

Title:

Assessing the frequency of microcystin biodegrader and mlrA gene detection in Lake Zurich

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Abstract (300 words maximum): :

Global warming and anthropogenic-induced alterations in nutrient ratios favour harmful algal blooms (HABs) in freshwaters, posing a threat to human and animal health. In Lake Zurich, the filamentous cyanobacterium *Planktothrix rubescens* benefits from lake warming and has become the dominant microbial organism, forming massive seasonal blooms. Abiotic stressors such as intense UV radiation and turbulences disrupt *P. rubescens* filaments, releasing the bioactive secondary metabolite microcystin (MC) into the surrounding matrix. Although physico-chemical transformation of MC is slow, concentrations of MC remain undetectably low throughout all seasons. Thus, we hypothesized that MC biotransformation must be a common trait in Lake Zurich. We assessed the seasonal and spatial dynamic of bacterial MC degraders in the context of *P. rubescens* population dynamics and investigated the ecological role of the only described MC degradation pathway via the *mlr* gene cluster. We used a dilution to extinction strategy coupled with the most-probable number method to determine the frequency and seasonal succession of microcystin-degrading bacteria in three water layers. Lake water samples were inoculated with lysed axenic *P. rubescens* filaments and MC concentrations quantified by HPLC-MS. The presence of *mlrA* gene in selected enrichments was examined with semi-nested PCR. Highest abundances of degraders was found in the upper hypolimnion during summer stratification. By early September, the degrader maxima shifted upwards, persisting in the metalimnion until late autumn, when thermal mixing caused equal distribution throughout the water column and induced a pronounced increase in degrader abundance. This coincides with the population pattern of *P. rubescens*. Detection of the *mlrA* gene in the most abundant fraction of MC degraders remained unsuccessful. In conclusion, our study highlights the dynamic interplay between *P. rubescens* proliferation and the seasonal abundance of MC degrading bacteria.