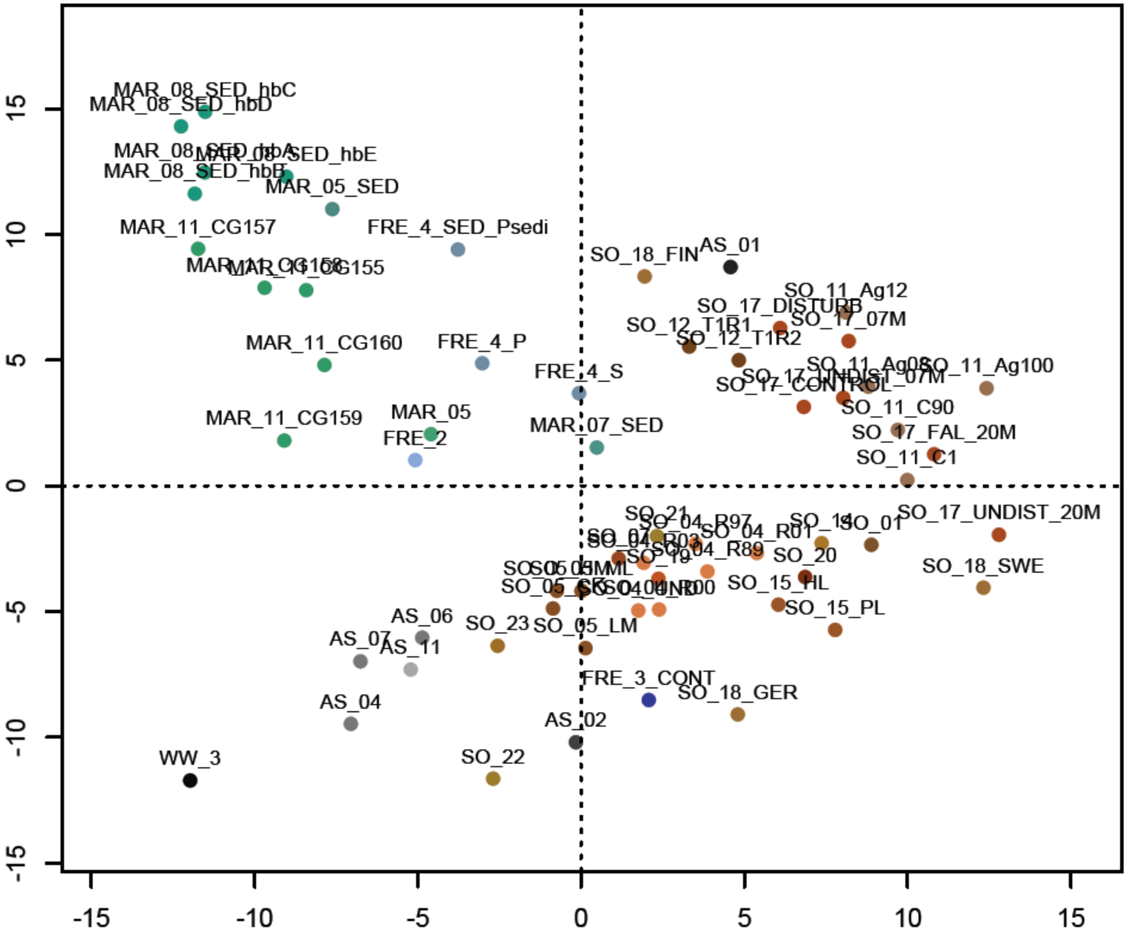
Denitrifier diversity

Bacteria
Eukarya
Archaea

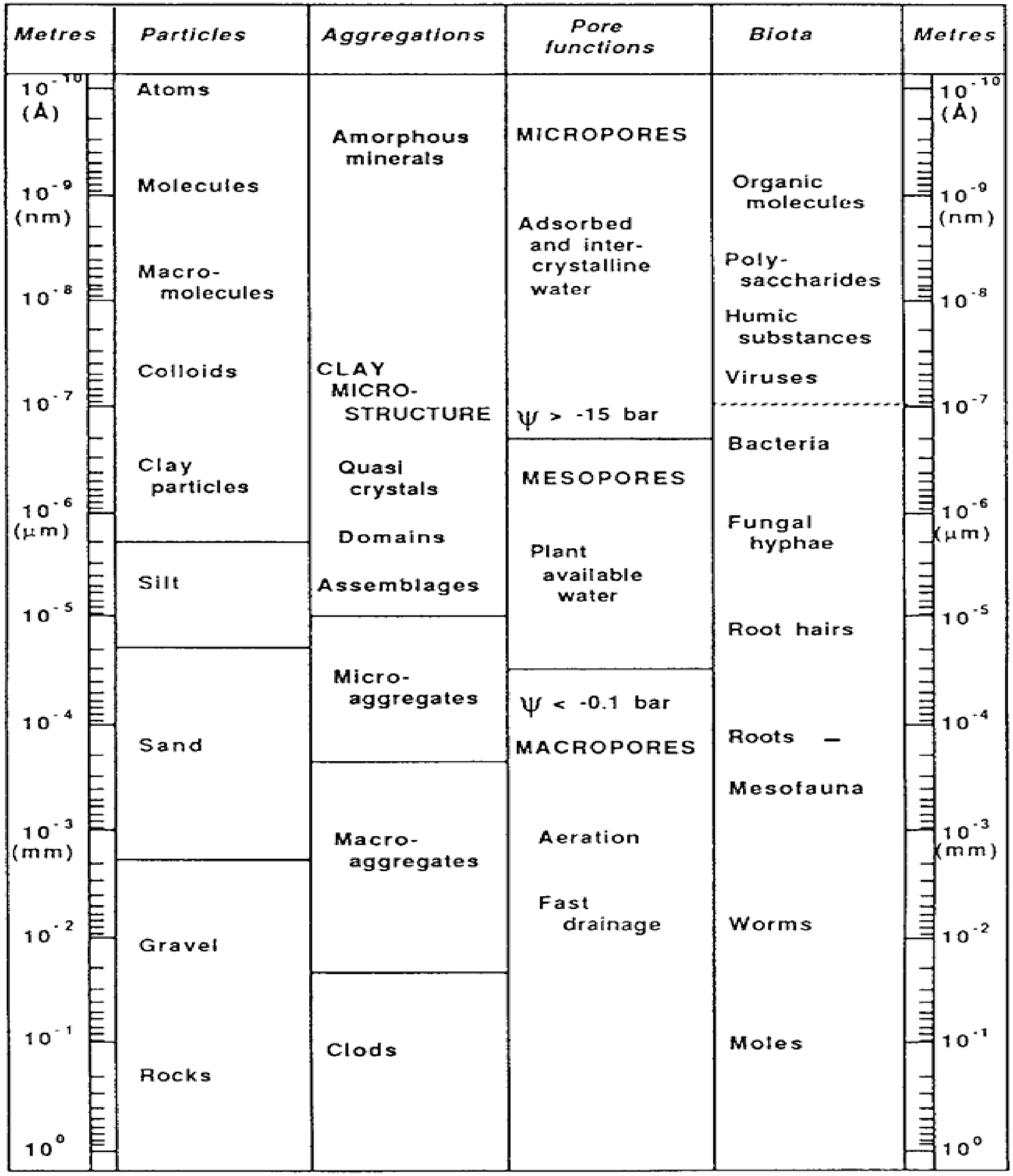


Denitrifiers

Salinity is a barrier



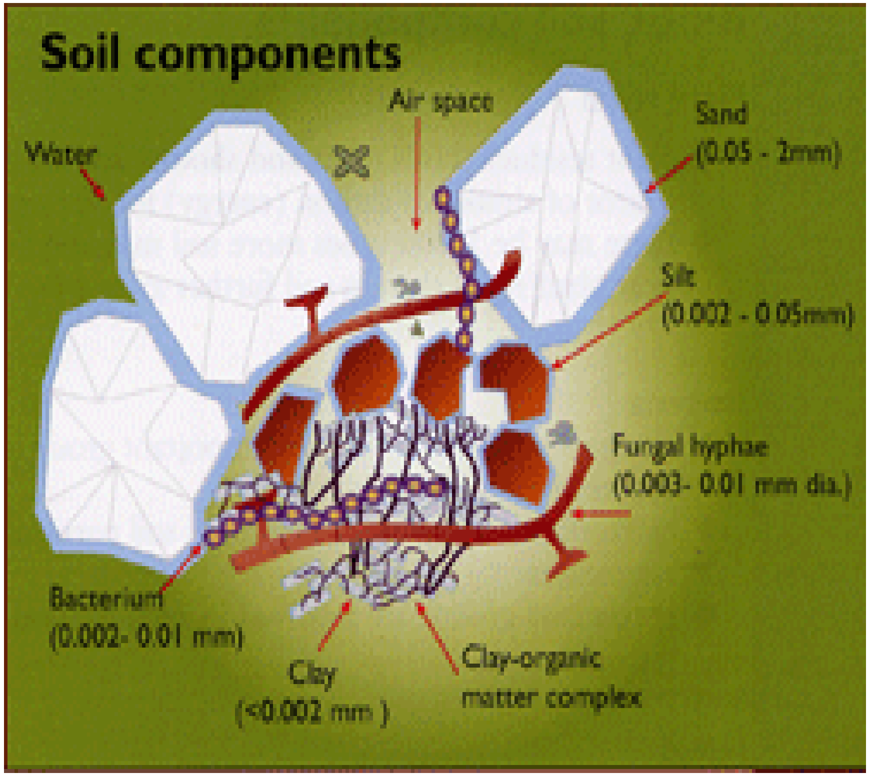
Scale in Soil Structure



Metres	Particles	Aggregations	Pore functions	Biota	Metres
10^{-10} (Å)	Atoms				10^{-10} (Å)
		Amorphous minerals	MICROPORES		
10^{-9} (nm)	Molecules			Organic molecules	10^{-9} (nm)
			Adsorbed and inter-crystalline water	Poly-saccharides	
10^{-8}	Macro-molecules				10^{-8}
	Colloids			Humic substances	
10^{-7}		CLAY MICRO-STRUCTURE	$\psi > -15$ bar	Viruses	10^{-7}
	Clay particles	Quasi crystals	MESOPORES	Bacteria	
10^{-6} (μm)		Domains		Fungal hyphae	10^{-6} (μm)
	Silt	Assemblages	Plant available water		
10^{-5}				Root hairs	10^{-5}
		Micro-aggregates			
10^{-4}	Sand		$\psi < -0.1$ bar MACROPORES	Roots –	10^{-4}
				Mesofauna	
10^{-3} (mm)		Macro-aggregates	Aeration		10^{-3} (mm)
10^{-2}	Gravel		Fast drainage	Worms	10^{-2}
10^{-1}		Clods		Moles	10^{-1}
	Rocks				
10^{0}					10^{0}

Scale in soil structure (Waters & Oades, 1991)

Soil as a habitat

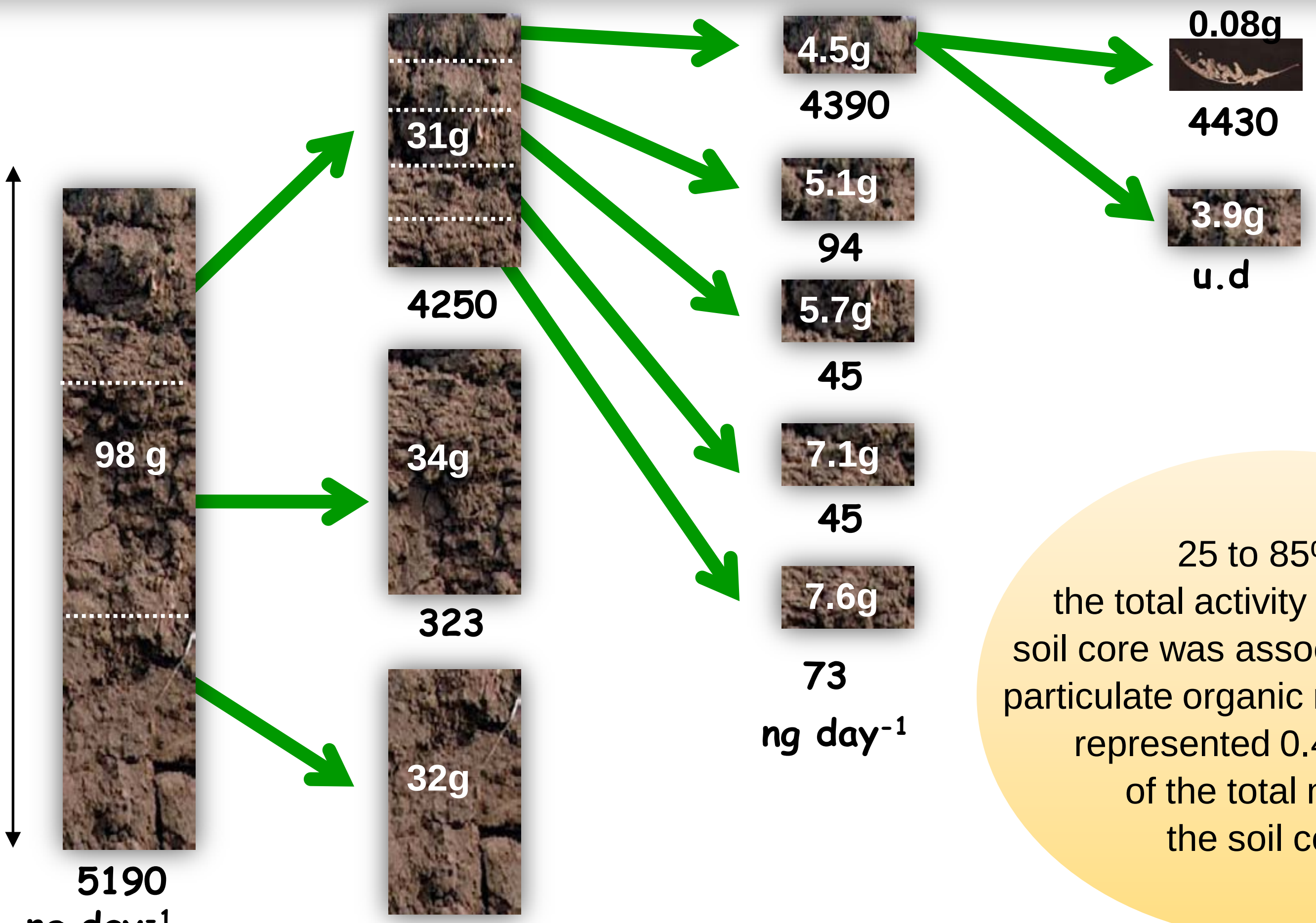


Clay soil area: 100 m^2/g

Bacteria: 10^8/g soil

Occupy 0.1-0.3% of the protective pore space

Hotspot of activity



Soil core
15 cm

98 g

5190
ng day^{-1}

31g

4250

34g

323

32g

499
ng day^{-1}

4.5g

4390

5.1g

94

5.7g

45

7.1g

45

7.6g

73

ng day^{-1}

0.08g

4430

3.9g

u.d

5190
100%

5070
98%

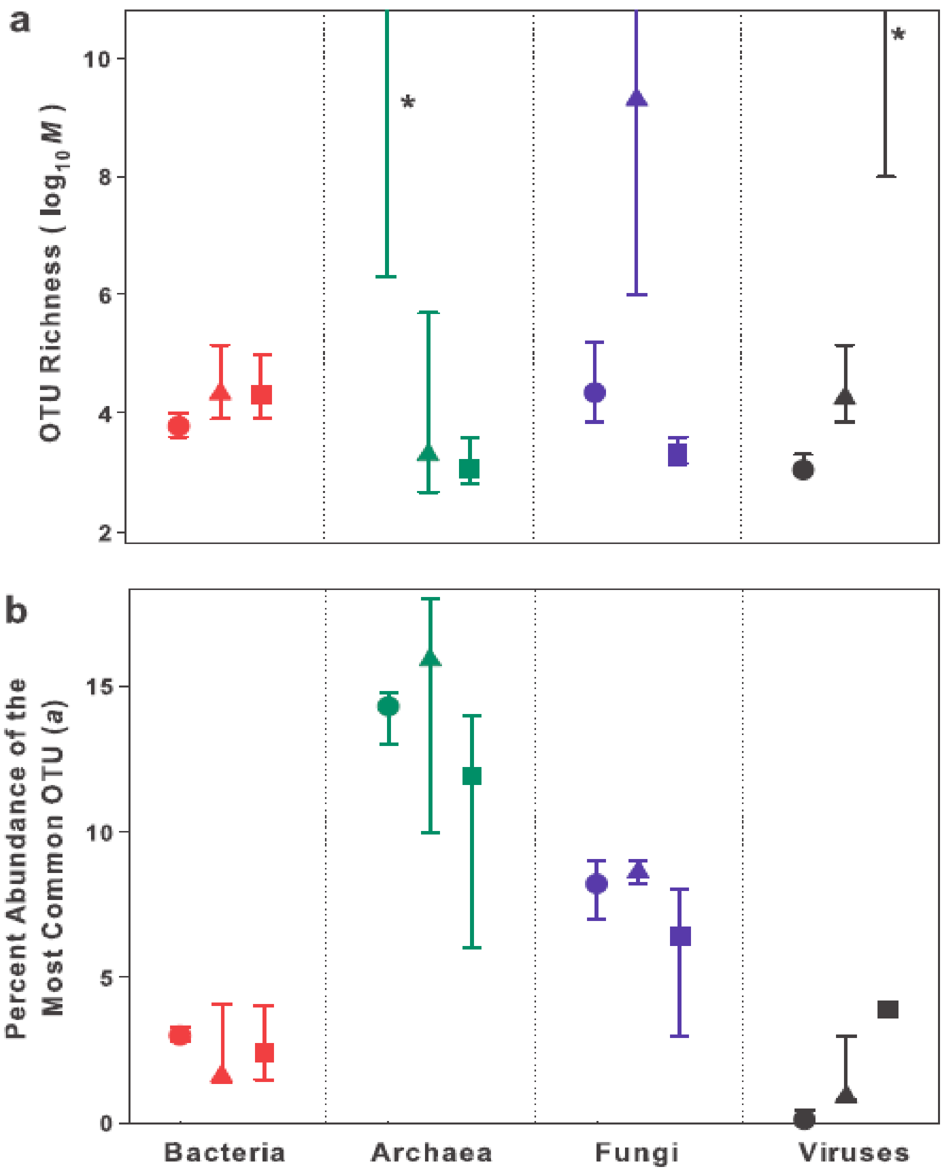
4660
90%

25 to 85% of
the total activity of the intact
soil core was associated with the
particulate organic material, which
represented 0.4 to 0.08%
of the total mass of
the soil cores.

Parkin. 1987.
Soil Sci. Soc. Am. J.
51:1194-1199

Soil microbial diversity

a) Estimation of OTU richness (Operational Taxonomic Unit)

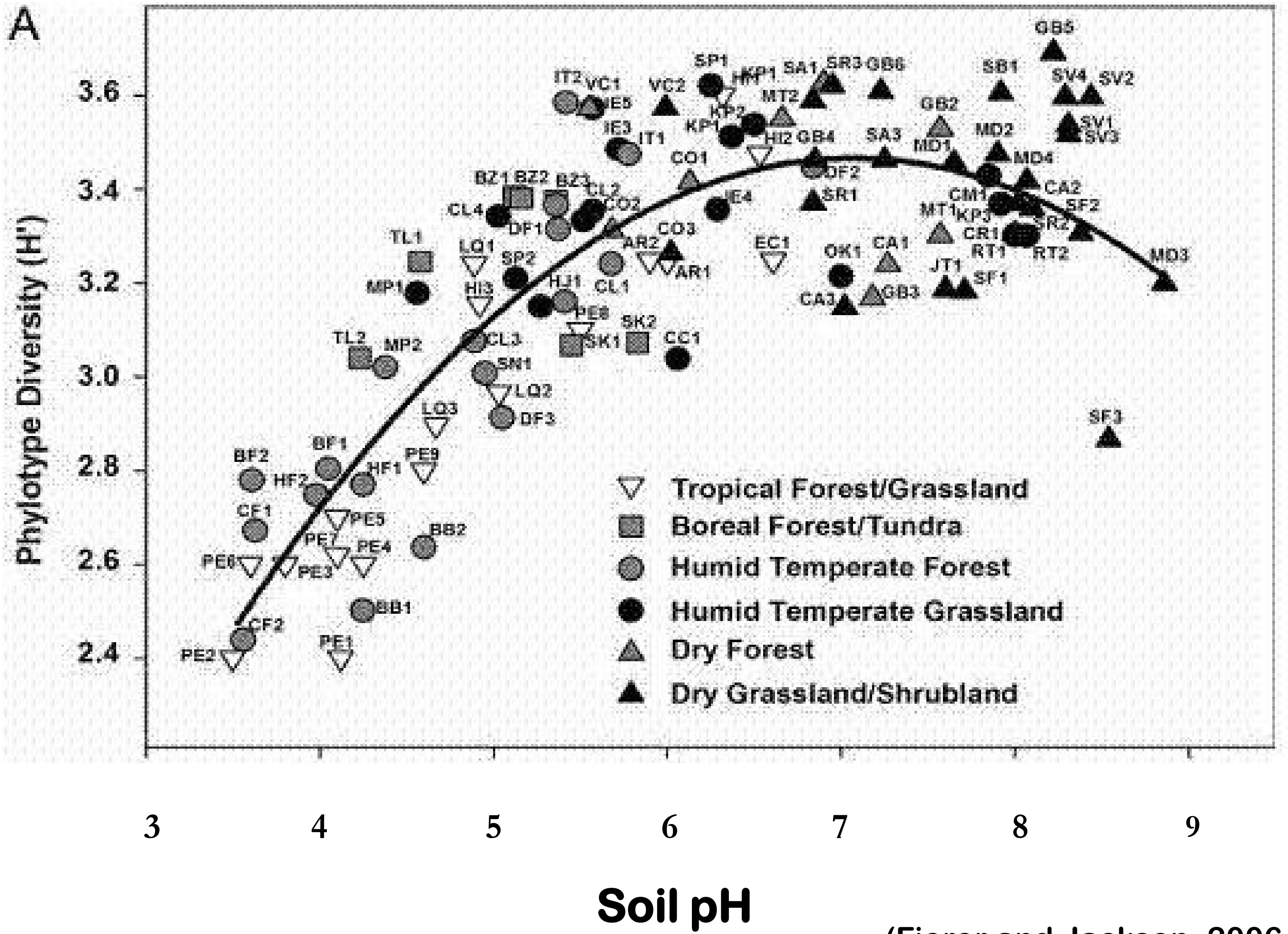


b) Abundance of the most common OTU

● desert
▲ prairie
■ rainforest

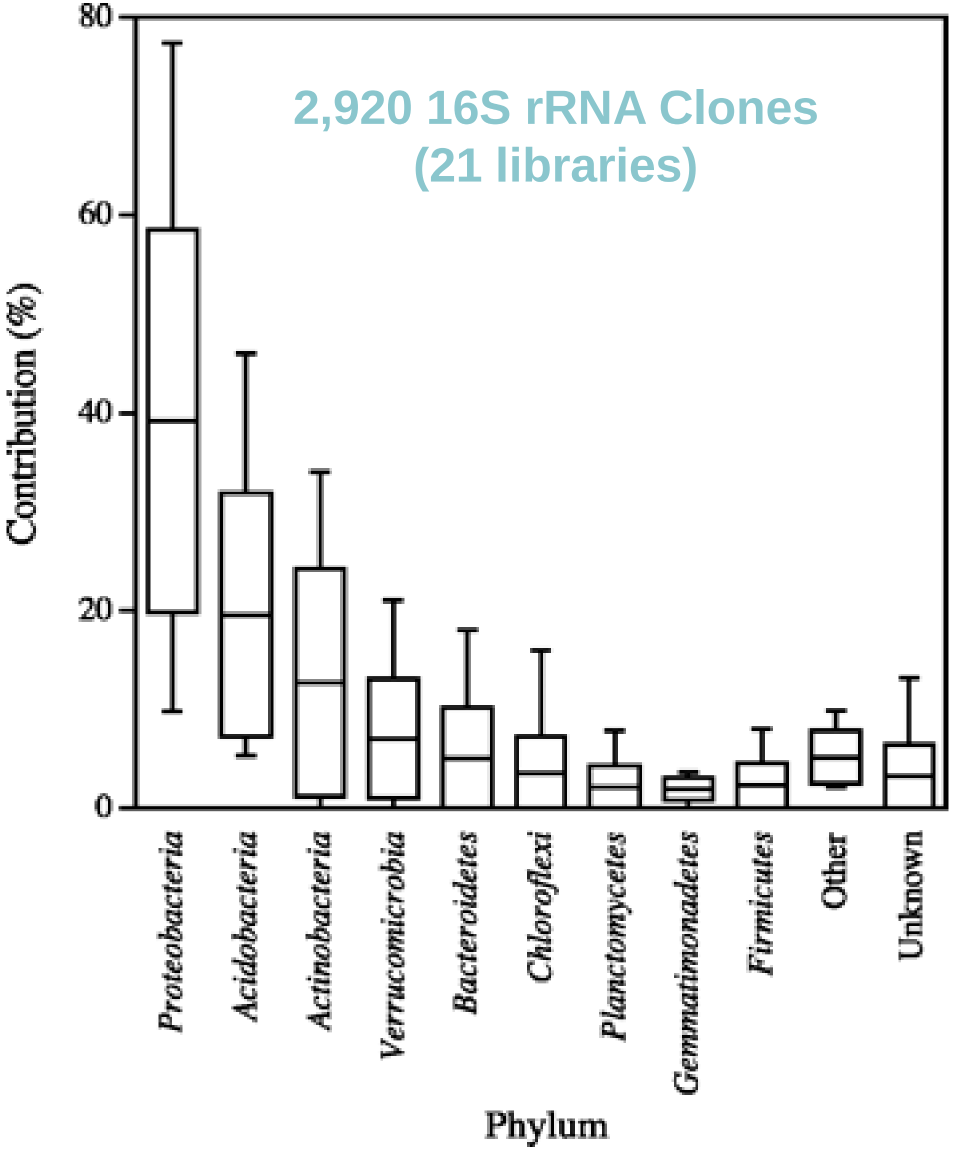
(Fierer et al., 2007)

pH – strong driver for bacterial community composition in soil



(Fierer and Jackson, 2006 PNAS)

Dominant bacterial phyla in soil

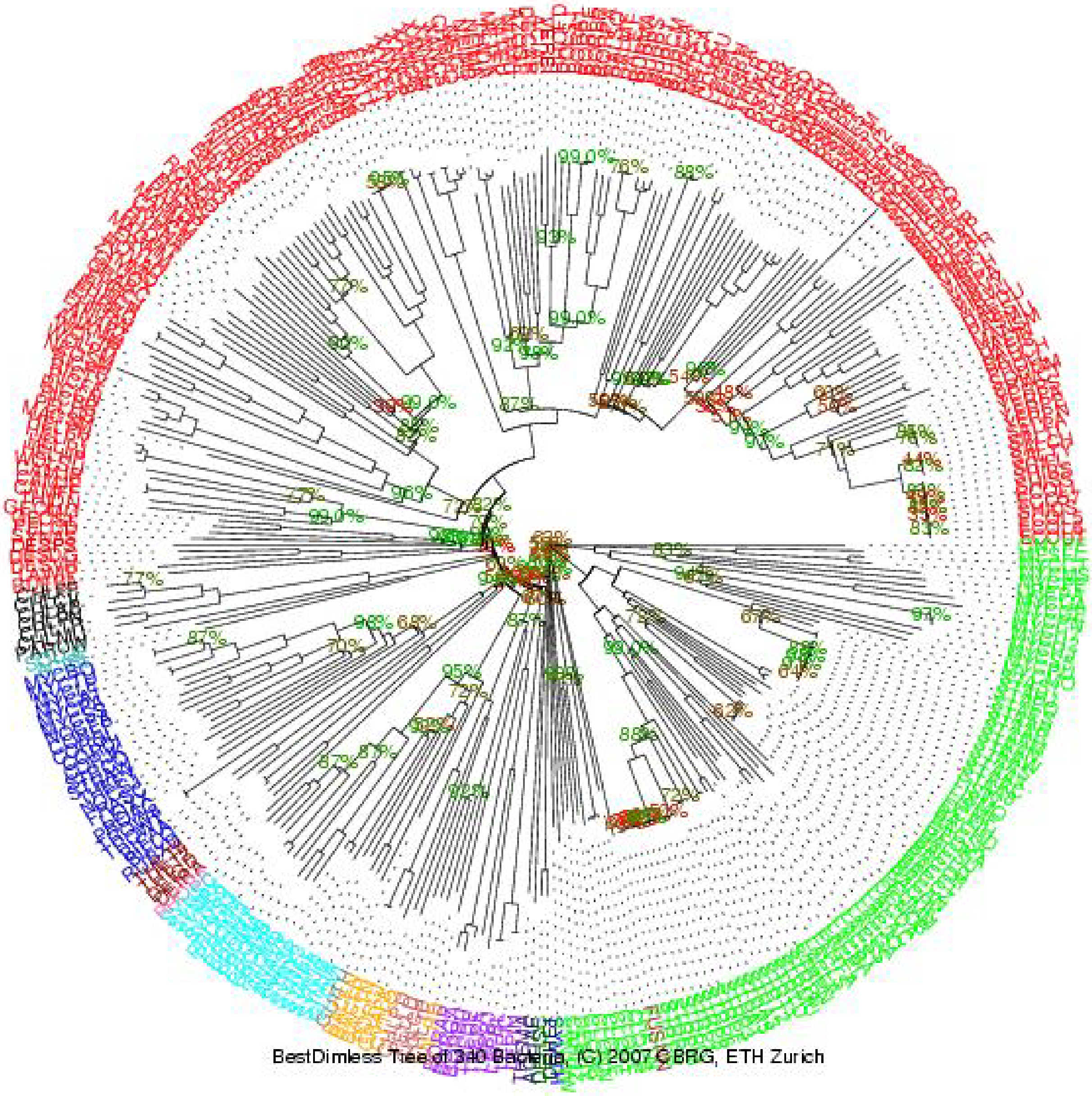


Ranked genomes:

Proteobacteria
Firmicutes
Actinobacteria
Cyanobacteria
Spirochaetes
Bacteroidetes

(Janssen, AEM 2006)

All Bacterial genomes, 2007, 340 species



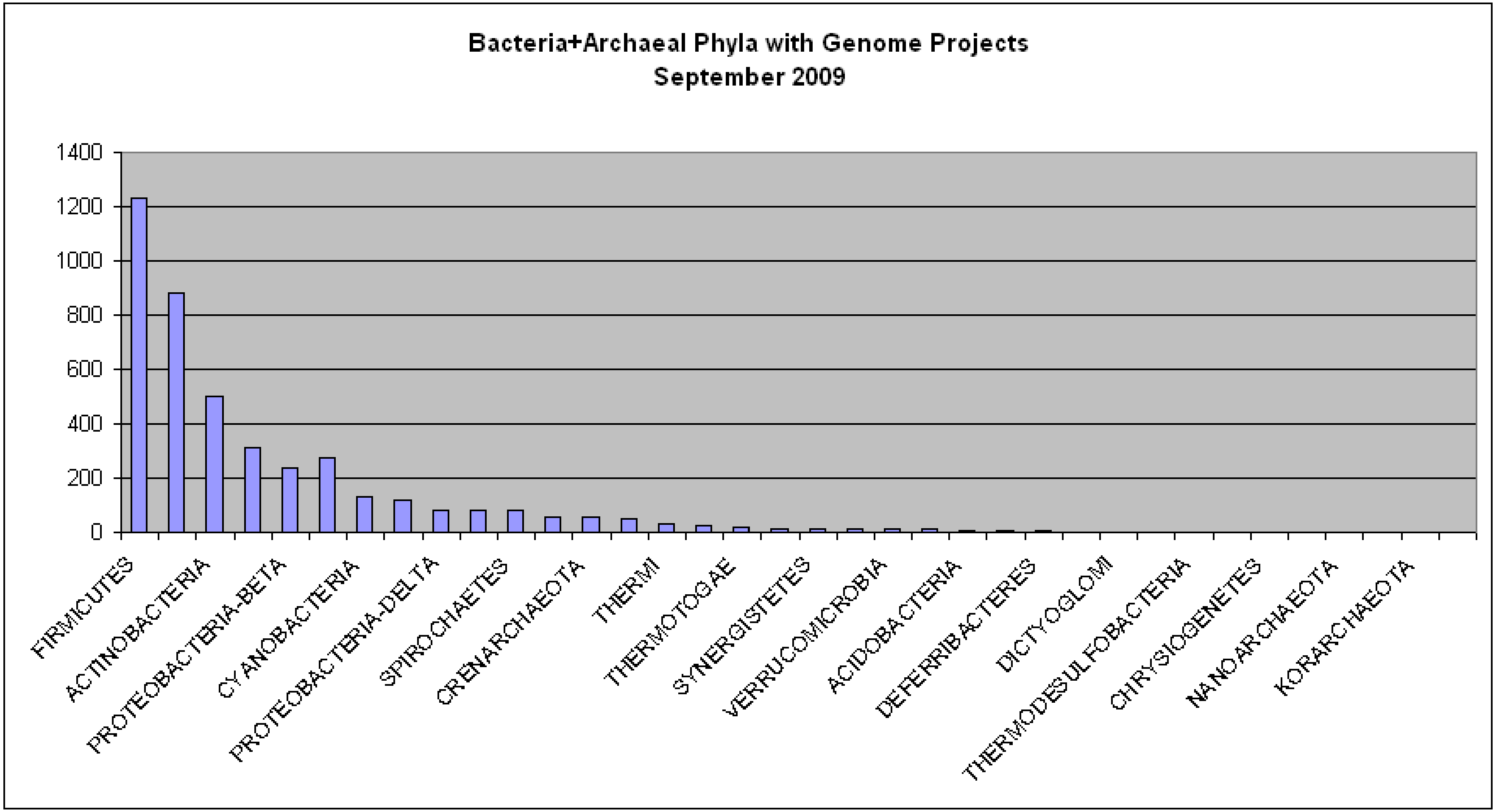
BestDimless Tree of 340 Bacteria, (C) 2007 CBRG, ETH Zurich

Color code:

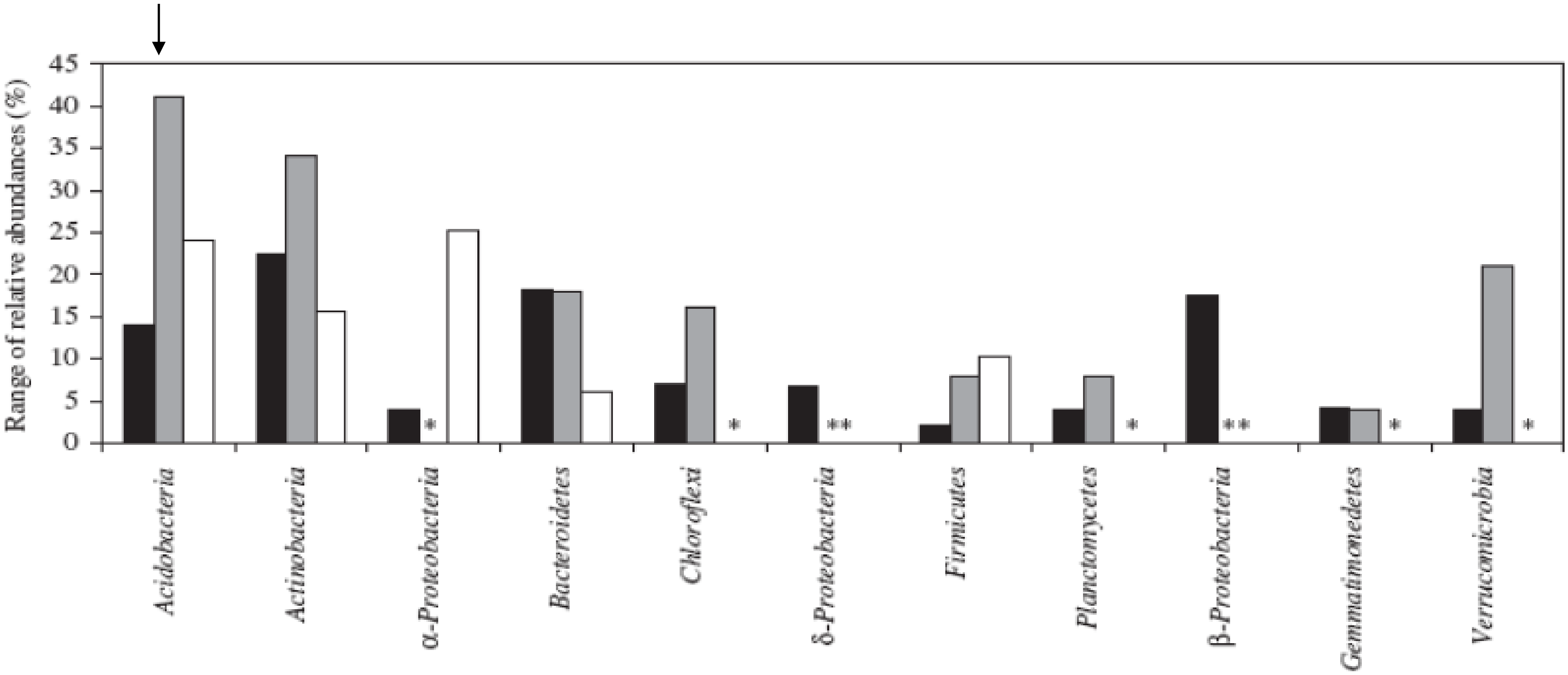
Proteobacteria
Firmicutes
Actinobacteria
Cyanobacteria
Spirochaetes
Bacteroidetes

Chlamydiae
Chlorobi
Deinococcus-Thermus
Acidobacteria
Chloroflexi
Aquificae
Fusobacteria
Planctomycetes
Thermotogales

Genome projects



Comparison between studies



■ 5 clone libraries (Youssef) ▨ 21 clone libraries (Janssen) □ qPCR (Fierer)

(Youssef et al. 2009 *ISMEJ*)

Taxa distribution in terrestrial ecosystems

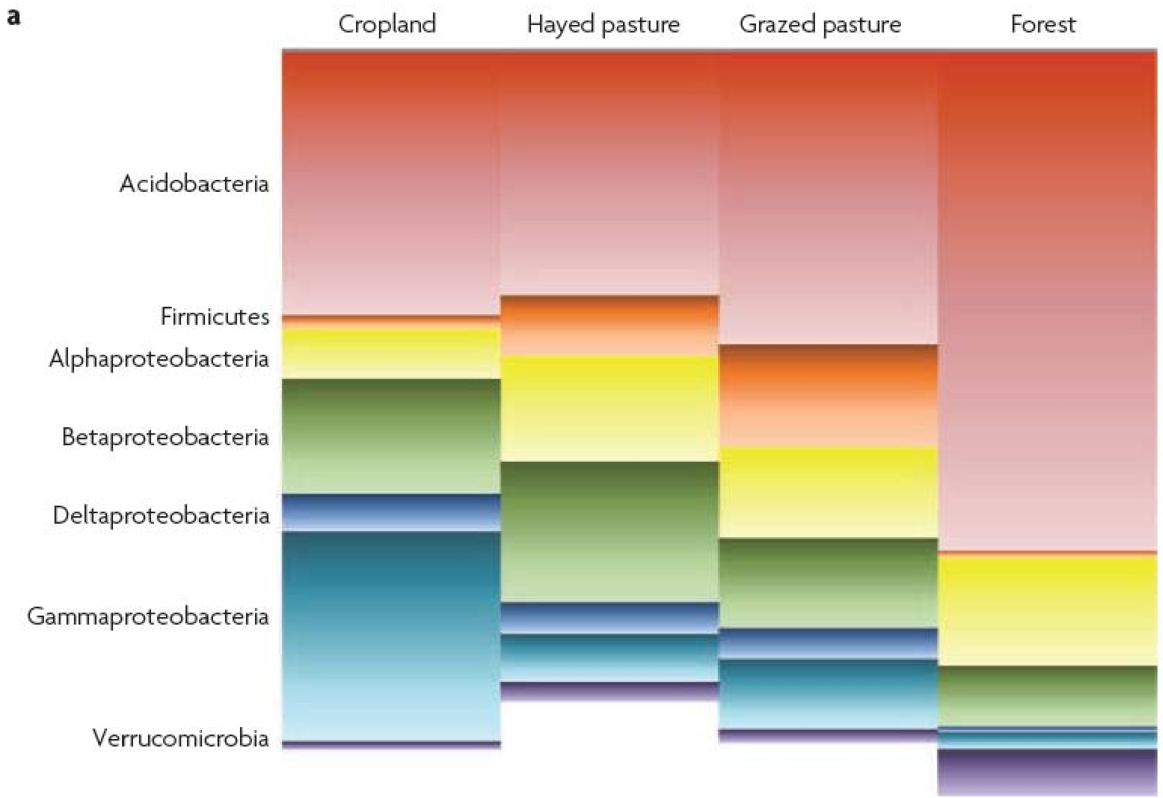
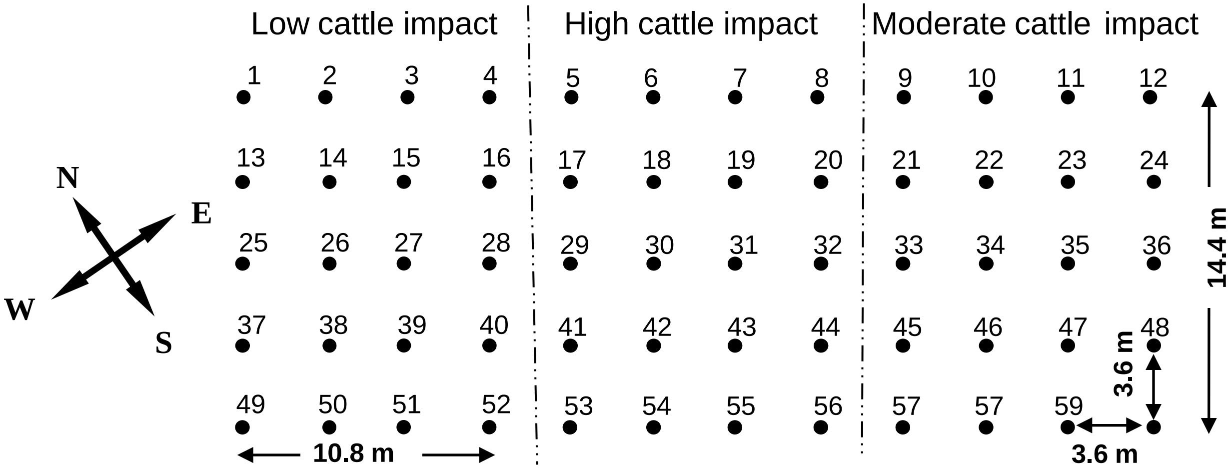


Figure 2 | **Niche differentiation at the phylum and class levels. a | The relative abundance of bacterial** taxa in bacterial communities in soil under different land management regimes (Jangid et al. 2008, SBB).

(Philippot et al 2009 NRM)

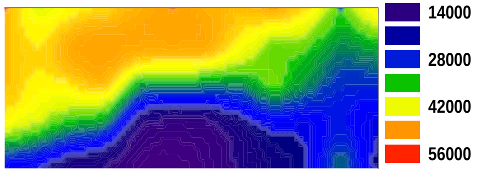
Do the dominant bacterial groups display spatial distribution patterns?



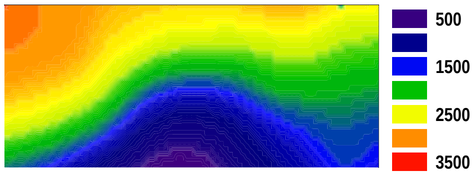
Abundance

Quantification of taxa at phylum or class level

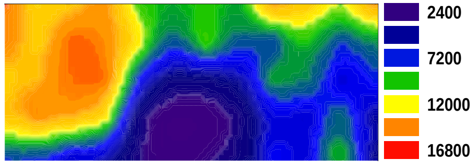
Total bacteria



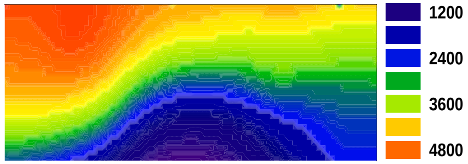
Acidobacteria



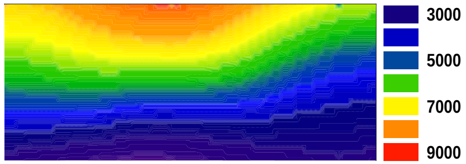
Actinobacteria



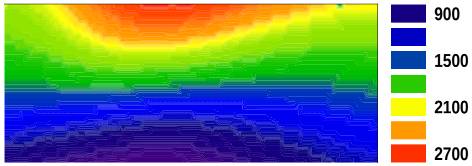
α-Proteobacteria



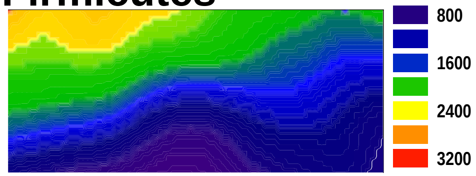
Bacteroidetes



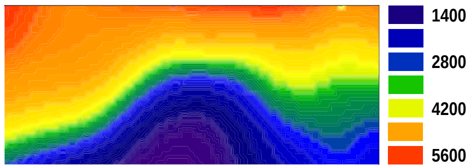
β-Proteobacteria



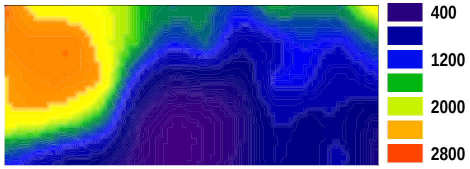
Firmicutes

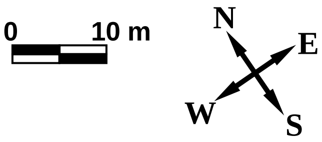


Gemmatimonadetes



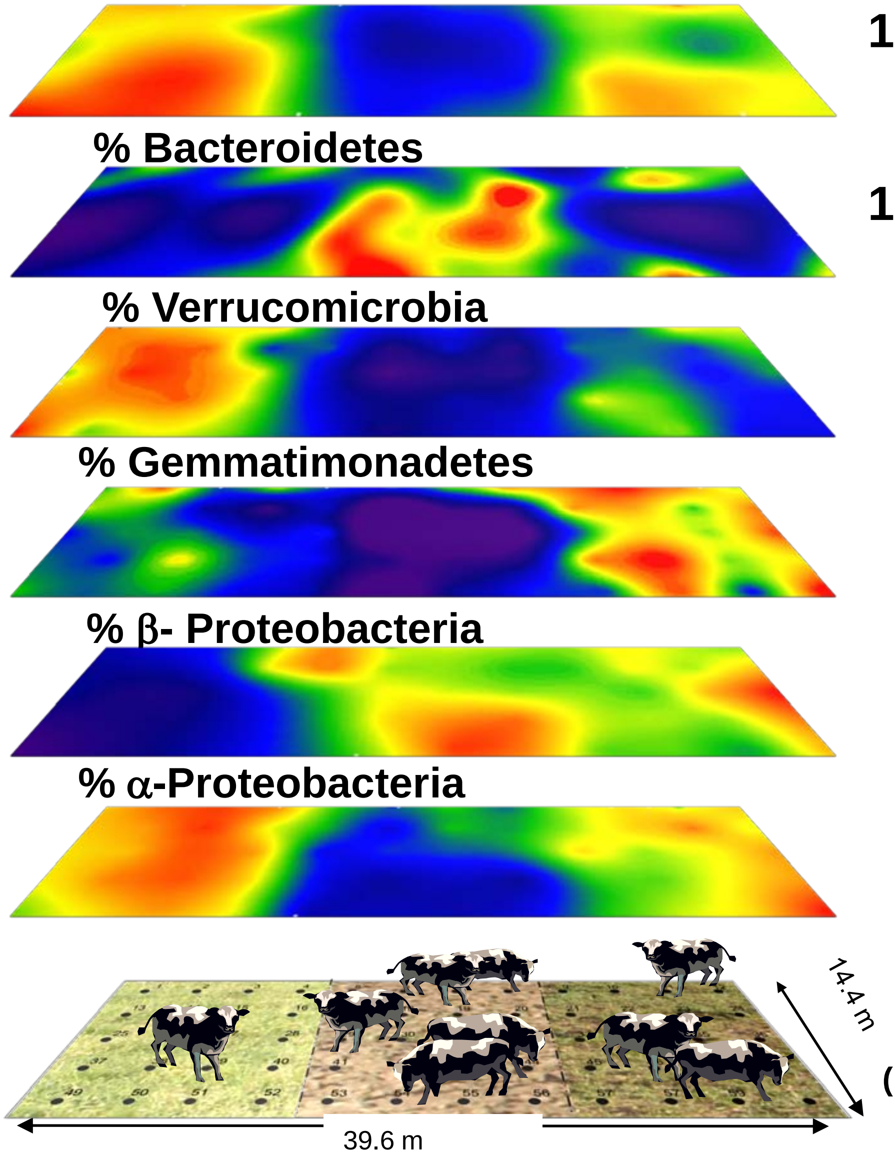
Verrumicrobia





(Philippot et al. 2009 *EM*)

Relative abundance



% Actinobacteria **10 – 40%**

% Bacteroidetes **12 – 24%**

% Verrucomicrobia **1 – 6%**

% Gemmatimonadetes **6 – 15%**

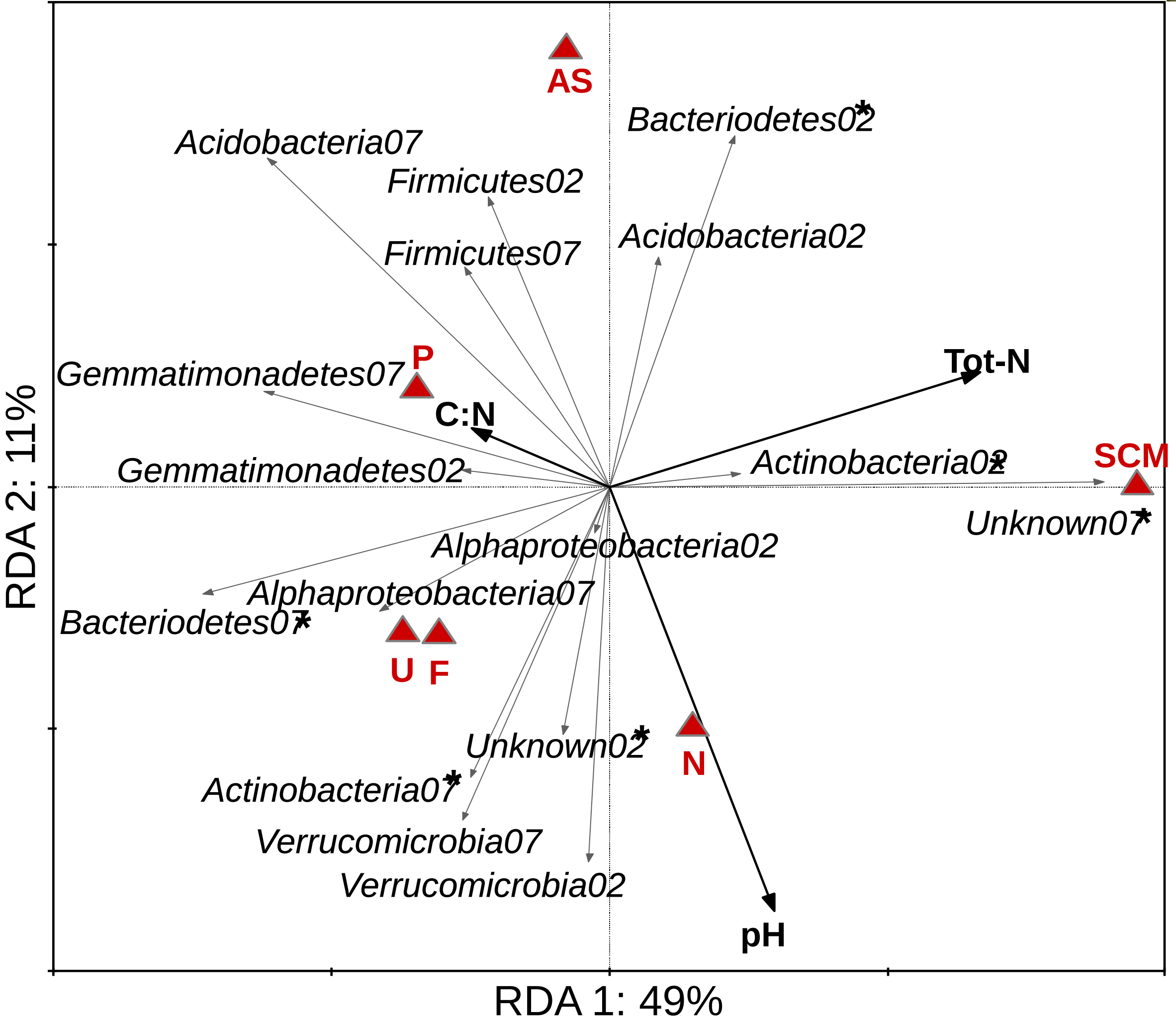
% β- Proteobacteria **3 – 7%**

% α-Proteobacteria **6 – 11%**

(Philippot et al. 2009 *EM*)

Higher taxa affected by management?

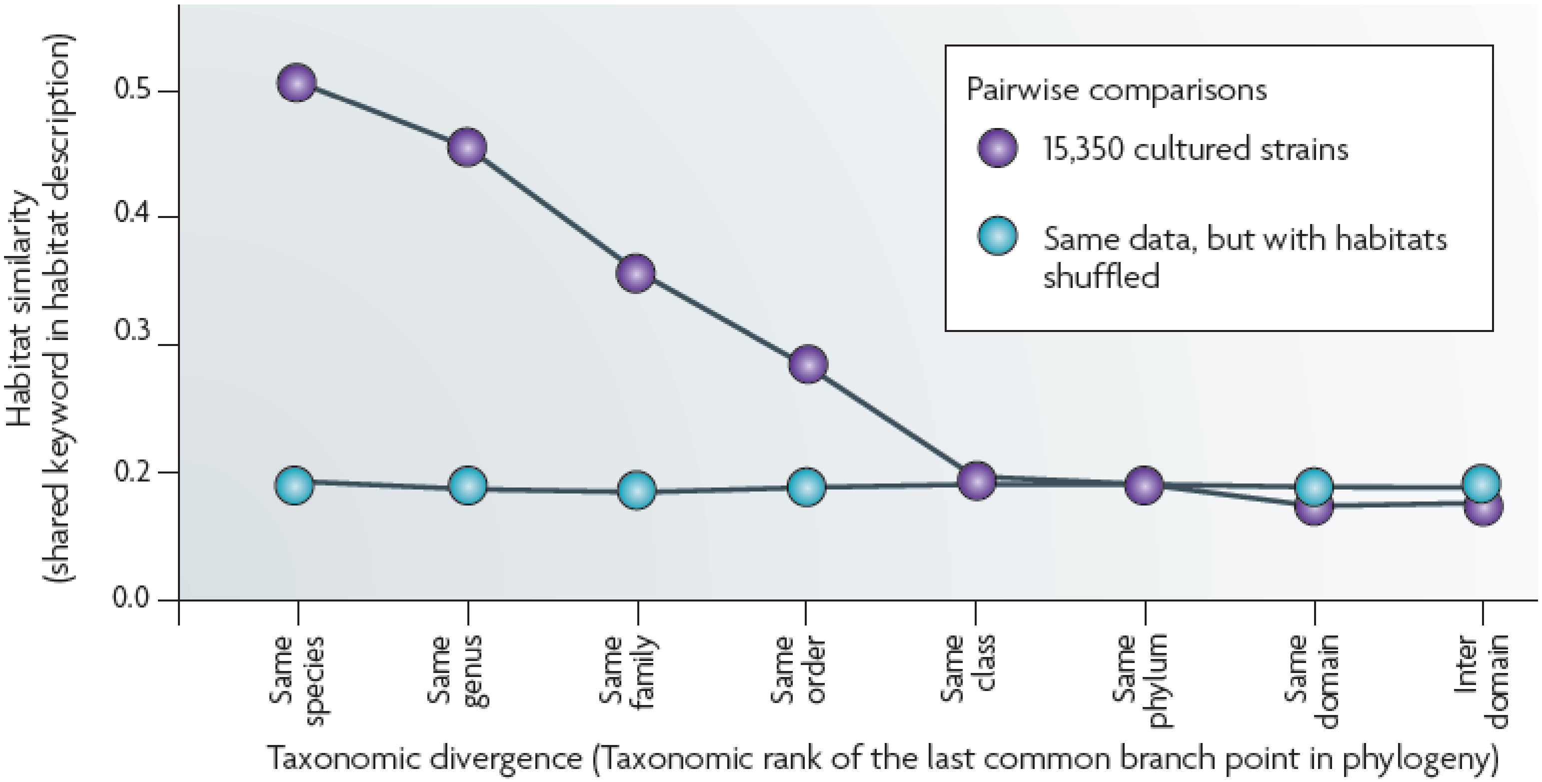
Years 2002 (02)and 2007 (07):



AS	Ammoniumsulfate
P	Peat
U	Unfertilized
N	Calcium nitrate
SCM	Soild cattle manure
F	Fallow, unfertilized

(Wessén et al. 2010 *SBI*

Habitat-phylotype associations

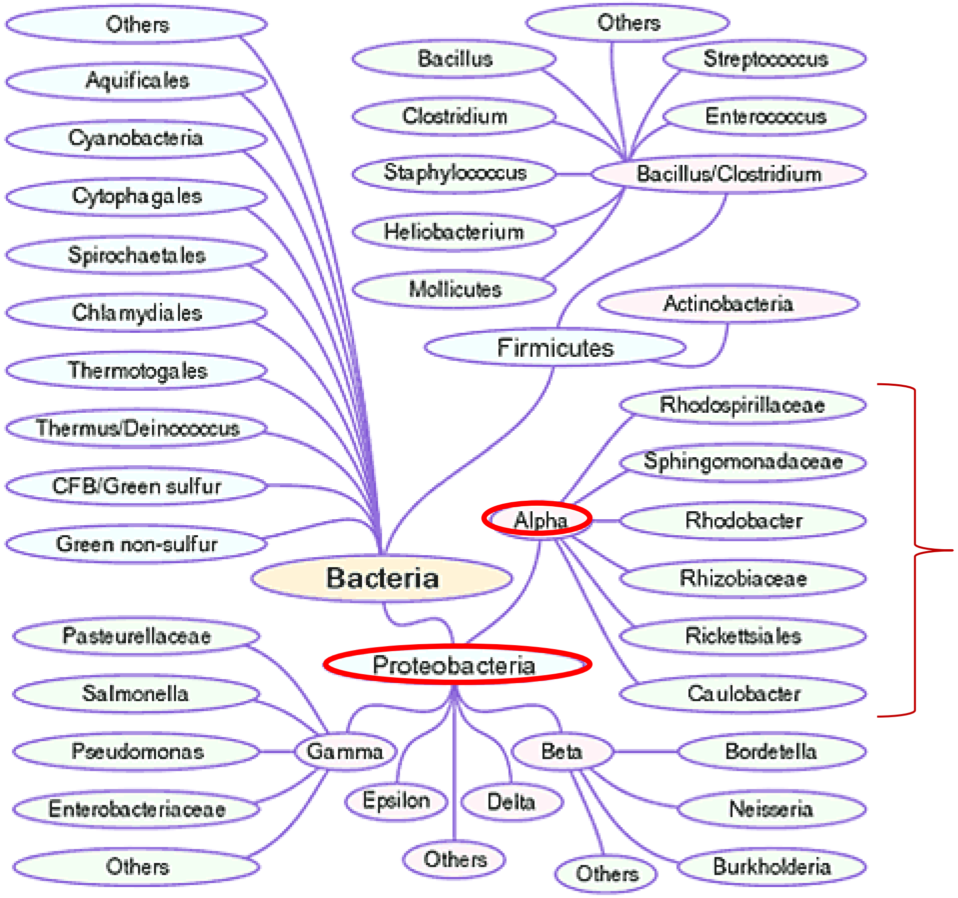


Habitat–phylotype associations. A comparison of cultured microbial strains, plotting habitat similarity against level of strain relatedness . For taxonomic ranks <order, the difference is significant ($P < 10^{-6}$) (Mering et al. 2007, Science).

(Philippot et al 2009 NRM)

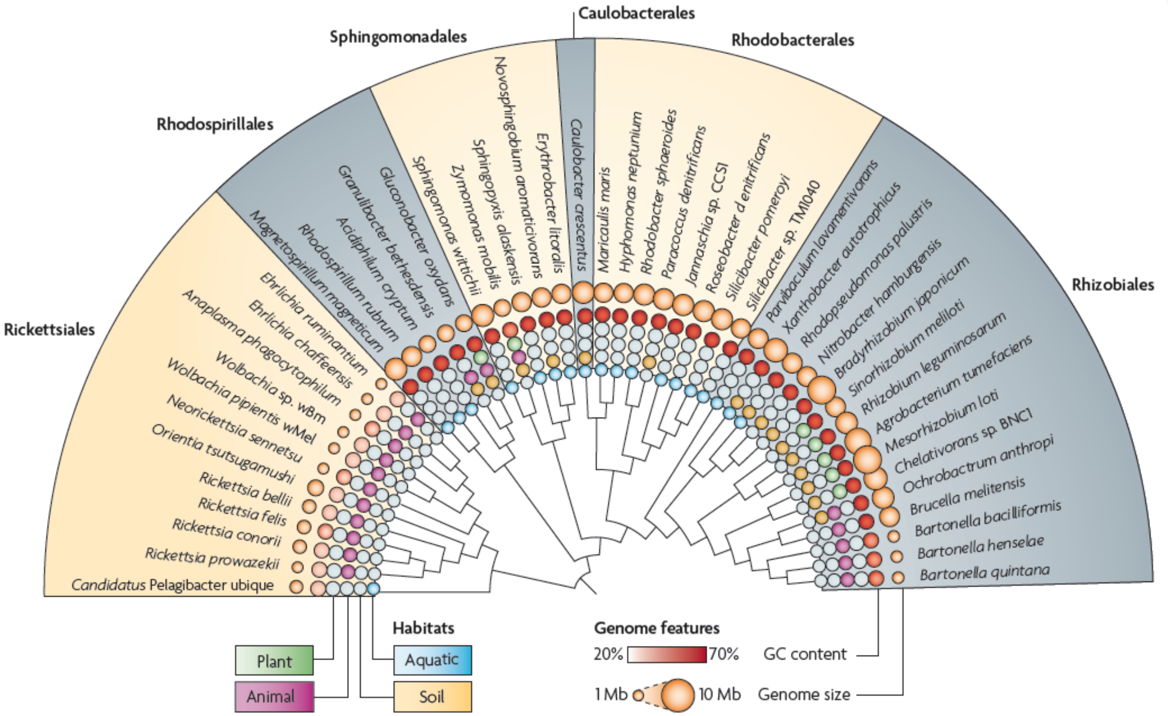
Ecological diversity within a lineage?

How much ecological diversity is there within a taxonomically defined bacterial lineage?



The class Alphaproteobacteria, which has more than 100 sequenced representatives, is one of the most ecologically diverse classes and is therefore a particularly good model system to use to address this question.

Habitat–phylotype associations for the α-proteobacteria



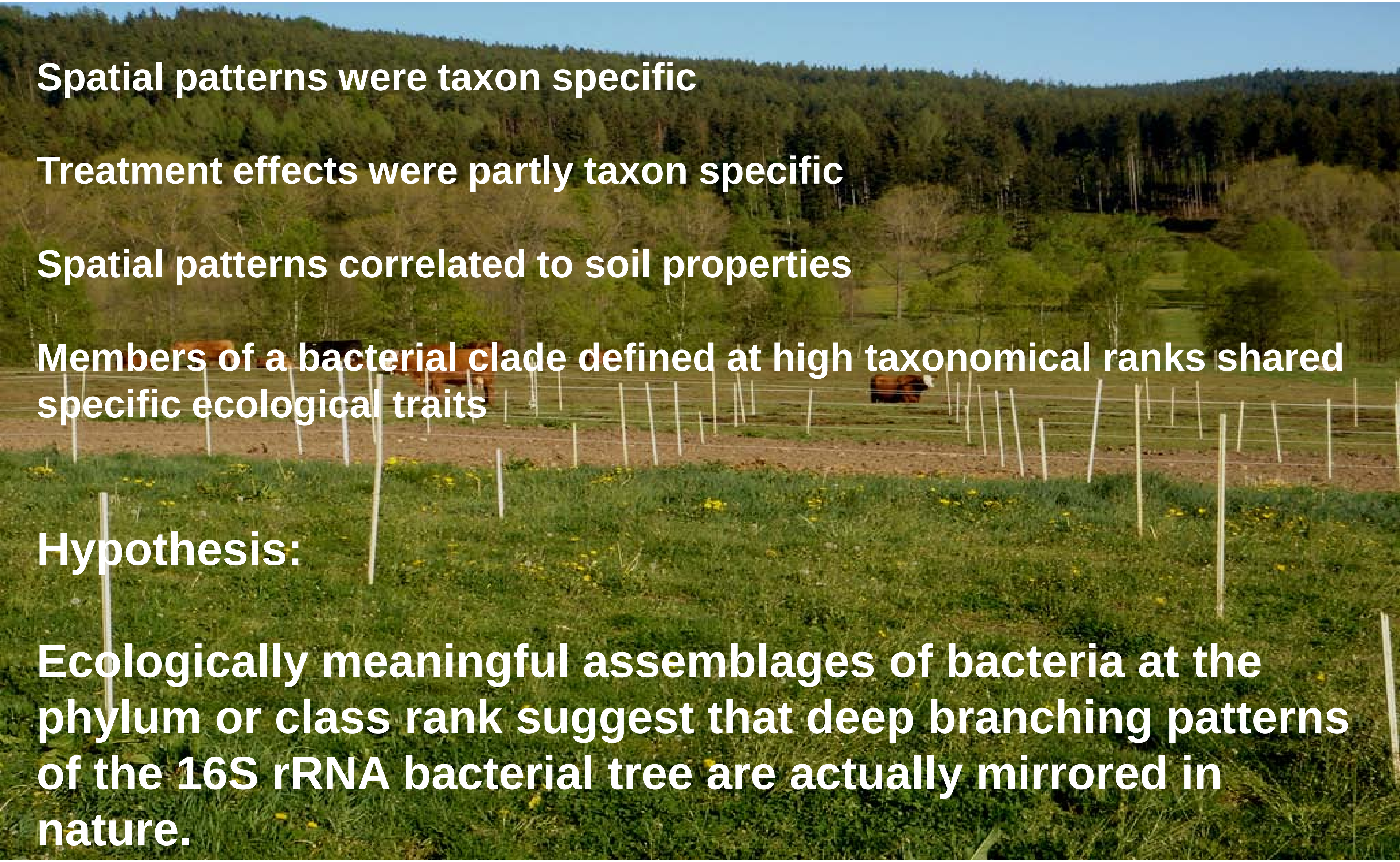
Ecological coherence in terms of habitat preference is manifested at genus and order level in the phylogeny (Ettema et al. 2009, Biol. Lett.).

- Adaptation to open/changing environments associated with genome size expansions and rapid changes in gene repertoires, whereas adaptation to isolated/stable environments reflected in reductive evolution.

- Differences in lifestyle correlate with variations in the genes encoding proteins that have functions associated with environmental interactions, such as regulation and transport

(Philippot et al 2009 NRM)

Conclusions and perspective



Spatial patterns were taxon specific

Treatment effects were partly taxon specific

Spatial patterns correlated to soil properties

Members of a bacterial clade defined at high taxonomical ranks shared specific ecological traits

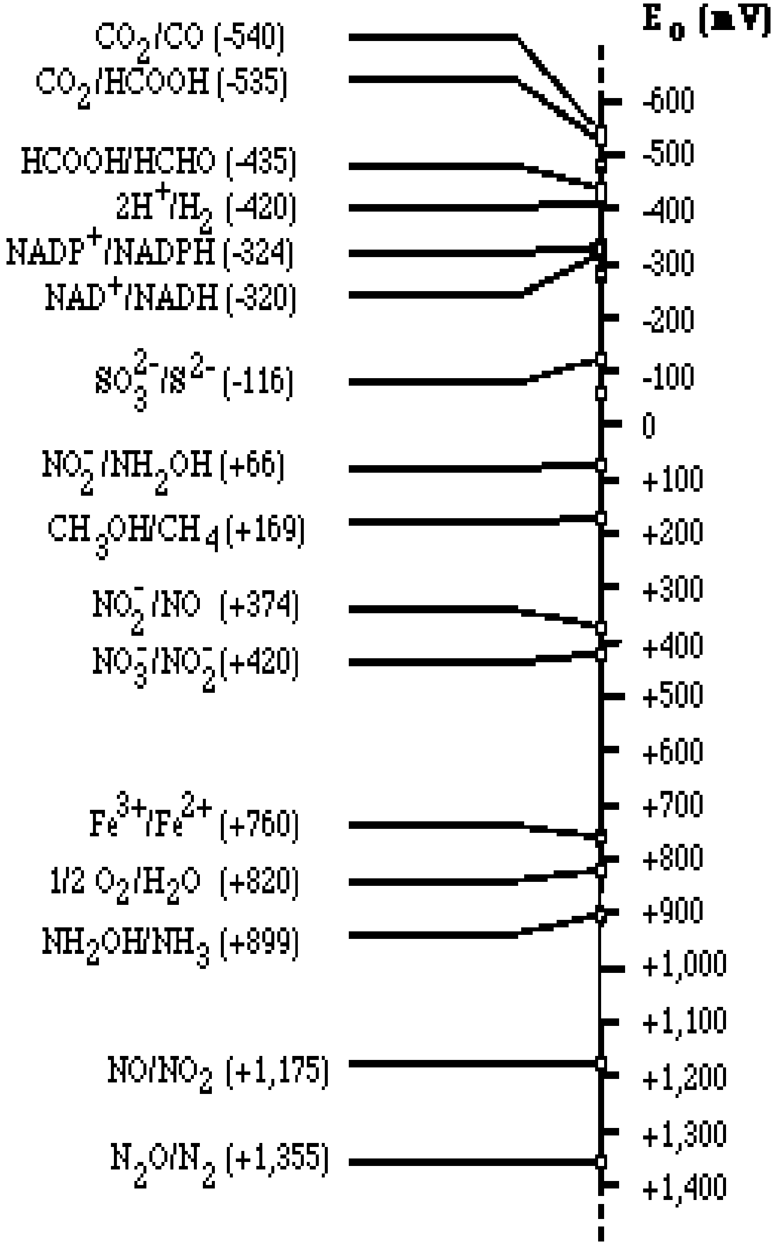
Hypothesis:

Ecologically meaningful assemblages of bacteria at the phylum or class rank suggest that deep branching patterns of the 16S rRNA bacterial tree are actually mirrored in nature.

Functional guilds

Bacteria

- Metabolic pathways
- Chemolitotrophs
- Phototrophs
- Autotrophs

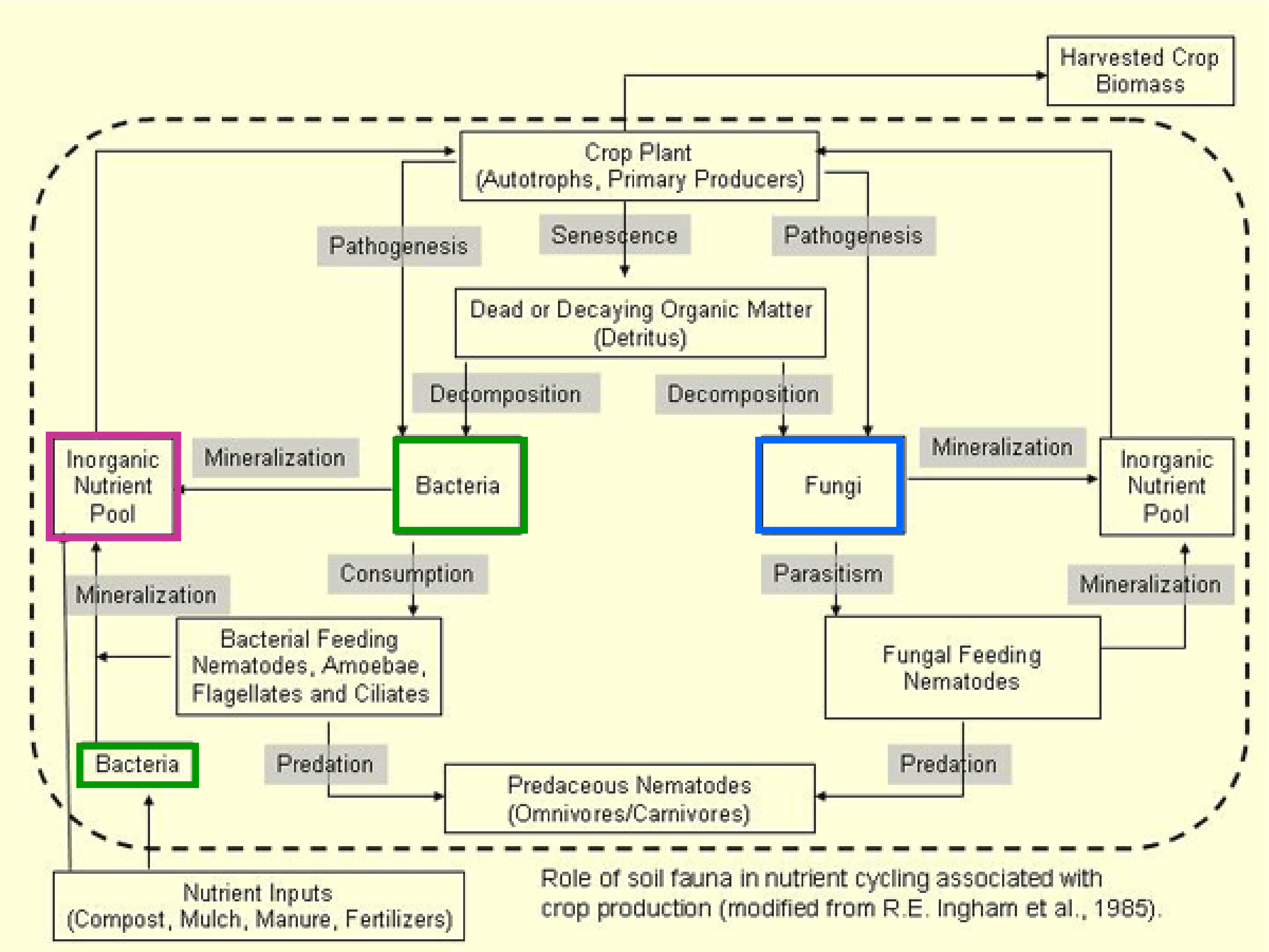


Functional groups of bacteria

Bacteria fall into four functional groups:

1. **Most are decomposers – degrade organic matter, cycle C and degrade pollutants)**
2. **A second group of bacteria are the *mutualists, e.g.* the nitrogen-fixing bacteria.**
3. **The third group of bacteria is the *pathogens*.**
4. **A fourth group, called *lithotrophs* or *chemoautotrophs*, obtains its energy from compounds of N, S, Fe or H instead of from C-compounds (Some are important to biogeochemical cycling and degradation of pollutants)**

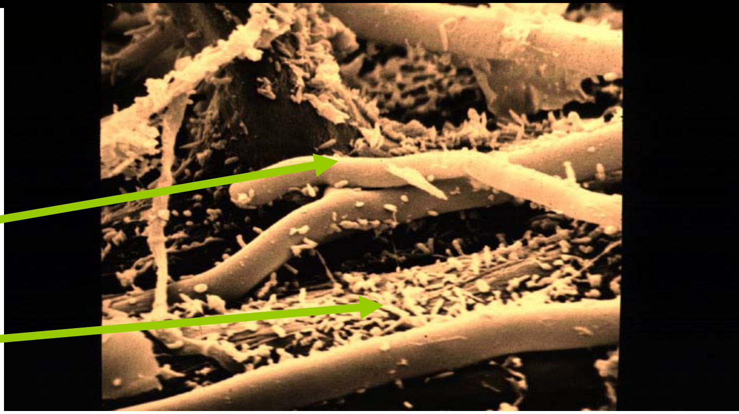
Bacteria in soil



Role of soil fauna in nutrient cycling associated with crop production (modified from R.E. Ingham et al., 1985).

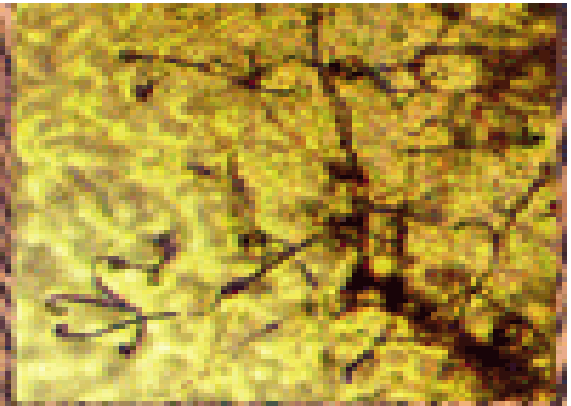
Bacteria in soil

- **Bacteria along with fungi, are the most important group in organic matter decomposition**



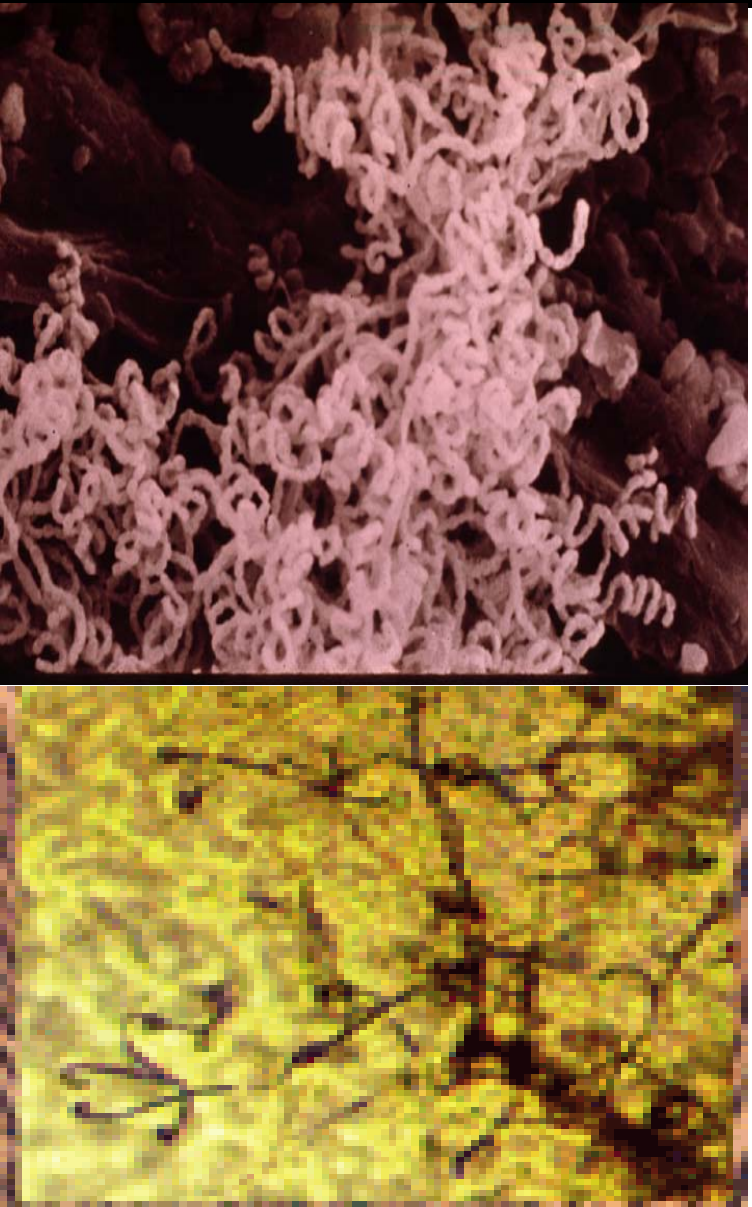
- **Extracellular compounds help bind soil particles into aggregates**

- **Specialized groups are involved in each portion of the N-cycle**



Actinobacteria with growth form similar to fungi produce compounds that give soil its distinctive aroma, important degraders

Actinobateria in soil



Bacteria with growth form similar to fungi.

Degrade recalcitrant compounds, such as chitin and cellulose

Active at high pH levels. Fungi are more important in degrading these compounds at low pH.

Produce compounds (geosmines) that give soil its distinctive aroma

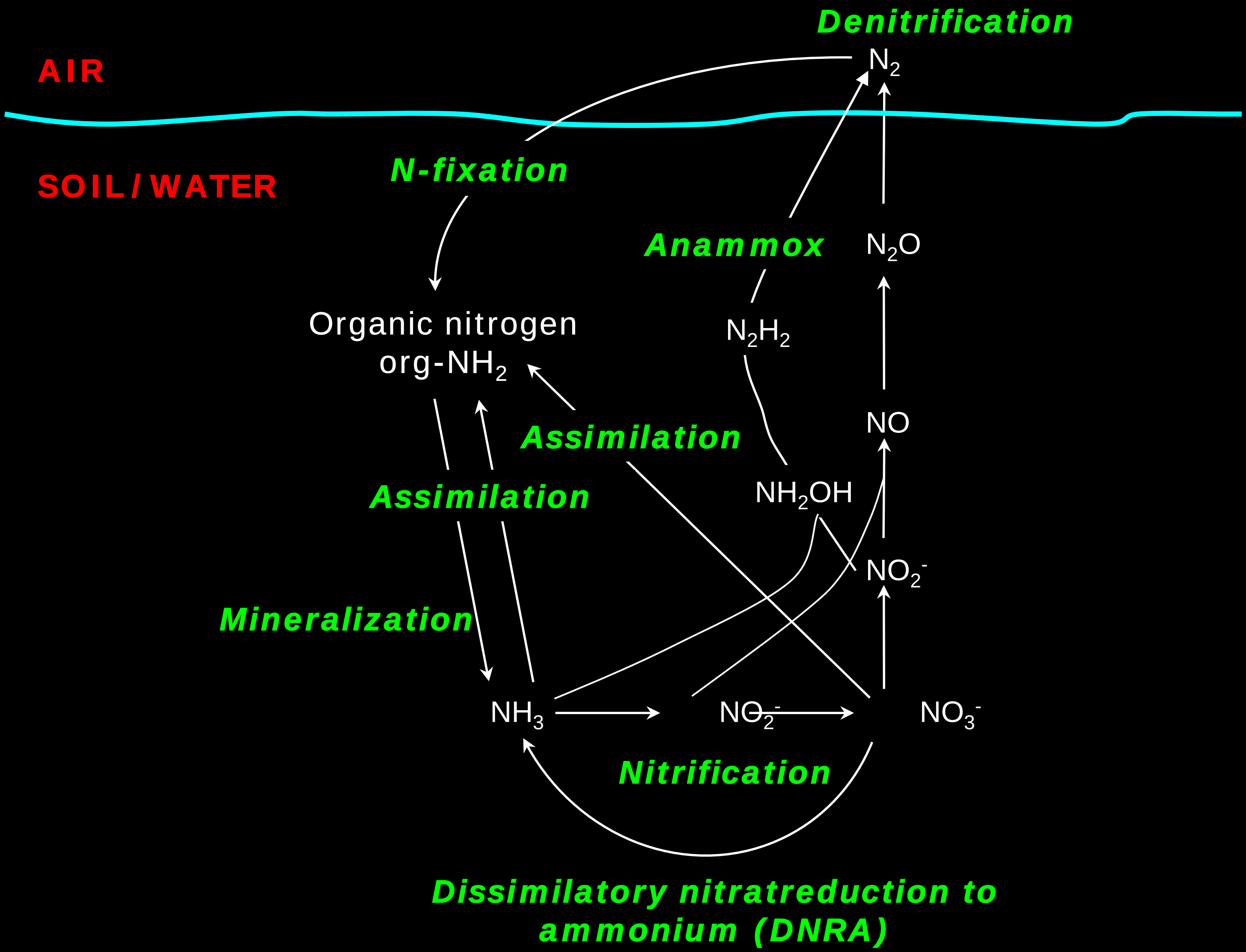
A number of antibiotics are produced by actinomycetes such as Streptomyces.

Bacteria in N-cycling

- **N-mineralization**
- **N-fixation**
- **Nitrification**
- **Anammox**
- **Denitrification**

Symbiotic N-fixation: *Bradyrhizobium japonicum* and soybean. Important nitrogen source for agriculture, especially in develeoping countries and organic farming.

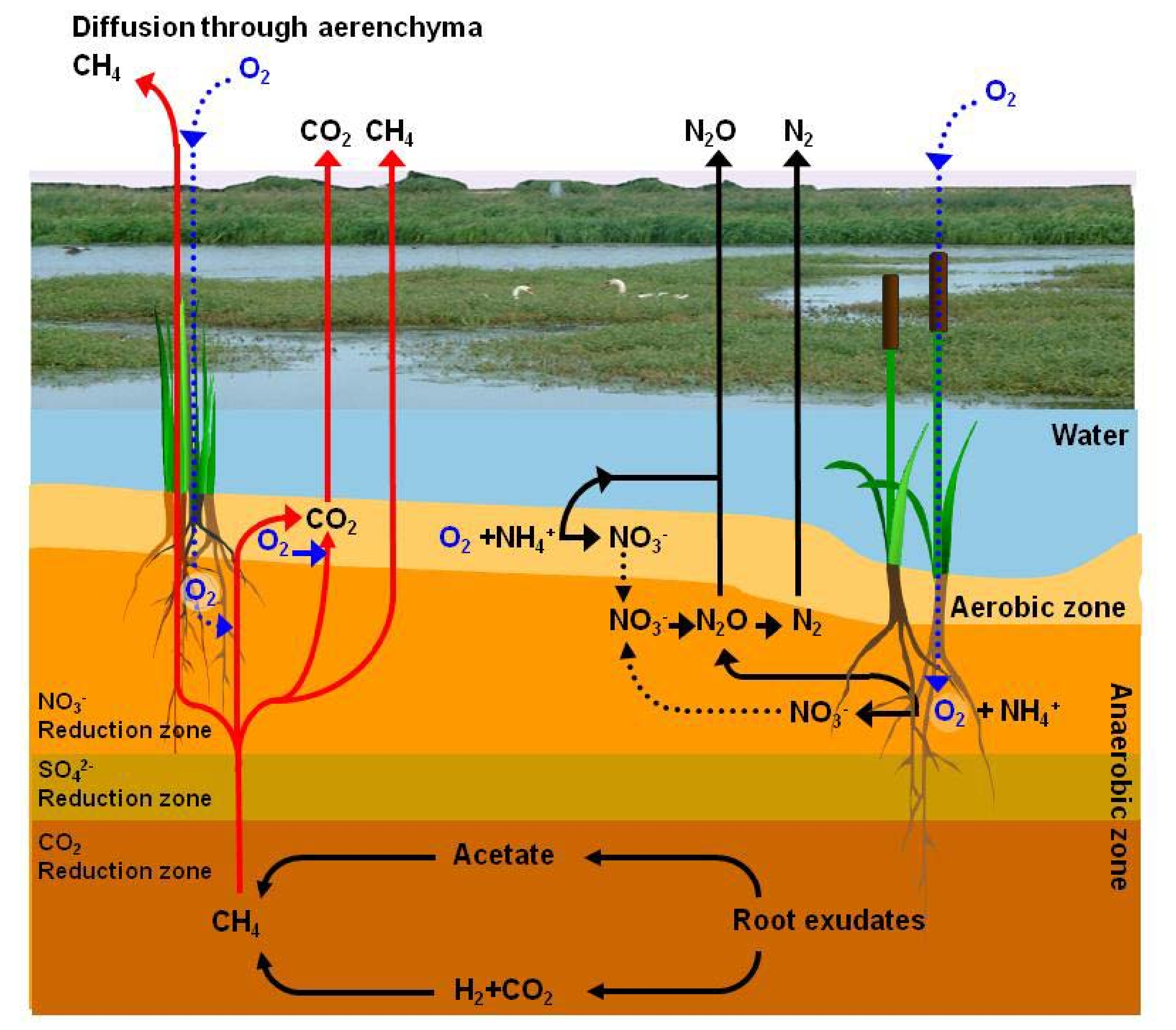
Bacteria in N-cycling



Degradation of xenobiotics

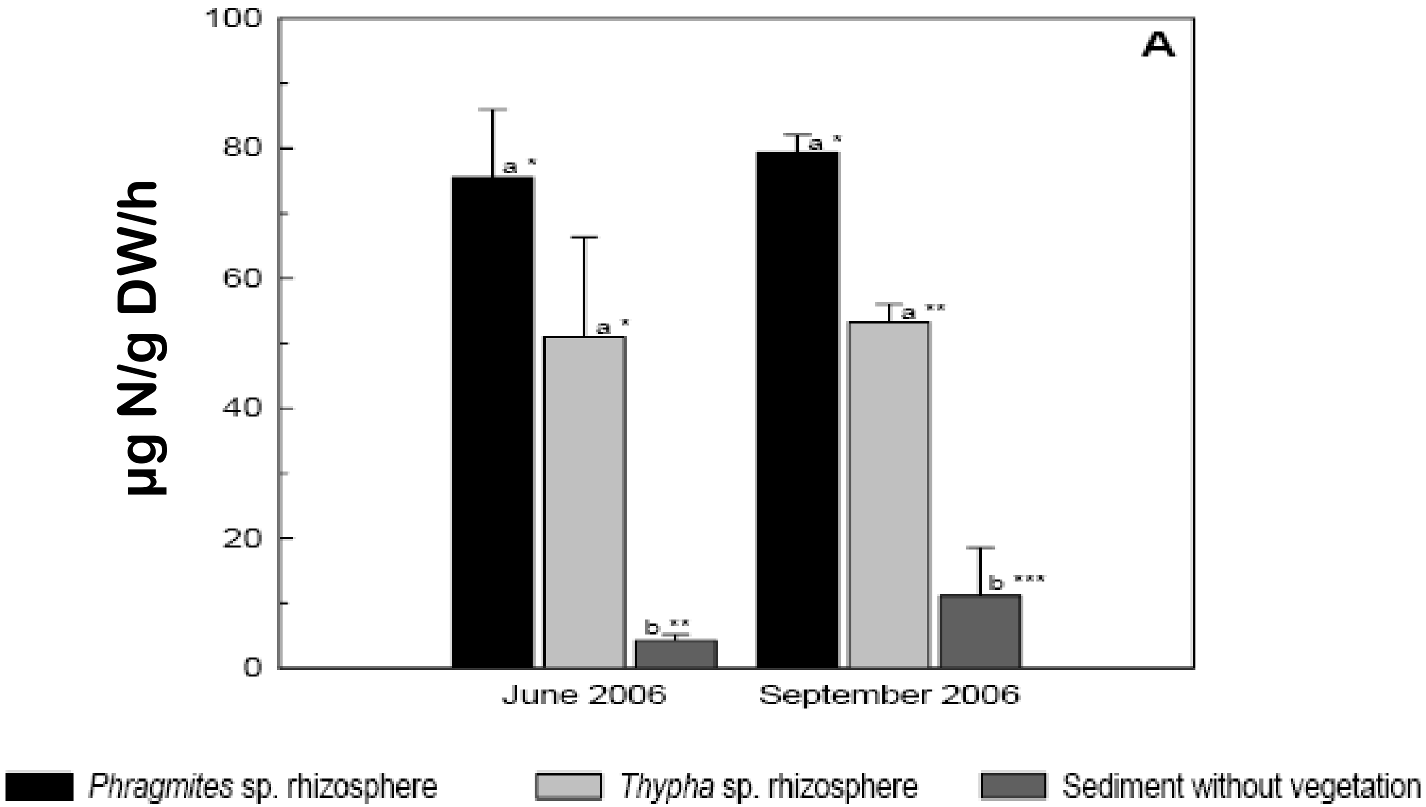
- Bacteria or fungi
- Metabolic or cometabolic or..
- Aerobic or anaerobic

Contaminated soil can be restored by microbes.



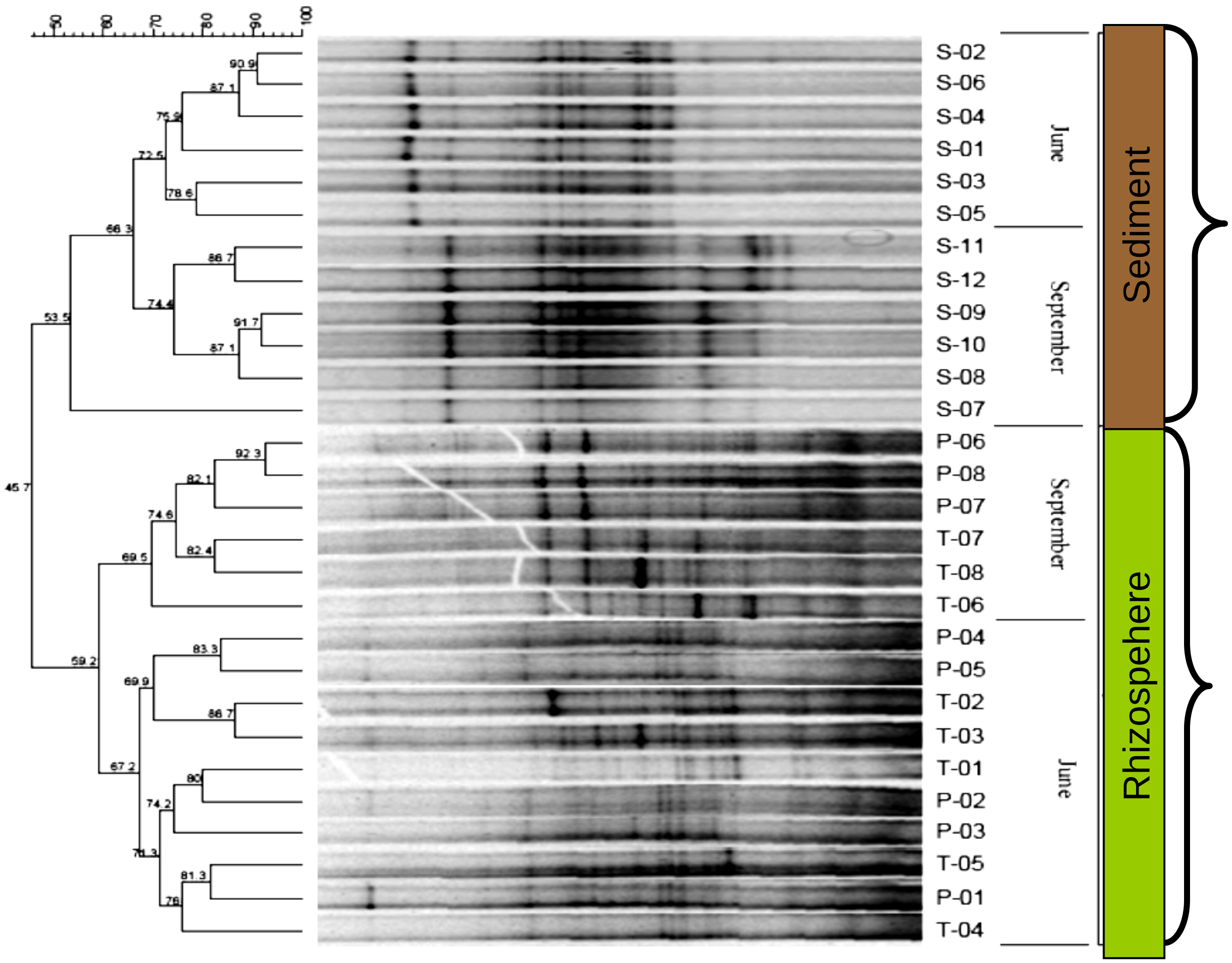
Philippot *et al*. 2009
Plant and Soil
321:61-81

Plants increase denitrification rates



Ruiz et al., 2009*, FEMS Microbiol. Ecol.*

Plants shape denitrifier communities (DGGE of *nosZ*)



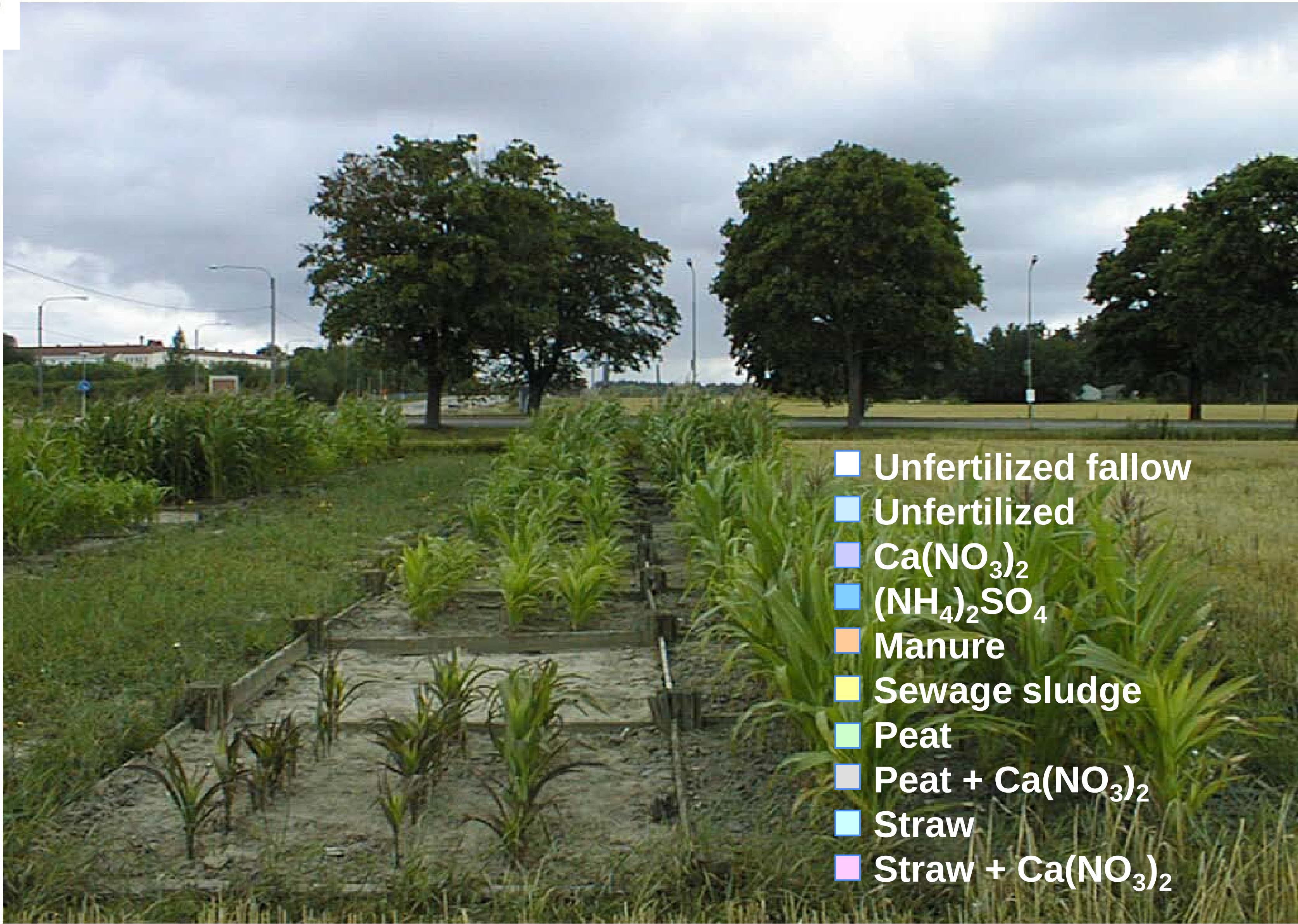
Low rates

High rates

Ruiz et al., 2009, *FEMS Microbiol. Ecol.*

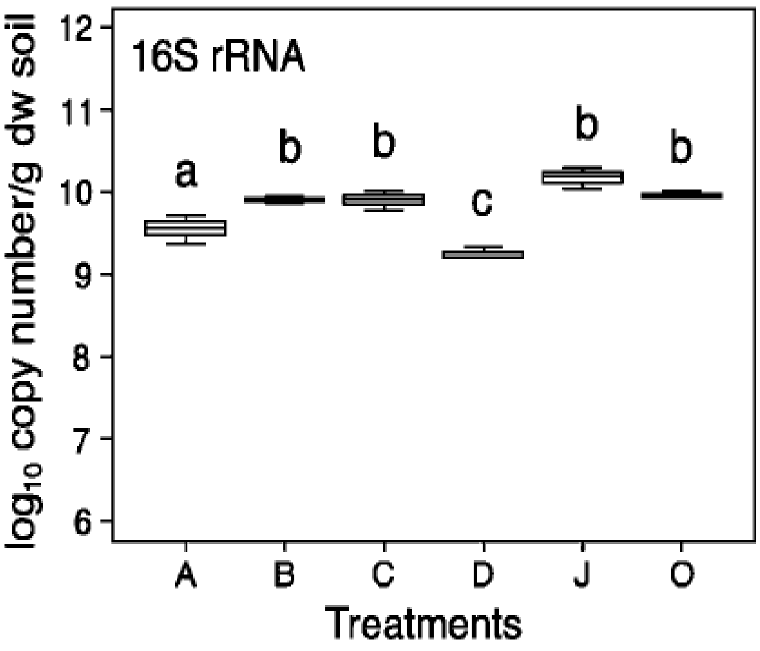
Effects by management?

Ultuna field trial

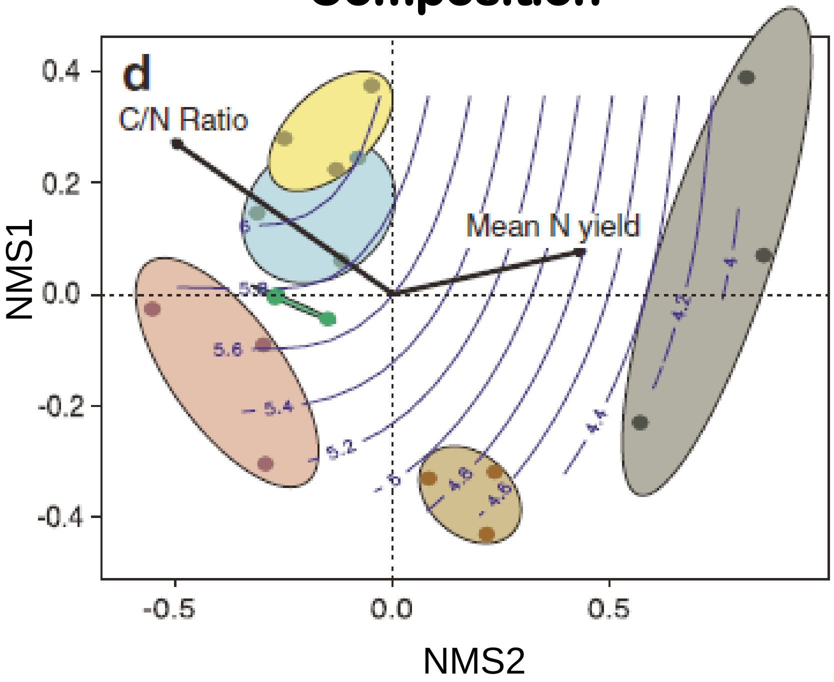


- ⬜ Unfertilized fallow
- 🟦 Unfertilized
- 🟪 $Ca(NO_3)_2$
- 🟦 $(NH_4)_2SO_4$
- 🟧 Manure
- 🟨 Sewage sludge
- 🟩 Peat
- ⬜ Peat + $Ca(NO_3)_2$
- 🟦 Straw
- 🟪 Straw + $Ca(NO_3)_2$

Bacterial communities are affected by fertilization in terms of size and structure:



Numbers



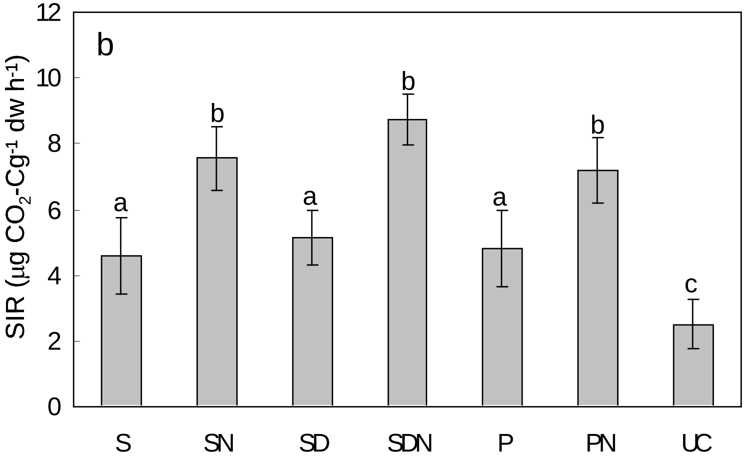
Composition

A Unfertilized bare fallow
B Unfertilized
C $Ca(NO_3)_2$
D $(NH_4)_2SO_4$
J Manure
O Sludge

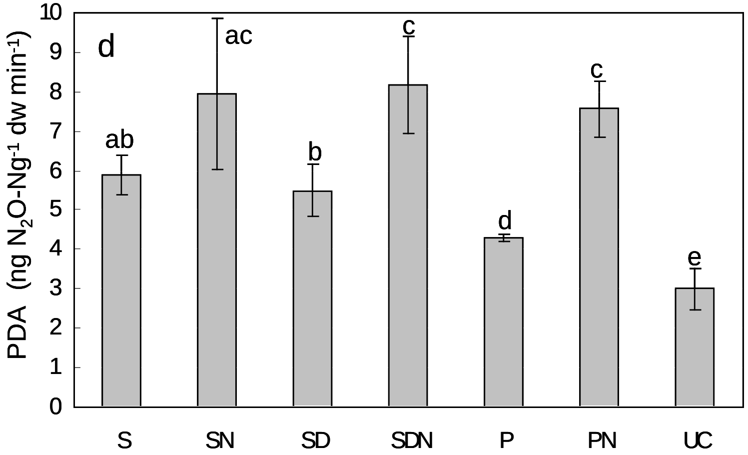
Hallin et al. 2009 *ISMEJ*

Microbial activity affected by management

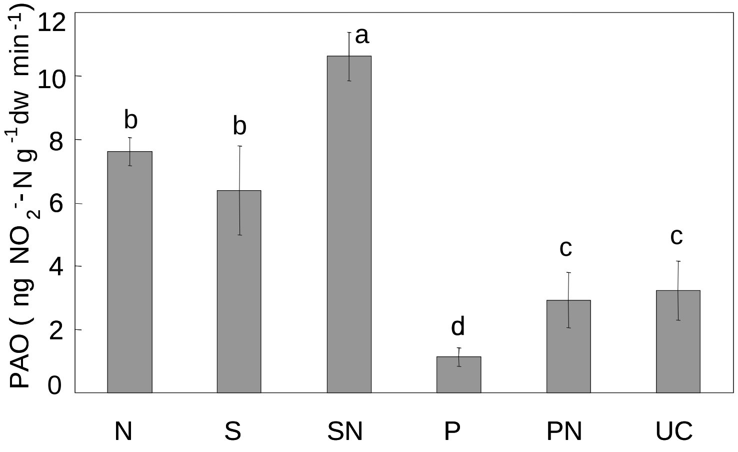
Respiration



Denitrification



Ammonia oxidation



To conclude

"We're taking soil samples today ... in other words, FIELD TRIP!"

Yippii…. Lots to discover

Isolation of bacteria

Understanding significance of diversity for:
- **ecosystem stability**
- **ecosystem resilience**

Soil-microbe ineraction

1. Predicting the impact of environmental change

2. Understanding consequences of change on biogeochemical cycling