Alpine lakes benthic viral community structure and diversity: a metagenomic and ecological approach

HORIZON 2020

Alpine lakes benthic viral community structure and diversity: a metagenomic and ecological approach

Informe

Información del proyecto

metaVir-Alp

Identificador del acuerdo de subvención: 704603

Sitio web del proyecto 🗹

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Proyecto cerrado

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Este proyecto figura en...

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¿Inmenso, complicado, (des)ordenado? Descifrando los secretos del cosmos

Periodic Reporting for period 1 - metaVir-Alp (Alpine lakes benthic viral community structure and diversity: a metagenomic and ecological approach)

Período documentado: 2016-11-01 hasta 2018-10-31

Resumen del contexto y de los objetivos generales del proyecto

Microbial communities are the main responsible of biogeochemical cycles (cycling of substances) in aquatic systems. These cycles can be strongly affected by human activities and thus by climate change with consequences on the release of greenhouses gases, such as CO2 and CH4. Viruses are a key and yet neglected component of these microbial communities. They kill and modulate the abundances of bacteria, archaea, protists and fungi, which are a dominant part of the biomass in aquatic systems. Through host lysis, they therefore have an impact on bacterial respiration, CO2 emission and nutrients cycles. Further, viruses are responsible for microbial evolution by selecting microbes resistant to infection and by genetic material transfer. Freshwater ecosystems represent only 0.01% of water on Earth and yet they are of great ecological importance supporting 6% of global biodiversity and offering a wide range of ecological services (e.g. irrigation, fishing, pasturing, tourisms, outdoor activities and hydroelectricity production). Freshwaters are among the most threatened ecosystems globally

Viral communities in freshwaters are globally under-studied, and virtually no information exists on Alpine lakes.

metaVir-Alp aimed to characterise the genetic diversity, structure and function of viral and bacterial communities in freshwater systems along an altitudinal gradient combining metagenomics, microbiology, and advanced computation. As model system, I used the threated Alpine lakes. Specifically, we focused on lake sediments that are hotspots of carbon cycling due to the large deposition of terrestrially derived carbon and the greenhouse gases outgassing (by microbial mineralization).

During the two years, three intensive and challenging sampling sessions (Pre-sampling 2017, Summer 2017 and Winter 2018) were carried out collecting water and sediment from two sites in 4 Alpine lakes along an altitudinal gradients (from 680m to 2000m). We compiled a comprehensive dataset with physico-chemicals data for each sampling point in each lake (D1). We produced a DNA bank of 34 microbial and 34 viral communities (D2), which is and will be used to perform highthroughput sequencing in order to have a comprehensive genetic characterisation of freshwater microbial and viral communities. This resource is a valuable information that will give an insight of the viral genetic diversity and function in freshwater. Further, the successful secondment at the Fondazione Edmund Mach generated also a productive collaboration on a side project on Cyanobacteria. Equally important, this fellowship allowed me to resume successful my career after two years of maternity leave, by completing a novel research project and acquiring key skills that permitted my career to go further.

Trabajo realizado desde el comienzo del proyecto hasta el final del período abarcado por el informe y los principales resultados hasta la fecha

The project started in November 2016. Working with environmental viruses involved many challenges both experimentally and computationally. Initially, we needed to understand how much material (particularly for sediment) we had to collect in order to have enough viral DNA to produce DNA libraries. Thus, we performed a pre-sampling session in March 2017 where we collected different amount of sediment and water at the three defined layers (Epilimnio, Thermocline, and Ipolimnio). In addition to viral DNA, we also extracted microbial DNA at various stage of the serial filtration (10 µm, 5 μ m and 0.22 μ m) involved in the viral enrichment protocol. The genetic material was then sequenced generating 5 viromes and 2 metagenomes through shotgun sequencing and 33 16S through amplicon sequencing. Data showed that the final viral fraction contained a substantial portion (from 10% to 40%) of microbial taxa recovered from filters used during the filtration process, and therefore particular care should be taken during the computational analysis of viromes. The presampling session results allowed us to design properly the summer and winter sessions and to produce a manuscript on methodological issues of viral enrichment protocol (In preparation). Summer and Winter field sessions covered 4 lakes, and samples were collected from water (3 depths) and sediment (Deliverable 1). Winter session was challenging as we sampled lakes ice covered. Lagorai lake, which is located at 2000 m, was particularly difficult since it was unreachable by car and covered by ice and 2 meters of fresh snow. We managed to reach it by helicopter and to collect two water samples and a sediment sample, helped by a skilled alpine guide. Tangential Flow filtration and centrifugation steps were used to produce our final viral-enriched fractions. Then, viral and microbial DNA libraries were generated for sequencing on Illumina HiSeq 2500. At this stage we faced a dilemma as viromes library kept failing. We, thus, performed extra experiments to find the right protocol and to characterise in detail the viral genetic material, such as the DNA High Sensitivity Bioanalyzer assay. After weeks of frustration, we found the right protocol and prepared 27 viral DNA libraries to run on an Illumina HiSeq 2500 platform (Deliverable 2). This generated a highly valuable viromes sequence database that will be analysed with a specific virus characterisation pipeline developed in our Lab. Two years project were not enough to accomplish all aims. The project was challenging and had a massive field campaign, which required a lot of time and energy. I am still working on WP3 and WP4. However, since my stay at the Computational Microbiology Lab is prolonged, I will be able to finish the analysis.

In addition to the training scope, the secondment at the Fondazione Edmund Mach generated an

interesting collaboration on the genetic characterisation of the Cyanobacteria Thyconema, an important species able to produce neurotoxins that are harmful for human and animal health. Further, three new microbial genomes of potential symbionts of cyanobacterial organisms were also recovered and assembled. Two peer-reviewed papers were published.

metaVir-Alp results were presented to the scientific public during two international conferences (FEMS and ISME). Dissemination to the non-scientific audience involved different outreach events, such as a seminar to a local High School and the participation to the "Notte del Ricercatore" at Museum of Science of Trento (MUSE).

Avances que van más allá del estado de la técnica e impacto potencial esperado (incluida la repercusión socioeconómica y las implicaciones sociales más amplias del proyecto hasta la fecha)

Work Package 1 and 2 has generated a comprehensive dataset of genetic information of viral and microbial communities with the associated metadata (abiotic variables of each community sample point) of four Alpine lakes. This is an unprecedented complete dataset of benthic microbial community of the threatened Alpine lakes. This data allow us through WP3 and WP4 to have a detailed characterisation of viral and microbial community composition and genetic diversity by means of phylogenetic analyses. We will also perform a cross-comparison among lakes of viromes and microbiomes in relation to sequences similarity and richness. Additionally, the temporal and spatial dimension that characterises the dataset permits to expand and validate the computational pipeline for virus developed in our Lab.

Alpine lake ecosystems have considerable cultural and socioeconomic values, and represent hotspots of biodiversity and carbon cycling. This project improved and deepened our understanding of microbial diversity and processes in sensitive Alpine lakes with implications for their conservation across EU countries.



Sediment sampling at Calaita Lake (1620 m)

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