Microbial diversity and processes in Lake Kivu (East Africa)

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SAME 12
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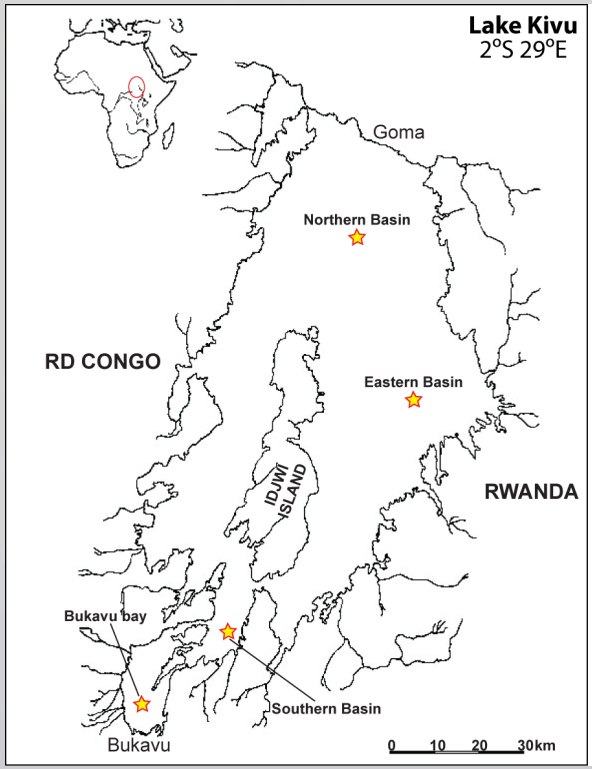
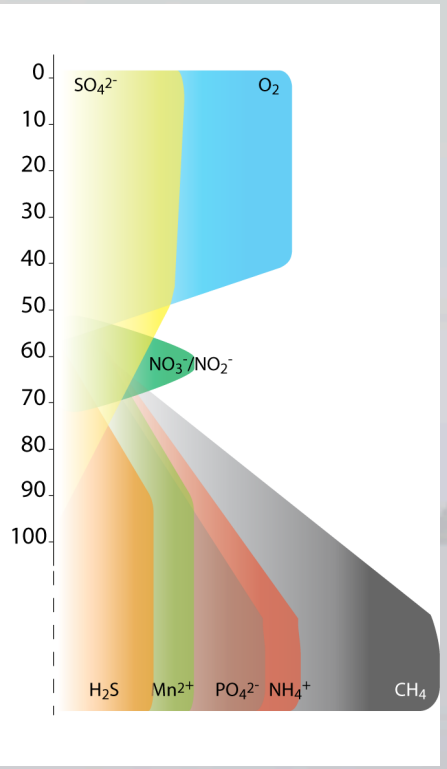
Main Characteristics

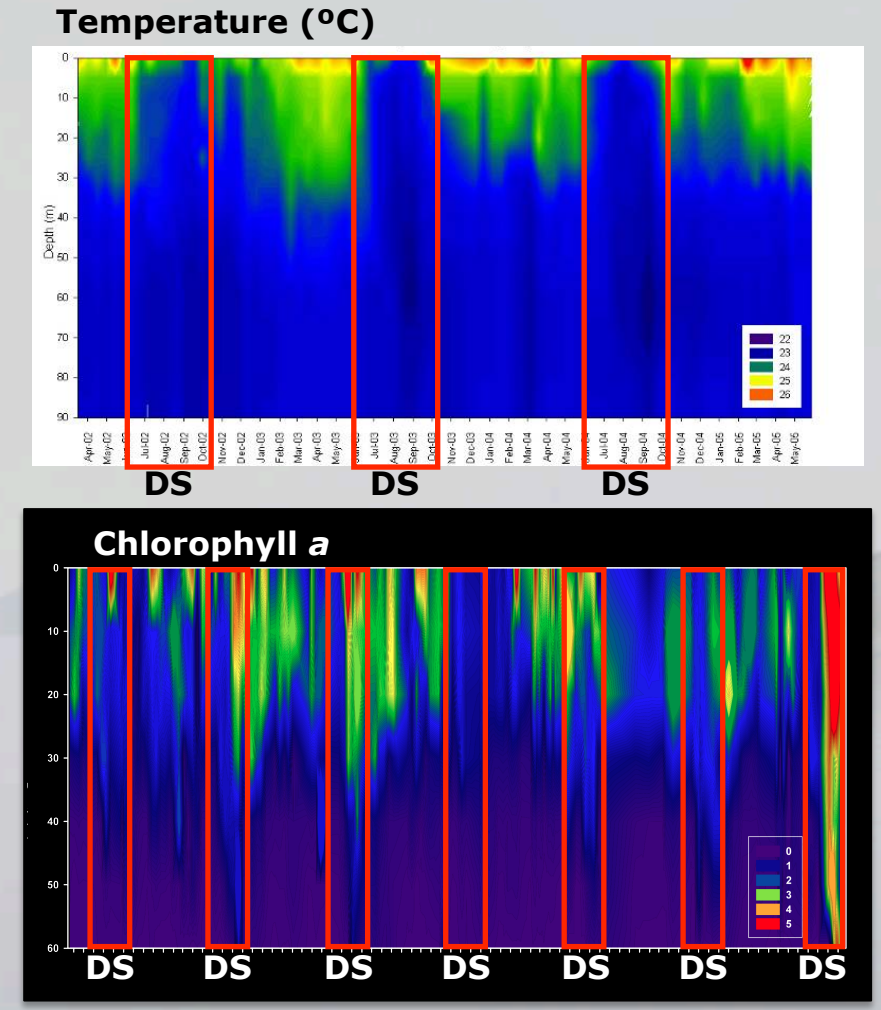




- Deep (max. depth 486 m)
- Oligotrophic
- Meromictic
- East african lake of volcanic origin
- **Oxic mixolimnion** (down to 50 m depth)

- Deep **anoxic monimolimnion** (50 to 486 m depth)
- High amounts of dissolved CO_2 and CH_4 in the monimolimnion
  - CO_2 (300 km^3): mainly volcanic origin
  - CH_4 (60 km^3):
    2/3 anoxic microbial reduction of CO_2
    1/3 anaerobic degradation of settling OM

Main Characteristics

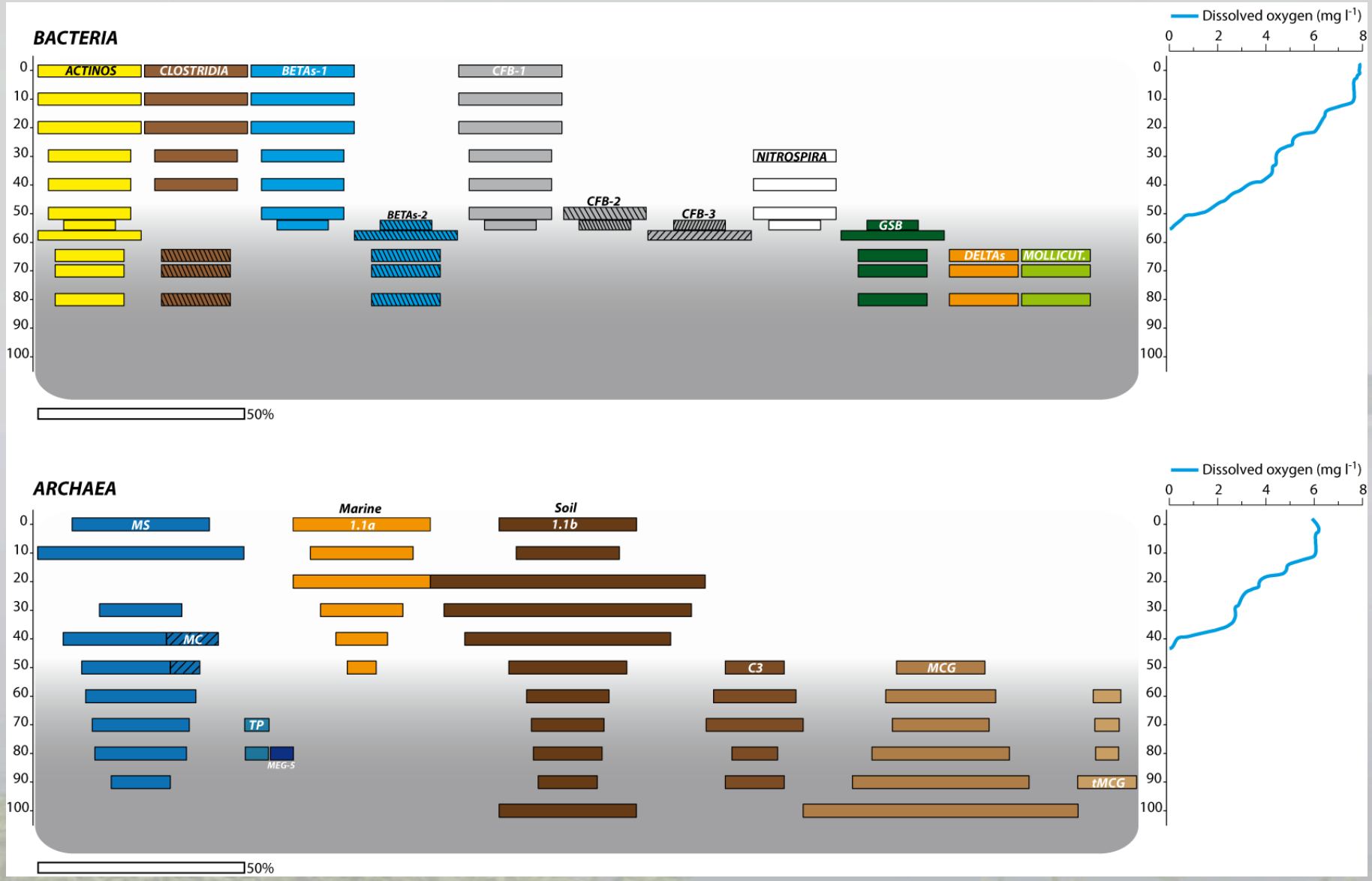


- Dry Season (June-September)
  - SE winds
  - lake **mixing** and thermal homogenization
  - Upwelling nutrients from deep waters
  - Phytoplankton development ([Chl*a*] ↑)
- Rainy Season (October-May)
  - lake is thermal **stratified**
  - No nutrient inputs into oxic layer
  - Little Phytoplankton development ([Chl*a*] ↓)

Snapshot on Community Structure and Diversity

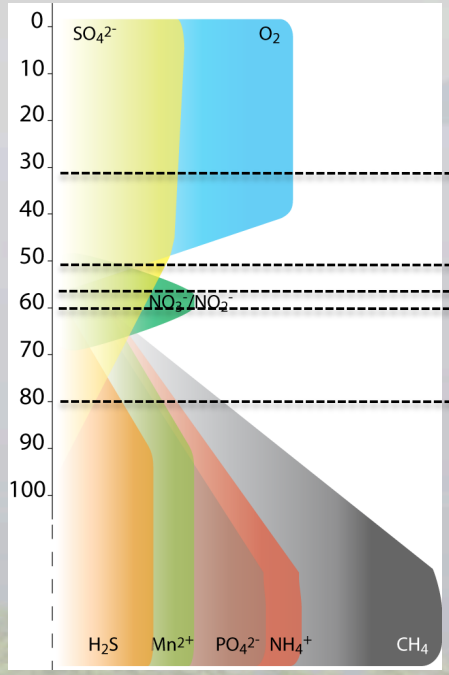
Recent studies analysed the prokaryotic community using DGGE fingerprinting

Snapshot on Community Structure and Diversity



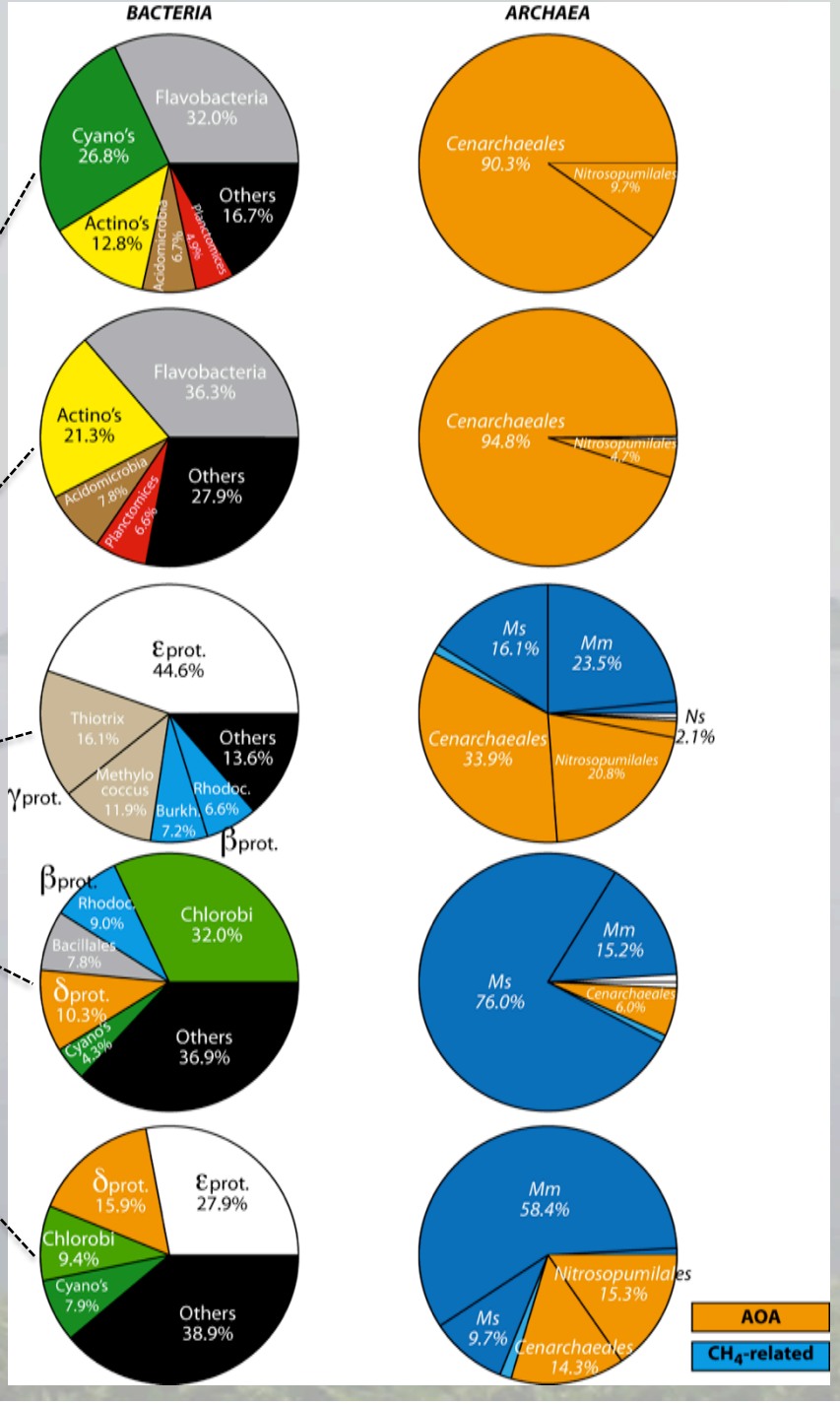
Bacterial (RS 2010) and archaeal (RS 2007) phylogenetic diversity and relative abundance of recovered OTUs after DGGE analyses of Lake Kivu water samples. The breadth of the bar indicates the percentage of OTUs related to the indicated phylogenetic group (to be applied only to the same depth at a time).

Snapshot on Community Structure and Diversity



454-pyrosequencing preliminary results

RS 2010
Northern Basin



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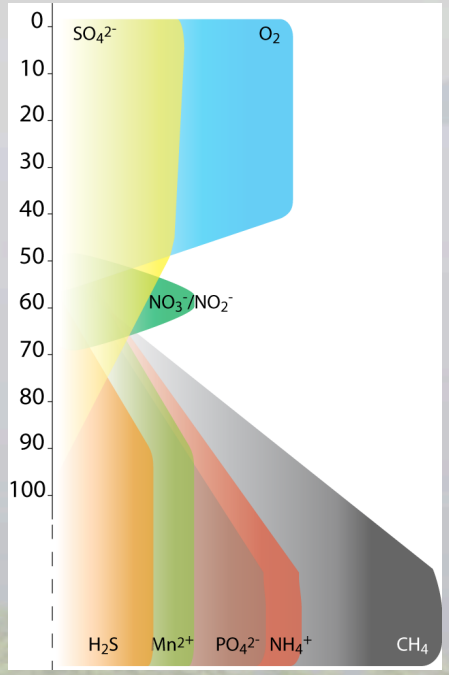

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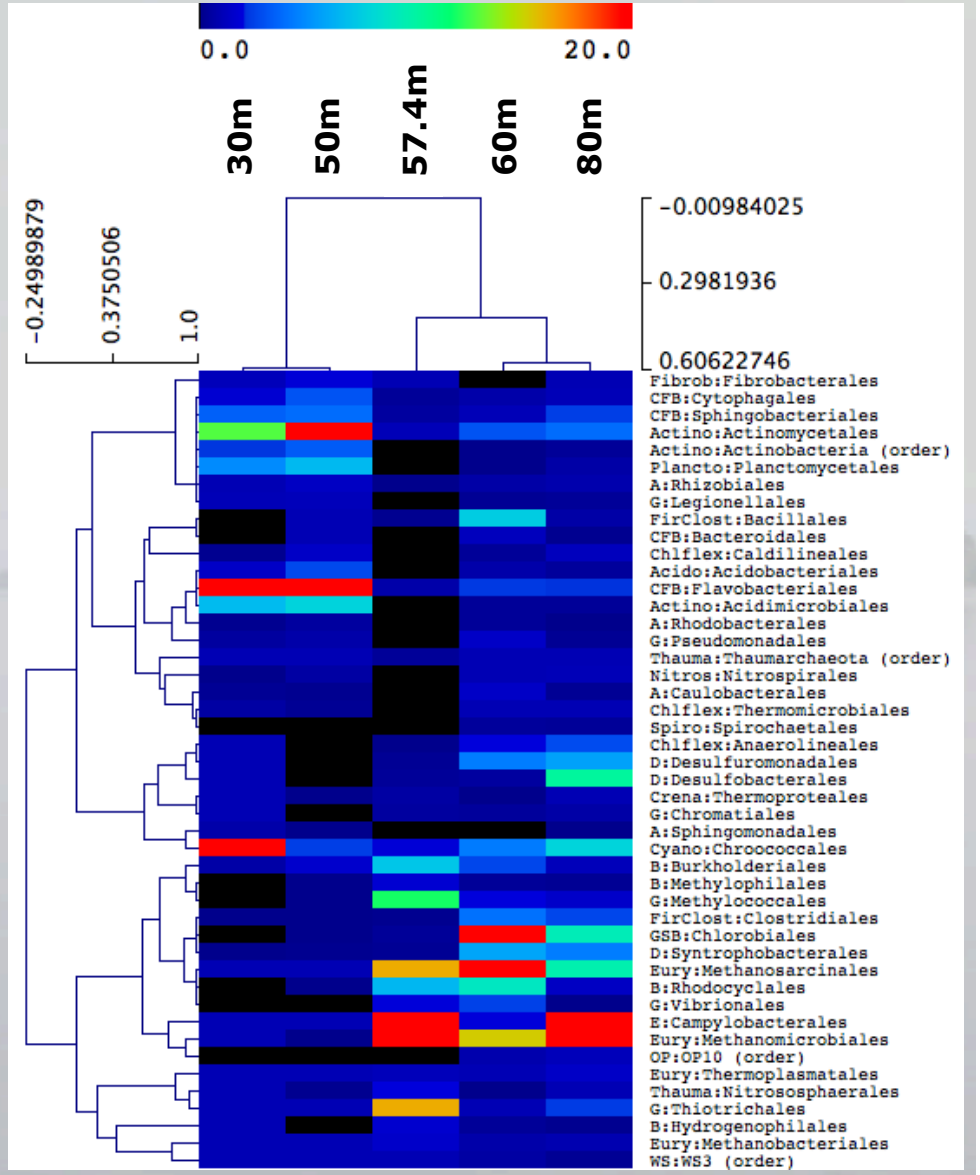


Double dendogram based on hierchical clustering with average linkage based on Spearman distance matrices of phylogenetic groups retrieved using 16S rRNA gene *454-pyrosequencing*

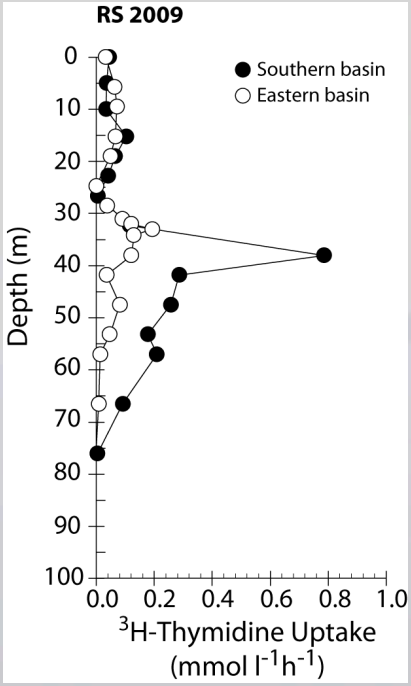
Snapshot on Processes in lake Kivu

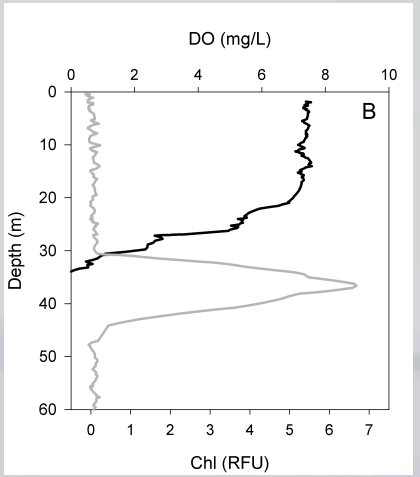
Indirect evidences of metabolic processes in lake Kivu

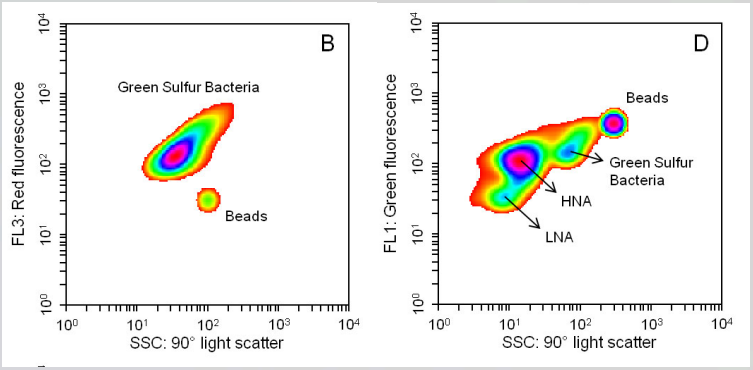
Snapshot on Processes in lake Kivu

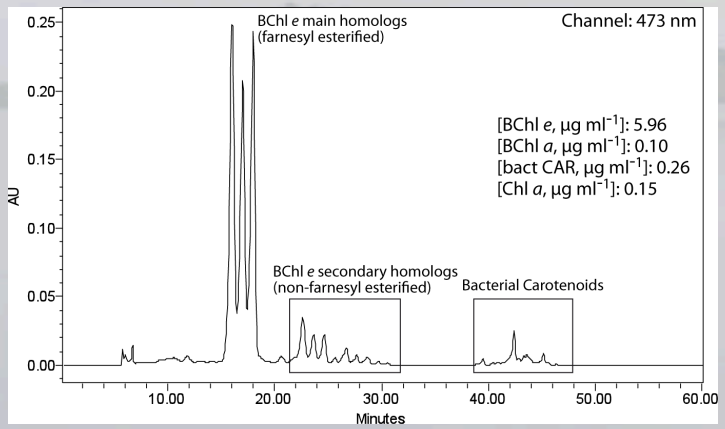
Microbial activity

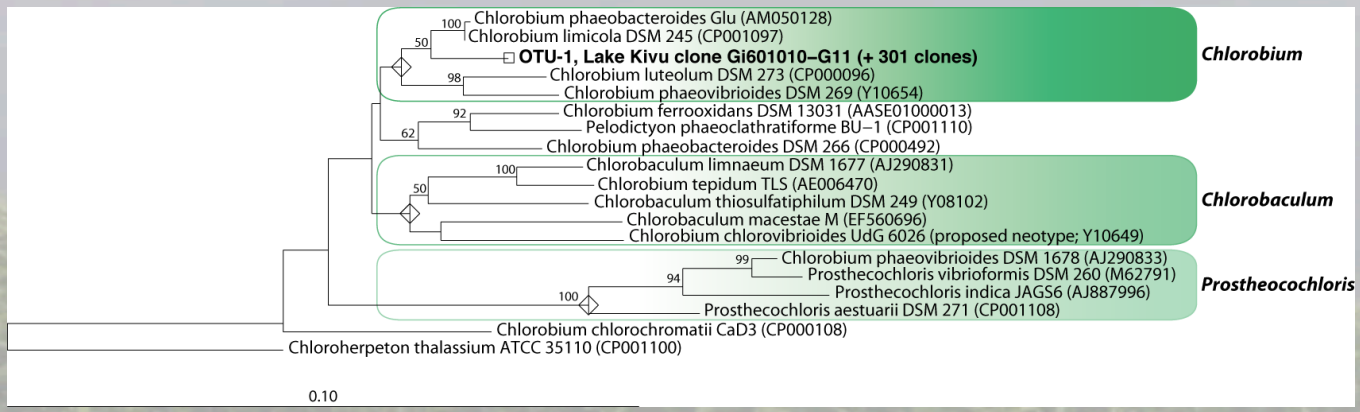
^{3}H-Thymidine uptake and Green Sulfur Bacteria signatures











Snapshot on Processes in lake Kivu

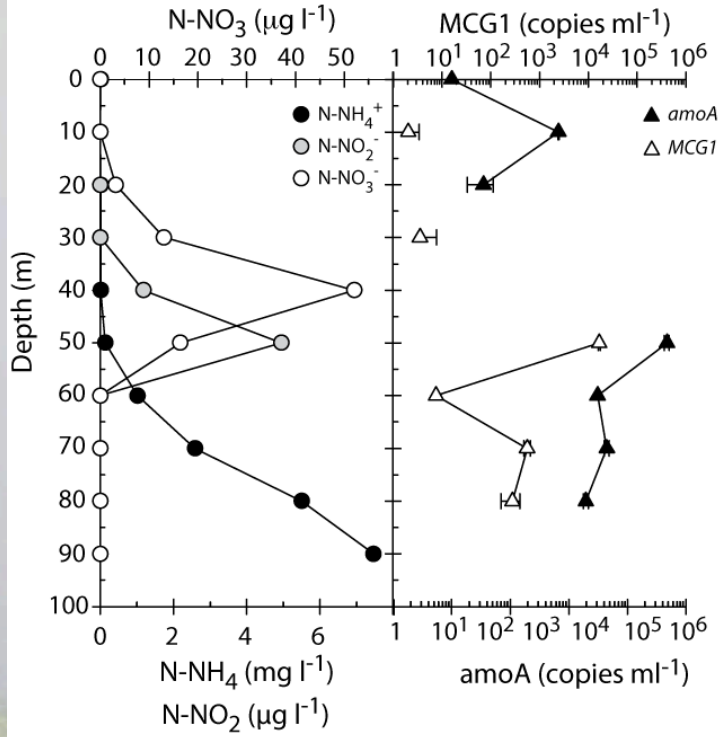
Microbial activity

Archaeal nitrification: ammonia monooxygenase (amoA) signatures

Gene Quantification

RS 2007

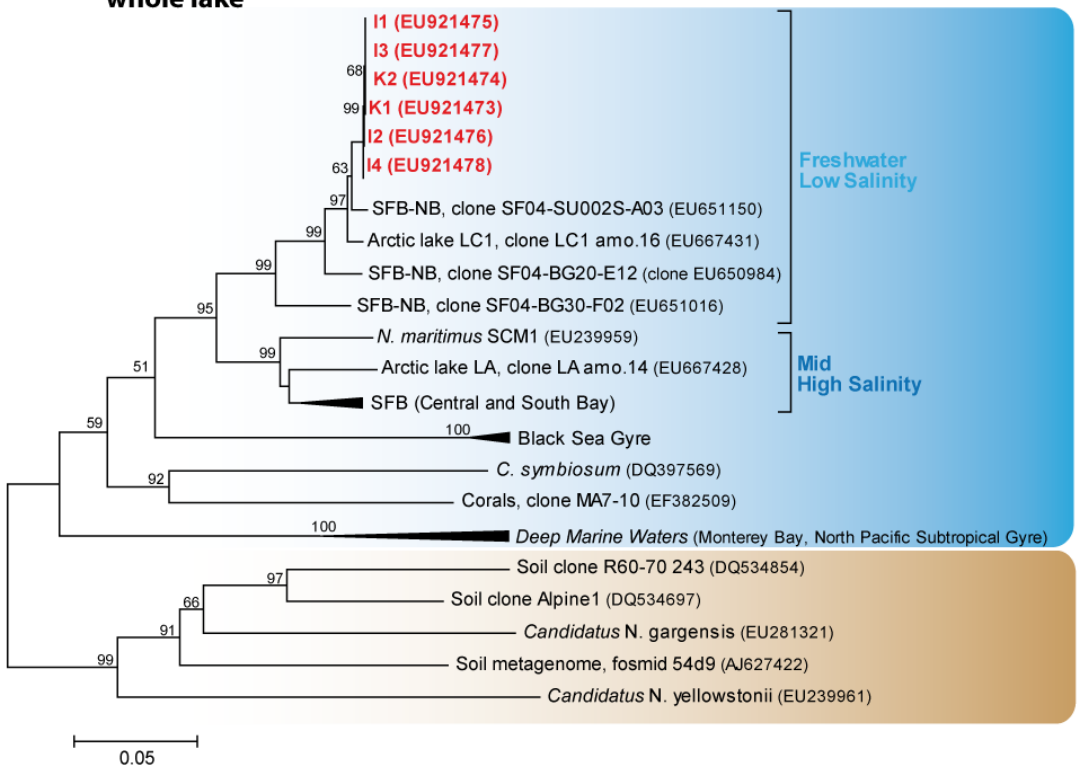
Southern basin



Gene Phylogeny

RS 2007

whole lake



Modified from Llirós et al 2010 AEM 76

Neighbour-joining phylogenetic tree for ***amoA*** sequences constructed using Tamura-Nei corrected distances. Wedge sizes are proportional to sequences condensed on them. The scale bar indicates 5% sequence dissimilarity.

Take home message

- Water column stratification induces a segregation of planktonic *Bacteria* and *Archaea* in the oxic and the anoxic water compartments.
- The chemocline, including an oxic-anoxic transition, a nitracline and a sulfidic zone, is a layer supporting intense microbial activity.
- Presence of Ammonia Oxidizing *Archaea*, Green Sulfur Bacteria, and *Epsilonproteobacteria* putatively link the C, N, and S cycles in the redoxcline of Kivu.
- Further studies are needed to fulfil global biogeochemical cycles and prokaryotic diversity knowledge on Lake Kivu.

Thank you for your attention

More knowledge on lake Kivu ... Lake Kivu: Biology, Ecology and Geochemistry
(Eds. Descy, Darchambeau & Schmid)
Springer, Aquatic Ecology Series
in progress

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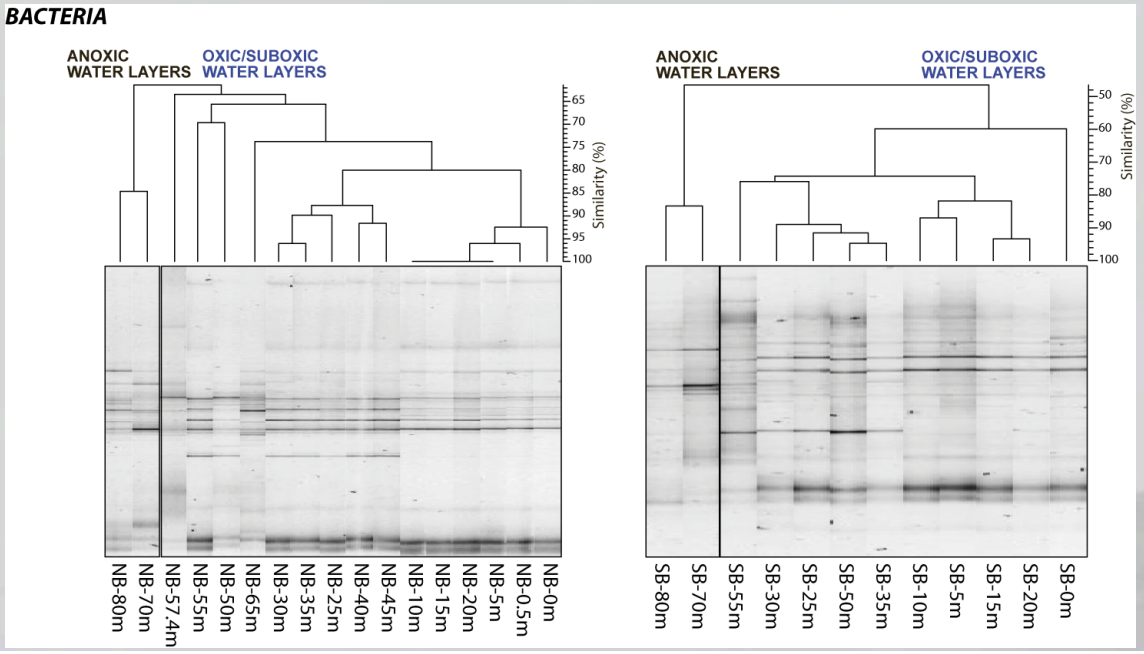

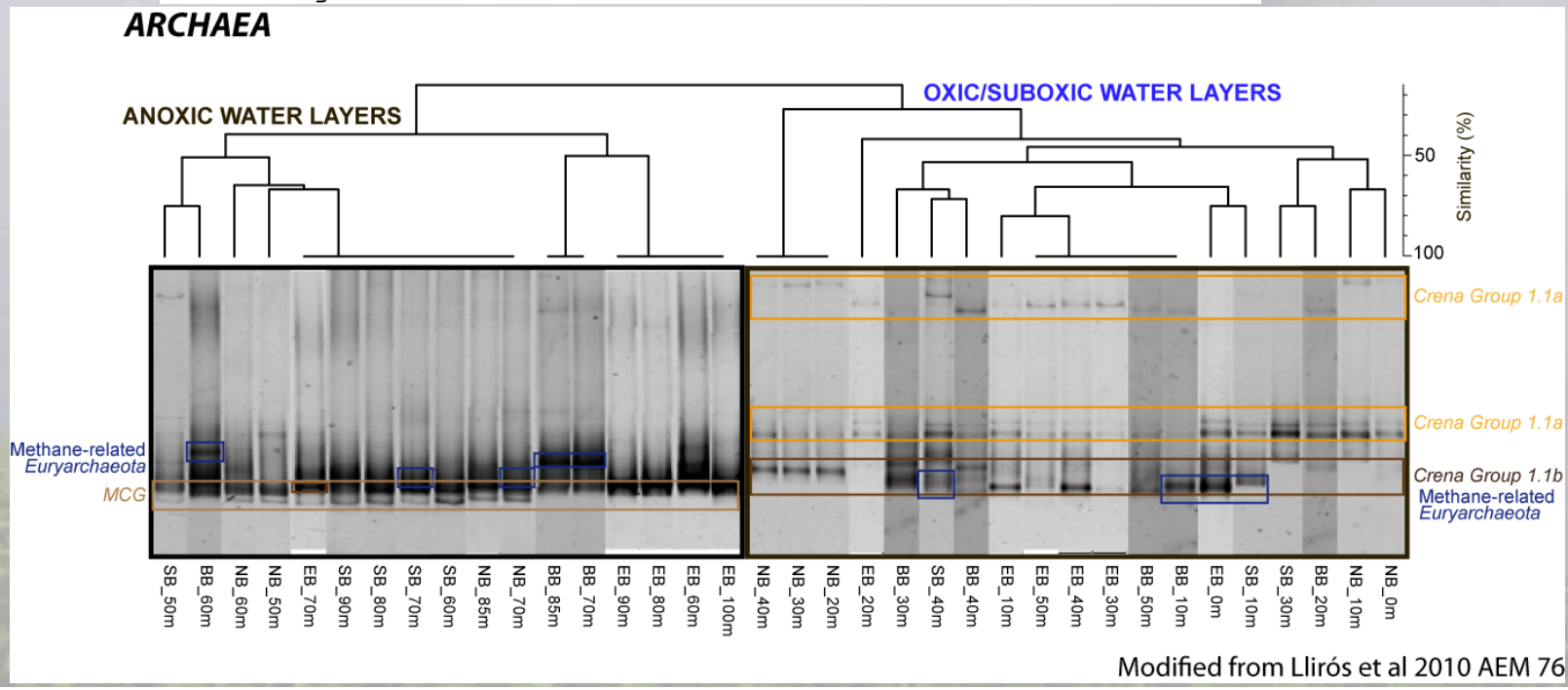

Modified from Llirós et al 2010 AEM 76

Snapshot on Processes in lake Kivu