Compte-Rendu de la réunion du 14 mai 2024

INTERREG FR CH (2024-2026) ALGA

ALGA WP1 Genes and Toxins meeting 14 May 2024

Present : Nicolas Tromas, Stéphan Jacquet; Valentin Vasselon; Mridul Thomas, Bastiaan Ibelings

Absent with notification: Carratalà Anna; Janssen, Elisabeth

The participants were invited to express their main interest in the topic. Next a discussion would follow where we see how we can benefit from each others activities.

Valentin

SynAqua

Samples taken from Synaqua could be useful to compare what was sampled 7 years ago (June 2017) compared to what will be done with ALGA

- SynAqua – share link for interactive maps
- https://synaqua.hub.inrae.fr/actions/cartographie/cartographie-des-rives-du-leman
- Revisiting some SynAqua sites for ALGA project (last done 2017 for diatoms)
- All the Synaqua deliverables are accessible here : https://synaqua.hub.inrae.fr/livrables
- You can download BenthoTorch and physico-chemical data associated to those samples provided by Frederic Rimet (Synaqua_Bentho_Physico.zip)
- We have preserved biofilms collected from stones from Synaqua project, they are preserved in 70% ethanol at 4°c (high risk of DNA degradation).
- We also have access to DNA extracted during the project with the Nucleospin Soil Kit from Macherey-Nagel. With Stephan we checked where they are stored and they are available but with low volume (around 15µL of DNA extract). Table with DNA concentrations can be provided once interested sites will be validated.

EcoAlps : another Interreg project names Eco-AlpsWater (EAW, 2018/2020) on several lakes and rivers within the Alpine space: https://www.alpine-space.eu/project/eco-alpswater/

- Valentin performed postdoc within this project on the benthic diatom part, but benthic and pelagic samples were collected to target several biological groups including Cyanobacteria (16S metabarcoding)
- Existing data for some lakes on toxins (LCMS-MS by Nico Salmaso) from 2019 / 2020
- Associated article : "DNA sequence and taxonomic gap analyses to quantify the coverage of aquatic cyanobacteria and eukaryotic microalgae in reference databases: Results of a survey in the Alpine region" https://www.sciencedirect.com/science/article/abs/pii/S0048969722022689 with associated data accessible here : https://zenodo.org/records/5822484
- I also attach a table of 16S metabarcoding results focusing Cyanobacteria on benthic and pelagic samples on French sites of the project (only pelagic for the Leman, but benthic and pelagic results on Bourget lake) : "eaw16S_data_12Oct2020_FR.xlsx".
- For more data and info, I would like to validate first with Nico Salmaso and Isabelle Domaizon before sharing, but pretty sure there will be no problem.
- Will share eDNA protocols from EcoAlps to
- Lake stone biofilm sampling from EAW project : https://www.protocols.io/view/lake-biofilms-sampling-for-both-downstream-dna-ana-kqdg35yjpv25/v1
- River biofilm sampling from EAW project : https://www.protocols.io/view/river-biofilms-sampling-for-both-downstream-dna-an-e6nvw9mjdgmk/v1
- As cyanotoxin analysis was performed on those biofilm samples, biofilm were first collected within sterile water and subsampled in 10mL aliquotes: 10 mL preserved in ethanol for DNA extraction, 10 mL for dry/wet determination and 10 mL filtered on GF/C filters prior -20°C storage for toxin analysis : see document to download "Eco-AlpsWater_Sampling_Cyanotoxins draft_20Dec2018.pdf"

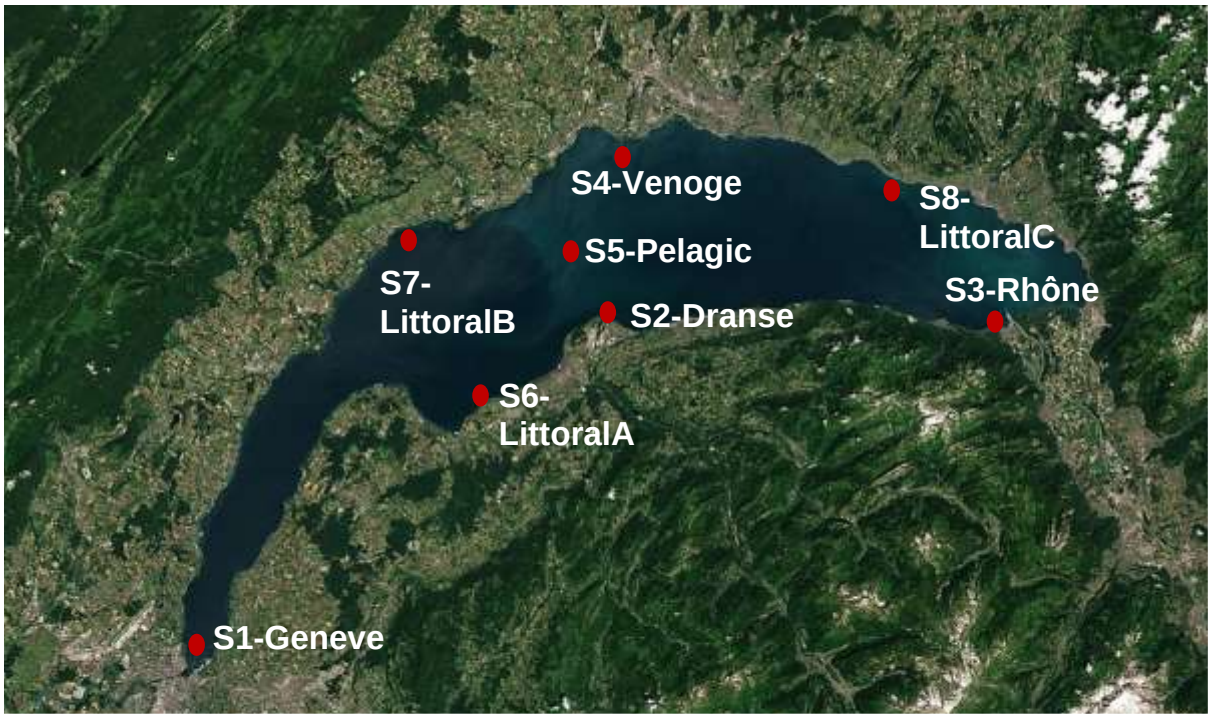
Plans for ALGA

- Sampling streams for benthic cyanobacteria in summer 2024 (Drance, Rhone, ...). The idea is on thhe 24th / 25th June to perform sampling of biofilms in the lake Leman following Synaqua positions close to rivers (Rhône, Dranse, maybe 1 or 2 small rivers) on the French side.
- We will also collect biofilm directly in the rivers, maybe 500m upstream from the lake.
- If samples have to be compatible with cyanotoxin analysis, we can use the EAW protocol or another protocol fitting with Eawag (Lilly) requirements.

Stephan: will help in choosing sites and assist in sampling with VV and NT

Nico

<u>Suggested</u> sampling for the snapshot based on ZABr:



Benthic cyanobacteria

- For the ZABR snapshot, the idea is to capture the sites where we would have more benthic cyano and also more toxic ones. Here, several sites will be samples - mouth with larger effluents as a priority (Dranse, Rhone) – porblay a small one too (Redon)
- To quickly get an answer of which cyanos are present in the mats, we could use long reads 16S to identify the cyano (we just have to take into account that short and long reads will be used for the DNA extraction). DNA extraction might be a bit more sensitive for long-reads as we don't want to extract several times the same sample. If we plan to do long reads, it might be good to directly use specific DNA extraction for this sequencing approach.
- With metaG, we would know much more accurately which toxin synthetase genes and genes associated with other secondary metabolites are present in the benthic cyanobacteria

Planktonic cyanobacteria

- About the planktonic ones, if there is more sampling, I might be interested in samples where Planktothrix could be "easily" isolated (individually – single filament) (if possible).

Bas / Anna / Lilly / Mridul (collaboration UniGe / EPFL / Eawag)

The idea is to share postdoc time – contract at UniGe – between the partners. We aim to find additional funding to extend the 2 year contract to at least 3 years. Focus is on planktonic phytoplankton including cyanobacteria, to ultimately link phenotypic (from image analysis pipeline in development) and genotypic data. Samples at high frequency taken from LeXPLORE.

- Ongoing collaboration with Anna Carratala and Elisabeth Jansen on planktonic cyanobacteria (16S) and their metabolites. We have two years of data taking samples from LeXPLORE
- Limited capacity at Eawag for toxin (known `WHO`toxins) from mats and plankton (in case blooms are observed)
- Sampling couple streams in CH (e.g. Aubonne, Versoix) for benthic cyanos – if Master students available to help out

Mridul: we should finalise protocols for standardised sampling, storage and analysis for metabarcoding and toxins (Lilly)