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Growth rates of pelagic fungi in contrasting marine environments

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Abstract

While fungi in soil and freshwater environments are well studied, the role of fungi in marine ecosystems has been overlooked. In recent years there has been a growing recognition of the crucial role that fungi play in marine ecosystem processes, including their contribution to nutrient cycling, decomposition and parasitic relationships with other organisms. However, their diversity and ecological functions are to this day still severely understudied and questions, such as biomass contributions and growth rates in their natural environment remain unanswered. Using a natural sea-water inoculum and cell detection via epifluorescence microscopy, this thesis aims to address this knowledge gap by measuring the growth of marine fungi in two contrasting environments. The study successfully established growth rates for pelagic fungi, with steady growth detected in all samples, emphasising the presence of active fungal communities in both temperate and polar marine environments. The nutrient-rich Antarctic waters exhibited significantly higher fungal growth rates compared to the Adriatic Sea, suggesting that nutrient availability is an influential driver of fungal production. While fungi displayed continuous growth during the incubations, viral and bacterial communities both exhibited an initial bloom followed by a rapid decline, with viruses being a little delayed. This suggests possible different ecological niches of fungi compared to bacteria and viruses. In conclusion, this thesis provides valuable insights into marine fungal growth dynamics and their interactions with other microbial groups, offering a crucial step towards understanding the ecological significance of fungi in marine environments.

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Introduction

The ocean is a remarkably complex and dynamic system, acting as a major carbon reservoir by sequestering large amounts of atmospheric CO_2. Through intricate biogeochemical processes, including the marine carbon cycle, the ocean plays a critical role in regulating the global carbon cycle and the Earth's climate (DeVries, 2022). A crucial component of the marine carbon cycle is the microbial loop. This process involves the transformation and recycling of dissolved organic matter by marine microbes, including bacteria, archaea, viruses and fungi, during which dissolved organic carbon (DOC) is incorporated into the marine food chain. To fully understand the complex biogeochemical cycles that sustain marine ecosystems it is essential to study the diverse and often unseen microbial communities that drive these processes (Jiao et al., 2024).

In the past, the field of marine microbial research has primarily focused on bacteria and archaea. Only in recent years, there has been a growing recognition of the crucial role that fungi play in marine ecosystem processes (Taylor & Cunliffe, 2016). Fungi are present in almost all ecosystems. In terrestrial and freshwater environments, they are already well studied as they are important degraders of organic matter. However, fungi in the marine environment have been largely overlooked, resulting in a significant gap in our current understanding of marine microorganisms (Breyer & Baltar, 2023).

Marine Fungi are a diverse group, present in a variety of habitats from coastal waters to the deep sea, with estimates suggesting there could be up to 10,000 species, yet fewer than 2000 have been described (Amend et al., 2019). Studies have shown that fungi dominate microbial biomass during certain conditions (Bochdansky et al., 2017; Gutiérrez et al., 2011) and it is assumed that they influence the flow of organic matter in the marine food web (Grossart et al., 2019). Fungi are heterotrophs and are commonly known to be important degraders of organic matter, using their ability to secrete extracellular enzymatic enzymes to break down large polymers. Not only are marine fungi able to degrade carbohydrates through the expression of carbohydrate-active enzymes (CAZymes) (Baltar et al., 2021), but also proteins, phosphorus and sulfur compounds. They are therefore hypothesised to be crucial contributors to biogeochemical cycles (Salazar Alekseyeva et al., 2022). Additionally, many marine fungal species act as pathogens and parasites, infecting phytoplankton as well as the macroscopic sea life (Yarden, 2014).

Moreover, marine fungi are a promising source of natural products with potential applications in medicine, agriculture and industry. These include compounds with antibacterial and anticancer properties, hydrophobins (Kempken, 2023) and enzymes capable of degrading environmental pollutants, making fungi a valuable resource for biotechnological research and development (Tortella et al., 2005). The study of marine fungi is an emerging field that bridges marine ecology, mycology and biotechnology. However, the role of fungi in the marine microbial loop is still not entirely clear and a lot of questions concerning diversity and function of marine fungi remain unanswered to date. Specifically, among others, there is limited

understanding of their biomass contributions, phylogenetic diversity, ecological functions and growth rates (Breyer & Baltar, 2023).

This thesis aims to measure the growth of marine fungi in natural environments and to establish growth rates of marine fungi. Fungal growth has been studied in other environments, such as soil, by measuring acetate incorporation into ergosterol (Rousk & Bååth, 2011), but to date there are no comparable studies for the marine environment. This study seeks to determine the first growth rates of pelagic fungi in the marine environment by employing a dilution technique. In this approach a seawater sample is filtered, creating a dilutant, to which an inoculum of unfiltered seawater is added, allowing microbial communities to regrow over time. While this method has commonly been used to measure phytoplankton (Landry et al., 1995) and prokaryotic growth (Worden & Binder, 2003), it has not yet been used to study fungal growth making this a novel approach in the research of marine fungi. CARD-FISH and Calcofluor-White staining were used following the dilution experiment to assess fungal abundance.

Furthermore, this thesis compares fungal growth to prokaryotic and viral abundance over time, highlighting potential interactions between these microbial groups. A comparison of fungal production in a temperate, oligotrophic environment and a polar environment will provide insight into the fungal communities of two distinctly different ecosystems with varying environmental factors, such as temperature and nutrient concentrations. While warmer temperatures usually support microbial growth (Ratkowsky et al., 1982) which could lead to larger fungal growth in the Adriatic Sea, it is hypothesised here that the nutrient-rich Antarctic will exhibit faster fungal growth.

By unravelling the growth dynamics of marine fungi and their interactions with other microbial groups, this research will enhance our understanding of fungal production and activity in the ocean, offering valuable insight into the roles fungi play in marine ecosystems and their potential contribution to marine ecosystems.

Methods

Sampling

The samples were obtained from two contrasting environments, the Adriatic Sea and the Antarctic Ocean using the same protocol (Table 1, Figure 1). Samples from the Adriatic Sea were taken at the coast of Rovinj in March and September of 2022, sampling from the surface layer. The samples were transported to Vienna to be processed. Samples from the Antarctic Ocean were acquired during the Antom II cruise in January 2022 using a CDT-rosette with Niskin bottles. Four stations (Station 2, 3, 4 and 6) were sampled during the cruise at two different depths, the surface (SUR) at 5m, and the deep chlorophyll maximum (DCM) between 16 and 29m (Figure 1). Samples were processed on the ship as explained below and frozen to be later analysed back in the laboratory in Vienna. Environmental data such as temperature, salinity and chlorophyll were measured on site for both experiments.

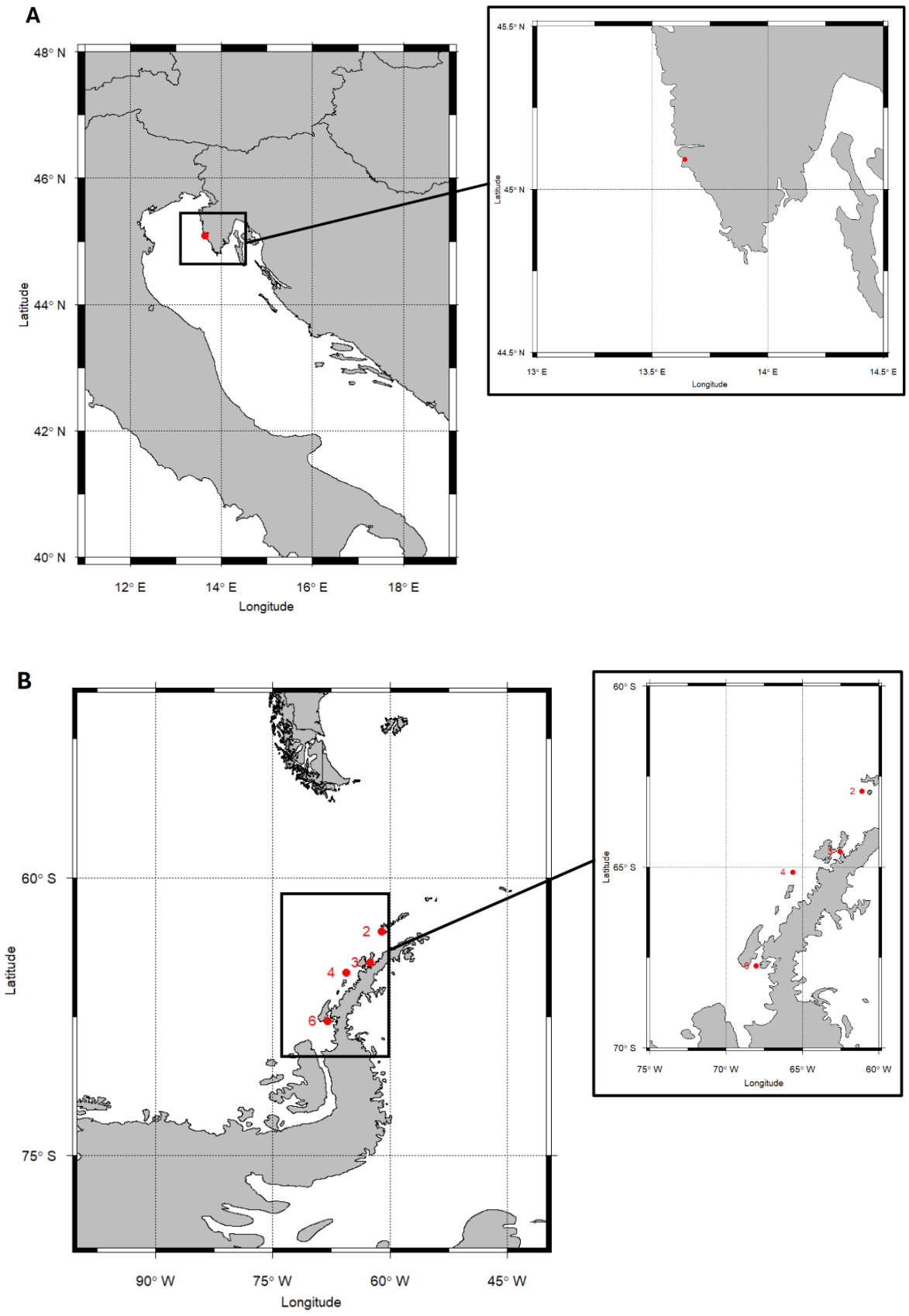

Figure 1: Sampling sites: A) The Adriatic Sea, where sampling took place at the coast of Rovinj and B) the Antarctic Ocean with the 4 sampled stations on the right.

Experimental Setup

The sampled water was filtered through a 0.22µm Inline polycarbonate filter using a peristaltic pump. The filtered seawater was then transferred to smaller bottles of around 2 l. 10% of inoculum (original unfiltered seawater) were added back into each bottle to perform the dilution experiment.

The experiments from the Adriatic Sea were incubated in shaker incubators in the dark at two different temperatures (10°C and 20°C for March, with 10°C being the in-situ temperature and 15°C and 25°C for September, with 25°C being the in-situ temperature). Subsampling of prokaryotic abundance and fungal abundance and biomass was carried out every 7 days for 8 weeks during the incubation. Furthermore, the experiments from September were sampled for viral abundance every 7 days. The experiments from the Antarctic Sea were incubated at 4°C in the dark and sampling was performed every 3 days for 9 days. 100-500ml of water were obtained from each bottle at every sampling point and fixed with 2% Formaldehyde. The samples were then stored in the refrigerator for at least 45 minutes. In the following, a circular manifold was used to filter the samples through a 0.2µm filter, which was placed on top of a 0.45µm support filter. The filters were frozen until further processing.

Calcofluor-White staining

The samples from Rovinj were stained with equal parts Calcofluor-White and KOH (10%). Calcofluor-White is a fluorescent dye that binds to chitin and cellulose in the cell walls of multiple organisms (Rasconi et al., 2009). Using the epifluorescence

microscope Zeiss Axio Imager 2 (1250× magnification, Carl Zeiss, Jena, Germany) 20 randomly chosen grids were examined in the DAPI channel for each filter, taking a picture of each grid. The fungi that were found on these grids were counted, and their diameter measured.

CARD-FISH

The samples from the Antarctic Ocean were analysed using CARD-FISH, which is a method commonly used for marine bacteria (Pernthaler et al., 2002) and has more previously also been applied to marine fungi (Bochdansky et al., 2017; Priest et al., 2021). The protocol used is a modified process published by Breyer et al. (2024), explained below, which and has been shown to be comparable to Calcofluor-White staining. Up to 6 samples were processed simultaneously. A culture of Isolate 64 (Antom II) was used as positive control. Only batches in which the control filter showed a positive CARD-FISH signal, meaning that at least 75% of counterstained fungal cells were also stained with Alexa 488, were analysed, otherwise the process was repeated.

Embedding:

The embedding-process protects the cells from being washed from the filter in the following steps. For this, the filters were placed onto 55µl of 0.1% Agarosesample-side down and are then positioned in an hybridisation oven for 15 minutes at 37°C to dry. 96% Ethanol was then poured over the filters to remove them. About 1/8 of each filter was then cut off for further processing.

Permeabilization:

To achieve cell wall permeability, which must be ensured for the probe to be able to diffuse into the cells, the filters were incubated in a buffer for 1 hour at 30°C on a heat shaker. This buffer contained 60 units Cellulase, 3.6 units Protease, 2 units Chitinase and 15 000 units Lyticase, dissolved in 1775 µL 1x PBS with 1% SDS at a pH of 6.5. The filters were then washed with MilliQ water twice, to remove residual enzymes.

Endogenous Peroxidase Inactivation:

In the next step, the filters were incubated in 0.01M HCl for 15 minutes in the dark to inactivate endogenous peroxidase. Incubation was followed by washing the filters in MilliQ twice, shortly immersing them in 96% Ethanol and fully drying them.

Hybridization:

The filters were put in an Eppendorfer tube along with 580µl Hybridisation Buffer (1800 µL 5M NaCl, 200 µL 1M TRIS-HCl, 1 g Dextran Sulfate, 5 µL 100% Triton X100, 2.0mL Formamide, 1 mL 10% Blocking reagent and 5.0 mL Sigma Water) and 20µl HRP probe. To specifically target fungal cells, PF2 probe was used. The tubes were then incubated for 3 hours in a hybridization oven at 46°C and slow rotation in the dark. During this step the horseradish-peroxidase (HRP) labelled probe diffuses into the cells and binds ribosomal RNA target.

Washing:

Afterwards, to remove the remaining hybridisation buffer, a washing buffer (2150 µL 5M NaCl, 1000 µL 1M TRIS-HCl, 500 µL 0.5M EDTA, 50 µL 10% SDS, 46.3 mL MilliQ-water) was preheated in the water bath to 48°C before adding the filters for 15 minutes. The filters were then incubated in 1xPBS for 15 minutes in the dark.

Amplification:

During the amplification procedure the fluorescence- marked Tyramide Alexa Fluor™ 488 (Thermo Fisher Scientific, MA, USA) stains all cells, where a HRP probe has been bound in the hybridisation step. An Eppendorf tube was filled with the amplification substrate consisting of 692µL amplification buffer (2g Dextran Sulfate, 8000µL 5M NaCl, 200µL 10% Blocking reagent, 11800 µL 1x PBS), 7µL of Solution A (200µL Amplification buffer and 1µL 30 % H_2O_2) and 1µL Alexa Tyramide 488. The filters were added to the tube and incubated in the hybridisation oven for 45 minutes at 46°C in the dark. Subsequently, the filters were incubated in 1xPBS for 15 minutes in the dark before washing them in MilliQ-water three times, shortly dipping them in 96% Ethanol and fully drying them.

Counterstaining and Detection:

Finally, the filters were mounted on the microscopy slides and counterstained with the general DNA dye 4W,6-di-amidino-2-phenylindole (DAPI). The filters were then examined using the same protocol as for the Calcofluor samples. Along with the DAPI channel the FITC channel was used to visualize the signal from Alexa 488.

Flow cytometry

To measure prokaryotic abundance 1ml of sample was fixed using 2% Formaldehyde at every sampling point and then frozen at -20°C. 100µl of these samples were later stained with SYBR-Green using 1µl of a working solution of 100x. After an incubation time of 10 minutes in the dark, prokaryotic abundance was measured with the Flowcytometer Accuri C6 at medium speed for one minute.

Additionally, viral abundance was measured for the samples from the Adriatic Sea in September. 1ml of water was sampled from each bottle at every sampling point and fixed with 20µl Glutaraldehyde (25%). The cryovials were then immediately placed in liquid nitrogen for around 30 seconds and finally transferred to the -80°C freezer. Before measuring, the samples were defrosted in lukewarm water. 250µl of the sample were diluted with 250µl TE-buffer (1x; pH 8.2-8.3) and stained with 5µl of a 1:200 SYBR-Green stock. The viral abundance was measured using the Flowcytometer FACSAria III.

Analysis

Data analysis and visualisation was performed using R and Microsoft Excel. Growth rates (GR) were calculated using the formula $GR = \frac{A_f - A_i}{t}$ where A_f represents the final fungal abundance (cells/l), A_i the initial fungal abundance (cells/l) and t the time (days). Furthermore, Turnover times (TT) were determined using the formula $TT = \frac{A_f}{GR}$, with A_f again being the final fungal abundance (cells/l).

Results

Environmental data revealed substantial water temperature differences between the Antarctic Ocean and the Adriatic Sea, ranging from approximately 1°C in the Antarctic to almost 25°C in the Adriatic. Additionally, significant seasonal variations in temperature were observed in Rovinj, with temperatures recorded at 10.5°C in March and 24.7°C in September. Considerable differences in chlorophyll levels were also noted between the two different regions, averaging 1.5µg/l in the polar and only 0.4µg/l in the temperate environment. Nutrient concentrations in the Adriatic Sea, however, exhibited minimal variation between March and September (Table 1).

Table 1: Environmental parameters and nutrient concentrations at the Adriatic Sea and the Antarctic Ocean across different Stations, depths (SUR: Surface, DCM: Deep Chlorophyll Maximum) and sampling periods.

Location	Station	Coordinates	Month of sampling	Layer	Depth [m]	Water Temperature at sampling [°C]	Salinity [PSU]	Chlorophyll [µg/l]	Nitrate [µmol/l]	Nitrites [µmol/l]	Ammonium [µmol/l]	Phosphorus [µmol/l]
Adriatic Sea	Rovinj	45°05'32.8"N, 13°38'26.5"E	March	SUR	1	10.5	38.80	0.43	0.2	0.09	0.27	0.04
Adriatic Sea	Rovinj	45°05'32.8"N, 13°38'26.5"E	March	SUR	1	10.5	38.80	0.43	0.2	0.09	0.27	0.04
Adriatic Sea	Rovinj	45°05'32.8"N, 13°38'26.5"E	September	SUR	1	24.7	38.57	0.38	0.2	0.04	0.20	0.04
Adriatic Sea	Rovinj	45°05'32.8"N, 13°38'26.5"E	September	SUR	1	24.7	38.57	0.38	0.2	0.04	0.20	0.04
Antarctic Ocean	2	62°55'0.6"S, 61°06'6"W	January	SUR	5	1.4	34.10	1.00				
Antarctic Ocean	2	62°55'0.6"S, 61°06'6"W	January	DCM	29	1.3	34.10	1.00				
Antarctic Ocean	3	64°34'25.2"S, 62°33'42"W	January	SUR	5	1.0	34.00	1.20				
Antarctic Ocean	3	64°34'25.2"S, 62°33'42"W	January	DCM	24	1.0	34.10	0.90				
Antarctic Ocean	4	65°08'48"S, 65°38'9"W	January	SUR	5	1.0	33.50	1.90				
Antarctic Ocean	4	65°08'48"S, 65°38'9"W	January	DCM	20	0.9	33.50	1.60				
Antarctic Ocean	6	67°44'33"S, 68°01'24"W	January	DCM	16	0.3	33.20	2.60				

Fungal abundance in the samples from the Adriatic Sea exhibited steady growth during the incubation, showing saturation towards the end of the experiment. Prokaryotes showed an initial bloom within the first few days, followed by a rapid decline and a subsequent smaller bloom. Viral abundance followed a similar pattern as prokaryotes, but with a slight delay relative to the first prokaryotic bloom, prior to a steady decline of viral abundance. Interestingly, there were no significant differences in growth patterns of bacteria and fungi at varying incubation temperatures, nor were there marked differences in growth between March and September (Figure 2).

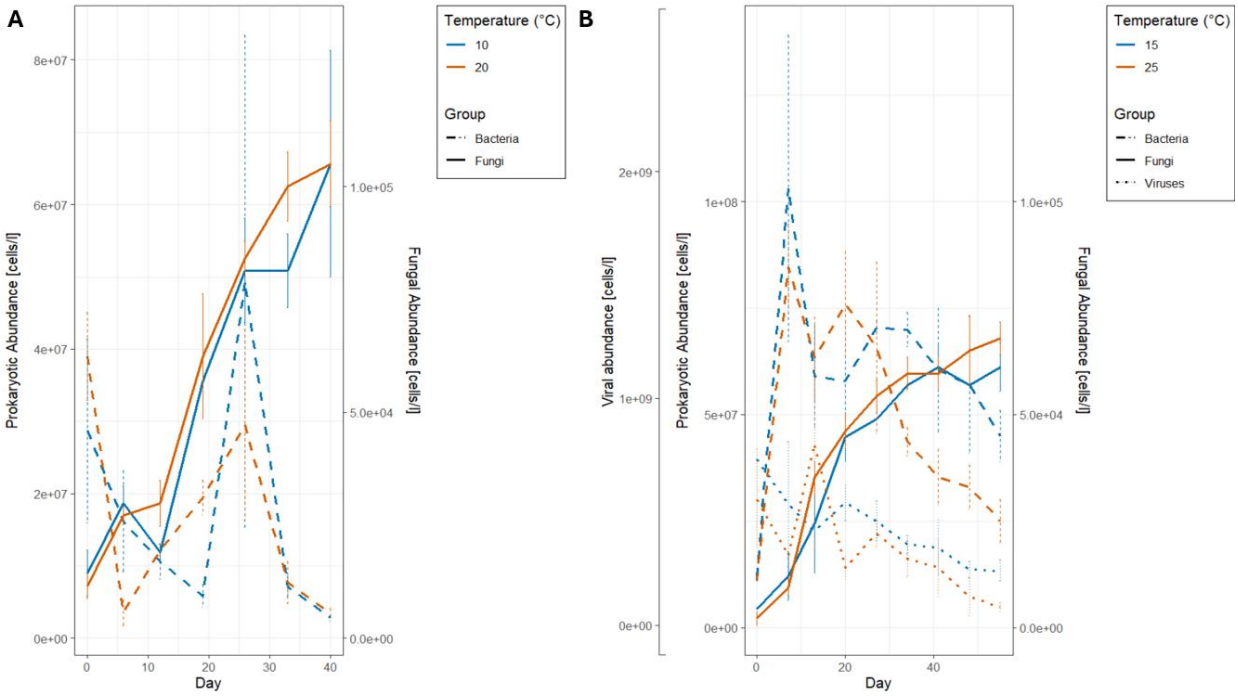

Figure 2: Fungal, Prokaryotic and Viral Abundance over time in the Adriatic Sea During (A) March and (B) September. Colours indicate different incubation temperatures.

A similar pattern of microbial growth was observed in the samples from the Antarctic Ocean. Fungal growth initiated slightly later than prokaryotic growth, with bacteria

exhibiting a rapid increase followed by slowing growth towards the end of the 9-day experiment. In contrast, fungal abundance continued to rise without reaching saturation. Notably, the fungal abundance at the end of the experiment was already significantly higher than that observed in the Adriatic Sea, even though it had not yet reached its saturation point (Figure 3).

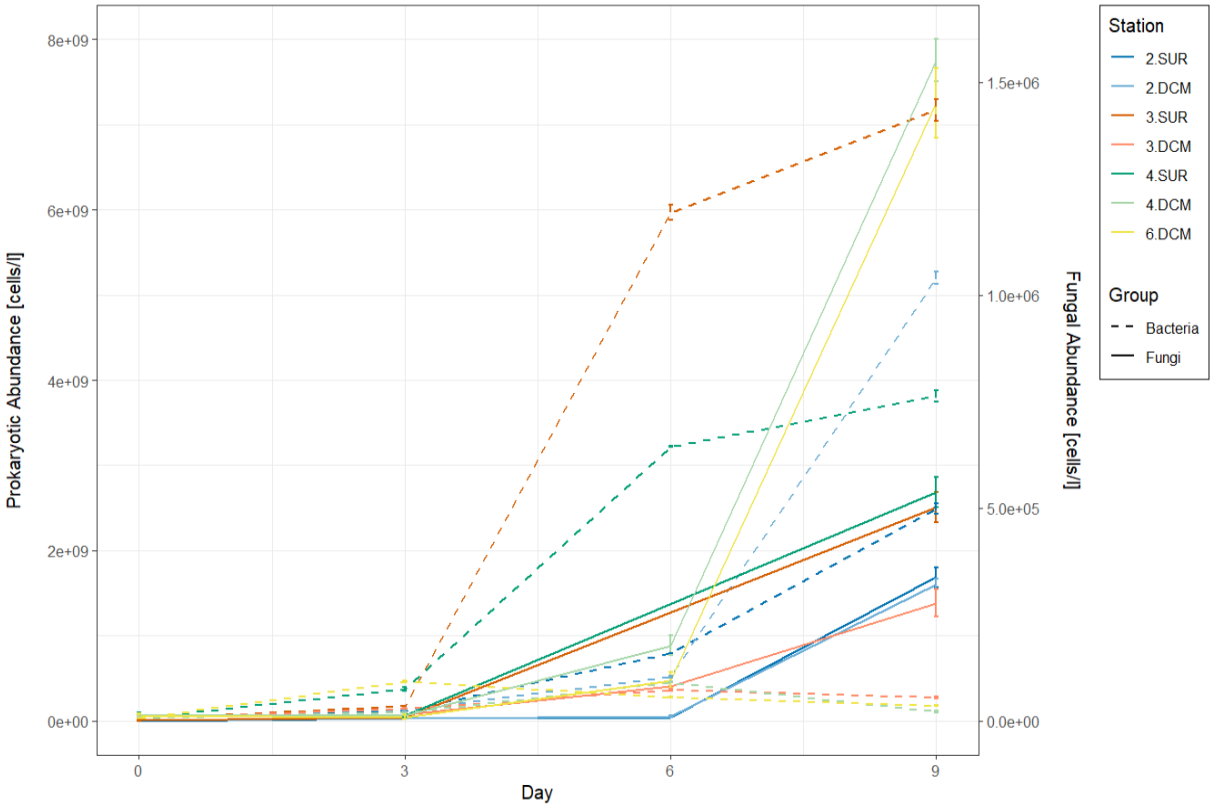

Figure 3: Fungal and prokaryotic abundance over time in the Antarctic Ocean. Colours indicate different stations and depths (SUR: Surface, DCM: Deep Chlorophyll Maximum).

The calculated maximum fungal abundance, biomass, growth rates and turnover times for the Adriatic Sea and the Antarctic Ocean were different. Fungal growth parameters were substantially higher in the Antarctic Ocean compared to the Adriatic Sea. For instance, the maximum fungal abundance in the polar environment was in

order of magnitude higher (1.54x 10^6 cells/l) than in Rovinj (1.05x 10^5 cells/l). Fungal biomass follows a similar trend to fungal abundance.

Growth rates of fungi in the Antarctic Ocean were also more than one order of magnitude higher, with values up to 5.64x 10^4 cells/l/day, compared to a maximum growth rate of 2.33 x 10^3 cells/l/day in the Adriatic Sea. Turnover times in the Antarctic Ocean were much shorter (averaging around 9 days), than in the Adriatic Sea (range between 44.95 and 59.17 days). However, maximum fungal biomass was similar across the two different environments with values between 2.2 and 4.29µg C/l, with only two exceptions of samples from the Antarctic Ocean (4 DCM and 6 DCM) with values above 16µg C/l. Only minimal differences in all measured growth parameters were observed between different sampling times in Rovinj (Table 2, Figure 4).

Table 2: Calculations of maximum Fungal Abundance and Biomass, Growth Rates and Turnover Times in the Adriatic Sea and Antarctic Oceans across different stations, depths (SUR: Surface, DCM: Deep Chlorophyll Maximum) and incubation temperatures.

Location	Station	Layer	Incubation Time [Days]	Temperature of incubation [°C]	Max. Fungal Abundance [cells/l]	Max. Fungal Biomass [µg C/l]	Growth Rate [cells/l/day]	Turnover Time [Days]
Adriatic Sea	Rovinj	SUR	40	10	1.05e+05	3.24	2.26e+03	46.40
Adriatic Sea	Rovinj	SUR	40	20	1.05e+05	2.39	2.33e+03	44.95
Adriatic Sea	Rovinj	SUR	55	15	6.11e+04	2.66	1.03e+03	59.17
Adriatic Sea	Rovinj	SUR	55	25	6.79e+04	3.19	1.19e+03	56.80
Antarctic Ocean	2	SUR	9	4	3.37e+05	2.63	3.74e+04	9.00
Antarctic Ocean	2	DCM	9	4	2.95e+05	2.20	3.25e+04	9.07
Antarctic Ocean	3	SUR	9	4	5.01e+05	2.90	5.55e+04	9.03
Antarctic Ocean	3	DCM	9	4	2.77e+05	2.55	2.97e+04	9.33
Antarctic Ocean	4	SUR	9	4	5.19e+05	4.29	5.64e+04	9.20
Antarctic Ocean	4	DCM	9	4	1.54e+06	16.31	1.70e+05	9.08
Antarctic Ocean	6	DCM	9	4	1.42e+06	18.57	1.56e+05	9.09

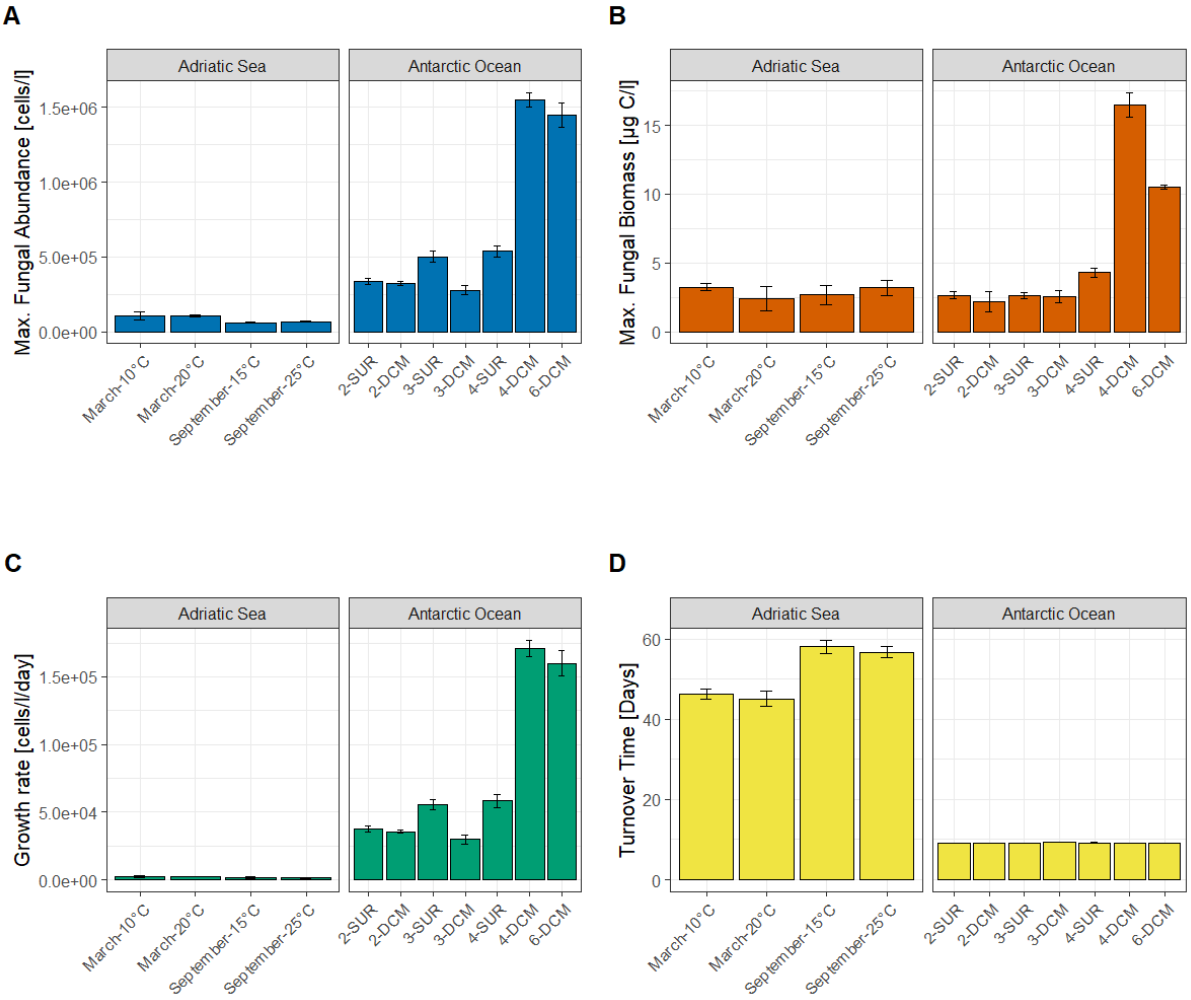

Figure 4: Calculations of Max. Fungal Abundance and Biomass, Growth Rates and Turnover Times in the Adriatic Sea and Antarctic Ocean across different stations, depths (SUR: Surface, DCM: Deep Chlorophyll Maximum) and incubation temperatures.

Discussion

This study successfully measured fungal growth in natural marine environments, establishing the first growth rates of pelagic fungi. Steady fungal growth over time was observed across all incubations, indicating active and abundant fungal communities at both sampling sites. Saturation occurred after approximately 35 days in the Adriatic Sea samples, suggesting a possible nutrient limitation. However, no saturation was reached in the samples from the Antarctic Ocean within the 9-day experiment duration. The overall observed growth rates range from 1.03×10^3 to 1.70×10^5 cells/l/day, with turnover times between 9 and 59 days. For comparison, a study by Rousk & Bååth (2011), in which acetate incorporation into ergosterol was used to estimate fungal growth, fungal turnover times in soil were estimated to be 20 to 580 days, depending on growth conditions. These numbers were found to be comparable to turnover times of fungi in freshwater systems growing on organic matter such as leaf litter and wood (Rousk & Bååth, 2011), indicating a relatively fast growth of marine fungi in comparison to fungi in other ecosystems.

As expected, the environmental conditions, including temperature and chlorophyll levels, were notably different at the two study sites. Growth was significantly higher in the Antarctic Ocean compared to the Adriatic Sea, with growth rates more than one order of magnitude greater and turnover times more than six times shorter in the Antarctic. This increased growth in the more productive, as shown by higher Chlorophyll levels, and nutrient-rich Arctic waters supports the hypothesis that nutrient availability is a more critical factor for fungal growth than temperature. This is

further underlined by the lack of significant differences in growth rates at varying incubation temperatures or seasons in the samples from Rovinj. Maximum fungal Biomass was very comparable across the two environments, potentially a result of the much longer incubation periods in the Adriatic Sea Experiments.

Prokaryotic populations exhibited an initial bloom within the first few days, followed by a rapid decline and a subsequent smaller bloom, which is a typical bacterial growth pattern (Maier, 2009). Viral abundance mirrored this pattern, with a slight delay relative to the first prokaryotic bloom, before steadily declining. These observations indicate potential correlations and interactions between viruses and bacteria in the sampled community, emphasizing their distinct dynamics within the marine environment (Rohwer & Thurber, 2009). In contrast, fungal growth followed a markedly different pattern, with their growth occurring gradually over time. These discrepancies in growth dynamics suggest that fungi operate on a different timescale and are less influenced by the activities of prokaryotes and viruses. This indicates potentially different ecological niches and strategies of fungi compared to the other studied microorganisms, despite the potential for nutrient competition (Grossart et al., 2019).

Several limitations should be noted. Potential bias could have arisen from the different methods used across the two environments, however Breyer et al, 2024 proved these methods to be comparable. The duration of the Antarctic experiment was not sufficient to observe saturation, which limits the insights into the maximum

growth potential of fungi in the Antarctic Ocean. Additionally, broader sampling across different locations and seasons would provide a more comprehensive understanding. Expanding the geographical and temporal scope would therefore be an interesting addition for future studies to build on these findings.

In conclusion, the findings suggest that marine fungi are actively growing in the marine environment. This study showed relatively short turnover times of marine fungi compared to fungi in soil, highlighting the potential ecological roles of fungi in this understudied environment. Growth rates were significantly higher in Antarctic samples compared to Mediterranean samples, likely due to the nutrient-rich and more productive Antarctic waters. Furthermore, the differing temporal scales of growth of fungi compared to bacteria and viruses suggest a lack of direct competition, while the correlations between bacterial and viral dynamics highlight their complex interactions within the marine ecosystem. Ultimately, this study provides valuable insights into the growth dynamics of marine fungi in their natural environment and their interactions within marine microbial communities, while demonstrating the need for further research in the field in order to obtain deeper knowledge on the ecological significance of marine fungi and their contributions to ecosystem dynamics.

Zusammenfassung

Während Pilze in Boden- und Süßwasserumgebungen gut erforscht sind, wurde ihre Rolle in marinen Ökosystemen bisher vernachlässigt. In den letzten Jahren wurde die wichtige Rolle der Pilze in marinen Ökosystemprozessen, einschließlich ihrer Beiträge zu Nährstoffkreisläufen, der Zersetzung organischen Materials und parasitären Beziehungen zu anderen Organismen, zunehmend anerkannt. Ihre Diversität und ökologischen Funktionen sind jedoch nach wie vor stark untererforscht, und Fragen wie Biomassebeiträge und Wachstumsraten in ihrer natürlichen Umgebung blieben bisher unbeantwortet. Mithilfe eines natürlichen Meerwasserinokulums und Zelldetektion durch Epifluoreszenzmikroskopie zielt diese Arbeit darauf ab, diese Wissenslücke zu schließen, indem das Wachstum mariner Pilze in zwei kontrastierenden Umgebungen gemessen wird.

Die Studie ermittelte erfolgreich Wachstumsraten für pelagische Pilze und konnte ein kontinuierliches Wachstum in allen Proben zeigen, was die Präsenz aktiver Pilzgemeinschaften sowohl in gemäßigten als auch in polaren marinen Umgebungen unterstreicht. Die nährstoffreichen antarktischen Gewässer wiesen signifikant höhere Pilzwachstumsraten im Vergleich zur Adria auf, was darauf hindeutet, dass die Nährstoffverfügbarkeit ein einflussreicher Faktor für die Pilzproduktion ist. Während Pilze kontinuierliches Wachstum zeigten, wiesen virale und bakterielle Gemeinschaften zunächst eine sehr starke Vermehrung, gefolgt von einem schnellen Rückgang auf, wobei Viren etwas verzögert reagierten. Dies deutet auf mögliche

unterschiedliche ökologische Nischen von Pilzen im Vergleich zu Bakterien und Viren hin.

Zusammenfassend liefert diese Arbeit wertvolle Einblicke in die Wachstumsdynamik mariner Pilze und ihre Interaktionen innerhalb mariner mikrobieller Gemeinschaften und stellt einen wichtigen Schritt zum Verständnis der ökologischen Bedeutung von Pilzen in marinen Umgebungen dar.

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