

## The community composition and diversity of epilithic bacterium and microalgae in a Japanese river system during irrigation season

\*Tohru Ikeya<sup>1</sup>, Chia-Ying Ko<sup>2</sup>, Elfrizson Martin Peralta<sup>3</sup>, Takuya Ishida<sup>1</sup>, Yoshitoshi Uehara<sup>1</sup>, Satoshi Asano<sup>1</sup>, Noboru Okuda<sup>1</sup>, Masayuki Ushio<sup>4,5</sup>, Shohei Fujinaga<sup>4</sup>, Ichiro Tayasu<sup>1</sup>, Tomoya Iwata<sup>6</sup>

1. Research Institute for Humanity and Nature, 2. Institute of Fisheries Science, National Taiwan Univ, 3. Department of Biological Sciences, Univ of Santo Tomas, 4. Center for Ecological Research, Kyoto Univ, 5. PRESTO, Japan Science and Technology Agency, 6. Faculty of Life and Environmental Sciences, Yamanashi Univ

The surface of river stones serves bacterium, microalgae, protozoas, and insect larvae as one of the major habitats in a river. These organisms are exposed to running river water in which discharged water, sediments and allochthonous organic materials are induced from upper sites. We conducted a cooperative research of the riverine benthos to assess the possible effect of anthropogenic effect of land use on water quality and microflora of epilithic communities in the Yasu River watershed in late spring. This study examined the site-specific variability of the bacterial and algal composition using MiSeq 16S rRNA gene sequencing and cell counting. These data were compared with a set of environmental parameters and photosynthetic pigments by multivariate ordination analyses.

The sequence data of amplicons after amplification of 16S hypervariable regions 3 were obtained by a MiSeq (Illumina) sequencer to collate with SILVA database using the USEARCH package and the pipeline. The yield of the amplification was so low at one of the 30 sites that the analysis was made at 29 sites for the OTU analysis. Because cyanobacterial OTUs comprised 342 OTUs in a total of 5545 OTUs, the rests were assumed as heterotrophic bacterium and were grouped separately. As high as 180 species of microalgae were also discriminated by an optical microscopy. The spatial distribution of both bacterial OTUs and microalgae indicates a cluster of upper stream sites where the concentration of phycoerythrin seems to be high. So, some environmental gradient is supposed to induce such site-specific distribution of bacterium, microalgae and phycobilin pigments. Non-metric multidimensional scaling (NMDS) showed that the distribution of autotrophic microbes, that are cyanobacterium and microalgae, have a significant correlation with water temperature, dissolved organic carbon, altitude, water current, land use, and turbidity, though cyanobacterium also have a significant correlation with pH whereas microalgae has a significant correlation with DO. In addition to water temperature, dissolved organic carbon, altitude, water current, land use, and turbidity, the stream order is included in significant factors for the distribution of heterotrophic bacterium.

Keywords: bacterium, microalgae, 16S, MiSeq