

## Conference Abstract

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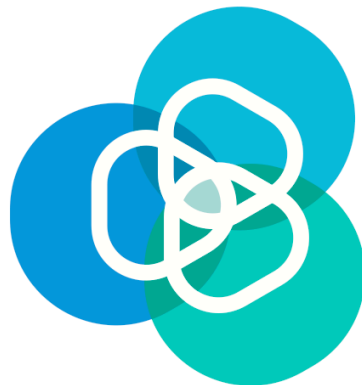
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# ParAqua Grantees Conference Abstracts Booklet

 Serena Rasconi, Ana Gavrilović

# ParAqua Grantees Conference

**1-2 September 2025, Zagreb (Croatia)  
and Zoom**



**PARAQUA**

**Abstracts Booklet**

# Challenges and possible solutions for detecting and identifying algivores in industrial facilities

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## ABSTRACT

One of the largest challenges that the microalgal industry is facing is the occurrence of microorganisms that are able to either improve the growth and the quality of the algal biomass or cause massive collapse of industrial algal cultures. Culture contamination with grazers and parasites that actively prey on microalgae as well as toxin-producing pathogens can cause important economic losses to the algal producers, rendering tons of algal biomass unfit to be either harvested or commercialized<sup>1</sup>. Grazers can be multicellular eukaryotes such as rotifers and small crustaceans or unicellular microorganisms. Among the latter, ciliates, (zoosporic) microflagellates, true amoebae (Amoebozoa) or microorganisms with amoeba-like life stages are common predators. Predation can involve engulfing the prey or sucking out the cellular contents, a behavior often dubbed as “vampirism” but has the technical term “myzocytosis”. Myzocytosis rather than simple endocytosis takes place when the prey is larger than what the predator can consume by surrounding it with its cell body. Although grazers are often heterotrophs such as ciliates (might also include Ciliophora and Opalozoa), amoebozoans, rhizarians (e.g., amoebae with filiform pseudopods), heteroloboseans and fungi (e.g., chytrids), other organisms such as dinoflagellates and chrysophyceans belonging to lineages able to carry out photosynthesis can become grazers as well. Apparently, many microbial lineages became algivorous by being able to digest chlorophyll and avoid its phototoxicity<sup>2</sup>. Other microorganisms can cause damage by becoming parasites, either endo- or ectoparasites. The latter seem to be often fungi, some of them belonging to known phytopathogenic taxa.

How can microalgal producers fight such a biodiverse menace to their algal cultures? Here are presented the challenges for detecting these biological contaminants as early as possible and its correct identification. What has become clear is that very often these culture-collapsing contaminants cannot be cultured without its prey or host, making their isolation quite challenging. Because of this, many of these contaminants have not been studied before, being absent from databases such as NCBI core\_nt, PR<sup>2</sup>, UNITE and Silva. Possible solutions and strategies will be presented in this talk that will include building new bioinformatic tools and sequence databases, mitigation protocols and early detection methods from molecular biology to microscopy and flow cytometry or the combination thereof.

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# Dissemination activities around the ParAqua database (2023-2025)

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## ABSTRACT

One of the deliverables of the ParAqua COST Action is the development of a dedicated database that collects and makes openly available data gathered from Action participants, complemented by an integrated e-science tool to support researchers and companies in making early, data-informed decisions for algal cultivation and parasite identification. This initiative responds to a key gap in aquatic biodiversity research, where data on parasitic and saprophytic microorganisms are missing or remain hidden into publications despite their potential to be combined and reused. Thanks to a dissemination grant, I presented the initial outcomes of this work at Biodiversity and Ecosystem eScience Conference (BeES) 2023 in Seville (Spain). At that stage, the ParAqua database was in its early development phase, with efforts concentrated on data collection, standardisation, and harmonisation. The abstract highlighted the importance of integrating heterogeneous data sources, including experiments, field observations, molecular data provided by Action participants. This contribution stressed that harmonisation was a prerequisite to ensure the interoperability, and long-term usability of the data. Feedback from experts in the field enabled us to refine the database structure and improve methodological choices. The conference also served as a platform to strengthen collaborations, in particular with LifeWatch ERIC. Together with colleagues from CNR and LifeWatch ERIC, the original abstract was extended into a full, citable, open-access publication<sup>1</sup>, and additional abstracts were later presented<sup>2</sup>. This effort amplified the dissemination potential, ensuring that the database concept and early methodology reached a broader community beyond the Action's direct participants. Two years later, at BeES 2025 in Heraklion (Greece), I presented an updated version of the ParAqua database<sup>3</sup>. The current release integrates both published and unpublished data on the detection of zoospore parasites, as well as their co-occurrence with host species derived from direct observations. At present, the database comprises 16,139 observations, including 352 confirmed host–parasite interactions, integrating data from literature reviews, molecular studies, and field observations. Built upon internationally recognised controlled vocabularies such as Darwin Core, the LifeWatch Traits Thesaurus, and Dublin Core, the platform ensures semantic consistency and interoperability with other biodiversity and ecological data infrastructures. The user-oriented design of the database provides a web interface that allows advanced search and browsing functions, alongside downloadable datasets in CSV format. Collectively, these features make ParAquaBase a versatile tool for advancing ecological and parasitological research and supporting applied contexts such as monitoring and managing algal cultivation systems. The ParAqua database directly contributes to the Action's overarching objectives by building a shared and openly accessible knowledge base. By collecting, harmonising, and disseminating high-quality data, the database promotes transparency, collaboration, and digital science practices in line with Open Science principles. As such, the ParAqua database embodies the Action's mission to fill knowledge gaps, foster interdisciplinary exchange, and provide sustainable tools for the aquatic research community.

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<sup>3</sup>LifeWatch ERIC. (2025). The LifeWatch ERIC Biodiversity and Ecosystem eScience Conference (BEES) 2025 – *Book of Abstracts*. *LifeWatch ERIC*. <https://doi.org/10.48372/0XWH-3K>

# Impacts of harvesting methods and medium recycling on rheology and composition of recycled medium and cell concentrates of *Limnospira platensis* semi-continuous cultures

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## ABSTRACT

When producing *Limnospira platensis* (Spirulina) it is essential to reuse the exhausted culture medium for sustainability reasons. However, this strategy is challenging given the negative effect the medium has on microalgal growth. While recycling helps reduce costs and environmental impact, it can also result in an increased risk of biological contamination. In this study, *Limnospira platensis* was grown in a semi-continuous mode with daily harvest and dilution ( $0.25 \text{ d}^{-1}$ ) for 50 days with medium refresh (control), or recycle after  $0.22 \mu\text{m}$  or  $10 \mu\text{m}$  filtration, or centrifugation. The concentration of extracellular polymeric substances (EPS) in the medium was 4- to 6-fold higher during semi-continuous growth when compared to batch mode and the highest after centrifugation. Medium recycling reduced growth rates by 30%, but productivity remained unaltered during the experiments ( $0.24 \text{ g L}^{-1} \text{ d}^{-1}$ ). EPS extracted from recycled media had similar compositions (mainly proteins and hydrocarbons) and no influence in the viscosity of solutions. The biochemical composition and rheology of cell concentrates varied widely, especially after centrifugation. The harvesting method affected the partitioning between free EPS in the medium and EPS adhered to the cell wall. If carefully applied to the microalgae industry, these findings can lead to cleaner and more sustainable biomass production. The experiments reported here were conducted during a short term scientific mission (STSM) focused on control strategies for parasitism risk in algal biotechnology, the aim of WG3. Given that no zoosporic parasites were found in the investigated cultures, the results were directed to other topics related to good practices in microalgal biotechnology.

# Industrial Biotechnology Algal Bank (IBAB): The biobank for industrial production, adding a new feature for the development of new products.

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## ABSTRACT

The microalgae production industry has experienced significant growth, driven by its potential to address global food and environmental challenges. Central to this expansion is the role of robust culture collections. On this view, the Industrial Biotechnology Algal Bank (IBAB) by Greencolab was created to ensure industrial partners and associates have rapid access to production-ready strains, reducing downtime from months to days. IBAB provides a comprehensive suite of services, including bioprospection, strain isolation and optimisation, taxonomic classification, and biochemical analysis, supported by facilities capable of scaling from 1L to 100L bioreactors. This new approach to culture collection presents a fresh perspective on biobanks, involving the maintenance of a small number of strains in various growth stages, ranging from cryopreservation to solid media, stagnant cultures in low volumes, and bubbling columns with cultures in the exponential growth phase. However, a significant threat to industrial-scale production is culture collapse caused by Harmful Biological Contaminants (HBCs), which can destroy cultures within days and lead to significant economic losses. Understanding the biology of these contaminants is crucial for developing effective mitigation strategies, yet challenges have hindered their study in maintaining and preserving them over the long term in a laboratory setting. To address this critical gap, the Contaminants Working Group from Greencolab is collaborating with the IBAB on the development of a dedicated HBC biobank by creating tailored cryopreservation protocols. This initiative focuses on optimising methods for the long-term storage of contaminants using different cryoprotectants. The goal is to develop standardised, species-specific protocols that ensure the viability and purity of HBCs without the need for continuous subculturing. This enters on the subject of the ParAqua COST ACTION by studying and tackling the conservation and research on zoosporic parasites that can be contaminants in microalgae production. By establishing a cryopreserved HBC biobank, IBAB will provide an invaluable resource for the research community and industry partners. This will facilitate the molecular and biological characterisation of contaminants, accelerating the development of early detection methods and effective mitigation strategies. This strategic expansion of our services will not only enhance the robustness of industrial microalgae production but also solidify IBAB's role as a key facilitator for innovation and sustainability in the blue biotechnology sector.

**Keywords:** Culture Collection, Biotechnology, Microalgae, Harmful Biological Contaminants, Cryopreservation, Biobank.

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# The ParAqua Podcast: promoting science communication in ParAqua and beyond

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## ABSTRACT

Over the last three years we have created and produced The ParAqua Podcast, a public facing science communication podcast for the ParAqua network. The format of the podcast is a short interview with a different guest each episode. Each episode consists of host led questions that focus on the career and research of the guest, often prompting discussion and interesting debate. One of the key aims of this podcast project was to educate the public about the role that parasites play in the environment and how they can be an important regulator of overall ecosystem health. We also aimed to provide guests with a new way of introducing their work to the general public as well as allowing scientists a convenient way of hearing about new research being done in the fields of aquatic and marine parasitology. In this way, we also aimed to challenge guests on the podcast by requiring them to make their research accessible to the layman, whilst still proving engaging content to a scientific audience. Furthermore, in a field that often relies on visual aids to demonstrate results and conclusions, this podcast also aimed to allow guests to develop their presentation skills for a purely audio format. To date 13 episodes have been published covering a range of topics related to parasitism and aquatic ecology. One key element of this podcast was the desire to have a diversity of speakers, from a range of backgrounds, scientific fields and career stages. This presentation will focus on the creation, implementation and successes of The ParAqua Podcast, with a shorter section at the end intended to demonstrate a bit of the process that goes into making a podcast and some feedback we have received from guests and listeners. We believe that the podcast has contributed greatly to Capacity Building Objective 6\* and 10<sup>^</sup>. Furthermore, it is our belief that this project represents a high value investment for ParAqua and COST EU as the episodes will remain free to listen via a range of publicly accessible streaming channels for decades to come.

\* Set-up and maintain an active communication strategy, through the use of various social media, press releases or public presentations to raise public awareness about the topics of interest in ParAqua.

<sup>^</sup> Inform and advocate to the public at large with factsheets, handbooks, databases, public events and scientific papers etc, thereby increasing awareness about the importance of biodiversity for healthy ecosystem functioning and biotechnology.

# Selection of species and strains of microalgae for different commercial applications

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## ABSTRACT

There is increasing commercial interest in the usage of microalgae for a wide variety of applications including nutrients and chemicals for food production, animal feed, aquaculture, biofuels and bioenergy, cosmetics, pharmaceutical products, biofertilizers, waste pollutant remediation, nutraceutical supplements such as omega-3 fatty acids, colorings, antioxidants and flavorings. These applications strongly depend on the characteristics and chemical composition of different microalgae species and strains. It is estimated that there are many thousands of microalgae species with different properties. In addition, strains of microalgae belonging to the same or closely related species could have different characteristics and significant differences in their chemical composition due to culturing in different environments and adapting to the different physical conditions of these environments. While most available microalgae strains remain largely uncharacterized, a substantial amount of research has been performed on a small number of strains with desirable characteristics.

Strain selection in algae is a complex decision-making process that requires careful consideration of numerous factors. This is a critical process that can make or break the success of commercial algae-based projects and industries. There are many factors that guide this crucial decision-making process, the most important being: tolerance to environmental conditions, growth rate in the culturing environment, biomass density achievable in culturing conditions, desirable product specificity, nutrient requirements, lipid content, genetic engineering potential, and compliance with local regulations.

The aim of this review is to present several examples of selection and usage of species and strains of microalgae for different commercial applications.

# Unravel the contribution of environmental variables triggering new host/parasite infection in the chytrid parasite *Staurastromyces oculus*

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## ABSTRACT

Chytrids are widespread parasitic fungi that infect aquatic primary producers, often reaching epidemic levels and reshaping host populations. Many species form resilient resting spores that endure unfavorable conditions and may trigger new infection cycles during algal blooms. However, the environmental cues driving germination remain unclear. We tested the effects of temperature, light, and host presence on germination dynamics using the model system *Staurastrum* sp. – *Staurastromyces oculus*. Resting spores were stored for 3 months under varied conditions (4°C vs. 16°C; light vs. darkness), then exposed to different combinations of these triggers. Germination and infection were tracked over 14 days via automated fluorescence microscopy. Preliminary results show that temperature increase after 4°C storage strongly induces germination, while light had no clear impact. Spores stored at 16°C showed no classic germination, yet infections occurred, pointing to low-level or sustained infection activity. These findings suggest chytrid resting spores may follow multiple germination pathways, with temperature and host cues playing key roles. This work presents the results of the ParAqua Short-Term Scientific Mission (STSM) titled “Microcosms experiments on resting spore germination cues with a phytoplankton-chytrid model system”, granted in July 2024 and carried on at the laboratory of Dr. Van den Wyngaert at the University of Turku. This work helped elucidate germination mechanisms in host-chytrid parasite system that were not yet elucidated, achieving the ParAqua goal of filling the knowledge gaps in zoospore ecology.

# Attending AlgaEurope conference with ParAqua Dissemination Conference Grant

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## ABSTRACT

Algae production is on the rise. Algae can be utilized for a broad spectrum of products, everything from feedstock for biofuels, biomaterials or biofertilizer production, to high-added-value for phyto-pharmaceuticals, cosmetics, food and animal feed. Full production is still hindered by several drawbacks, one of them being the mitigation of infections in algae systems, especially when using wastewater as a nutrient source.

Annual AlgaEurope conference<sup>1</sup> gathers experts from all fields dealing with algae, from academia to industry, from governance to communities. Many of the attending participants struggle with culture infections, thus results of ParAqua would be welcome for their business and attempts to explore higher production potential.

AlgaEurope conference was visited by 425 delegates and 225 companies from 44 countries. There were 289 submitted abstracts, 148 posters and more than 90 speakers. ParAqua presentation<sup>2</sup> was scheduled for the last day of the conference, nevertheless, there was a great interest for the topic after the talk.

After the speech, there was interesting discussion about the possibilities the topic of the ParAqua COST action brings to the algae production area. For example, there was an interest about using zoosporic parasites as a controlling agent for microalgae infections in macroalgae production. There was also a question about utilisation of spores for products. Several delegates were interested if we can help them with specific infection problems in their cultures (from laboratory to open-cultivation ponds). Few delegates discussed symbiotic relationships of algae with other microorganisms, stressing the possibility of cooperation between organisms, not only parasitic action.

Because of the ParAqua project communication at the conference, several participants joined the ParAqua action. Many were keen to join our events and workshops, helping us with surveys, and there is still on-going discussion on the subject till this day. In the AlgaEurope community, ParAqua has a reputation of a good and successful action, and is frequently cited by the speakers on the subject of culture infections.

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# Science communication through visual storytelling: promoting ParAqua's mission via video dissemination

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## ABSTRACT

MicrobEco actively participated in the scientific communication activities of the COST ParAqua action, with a particular focus on video production and visual dissemination. In particular, thanks to two Virtual Mobility (VM) grants from ParAqua, professional video content was produced to support the action's visibility and dissemination strategy. These projects were designed to raise awareness of ParAqua's activities, improve public understanding of the scientific work carried out within the network, and promote connections between researchers, stakeholders, and the general public. The first VM grant focused on the international ParAqua conference held from the 15th to 17th of April 2024, in Dubrovnik. The resulting videos documented the key moments of the meeting, including formal sessions and informal interactions, to provide a visual summary of the conference. The second VM was dedicated to the Workshop Regulation of Culture collections, strains preparation and characterisation held in Verbania, which combined theoretical lectures and hands-on laboratory work. The video outputs from the workshop aimed to highlight both the scientific content and the dynamic, multidisciplinary nature of the training activities. The methodological approach adopted throughout both projects was participatory and adaptive. In the first VM, participants actively contributed by sharing their own visual materials from the conference, which were then curated and edited into coherent video narratives. The second project involved direct on-site filming and editing. All videos were designed for broad accessibility: subtitles, clear explanatory descriptions, and social-media-friendly formats (including vertical 9:16 cuts) ensured that content could be effectively shared across platforms such as YouTube and Instagram. The overarching goal was not only to document but to translate ParAqua's work into a visual product addressing diverse audiences. The outcomes of both projects strongly support the core objectives of ParAqua, namely foster collaboration, strengthen a multidisciplinary research network, and increase visibility at both the scientific and societal levels. The videos promote knowledge exchange, reinforce ParAqua's identity through consistent branding, and serve as reusable communication assets for outreach and stakeholder engagement. Virtual mobility grants addressing the production of video for digital media were therefore immediately translated into a concrete contribution to ParAqua's objectives.

## REFERENCES:

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<https://www.youtube.com/watch?v=bl1Qty9pMCO>  
<https://www.youtube.com/watch?v=IFrFktdW-il>

# Phytoplankton under pressure - How environmental factors drive phytoplankton parasitism

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## ABSTRACT

Fungal parasitism by chytrids is emerging as a key process influencing phytoplankton population dynamics, biodiversity, and nutrient transfer in aquatic ecosystems. Despite their ecological importance, chytrid parasites remain understudied, particularly in natural freshwater environments, where baseline data on their prevalence, host range, and environmental drivers are limited<sup>1</sup>. In this study, we investigated the dynamics of chytrid infections in three shallow freshwater bodies in southern Poland over six consecutive years (2019–2024). Samplings were conducted monthly or fortnightly from April to October, with infections identified using dual staining (Calcofluor White and Wheat Germ Agglutinin) and epifluorescence microscopy<sup>2</sup>. Chytrids were detected in all three water bodies, with infections observed across multiple phytoplankton groups, including green algae (*Desmodesmus* spp. and *Mougeotia* sp.), the diatom *Asterionella formosa*, and cyanobacteria such as *Aphanizomenon* spp. including *A. gracile*. Generalized Linear Model (GLM) showed that water temperature, pH and concentrations of nitrates and phosphates were the strongest predictors of infection occurrence. Despite detection in all three water bodies, recurrent and high-prevalence infections were limited to one site, where the seasonal cycle remains undisturbed. Infection prevalence (IPC) ranged from 0 to 20%, peaking during the summer months (June – August), with green algae showing the highest infection rates. IPC correlated positively with temperature, precipitation and the presence of cyanobacterial blooms, highlighting a complex interaction of abiotic and biotic drivers. The insights gained through this research directly contribute to the goals of the ParAqua COST Action by addressing current data gaps on zoosporic parasites in freshwater systems and clarifying how abiotic and biotic conditions shape their ecological roles. The resulting dataset contributes to the ParAqua central occurrence database, providing a foundation for future modeling and comparative studies. Finally, the identification of key environmental drivers may contribute, in the future, to the development of a risk assessment tool for predicting infection risks and dynamics. By expanding our understanding of chytrid-parasite interactions in natural systems, this work contributes to ParAqua's broader mission to improve monitoring, predictive capacity, and management strategies for parasitic infections.

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# Two years of social media outreach: a comparative analysis

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## ABSTRACT

In an increasingly digital world, social media has become an essential tool for scientific networks like COST Actions to foster collaboration, share research outcomes, and reach broader audiences. Two years ago, a baseline analysis was conducted on the social media presence of the ParAqua COST Action, assessing general metrics across Facebook, Instagram, Twitter (now X), and LinkedIn. This analysis aimed to evaluate the online visibility, audience engagement, and dissemination effectiveness of the network's outreach efforts.

The current study revisits the same platforms to assess how the social media metrics have evolved over time. Using publicly available data and social media analytics tools, the metrics such as follower growth, post reach, engagement rates, and interaction types were analyzed. The longitudinal comparison provides insights into the digital development of the network, highlighting trends, strengths, and areas needing improvement. These findings reflect broader patterns in science communication and provide a conceptual framework for how networked scientific communities grow their digital presence over time.

This work directly supports ParAqua's main objectives, particularly its focus on strengthening collaboration and knowledge dissemination within and beyond the network. By evaluating the effectiveness of communication strategies, we contribute to improving visibility, transparency, and stakeholder engagement across the Action. The findings offer actionable recommendations for ParAqua members and similar initiatives seeking to enhance their impact through social media.

# A/Biotic factors driving zoosporic fungal disease on phytoplankton

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## ABSTRACT

Zoosporic parasite species belonging to the aquatic fungi Chytridiomycetes often target living phytoplankton in marine and freshwater environments. Abiotic variables potentially influence parasite spread, e.g. water salinity, while host microbiome might represent a biotic variable providing protection towards parasitic infection. In this study, we tested whether salinity influenced the infection dynamics of zoosporic parasites on phytoplankton. Moreover, in order to study the implication of the host microbiota in driving infection, we tested whether epibiotic bacterial communities associated to the host changed after infection with zoosporic parasites. The experimental design to test the abiotic variable included three different salinities: 20%, 36% (the salinity they live in the environment) and 45%. The available culture of the dinoflagellate *Alexandrium minutum*, maintained at 36%, was acclimated to water salinities of 20% and 45% for two weeks. Then, each culture was infected with active zoospores of the chytrid parasite *Dinomyces arenysensis*, in triplicate, and incubated in a culture chamber. Considering that the life-cycle of *D. arenysensis* lasts about 3 days, we quantified the infection prevalence 3 and 6 days after co-culture, to measure the first and second round of infection. Direct observation of the infected cultures highlighted that new parasite sporangia were present at each salinity since the first timepoint. Infection prevalence increased from the first infection round to the second, in all cases, indicating actively growing and spreading of zoosporic parasites. However, we recorded a higher increase of infections in cultures at 36% salinity, indicating an optimal disease dynamic at the salinity that the parasite is adapted to. In order to investigate changes in the microbiota of phytoplankton affected by parasitic disease, we sampled surface water at Port Ginesta (Barcelona, NW Mediterranean) and artificially infected three replicates of its phytoplankton community with active zoospores of *D. arenysensis*. After incubation in a culture chamber, we size-fractionated samples through 3 $\mu$ m and 0.2 $\mu$ m filters at three timepoints: days 3, 6 and 9 after infection. We extracted community DNA and used 16S rRNA metabarcoding to assess the bacterial diversity associated to the hosts or free-living, and performed microscopy observations to evaluate host abundance and infection prevalence. Preliminary observations highlighted that phytoplankton was infected by zoosporic parasites six days after the introduction of chytrids to the community, and we observed a complete absence of dinoflagellates nine days after infection. Data from the microbiota molecular diversity are currently still being processed, and will potentially highlight changes in the phycosphere epibiotic community of infected and not infected phytoplankton. This work was carried out within the framework of a short-term scientific mission funded by the ParAqua COST Action. It fulfilled the primary aim of the action, dedicated to the generation of a collaborative network of scientists across Europe working on the topic of zoosporic parasites. Moreover, the experimental work was designed to contribute to the understanding of environmental drivers underlying the dynamic of zoosporic diseases, a major objective of ParAqua. Ultimately, this collaboration allowed for introduction of three parasitic chytrids in the MEGic culture collection, another major objective of this Action.

# Effects of climate change-driven temperature increase on brown algae-parasite interactions

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## ABSTRACT

The effects of climate change are becoming more and more obvious in a wide variety of ecosystems. One example is the increase in overall water temperatures in the world's oceans. In this work, two perspective scenarios of a potential temperature increase were used to test the response of a laboratory-scale pathosystem involving the brown alga *Macrocystis pyrifera* and two oomycetes, *Anisolpidium ectocarpii* and *Eurychasma dicksonii* (strains Eury05 and Eury96), and the phytomyxid *Mauullinia ectocarpii*, infecting it. We used complementary molecular (qPCR) and microscopic (bright-field and fluorescence microscopy) methods to assess the influence of temperature on the growth and infection phenotype of the pathosystem at 10 °C, 15 °C and 20 °C.

The results obtained show that different parasites have different temperature optima. In particular, the infection potential of *E. dicksonii* and *M. ectocarpii* declined with increasing temperature and was absent at 20 °C, whereas *A. ectocarpii* appeared to be favoured by higher temperatures. The host alga *M. pyrifera* itself also showed structural reactions to the increased temperature. Phenotypical evaluations revealed an influence at 20°C on the growth of the algal gametophytes, but also on the shape and structure of the cells. According to these observations, the effects of changing temperatures are likely to be mediated in a species-specific way in parasite-host interactions, with potential consequences for coastal ecosystems.

As part of a Short-Term Scientific Mission at the Muséum national d'Histoire naturelle (MNHN) in Paris, supported by the ParAqua COST Action, we are adapting a high-throughput microscopy and image analysis workflow to quantify cellular responses to infection. These responses include nuclear morphology, cell wall thickening and growth dynamics. The aim is to work on cost-effective methods for the early detection of zoosporic parasites, even at low abundances, and for evaluation of infections.

This work contributes to the establishment of a knowledge hub on host–parasite diversity and infection dynamics, supporting ParAqua's broader goal of developing predictive tools and protocols for managing infections with zoosporic parasites. By demonstrating divergent parasite responses to warming, it provides essential baseline knowledge for monitoring, risk assessment, and management in both natural brown algal populations and aquaculture systems.

# An example of sample preparation methodology for metabarcoding of different microalgae communities

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## ABSTRACT

Microalgae, including eukaryotic algae and cyanobacteria, form a diverse group of microscopic unicellular photosynthetic organisms that inhabit almost all ecological niches. High growth rate, simplicity of the cultivation process with minimal water consumption, reduction of atmospheric CO<sub>2</sub>, possibility of year-round production in large outdoor facilities and photobioreactors as well as low production costs are their main advantages compared to other raw materials. For these reasons, microalgae are continuously being researched and cultivated for the extraction of food supplements, pharmaceuticals, and other industrially important bioactive substances due to their complex metabolic capacities. Contamination of microalgae cultures is one of the main problems currently affecting the development of industrial microalgae cultures. Numerous data have been reported on negative effects of contaminants, such as parasites in microalgae cultures. Timely detection of parasites in the culture is important because they can potentially cause the death of microalgae cultures and thus cause economic losses<sup>1</sup>. DNA barcoding allows for the identification of individual algal species or individual algal contaminant while DNA metabarcoding reveals detailed identification of microbial community dynamics in microalgal-based samples, including different contaminant groups. For both types of analysis, it is necessary to select/develop appropriate biomarkers, as they amplify differently and have different levels of efficiency (specificity). The analysis of the publications showed that 12 different markers (different nuclear regions 18S and ITS, plastid regions of *rbcL*, 23S and 16S) were used in metabarcoding methodology studies of eukaryotic freshwater microalgae communities. Among them, the most frequently used were the V4 and V9 regions of 18S rRNA and *rbcL*<sup>2,3</sup>. The main objective of this work was to adjust/adapt, test and describe in detail the protocol for the preparation of samples of different microalgae communities (from commercial algae cultures and intentionally contaminated by culturing under inappropriate environmental conditions) for metabarcoding using region V4 of 18S rRNA in order to detect potential fungal contaminants. The results of protocol adaptation showed that the addition of lysozyme to the manufacturer's standard protocol increase the efficiency of microalgae cell wall degradation allowing for more efficient DNA extraction. Different amounts of extract were obtained from industrial samples (more concentrated – higher number of algae cells) and experimental samples (less concentrated – lower number of algae cells). However, both types of samples were successfully applied for PCR amplification of the target V4 region of 18S rRNA, which was confirmed by preliminary metabarcoding results that showed different diversity between different types of samples.

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# FunAqua: a global DNA-based database of aquatic fungal biodiversity in water and sediments

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## ABSTRACT

Aquatic fungi play a significant role in the functioning of aquatic ecosystems as decomposers, parasites, pathogens and mutualists. However, despite their ecological importance, they are under researched in comparison to other aquatic microorganisms and terrestrial fungi. They are underrepresented in sequencing databases<sup>1</sup> and there is an abundance of dark taxa found in aquatic environmental samples<sup>2</sup>. To support research into aquatic fungal biodiversity, the University of Tartu and the Estonian University of Life Sciences established a collaborative project entitled FunAqua in 2018. The project aims to (1) build and publish a metabarcode database for eukaryotes found in sediment and filtered water samples; (2) describe environmental factors affecting aquatic fungal community composition and diversity. With this presentation we introduce the FunAqua project, focusing on the metabarcode dataset derived from 1,080 sediment samples and 1,299 filtered water samples. Additionally, we will give an overview of Victoria Prins' participation at the 14<sup>th</sup> Symposium for European Freshwater Sciences (20.07-25.07.25, Türkiye) supported by the Inclusiveness Target Country (ITC) Conference Grant.

Sampling was conducted between 2018 and 2024 by voluntary contributors. The sampling points (n = 1,456) spanned all continents across 87 countries. We designated the sampling points to 10 biome types based on generalized categorization. From these biomes freshwater lakes had the highest number of samples (n = 1,041) followed by freshwater rivers (n = 765), saltwater marine biome (n = 336) and brackish marine biome (n = 157). We PCR-amplified the internal transcribed spacers (ITS) region of the rRNA operon along with the flanking 18S V9 region for barcoding purposes. Libraries were sequenced at the Oslo University on the PacBio Sequel instrument. In total, 137,887 high-quality OTUs were produced. The fungal kingdom was the most OTU-abundant kingdom with 50,175 OTUs (36% of OTUs). From sediment (n = 1,060) and water filter (n = 1,212) samples, 34,170 and 26,296 unique fungal OTUs were produced respectively. We identified 37 fungal phyla, 133 classes, 331 orders, 761 families, 2 550 genera and 3 985 species. The most abundant phylum was Ascomycota (35.6 % of fungal OTUs), followed by Rozellomycota (21.6%), Chytridiomycota (14.7%) and Basidiomycota (13.6%).

As FunAqua aims to investigate environmental drivers of aquatic fungal biodiversity, it aligns closely with the objectives of the ParAqua COST Action. FunAqua's research includes the ecologically significant zoosporic fungal parasites, which are a central focus of ParAqua. While ParAqua seeks to develop early detection methods through DNA-based tools, FunAqua contributes directly by the development of metabarcoding techniques, building a comprehensive aquatic fungal database, and conducting biodiversity analyses of aquatic fungi.

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