Title:

Exploratory isolation of viruses revealed diverse phage repertoire in alpine streams

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Abstract (300 words maximum): :

Streams are lifelines that perfuse Earth's landscape. Crucially, complex microbial communities organised as biofilms, colonise streambeds, drive critical ecological processes, and regulate biogeochemical cycles. While the global impacts of stream biofilms are increasingly recognised, viruses that infect bacteria to propagate - namely bacteriophages (phages) - remain largely unexplored. Here, we present a pioneering effort to isolate and characterise phages derived from alpine stream environments. Briefly, we collected >120 L of water from a Swiss mountain stream which was filtered and concentrated by 100-fold via tangential flow. We then screened the samples on 30 bacterial hosts isolated from mountain stream biofilms using soft-agar overlay where visible plaques caused by phage-killing on bacterial lawns, were cored and doublepurified. Our efforts yielded 39 phage isolates spanning across 7 bacterial host species. The majority were represented by phages infecting Rahnella and Massilia genera; both of which are common members of stream biofilms. We also observed diverse plaque morphologies and electron microscopy imaging revealed myoviruses and siphoviruses within our collection. We next sequenced and annotated our phage isolates and report genome sizes ranging from ~40 to 200 kb. Intriguingly, closer inspection of Rahnella phage genomes implied a microdiverse viral group defined by the varying presence of coding regions and auxiliary metabolic genes that could potentially "benefit" their host. This viral microdiversity could reflect on phage adaptation towards microdiverse bacterial communities, previously reported in oligotrophic mountain streams. Collectively, our exploration revealed an untapped assortment of phages in alpine streams. We envisage to continue expanding our phage library with the endeavour to next investigate their functional impact on stream biofilm communities.