Title:
Identification of ecologically relevant microcystin degraders in Lake Zurich

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Abstract (300 words maximum): :
Rare bacteria that rapidly respond to substrate pulses (copiotrophs) have higher and more diversified functional potential than the abundant oligotrophs. In Lake Zurich, the filamentous cyanobacterium Planktothrix rubescens will cause such seasonal maxima in available organic matter during the breakdown of their metalimnetic summer population due to abiotic stressors. The onset of autumnal thermal mixing entrains P. rubescens filaments in the turbulent upper water layers, leading to annual blooms, but also exposing them to higher shear forces and unfavourable irradiation levels. One compound released by disrupting cyanobacterial cells is the bioactive secondary metabolite microcystin (MC), a recalcitrant heptapeptide toxic to most eukaryotes, including humans. However, concentrations of MC in Lake Zurich are undetectably low, despite the size and seasonal fluctuations of the P. rubescens population, suggesting efficient microbial MC biotransformation. Applying a most-probable number approach, we found that the estimated concentrations of MC degraders in Lake Zurich were seasonally and spatially highly variable, ranging from <1% of the total bacterial community in depths mostly void of P. rubescens during lake stratification to up to 10% throughout the upper water column after autumn mixing. Over this latter period, we enriched the abundant fraction (>1%) of the lake community in batch cultures. In these experiments, lysed axenic P. rubescens filaments were replaced by pure MC as substrate to promote the formation of simplified MC degrading consortias. We performed flow cytometry and MC measurement for all cultures before conservation for subsequent sequence and bioinformatic analysis. The number of communities obtained reflected our MPN estimates, with highest growth success after onset of autumn mixing. Surprisingly, we detected MC removal for only every third community after 11 inoculation days. Planned work includes the long-read sequencing of 16S rRNA genes from selected enrichments by Oxford Nanopore MinION to identify those bacteria that are involved in or profit from MC biotransformation.