

Eawag Seminar Invitation

Composition, turnover, and acclimatization of ocean microbial communities at global scale

Speaker **Prof. Shinichi Sunagawa**
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When **March 15, 11.00 – 12.00 a.m.**

Where **Forum Chriesbach, room C20, Eawag Dübendorf**

Abstract Marine microbial communities cope with a variety of environmental gradients that impact their global distribution, community structure, and transcriptomic activity. Recent surveys have shown that microbial community compositions in tropical, sub-tropical, and temperate waters are largely governed by seawater temperature. Notably, the rate of seawater temperature change is highest in Arctic regions, which are generally more challenging to access. Thus, a better description of microbial diversity in these regions and an improved understanding about microbial responses to temperature change at global scale are important goals. Here, we analyse an extended dataset of 367 metagenomes and metatranscriptomes from 126 globally distributed sites collected during the Tara Oceans Expedition (2009-2013). This dataset covers a latitudinal range of 143° across all main oceanic regions including the Arctic Ocean. On both hemispheres, we observe a strong separation of the polar oceans at around 60°, which is congruent in taxonomic and gene functional composition, as well as community gene expression. An integrated analysis of metagenomic and metatranscriptomic data, using a newly established ocean microbial reference gene catalog of 47 M genes, reveals that the relative contribution of organism composition changes and gene expression changes differs across the global ocean as a function of temperature and/or latitude. The results are expected to help us differentiating responses of marine microbes to the impact of ocean warming.