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A harmonised dataset of field observations on zoosporic parasites infecting aquatic primary producers

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Abstract Zoosporic parasites are a polyphyletic group of microorganisms characterised by a motile spore stage, which play a crucial ecological role in aquatic environments. They are known to influence population dynamics of aquatic primary producers, nutrient cycling, and energy transfer within microbial food webs. Despite their importance, data on their

diversity, distribution, and interactions with their hosts remain sparse and fragmented. Here, we present a harmonised dataset of field observations on zoosporic parasites infecting aquatic primary producers. The dataset integrates both published and previously unpublished records, encompassing more than 4427 observations collected between 2007 and 2021 across 28 sites in Europe and North America. It includes data for 91 unique parasite taxa, along with confirmed and putative parasite–host associations derived from direct microscopic or molecular evidence. All records were standardised using the Darwin Core schema to

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ensure interoperability and long-term usability. This open-access resource provides a foundation for comparative and meta-analytical studies on parasite–host ecology, biodiversity assessments, and industrial applications related to algal production systems.

Keywords Co-occurrence · Algae · Diatoms · Fungi · LifeWatch · Chytridiomycota · Phytoplankton · Cyanobacteria · Macroalgae

Introduction

Zoosporic parasites are a polyphyletic group of microorganisms which have in common the presence of a motile spore stage in their life cycle, and comprise different taxonomic groups like Chytridiomycota, Oomycota, Phytomyxea, and Syndiniales (Thines et al. 2025; Van den Wyngaert et al. 2025a, b). Their interactions with primary producers have been widely documented, showing that they significantly influence the population dynamics of both freshwater and marine algae. Under certain conditions, particularly during phytoplankton blooms, epidemic outbreaks of parasitic Chytridiomycota (chytrid) lead to their dominance within fungal communities (Rasconi et al. 2012; Van den Wyngaert et al. 2022; Van den Wyngaert et al. 2025a, b; Wurzbacher et al. 2010). Similarly, Syndiniales also often dominate the relative abundance in global protist communities (Clarke et al. 2019; Cleary & Durbin 2016; Guillou et al. 2008). Zoosporic parasite epidemics can regulate phytoplankton populations and contribute to nutrient cycling in different aquatic habitats (Gleason et al. 2011; Ibelings et al. 2011; Kagami et al. 2014; Klawonn et al. 2021). Specifically, zoosporic parasites contribute to organic matter transfer in aquatic ecosystems through specific pathways like the “mycoloop,” where trophic transfer of matter locked in inedible phytoplankton species is undertaken by dissemination of nutrient-rich zoospores (Grami et al. 2011; Kagami et al. 2014; Rasconi et al. 2014), and the “fungal shunt,” which tightens the coupling of the microbial food web (Klawonn et al. 2021). These zoosporic parasite-mediated material and energy flows are likely still underestimated as biomass estimates of zoosporic parasites in natural conditions remain sparse (Gsell et al. 2022).

Fungal and other zoosporic parasites also play critical roles in unique environments. In acid mine drainage ecosystems, they work symbiotically with algae to support sulfate-reducing bacteria and assist in metal immobilisation (Das et al. 2009). In polar environments such as the Antarctic, various fungal taxa have been detected from macro- (Martorell et al. 2021) and micro-algae (Ilicic et al. 2022), suggesting potential for novel taxa discovery and applications in biotechnology. In Arctic and sub-Arctic regions, chytrid fungi parasitise diatoms, potentially influencing food web dynamics (Hassett et al. 2017; Ilicic et al. 2024; Kilias et al. 2020). Beyond their role in natural ecosystems, zoospore parasite outbreaks pose substantial economic challenges to the microalgae biotechnology industry. In algal biomass production systems, parasite invasions often necessitate mechanical or chemical disinfection, leading to major disruptions, production losses, and increased operational costs (Asatryan et al. 2019; Carney & Lane 2014).

Despite their ecological significance and industrial relevance, aquatic parasitic microorganisms remain understudied and underrepresented in biodiversity records. Data on the detection of parasites of primary producers are not systematically collected or shared. For instance, the Global Biodiversity Information Facility (GBIF—<https://www.gbif.org/>) lists only 44,974 observations of Chytridiomycota, accounting for just 3% of aquatic fungal records, while aquatic groups such as Bigyra, Oomycota, and Perkinsea collectively total 98,930 observations. These numbers are not comparable to the vast number of observations recorded for terrestrial parasitic microorganisms, highlighting the clear disparity in efforts to detect microbial biodiversity across environments (Grossart & Rojas-Jimenez 2016). For these reasons, freshwater and marine environments represent priority targets for the assessment of microbial biodiversity. Understanding their presence, phenology, and interactions with their host and environmental cues is essential for both ecological research and industrial applications. Identifying the drivers of their occurrence and proliferation could help regulate parasite populations in both industrial and natural environments.

Here, we present a dataset compiling both published and unpublished observations of aquatic zoosporic parasites, focusing on presence/absence

data and their co-occurrence with hosts as inferred from direct observation. Although still limited in terms of taxonomic and geographical coverage, this dataset helps bridge current knowledge gaps regarding the biodiversity and distribution of aquatic parasites and their hosts. With this datapaper, we aim to raise awareness to the fragmented and incomplete representation of aquatic zoosporic parasite diversity and occurrence data and want to encourage the use of the presented data platform to centrally store data on aquatic zoosporic parasites with a unified metadata description approach ensuring FAIR usability. In addition, we call for increased systematic and coordinated efforts in data collection, standardisation, and sharing to achieve a comprehensive understanding of these ecologically important interactions. This dataset represents an example of such efforts that can be used as foundation to expand current initiatives in this field (Rasconi et al. 2022; Tarallo et al. 2024).

Methods

The data collection effort began as part of the COST Action ParAqua (Rasconi et al. 2022), a COST-funded European network which aims at compiling and disseminating comprehensive data on the occurrence of zoosporic parasites and their interactions with their hosts in aquatic environment. The data used in this study were sourced from both published works (Alacid et al. 2020; Fernández-Valero et al. 2022; Gsell et al. 2013; Karpov et al. 2021; McKindles et al. 2021; Rasconi et al. 2012; Reñé et al. 2021a, b; Reñé et al. 2017a, b; Reñé et al. 2017a, b; Reñé et al. 2022; Reñé et al. 2021a, b; Van den Wyngaert et al. 2022; Sprong et al. 2023) and unpublished observations contributed by ParAqua members. The data collection focused on parasite-host interactions and the presence of parasite species in the environment. The collected data comprise a list of identification of zoosporic parasites of aquatic primary producers collected from natural environments, along with observations of confirmed or putative parasite-host interactions. The identification of the parasitic taxon is based on microscopy observation and/or molecular sequence or inferred by previous literature.

Where available, we also recorded additional information, such as the ecosystem type and the

geographical context of each observation. For geographic coordinates, the original latitude and longitude were recorded and standardised to decimal coordinates. The coordinates were then manually checked for consistency with the locality reported in the original reference. Additional geographical context information was retrieved where possible.

The organism abundance is also reported and retained in its original format, along with details of the methodology used for quantification. The organism quantity was converted into presence/absence data (if the organism quantity is zero, it is marked as “absent”, if greater than zero, it is marked as “present”).

The full taxonomy of species—including phylum, class, order, family, and genus—was derived from Van den Wyngaert et al. (2025a, b) and verified for accuracy against internationally recognised taxonomic backbones such as WoRMS, Catalogue of Life and AlgaeBase and manually counterchecked by expert review. The classification of Fungi is aligned with Tedersoo et al. (2018). The original description of the species (i.e. verbatim scientificName) and the coordinates (verbatimCoordinates) are reported in the tables to ensure the accuracy of the information provided.

To ensure data interoperability and facilitate reuse, we adopted Darwin Core (Wieczorek et al. 2012) to standardise terminology and harmonise the collected variables.

A table summarising each variable, its definition, and the standard terminology used is provided as supplementary material. The dataset was formatted as a column-oriented table in CSV (UTF-8) format and is publicly available under a CC BY 4.0 licence at <https://data.lifewatchitaly.eu/handle/123456789/326353>. The associated metadata are described using the Ecological Metadata Language (EML 2.2.0) standard in extensible markup language (.xml) format.

Results

The dataset comprises 4427 observational records from 7 data sources, 3 of which were unpublished before. The dataset encompasses 91 unique taxa. The lowest determined taxonomic rank varied among records. The taxonomic description includes 44 taxa

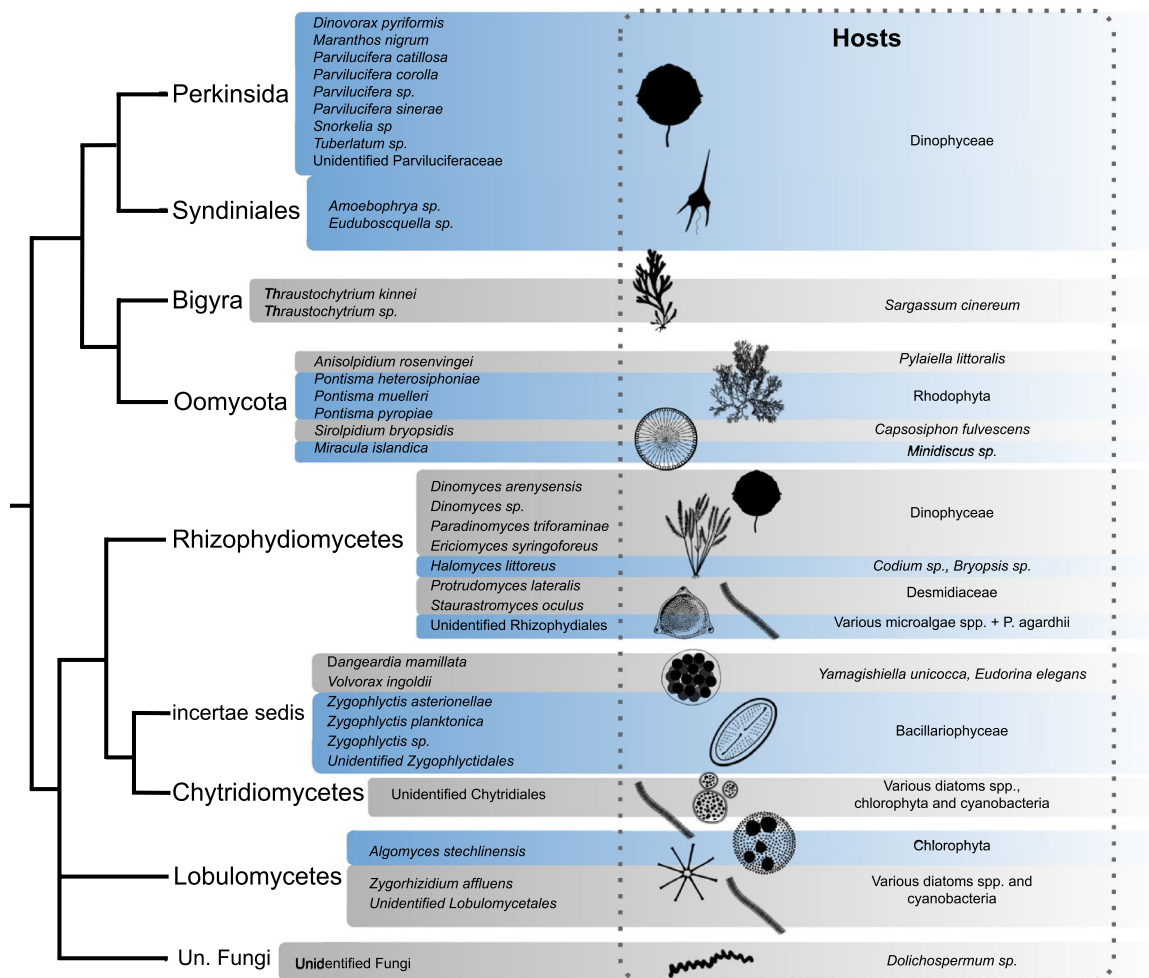


Fig. 1 Cladogram illustrating the phylogenetic relationships among the taxa included in this study and their associated confirmed or putative hosts. Blue and grey shading indicate distinct host groups

identified at the species level, 14 at the genus level, 3 at the family level, 29 at the order level, and 1 unidentified fungal taxon not assignable to any known fungal phylum (Fig. 1).

The geographic distribution of the dataset is defined by a bounding box ranging from latitude 59.92 to longitude -84.51 (Fig. 2). The collected samples originate from 28 unique locations across seven countries (Fig. 2): Finland ($n=4$ observations), France ($n=990$ observations), Germany ($n=1517$ observations), the Netherlands ($n=505$ observations), Spain ($n=34$ observations), the

United Kingdom ($n=1350$ observations), and the USA ($n=27$ observations).

In terms of temporal coverage, the dataset spans over a period of 14 years, from 2007 to 2022, with a 5-year gap between 2010 and 2015.

We recorded 123 unique parasite-host interactions, either putative or confirmed by microscopy observations.

Regarding the host diversity, a total of 37 unique host taxa were identified, belonging to four major groups (Fig. 1): diatoms (Bacillariophyceae – Stramenopiles), dinoflagellates (Dinophyceae), Cyanobacteria (Nostocaceae

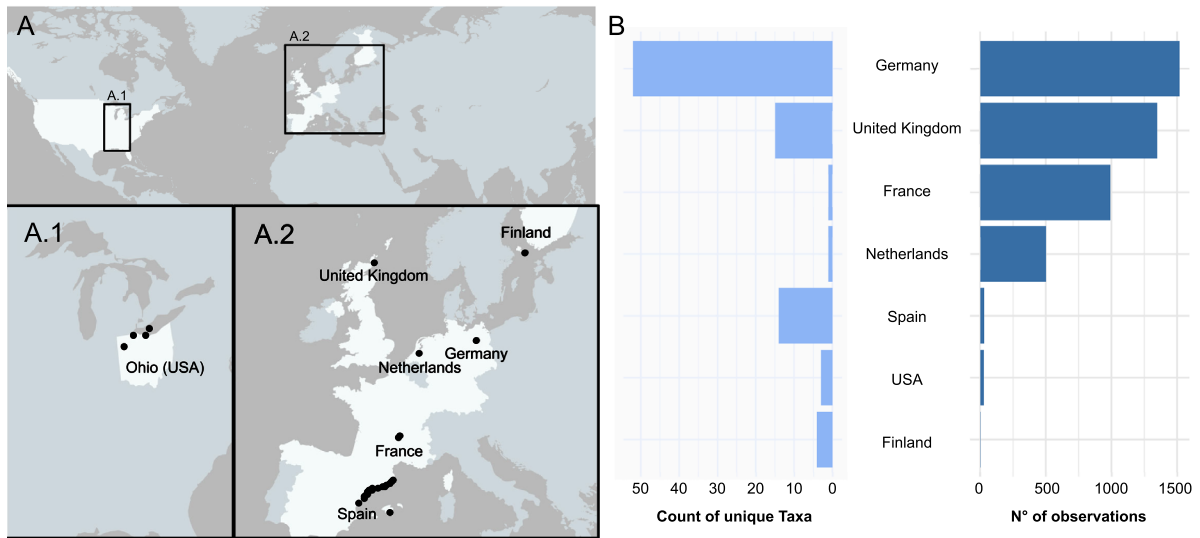


Fig. 2 **Panel A** Geographical distribution of parasite observations; each point represents a distinct sampling locality; **Panel B** Number of unique taxa (left axis, light blue bars) and total

number of observations (right axis, dark blue bars), grouped by country of sampling

and Oscillatoriothycidae), and green algae (Chlorophyta–Viridiplantae).

Discussion and conclusion

By exploring the interactions between parasites and their hosts, researchers are gaining valuable insights into ecological stability, biodiversity, and the structure of aquatic ecological networks. The study of aquatic primary producers parasites extends beyond academic interest; understanding host-parasite interactions is fundamental for sustainable resource management and biotechnology (Carney and Lane 2014). Through the ParAqua COST Action, we initiated a harmonised approach to data collection (Tarallo et al. 2024). These datasets form part of this effort, and one of the aims was to showcase the value of compiling and publishing such dataset as a harmonised and FAIR resource.

Additionally, we have compiled molecular data related to parasite-host systems and developed a dedicated database to host these data (Van den Wyngaert et al. 2025a, b). All data are provided as open, accessible, and citable resources in accordance with the FAIR principles. A browsable database interface is currently in preparation to enable

structured queries and facilitate the download of all observations.

The current data we gathered also highlights important geographic gaps, particularly the need to assess zoospore parasite occurrence and impacts beyond Europe and the United States.

At present, the data gathered do not represent the full diversity and distribution of zoospore parasites. The compiled data reflect differences in sampling strategies, species identification methods across contributing studies, and the availability of data among the researchers involved in the project as well (Rasconi et al. 2022). Additionally, variation in the underlying research focus has resulted in datasets that either provide biodiversity snapshots or long-term time series of single host–parasite interactions. For these reasons, we have not yet attempted to analyse large-scale patterns in zoospore parasite occurrence or impacts. However, we anticipate that future integration across spatial and temporal scales will enable such analyses.

We actively encourage further data contributions to expand and refine this initiative. As the database grows, it has the potential to become a key resource for pattern detection, ecological modelling, and a deeper understanding of zoospore parasite dynamics in aquatic ecosystems.

We envision that this FAIR-ready database will support investigations into the geographic and temporal distribution of zoosporic parasites and, ultimately, enable the exploration of large-scale patterns in their diversity and occurrence.

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Author contributions All authors contributed to the provision and harmonisation of data. AT drafted the manuscript and prepared the figures. All authors reviewed and approved the final manuscript.

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Data availability The datasets generated during the current study are publicly available at: <https://data.lifewatchitaly.eu/handle/123456789/326353>

Declarations

Conflict of interest The authors declare no competing interests.

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