

## Zooplankton as refuge for invading bacteria

It has long been known that zooplankton species, such as daphnids and rotifers, are populated with bacterial epibionts. Nonetheless, studies on the impact of non-parasitic bacteria are still scarce. In this study we analysed the consequences of this colonisation on the distribution of potentially pathogenic and antibiotic resistant bacteria in freshwater systems. This is based on the hypothesis that potential pathogens have a selective advantage when growing in biofilms, as has been shown in clinical settings. Thus we postulate that attaching to animals might allow potential pathogens, e.g. deriving from the efflux of a waste water treatment plant (WWTP), to survive in freshwaters. Additionally the movement of the animal transports the bacteria away from the point-contamination to more pristine waters.

We experimentally show that, if added to a natural bacterial community, *Escherichia coli* attaches to daphnids and derives particularly well in the gut of the animals, where they naturally do not form part of their microflora, whilst decreasing in abundance in the surrounding water. Moreover, the presence of daphnids decreased the abundance of a tetracycline resistance gene (*tetA*) in the surrounding water, whilst a higher number of *tetA* gene copies were detected in the animals. In addition we tested whether zooplankton species form a surface for the horizontal gene transfer, of e.g. antibiotic resistant genes, from one *E. coli* strain to another. In order to expand our hypothesis to natural environment we sampled Lake Maggiore at three points with increasing distance to an inflow of a WWTP and compared the microbial community on various zooplankton species as well as on stones and in the sediment. Whereas similar relationships have been described in marine systems, e.g. *Vibrio cholera* and Copepods, this is the first study that confronts the potential role of zooplankton in the spread of potential pathogens in freshwater systems.

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