

Effects of the graphene photocatalysis treatment on microbial eukaryotic community structure in Lake Xingyun, southwestern China

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eDNA analysis of microbial eukaryotic composition

The microbial eukaryotes structures with and without the graphene photocatalysis treatment in Lake Xingyun are compared using eDNA. Our results shown in Fig. 1 and 2.

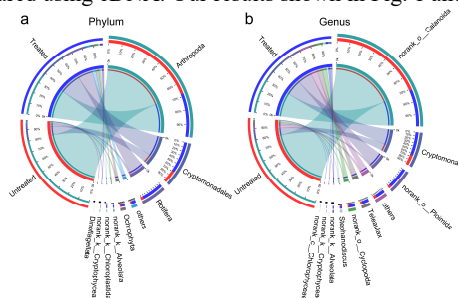


Fig 1: The eukaryotic composition of all water samples. Wilcoxon rank-sum test bar plot on Genus level

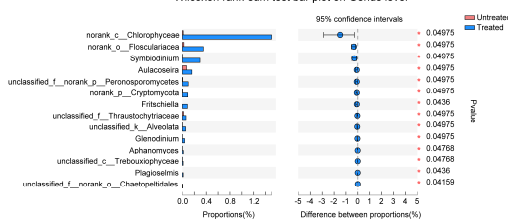


Fig 2: Comparison of eukaryotic composition between the untreated and treated groups at genus level.

Discussion of Results

The eutrophication of aquatic environments has become a worldwide problem[1] and the microbial eukaryotes are important in aquatic ecosystem functioning[2]. The graphene photocatalysis is a new method to control eutrophication and the microbes compositions the mechanisms remain to be understood. Our study provides the first insight into diversity patterns of microbial eukaryotes in Lake Xingyun using eDNA, which is a powerful tool for detecting diverse microorganisms[3].

[1] Paerl *et al.* (2013) *Science* **342**(6157), 433-434. [2] Fuhrman *et al.* (2009) *Nature* **459**(7244), 193-199. [3] Song *et al.* (2015) *Journal of Basic Microbiology* **55**(10), 1203-1211.