

Lake water as reservoir of antibiotic resistance genes constitutively present within the natural microbial community

The fate of antibiotic resistance genes (ARGs) in environmental microbial community is largely unknown although ARGs can constitute a threat for human health. In order to understand the dynamics and the relations of ARGs with biotic and abiotic factors in aquatic environment, we sampled water for 1.5 year in four stations of Lake Maggiore; for one of them (Ghiffa), we also sampled water from the whole water column. Moreover, for Ghiffa station, limnological parameters and prokaryotic cell abundance were determined. Each water sample was filtered and processed for the presence of twelve ARGs by PCR and, for the positive ARGs, qPCR protocols were developed. In order to investigate the relations between ARGs profiles and microbial community composition, we also sampled water every day for one week in Pallanza station. The DNA recovered during both the 18 months' (long term) and the week (short term) monitoring were analyzed for the presence and abundance of ARGs and for the microbial community composition by 16SrDNA Illumina sequencing. Four ARGs were detectable in all stations during the whole sampling campaign, for instance tet(A) and sulII genes resulted quantifiable in more than half of the samples, and their abundance was positively correlated to oxygen and negatively to chlorophyll a, while str(B) and blaCTXM were present but rarely quantifiable. The composition of the microbial community was stable during the week while a seasonality was observed during 1.5 year of analysis. Moreover a potential relation between the presence of blaCTXM and the abundance of Flavobacteria was observed. All together, these results suggest the Lake as reservoir of ARGs fixed within the natural microbial community, thus it can constitute a hazardous hotspot for the transmission of antibiotic resistance to human pathogens.

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