

The examination of environmental factors on the community composition of riverine bacteria and microalgae in an epilithon during irrigation season in the Yasu River, Japan

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We analyzed the composition of bacteria and microalgae which were collected at the 29 sampling sites at the Yasu River in late spring, 2016, in order to assess the possible effect of anthropogenic effect of land use on the microflora of epilithic communities. The analyses were made with MiSeq 16S rRNA gene sequencing and cell counting for the bacteria and microalgae, respectively. A control data set was obtained at the same sampling sites at the Yasu River in 2012 to elucidate the general and seasonal dynamics of the microbial and algal communities.

The previous examination has shown that both the microbial and algal communities in the Yasu River watershed during irrigation season showed site-specific differences. 1) The important environmental gradients for microbial communities may be formed by land use. 2) The important parameters were temperature, DOC, current, and PP of EOM. 3) The spatial pattern of phycobilin occurrence was consistent to the β diversity deduced from algal counts and metagenomics. The further analyses of the bacterial and algal taxa have shown site-specific occurrence of particular groups during irrigation season, which suggest that particular functional groups determined the spatial pattern of species diversity in response to the environmental factors, such as nutrient, temperature and turbidity.

Keywords: bacteria, microalgae, 16S, MiSeq