

# Bioinformatics Seminar Series

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14:00-15:00

Contact: Hiroyuki Ogata (ogata@kuicr.kyoto-u.ac.jp)

### Microbial ecology in deep freshwater lakes

#### Dr. Yusuke Okazaki

*Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology*  
y.okazaki@aist.go.jp

#### **Abstract**

Although freshwater ecosystems occupy a small portion of the earth's surface, these areas cycle petagrams of carbon per year globally and are of great importance to humans as drinking water sources. Compared with shallow freshwater ecosystems, deep lakes are fewer in number but are larger in water volume and characterized as a place for important biogeochemical cycles. Further, deep lakes are vulnerable to anthropogenic impacts such as climate change and eutrophication. Microbial processes are keys to understanding these ecological and biogeochemical mechanisms. In this seminar, I will present an overview of my works, which have been focusing on the unique diversity and ecology of the bacterioplankton in deep freshwater ecosystems. Further, I will introduce a future perspective of my research, which is going to exploit a huge genomic dataset generated from multiple deep lakes to challenge research topics beyond the microbial ecology of deep freshwater lakes.

#### References

- 1) Okazaki Y, Hodoki Y, Nakano S. (2013) Seasonal dominance of CL500-11 bacterioplankton (Phylum Chloroflexi) in the oxygenated hypolimnion of Lake Biwa, Japan. *FEMS Microbiology Ecology*, 83: 82-92.
- 2) Okazaki Y, Salcher MM, Callieri C, Nakano S. (2018) The broad habitat spectrum of the CL500-11 lineage (phylum Chloroflexi), a dominant bacterioplankton in oxygenated hypolimnia of deep freshwater lakes. *Frontiers in Microbiology*, 9: 2891.
- 3) Okazaki Y, Nishimura Y, Ogata H, Yoshida T, Nakano S. (2019) Genome-resolved viral and cellular metagenomes revealed potential key virus-host interactions in a deep freshwater lake. *Environmental Microbiology*, 21: 4740-4754.
- 4) Hiraoka S\*, Okazaki Y, Anda M, Toyoda A, Nakano S, Iwasaki W\*. (2019) Metaepigenomic analysis reveals the unexplored diversity of DNA methylation in an environmental prokaryotic community. *Nature Communications*. 10: 159.