

Eukaryotic communities in drinking water distribution systems around the globe: composition and influencing factors

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Eukaryotes are ubiquitous in natural environments where they play an important role in microbial communities. However, information regarding their presence and functional potential in drinking water distribution systems is scarce, as well as the knowledge regarding what factors affect these micro-organisms. In this study we explore the diversity of eukaryotes present in drinking water distribution systems by analyzing DNA sequences retrieved from metagenomic analyses of drinking water samples collected in distribution systems spread in four continents. Starting from this dataset, we identified the eukaryotes present in these systems and provided an evaluation of the factors (e.g., water quality, geographic distance) affecting their compositional and functional potential diversity, highlighting, also, characteristic taxonomic and potential functionality changes caused by design factors, e.g., the type of water source and the disinfection strategy employed. Our analysis identified more than 40 eukaryotic phyla, being *Arthropoda*, *Rotifera* and *Basidiomycota* often the most detected. Eukaryotes linked with putative pathogens growth, as free living amoebas, were detected in most systems, indicating their pervasive presence in drinking water systems. Specific system characteristics affected the identified phyla. For example, even in the presence of exhaustive water treatments, systems fed by surface water presented often a large fraction of phototropic micro-organisms (e.g., *Bacillariophyta*). In addition, eukaryotic communities are influenced by physico-chemical water quality parameters, with residual disinfectant exhibiting a primary importance. Overall, this study advances our understanding of drinking water distribution systems microbiology, clarifying the microbial ecology of eukaryotes and highlighting the factors affecting their presence and functionality.