Geophysical Research Abstracts Vol. 21, EGU2019-12574, 2019 EGU General Assembly 2019 © Author(s) 2019. CC Attribution 4.0 license.



## Microbial diversity in the deep subsurface of Lake Ohrid

Camille Thomas (1), Alexander Francke (2), Bernd Wagner (3), and Daniel Ariztegui (1)

(1) University of Geneva, Department of Earth Sciences, Geneva, Switzerland (camille.thomas@unige.ch), (2) School of Earth and Environmental Sciences, University of Wollongong, Wollongong NSW, Australia (afrancke@uow.edu.au), (3) Institute of Geology and Mineralogy, University of Cologne, Cologne, Germany (wagnerb@uni-koeln.de)

Lake Ohrid (Macedonia) has been the target of an ICDP drilling to investigate evolution dynamics and paleoclimatic changes recorded in the oldest lake in Europe. The 584 m of sediment archive obtained in 2013 (DEEP core) show clayey to silty lithologies, differing between glacial and interglacial stadials. Previous studies have highlighted changes in climatic conditions resulting in differential biogeochemical cycling the lake and shallow sediment (Francke et al., 2016; Just et al., 2016). Microbial communities are the main actors of this biogeochemical cycling and their activity results in early diagenetic transformation in the sediments. Geomicrobiology studies have shown that climatic conditions strongly influence the sedimentary microbial diversity (Vuillemin et al., 2018). We here investigated this diversity using 16S rRNA gene sequences along the upper ca. 200 m of the DEEP core from Lake Ohrid.

Results show that Atribacteria, Betaproteobacteria, Bathyarchaeota and to a lower extent Dehalococcoidia phyla structured the community but their occurrence appears to be independent from each other. Atribacteria and Bathyarchaeota together with Dehalococcoidia have been described in the rare investigations of deep lacustrine biosphere (Vuillemin et al., 2018) and were also commonly encountered in ocean sediments. Their metabolic versatility is adapted to low energy environments where they can realize the fermentation of various substrates (sugars, propionate and amino acids). Betaproteobacteria-associated sequences were often co-occurring with cyanobacterial sequences that suggest preservation of ancient DNA from the water column.

We compared the richness and diversity of all phyla with environmental parameters measured in corresponding intervals to test for the relationship between paleoenvironmental conditions and the subsurface biosphere. We found no significant relationship between any phylotypes and given environmental parameters, nor with sediment age or glacial-interglacial stadials. Our preliminary results support a weak recording of early diagenetic processes and their actors by bulk prokaryotic sedimentary DNA in Lake Ohrid, which might suggest rapid turnover and replacement by specialized low-energy clades of the deep biosphere.

Francke, A., Wagner, B., Just, J., Leicher, N., Gromig, R., Baumgarten, H., Vogel, H., Lacey, J.H., Sadori, L., Wonik, T., Leng, M.J., Zanchetta, G., Sulpizio, R., and Giaccio, B., 2016, Sedimentological processes and environmental variability at Lake Ohrid (Macedonia, Albania) between 637 ka and the present: Biogeosciences, v. 13, no. 4, p. 1179–1196, doi: 10.5194/bg-13-1179-2016.

Just, J., Nowaczyk, N.R., Sagnotti, L., Francke, A., Vogel, H., Lacey, J.H., and Wagner, B., 2016, Environmental control on the occurrence of high-coercivity magnetic minerals and formation of iron sulfides in a 640ka sediment sequence from Lake Ohrid (Balkans): Biogeosciences, v. 13, no. 7, p. 2093–2109, doi: 10.5194/bg-13-2093-2016. Vuillemin, A., Ariztegui, D., Horn, F., Kallmeyer, J., and Orsi, W.D., 2018, Microbial community composition along a 50 000-year lacustrine sediment sequence: FEMS Microbiology Ecology, , no. February, p. 1–14, doi: c.