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Evaporation as a Key Process in Thermoregulation of Shallow Coral Reef Environment: From Local Micrometeorology and air-sea Exchange to Marine Heat Waves Under Different Geoclimatic Regions

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Coral bleaching events are more frequent and severe as global temperatures rise and marine heat waves are more frequent. However, quantifying the surface energy fluxes in coral reefs at various geoclimatic regions and the mechanisms by which the air-water interactions regulate water temperature is rare. We measure surface energy fluxes over coral reefs using Eddy Covariance towers in two contrasting geo-climatic regions: The typical setup of humid/tropical coral reefs (Heron Reef, Great Barrier Reef, Australia) and the rarer desert coral reef (Gulf of Eilat, Israel). We analyze how the surface heat fluxes regulate the temperature of shallow coral reef environments. We show that in the desert reefs, the dry air overlying the shallow coral reef results in extremely high evaporation rates which in turn results in extensive cooling of the water. In humid/tropical reefs, evaporation is suppressed by humidity and is limited in the ability to offset the heating of the water. The extreme difference in evaporative cooling in desert versus tropical reefs is key in the response to marine heat waves. We conclude that evaporative cooling is a key mechanism protecting coral reefs located in deserts from extreme high-water temperatures, thereby representing possible thermal refugium for corals against background global warming.

The potential contribution of SAR11 to global warming via methyl-phosphonate biosynthesis

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Many marine regions are characterized by extremely low concentrations of bioavailable phosphate (P), thereby limiting the primary and secondary microbial productivity that forms the base of the oceanic foodweb. Nevertheless, tiny genome-streamlined bacteria thrive in these conditions by utilizing alternate forms of phosphorus such as phosphonates (PHNs). Interestingly, when one such PHN type, methyl-phosphonate (MPn), is degraded by bacteria to retrieve P as a nutrient, methane is also released, and the latter is a potent greenhouse gas. Greenhouse gases are causing an increase in temperature that causes ocean stratification, which in turn results in phosphate limitation and further MPn degradation. Very little is known about PHN production, even though the presence of relatively high standing stocks of PHN in marine dissolved organic matter (DOM) suggests that these compounds are constantly produced in ocean surface water. The main source of MPn in DOM is still to be discovered. Here, we propose to test whether the most abundant heterotroph of the global surface ocean, the SAR11 clade, represents the primary source of PHNs that accumulate in marine DOM, and thus may play a role in global warming via both MPn biosynthesis and degradation. To reach this objective we are combining microbiology (culturing of the fastidious SAR11 bacteria: strain HTCC7217 that harbors genes for MPn biosynthesis) and advanced organic chemical analysis (chemical purification and identification of PHN-macromolecules produced). Further, we will test the environmental conditions that trigger MPn biosynthesis.

Stratification sensitivity of a monomictic subtropical lake to expected climate changes

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Located in a highly sensitive subtropical climate area, according to the IPCC reports, Lake Kinneret will be exposed to extreme changes in the next few decades. Lake Kinneret is a warm monomictic lake, which is thermally stratified throughout most of the year and mixes thoroughly each winter when the epilimnion water temperature reaches equilibrium with the hypolimnion water temperature by surface cooling and turbulence. Using high-resolution atmospheric projections obtained from the CORDEX RCP4.5 simulation to force a 3D limnological model, we show significant changes in the stratification and circulation of the lake over the next 50 years. As air temperature is expected to rise by up to 2.5°C in winter and autumn by 2070, the water column full mixing is expected to be suppressed. Unmixed years are expected to appear more often and full mixing will be re-activated just when cold enough winter conditions allow a full water column turnover. Lack of mixing between the epilimnion and the hypolimnion may create a depleted oxygen environment in which very few organisms can live in, hence, it might strongly affect the lake's present ecological system, its sustainability, and its water quality. Stratification Index analysis results show that Lake Kinneret will remain stratified throughout the year 20%-30% of the time in 2030-2070 under climate change scenario RCP4.5. However, abrupt cooling of the lake surface due to enhanced latent heat loss was observed in the model results around the year 2065 and expect to restrain the dramatic change in the lake stratification.

Global trends of echinoid mass mortalities – insights from *Echinocardium* from the Eastern Mediterranean Sea

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Mass mortality events (MMEs) have been occurring since the dawn of time. However, in contrast to terrestrial events, most marine MMEs remain undetected due to the inaccessibility of most marine environments. Here we summarize 314 studies of echinoid MMEs dating back to 1888 and include citizen-science reports, social media, and newspaper articles. We formulate five potential mechanisms driving echinoid MMEs and calculate their relative abundance. We then provide the first reports of echinoid MMEs in the Eastern Mediterranean, compiling *in situ* observations, molecular, morphological, and environmental data, to illustrate a decade-long history of ongoing localized MMEs in the region. We found five main mechanisms driving echinoid MMEs: 1) catastrophic events (25%), 2) algal blooms (9.6%), 3) pathogenic activity (16.9%), 4) temperature and tides (39%) and 5) human activity (9.6%). Along the Israeli coastline, four MMEs of irregular echinoids of the genus *Echinocardium* are reported between 2011 and 2020. Using the Israeli MMEs as a case study to scrutinize the abovementioned mechanisms, we analysed skeletal remains collected during one of the MMEs, meteorological and remote-sensed environmental data (Chlorophyll *a*, sea surface temperatures, and precipitation) collected during the weeks prior to the MMEs. While none of the environmental parameters alone could be identified as the sole contributor to the Israeli MMEs, the mortality events were always recorded near the outlet of polluted rivers or adjacent to major power stations – suggesting pollution from human activity as the main source of these mortalities. Observations from the warm Eastern Mediterranean may predict the future of the western parts of the Mediterranean as global warming accelerates and human activity intensifies.

Influence of temperature on cyanobacteria-phage interactions

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In marine environments viral infection is a major biological factor involved in the regulation of microbial communities. Nevertheless, both viruses and their hosts also interact with their environment which affects cellular processes. Over the past few decades, studies have demonstrated the effects of abiotic factors (such as temperature or irradiance) on virus-microbe interactions. These parameters play a considerable role in infection dynamics, and can dramatically alter the outcome of the interactions. Elucidating how environmental parameters regulate host-virus interactions is thus of prime importance to unveil how they coexist in the oceans. Marine cyanobacteria of the genera *Prochlorococcus* and *Synechococcus* are highly abundant and contribute greatly to primary production. The viruses that infect them, the cyanophages, are considered to be main drivers in their mortality, diversity and evolution. To date, their responses to temperature have never been investigated. In this context, my research focuses on the interplay between cyanobacteria and their phages under this environmental variable. Here I will present the influence of temperature on cyanophage decay and infection properties. The results showed that decay of infectious cyanophages is faster at high temperature than at low temperature and that this loss of infectivity is not coupled with particle degradation. Moreover, temperature can modify the host-range of cyanophages. Several *Synechococcus*-phage systems displayed shifts in resistance/sensitivity when grown under different temperatures. Interestingly, temperature did not affect *Prochlorococcus*-phage interplays. This study will contribute to a better understanding of the role of temperature in the control of cyanobacterial-cyanophage interactions in the oceans.

Enrichment of nutritional compounds in seaweeds via abiotic stressors in integrated aquaculture

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Seaweeds may contain significant amounts of essential proteins, carbohydrates, and minerals, offering an alternative, sustainable, healthy food source from the sea. However, there are yet challenges impeding their full exploitation. Our study presents an innovative, two-step aquaculture approach integrating seaweeds and finfish, dedicated to enrich seaweeds with nutritional compounds. The approach involves diverting fish effluents rich in nutrients into a series of seaweed cultivation tanks. Then, the seaweeds were exposed to short-term abiotic stressors (namely, high irradiance, nutrient starvation, and high salinity) to stimulate synthesis of desired ingredients in their tissues. Our methodology enabled high growth rates of up to 25% seaweed biomass increase per day, with significant enhancements in the amount of protein, starch, and minerals within days. Moreover, the seaweeds presented elevated bioremediation capabilities assimilating the ammonia nitrogen, NO₃ and PO₄ with high uptake rates, and with 50–75% removal efficiencies. Industrial relevance: The rising public awareness to quality of healthier food products has stimulated growing demand for seaweed supply. Our new approach suggests a promising direction toward the transition from seaweed production of raw, commodity seaweed biomass, to a tailored production of functional seaweeds, enriched with valued compounds that can be utilized in the emerging food and health industries.

33 days later: The infection process and molecular analysis of a myxozoan parasite in tilapia

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Myxozoans are microscopic, eukaryotic, obligatory endoparasites that have been placed recently within the phylum Cnidaria. Although they have a reduced genome and body structure, they retain complex life cycles, infecting both vertebrates and invertebrates. Recently, we identified a new myxozoan species, *Myxobolus bejeranoi*, as the causative agent of up to 40% mortality in commercial cultures of hybrid tilapia, *Oreochromis aureus* (blue tilapia) X *Oreochromis niloticus* (Nile tilapia). Our main objective is to molecularly characterize the parasite and to understand its infection specificity to tilapia species. We have assembled a draft genome and de-novo transcriptome of *M. bejeranoi*, from infected fish gills, extracted DNA and RNA. Since the sequencing data was contaminated from the fish host, we used various bioinformatic tools and pipelines to “refine” the genome and transcriptome and to better characterize this parasite’s genome. In order to understand the parasite’s infection specificity to its fish host, we tested the infection rate of *M. bejeranoi* in hybrid tilapia species and the purebred parent species. Our findings indicate that the susceptibility of hybrid tilapia to *M. bejeranoi* infection is similar to its purebred parent blue tilapia, while the other parent, Nile tilapia, is resistant. Understanding this parasite can inform broader evolutionary processes of myxozoan parasites within Cnidaria and may contribute to fish aquaculture stability, which is an essential food source around the world.

In-depth characterization of diatoms succession and community composition over seasonal transitions in the oligotrophic Gulf of Aqaba-Eilat

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Diatoms are a main group of phytoplankton, which estimated to drive about 20% of global primary productivity. Diatom cells often dominate high nutrient settings. However, they are found throughout the oceans including in low nutrient, stratified areas. The Gulf of Aqaba/Eilat (GoA) is an oligotrophic narrow basin in the northeastern-most section of the Red Sea. Oceanographic conditions in the GoA alter between nutrient-limited summer stratification and winter mixing that lead to entrainment of nutrients to the photic layer. The microbial community in the GoA is mainly dominated by cyanobacteria groups through summer. During winter, influx of nutrients by mixing enables the formation of a phytoplankton bloom at the onset of spring. Yet, the diversity, succession and contribution of diatoms remains unknown, limiting our understanding of the significance of such important primary producers in the GoA ecosystem. To address this, a routine bi-weekly sampling was performed in the offshore Station-A in Eilat. Sampling included seawater collection and acquisition of environmental parameters. Thus far, analysis of one season revealed a dynamic and diverse assemblage, with high year-round abundances of species of the minute Thalassiosiraceae family and the pennate *Cylindrotheca closterium*, peak of chain-forming *Chaetoceros* genus during winter, and of additional chain-forming species of *Leptocylindrus* in early spring. Summer assemblages included mainly members of *Rhizosolenia*, and the pennate *Pseudo-nitzschia delicatissima*. Together with ongoing quantitative pigment and metabarcoding analyses (18 S), our study will serve as baseline for understanding the morpho-genetic diversity, seasonal succession and ecological role of diatoms in the gulf's ecosystem.

Morphological performance and natural products diversity of *Asparagopsis taxiformis*

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Asparagopsis spp belongs to the family of Bonnemaisoniaceae, a red algae (Rhodophyta), the largest group of marine seaweeds. It is present in the Israeli coastline by the species *Asparagopsis taxiformis*, widespread throughout the world and one of the 'worst invasive in the Mediterranean Sea'. *A. taxiformis* is a rich source of natural products, used by the algae as a natural defensive mechanism against herbivores and bacteria. Its halogenated compounds are known to have potent antifungal, antibacterial and antiprotozoal activity. Here, we explore the variations between three major tissues of *A. taxiformis* named blade, stipe, and holdfast collected at the rocky shore of Tel Shikmona, Haifa, Israel. Morphological performance and localization of natural products in algae's cells were examined using light microscopy, histology staining, scanning electron microscopy, Fluorescence and Lightsheet microscopy. Chemical diversity of annotation natural products was evaluated by LC-MS/MS based-metabolomics, highlighting the unique characteristics of each selected tissue.

Wastewater surveillance as the first line of defence against polio outbreaks

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Israel conducts routine wastewater surveillance for Poliovirus since 1988. In September 2021, wastewater samples collected from Jerusalem region at more than one site became positive for ambiguous type 3 Vaccine-Derived Poliovirus (VDPV) with increasing frequency. On late February, 2022, a VDPV3, genetically related to the environmental surveillance samples, was isolated from a stool sample collected in Jerusalem from a non-immunodeficient, unimmunized child who developed Acute Flaccid Paralysis, confirming that the VDPV3s were circulating rather than immunodeficiency related VDPV3s. Later this year, poliovirus type 2 was detected by the wastewater surveillance in three non-overlapping regions in the Jerusalem region. Sequencing showed genetic linkage among isolates and accumulation of mutations over time, with few isolates defined as type 2 VDPV. This demonstrates the emergence and potential circulation of type 2 VDPV in a high-income country with high vaccine coverage and underscores the importance of routine wastewater surveillance during the polio eradication.

Stories from the growth phenotypes- metabolic adaptations across phylogeny in heterotrophic marine bacteria.

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The microbial diversity across the global oceans is among the driving factors that shape the character of the biome associated with it. Through processes that range in function from enabling nutrient availability to geochemical cycling, bacteria play a crucial role in upholding the possibility of marine life in its known complexity. We are using a diverse library of marine heterotrophic bacteria to understand the factors that govern the thriving of bacteria under various ocean conditions and the strategies that enable them to survive in different niches. We are characterizing growth dynamics under various conditions, defining their metabolic adaptations and quantifying processes such as motility, biofilm formation and mortality. We are comparing these measurements to identify how they are related to their genomes and phylogeny.

An algal-bacterial synthetic community reveals a novel ‘protection’ phenotype in abundant marine bacteria

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Emiliania huxleyi is a unicellular micro-alga forming massive oceanic blooms that swarm with heterotrophic bacteria. The blooms collapse after a couple of weeks in a process largely attributed to viral infection. However, various laboratory algal-bacterial co-culture systems demonstrate that bacteria can also trigger algal death. Co-culture systems are extremely reduced to allow tightly controlled conditions, but they lack the bacterial complexity of the ocean. To study bacterial pathogenicity in an ecologically relevant context, there is a need to increase the complexity of co-cultures. In this work we investigate whether *Phaeobacter inhibens*, a known *E. huxleyi* pathogen, is able to induce algal death in the presence of a complex bacterial community. We show that an *E. huxleyi*-associated bacterial community protects the alga from the pathogen, although the pathogen naturally occurs within the community. To study how the bacterial community regulates pathogenicity, we reduced the complex bacterial community to a five-member synthetic community (syncomm). The syncomm is comprised of a single algal host and five bacterial species that represent major bacterial groups that are naturally found associated with *E. huxleyi*. We discovered that a single bacterial species in the reduced community, *Sulfitobacter pontiacus*, protects the alga from the pathogen. We further found that algal protection from *P. inhibens* pathogenicity is shared among several *Sulfitobacter* species. Algal protection by bacteria might be a common phenomenon with ecological significance, which is overlooked in reduced co-culture systems.

Dissolved aluminium dynamics in response to dust storms, wet deposition, and sediment resuspension in the Gulf of Aqaba, northern Red Sea

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Dissolved aluminium (Al) is a primary tracer of atmospheric deposition to the open ocean. However, the impact of short-term environmental perturbations such as dust storms, sediment resuspension and rainfall events on the oceanic water column is poorly constrained due to the low temporal resolution sampling in open ocean settings. The Gulf of Aqaba (GoA), Red Sea, is a highly accessible deep oligotrophic water body featuring exceptionally high atmospheric deposition fluxes delivered by dust storms, which constitutes as the main terrigenous input to the GoA surface water. Here, we present a time series of dissolved Al and silicate concentration profiles sampled during 2017 and 2018, with a particular focus on daily time scale dust storms, episodes of sediment resuspension and rain events. We evaluate the results in conjunction with high temporal resolution measurements of airborne aerosols and sediment trap-based water column sinking particulate fluxes. Counter-intuitively, mixed layer Al (Al_{ML}) inventories decrease with increasing aerosol loads, with dust storms promoting intense Al scavenging, abruptly driving down Al_{ML} by up to 14%. Similarly, a sediment resuspension event triggered a decrease of 34% in the Al water column inventory. By contrast, wet deposition may enhance the soluble Al flux from mineral dust by a factor of 11. The results demonstrate that atmospheric deposition in the oceans acts as a long-term source for Al while concomitantly serving as a short-term sink. The in-situ insights presented here may be used to understand and quantify the true impact of abrupt environmental events on water column chemical compositions.

Testing solutions to limit species introduction through the Suez Canal

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A recent hydrodynamic modeling study of the water flow through the Suez Canal suggests that species migration along the canal is affected by seasonal differences in the water levels between the Mediterranean and the Red Sea. Northward flow, facilitating Lessepsian migrations, is driven by the high Red Sea levels during most of the year. In contrast, southward flow occurs during the late summer months, when the water level in the Mediterranean is higher than that of the Red Sea, supporting Anti-Lessepsian migrations. Although a similar flow pattern is evident at least since the 1920s, most Lessepsian species appeared after the 1970s. The common explanation is that until the 70s the Great Bitter Lake salinity, located in the center of the canal, exceeded the lethal salinity values of most species, therefore acting as a species introduction barrier. It was hypothesized that layers of salt deposits that served as the salinity source were dissolved in the 1970s, resulting in the currently sea-like lake salinities. Here we analyze operational suggestions that will increase the lake salinity to limit future introductions. Numerical solutions of the water and salinity mass balance equations were used to test two suggestions: (1) discharging desalination brine into the Bitter Lake; and (2) building marine locks to reduce the canal water flow rates. The results indicate that only unrealistic volumes of desalination brine will impact the lake salinity, while constructing marine locks can provide a plausible solution for restoring a “salinity barrier” in the lake within 5-10 years.

Seasonal patterns of inorganic and organic nitrogen uptake by phytoplankton in the Eastern Mediterranean Sea

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In the nutrient-depleted Eastern Mediterranean Sea (EMS), Dissolved Organic Nitrogen (DON) may be critical for sustaining the base of the food-web. Urea is a readily available organic form of nitrogen. Currently, the natural role of urea in the EMS is unknown, and is the purpose of this study. Specifically, its availability to phytoplankton and bacteria compared with that of the inorganic ammonium (NH_4) and nitrate (NO_3). The study was conducted during two contrasting seasons, Autumn 2021 which represented extreme period of Nitrite+Nitrate (N+N) depletion (July 2020-November 2021) and Winter/Spring 2022 after a major deep winter mixing (December 2021-April 2022) with N+N decreasing gradually until in June 2022 it returned to below detection limits. Two sets of seasonal microcosm N enrichments experiments were performed to assess potential and field uptake rates of dissolved N species. During 48 hours of incubation, by measuring chlorophyll, bacterial abundance and N uptake, we compared microbial consumption of varying concentrations of urea, NO_3 , and NH_4 using excess Phosphate. These experiments showed that the potential uptake of NH_4 was dominant in all the experiments conducted, with urea generally slightly more available than nitrate. In-situ uptake rates of N compounds during 4 hours of incubation were assessed using ^{15}N and ^{13}C isotopes. These showed that when inorganic nutrients were essentially depleted, urea was the major N species taken up albeit at low rates. In spring 2022, the major uptake was nitrate. This coincided with the period when nitrate was the major N species in the water column, and we hypothesized that autotrophs adapted to utilize nitrate dominated the phytoplankton community.

Morphological changes in the coastline of Herzliya, in the years 1946-2022

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Herzliya Marina was built between 1992-1990 on a straight and smooth sandy beach. The marina's main breakwater protrudes into the sea about 500 m from the shoreline and its head stands in a water depth of about 6 m. In order to prevent beach erosion north of the marina, three detached breakwaters were built, each 100-150 m long, in 3 m water depth, about 200 m from the shoreline. A previous study, which used aerial photographs, found that before the marina construction the width of Herzliya's beach retreated 12-16 m during the years 1965-1979 and expanded 15-25 m in the years 1979-1990. Between 1990 and 1997, however, the coastal segment located 1-2.5 km north of the marina's lee breakwater, as well as the segment located 0.5-1 km south of its main breakwater had eroded by 12-18 m (decrease of 35% to 45% of the beach width). However, the shore behind the detached breakwaters and that just south of the marina had broadened to an average extent of 53 m (131%) and 11 m (126%) respectively. Since the study by Zviely (2000), morphological changes have continued to develop on the Herzliya beaches, south and north of the marina, which have been documented in detail using high-resolution aerial photographs and satellite images, as well as field measurements. Moreover, over the years, digital mapping techniques have been significantly improved. The large amount of data collected over the past 25 years and the improvement in mapping techniques, allow the current study to assess the changes that occurred in Herzliya's coastline over a longer period of time and achieve a more accurate location of the coastline.

Characterizing Mg isotopes behaviour in coastal aquifers

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Groundwater-derived solute fluxes to the ocean have long been assumed static and subordinate to riverine fluxes in marine isotope budgets. However, it was shown recently that they may play a significant role in ocean chemistry. The chemical composition of those solutes is affected by mixing between fresh and saline water bodies and by water-rock interaction, which also depends on the intruding seawater residence time and flow path. This study attempts to determine the geochemical processes governing different coastal aquifers in the context of the groundwater flow and water-rock interaction time-scale using the Nitzanim coastal aquifer (located at the Nitzanim nature reserve, in the southern part of Israel's coastal plain) and the shallow aquifer at the Indian River Bay, Delaware, USA, as case studies. Here, we present the groundwater's major and trace elements and Mg isotope compositions ($\delta^{26}\text{Mg}$ values) in coastal groundwaters, to constrain the importance of groundwater discharge for the magnitude and isotope composition of terrestrially derived solute fluxes to the ocean. The natural conditions in the Nitzanim nature reserve, and a cross-section of monitoring boreholes perpendicular to the shoreline, made it suitable to track groundwater-seawater interactions in the carbonate-rich silicate aquifer. Samples were collected from onshore boreholes at a distance of 710, 230, and 70 meters from the shoreline with a depth range of 0-73 meters below the groundwater level. The Indian River Bay, Delaware, is a shallow estuary on the Atlantic Coastal Plain comprised primarily of Pleistocene sands, with some silt and clay. Groundwater samples were collected from seepage meters and piezometers along a cross-section. The behavior of major cations concentration in the groundwater samples of our two study areas represents a non-linear mixing between fresh, meteoric groundwater and local saline seawater, i.e. enrichment in Mg^{2+} , Ca^{2+} and Sr^{2+} , and depletion in K^{+} and Na^{+} . Our preliminary $\delta^{26}\text{Mg}$ data of the Nitzanim study area show values similar to seawater near the coast, while values are more negative away from the coast, towards the fresh, meteoric end member, suggesting a contribution of Mg from dissolution of ^{24}Mg -enriched carbonates by freshwater. Also, the $\delta^{26}\text{Mg}$ value of most samples with intermediate salinities is more negative than the expected mixing line between seawater and freshwater, probably due to the influence of additional water-rock interactions. In contrast, the $\delta^{26}\text{Mg}$ data from the study area in Delaware mostly overlap (within errors) to the average $\delta^{26}\text{Mg}$ value of seawater, probably due to Mg contribution from both ^{24}Mg -enriched carbonates and ^{26}Mg -enriched silicates, or Mg contribution by sea-spray, bringing the freshwater end-member to a $\delta^{26}\text{Mg}$ value similar to seawater.

Benthic fluxes of dissolved barium from the sediments of the South East Mediterranean

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Dissolved Ba in the ocean shows bio-intermediate nutrient like vertical distributions, similar to those of Si, and Alkalinity. Due to the involvement of Ba in various biogeochemical processes, it is used as tracer of freshwater input, productivity, and Ba:Ca ratios of foraminifera skeletons for paleo-alkalinity and paleo-salinity. However, the present-day oceanic budget of Ba is poorly constrained, which leads to uncertainty in its use as a proxy. Riverine, SGD, benthic, hydrothermal fluxes are considered to be the main sources of dissolved barium, whereas the formation of barite is a sink. Among these, the benthic Ba flux from the continental shelf sediments is poorly constrained. The goal of this study is to quantify the benthic fluxes of dissolved Ba from the sediments of the south-eastern Mediterranean Sea. To achieve this goal, porewater was extracted from two 40 cm cores, and were analysed for their Ba, SO₄, Cl, and alkalinity concentrations. The results show the Ba and alkalinity concentration increase with depth from the sediment-water interface, whereas SO₄ concentration decreases with depth. A 1D diffusion equation was used to estimate the benthic Ba flux. The estimates shows that the rate of Ba release from Mediterranean shelf sediments (745 $\mu\text{mol}/\text{m}^2/\text{yr}$) is significantly higher than the Peru (314 $\mu\text{mol}/\text{m}^2/\text{yr}$) and California (450 $\mu\text{mol}/\text{m}^2/\text{yr}$) continental margin sediments, but lower than the arctic shelf (4000 $\mu\text{mol}/\text{m}^2/\text{yr}$) and North Atlantic shelf (4040 $\mu\text{mol}/\text{m}^2/\text{yr}$). Outcome of this study, hence, signify the importance of benthic sources of Ba from the continental shelf sediments to the overlying sea water.

The effect of marine sponges on a coastal carbonate system

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The oceanic buffer system has a crucial role in regulating the CO₂ content of the earth's atmosphere as well as the pH of the ocean. Coastal ecosystems are among the most dynamic and bio-geochemically active marine zones, but the controls of the oceanic buffer system in these environments are less understood. Marine sponges are sessile filter feeders that recycle vast amounts of water and specialize in filtering particulate and dissolved organic matter, making it available to other benthic organisms, a process sometimes referred to as the 'sponge carbon pump'. Where sponges form dense populations, sponge communities are expected to have a substantial effect on the DIC pool and the coastal carbonate chemistry. Yet, this effect has not been thoroughly studied so far. To narrow this knowledge gap, I quantified, in situ, the pumping rates, DIC concentrations, and the pH in the water inhaled and exhaled by four dominant sponges species from the emblematic, sponge-dominated, coralligenous community of the northwest Mediterranean. These individual-based data were scaled up using sponge oscula abundance and size distribution obtained from benthic surveys to calculate the DIC flux mediated by the sponge community of a vertical wall. The scaled-up fluxes are contrasted with estimates of the overall DIC flux from the same wall, which were independently estimated using high-resolution measurements of cross-wall hydrodynamic and DIC concentration gradients. Overall, this study is expected to yield a first-order estimate of the effect of a north Mediterranean sponge community on the local carbonate system.

Specificity and dynamics of early microbial colonization on common plastic polymers in a marine environment

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Millions of tons of plastic litter end up in the oceans every year where it is gradually broken down into small particles. This plastic debris serves as substrates for the colonization of a variety of prokaryote and eukaryote organisms. Several studies have used a DNA metabarcoding approach to characterize the taxonomic composition of the plastic microbiome. However, very little is known about microorganisms with a specific preference for different plastic polymers over non-plastic natural/artificial substrates. We designed a controllable experiment set up in a marine aquarium in which we monitored early microbial colonization on four abundant plastic polymers (Polyethylene- PE, Polypropylene - PP, Polyethylene terephthalate- PET, and Polystyrene- PS) as well as on wood and glass. The plastic microbiome taxonomic composition was analyzed 2, 7, 14, 30- and 90-days post-incubation initiation. We used the full 16S rRNA gene as a barcode for bacteria, which was amplified and sequenced with the Nanopore MinION system. Our results demonstrated the specificity of certain bacterial genera such as *Alcanivorax* to specific plastic polymers at the early biofilm stage, particularly polyolefin polymers, PE, and PP. The relative abundances of a variety of different *Alcanivorax* species followed a similar pattern of expression between PE and PP over the time of the experiment. This research may shed light on the formation and structure of the plastic microbiome in its early development stages and may help in the identification of plastic biodegrading species.

Massive colonization of ascidians on sandy bottom of the East Mediterranean littoral

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Sandy bottom comprises most of the littoral zone of the East-Mediterranean, yet the ecology and function of its inhabitants is understudied. In comparison to the rocky environment, organisms inhabiting sandy habitats face limited organic resources, continuous sedimentation, and abrasion by loose particles. A massive colonization by the invasive solitary ascidian *Microcosmus exasperatus* (Family: Pyuridae) of the sandy bottom (15-20 m depth) in front of Michmoret was sighted by students of the Underwater Research Methods course in the Faculty of Marine Science, Ruppin Academic Center. Visual inspection reveals that specimens have settled mostly on polychaete tubes (>90%) and other hard objects, sometimes forming aggregations of 2-10 specimens that may facilitate the settlement of more individuals. The non-indigenous colonial ascidian *Polyclinum constellatum* (Family: Polyclinidae) was also present in lower numbers. Preliminary surveys suggest average densities of 1 ± 0.2 (95% CI) individuals of *M. exasperatus* m⁻² at depth >15 m. Similar densities were observed in six different stations spread over five km. The estimated filtration capacity of this population is considerable, likely over 100,000 cubic meter per square km a day. It is currently unknown whether this colonization is new, and if the population is persistent through the year or has a seasonal cycle. We plan to continue monitoring this population through monthly density surveys and survivability surveys after winter storms and will appreciate any past and future observations of this phenomena in other sandy bottom locations.

Impact of viral infection on calcification and nutrient uptake rates of the bloom-forming coccolithophore *Emiliana huxleyi*

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The coccolithophore, *Emiliana huxleyi*, is the most productive marine calcifying phytoplankton in the oceans and forms large-scale blooms in the oceans impacting both marine ecosystems and global biogeochemical processes. During calcification, *E. huxleyi* cells consume seawater alkalinity, which in turn changes the carbon stoichiometry in the upper ocean and directly affects air/sea CO₂ exchanges, thus influencing climate. Specific lytic viruses (*Emiliana huxleyi* virus, *Ehv*) have been shown to be major biotic factors driving the termination of blooms. At the cellular level, the viral infected cell (the virocell) shows an altered metabolism likely optimized for viral production and egress. This likely causes both alterations in nutrient demands and changes in the stoichiometry in the host virocell as the lytic cycle progresses. Given the large-scale of bloom spanning across hundred to thousands of km² in the ocean, such shifts in the cellular requirements and composition will likely influence higher trophic levels feeding on infected cells, but also the biogeochemical cycling of nutrients and marine carbon chemistry dynamics. In this work, we aim to test *in vitro* using cultured *E. huxleyi* and *Ehv* strains, the impact of viral infections on the alkalinity, nutrient uptake rates and cell stoichiometry over infection dynamics. The results of this work will improve the current understanding of the role of coccolithophores but particularly viruses as key agents influencing the ecology and biogeochemistry of marine ecosystems.

Heterogeneous reactions and their effect on dissolved inorganic carbon and total alkalinity

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The ocean's carbonate system has been well-studied over recent decades due to its important roles in the global carbon cycle, anthropogenic influences, and climate modulation. The ocean's dissolved inorganic carbon (DIC) and total alkalinity (TA) constitute main parameters of the carbonate system, and determine the seawater tendency to absorb, or release CO₂ from the atmosphere. Recent studies have shown that heterogeneous reactions between dissolved ions and solid particles significantly affect the TA and DIC in some regions of the ocean. Nevertheless, no systematic research targeting the effect of heterogeneous reactions on the TA and DIC budgets has been conducted. This study aims to close this knowledge gap by combining laboratory experiments, in which the effect of a variety of local sediments on TA and DIC is examined, and in-situ measurements in the Gulf of Aqaba (GOA). The latter include monthly DIC and TA profiles, as well as a focused campaign aiming to study the effect of resuspension events on the water column's DIC and TA. Laboratory experiments conducted thus far have shown that suspension of local sediments in the GOA seawater leads to a decrease of both DIC and TA. The ratio between the decrease in TA and the decrease in DIC is ~ 2 , which indicates that the main mechanism responsible for the decrease is heterogeneous CaCO₃ precipitation. This observation provides robust evidence supporting our hypothesis and warrants further research of the significance of heterogeneous reactions in ocean waters.

Degradation in geomechanical properties in marine sediments enriched with organic matter

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As organic matter is buried in marine sediments, its content and availability control a series of anaerobic respiratory processes in the sediments. While chemical and physical processes proceed within the shallow sediments, both the pore water and the sediments' mineralogical composition alter. Although the biological and geochemical aspects of this early diagenesis processes have been studied for years, the sediments mechanical change remains unclear. Particularly, the change of shear strength and therefore the sediments' stability. Incubation experiments were conducted on undisturbed sediment cores to investigate the change in shear strength and consolidation following sulphate and iron reduction. Modern-day sediments from the Gulf of Aqaba (Eilat) were used due the known oligotrophic environment. The cores overlying water were enriched with dissolved organic matter as a source of dissolved organic carbon. The cores were sealed under anoxic conditions for 3 months. Porosity played an important role in the undisturbed cores limiting the depth to which diffusive and microbial process can occur. Geochemical analysis of the pore water identified that the upper 5 cm in all cores reached sulphate and iron reduction conditions and Fe and H₂S excess was detected. Between 5 to 10 cm the reduction derivatives were diffused down or up core. At the depth of ~ 7 cm a calcite precipitation was indicated. Direct shear tests and consolidation tests showed trends of a shear strength decrease and a void-ratio increase for samples containing the dissolved organic matter. The results provide an understanding for the long-ignored influence of early diagenesis conditions on the geotechnical parameters.

Population collapse of echinoderms in the Gulf of Aqaba

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The phylum Echinodermata is ecologically fundamental to maintaining a functional and stable ecosystem. Sea urchins, which are predominantly grazers, regulate algae accumulation on coral reefs, clearing space for scleractinian corals to grow. Sharp changes in sea urchin populations are the main driver of ecosystem phase shifts in coral reefs. The best-known example of such sea urchin-driven phase shift is the dramatic and destructive alternation of Caribbean coral reefs in the early 80's – from reef-building corals dominance to algae fields – due to the population collapse of the local sea urchin *Diadema antillarum*. In the present study, we assessed the echinoderm community in the Gulf of Aqaba (GOA), Red Sea, using field surveys conducted for over a decade between 2007-2021. The latest data point to a dramatic decline in the population size of *Diadema setosum*, the most dominant echinoid species in the GOA. Extreme southern storms in the years 2009, 2010, and 2020 led to sharp declines in sea urchin population size in shallow waters, albeit with a varying effect on different species. Broadly, our data points to an overall consistent decline in echinoid population size for most species in the GOA. Today, the abundance of 75% of key echinoderm species is at its lowest level since the recording began. These results point to an alarming and ongoing decline of the main regulators of the seasonal algae blooms in the GOA and place the coral community of the GOA in clear and immediate danger.

Natural products of marine origin for the treatment of colorectal and pancreatic cancers: mechanisms and potential

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Gastrointestinal cancer refers to malignancy of accessory organs of digestion, and it includes colorectal cancer (CRC) and pancreatic cancer (PC). Worldwide, CRC is the second most common cancer among women and the third most common among men. PC has a poor prognosis and high mortality, with 5-year relative survival of approximately 11.5%. Conventional chemo-therapy treatments for these cancers are limited due to severe side effects and the development of drug resistance. Therefore, there is an urgent need to develop new and safe drugs for effective treatment of PC and CRC. Historically, natural sources, plants in particular, have played a dominant role in traditional medicine used to treat a wide spectrum of diseases. In recent decades, marine natural products (MNPs) have shown great potential as drugs, but drug leads for treating various types of cancer, including CRC and PC, are scarce. The aim of the present study is to identify natural products from marine origin that have anti-cancer activity. The study includes the extraction of natural products (algae and marine bacteria) by chromatographic methods, analytical characterization using mass spectroscopy and examination of biological activity in cancer cell cultures from the source of the colon and pancreas in in-vitro systems. The results indicated that exposure of colorectal and pancreatic cancer cells to the red seaweed *Asparagopsis taxiformis* extract, reduced cell viability in a dose dependent manner. Further studies are needed in order to identify the structure of the active compounds. The contribution of this research lies in the detection of new compounds from marine origin with anti- cancer activity. Moreover, understanding the molecular mechanisms by which these molecules act on cancer cells from the colon and pancreas origin can lead to the development of new strategies to activate those pathways and develop novel approaches of treating cancer.

Intraseasonal oscillatory modes in the Eastern Mediterranean Sea

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The intraseasonal oscillations (ISOs) in sea currents in the eastern Mediterranean Sea near the central coast of Israel were analyzed by examining the velocity components of the sea currents at different depths as measured by Acoustic Doppler Current Profilers located at various depths between 0 - 675m. The total period covered by the observations was from December 2016 to May 2018. Prominent intraseasonal oscillations, much stronger than tidal velocity components, were observed in the upper part of the sea, at 30-70 m. The amplitudes of these oscillations are between 4-10 cm/s and their periods are 7, 11, 22, and 34-36 days. The strongest oscillations are found in the boreal winter. The ISOs in the sea currents were apparently induced by corresponding oscillations found in atmospheric wind velocity over the eastern Mediterranean at the surface, 500 and 250 hPa, as suggested by the high correlations, 0.6-0.9, between the wind velocity components of the oscillatory modes in the atmosphere and the velocity component of the oscillatory modes in the sea currents with similar periods. We propose that the source of the ISOs in the atmosphere over the eastern Mediterranean is the South Asia Jet wave train. The track of this wave train passes over the eastern Mediterranean, and the periods of the ISOs in the wave train are in the same band as the oscillations found here.

Golgi-related proteins in symbiotic bacteria may enable evasion from host-phagocytosis

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Sponges harbor abundant and diverse microbial communities, which supports the host health and ecology. Symbiont genomes have adapted to fit the physical, chemical, and biological conditions found inside the sponge, that differ from those experienced by bacteria living in seawater. Genomic adaptations of sponge symbionts have been investigated for Thaumarchaeota, Cyanobacteria, Verrucomicrobia and Chloroflexi. Shared symbiotic features included enrichment of restriction and modification systems, suggested to protect symbionts from invading DNA. Actinobacteria have been studied mainly using cultured strains in terms of biotechnology potential of secondary metabolites. However, the genomic adaptations of uncultured Actinobacteria to the symbiotic lifestyle have not been investigated. Here, we constructed a phylogenomic tree on 352 Actinobacteria (160 sponge-symbiotic and 192 from diverse free-living environments). Actinobacteria sponge symbionts are found affiliated mostly to the class Acidimicrobia. From this class, we selected genomes from the Genus UBA11606 and separately within the Family TK06, for a comparative genomics analysis between symbionts and free-living. Interestingly, the gene GPP34, a eukaryotic-like protein related to the Golgi apparatus, was found enriched in symbiotic Actinobacteria. Further, it was also found widespread across sponge symbionts of diverse taxonomy background, while mostly lacking in their free-living counterparts. This protein was previously reported in a pathogen-host system to bind to phosphatidylinositol-4-phosphate present in eukaryotic cells, interfering with phagocytosis related mechanisms. We hypothesize that sponge symbionts may use a similar strategy to be able to inhabit sponges.

Linking marine viruses to their native hosts using single-cell transcriptomics

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The discovery of giant viruses, with their immense size and complex metabolic pathways, has revolutionized our perspective on the viral world and on cell biology in general. We now know that viruses are far more complex than we had thought and that they play a significant role in global ecology. Giant viruses routinely infect marine phytoplankton—unicellular photosynthetic organisms that are responsible for 50% of annual primary production. As phytoplankton form the basis of the marine food web, their consequent death by giant virus infection has profound importance to the marine ecosystem. Many studies in recent years have focused on the life cycle of giant viruses within marine phytoplankton and revealed their abundance in the ocean through metagenomic analysis. However, we still know very little about their ecological role and their native hosts. To shed light on host-virus interactions in the marine environment, we developed a novel approach to detect active viral infection on a single-cell resolution from a natural sample. We performed 10X single-cell RNA-seq of natural plankton communities and detected actively infected cells of diverse species. We identified the infected cells and assembled single-cell transcripts from each cell, and managed to identify the target hosts and their specific viruses. We managed, using this method, to identify new pairs of hosts and viruses that were never described before. We foresee that this novel approach can be used in samples obtained from the natural environment to disentangle the host-virus interactions within an oceanic algal bloom.

Sustaining fish populations through Ecosystem based fisheries management- EcoScope

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Fisheries exploitation has been a major driver of fish population dynamics, while overfishing is the main cause of fish stock depletion at a global scale. Existing fisheries management practices (based on single- or multi-species approaches) have been unsuccessful in sustainably conserving fish stocks. Commercial and recreational fishing strongly impact all levels of biological organisation and community structure raising a pressing need for a holistic approach to managing fisheries. Ecosystem Based Fisheries Management (EBFM) recognizes the combined physical, biological, economic, and social trade-offs affecting the fisheries sector, and the need to address these trade-offs when optimizing fisheries yields. International conventions and agreements require that marine exploited populations have to be managed in a way that their biomass is large enough to produce maximum sustainable yields (MSY) for fisheries. To assist in the transition and application of EBFM in the European seas the EcoScope project will develop an interoperable platform and a robust decision-making toolbox, to promote an efficient, ecosystem-based approach to the management of fisheries. The EcoScope Platform will organise and homogenise climatic, oceanographic, biogeochemical, biological and fisheries datasets to a common standard type that will be available to the users through interactive mapping layers. The EcoScope Toolbox, will host ecosystem models, socio-economic indicators, fisheries and ecosystem assessment tools, and indicators for examining fisheries management and marine policy scenarios. The EcoScope project will incorporate methods for dealing with uncertainty, promoting efficient, holistic, sustainable, EBFM that will aid towards restoring fisheries sustainability providing an effective toolbox for decision makers and end-users.

Striking recovery of the reef fish community after an extreme storm event in the Gulf of Aqaba

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Storms are among the most common disturbances within coral reef ecosystems. However, their effects on reef fish diversity can be either negative or positive. In the Gulf of Aqaba, storms are extremely rare, yet in March 2020 strong storm surge hit the coast of Eilat, causing severe damage to the coral reef and shore infrastructure. Using data collected from 78 reef knolls surveyed repeatedly since 2015, we explore the storm's effects on the structure and spatial heterogeneity of the fish community across multiple scales. We found a post-storm decrease in fish density and an increase in community evenness. Yet, storm impacts differed considerably between close sites with varying conservation efforts and visitor pressure. The fish community showed striking recovery and regained baseline richness, abundance, and diversity values within a year. The resilience of the unaccustomed reef fish community to storm disturbance suggests that conservation efforts should focus on managing and mitigating local human stressors such as shoreline modification, intensive diving pressure, and the prevention of oil spills. Additionally, those findings stress the importance of a long-term monitoring program that can assess the response of reef fish communities shortly after disturbances events.

Heterotrophic Diazotrophs in River-Lake Ecosystem: Contribution, Abundances, and Rates

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Previous studies have indicated that aggregates are hotspots for heterotrophic N₂ fixation in marine environments. However, the knowledge of heterotrophic N₂ fixation in freshwater ecosystems is limited, especially those associated with aggregates. In our study, N₂ fixation rates were quantified by measuring the assimilation of ¹⁵N₂, while the diazotrophic community was identified by *nifH*-based amplicon sequencing. Additionally, diazotrophs were localized and quantified within the aggregates via immunolocalization of the nitrogenase enzyme. N₂ fixation rates in the Jordan River (0.04 – 0.25 nmol N L⁻¹ d⁻¹) were mainly ascribed to heterotrophic diazotrophs associated with aggregates (47-100 % of total N₂ fixation). In the Sea of Gallie Lake, N₂ fixation rates especially were (36 – 86 %) attributed to phototrophic diazotrophs. The newly developed method of quantifying diazotrophs by immunolocalizing nitrogenase enzyme showed higher abundances of diazotrophs in the midstream and downstream seasons. Interestingly, despite high nitrogen fixation rates in the lake, the abundance of diazotrophs was lower than in the river. The specific N₂ fixation was significantly higher in the lake compared to the river. Our results suggest that lake diazotrophs are more energetically efficient than the river. *nifH* sequences analysis highlighted the differences in the diazotrophic communities found as free-living or associated with aggregates along the river-lake transect. Immunolocalization micrographs indicated that river aggregates comprised clusters of heterotrophic diazotrophs, while numerous phototrophic diazotrophs were localized on the lake particles. The results and corresponding insights indicate that heterotrophic diazotrophs associated with aggregates have a central contribution to total N₂ fixation in various freshwater environments.

A physics based model of swarming jellyfish

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We use a model of active Brownian particles to simulate the swarming behaviour of jellyfish. We address the phenomena of counter-current swimming, avoidance of turbulent flow regions and foraging. Corresponding mechanisms are motivated from observations of jellyfish swarming. The model characteristics is tested in three paradigmatic flow environments. The generic modelling framework that stands behind the simulations can be augmented to incorporate physiological details of single individua and it can be scaled up to large swarms of jellyfish.

Methanogenesis characterization in thawing permafrost

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Methane (CH₄) gas is the second most important greenhouse gas after CO₂, and ~28 times more effective than CO₂, and as such, it contributes to the rise in global warming. Thermokarst lakes, which are a hotspot for methane emissions, formed by permafrost soils thawing. These lakes are located in the arctic circle and contain high content of organic matter due to the freezing conditions the original soil was kept in since the last ice age (18,000 years). The thawing allows the microorganism population to grow and consume the organic matter which becomes available for methane production. The emitted methane contributes to the greenhouse effect and creates positive feedback. Today, our knowledge about the thermokarst lakes is lacking and the mechanisms, which produce the methane in these lakes, are uncertain. The goal of my research is to understand what are the controls on the onset of methanogenesis and to quantify the methanogenesis rates constraining their depth distribution, pathways, and response to warming. To achieve these goals, I plan to use fieldwork and an experimental approach. I will explore the process in two thermokarst lake types in central Alaska, a young and actively expanding lake and an older lake that is no longer expanding. Porewater profiles, as well as various sediment parameter profiles, will be performed to attain geochemical wide knowledge of the research area. In addition, I will conduct two types of incubation experiments. The first is a long-term slurry incubation experiment to study the onset of methanogenesis and its mechanisms. It will contain slurries from the permafrost front and 2 phases of permafrost thawing stages. I will perform different manipulations and use isotopic labeled acetate and bicarbonate to follow the main pathways of methanogenesis. The second incubation experiment will include sediment from different depths and spatial distribution and will use to quantify the accumulation of methane with time. A preliminary experiment was conducted in Lake Kinneret in northern Israel to test the methods and the measurement techniques.

Diversity in Dissolved Organic Matter Utilization by Heterotrophic Marine Bacteria

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Heterotrophic marine bacteria utilize and recycle dissolved organic matter (DOM), impacting biogeochemical cycles. It is currently unclear to what extent different DOM components can be utilized by different heterotrophic clades. Here, we ask how a natural microbial community responds to macromolecular pools that comprise much of the biomass of living organisms, and are expected to be released upon death as DOM. Surface seawater from the Eastern Mediterranean were amended with 6 defined media comprising either peptides, amino acids, amino sugars, oligosaccharides, mono sugars or organic acids. These were compared to control un-amended seawater and to seawater amended only with inorganic nutrients (N+P: NH₄ and PO₄). Total bacterial counts and productivity increased after 24 hours for all treatments except the control, but glucose and ATP uptake were more variable. The control and N+P were mostly dominated by Alphaproteobacteria, while the macromolecular pools additions were dominated by Gammaproteobacteria. Several families specifically increased in some treatments: peptides promoted a relative increase in Pseudoalteromonadaceae, oligosaccharides promoted both Pseudoalteromonadaceae and Alteromonadaceae, and most other treatments were dominated by Vibrionaceae, especially amino acids and amino sugars. While some results were consistent with laboratory experiments, for example Pseudoalteromonadaceae favoring peptides, other clades behaved differently. Alteromonadaceae, for example, grew well in the lab on many substrates but dominated in the field only when oligosaccharides were added. These results highlight the diversity in DOM utilization among heterotrophic bacteria and complexities in the response of natural communities, where community composition may be influenced by other factors such as competition.

Microplastic interaction with marine biological systems

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Micro plastic (MP) particles are often transported from the water column to marine food webs by filter-feeder organisms which play an important role in benthic-pelagic coupling. The ingested MP may accumulate in the gut or may pass through the digestive system where they are subject to different pH fluctuations and to various digestive enzymes, ultimately excreted within the organism's feces. Feces sink down the water column transporting carbon to deeper waters, therefore acting as a vector of MP through marine zones. Ascidiaceae (Chordata, Ascidiaceae) are highly efficient filter-feeders, able to remove even minute particulate matter from the water column. Therefore, they present fundamental opportunities for understanding the interaction of plastic debris with marine organisms. Here, we use engineered MP particles of high environmental relevancy, to examine the consequences of transit through an organism's digestive system. Engineered MPs were prepared by subjecting crashed plastics to various degradation processes imitating the natural oxidation, thermal, and mechanical degradation. We examined the changes of the particle's surface area, size, morphology and surface functionality. We used both biodegradable and non-biodegradable plastic, synthesized from bulk plastic everyday products. These particles were fed and later extracted from the feces of two solitary ascidian species: *Styela plicata* collected from the Mediterranean, and the Red Sea *Polycarpa mytiligera*. We developed a protocol for MP extraction from ascidian feces while minimizing contamination of undigested MP. Our preliminary results reveal that the extracted MP (following digestion by ascidians) had a rough surface area coated by organic matter. This change in surface area and functionality may later influence the MP availability to other organisms. Currently, we examine the effect of MP on ascidian digestion system and feces. Overall, as MP transfer through marine food webs across marine ecosystems, it is essential to promote the understanding of the consequences of biological digestion.

CultureLED: A 3D printer-based LED illumination cultivation system for multi-well culture plates

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Algae are a source of plant-based products such as pigments, lipids, and carbohydrates. Although algae cultivation techniques have evolved and improved, a vast amount of research is still needed to achieve a better understanding of these organisms and their biochemical and molecular mechanisms. Like other photosynthetic organisms' cultivation methods, there is a growing need for affordable, flexible, and easy to control research systems. Additive manufacturing revolutionized design and development processes as it became widely available, allowing the creation of complex shapes, enabling mass customization, supporting low-volume manufacturing and distributed production. The emergence of open-source designs and electronics components combined with 3D printing applications have the potential to open new methods for plant cultivation. Our work describes CultureLED, a well plated cell culture system that can be mounted on an orbital shaker or positioned on a shelf. It is based on low-cost commercial off-the-shelf components for low production cost, simplicity, design flexibility allowing controllable light conditions. The CultureLED utilizes programmable light-emitting diodes (LEDs) for application of different light patterns, intensity, and duration. The system is not limited to algae and can be used as an experimental platform for understanding the effect of light on plant cells and other small sized organisms/microorganisms.

Characterizing soft substrate fish communities along the Israeli coastline

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The Levantine basin, including the Israeli coastline, is characterized by mostly soft bottom habitat. While most studies on fish communities in this region have focused on hard bottom environments, there is only little information on the soft bottom and this habitat is underrepresented in marine protected areas. The overall aim of this study is to characterize spatial and temporal patterns in the fish communities over soft bottoms environments to improve the conservation of this habitat and facilitate the establishment of new marine protected areas. For this we used baited remote underwater stereo-video (BRUV's), visual surveys by divers using a tow-board, and Hydro-Acoustic survey with SIMARD-EK-80 echosounder. The surveys were conducted across 7 sites along the Israeli coasts. Results revealed a general increase in diversity and abundance from South to North. This pattern was similar for both indigenous and non-indigenous species. Importantly, our surveys uncovered hitherto unknown meadows of the seagrass *Cymodocea nodosa*. Seagrass meadows are unique and important habitat that supply high complexity, serves as a nursery for many species and help stabilize the substrate. Understanding the soft bottom environment is crucial for making informed decisions about protection of this important marine habitat.

Establishing baseline assessment levels for monitoring coastal heavy metals using foraminiferal shells: A case study from the Southeastern Mediterranean

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One of the challenges in monitoring the marine coastal environments is quantifying the magnitude and duration of pollution events. This study introduces a new concept of defining heavy metal (HM) baseline assessment levels (BAL) in coastal environments using foraminiferal shells. We demonstrated the potential of this approach by examining a nature reserve along the Mediterranean coast of Israel. Our previous investigation of this site in 2013-2014 using foraminiferal single chamber LA-ICPMS created a dataset consisting of HM measurements of two species, *Lachlanella* and *P. calcariformata*. This database was used to establish the BAL of Zn, Cu and Pb, associated with anthropogenic sources. In February 2021, an oil spill event affected the entire Mediterranean coast of Israel, and included an out wash of tar onto the shore. The event provided a unique opportunity to test the applicability of foraminiferal BAL by revisiting the previously studied site. Our strategy was to compare whole shell ICP-MS measurements of the two species collected shortly after the event and six months later, and compare them with the established BAL values. Our results revealed a significant increase (2-20 folds) in Zn/Ca, Cu/Ca, Pb/Ca ratios between 2013-14 and 2021. Among these, the increase in Pb/Ca is the most substantial. This implies a possible linkage between the oil spill event and the substantially elevated metals/Ca ratios measured by the foraminifera in 2021. This observation confirms that once BAL values are established, the analysis of bulk shell ICP-MS is effective for monitoring HM contamination of coastal environments.

Microbial diversity and antibacterial traits of the mesophotic sponge *Calyx nicaeensis*

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Marine sponges are famous for hosting rich microbial communities that can comprise up to 40% of the sponge volume and are a major source of bioactive compounds from the marine environment. The sponge secondary metabolites are important for its survival, and frequently these metabolites are synthesized by the sponge-associated bacteria. It is well-known that new antimicrobial compounds are urgently needed because the extensive use of antibiotics caused bacterial resistance. Sponges from less explored habitats could be a promising source for such compounds. *Calyx nicaeensis* (Porifera, Demospongiae, Haplosclerida) is a rare, endemic Mediterranean sponge found in the mesophotic region on the Israeli coast. Scarce information is known about *C. nicaeensis* secondary metabolites and has never been studied in specimens from Eastern Mediterranean and the mesophotic region. Moreover, *C. nicaeensis* associated bacteria have yet to be cultivated, and it is interesting to reveal their diversity, and understand the bacterial interspecific interactions. Bacteria were cultivated from two sponge specimens, on solid media. Isolates were chosen based on different morphology resulting in 317 isolates. Each morphologically different colony was isolated and identified by 16S rDNA. Based on EZtaxon database, isolates were grouped to 90 OTUs. To understand the interspecific interactions among the cultivated sponge-associated bacteria a competition assay was performed. This test enables to determine the ranks of competitive capability of bacteria for further antibacterial compound investigations. The highest-ranking bacteria were chemically extracted, and the extracts have undergone a disk assay for antibacterial activity.

Characterization of a novel fungal-algal symbiosis on polyethylene surfaces in the Mediterranean Sea

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Recent advancements in marine sciences offer us a unique look into marine plastic-colonizing organisms which creates an ecosystem termed the “Plastisphere”. Terrestrial fungal-algal interactions have been characterized in the rhizosphere and lichens but very little is known about similar relationships in the marine environment. In this work, I aimed to characterize novel marine symbiotic relations on plastic surfaces in the Mediterranean Sea. Polyethylene bags that were submerged in Herzliya marina water for a period of one month were covered with a network of filaments that seemed to serve as a basis for the colonization of several diatom species. To test whether the filaments are fungi hyphae I applied lactophenol cotton blue (LFCB) stain on the filaments, which specifically bind to sugars in the fungi’s cell wall. The staining confirmed that the filaments are fungi hyphae. I used light microscopy and High-Res Scanning electron microscopy to further characterize the fungal-diatom symbiosis relationships and for the identification of the diatom genera. Diatom and reproduction events counts indicated that the relations are facultative. To identify the fungi taxa, we amplified the Internal Transcribed Spacer (ITS) fungal barcode and sequenced it with an in-house nanopore MinION platform. The sequencing results identify a single unknown fungal species of the Ascomycota phylum. This work shed light on a novel marine fungal-algal symbiosis that may be common on plastic as well as other marine surfaces.

Effects of crude oil and gas condensate spill on coastal benthic microbial populations

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Marine sediments are ecologically-important environments that act as a long-term depository for different contaminants from natural and anthropogenic sources. We investigated the response of crude-oil and gas-condensate spills on benthic microbial populations in the oligotrophic southeastern Mediterranean Sea using costume-design benthocosms. Additions of crude-oil and gas-condensate significantly changed the sediment's chemical properties, with ~2 fold elevated levels of total organic carbon (TOC) and up to ~6 fold higher concentration of total polycyclic aromatic hydrocarbons (Σ PAHs) relative to unamended sediments. Naphthalene and benzo(a)pyrene were the dominant species comprising the PAHs in both the crude-oil and gas-condensate treatments (29-43% and 26-35%, respectively). Porewater PO₄ drastically declined throughout the experiment, whereas NO₂+NO₃ decreased ~100 days post hydrocarbons addition and then increased in the remaining ~100 days till the conclusion of the experiment. This temporal variability in NO₂+NO₃ hint that hydrocarbon pollution may affect the interplay between benthic denitrification and N₂ fixation, thus affecting nutrient limitation for benthic heterotrophic bacteria and phytoplankton. Moreover, our results show that crude-oil and gas-condensate usually lead to a decline in benthic autotrophic microbial biomass (50-80%), while heterotrophic bacterial abundances remained unchanged, and bacterial production rapidly increased (maximal 1600%, crude-oil>gas-cindensate). These affects were prolonged and lasted several months post hydrocarbons addition, highlighting the sediments as repository for oil contaminants. Amplicon sequencing of the 16S rRNA gene revealed hydrocarbonoclastic bacteria including Methylophaga, Ponticaulis and Alcanivorax genera post crude-oil addition and Actinobacterota 67-14 lineage following gas-condensate amendments. Our results may enable applying a better science-base environmental policy of the benthic marine environment.

Functional morphology of the smallest oceanic predators

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Small heterotrophic flagellates (sHF) are the chief microbial predators and nutrient recyclers in the open ocean. Survival of different sHF groups depends on their ability to gather scarce food, which in its turn depends on their morphological adaptations to feeding. We examined the sHF morphologies in the largest, most oligotrophic South Pacific and Atlantic (sub)tropical gyres and adjacent mesotrophic waters. On four research cruises, the sHF cells were flow cytometrically sorted from bacterioplankton and phytoplankton to observe their fine morphological features using electron microscopy. The sorted sHF comprised unikont choanoflagellates and heterokont biflagellates numerically at ~1-to-10 ratio. Loricated choanoflagellates showed a tendency for lighter silicification of loricae in oligotrophic waters. Of the four differentiated morphological types of heterokonts present in all sampled regions of the open ocean, the smallest heterokont was predominant. Contrary to other heterokonts, tinsel flagellum of this smallest heterokont was too short to propagate even a single wave and hence to trail the cell in one direction. Instead, the smallest heterokont is predicted to tumble screening its surrounding for food. Combined with its tiny size, such trajectory motion presumably increases the chances of the smallest heterokont to capture scarce food in the open ocean. Its distribution and abundance in vast oligotrophic areas of the ocean make this smallest heterokont a likely candidate to be the most abundant predator on Earth.

Israel National Culture Collection of Algae (INCCA)

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In aquatic systems microalgae constitute the base of the food web. Climate change and anthropogenic activities affect the micro-algae populations in these ecosystems, causing a decrease in biodiversity, increasing frequency of harmful algal blooms, invasion of new species and loss of endemic algae. The Israel National Culture Collection of Algae was established to conserve the country's microalgae biodiversity, and to function as a resource of knowledge and live material. Our goal is to identify, document, isolate and preserve Israel's algae biodiversity for research, environmental rehabilitation, aquaculture, industry and education. Presently INCCA contains a total of 146 strains from different phyla, identified by morphological and molecular taxonomy based on the *rbcL* and the *rRNA SSU-ITS* sequences. Most of the strains belong to the chlorophyta (38%), cyanobacteria (35%) and the charophyta (16%). In contrast to most algal culture collections, for a majority of the strains ecological data from the site and time of sampling are available. One of the results of "The Nagoya Protocol" agreement, that came into effect in 2014, are the restrictions on the transfer of microorganisms between countries. This restriction reinforces the need for a certified national culture collection to preserve the biodiversity of algae in the country, especially for endangered species. INCCA allows the various consumers access to knowledge and cultures of algae that have been isolated professionally and with great skill and preserved under suitable conditions for each alga.

Lagrangian Pathways of the Mediterranean Outflow Water

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The Mediterranean Sea outputs approximately 1 Sverdrup of water into the Atlantic Ocean at the Straits of Gibraltar, which sinks and spreads throughout the North Atlantic as the distinctly saline Mediterranean Outflow Water (MOW). Its possible effect on the flow structure and as an amplifier for North Atlantic Deep Water formation has been discussed for decades. However, an overview of the statistics and timescales of Lagrangian pathways taken by the MOW throughout the Atlantic is lacking. We produce and analyze synthetic Lagrangian trajectories released from the Gulf of Cadiz into reanalysis velocity data from 1980-2020, comparing 5-day, monthly, monthly climatological, and annual climatological data. No significant difference is found between the 5-day versus the monthly full data. However, pathways statistics of the climatological flows are qualitatively and quantitatively different from the full data, signifying the importance of small scales, transient eddies, and interannual variability in controlling the spread, with a different role for each contributor.

Thermo-haline threshold and the future proliferation of symbiont bearing foraminifera as ecosystem engineers

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Tropical calcifiers are key organisms for understanding marine ecosystem responses to global changes. Rising sea surface temperatures are affecting symbiont-bearing tropical calcifiers such as corals and Large Benthic Foraminifera (LBF). In many ecosystems, parallel to warming, local salinities vary considerably along the shallow coastal settings, and the combined effect of such multiple stressors may be far greater than those of temperature alone. Laboratory culture experiments were used to evaluate the combined thermohaline tolerance of one of the most common LBF species and carbonate producer, *Amphistegina lobifera*. The experiments were done under ambient (39 psu) and modified (30, 45, 50 psu) salinities and at optimum (25 °C) and warm temperatures (32 °C). Calcification of the *A. lobifera* holobiont was evaluated by measuring alkalinity loss in the culturing seawater, as an indication of carbonate ion uptake. The symbiont's photosynthetic performance was determined by measuring dissolved oxygen. We further evaluated the growth of *Peneroplis*, which is known to tolerate high temperatures, under elevated salinities. The results show that the *A. lobifera* exhibits optimal performance at 39 psu and 25 °C, and its growth is significantly reduced upon exposure to 30, 45, 50 psu and under all 32 °C treatments. Salinity and temperature exhibit a significant interaction, with synergic effects observed in most treatments. Our results confirm that *Peneroplis* has a higher tolerance to elevated temperature and salinity compared to *A. lobifera*, implying that a further increase of salinity and temperatures may result in a regime shift from *Amphistegina* to *Peneroplis* dominated assemblages.

Trichodesmium populations from the Red Sea host a unique consortium of bacteria enriched in interactive pathways that mine nutrients from dust

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The oligotrophic and particle-rich Red Sea receives a significant amount of nutrients from dust deposition, including particulate Fe and P. With climate models predicting an increase in dust emissions, one organism expected to benefit is the globally important cyanobacteria *Trichodesmium* which forms vast bi-annual surface blooms. Due to their photosynthetic and nitrogen-fixing machinery, *Trichodesmium* are key players in the biogeochemical cycling of C and N within tropical and subtropical oceans. *Trichodesmium* form colonies that harbour a unique mechanism attuned to the capture, centering and processing of dust within its core. By hosting a microbial network of associated bacteria, *Trichodesmium* colonies harbour pathways that can mine dust for nutrients that are still poorly characterized. This study explores these processes using metagenomics, in combination with metaproteomics, to assess their diversity and taxonomic contribution. We focused on key particle-related processes including siderophore-biosynthesis genes, reductive phosphorus uptake and nitrogen-metabolism pathways. Our findings suggest that these traits within *Trichodesmium* colonies belong to a diverse assemblage rather than a select bacterial group that potentially complete these pathways through interaction. The diversity of these pathways has important ecological implications, improving their resilience and its ability to impact biogeochemical fluxes in light of a globally changing ocean.

Phycobilisome light-harvesting efficiency in natural populations of the marine cyanobacteria *Synechococcus* increases with depth

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Cyanobacteria of the genus *Synechococcus* play a key role as primary producers and drivers of the global carbon cycle in temperate and tropical oceans. *Synechococcus* use phycobilisomes as photosynthetic light-harvesting antennas. These contain phycoerythrin, a pigment-protein complex specialized for absorption of blue light, which penetrates deep into open ocean water. As light declines with depth, *Synechococcus* photo-acclimate by increasing both the density of photosynthetic membranes and the size of the phycobilisomes. This is achieved with the addition of phycoerythrin units, as demonstrated in laboratory studies (Kolodny 2021). Extending our research to natural environments, we probed *Synechococcus* populations in an oligotrophic water column habitat at increasing depths (Kolodny 2022). We observed morphological changes and indications for an increase in phycobilin content with increasing depth, in summer stratified *Synechococcus* populations. Such an increase in antenna size is expected to come at the expense of decreased energy transfer efficiency through the antenna, since energy has a longer distance to travel. However, using fluorescence lifetime depth profile measurement approach, which is applied here for the first time, we found that light-harvesting quantum efficiency increased with depth in stratified water column. Calculated phycobilisome fluorescence quantum yields were 3.5% at 70 m and 0.7% at 130 m. Under these conditions, where heat dissipation is expected to be constant, lower fluorescence yields correspond to higher photochemical yields. During winter-mixing conditions, *Synechococcus* present an intermediate state of light harvesting, suggesting an acclimation of cells to the average light regime through the mixing depth (quantum yield of ~2%). Given this photo-acclimation strategy, the primary productivity attributed to marine *Synechococcus* should be reconsidered.

Environmental impact of cathodic protection on the local benthic biogeochemistry: a case study from Gulf of Aqaba

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The Gulf of Aqaba (GoA) is a commercial corridor and a hotspot for scientific research and tourism. However, being an economically strategic location, the GoA faces the stress of commercial activities and offshore installations. Given this, this study is motivated to study the probable impact of remnants of cathodic protection (CP) assembly on the Kazza open beach. The Kazza open beach has visually contrasting sediments of red and black color and seepage of gas bubbles of unknown nature. It is suspected that this is caused by remnants of a CP that protect an old docking point. The area is investigated and mapped for various biogeochemical analyses. The pore-water chemistry of patches reveals high Fe^{2+} and Mn^{2+} concentrations in red and black patches respectively with higher, Ca^{2+} and Sr^{2+} and but lower other major concentrations in both patches. Interestingly the alkalinity and dissolved inorganic carbon (DIC) values for the red patch were also found to be very high compared to the black and control areas. We suggest the high Fe^{2+} and Mn^{2+} concentration in the red might be due to local reduction of sedimentary Fe and Mn caused by remnants of passive sacrificial or active anode of CP. The high DIC values might be due to the dissolution of carbonate minerals caused by the lowering of pH due to the oxidation of Fe^{2+} at the sediment-water interface. These findings suggest a probable impact of CP on the local biogeochemistry hence subsequently affecting the local ecosystem.

The role of *Octopus vulgaris* saliva in wound healing and arm regeneration

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The soft and vulnerable body of the octopus, possess a great challenge for its survival. An encounter with prey such as crabs or predators like sea turtles, occasionally result in arm amputation. Remarkably, an amputated arm is regenerated within weeks. These capabilities are evidence of very efficient regeneration mechanisms. Lab observation revealed that when an octopus injures its arm, it inserts the amputated tip into its mouth for consecutive short periods and repeats this behavior for hours. This stereotypic behavior has led us to hypothesize that some components of the saliva are essential for the regeneration process. To test this hypothesis, we first investigated the role of saliva in arm regeneration through morphological examination. We compared the regeneration efficiency of two amputated arm tips. On one arm we placed a sleeve that covered the whole stump thereby restricting insertion of the tip in to the mouth while, in the control the sleeve did not cover the amputated tip. Regeneration was monitored with a dissecting microscope. The results revealed a decrease regeneration rate in the arms that were prevented from exposure to the saliva. We then proceeded to identify the regenerative enhancer compounds and test the possibility that the octopus' saliva enhances regeneration of other organisms as well. We fractionated the saliva by HPLC and the fractions were tested on planarian regeneration. Several fractions were found to enhance planarian regeneration. The project contributes to the field of regeneration research and may provide new lead compounds with medical potential for wound healing.

Dissolved trace metals and Pb and Th isotope dynamics between the continental shelf and the deep and warm ultraoligotrophic eastern Mediterranean

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The land to ocean gradient in the chemical composition of seawater is controlled by boundary exchange processes, a term that reflects the combined effect of lithogenic and dissolved terrigenous fluxes, particle-dissolved exchange, oceanic biogeochemical processes, and the interplay with open ocean water masses. Here, we report for the first time dissolved trace metals, rare earth elements, nutrients, ^{232}Th and ^{230}Th concentrations, and the Pb isotopic composition of seawater profiles sampled during two cruises carried out in April 2018 and June 2021 between the northern offshore of Israel and the deep and warm oligotrophic eastern Mediterranean Sea. The results display elevated concentration of terrestrial trace elements and Pb isotopic signal associated with terrestrial input along the continental shelf. An enrichment in Zn, Cd, Ni, ^{230}Th and NO_3 and a depletion in ^{232}Th and Pb concentrations was observed along intermediate depths. These imply that a shelf-break sourced intermediate nepheloid layer acts as both a source and a sink for trace metals through partial dissolution and scavenging. The ^{230}Th and ^{232}Th are used to evaluate scavenging intensity and first order residence times and dust fluxes. Th isotopic composition estimate terrestrial impact on first order dust fluxes up to 100 km from shore. The different trends in dissolved elemental concentrations, as well as Pb and Th isotope distributions, observed between the two cruises emphasize the dynamic nature of continental margin environment as varying atmospheric, terrestrial and anthropogenic inputs may transiently alter elemental water column distributions and potentially impact open water biogeochemical cycles.

Carbon isotopes ($\delta^{13}\text{C}$) as a tool to study carbon uptake by *Halophilla stipulacea*.

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Seagrasses are one of the most efficient natural carbon sinks in the marine ecosystem as a result of their ability to absorb and store carbon dioxide. Therefore, future understanding of the carbon fixation processes in seagrasses may improve our ability to mitigate the current increasing atmospheric CO_2 . Unlike terrestrial plants however, the carbon uptake mechanism in seagrasses during photosynthesis is not entirely clear. Here, we aimed to get a broader picture of what affect the carbon isotopic fractionation during seagrass photosynthesis. In this geochemical-based study, *Halophilla stipulacea* from the Gulf of Aqaba was sampled. We then performed mesocosm together with in-situ experiments to study factors affecting photosynthesis. Using $\delta^{13}\text{C}$ analyses this study track the change of carbon isotope composition of the dissolved inorganic carbon and *H.stipulacea* biomass during photosynthesis under different conditions, such as enrichment of CO_2 , hydroponic growth, and enriched organic matter in the sediment. Among other marine primary producers, seagrass has the most enriched $\delta^{13}\text{C}$ values. The mean carbon isotope value of *H.stipulacea* in its local conditions is -8.2‰ for leaf and for roots is -9.1‰. A mesocosm experiment indicates that the rhizosphere partially affects the leaf isotopic signature. Compared with local growth $\delta^{13}\text{C}$ values, enriched organic matter sediment produced deplete $\delta^{13}\text{C}$ leaf values, while hydroponic treatment made no significant change between leaf and root values. By studying the factors that affect carbon isotopic values and understanding the sediment water column dynamic, new information will be revealed about the process of carbon fixation.

Red Sea is the cradle of octocoral research: Taxonomy of the genus *Cladiella* (Octocorallia)

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Soft corals of the genus *Cladiella* Gray, 1869 are common on the Indo-Pacific coral reefs, as well as in the Red Sea. At present, 63 morphospecies of the genus are listed in WoRMS, among them, 24 species were originally described from the Red Sea. The only existing taxonomic revision of the genus is by Tixier-Durivault, 1948. The goal of the current study is to re-examine using light and scanning electron microscopy (SEM) the *Cladiella* type-material from the Red Sea to validate the morphological features present in each species. The diagnostic features of the types include colony morphology, shape, and size-range of their sclerites. The sclerites of all examined species include dumbbells, most species also have polyp sclerites featuring a figure-eight morphology. SEM examination provided for the first time the detailed sclerite morphology for the Red-Sea types. In some cases, the findings correspond to the descriptions in Tixier-Durivault's revision, such as *C. hicksoni* (Tixier-Durivault, 1944) but for others they are contradictory when sclerites was examined morphology such as *C. pachyclados* (Klunzinger, 1877). Our findings for *C. pachyclados* correspond to Klunzinger's original description but Ehrenberg's description of *C. brachyclados* (Ehrenberg, 1834) is incomplete, therefore a comparison to the current findings cannot be made. The re-examination of *Cladiella* types, along with the collection of relevant fresh material from the type localities, is the first step to link each morphospecies to a molecular taxonomic operational unit (MOTUs). The study is critical to delineate species boundaries and to recognize biodiversity patterns across different biogeographic regions.

Fine-scale structuring of surface picophytoplankton communities in the ultra-oligotrophic Southeastern Mediterranean Sea

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The spatial distribution of phytoplankton is characterized by distinct fine-scale (1-100km) patchiness associated with mesoscale and sub-mesoscale ocean dynamics. While fine-scale patchiness in total phytoplankton biomass is often observed in satellite and in-situ data, fine-scale structuring of phytoplankton communities is still rarely documented, limiting our ability to accurately characterize ocean biodiversity. Here we show results from a high resolution study aimed at characterizing fine-scale variations in the community composition of picophytoplankton inhabiting the summertime surface waters of the Southeastern Mediterranean. Combining high resolution (30m) Landsat imagery and in-situ measurements along two transects, we show that in the ultra-oligotrophic conditions characterizing this region picophytoplankton may be assembled in fine-scale patches that significantly differ in their community composition. The separated patches are also characterized by distinct signatures in the surface temperature and salinity space, providing observational evidence to the phytoplanktonic landscape being organized in segregated fine-scale assemblages that differ in their life history. Our results indicate that fine-scale variability patterns and the processes underlying their formation should be considered when investigating ecological and biogeochemical processes in oligotrophic waters, and demonstrate the potential of harnessing very high resolution satellite data (~10 m) for that purpose.

Air Water Interactions Along the Dead Sea Rift (AWI-DSR) Geoclimatic Gradient

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Rifts, tectonic depressions, stretches along continents and typically collect a wide variety of waterbodies, including wetlands, lakes, terminal lakes and locked seas. Here we exploit the waterbodies along the Dead Sea Rift, which vary by geo-climatic settings (from humid Mediterranean to hyper-arid), water depth, water salinity, etc., by simultaneously measuring surface heat, gas and momentum fluxes using Eddy Covariance towers. These waterbodies are subjected to similar radiative forcing. We show that in the two desert waterbodies differ significantly by surface heat flux partitioning: In the Gulf of Eilat (extension of the Red Sea), the evaporation rate is three times larger than in the Dead Sea (a hypersaline terminal lake), this is due to the effect of water salinity in reducing water vapor pressure. In the two northern water (Lake Kinneret and Agmon Hula), which resides in the more humid, Mediterranean region, the evaporation rate is suppressed by humidity, in comparison to the Gulf of Eilat. These two waterbodies differ by their depth, which determines the dynamics of evaporation, surface heat fluxes and thermoregulation. We analyze the role of the timing of the Mediterranean Sea Breeze on evaporation rate. This observational setup, of concurrent measurements of air-water interactions along the gradients within the Dead Sea Rift provides a rare opportunity to quantify various aspects of water management policies, the formation of rocks within these waterbodies, the effect of local micrometeorology and synoptic scale circulation on the waterbodies and their surroundings.

Towards global quantification of seawater circulation in coastal aquifers

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Submarine groundwater discharge (SGD) is significant to coastal water chemistry and ecology. Nonetheless, the majority of SGD flux to the ocean comprises circulated seawater. This study deals with seawater circulation in coastal aquifers on a global scale in order to assess solute fluxes through SGD into the ocean. While the circulated seawater does not affect the water budget, it has a much higher impact on the ocean solutes budget due to water-rock interactions. We present a global assessment of saline SGD mechanisms' role using numerical simulations and analytical calculations. The numerical model simulates three main circulation mechanisms in coastal aquifers: density-driven circulation (long-term), tidal-driven nearshore circulation, and tidal pumping (short-term), while we calculate the wave-driven benthic exchange flux analytically using the same settings of the numerical model. The model tests the typical range of geohydrological parameters such as hydraulic conductivity, hydraulic gradient, tidal amplitude, and more. Our results revealed that: (1) increasing hydraulic conductivity increases the density-driven and decreases the tidal-driven nearshore circulations; (2) increasing the hydraulic gradient (or freshwater recharge) has no significant effect on the density-driven circulation while it slightly decreases the short-term nearshore circulation; (3) tidal pumping fluxes are a relatively large fraction of the overall SGD flux (30%-60%). Together with global hydraulic parameter distributions, the model results enable assessing the global SGD component of seawater circulation. Preliminary results reveal that the total density-driven SGD is about 0.5-1% of the river fluxes to the oceans. Based on the enrichment of calcium in the long-term SGD component, our global assessment of the calcium flux through density-driven flow may reach the same calcium flux through rivers into the ocean.

The Algal-Bacterial Extracellular Matrix

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Phytoplankton, namely micro-algae, are abundant in all aquatic environments. Phytoplankton account for about half of the primary production worldwide, and play a crucial role in marine food webs. Phytoplankton exude a variety of molecules that attract heterotrophic bacteria, actively shaping the bacterial population surrounding them. The close algal-bacterial association affects phytoplankton physiology and bloom dynamics. Many phytoplankton species exude large amounts of extracellular polymers, forming a dense, gelatinous matrix. This matrix serves as a 'hot-spot' for bacterial activity; it supplies nutrients, sanctuary and can serve as a basis for the formation of multicellular structures- such as bacterial biofilms. Algal-bacterial assemblages, held together by an extracellular matrix (ECM), create unique microenvironments and facilitate intimate interactions. Many natural phenomena, such as marine snow, are mediated by algal-bacterial communities bonded by an ECM. Do algae alone produce the ECM? Do bacteria contribute extracellular components? Using the ecologically relevant interaction between the bacterium *Phaeobacter inhibens* and the micro-alga *Emiliana huxleyi*, we examine the process of algal-bacterial matrix formation in order to characterize its structure and composition. We show that algae and bacteria form joint multicellular structures. *E. huxleyi* exudes molecules that promote the shift of bacteria from motile, free-living single cells, to adherent sessile cells. Once sessile, bacteria form complex multicellular structures held together by a bacterially produced ECM. In co-cultures, bacteria attach directly onto the algal cell or to polymers that are released by algae. The algal-bacterial ECM promotes increased aggregation and exhibits a unique composition, compared to matrix in monocultures.

How barnacles cope with the copepods ability to detect feeding currents and escape

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Sessile barnacles feed by sweeping their basket-like cirral fan, intercepting suspended prey within the swept volume. A primary component of the diet of adult barnacles is copepods, but copepods are sensitive to fluid disturbances and capable of escaping. How do barnacles manage to capture copepods? We examined this question by quantifying the feeding current of ~1-cm sized *Balanus crenatus*, and by studying the tracks of captured copepods and the escape positions of evading copepods. The barnacle produces a feeding current that leaves the barnacle in a powerful downstream jet. Water arriving to the barnacle comes both from behind and from the sides. The flow from the sides represents quiescent corridors where the fluid rate of deformation is often below the deformation rate required to elicit an escape. In contrast, flow arriving from the back is characterized by high deformation rates. Accordingly, we found that most captured copepods arrived through the quiet corridors, while most copepods arriving from behind managed to escape. It is the unique feeding flow architecture that allows feeding on evasive prey. We used the Landau-Squire jet solution to describe the feeding current. We found that the model reproduces the essential features of the feeding current, including the quiescent lateral feeding corridors. However, the model suggests that smaller barnacle specimens operating at lower Reynolds numbers will produce a fore-and-aft symmetric feeding current without the lateral quiescent corridors. This would suggest a yet-to-be-examined ontogenetic diet shift from non-evasive prey to inclusion of evasive prey as the barnacle grows.

Collective Oriented Swimming in Jellyfish

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Jellyfish swarming causes a nuisance for bathers, harms fisheries, and clogs water intake pipes of onshore infrastructure. Despite these considerable disturbances to human and economic activity, little is known about the collective behavior and movement routes of swarms which impedes predictive and mitigative efforts. Many previous studies on jellyfish swimming were conducted in a laboratory setting under still-water conditions and have focused on individual jellyfish behavior and performance, rather than the collective behavior of naturally occurring swarms. Here, we utilized drone footage along the Israeli Mediterranean coast over a period of three years to study the motion and orientation of large ($> 40\text{ cm}$ in diameter) individual *Rhopilema nomadica* jellyfish in naturally occurring swarms. Our results show that aggregated jellyfish near the surface align their body orientation to the same direction ($\pm 60^\circ SD$). In most of our observations the average orientation of jellyfish was to the west ($177^\circ \pm 36.7^\circ SD$; 3,000 jellyfish in 48 observations), away from the coast. Swimming speed was often larger than the ambient water speed and therefore affected jellyfish trajectories and the movement of swarms. Oriented swimming potentially extends the swarm's life span, compared with random orientation. We hypothesize that the direction of ocean waves may serve as an external cue to orient individual jellyfish. Such offshore collective orientation may be evolutionarily advantageous, as it reduces the risk of stranding and increases the likelihood of sexual reproduction. These findings suggest that jellyfish swimming should be incorporated into models used to predict swarm progression to mitigate potential harms.

The role of symbiont bearing benthic foraminiferal biomineralization in coastal environments undergoing warming

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Benthic foraminifera are unicellular marine eukaryotes that produce an exoskeleton made from calcite that contribute to 4% of the total carbonate production in the modern oceans. Specifically, symbiont bearing Large Benthic foraminifera (LBF), that are very common to the shallow tropical-subtropical environments, are responsible for 80% of total production by benthic foraminifera. In our research, we focus on assessing the present and future role of LBFs from shallow Eastern Mediterranean shelf, which harbor and extremely diverse and abundant LBF (100 specimens per 5cm²) and is at the forefront of ocean warming. For this study, ecological samples were collected throughout a year to (i) establish the key LBF species in these environments (ii) calculate average foraminifera density (iii) seasonal assemblage composition and (iv) size fraction analysis on the foraminifera assemblage. These parameters were used to establish model growth curves of dominant LBF species and combined with the seasonal population dynamics to compute overall carbonate production potential for each species. Additionally, these species were grown under a temperature gradient in controlled laboratory conditions where the holobiont health was monitored through carbonate production (alkalinity anomaly method) and net photosynthetic activity (dissolved oxygen) to establish the thermal sensitivities of the different LBF species and their algal symbionts, respectively. The carbonate production estimation combined with data on algal substrate preferences and holobiont thermal thresholds are used to gain insight on the future of the dominant players of the community and possible species turnover in these coastal environments.

Seasonal and vertical tidal variability in the south-eastern Mediterranean Sea

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Currents and pressure recorded from the DeepLev mooring site, and velocities derived from surface drifters, are analyzed to identify the six main tidal constituents (Msf, O1, K1, UPS1, M2, and S2) in the Eastern Levantine Basin. Harmonic and spectral analysis on seasonal segments of currents and pressure reveal dominant semidiurnal sea-level variability as well as diurnal tides with seasonal variability, and significant diurnal currents with weak semidiurnal currents in all seasons. The most dominant tidal constituent seen in both the harmonic and spectral analysis from the pressure dataset is the M2 (12.4 hr), while for the currents, it is the UPS1 (21.5 hr). Results of the analysis of pressure datasets generally agrees with previous models and observations, while the current trends are different than those reported before. Seasonal analysis of the moored dataset provides insights into the characteristics of the local tidal regime, and its interactions with seasonal phenomena. Additionally, an analysis of different lengths of datasets with regards to the Rayleigh criterion provides evidence of the temporal constraints needed to adequately resolve the tides using surface drifters.

Infection by the parasite *Myxobolus bejeranoi* (Cnidaria: Myxozoa) suppresses the immune system of hybrid tilapia

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Myxozoa (Cnidaria) is a large group of microscopic obligate endoparasites that can cause emerging diseases, affecting wild and farmed fish populations. Recently, the myxozoan *Myxobolus bejeranoi* was found to infect the gills of hybrid tilapia (Nile tilapia (*Oreochromis niloticus*) X Jordan/blue tilapia (*O. aureus*)), at more than 50% prevalence leading to high mortality rates. Here, we used comparative transcriptomics to elucidate the molecular processes occurring in the fish host following infection by *M. bejeranoi*. Fish were exposed to pond water containing actinospores for 24 hours and the effects of minor, intermediate, and severe infections on the sporulation site, the gills, and on the hematopoietic organs, head kidney and spleen, were compared. Enrichment analysis for GO and KEGG pathways indicated immune system activation in gills at severe infection, whereas in the head kidney a broad immune suppression included deactivation of cytokines and GATA3 transcription factor responsible for T helper cell differentiation. In the spleen, the cytotoxic effector proteins perforin and granzyme B were downregulated, while insulin, which may function as an immunomodulatory hormone inducing systemic immune suppression, was upregulated. These findings suggest that *M. bejeranoi* is a highly efficient parasite that disables the defense mechanisms of its fish host while prolonging host cell life which enable its proliferation.

Impacts of the desalination industry on coral reefs: effects of antiscalants on hard and soft corals

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Arid and semi-arid countries are under severe water-stress and rely on desalination for freshwater production. Desalination plants are a potential threat to the marine environment as their waste is discharged back into the sea. Antiscalants (AS), comprised of polyphosphonates or polymer-based materials, are widely used in the desalination process and are part of the brine-waste. Many water-stressed countries host coral reefs, so identifying the sensitivity of different reef species to desalination waste and its common components is important. In this study, we tested the impacts of polyphosphonate-based and polymer-based ASs (0.025ml AS/L) on the hard coral *Montipora capricornis* and on the soft corals *Xenia umbellata* and *Litophyton* sp in two experiments. After two weeks of exposure, hard corals from both ASs presented severe tissue damage, lower photosynthetic efficiency, and higher bacteria abundance. Polyphosphonate-based AS enhanced oxidative stress on *M. capricornis* and on the soft coral *X. umbellata*. *Litophyton* sp. showed oxidative stress signals under polymer-based AS and increased bacteria abundance under both types of antiscalants. Both soft corals had lower bacteria activity under AS. In general, polyphosphonate-based AS induced physiological stress in the hard coral *M. capricornis* and the pulsating soft coral *X. umbellata*, while the soft coral *Litophyton* sp was more sensitive to polymer-based AS. Oxidative stress and increased bacteria abundance seems to be the main drivers of the physiological effects observed. Water scarcity is a global issue, so it is imperative to investigate the best approaches to monitor and mitigate impacts of desalination technologies on marine ecosystems.

The Effect of Mineralogy on CO₂ Capture by Enhanced Limestone Dissolution

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Climate change is one of the biggest threats to the everyday lives of people worldwide. The very high CO₂ emissions scenario projects a warming of 4 °C by the end of 2100 . The 2015 Paris Agreement aimed to limit global warming to less than 2 °C, ideally below 1.5 °C, by the end of this century. However, the current and pledged reductions will likely not be enough, and additional CO₂ mitigation strategies are needed. In this research, I examine a CO₂ capture method using an enhanced dissolution of limestones with seawater. During the process of CO₂ dissolved in seawater, acidity increases, increasing the rate at which limestone dissolves. As a result of the limestone dissolution, the acidity decreases, and dissolved CO₂ becomes HCO₃⁻, which does not exchange with the atmosphere, thus capturing the gas CO₂. This process is natural, spread over a millennial time scale. In order to adapt it to the immediate needs of our times, I built an experimental system through which I accelerated the process using limestones with different mineralogy. The experimental results show the method has feasible development potential: in every experiment performed there was an increase in DIC and TA values suggesting that indeed CO₂ had been captured. Another conclusion that emerges from the results is that the variety of limestones suitable for this method is wide, making it more feasible for widespread application.

A new genetic lineage of *Asparagopsis taxiformis* (Rhodophyta) in the Mediterranean Sea: as the DNA barcoding indicates a recent Lessepsian introduction

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Asparagopsis taxiformis (Delile) is a red marine macroalga (Rhodophyta) with high invasive potential and broad worldwide distribution. In the Mediterranean Sea, *A. taxiformis* was reported before the opening of the Suez Canal and is comprised of two different cryptic lineages, named L2 and L3. As for the Israeli Mediterranean Sea (IMS), *A. taxiformis* benthic populations have seemingly expanded with several large seasonal blooms recorded in recent years. However, neither ecology nor molecular substantial studies have been conducted for this particular geographical area. In this study, randomly samples specimens of *A. taxiformis* and preserved herbarium samples collected from the IMS in the past, were all barcoded and taxonomically identified using three molecular genetic markers (LSU, *cox2-3* spacer, and *rbcL*). We found a cryptic lineage 4 (L4) of *A. taxiformis* first reported here for the Mediterranean Sea, and previously described for the western Indo-Pacific and Hawaii. Herbarium samples confirmed the presence of L4 as early as 2013. Comparative assessment of *cox2-3* spacer marker indicates 100% similarity to sequenced L4 samples from Egypt in the Red Sea. The IMS *cox2-3* spacer sequences differed from previously sequenced samples from the Mediterranean Sea by 2.3% and 3.9% bp, compared to L3 and L2 Mediterranean populations, respectively. Altogether, our results strongly indicate a Lessepsian migration route for *A. taxiformis* L4 with yet unknown consequences for the local marine ecosystems.

Characterizing a novel methionine synthase that underlies bacterial lag phase shortening

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The resources and nutrients in the ocean are available intermittently, forcing bacteria to grow in a 'Feast and Famine-fashion'. Algae can provide nutrients and algal compounds, which can be metabolized by bacteria. During lag phase, bacteria synthesize the essential cellular machinery to utilize these resources and prepare the cell to proliferate. Therefore, the bacterial ability to rapidly commence growth when nutrients become available (duration of the lag phase) is a critical step in competing on resources and outgrowing competitors. Previous data from our lab indicate that Dimethyl sulfoniopropionate (DMSP) and other methylated compounds secreted by the microalgae *Emiliana huxleyi*, trigger a shortening of the lag phase in the bacterium *Phaeobacter inhibens*. It appears that algal methylated compounds could function as methyl group donors during bacterial de novo methionine biosynthesis. Here, we corroborate that *P. inhibens* possess a Methionine synthase (named Bmt), which can harvest methyl groups directly from DMSP to synthesize methionine, promoting earlier growth. Furthermore, under stress conditions DMSP even further shorten the bacterial lag phase. Our data suggest that DMSP and additional methylated compounds confer an advantage to *P. inhibens* and other bacteria, that can harvest essential methyl groups and expedite the transition from lag phase to exponential growth.

The plastisphere ecosystem: the geographical and seasonal effect on microplastic microbiome

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Floating microplastic debris (<5 mm) have been found in almost all marine environments around the world. Due to their high durability at sea, plastic polymers such as polyethylene, polypropylene and polystyrene serve as stable substrates for the colonization of diverse communities of marine organisms. In this study we aimed to characterize and compare the marine microplastic and its bacterial microbiome in contrasting seasons (Winter and Summer) between two separate marine environments – along the Israeli coast of the Mediterranean Sea (IL), and the Portuguese coast of the Atlantic Ocean (PT). At both locations microplastics and surrounding water were sampled in triplicates. State-of-the art DNA metabarcoding methodology was used for the characterization of the microplastic microbiome. Additionally, the physical environmental parameters, including the microplastic itself were analyzed and compared using the same methods for both locations. In similar to previous studies, our results suggest that the geographical location is the strongest source of microplastic microbiome variation followed by the season. While few reoccurring bacteria have been identified in the samples from the two marine environments, most genera were significantly enriched in either one of them. The overall plastisphere microbial composition of the samples from the two environments was different and showed different seasonal effects. These results suggest that the plastisphere is composed of multiple different ecosystems that are defined by multiple environmental factors of their specific geographical locations.

Early behavioral shifts of parrotfish prior to an extreme weather event

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With modern climate change, extreme weather events are increasing in frequency and intensity. Little is known on how individuals respond during extreme weather events and their recovery in the following days. Extreme weather events may be particularly challenging for mobile, territorial animals that follow consistent spatiotemporal patterns. We analyzed high-resolution data to infer behavioral patterns in parrotfish (*Scarus fuscopurpureus*) before, during, and immediately after a surge storm that devastated a shallow reef in the northern Gulf of Aqaba. Interestingly, we found that several individuals exhibited a marked shift in diel activity patterns as early as 10 days prior to the storm. We also found that tracked fish resumed normal activity patterns as early as one day after the storm, despite discernible changes to the reef they inhabit. This is one of the first documentation of anticipatory behaviors in wild animals. Results suggest that reef fish may become aware of surge storms far earlier than expected, and allude to the presence of environmental cues marking the approach of a storm. Early response to such extreme events is likely to increase the survival rates of individual parrotfish, whose functions are vital for the recovery of the reef in the aftermath.

The discovery of chloroplast harvesting in miliolid foraminifera (Rhizaria) implies that kleptoplasty is a precursor to a full algal symbiosis

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During their evolution, benthic foraminifera (unicellular eukaryotes) have acquired autotrophy many times, establishing symbiotic relations with various groups of algae and, in some species, sequestration of chloroplasts forming different models of kleptoplasty. To date, kleptoplasty has been documented exclusively in the benthic rotaliid lineage. We report the discovery of a diatom kleptoplasty in a shallow water miliolid foraminifera, *Hauerina diversa*. To elucidate this adaptation, we visualized many intact chloroplasts in clustered structures within the foraminiferal cytoplasm using transmission electron microscopy. Primary production estimates using isotopically labeled $\text{NaH}^{14}\text{CO}_3$ as a carbon source confirm the photosynthetic activity of the 'stolen' chloroplasts inside the host cell. Molecular analysis of 18S rDNA shows that *H. diversa* branches as a sister to the ancient miliolid family Alveolinidae that harbors centric diatom symbionts. Metagenomics confirms that the harvested chloroplasts belong to the same centric diatoms, subclass Coscinodiscophycidae. Until now, kleptoplasty and symbiosis with living algae have been only documented in different groups of organisms and various foraminiferal families. Our results reveal for the first time that both mechanisms occur in closely related groups and share the same symbionts origin, which supports the hypothesis that kleptoplasty might be a precursor for establishing successful algal symbiosis.

Thermal performance of the recently invading alien *Diadema setosum* on Israeli Mediterranean Reefs

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Climate change and bioinvasions are major drivers of ecosystem change, and the Israeli coast is a hotspot of both. Native sea urchin populations have collapsed on this coast in the past few decades due to warming and competition for food with invasive rabbitfish. Recently, an alien Red Sea urchin, *Diadema setosum*, is becoming abundant in the Levant, with reported high densities in the south Aegean and Cyprus. In Israel it was first observed in Tel Aviv in 2017, but in the past two years more observations have been reported. We aim to follow its populations and assess its thermal tolerance to current and future seawater temperatures in order to understand its possible ecological role as a grazer in the ecosystem. For that, we monitor its densities with seasonal SCUBA surveys on Shikmona, Michmoret and Achziv subtidal reefs at depths of 3-5 and 8-12 m. The winter-spring 2022 survey revealed populations of tens of individuals, mostly clustered, in some locations, but it cannot be considered highly abundant yet. To evaluate the thermal vulnerability of *D. setosum*, temperature performance curve was developed in mesocosm experiments over a 24-34°C temperature range. Oxygen consumption by the urchins was used as a proxy for stress caused by the temperature range. Results so far indicate, beside a survival rate of 100%, an increase in oxygen consumption up to 30°C and then decrease, in an incubation conducted after 7 days of exposure. Incubation after another week reveals some recovery in all treatments, suggesting a potential acclimation capacity.

Climate change impact on Lake Kinneret ecosystem

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The Mediterranean region is one of the most sensitive areas to climate change. Various scenarios predict that in the coming decades, this region will suffer precipitation reduction, temperature increase and extreme events. These changes are expected to impact the Lake Kinneret ecosystem structure and function, such as phytoplankton species composition and water quality, that in turn might compromise key ecosystem services including drinking water supply and tourism. The question arises – can the Kinneret ecosystem maintain its structure and function, i.e. is it resilient? When ecological resilience is low, the ecosystem can reach a tipping point, and undergo irreversible changes to its structure. Lake models enable virtual experiments to examine ecological questions. Applying multiple independent models to a given lake system, also termed 'ensemble modelling', has an advantage as it addresses the inherent uncertainties in individual model projections. This approach may thus result in higher predictive power than when a single model is used. In this study we show results of running two lake models (WET and DYRESM-CAEDYM) on several 50-years climate scenarios for Lake Kinneret. The two models are one dimensional, hydrodynamic biogeochemical deterministic models, consisting of 5 phytoplankton and 3 zooplankton groups. Climate scenarios included gradual temperature raise and increased heat waves. For each scenario, 1000 meteorological time series data were generated and used as forcing for the lake models. Expected changes in physical and biogeochemical properties of Lake Kinneret are shown together with the prediction uncertainty.

The fate of Mediterranean reef biodiversity under rapid ocean warming: lessons from thermal performance experiments

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Climate change is a global threat to marine biodiversity but some regions are more vulnerable than others. The coastal waters of the southeastern Mediterranean represent the trailing (warm) distributional edge of native Mediterranean species where thermally sensitive species can be strongly impacted by warming. They are also a hotspot of climate change and bioinvasions that have already led to dramatic shifts in regional biodiversity. Warming of 2-3 degrees, much higher than the global average, have occurred in the past few decades in the area, and the populations of dozens of native species have collapsed while tropical alien species flourish. As a result, some taxonomic groups, like molluscs, are totally dominated today by tropical alien invaders. Recent regional assessment of future warming project additional 4 degrees of warming by the end of the century, under the business-as-usual scenario of human conduct and global emissions. We have conducted a series of experiments over the past decade testing the thermal performance of more than a dozen invertebrate and macroalgae species under a wide range of temperatures. These experiments reveal that most, but not all native species that are still present are under thermal stress when exposed to current summer temperatures, and may face regional extirpation under future conditions, while tested tropical alien showed much greater resilience, suggesting that this trend of biodiversity shift towards thermophilic alien species domination will continue. The apparent and possible future implication to reef ecosystem functioning and the success of conservation actions will be discussed.

***In vitro* gold nanoparticle synthesis using *Phaeodactylum tricornutum* cultures with image analysis particle characterization**

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Diatoms are one of the most diverse groups of unicellular eukaryotic phytoplankton, mostly known for their silicate cell wall. Members of this group are found in terrestrial, marine, and freshwater habitats. One of the main diatom model species is *Phaeodactylum tricornutum*, which is characterized by fusiform cell morphology and a cell wall poor in silica content, compared to other species. Gold nanoparticles (AuNPs) have received great interests in areas of sensing, imaging and diagnostics due to their unique optical and chemical properties. Currently, green synthesis of AuNPs by *Phaeodactylum tricornutum* can become an alternative manufacturing method. In this study, *in vitro* synthesis using *P. tricornutum* cultures grown under different light regimes, has been examined. Au³⁺/AuNPs had a moderate toxic effect on cultures' growth but when combined with flashing light regimes, growth was significantly reduced by almost 50%, showing a strong synergistic effect between light regime and Au³⁺ supplementation. Digital imaging of the diatom cells via scanning electron microscope was followed by particle quantification and characterization. It was concluded that cultures grown under continuous light yielded smaller amounts of AuNPs and that the different light regimes have affected the dimensions of AuNPs, with larger particles being formed under flashing light. Nevertheless, 99.8% and 97.7% of the AuNPs were in the particle-size distribution of 1-100nm for continuous and flashing light regimes, respectively.

The discharge of gas-saturated brines fuels the chemosynthetic ecosystem in the deep Eastern Mediterranean Sea

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Diverse, understudied biota maintain the vital services of the vast deep hydrosphere. In this dark, energy-limited environment, the natural discharge of fossil hydrocarbons from the seabed fuels chemosynthetic productivity and nourishes flourishing communities in cold seep ecosystems. These seeps may play a key role in the functionality of the oligotrophic basins, such as the Mediterranean Sea offshore Israel. Using deep-sea-going robotics, we discovered and sampled hydrocarbon-rich, warm, brine pools at a water depth of 1150 m within Palmahim Disturbance, 60 km offshore Israel. Our observations reveal that this extremely productive system, where primary productivity of $\sim 700 \mu\text{g C L}^{-1} \text{d}^{-1}$ at the brine-water interface exceeds that of the entire water column, accommodates rich chemosynthetic communities where microbial biofilms, as well as tubeworms and mollusks, whose nutrition fully relies on their microbial partners, thrive en masse. The finding of a deep-sea shark nursery and large numbers of seldom-seen organisms, such as the deep-sea echinoderm *Gracilechinus elegans*, suggests that this rare habitat has a broad ecological impact. We investigated the functionality of this ecosystem, focusing on microbes, both free-living and symbiotic, using omics. We show that microbes cooperate to catalyze the cycling of methane, sulfur and nitrogen (present in the millimolar range in brines and adjacent sediments), fix carbon and degrade organics in this hotspot of biotic interactions and metabolic innovation. Our discoveries, which lead to the recent declaration of the first deep-sea marine reserve offshore Israel at the Palmahim Disturbance, highlight the importance and potential of deep-sea research.

Deciphering stress resilience and programmed cell death mechanisms in marine diatoms

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Oceanic diatoms are unicellular algae, contributing ~20% of global photosynthesis. They form large-scale blooms which impact global nutrient recycling. Bloom dynamics include exponential cell proliferation, followed by a synchronized demise attributed to different stressors as nutrient deprivation, viruses and grazers. Diatom mortality has some characteristics of programmed cell death (PCD), yet, cellular machinery mediating unicellular organisms PCD as diatoms are understudied. We characterize novel genes involved in stress resilience and PCD in the model diatom *Phaeodactylum tricornutum*. Using CRISPR-Cas9, we knocked-out three metacaspase genes presumably involved in PCD due to structure similarity to caspase, a key protease in animal PCD. Mutants grew slowly than WT, and showed higher mortality rate after heat and H₂O₂ stress, mimicking environmental conditions which induce oxidative stress. Thus, metacaspases have a possible unexpected vital role involving protein aggregates disposal, as opposed to their common suggested role in algal PCD. Furthermore, to expand candidate genes involved in stress acclimation and death, we investigated an RNA-sequencing dataset from H₂O₂-treated *P.tricornutum*, to study the role of genes upregulated in subpopulations with two contrasting cell fates, death and survival. We then used an available mutant library of the model *Chlamydomonas reinhardtii* to validate mutant phenotypes in selected orthologues upregulated in each subpopulation. Ascorbate-peroxidase knockout lines died more than WT under H₂O₂ stress, while Cathepsin-X knockouts died less. Finally, candidate genes were knocked-out in *P.tricornutum*. Their phenotypes are currently being characterized. By combining targeted and untargeted genetic approaches, we aim to reveal cellular pathways mediating phytoplankton death in the ocean.

Growth and threats of eastern Mediterranean turtles in their epipelagic phase

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Sea turtles are endangered marine reptiles, spending majority of life stages at sea. Habitats impacted by anthropogenic exploitation endanger populations often to the brink of extinction. During the post hatchling to juvenile life stages, turtles occupy pelagic habitats, using floating materials or flora that create a passive transport method and a focal point of threats. Since 2017, Israel's Sea Turtle Rescue Center (ISTRC) had observed an increasing number of juvenile Loggerheads (*Caretta caretta*) and Green sea turtles (*Chelonia mydas*), injured or dead, due to neck and limbs' entanglement in polypropylene (PP) woven sacks. The unraveled threads suggest sacks are being cut and thrown to sea intentionally, and the turtles presumably use them as their floating habitat. Most entanglements (76%) occurred between June - September. Hypothesizing PP sacks presence only during summer, accentuate voyages or seasonal cargo. The main conservation resources are used for the prosperity of marine turtles' reproduction onshore and although it is critical for recruitment, the fragile pelagic stage is not in the center of research and conservation attention. Numerous challenges are concerning long term work in pelagic transitory habitat, with small individuals whose movement is environmentally dependant and is thus unpredictable. These difficulties create a gap of knowledge regarding their passive migration distribution, its exact duration, growth rates, diving patterns, nutrition and more, resulting in conservation difficulties. This research used ISTRC's database, enlarged by sack-entangled patients, to reveal novel developmental biology in month-specific growth curves of Loggerhead and Green sea turtles in their first years of life.

Modeling a fish species-specific preference using low volume data, a new perspective for constructing artificial reef

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Worldwide coral reefs' deterioration is reflected in the destruction of shelters in diverse marine environments. The absence of suitable shelters for coral-reef fish communities might undermine marine ecosystems' stability. Artificial shelters (AS) are suggested as a solution, yet, constructing successful shelters for reef-fish is a great challenge due to the large variety of needs of the different species. Preference of each species for shelter differs between species and furthermore, differs within the same species at varying local coral reefs. Thus, planning a successful AS requires a detailed local per-site study of the reef-fish assemblage, composition, and nutritional needs. Studying the community of coral-reef fish in Katzaa (Gulf of Aqaba), between January 2021 and April 2022, led to a particular method for characterization of reef-fish species-specific preferences for shelters, using low volume data (insufficient for any statistical test). We grouped individual species of reef-fish by systematic (families) and functional division (dietary group). Later, we examined the preference of each group using a-parametric tests and combined the obtained groups to develop a profile for each of the dominant species in the study site. Altogether, we developed profiles for 17 species' preferences that were accurately verified with the reef-fish counts from the Katza surveys for each of the species. We propose this method to allow researchers to examine their particular design and location of artificial shelters locally, with minimal effort and a low budget. Consequently, this method will increase the efficiency and success of recruitment and settlement of reef-fish to the artificial shelters.

Exploring the phenotypic landscape of algal resistance to lytic viral infection

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Phytoplankton are unicellular photoautotrophs that form the basis of marine food webs and account for ~50% of the global net primary production. Phytoplankton can form large-scale oceanic blooms, which play key roles in global biogeochemical cycles. The seasonal blooms are often terminated by lytic viruses, yet some “seed” population can survive viral infection and serve as the next bloom inoculum. In recent years, an arsenal of resistance mechanisms and active defense systems against viruses was discovered in bacteria. However, in diverse algal lineages, resistance mechanisms against viruses are poorly understood. Here, we investigated molecular components of resistance mechanisms in the tractable host-virus model system, the bloom-forming algae *Emiliana huxleyi* and its large dsDNA virus, *E. huxleyi* virus (EhV). We generated extensive transcriptomic datasets of algal strains that exhibit a spectrum of resistance and susceptibility phenotypes to viral infection. By 3' RNA sequencing we compared the inherent differences in gene expression between the susceptible and resistant strains, and identified potential genes related to resistance. Next, we conducted bulk 3' RNA-seq analysis during a detailed time course of viral infection, through the stages of population demise and recovery. We are currently analyzing the cellular response of *E. huxleyi* to infection and aim to track the transcriptomic patterns of the newly discovered resistance-related genes. This work will shed light on algal resistance mechanisms to viral infection, how they emerge in the population and how they shape bloom succession in the ocean.

Chemical signalling in the ocean: Exploring the role of DMS in marine food webs

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Marine phytoplankton produce the sulfuric gas dimethyl sulfide (DMS), which is emitted to the atmosphere and promotes cloud formation. DMS is also key biochemical signal mediating diverse trophic interactions in the ocean. Yet, its role during microbial predator-prey interactions remains elusive, with contradicting evidence for its contribution to either algal chemical defense or as a chemoattractant of grazers to prey cells. We investigated the signaling role of DMS during zooplankton-algae interactions by genetic and biochemical manipulations of the algal DMS-generating enzyme, dimethylsulfoniopropionate lyase (DL), in key algal model species. We inhibited DL activity in the bloom-forming haptophyte *Emiliana huxleyi* cells using a novel selective DL-inhibitor. Alternatively, we enhanced DL activity by overexpression in the non-DMS producing diatom *Thalassiosira pseudonana*. We found that the algal DL activity did not serve as an anti-grazing chemical defense, but enhanced grazing by *Oxyrrhis* and other micro- and mesozooplankton, including ciliates and copepods. Consumption of algal prey with induced DL activity also promoted *Oxyrrhis* growth. The paradoxical role of the algal DMS revealed here, acting as an 'eat-me' signal for grazers, may be ecologically important and prevalent during prey-predator interactions at sea. Our findings raise fundamental questions regarding the evolutionary retention of the DMS-generating enzyme in phytoplankton. Therefore, we are currently mapping the phylogenetic and global biogeographic distribution of the DL enzyme, which will allow to develop model systems and genetic tools needed to interrogate the yet unknown cellular role of DL, and to better understand its function(s) as a key enzyme in marine environment.

Annual dynamics of cyanophages and their hosts in the Sargasso Sea

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Cyanobacteria of the genera *Prochlorococcus* and *Synechococcus* are widely distributed across different oceanic regions and display well described seasonal dynamics due to changes in environmental conditions. Phages that infect cyanobacteria belong primarily to the T4-like myoviruses and T7-like podoviruses families. To understand cyanobacterial-cyanophage population dynamics in the Sargasso Sea, we are sampling monthly at the Bermuda Atlantic Time-series (BATS) station, located in the northwest Sargasso Sea. This is an oligotrophic gyre system in which *Synechococcus* is most abundant in the spring and *Prochlorococcus* is most abundant in the summer-fall. Data on cyanophage abundances and distribution are still very limited for nearly all parts of the oceans and are non-existent for this region. In this project I am evaluating the seasonality of cyanophage abundances in the photic zone. I found that during the annual cycle of 2021 the T4- and T7-like cyanophages abundances were at least one order of magnitude higher than their cyanobacterial hosts, *Prochlorococcus* and *Synechococcus*. T7-like abundances were higher over most depth profiles except for the March profile when T4-like were higher at all depths. The abundances of both cyanophages increased toward the end of the summer, but their peaks did not overlap, occurring in different months. The annual peak in abundance for T4-like cyanophages was in August at 100 meters. T7-like abundances reached their annual maximum in October at 100 meters. This data suggests that these two cyanophage groups abundances are driven differently by biotic and abiotic annual environmental changes.

Impacts of brine waste from the desalination industry on the benthos: from seagrass and bacteria to seabed geochemistry

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Seawater desalination is a frequently used technology to produce freshwater in arid and semi-arid regions. However, the process of desalination comes with a potential environmental price. A hypersaline brine byproduct that often includes various chemicals such as antiscalants. is usually discharged back into the coastal environment, where the dense plume sinks to the bottom and flows over the seabed, affecting all nearby marine environments. Currently little is known on the impacts of antiscalants on marine benthos, specifically tropical seagrass, benthic bacteria, and porewater chemistry. A four week, mesocosm experiment was carried to determine the impacts of 5 ppm polyphosphonate antiscalant and 5 ppm polyphosphonate with 5% above ambient salinity on the seagrass species *Halophila stipulacea*, benthic bacteria, and porewater chemistry. Seagrass morphometrics such as leaf surface area, weekly growth rates, photosynthetic efficiency, and respiration were collected after 0, 1, 2, and 4 weeks. Porewater was collected from a sediment depth of 10 cm where alkalinity, PO₄, NH₄, dissolved inorganic carbon (DIC) were measured. Results showed few differences in seagrass parameters. Respiration in the antiscalant only treatment compared to the control and antiscalant with salinity (38.1% and 32.2% higher, respectively). PO₄ for both antiscalant treatments was higher (antiscalant: +123%; antiscalant+salinity: +159.4%) in the water column compared to the control. These results indicate that after 4 weeks, minimal differences occurred in the seagrass, while water chemistry was altered. The outcome of this research will allow better management practices of seawater desalination.

Effects of habitat traits and structural configuration on fish communities in an Eastern Mediterranean rocky reef

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Habitat-species interactions shape fish communities, and therefore are a critical component for efficient resource management, conservation efforts and coastal planning. At a local scale, structural traits such as reef complexity, can create preferable niches for individual fish. In parallel, wider-scale traits such as habitat connectivity, corridors or fragmentation, are likely to affect species' populations and the overall fish community. Therefore, characterizing species-habitat interaction requires a multi-scale approach. In this work we'll be addressing both local and wide-scale habitat traits by developing novel techniques for habitat classification using high-resolution Synthetic Aperture Sonar (SAS) and bathymetry layers. Three major applications are developed: (1) The SAS images provide divers with a map such that divers can precisely identify their location at the reef *in-situ*. (2) The bathymetry layer allows us to identify the full gradient of various complexity indices – at multiple scales, and (3) the classification scheme allow us to calculate ecological functions at multiple scales. We will use Eastern Mediterranean fish communities as a study case from which we will develop a general framework for future studies of habitat-species modeling in other marine environments.

The ecological impact of viral infection on algae accompanying microbiome during algal blooms

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Primary production in the ocean is the basis of the marine food web. This production is attributed to various phytoplankton species that ultimately drive the marine ecosystem. The coccolithophore *Emiliana huxleyi* is an abundant phytoplankton species that form massive blooms that cover extensive ocean areas. These blooms are thought to be terminated following infection by a specific virus, the *E. huxleyi* virus (EhV). *E. huxleyi* metabolism is rewired upon viral infection to create a unique metabolic landscape. *E. huxleyi* bloom demise is accompanied by a massive release of unique dissolved organic carbon (DOM), including a labile source of carbon that is consumed by heterotrophic bacteria. We hypothesize that the metabolic composition of the DOM can significantly affect bacterial assemblages. Nevertheless, the impact of viral-induced DOM (vDOM) on bacterial composition and physiology is not clear. Here, we aimed to elucidate the effect of vDOM on its consumers, especially heterotrophic bacteria. We are especially interested in understanding whether constituents of the vDOM can induce specific bacterial lifestyles, such as pathogenicity towards the algae. For this, we apply various bioassays to characterize the effect of vDOM on bacterial community physiology, metabolism, and diversity. We aim to understand better the molecular and metabolic basis of the algae-virus-bacteria tripartite interaction.

Measuring Surface Velocities and Waves from Unmanned Aerial Vehicles

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Sea surface velocity is an important parameter in transport of pollutants, plankton, and nutrients. Likewise is the sea state, i.e., spectrum of surface waves, which affects material transport as well as air-sea exchange of gases and momentum. However, in-situ measurements of these two parameters are often hindered by technical difficulties and are limited in their spatial coverages. Here we present a novel framework for simultaneous retrieval of surface currents and wave spectrum, from videos taken from Unmanned Aerial Vehicles (UAVs, or drones). Due to their low cost, easy deployment, high mobility and large spatial coverage, UAVs have important advantages over traditional methods used for these purposes. We build on a recently developed open software for calculating surface currents from UAV video, and generalize it to perform wave spectrum estimation as well. We offer several methodological developments to improve robustness to various skylight and wave (e.g. sunglint and wave foam) conditions. Finally, we validate and estimate the accuracy of both methods (UAV current measurement was previously validated mostly in rivers or channels) using UAV and in-situ data which we collected in several Israeli coastal and continental shelf locations.

Basin Scale to km Scale Variability of the East-Mediterranean Upper Sea Circulation

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The East Mediterranean Sea circulation has been observationally characterized in terms of its basin scale flow (e.g. wind gyres) and “mesoscale” (~50 km size) eddies. Smaller scales (“submesoscale”) were rarely observed, as they are smaller than typical ship sections sampling resolution. However, submesoscale eddies and fronts have been shown to strongly influence larger scale circulation elsewhere, as well as material transport, with important implications for marine biogeochemistry and for pollutant dispersion. To examine submesoscale circulation and its interaction with larger scale circulation in the region, we conduct high resolution numerical modelling of the East Mediterranean Sea, resolving spatial scales from basin scale to 1 km scale. We find that a continuous boundary current propagates along the East Mediterranean continental slope region, rather than several disjointed regional boundary currents. The boundary current continuously generates mesoscale and submesoscale eddies in the region, which are often shed into the interior. Moreover, the eddy shedding typically occurs near several identified bathymetric capes. Submesoscale eddies and fronts of sizes as small as resolved by the model (~1km) densely populate the mixed layer during winter months and are associated with higher magnitudes of velocity and density gradients compared to their larger counterparts. We analyze the spatiotemporal distribution of kinetic energy (i.e, the energy spectrum), as well as the cross-scale energy transfers. In the mixed layer, submesoscale and mesoscale eddies transfer their kinetic energy to larger scales during winter, while submesoscale fronts and filaments transfer their energy to even smaller scales. Under the mixed layer, in the permanent pycnocline, wind-generated internal waves are shown to dominate the variability.

Nutrient concentration or nutrient ratio? The effect of media composition on *Prochlorococcus* growth and decline

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Dissolved nutrients in the ocean, mainly Nitrogen (N) and Phosphorus (P), play major roles in stimulating growth and primary production, thus ensuring life in the sea. Common mathematical models of bacterioplankton growth predict that growth rate will only be affected by extracellular nutrient concentrations near the K_m of the uptake mechanism, yet this has not been tested experimentally. We asked whether *Prochlorococcus*, a globally abundant model cyanobacterium, can respond to high media nutrient concentrations or changes in media N:P ratio in batch culture through changes in growth rate. We examine two alternative hypotheses; i) Growth yield (maximum biomass) in lab cultures depends on media nutrients concentrations, but growth rate does not. ii) Both yield and growth rate change as a function of media concentrations, and specifically the N:P ratio. Three *Prochlorococcus* strains were studied, isolated from two different niches: High-light-adapted MED4 and MIT9312 grow at the ocean surface, where nutrients are scarce, and low-light-adapted MIT9313 grows deeper in the water where nutrients are more available. All strains were grown in multiple nutrient conditions: Pro99 (nutrient-replete medium), low N, low P and low N/low P media. MED4 and MIT9312 (HL) and MIT9313 (LL), show distinct death patterns between N and P starvation. N starvation results in a sharper and faster decline compared to P starvation, and both MED4 and MIT9312 seem to survive longer under P-starvation compared to MIT9313. To conclude, it seems that different *Prochlorococcus* strains respond and adapt uniquely to nutrient limitation, possibly as a result of niche-adaptation

The Swimming Velocity of the *Rhopilema nomadica* Jellyfish

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Our study of jellyfish swimming along the Israeli coastline suggests that the jellyfish swimming speed and sea currents are often similar in magnitude. Consequently, the transport of jellyfish swarms is a result of a vector summation between the jellyfish swimming velocity, \vec{V}^s , and the sea current, \vec{V}^c . A library review shows that despite the significant impact of jellyfish, very little field information is available about jellyfish swimming. Here we try to narrow this knowledge gap by measuring the swimming velocity of *Rhopilema nomadica* Jellyfish individuals at sea. Stabilized drones were launched from a small research vessel during jellyfish blooms in summer 2020. Following calibration, video images captured by the drones were analyzed and the horizontal position of *R. nomadica* individuals was obtained. Linear trajectories were curve fitted to calculate the horizontal velocities, \vec{V}^m , in the drone (world) frame of reference. The instantaneous current velocity in the vicinity of each jellyfish was obtained using the measured velocity and the orientation angle of jellyfish pairs. Each pair resulted in a measurement of the instantaneous water velocity. A comparison between the current velocity measured by the new jelly-pair method and the water velocity obtained by other means (an ADCP and drifters) shows a satisfactory agreement. The swimming velocity was obtained by subtracting the current velocity from the measured velocity, $\vec{V}^s = \vec{V}^m - \vec{V}^c$. We will show results of *R. nomadica* swimming velocity, correlate them with jellyfish size and pumping frequency, and compare the findings with solutions of a jellyfish swimming model.

Air-water interactions regulating water temperature of lakes: direct observations (Agamon Hula, Israel) and analytical solutions

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Air-water interactions regulate lake-water temperature by balancing the rate of change of water temperature (stored heat) with the incoming and outgoing heat fluxes, which are functions of water temperature and external forcing. Yet, there is a large knowledge gap in quantifying the thermoregulation of a lake, and especially managed lakes, which is hypothesized to be related to both external environmental forcing and management decisions on lake depth and water inflow. Here we explore the thermoregulation of a restored and managed Mediterranean lake (Agamon Hula, Israel), by direct measurements of all major heat fluxes. We interpret the results with a rigorous analysis of the thermoregulation equation, obtained by formulating the energy balance equation in terms of water temperature. The equation shows how water temperature of a lake shifts toward steady state, scaled by the lake's response time. Where the steady-state temperature was reached, it was controlled by external environmental forcing and not by lake depth. Whereas the thermal response time to re-attain steady state, following an abrupt change in various environmental conditions, is controlled by water depth. The lake-temperature response to pre-defined oscillations of the environmental forcing showed that the amplitude of water temperature fluctuations and the time delay from steady-state are controlled by the ratio between the environmental forcing's time period (diurnal, seasonal or other cycles) and the thermal response time of the lake. The summertime measured CO₂ fluxes of Agamon Hula revealed the lake acts as a CO₂ source

Exploring the interplay between virus infection and host ecophysiology in marine diatoms

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Diatoms are among the most globally distributed and ecologically successful organisms in the modern ocean. These eukaryotic, photosynthetic microbes are key players in the carbon cycle, contributing ~20% of global primary production. With an obligate requirement for silicon (Si) for cell wall formation, diatom biogenic silica also ballasts the vertical flux of carbon out of the surface ocean. We understand very little about the unique viruses that infect diatoms, despite the potential to transform diatom-mediated biogeochemical cycling. Recent findings suggest that environmental factors can dramatically shape diatom host-virus interactions, yet we lack mechanistic knowledge of ecophysiological pathways that underscore virus infection in these organisms. Using the model, bloom-forming diatom, *Chaetoceros tenuissimus*, we are exploring the interplay between host ecophysiology and infection dynamics. We found that the onset of virus-mediated diatom mortality is accelerated by the degree of phosphorus limitation. Interestingly, in phosphorus-limited cultures, we also observed higher alkaline phosphatase activity in infected cultures, suggesting differential regulation of the phosphorus limitation response during viral infection. In addition, given that diatom silicification is impacted by nutrient availability and host ecophysiology, we are testing whether the diatom cell wall constitutes a physical barrier to viral entry. Using a range of environmental conditions to manipulate biogenic silica thickness and morphology, we are exploring mechanisms of viral entry and replication. These findings highlight the interplay between the environment and host-virus dynamics, providing insight into the underlying mechanisms that drive virus infection of diatoms in the ocean.

Identification of *Desulfuromonas carbonis* Metabolites that are Secreted in Response to Electron Acceptors

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Chemical profiles in anaerobic porewater of organic-rich sediments indicate that various microbes use several electron acceptors in the anaerobic dissimilatory respiration. One of those bacteria is *Desulfuromonas carbonis*. Here we investigated the changes in secretion of these metabolites due to the presence of various common electron acceptors (EAs), focusing on microbial secondary metabolites that are used in bacterial signaling processes.

Pure cultures of *D. carbonis* were incubated with several different electron acceptors, extracted by solid-phase extraction methods, and examined by liquid chromatography-tandem mass spectrometry (LC-MS\MS). The LC-MS\MS data was analyzed using the global natural products social molecular networking (GNPS) online platform, to identify potential bacterial signals that may play a role in population-wide processes related to the use of EAs to enhance fitness. We examined the presence of such compounds in complex cultures containing *D. carbonis*, natural anoxic lake sediment, and iron oxide, in order to mimic their ecological niche. Our results indicate that bacteria produce unique metabolites depending on the presence of different EAs in the cultures. Indole-3-carboxaldehyde (ICA) was found in significant amounts in iron-oxide containing cultures. This compound has been found to play a role in tryptophan metabolism and is known to affect chemical communication among various bacterial species. Incubation of *D. carbonis* with increasing amounts of iron resulted in decrease production of ICA. These results establish the potential of ICA to be involved in natural processes specific to dissimilatory iron reduction. We will continue to investigate these processes and the connection between ICA signaling and iron.

Feel the pulse: soft coral kinesics through ontogeny and symbiosis

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Octocorals are abundant in coral reefs, inhabiting hard substrate from the Indo-Pacific to the Red Sea. Although they grant brilliance and high biodiversity to the reef as their stony counterparts, they are understudied. Several species of the family Xeniidae are characterized by the unique pulsation of their polyps. Such rhythmicity turns a motionless reef into an animated and mesmerizing structure. Moreover, pulsation is of biological importance that has been noted and studied throughout the past 200 years. Yet, the ontogenetic aspects of this phenomenon have remained uninvestigated. The goal of this study is to examine the development of pulsation in early life stages of the soft coral *Heteroxenia fuscescens*, also in relation to algal symbiont acquisition by the sexual offspring. For this purpose, adult colonies are collected from the shallow reefs of Eilat, transferred to an outdoor flow-through tank and monitored for planulation. Released planulae are collected and transferred to laboratory for settlement and metamorphosis. Simultaneously, several polyps are detached from parent colonies for endosymbiont cell isolation. Part of the newly settled primary polyps are infected with parental algal isolates, others are kept azooxanthellate. Metamorphic events and commencement of pulsation are monitored and photographically recorded. Hitherto findings indicate that zooxanthellate polyps perform continuous and synchronous pulsation within 8-14 days post-metamorphosis, whereas azooxanthellate polyps limit or cease movement. The sole dependence of xeniid corals on their endosymbionts for energy supply contributes to the significance of the crucial host-algae relationship. Thus, emphasizing the need to highlight ontogenetic aspects of the pulsation process.

Feeding strategy and dietary preference shape the microbiome of epipelagic copepods in a warm nutrient-impooverished ecosystem

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Copepods provide a rich organic microenvironment allowing the settlement and proliferation of microorganisms, forming dynamic microbial hotspots in the oceans. Such symbiotic associations in the plankton were previously hypothesized to be especially developed in warm oligotrophic seas, as they may serve as alternative sources of nutrients in biologically-poor waters. Aiming to better understand how copepod microbiomes are shaped in an oligotrophic sea, we characterized microbiota associated with three dominant coastal epipelagic copepod species in the ultra-oligotrophic Eastern Mediterranean Sea using amplicon sequencing of the 16S rRNA gene. Our results show that copepod-associated microbial communities were host-specific rather than determined by seasonal environmental changes. In the filter-feeding copepod with a tendency to herbivory, *Temora stylifera*, microbial diversity was low and relatively stable throughout the year. In contrast, omnivorous copepods, the ambush-feeding *Oithona nana*, and the mixed-feeding *Centropages ponticus* harbored more diverse microbiomes dominated by transient taxa. We suggest that filter-feeding strategy and narrow food spectrum can limit copepod-microbe interactions, while the ambush and mixed feeding strategies combined with omnivory confer higher microbial diversity. Filter feeders may reduce the recruitment of opportunistic microbes by maintaining high fidelity associations, as indicated by the large number of core taxa in *T. stylifera*. We underline the importance of the copepod-microbe associations in nutrient-impooverished ecosystems, based on predicted enrichment of nitrogen metabolism in the core microbiome, mostly during summer when the shallow coastal waters are nitrogen-depleted.

Aerobic methanotrophic activity stimulates iron reduction in lake sediments

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Recent observations from shallow anoxic lacustrine sediments around the world show an unexpected presence of bacterial methanotrophs, usually typified to be aerobic, together with anaerobic microorganisms, such as methanogens and iron reducers, which may result from undetectable traces of oxygen or a yet to be understood biochemical process producing oxygen. Both *mcr* gene-bearing archaea and *pmoA* gene-bearing bacterial methanotrophs were suggested to mediate methane oxidation in Lake Kinneret sediments. In these sediments, iron reduction was shown to be coupled to methane oxidation; however, with an unclear mechanism linked to methanotrophy. Here we show a new set of geochemical and microbial data from slurry experiments that tested the oxygen exposure effect on this aerobic and anaerobic activity. The exposure to oxygen (up to 1%) promoted aerobic methanotrophy, and surprisingly, an increase in net iron reduction in the anoxic lake sediments. The iron reduction was microbially mediated and performed by either *Desulfuromonas*, *Geobacter*, or *Methylomonas*. The experiments provide insight into the complex life and biogeochemical cycles in anoxic lake sediments.

Nitrate as a control on methane emissions from Lake Kinneret sediments

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Methane (CH₄) production and consumption in lake sediments is controlled by many chemical, geological and biological factors. As an important greenhouse gas, monitoring methane emissions and studying the natural controls on its consumption within lake and marine sediments, is important for better understanding methane cycles. One control on methane release to the atmosphere is the presence of electron acceptors such as sulfate, iron, nitrate etc. These are related to anaerobic microbial oxidation of methane (AOM). This study was conducted to evaluate the potential of nitrate as a sole electron acceptor for AOM in a controlled sediment-water mesocosm. Over a water mesocosm redox conditions, chemical and biological samples were taken daily to identify possible pathways for AOM and other respiratory processes. Methane and Fe(II) decrease seems to be coupled to nitrate addition, indicating either direct or indirect processes such as nitrate reduction through iron oxidation, nitrate dependent AOM and more. The fact that CH₄ keeps decreasing after depletion of nitrate points towards possibly methane oxidation by Fe(III) reduction which was seen possible in Lake Kinneret sediments in previous studies. Further investigation on nitrate/nitrite and iron coupling is required to get a better understanding of AOM processes and other microbial mechanisms related to the nitrogen cycle in such environments.

The role of submarine groundwater discharge in the ocean carbon budget

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Israel Ocean chemistry is dictated by weathering and transporting elements from the land to the ocean and their removal through precipitation and adsorption. Submarine groundwater discharge (SGD) may release large amounts of trace metals, nutrients, carbon, and other dissolved species to the coastal ocean. The element fluxes may be comparable to surface water flow due to groundwater interaction with the aquifer sediments and the high ratio between rock and water. Recent attempts to calculate the carbon and alkalinity ocean budget have shown that riverine DIC input and marine carbonate burial cannot be balanced by alkalinity delivered via submarine groundwater. This deficit in the ocean's alkalinity mass balance may be attributed to insufficient knowledge of the carbonate and alkalinity contributions through SGD, particularly seawater circulation in the aquifer. Our study shows a contribution of alkalinity during long-term seawater circulation in aquifers, both in Indian River Bay (Delaware) and in the East Mediterranean coastal aquifer. As part of this research, we collected an extensive data archive on coastal aquifers worldwide. This data is used to characterize the interactions between groundwater and country rocks depending on the type of rock and how they may impact water alkalinity and dissolve carbon. Understanding these geochemical processes allows us to estimate carbon species, alkalinity fluxes, and budgets into the ocean. It is essential to understand the ocean's alkalinity buffer system budget in order to understand carbon sources and sinks, along with climate feedback mechanisms.

Surviving Starvation: Metabolic Mechanisms of Interaction between Phototrophs and Heterotrophs

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Prochlorococcus are a clade of photosynthetic marine cyanobacteria, which are highly abundant in the oligotrophic (nutrient poor) waters of the world oceans and are responsible for a large portion of global carbon fixation. *Prochlorococcus* can grow in the lab but quickly die off when facing nutrient stress. They can, however, survive nutrient starvation for months in the presence of some heterotrophic marine bacteria. We hypothesize that the key to this remarkable survival is cross feeding and nutrient recycling between the phototrophic and heterotrophic partners. We employ a combination of Genome-scale metabolic models (GEMs), transcriptomic and proteomics to identify nutrients exchanges driving this synergistic interaction.

Photosynthesis, respiration, and mixing rates in the Gulf of Aqaba

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The supply of nutrients into the photic zone, photosynthesis, and re-mineralization of organic material, are basic geochemical properties of aquatic environments. Here, we estimate the rates of these processes in the northern Gulf of Aqaba. To do so, we rely on the fact that while the Gulf is thermally stratified, it experiences deep mixing every 7-10 years. On such events, the mixed layer deepens to the bottom of the basin, thus exposing the deep water-column to photosynthesis and air-sea gas exchange. Consequently, nutrients concentrations decrease, while dissolved oxygen (O_2) increases. Once the water column re-stratifies, nutrients and O_2 concentrations below the thermocline are governed by re-mineralization of sinking organic material, and by water-exchange with the photic zone. To calculate the rates these processes, we fitted a differential equation, which included a term for each process, to nutrients and O_2 data from the longest stratified period recorded in the Gulf, between 2012 and 2022. All the parameters we tested (O_2 , nitrate, phosphate, and silica) showed good agreement to the equation ($R^2 = 0.7 \pm 0.2$), and yielded similar water-exchange coefficients, which averaged $1.3 \pm 0.3 \text{ m}^2 \text{ d}^{-1}$. Based on this water-exchange parameter, we estimated a nitrate flux of $0.2 \times 10^{-3} \text{ mol N m}^{-2} \text{ d}^{-1}$ into the photic zone. Because nitrate concentration in the photic zone of the Gulf is close to zero during stratification, this flux provides a basin-scale estimate for new production in the Gulf.

The invasive echinoid *Diadema setosum* (Leske, 1778) - reaching population outbreak phase in the Eastern Mediterranean Sea

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The Mediterranean Sea is a unique habitat. Its relative isolation and distinct characteristics create an exceptional ecosystem recognized as a marine biodiversity hot-spot with remarkable endemism rate. Yet, local biodiversity is threatened, mainly due to a massive invasion process: The opening of the Suez Canal allowed more than 800 non-indigenous species to migrate from the Red Sea to the Mediterranean, in a process termed Lessepsian Migration. *Diadema setosum*, one of the most ubiquitous echinoids in the Red Sea, was first documented in the Levantine basin in 2006. As it primarily feeds by algae grazing on hard substrates, *Diadema* are often recognized as environmental engineers, capable of altering the structure of entire benthic communities. Here we follow the invasion dynamics of *D. setosum* in the Eastern Mediterranean Sea from its initial appearance to its recent population growth shown since 2019, which implies population outbreak. We combined sampling, extensive survey data and citizen-science reports to depict the invasion's current status and scope. We used molecular data from Mediterranean collected specimens to identify the genetic makeup of the invaders. The results illustrate the presence of a single genetic clade in the area, matching the Red Sea clade, reinforcing the invasion's origin. In contrast to other alien species in the region, the ecological footprint of *D. setosum* poses a clear and immediate threat to the entire Levantine Basin, calling for rapid and coordinated action at both national and regional scale.