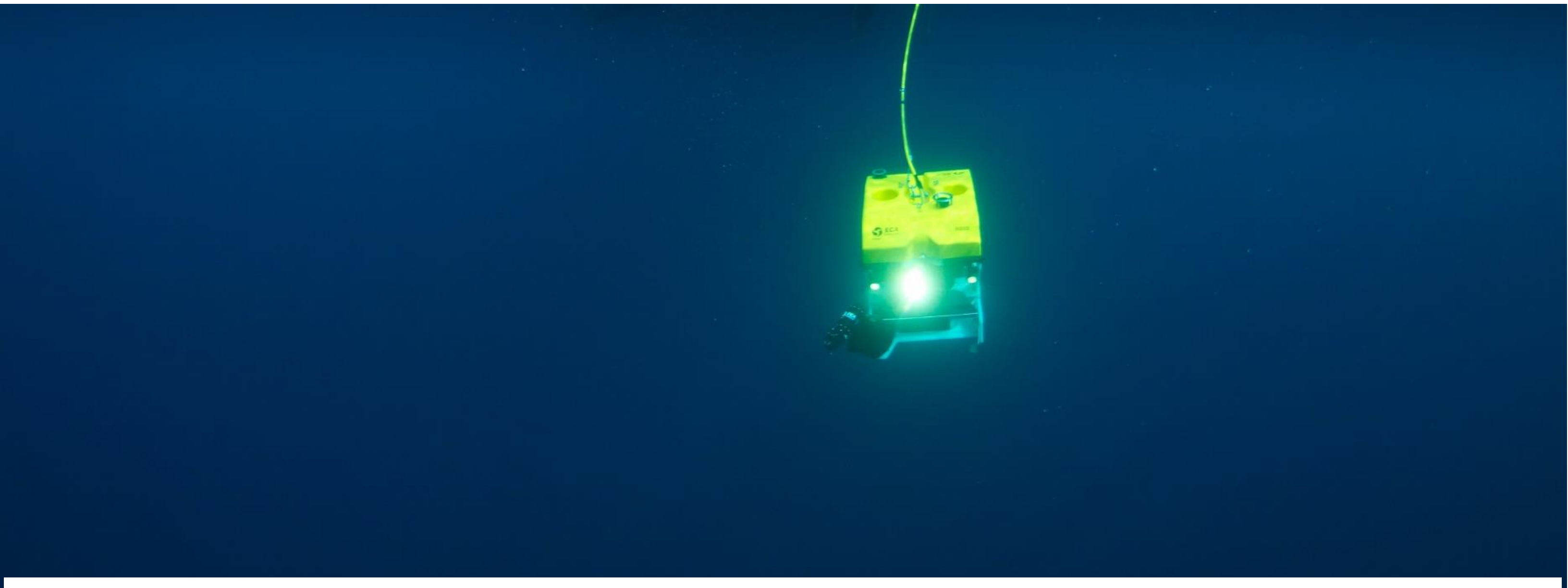
The Israeli Association for Aquatic Sciences

Book of Abstracts



IAAS-IOLR joint Annual meeting

Eilat 2024

The Israeli Association
for Aquatic Sciences

חקר ימים ואגמים לישראל
ISRAEL OCEANOGRAPHIC & LIMNOLOGICAL RESEARCH

The Israeli Association for Aquatic Sciences wishes to the thank to the following institutes, ministries and companies. This year's meeting is a special meeting, joint to the association and the Israeli Oceanographic and Limnological Research institute. The meeting is happening at the end of a year that was challenging in many ways for students, researchers and their families. Therefore, the association particularly grateful for the special contribution coming from these institutes that made it possible to provide scholarships and grants for students in reserve service and\or their partners.

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Image: Yoav Lindman

Pacific cold-tongue bias in CMIP linked to shifts in extratropical subduction zones

O. Ariel (1), **O. Adam** - alhanab.sweetie@gmail.com (1), M. Shourky (1), and H. Gildor (1)
1) Hebrew University

The Equatorial Pacific Cold Tongue (CT) bias is a systematic sea surface temperature (SST) bias, that persists through all generations of comprehensive climate models. Recent works suggested that extratropical SST biases contribute to the CT bias, mediated by the wind-driven ocean overturning circulation in the Pacific. However, as shown here, the northern and southern hemispheric `eastern exchange windows', which are the dominant extratropical source for water upwelling in the Equatorial Pacific, are not characterized by cold SST biases. Here we explore these links using Lagrangian back trajectory analysis in 32 models participating in phases 5 and 6 of the coupled model intercomparison project (CMIP5/6), and four ocean reanalyses. Consistent with previous works, we find that Equatorial Pacific upwelling is sourced primarily from late-winter subduction in the extratropical eastern exchange windows. We also find that climatological dynamical fields dominate the probability distribution maps linking extratropical subduction with upwelling in the CT. Variations across CMIP5/6 models and between CMIP5/6 models and reanalyses consistently point to poleward shifts of both the south- and north-eastern exchange windows into colder extratropical waters as a likely key contributing factor to the CT bias, which, due to the strong meridional SST gradients in the extratropics, can drive CT biases even with no extratropical SST biases. Cool biases in the northern extratropics, which partially overlap with the north-eastern exchange window, also contribute to the CT bias. Trajectory duration varies considerably across models and between models and reanalyses, but is not consistently related to the CT bias

Quorum sensing-based biosensors for monitoring bacterial populations in aquaculture

D. Aizman - aizmandaniel@gmail.com (1,2), R. Ben Israel (1), L. Androsiuk (1,2), S. Tal (2)
1) Marine Biology and Biotechnology Program, Department of Life Sciences, Ben-Gurion University of the Negev, Eilat Campus, Israel
2) Israel Oceanographic & Limnological Research Ltd., National Center for Mariculture, Eilat, Israel

The growing demand for farmed fish and the exhaustion of open-sea fishing resources have driven the development of intensive aquaculture methods in land-based ponds. However, these intensive farming practices are highly vulnerable to disease outbreaks, necessitating constant monitoring of pond conditions. The current monitoring systems are effective in tracking physical and chemical parameters, but there is a need for real-time detection of biological contaminants. To address this gap, our research focuses on developing biosensors that utilize quorum-sensing molecules to monitor pond bacterial populations. These sensors are engineered to activate reporter gene expression, enabling the detection of various quorum-sensing compounds. Our goal is to incorporate these biological sensors into a microfluidic device for continuous, real-time monitoring of bacterial populations.

We demonstrated proof-of-concept sensors for Gram-negative Vibrio and *Pseudomonas aeruginosa*, and now extending the work to Gram-positive *Bacillus subtilis. B. subtilis* quorum sensing involves the ComX pheromone, which is post-translationally processed by ComQ to become active. When the extracellular concentration of ComX reaches a threshold, it activates the transcription factor ComA via a cascade of biochemical reactions. ComA controls the expression of ComX and ComQ as positive feedback. I will present our cloning strategy, replacing ComQ with GFP, and preliminary results for *B. subtilis*. As part of this effort, I designed a plasmid with overlapping regions for assembly and a GFP gene for fluorescence-based reporting. The plasmid was successfully assembled and is now being used in our biosensor development.

Consistent nonlinear stochastic evolution equations for wave shoaling source term implementation in WaveWatch-III

A. Akivis - alonlopo@gmail.com (1), T. Vrecica (2), I.-Y.Toledo (1)
1) School of Mechanical Engineering, Tel Aviv University, Israel
2) Mathematical Institute, Serbian Academy of Sciences and Arts, Serbia

Accurate prediction of wave dynamics in shallow and intermediate waters is critical for coastal engineering, environmental management, and civilian pleasure activities. While linear wave models can predict deep-water conditions effectively, they often fall short in regions where nonlinear interactions become significant. Nonlinear interactions such as triad wave interactions, particularly during shoaling, play a crucial role in the evolution of the wave spectrum and the generation of infra-gravity waves. In this work, we extend the third-generation spectral wave model WAVEWATCH III (WW3) by implementing a nonlinear source term based on the triad interaction formulation derived in Vrecica and Toledo (2016) (hereinafter referred to as CDB model). This formulation captures the triad wave interactions, providing an improved representation of energy spectra evolution during wave shoaling. The model was tested across various benchmark cases and compared to previous deterministic models and measurements. Our enhanced WW3 model demonstrated an ability to simulate wave triad interactions, particularly in intermediate water depths, where nonlinear interactions play a critical role in spectra evolution. This study demonstrates the potential of implementing the CDB model into widely used ocean wave models, enhancing their ability to provide a more realistic representation of coastal processes and improving the overall results.

Elucidating mechanisms of bacterial pathogenicity towards Emiliania huxleyi

N. Albocher-Kedem - nitsan_ak@weizmann.ac.il, T. Sharon Nir-Zadock, B. Dassa, A. Vardi

Phytoplankton are unicellular, photosynthetic microorganisms that dominate the ocean's primary production. The cosmopolitan coccolithophore *Emiliania huxleyi*, a unicellular eukaryotic alga responsible for some of the most significant oceanic algal blooms, covers thousands of square kilometers and plays a vital role in the global carbon and sulfur cycles. Sulfitobacter D7 was isolated from an *E. huxleyi* bloom in the North Atlantic and exhibits a lifestyle switch from mutualism to pathogenicity, which is presented in algicidal effects against *E. huxleyi* upon co-culturing. However, little is known about the bacterial molecular mechanism of pathogenicity against the algae. In our attempt to reveal this molecular switch, we constructed a transposon mutant library of Sulfitobacter D7. Then, we tested these mutants for changes in their virulence toward *E. huxleyi* by conducting a high throughput screening of co-culture dynamics. We found several exciting candidate genes involved with the virulence of Sulfitobacter D7 toward *E. huxleyi*. Studying the molecular basis for alga-bacterial interactions will provide insight into the ecological significance of these interactions in determining cell fate in algal blooms and how it may control the fate of carbon and sulfur in microbial food webs.

Monitoring the epilithic algae and cyanobacteria of lower jordan river

A. Alster - alster@ocean.org.il (1), R. N. Kaplan-Levy (1), E. A. Ben-Orr (1) and S. Barinova (2)
1) Israel National Culture Collection of Algae (INCCA), Kinneret Limnological Laboratory, Israel Oceanographic & Limnological Research, Israel
2) Institute of Evolution, University of Haifa, Israel

The Epilithic community of algae and cyanobacteria from Lower Jordan has been monitored since 2021 with the aim of studying the species diversity and estimating the ecosystem status. Monthly samples were collected from eight stations, starting at Lake Kinneret outflow and extending south till Menahemia. The epilithic biofilm was scraped off stones from each station and identified using light microscopy. From 2024 onwards, scanning electron microscopy was also employed to identify diatom populations in the biofilm. During the study period, about 100 epiphytic species were identified in the river. The river's epilithic community primarily consisted of *Cyanobacteria, Bacillariophyta, Ochrophyta*, and *Chlorophyta*, while *Charophyta, Euglenozoa*, and *Miozoa* species were occasionally found in the northern stations, carried by the flow from Lake Kinneret. In addition, seasonal variations were observed: while the summer-autumn period was characterized by a high presence of Cyanobacteria, Ochrophyta, and Chlorophyta species, the winter-spring period was dominated by *Bacillariophyta*. The spatial distribution of epilithic populations along the stream showed that *Heterococcus* sp. (Ochrophyta), *Tapinothrix janthina*, and *Chroococcidiopsis* sp. (Cyanobacteria) were present at all sampling stations and appeared typical of the Lower Jordan ecosystem. Bioindicator species of brackish water, such as *Uronema confervicola*, *Ulva torta* (Chlorophyta), and *Entomoneis paludosa* (Bacillariophyta), were observed only after the Saline Water Carrier entered the river. Estimation of the organic water pollution along the river using algae and cyanobacteria as bioindicators show an increase in pollution levels as the water flow moves further from Lake Kinneret.

The effect of the organic plasticizer TXIB on the coral *Stylophora pistillata*

M. Am-Shalom - maiams@post.bgu.ac.il (1), R. Kanfy-Weinberger (1), E. Winter (2) and A.Kushmaro (2)
1) Department of Civil and Environmental Engineering, Ben Gurion University
2) Avram and Stella Goldstein-Goren Department of Biotechnology Engineering, Ben Gurion University

Many organic pollutants have been reported entering the Gulf of Aqaba (GoA), possibly affecting reef health. To assess possible effects of common micro pollutants we sampled pore water in a number of sites and carried out analyses using gas chromatography-mass spectrometry. (GC-MS) analysis revealed a number of contaminants including 2-ethylhexanol, 2,4-dimethylbenzaldehyde, and 2,2,4-Trimethyl-1,3-pentadiol-diisobutyrate (TXIB) a plasticizer, were frequently found in the GoA. This leads to the question does TXIB affect the local fauna. We exposed planulae of the common coral *Stylophora pistillata*, under controlled laboratory conditions, to assess possible effects of exposure to TXIB. Ten planulae were maintained in glass petri dishes each with different concentrations (0.01, 0.1, 1 ppm) of TXIB in AFSW (Artificial Filtered Sea Water), at 19oC. Due to poor solubility in seawater, TXIB was solubilized in DMSO. An additional ten planulae were maintained in AFSW with DMSO as control at the same temperature. Three days after exposure, effects were assessed using fluorescence and transmission electron microscopy (TEM). Effects included bleaching degradation of chloroplasts, notably the thylakoid membranes, indicates oxidative stress and metabolic dysfunction within coral cells. This research contributes to understanding the risks posed by SGD pollutants and provides valuable insights to guide future conservation efforts in marine environments experiencing similar stressors from human activities.

Insights into microbial dispersal, abundance and viability in sea-spray aerosols across the East Mediterranean Sea

B. Ankri - Benankri818@gmail.com, E. Rahav and B. Herut

Sea spray aerosols (SSA) are known to play a significant role in transporting microbes and other cells over long distances. Limited knowledge exists regarding the environmental and biological factors that govern the survival of these microbes after being deposited back in surface oceans. Here, we generated SSA using a bubble-bursting experimental system and investigated the abundance and viability of its respective airborne prokaryote. To this end, surface water was pumped continuously along a natural trophic gradient in the Levantine Basin, Eastern Mediterranean Sea onboard the RV Meteor (cruise M197), as well as under laboratory settings using different water 'types' (e.g., oligotrophic vs N+P enriched). Overall, airborne microbes in the sea-spray ranged from 1.2×10^4 to 66×10^4 cells m^{-3}, with viable cells ranging from ~5-33% (median ~21%). The degree of viable cells followed the natural oligotrophic gradient typically found in the Levant, with a low percentage of viable cells found in ultra-oligotrophic locations south of Cyprus (median ~14%) that gradually increased till Sicily (median ~21%). In agreement, laboratory experiments showed that airborne bacterial productivity was ~50% higher in eutrophic water compared to oligotrophic. Our results provide insights into the factors enabling the viability of airborne bacteria emitted via sea spray.

Pollutant concentrations in urban runoff during rainfall events in the gulf of eilat

R. Armoza-Zvuloni - rachel@adssc.org (1), R. Shem-Tov (1), S. Kan (1), G. Antler (2), T. Rivlin (3), T. Mass (4), Z. Zemah Shamir (4), S. Zemah Shamir (5)

1) Dead Sea and Arava Science Center, Yotvata
2) Department of Earth and Environmental Sciences, Ben-Gurion University of the Negev, Be'er Sheva, Israel. The Interuniversity Institute for Marine Sciences, Eilat, Israel
3) The Interuniversity Institute for Marine Sciences, Eilat, Israel
4) Morris Kahn Marine Research Station, The Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel
5) Reichman University, Herzliya, Israel

The coral reefs in the Gulf of Eilat have been shown to exhibit high resilience to stress conditions. However, increased variability and intensity of stressors could irreversibly damage the reefs. Some of the stress factors threatening the reef ecology stem from the city of Eilat's proximity. A major threat to the ecosystem is pollutant enrichment. One significant untracked source is urban runoff, which flows into the Gulf during rain and flood events. In this study, we monitored rain and flood events. We measured rain intensity and sampled runoff at 12 sites along the shoreline prior to its entry into the Gulf during three rainfall events, then characterized the composition and concentration of pollutants. We found that pollutant concentrations in urban runoff changed as the rainy season progressed. In the first event following summer, concentrations of metals, nutrients, and particulate matter were at their highest, then declined in subsequent events. Average nitrogen concentrations reached 920 µM in the first event, then dropped to 570 and 180 µM in the second and third events, respectively. Similarly, lead ranged from 90 to 40 µg/L, copper from 120 to 25 µg/L, and chromium from 110 to 40 µg/L. Particulate matter ranged from 5 to 3.3 g/L, with 15 to 11% organic content. High concentrations of nitrogen and metals in runoff entering the Gulf may weaken the ecosystem's resistance to stress, particularly with rising water temperatures. To better estimate pollutant levels, assessing runoff generation potential under different storm scenarios is essential.

Koinonema galileica spec. nov. (Oscillatoriales): a newly identified cyanobacterium invading the benthos of lake kinneret

R. N. Kaplan Levy (1), A. Alster (1), **E. Arogety Ben-Orr** - emily.bo@ocean.org.il (1) and J. Kaštovský (2)

1) Israel National Culture Collection of Algae (INCCA), Kinneret Limnological Laboratory, Israel Oceanographic & Limnological Research, Israel.
2) Department of Botany, University of South Bohemia, České Budějovice, Czech Republic.

In this study, we report the identification and characterization of a novel cyanobacterium from the order Oscillatoriales, *Koinonema galileica* spec. nov., that invaded the benthic zone of Lake Kinneret in May 2023. This species was first observed along the littoral zone of the southwestern Lake Kinneret shores, slowly expanding to the lake outflow all the way to the Lower Jordan River. Since then, it was observed also in the northwestern shores up to Tabha in January 2024. Specimens were isolated from several locations and subjected to comprehensive morphological and genetic analyses. Microscopical examination revealed blue-green, homogeneous granulate trichomes. The central part of the filament was wider, with cells that were distinctly wider than they were long, measuring 8.4-10 (up to 12.2) µm in width and 3.0-5.6 (up to 6) µm in length. Amplification and sequencing of the 16S rRNA revealed that this species belongs to the genus *Koinonema* with 99% identity, its intragenic space (ITS) contains two tRNA sequences and it shares only 96.6% with the holotype species *Koinonema pervagatum* B. Buch et al, 2017. The genetic potential to produce cyanotoxins was tested and found negative for the hepatotoxins cylindrospermopsin and microcystin, and the neurotoxin anatoxin-a. The occurrence of benthic cyanobacterial blooms has not been recorded in Lake Kinneret for at least a decade. The bloom that emerged at the end of May 2023 and persisted for several months highlights the need for research on the phytobenthos of Lake Kinneret, a subject that has not been explored since 1974.

Influence of temperature on cyanobacteria-cyanophage interactions

L. Arsenieff - l.arsenieff@live.fr (1) and D. Lindell (1)
1) Faculty of Biology, Technion - Israel Institute of Technology

Over recent decades, studies have demonstrated the effect of temperature on virus-phytoplankton interactions. Variations of this abiotic parameter can dramatically alter the outcomes of their interplay, involving changes in host susceptibility, infection properties, or even in viral-life strategy. Elucidating how temperature is involved in the control of host-virus interactions is thus of prime importance. In marine systems, cyanobacteria of the genera Prochlorococcus and Synechococcus are substantial contributors to primary production. The cyanophages that infect them are considered to be the main drivers in their mortality, diversity, and evolution. Despite the ecological importance of cyanophages, their responses to temperature have not been examined to date. Here we report on the interplay between cyanobacteria and their phages as a result of changes in this environmental variable, with experiments performed at 17°C, 21°C, and 26°C. Infection dynamic experiments showed that temperature impacted the viral cycle of a cyanophage, with a latent period twice as long at the lowest temperature compared to the highest temperature. We further investigated the influence of temperature on the host-range of cyanophages. We observed distinct changes in infection patterns, with several *Synechococcus*-cyanophage systems displaying shifts in resistance/sensitivity when grown at different temperatures. Interestingly, temperature did not affect the Prochlorococcus-cyanophage interactions tested. Our study reveals that temperature can affect virus-host systems at different levels and that the effects vary between interactions. Our findings raise questions on the mechanisms involved in the resistance/sensitivity shifts and how temperature influences them.

Recycling of crop waste through growth of black soldier fly larvae: A sustainable source for fish feed

M. Arumugam - arummani@post.bgu.ac.il (1, 2), G. Atieno (1), M. Gulwe (1), P. Odoyo (1), G. Winters (3), D. Zilberg (2) and S. Penno-Winters (1)
1) Central and Northern Arava R&D,
2) Ben Gurion University
3) Dead Sea and Arava Science Center

Utilizing agricultural crop waste to cultivate black soldier fly (*Hermetia illucens*) larvae (BSFL) presents a sustainable and circular solution for waste management and aquaculture nutrition. Including BSFL in fish diets aligns with sustainable aquaculture practices, reduces reliance on overfished marine resources, and lowers the environmental impact of feed production. Moreover, BSFL not only supports sustainable fish production but also contributes to global food security by enhancing the efficiency of waste-to-feed conversion systems. BSF larvae grow on various organic waste materials, including crop and plant residues, efficiently reducing the waste into dense, nutrient-rich compost. Our studies support that different agricultural wastes affect BSFL growth rates and larvae proximate compositions. The protein and lipid-rich BSFL meal has shown remarkable potential as a fish feed ingredient, containing essential amino acids, fatty acids, and minerals, all crucial for optimal fish growth and development. In feeding trials incorporating up to 20% BSFL meal, we showed that the growth of Nile tilapia (*Oreochromis niloticus*) was supported with no adverse effects. Beyond its nutritional values, BSFL are rich in bioactive compounds such as lauric acid, which have been proven to have anti-microbial properties and enhance immune function. Metabolites, like lauric acid and antimicrobial peptides, play a pivotal role in boosting fish health by strengthening their innate immune defense, promoting gut health, and reducing susceptibility to bacterial and parasitic infections. BSFL extracts have been shown in our studies to suppress bacterial and fungal growth, including Streptococcus iniae, a common bacteria causing infections in tilapia.

Micritization in the Persian Gulf – Abu Dhabi: Chemical precipitation or physical boring activity?

A. Ash - almog.ash@mail.huji.ac.il (1), A. Torfstein (1, 4), G. Antler (2, 4), T. Cao (3), T. Rivlin (4), M. Alsuwaidi (3), S. Morad (3), B. Lazar (1), M. Stein (1)

1) Institute of Earth Science, Hebrew University of Jerusalem, Edmond J. Safra Campus, Givat Ram, Jerusalem 9190401.
2) Department of Earth and Environmental Sciences, Ben-Gurion University of the Negev, David Ben Gurion Blvd 1, Beer-Sheva 8410501
3) Department of Petroleum Geosciences, Khalifa University, Abu Dhabi, Post Box: 127788.
4) The Interuniversity Institute of Eilat, Eilat 8810302

The solidity and porosity of calcium carbonate rocks are of great interest in fields such as reservoir evaluation, groundwater flow, and civil engineering. Micritization (an early diagenetic process converting carbonate shells and skeletons into micro-grained carbonate) affects these rocks characteristics, though its exact mechanisms are poorly understood. The coastal environments of Abu Dhabi provide “natural laboratories” to study micritization, as they resemble the low-angle calcium carbonate ramps that were widespread in epeiric seas during the geological past. In this study, we examine calcium carbonate mud and correlating porewater from a variety of depositional environments such as mangroves, tidal channels, sabkhas, and offshore locations to better understand micritization. To tackle this problem, we are employing sedimentological, mineralogical, and various geochemical methodologies. Preliminary results show that most of the calcium carbonate mud is composed of low-magnesium calcite, with little to no aragonite. This finding contrasts with other studies on calcium carbonate ramps in which the carbonate mud is comprised of high-magnesium calcite. Micritization increases with depth, particularly in tidal channels, and is associated with physical erosion by endolithic fauna. Crystal structures in the sabkhas indicate that chemical precipitation is more prevalent there. The porewater in all sampled environments shows a distinct DIC to alkalinity slope of 1, suggesting that chemical processes such as calcium carbonate precipitation/dissolution in an open system, sulphate reduction/sulphide oxidation, etc., are occurring alongside the physical boring activity. Mass balance and thermodynamic simulations are conducted to identify and quantify the possible geochemical processes.

A matter of choice: The interactions between foraminifera and their seagrass host, *Halophila stipulacea*

J. Masawa (1, 2), G. Winters (1, 3), M. Kaminer (1), A. Szitenberg (1), M. Gruntman (2) and **S. Ashckenazi-Polivoda** - sarit@adssc.org (1, 3)

1) The Dead Sea and Arava Science Centre, Masada National Park, Mount Masada, Israel
2) School of Plant Sciences and Food Security, Porter School of the Environment and Earth Sciences, Tel Aviv University, Tel Aviv, Israel
3) Eilat Campus, Ben-Gurion University of the Negev, Eilat, Israel

Seagrasses and foraminifera serve as essential bioindicators for monitoring marine ecosystems. Seagrass meadows, like those formed by *Halophila stipulacea*, play a vital role as ecosystem engineers and in blue carbon sequestration. In sub/tropical waters, benthic foraminifera are among the most abundant epiphytic organisms inhabiting seagrass meadows. Yet, their ecological interactions with seagrasses remain understudied. This study explored the association between foraminifera and the tropical seagrass species *H. stipulacea*, aiming to determine whether these interactions are facilitative or random. For this, we performed a "choice" experiment, where foraminifera offered a choice to settle on *H. stipulacea* plants or plastic "seagrasses" plants in both roots and shoots. Seagrass and sediment samples from the Gulf of Aqaba-Eilat were planted in mesocosms and controlled for salinity (40 ppm), light (100 µmol photons m^2/s), and temperature (25°C). Over 30 days, plants were analyzed for foraminiferal settlement. At the end of the experiment, a microbiome analysis was performed to identify possible variances in the microbial community and diversity of the substrates. Results showed significantly higher foraminiferal abundance and diversity on *H. stipulacea* than plastic plants, particularly older shoots. Microbiome analysis revealed that *H. stipulacea* supported a richer microbial community than plastic substrates, with older shoots correlating to higher foraminiferal abundance, possibly due to biofilm richness. These findings suggest a facilitative relationship between *H. stipulacea* and foraminifera, likely mediated by the microbial diversity on seagrass surfaces. This study highlights the need to protect seagrass meadows, which support foraminiferal diversity, especially as global changes threaten these critical ecosystems.

Long-term wave climate statistics in Eilat

D. l. Bar (1), **S. Asher** - shaiashe@technion.ac.il (1), A. Levin (1), M. Sladkevich (1)
1) Israeli Coastal and Marine Engineering Research Institute (CAMERI)

Until now, no long-term wave-climate statistics of the northern Gulf of Eilat have been reported in the literature. This study, conducted by the Israeli Coastal and Marine Engineering Research Institute (CAMERI), presents a first-of-its-kind analysis of the northern Gulf of Eilat's wave climate, incorporating in-situ measurements, numerical modeling, and literature surveys. Wave measurement in Eilat began in 2021 (National Monitoring Program at the IUI) using a single pressure sensor, followed by the deployment of a directional Datawell buoy in April 2023 by CAMERI. The measurements show that waves exceeding a height of 0.3-0.5 m are primarily generated by southern winds, most of which occur between October and April. During its 1-year deployment, CAMERI's buoy recorded five events with a significant wave height (Hm0) above 0.5 m. Since the measurement data only cover a few years, they are insufficient to underpin long-term statistics. Instead, the data were used to calibrate a WAVEWATCH III® hindcast model, powered with COPERNICUS ERA-5 re-analysis winds, which was then used to synthesize a 21-year wave time series. 118 events with Hm0 of at least 0.9 m were identified in the modeled time series with an average duration of 35 hours. The model generated five events with wave heights above 2 m and a peak wave period of ~7-9 s, four of which were observationally reported in the literature. The most extreme event (Hm0=4.5 m) occurred on 13.03.2020. While wave events over 0.5 m are infrequent, significant storms do occur, with potential implications for coastal management in the region.

Seaweeds of the Israeli Seas: exploring ecological and biotechnological potential

D. Y. Ashkenazi - doronashkenazi1@gmail.com (1,2), A.r Abelson (1, *), Á. Israel (2, *)
* Equal contribution
1) School of Zoology, Tel Aviv University, Ramat Aviv, Tel Aviv-Yafo 69978, Israel.
2) Israel Oceanographic & Limnological Research Ltd. (PBC), Tel Shikmona, P.O. Box 9753, Haifa 3109701, Israel.

Marine macroalgae (seaweeds) have developed unique bioactive compounds that have enabled their survival for millions of years, holding great potential for human benefits. For the Israeli Mediterranean Sea however, no systematic ecological surveys of seaweeds have been published since the late 1990s, and chemical analyses of local species are limited. This study presents a long-term ecological survey of natural seaweed populations along Israel's intertidal coastline, examining biodiversity and spatial-temporal dynamics. Additionally, it provides a seasonal chemical analysis of local dominant seaweed species, assessing their nutritional and health-associated metabolites.

The survey covers six sites, including the Mediterranean Sea and Eilat, with 350 specimens collected, identifying 60 species. A notable bloom was observed only during the spring season. Seasonal variations significantly impacted the seaweeds chemical composition, though the trends were not consistent across all species. Generally, higher protein content was found during winter, while antioxidant capacity peaked in spring. Phenolic compounds and sunscreen molecules did not show clear seasonality.

These results suggest optimal harvesting seasons and ideal growth conditions for specific compounds, highlighting the sustainable potential of seaweeds for aquaculture and biotechnology.

An innovative sustainable aquaculture technology will also be presented, demonstrating how the nutritional and medicinal value of seaweeds can be controlled and enhanced.

In summary, we hypothesize that the extreme abiotic conditions along the Israeli Mediterranean shoreline may foster unique regional seaweeds with distinct chemical characteristics. These qualities could be harnessed for superfood, cosmetic, nutraceutical, and pharmaceutical applications, particularly in the context of sustainable resources in times of climate change.

The statistics of Eastern Mediterranean Sea currents

Y. Ashkenazy - ashkena@bgu.ac.il (1), H. Gildor (2), A. Solodoch (2)
1) Department of Environmental Physics, BIDR, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, Israel
2) The Institute of Earth Sciences, The Hebrew University of Jerusalem, Israel

We examined the probability density function (pdf) of current speeds in the Eastern Mediterranean Sea, near the central coast of Israel. The currents cover depths from the surface to over 1.3 km and span a time period from November 2016 to December 2019. We estimated the parameters of three typical distributions that are usually used to model the pdfs of currents and wind speed; the investigated pdfs are the Weibull, the General Extreme Value, and the Generalized Gamma distributions. We find that the three-parameter Generalized Gamma distribution best describes the pdfs of the speed-measured currents. We also find that the distribution parameters at the abyssal ocean (more than 1 km) are different than those of shallower depths, possibly pointing to a decoupling of the abyssal levels from the upper part of the ocean. Comparison of the measured current speed pdfs to current speed pdfs of high resolution (1 and 3 km) general circulation model (ROMS) simulations point to significant discrepancies. We show that these discrepancies are rooted in the low frequencies of the model's currents.

Algae4IBD-Algae as a sustainable source for functional food bridges the realms of health and tenvironment

D. Avni - avnidorit@gmail.com (1)

1) MIGAL Galillee Reaserch Institute

The consumption of Western diets, characterized by highly processed, high-sugar, and high-fat foods, has been linked to disruptions in gut microbiome composition and the onset of chronic inflammation, a key driver of non-communicable diseases (NCDs) as Inflammatory Bowel Disease (IBD)1. Additionally, with global challenges such as climate change and food security concerns, transitioning toward sustainable and health-conscious diets becomes imperative2, aligning individual well-being with environmental stewardship.

The EU-founded Algae4IBD project, composed of 21 partners, underscores the pivotal role of microalgae and macroalgae-based extracts as an unparalleled source of bioactive compounds endowed with anti-inflammatory, antioxidant, and prebiotic properties3,4. Algae4IBD consortia created the Algae4IBD bank, a diverse repository of 150 microalgae and macroalga, prepared various extracts (including ethanol, ethyl acetate, hexane, and water-based extracts), and rigorously screened them for their multifaceted bioactivities, encompassing anti-inflammatory, antioxidant, prebiotic, and antimicrobial effects.

Key pro-inflammatory cytokines, Tumor Necrosis Factor-alpha (TNF-α) and Interleukin (IL)-6, central in chronic inflammation and IBD pathogenesis, were the focus of assessment properties by cell-based analysis in both prevention and treatment models, alongside complementary health-related attributes. Promisingly, several microalgae and macroalgae-based extracts exhibited potent anti-inflammatory properties, offering potential in both the prevention and treatment of inflammation. Concurrently, these extracts displayed prebiotic, antimicrobial, and antioxidant activities, reinforcing their holistic health potential.

Interestingly, some of the promising algae are commercially available, and some are understudied. We have further fractionated the promising algae in order to identify the active compounds leading to new discoveries.

In summary, these findings highlight the profound and compelling bioactivity of microalgae and macroalgae. These extracts are powerful agents that mitigate inflammation, fortify gut health and preserve microbiome homeostasis.

The incorporation of these extracts into daily food products emerges as a promising strategy to mitigate chronic diseases while safeguarding the delicate balance of our planet's ecosystem.

This research bridges the realms of health and environmental responsibility, offering a compelling narrative for sustainable, health-enhancing diets.

Unraveling the Role of the Immune System in Coral Bleaching

E. Azarov - elenaaza@post.bgu.ac.il (1), S. Barkan (1), S. Talica (1), O. Gershini-Yahalom (1), B. Rosental (1)
1) Ben Gurion University of the Negev, The Shraga Segal Department of Microbiology, Immunology and Genetics

Coral reefs are an important ecosystem, supporting the ocean's biodiversity by harboring a quarter of all marine life.

Corals are marine animals in the subclass Hexacorallia. They live in a symbiotic relationship with an intracellular algae that provides most of the nutrients they need to survive. When exposed to heat stress the coral cells expel the algae living within them, a phenomenon known as coral bleaching. If the warm temperatures persist, the algae won't re-enter the coral cells, potentially leading to its death.

There are theories that during heat stress, the algae produce reactive oxygen species (ROS), harming host tissues until being expelled. However, we found that during heat-stress induced bleaching the immune activation markers ROS and Nitric Oxide (NO) are elevated in phagocytic cells of an Hexacorallian model; symbiotic and apo-symbiotic sea anemone *Exaptasia diaphana* (*E. diaphana*). These results suggest that the immune cells are at the base of ROS and NO induction, which could lead to the bleaching phenomenon.

Furthermore, with our development of cellular algae intake assay with apo-symbiotic E. diaphana cells we demonstrate that during heat stress the endosymbiosis process is being inhibited, compared to the phagocytic activity that is shown to be elevated.

Elucidating the relationship between virus infection and cell-cycle regulation in marine diatoms

L. Bamshid - linoybamshid@gmail.com (1), A. Tzur (1), D. Spungin (1), C. F. Kranzler (1)

Diatoms are a diverse group of eukaryotic phytoplankton, contributing ~20% of photosynthesis on Earth and forming the base of marine food webs. Distributed across a wide range of oceanic regimes, from coastal to offshore waters, diatoms translate diverse environmental signals to efficiently regulate cell-cycle progression and cell division in the water column. Diatoms are also infected by an enigmatic group of RNA viruses, yet how these viruses shape diatom bloom dynamics and community structure is poorly understood. While there is substantial evidence that viruses can alter the cell-cycle in mammalian and plant systems, how virus infection might interface with cell-cycle progression in diatoms is unknown. Here, using the model bloom-forming, centric diatom, Chaetoceros tenuissimus and the RNA virus, CtenRNAV, we found that virus infection substantially remodels cell-cycle phase distribution, generating a higher proportion of S and G2/M phases. CtenRNAV infection was also accompanied by transcriptional shifts of multiple cell-cycle related host genes, apparent within a day post infection. In addition, we measured faster virus replication in cultures which were artificially arrested at S and G2/M phase, suggesting that specific phases of the cell cycle are more permissive to the CtenRNAV virus life cycle. Consistent with prior studies, we also found that cell-cycle progression in C. tenuissimus is regulated by both light and silicon limitation, resulting in a G1/S and S phase arrest, respectively. Together, these findings provide insight into the interplay between virus infection and cell-cycle regulation in diatoms, advancing our understanding of how viruses might interface with diatom bloom dynamics across diverse environments in the ocean.

The hunger games – a glimpse into larval fish prey capture behavior in-situ in aquaculture

S. Bar - shirbar@tauex.tau.ac.il (1, 2), L. Levy (2), S. Avidan (3), and R. Holzman (1, 2)
1) School of Zoology, The George S. Wise Faculty of Life Sciences, Tel Aviv University
2) The Interuniversity Institute for Marine Sciences in Eilat
3) School of Electrical Engineering, The Iby and Aladar Fleischman Faculty of Engineering, Tel Aviv University

Larval fish rearing is a sensitive and expensive stage in the fish production chain, requiring close monitoring of the fish environment and costly live feed. Nevertheless, larval survival rates remain low (<30%) even under optimal conditions.

Basic research implicated the inefficient feeding behavior of early-stage larval fish as a potential driver of this mortality. However, how this behavior is affected by variations in environmental conditions is poorly understood. Monitoring larval feeding in aquaculture is traditionally done by indirect methods (e.g., gut content analysis) which provide no insight into the underlying physical and behavioral mechanisms.

We investigated age-dependent effects of temperature, pH, and O_2 on larval fish feeding by filming in situ in rearing pools at the Ardag Hatchery, Eilat. We tracked these parameters and the prey strike rate for 17 cohorts of Sparus aurata larvae throughout their ontogeny; collecting 268 high-speed videos (each >5 minutes). We then constructed an AI-based pipeline to detect feeding strikes within this massive dataset.

In the pools, strike rates were similar and low across age groups, irrespective of pH and oxygen levels, but increased significantly with increasing temperature. When compared to the strike rates observed in the laboratory, the rates in the pools were ~50% lower.

From an applied perspective, our AI pipeline for identifying feeding strikes far surpassed the performance of manual analysis, both in terms of time efficiency and in feeding event detections. The tool is now being further developed to help investigate larval fish feeding behavior at larger scales.

Freshwater diazotrophy at the global scale: From abundance, N_2 fixation rates and diversity to the factors that control them

E. Bar-Zeev - edobarzeev@gmail.com (1)

1) Zuckerberg Institute for Water Research, The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sde Boker Campus, 84990, Israel

New evidence and previous estimations indicate that dinitrogen fixation by diazotrophs may play a central role in the freshwater biosphere along the ecological scales. And yet, little is currently known on freshwater DIAZOTROPHY, namely the diversity, abundance, and N_2 fixation rates across the global freshwater ecospace, while even less is known on the environmental factors that control them. This research was based on a comprehensive global sampling effort by a scientific network and state-of-the-art analytics. Each partner received a costume-made sampling kit that was sent back to BGU to Quantify the number of diazotrophs via a new immunolabeled flow-cytometry approach, (ii) Identify the diazotrophs via MiSeq of the nifH gene and (iii) Measure N_2 fixation using the $15N_2$ technique. Our lates results from the global freshwater ecospace indicate that the number of diazotrophs is highly variable (<5 x1010 L-1), yet generally less than 12% of the total bacterial count. N_2 fixation rates were overall low, yet few hotspots were located with rates ranging from 10-50 nmol L-1 d-1. These N_2 fixers were highly diverse (α diversity up to 7.5) and often dominated by non-cyanobacterial diazotrophs. It could be deduced that freshwater diazotrophy is highly dynamic and is significantly impacted by the surrounding land use. Altogether, these global results and corresponding insights highlight the need to further delve into the spatiotemporal contribution of diazotrophy to freshwater primary and secondary productivity at the global scale.

Unveiling the microbiome of *Rhopilema nomadica*: from broad-scale patterns to endozoicomonas genomic insights

N. Barak - barak.noga22@gmail.com (1), T. Lotan (1) and D. Sher (1)
1) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel

Jellyfish blooms are a worldwide phenomenon, impacting marine ecosystems and human activities on a broad scale. Jellyfish blooms often disappear rapidly, with the causes of their demise mostly unknown. To test whether the microbial population contributes to bloom demise, we characterized the microbiome of *Rhopilema nomadica*, the most common jellyfish in the Eastern Mediterranean Sea. We assessed changes during multiple seasons and stages of the bloom, examining them in light of natural variability across jellyfish tissues, sizes, and sexes.

We revealed that the *R. nomadica* microbiome is less complex than the surrounding seawater, with a small number of dominant taxa. Interestingly, seasonal shifts were observed. While the winter bloom was dominated by *Tenacibaculum*, the late bloom showed a shift toward Unclassified *Rickettsiales* and *Endozoicomonas*, accompanied by a significant decrease in diversity. Endozoicomonas, a prevalent cnidarian bacterium, has been mostly studied in coral, where its role is still debated, ranging from symbiotic to potentially pathogenic. Our 16S analysis revealed that the same Endozoicomonas ASV is present in multiple jellyfish species across diverse geographical locations, indicating a widespread distribution. Building on these findings, we isolated, sequenced, and assembled 11 complete *Endozoicomonas* genomes from different tissues of different *R. nomadica* individuals. These genomes provide a crucial resource for exploring the ecological roles of *Endozoicomonas* in jellyfish. We are currently investigating the potential functions of these genomes and comparing them with coral-derived strains. This will help us better understand how *Endozoicomonas* interacts with cnidarian hosts with possible implications for jellyfish bloom dynamics and broader cnidarian-microbe relationships.

Investigating the role of the immune system in coral bleaching

S. Barkan - barksh@post.bgu.ac.il (1), A. Azarov Hirsh (1), B. Rosental (1)
1) Ben Gurion University of the Negev

Rising seawater temperatures have increased coral bleaching events worldwide, an event in which the coral’s symbiotic algae is expelled. This bleaching effect is detrimental for coral reefs. Previous research on coral heat stress induced bleaching found that different immune genes were differentially regulated and suggested immune activation. This led to the assumption that the immune response is a consequence of bleaching. Previously, we discovered phagocytic immune cells in Hexacorallia, a subclass containing stony corals and sea anemones. Furthermore, these immune cells increased their activity when we exposed them to heat stress. We then aimed to separate the two processes of phagocytosis vs. algae intake for symbiosis. To test this, we have used a Hexacorallia model system: the sea anemone Exaiptasia diaphana – which can be reared with and without symbiotic algae. We developed a cellular algae intake assay to test the effects of heat stress on symbiosis. We saw that while exposure to heat stress increases phagocytic activity, that same stress reduces algae intake. We then asked whether activation of the immune system could lead to algae expulsion. To this end, we injected immune activators into whole polyps and measured algae expulsion. We found that immune activation on its own might cause algae expulsion similar to that of heat stress. Hence, our data provides the basis for further study into heat induced immune activation in corals and sea anemones. We aim to elucidate the mechanisms in which immune activation leads to the destruction of symbiosis between the host and their symbiotic algae.

Activation of GABA-B receptor signaling affects cilia tubulin post-translational modifications in the sea anemone *Nematostella vectensis*.

E. Beck - efratbeck95@gmail.com (1), T. Lotan (1),
1) University of Haifa

The cilium is a highly preserved organelle found in most eukaryotic cells. It plays a crucial role in the propulsion of fluids and the motion of aquatic organisms through its motile form. The cilium, composed primarily of microtubules, undergoes post-translational modifications (PTMs) such as acetylation, glycylation, polyglutamylation, and tyrosination, affecting its length, stability, flexibility, motility, degradation rate, and beating pattern. Defects in the cilia can lead to various illnesses and disorders in humans, collectively known as 'ciliopathies'. To study ciliogenesis, we utilized the sea anemone Nematostella vectensis as a model organism. At the larval stage, the planulae are covered in motile cilia which facilitate their mobility within the aqueous medium. Our research indicates that planula ciliogenesis is influenced by GABA-B receptor signaling. Exposure to the GABA-B agonist baclofen resulted in a reversible arrest of planula mobility, development, and metamorphosis. Transcriptomic analyses on baclofen-treated and untreated control planulae revealed changes in the expression of genes linked to ciliary structure and transport. Further analysis using specific antibodies against tubulin modifications demonstrated that the levels of certain PTMs were altered upon baclofen treatment. Subsequently, we propose N. vectensis as a potential evolutionary model for studying cilia development and modifications, leveraging its phylogenetic position within the Cnidaria group.

Influence of shelter level in breakwaters on coral survival and settlement

A. Ben Natan - almog100560@gmail.com (1, 2) and N. Shashar (1)
1) Marine Biology and Biotechnology Program, Department of Life Sciences, Ben- Gurion University of the Negev, Eilat Campus, Beer-Sheva 84105, Israel
2) The Interuniversity Institute for Marine Science, 8810302 Eilat, Israel

With the increasing global population and migration toward coastal regions, there is a rising demand for coastal urbanization, including the development of living spaces, ports, tourism infrastructure, and general coastal defenses. However, climate change, characterized by higher currents, waves, and increased storm frequency, poses a significant threat to man-made structures. Consequently, the need for effective coastal defense structures (CDS) is becoming increasingly urgent. Traditional CDS, typically composed of hard units designed to block and divert wave and current energy, often fail to support diverse and abundant marine communities due to their impact on current and sediment transport, the introduction of invasive species, and the loss of natural habitats. Nonetheless, reports of diverse marine communities on breakwaters and seawalls suggest that these structures may unintentionally function as artificial reefs.

This study examines the effects of location on coral communities within a breakwater, specifically investigating the relationship between protection and coral fragment survival, larval settlement, and water motion (flow speed) across three distinct niches: exposed, semi-sheltered, and sheltered. Coral survivability was assessed through fragment planting, while recruitment was monitored using ceramic tiles. Flow speed was measured across the defined niches to evaluate water motion dynamics. Additionally, concrete barrier structures were placed in Exposed niches to test whether artificially added protective elements could enhance coral fragment survival.

Results indicated that there was no difference in coral settlement between niches. Similarly flow speed remained consistent between Exposed and Sheltered niches due to vortex formation in the sheltered zones. Survival analysis revealed variability between niches, with the addition of artificial shelter barriers leading to the highest increase in coral fragment survival on the breakwater.

This study contributes to the development of methodologies aimed at enhancing coral survivability, potentially transforming artificial barriers into functional artificial reefs.

Intracellular calcification of coccolith calcite revealed by cryo electron tomography

O. Ben-Joseph - ozbenjoseph@weizmann.ac.il (1), L. Aram (1), K. Rechav (2), N. Varsano (2), A. Gal (1)
1) Department of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, 7610001, Israel
2) Department of Chemical Research Support, Weizmann Institute of Science, Rehovot, 7610001, Israel

Many marine organisms produce crystalline materials with great precision, producing nature's most elaborate mineralized structures. A hallmark of biologically controlled crystallization are coccoliths, the mineralized scales which cover the surfaces of coccolithophores - ecologically significant, unicellular marine phytoplankton group. The coccolith scales consist of uniform calcium carbonate crystals assembled into intricate species-specific crystal arrays. While crystal formation is known to take place intracellularly, it is unclear what factors regulate this intricate crystallization reaction. Here, we study the intracellular morphogenesis of holococcoliths by tracking the growth of coccolith crystals using in situ cryo electron tomography. In the method, cells are preserved at their native state by rapid vitrification and are imaged at this state with nanometric resolution. We show that crystallization takes place in a small vesicle environment, where forming crystals are associated only with a simple and clear solution. These finding indicate that holococcolith morphogenesis is primarily regulated by the vesicle solution chemistry and not by surface templating or membrane molding. Such mode of morphogenesis could be readily affected by shifts in seawater chemistry.

High-resolution redox dynamics and microbial metabolic responses to electron donor/acceptor gradients at the pelagic chemocline of Lake Kinneret

O. Bergman (1, 2, 3)

1) Kinneret Limnological Laboratory (KLL), Israel Oceanographic and Limnological Research (IOLR), Israel
2) Department of Earth and Environmental Sciences, Ben Gurion University of the Negev, Israel
3) Water and Environmental Research Center, University Alaska Fairbanks, Fairbanks, Alaska USA

The pelagic chemocline of thermally stratified and meromictic lakes delineates the interface between oxic-anoxic water layers and is characterized by sharp chemical gradients. In this dynamic environment, physiological adjustments to changes in electron acceptor/donor availability are critical for the survival of microorganisms with oxygen availability playing a significant role. The goal our study was to identify metabolic activities within the complex microbial community, at the pelagic chemocline of Lake Kinneret (LK) along the transition from oxic to anoxic conditions as a function of electron donor/acceptor concentration. We aimed to 1. monitored the time space evolution of the pelagic chemocline of LK by a novel high resolution syringe sampler, 2. Quantify relevant electron acceptors and donors in the vicinity of the chemocline by wet chemical analysis of the syringe samples and by parallel multiprobe measurements and 3. Quantify key functional gens at the chemocline of LK by molecular analysis of the microbial community collected via filtration of the syringe samples. Our results reveal exciting and often overlapping gradients of methane, oxygen, ORP, ammonium, nitrite, nitrate and sulfide - within the 1.6 m water column, sampled at a 10 cm resolution. Utilizing primers of various functional genes related to the methane, nitrogen, and sulphate cycles we show that changes in electron donor/acceptor concentration are reflected in microbial function. These findings highlight the intricate relationship between microbial metabolic activities and steep electron donor/acceptor gradients present at the chemocline at high resolution and provide new insights into the adaptive strategies of microbial communities.

"Location location location!" - The potential impact of hydrocarbon exploration in the Israeli Mediterranean on natural and socioeconomic assets

A. Pertzelan (1) and **I. Bernshtein** - iberensht@univ.haifa.ac.il (1)

1) Department of Marine Biology, Charney School of Marine Sciences, University of Haifa

The exploration and extraction of hydrocarbon resources in the Israeli Mediterranean Sea, particularly from fields like Tamar and Leviathan, pose significant environmental and socioeconomic risks. This study assesses the potential impact of hydrocarbon spills from six proposed exploration blocks, using advanced oil spill modeling techniques (OpenOil and OceanDrift) to simulate multiple scenarios. By analyzing the spread of oil and condensate under various seasonal conditions, we evaluate the risks posed to eleven critical natural and socioeconomic assets, including marine protected areas (MPAs), desalination plants, beaches, estuaries, and ports.

The results reveal that spills originating from Zone E, particularly Block E65, have the most substantial potential for damage, especially to coastal infrastructure and northern MPAs. The simulation also highlights the heightened risks during summer months and storm events, with crude oil posing more severe long-term impacts than condensate. Additionally, coastal desalination plants and aquaculture farms face prolonged exposure to oil concentrations that could significantly disrupt operations. Our findings emphasize the need for enhanced regulatory safeguards, including expanded exclusion zones and contingency planning, to mitigate the risks associated with offshore hydrocarbon development.

Fine-scale structuring of a southeastern Mediterranean jellyfish swarm

H. Berman - hadarberman@gmail.com (1), D. Malul (2,3), V. Verma (6), A. Solodoch (4), T. Lotan (5), D. Sher (5), R. Barkan (6), Y. Lehahn (1)

1) Department of Marine Geosciences, The Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel
2) Civil and Environmental Engineering, Technion IIT, Haifa, Israel
3) The Inter-University Institute for Marine Sciences, Eilat, Israel
4) Institute of Earth Sciences, The Hebrew University, Jerusalem, Israel
5) Department of Marine Biology, The Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel
6) Department of Geophysics, Tel-Aviv University, Tel-Aviv, Israel

Jellyfish pose significant threats to tourism, clogging desalination and power plants, and impacting ecosystems, including fisheries. Understanding their spatial distribution and swarm behavior is crucial for science-based sustainable coastal management. Although swarm behavior has been studied at various spatial scales, observing jellyfish distribution at the sub-mesoscale level is challenging. To date, it has been impossible to monitor them from space due to the relatively coarse resolution of satellites. In this study, we combine aerial imagery, satellite data, and numerical modeling to infer jellyfish swarm behavior at the sub-mesoscale level.

Over three consecutive days, flights captured images of jellyfish along the Israeli Mediterranean coast. These images were converted to jellyfish counts, creating a spatial map of jellyfish concentration for each day. Sentinel-3 satellite chlorophyll data was used as a proxy for the ambient (passive) flow. Particle tracking (OceanParcels) coupled with a regional oceanic model (ROMS) was used to compare our findings with a jellyfish swimming model developed previously for smaller scales.

Our results indicate that the heart of the jellyfish swarm is found approximately 2 km from shore, corresponding to regions where chlorophyll levels decrease to very low values. We found that the northward movement of jellyfish in the Mediterranean Sea is similar to that of chlorophyll away from shore, suggesting that their northward movement is predominantly driven by ambient flow. Finally, our model results suggest that in the sub mesoscale, jellyfish swimming differs from that found for short timescales.

The development of feeding behavior in gilthead seabream larvae

A. Bitan - amir.bitan@ocean.org.il (1) N. Mizrahi (1,2), L. Koch (1), M. Chacon (1), W. Koven (1), A. Tandler (1)
1) Israel Limnological & Oceanographic Research, National Center for Mariculture, P. O. Box 1212, Eilat 8811201 Israel
2) Department of Life Sciences, Ben-Gurion University of the Negev, Eilat, Israel

Regulation of feed intake is an interplay of both central and peripheral mechanisms. The aim of this study was to evaluate the age-related response to food of appetite regulators and feeding behavior in gilthead seabream (*Sparus aurata*) larvae by comparing it with the response in adults. This may shed light on the development of feeding behavior in larvae and if it responds to satiety signals during the critical period of larvae development, at the onset of exogenous feeding. Cocaine- and amphetamine-regulated transcript (CART) is a potent hypothalamic anorexigenic neuropeptide. We identified six paralogs of CART in seabream and evaluated the relationship between their expression, the expression of other genes related to appetite regulation and to successful feeding. By comparing larvae that were fed or not at 7 days post hatch (DPH) we found, prior to feeding, a significant and timely increase in the relative expression of several appetite regulating genes suggesting an anticipatory response of appetite regulation at this early life stage. Larvae behavioral response to the presence of prey was significant only from 5DPH and evaluation of successful feeding revealed an exponential increase in food consumption with larvae age from 3DPH. However, delayed first feeding from 3DPH to 8DPH was found to have a significant negative effect on successful feeding. We therefore identified three CART paralogs that can be used as common markers for satiety in both larvae and adult gilthead seabream that can be used to asses satiety levels in larvae at different habitats or in aquaculture facilities.

Distribution and uptake of urea by microbial community in the S. E. Levantine basin

Blachinsky, A., Ben-Ezra T., Tsemel, A., Gozali, S., Tchernov, D., Altabet, M., Berman-Frank, I., Krom M.D.

Urea is a potentially important bioavailable organic N compound which can be directly utilized by some photoautotrophs and/or remineralized to ammonia. In this study, the distribution of urea was determined in the upper water column of the S.E.Levantine basin during three consecutive periods: a thermally stratified oligotrophic period depleted in dissolved inorganic nitrogen (DIN) and phosphorus (DIP); temporary mesotrophy subsequent to a winter storm which injecting a major pulse of nutrients into the photic zone; decline in inorganic nutrients during the subsequent seasonal thermal stratification. Urea and dissolved inorganic nitrogen (DON) concentrations peaked during the winter period after Storm Carmel (Dec 2021) and decreased during the following summer. We show evidence of urea removal in the zone at the top of the nutricline, a zone of high nitrification rates, with increased urea below that depth. Our study showed that bioavailable nitrogen was predominantly taken up by the microbial populations in the following order ammonia>urea>nitrate, excluding immediately after Storm Carmel when the preferred utilization of nitrate>urea. The in-situ uptake ratio of inorganic C/Bioavailable N ranged from 1.5 to 4 while the measured C:N ratio was 8-10. We hypothesize that this discrepancy results from microbial utilization of dissolved organic carbon, not labelled by the spiked $NaH^{13}CO_3$, and thus not accounted for. The highest rates of in-situ uptake of bioavailable N was for urea, a significant component of the DON pool, which emphasises the importance of DON uptake as a source of N in the extreme inorganic nutrient depleted SE Levantine basin.

Characterizing the ocean data ecosystem - a review for the new ocean data professional

M. Bloch Haimson - maya.bloch@gmail.com (1), Y. Lehahn (1), T. Sagi (2)
1) Leon H. Charney School of Marine Sciences, University of Haifa, Haifa 31905, Israel
2) Department of Information Systems, University of Haifa, Haifa, IL. Department of Computer Science, Aalborg University, Aalborg, DK

The ability to comprehensively utilize the growing amount of available ocean data is hindered by the difficulty to integrate different datasets. Current approaches rely on manual processes, limiting utilization of ocean data at scale. The Ocean Data Integration Initiative (ODINI, https://odini.net/) project is aimed at addressing this challenge by providing key missing tools and methods currently limiting the automation of the ocean data integration process. As part of the ODINI project, we set out to map the current status of the ocean data ecosystem. We aim to characterize and map the ocean data ecosystem in a robust and comprehensive manner, according to commonly used data ecosystem definitions. The approach we take consists of: Define the notion of a data ecosystem and provide examples from other fields. 1. Explore the concept of data ecosystem in ocean research. 2. Propose a model and map of the ocean data ecosystem. 3. Review state-of-art ocean data sources and their product offering. We propose that by mapping the ocean data ecosystem: It will be possible to identify the key barriers, trends and unanswered user needs of the marine research community. Identifying the market and user needs is a necessary first step before deciding which solutions in the field of marine research data need to be prioritized and designed. Mapping the ocean data ecosystem and state-of-the-art examples will facilitate ocean data professionals, new to the field, to familiarize with the ocean data sector and will assist them to provide solutions to key technological and knowledge challenges.

Non-invasive dna sampling of commercially valuable sea cucumbers: a tool for aquaculture sustainability in the gulf of aqaba

M. Bonomo - mai.bonomo@gmail.com (1,2), Dr. O. Bronstein (1,2)
1) Tel Aviv University
2) Steinhardt Museum of Natural History

The Gulf of Aqaba is home to a rich diversity of echinoderms, including commercially valuable sea cucumber species. Despite their economic importance, the biodiversity and species composition of these sea cucumbers remain undercharacterized. Conventional DNA sampling methods for identifying species are often invasive, labor-intensive, and impractical in the remote or highly regulated areas of the Red Sea, where destructive sampling is prohibited. This presents a challenge for aquaculture management, which requires accurate species identification to ensure sustainable harvesting and cultivation.

In this study, we applied a non-invasive, underwater DNA sampling method using sterile swabs to survey the sea cucumber populations in the Gulf of Aqaba. This method, designed to be efficient and non-destructive, allows for larger sample sizes per dive and facilitates high-throughput DNA analysis. Our approach successfully collected and sequenced DNA from multiple commercially important sea cucumber species. The results provide a clearer understanding of their species diversity, which is crucial for supporting sustainable aquaculture practices and resource management in the region. This technique offers a scalable, cost-effective solution for ongoing biodiversity monitoring and the sustainable development of sea cucumber aquaculture.

A multi-proxy record of Holocene continental slope processes at the Dor Disturbance

R. Bookman - rbookman@univ.haifa.ac.il (1), Y. Harmon (1), Y. Makovsky (1), M. Kanari (2), E. Boaretto (3), E. Garrett (4), S. Avnaim-Katav (2),

1) Dr. Moses Strauss Dept. of Marine Geosciences, Charney School of Marine Sciences, University of Haifa, 31905 Mount Carmel, University of Haifa, Haifa, Israel Israel
2) Oceanographic and Limnological Research, Tel Shikmona, Haifa 3108001, Israel
3) D-REAMS Radiocarbon Laboratory, Weizmann Institute of Science, 234 Herzl Street, 7610001 Rehovot, Israel
4) Department of Environment and Geography, University of York, Heslington, York, YO10 5NG, United Kingdom

Continental margins sedimentary records reveal regional climate-ocean trends and identify mass transport deposits (MTD) and reflect the regional paleoclimate and paleoseismicity. This study used two radiocarbon-dated piston cores collected from the shelf edge (122 m) and mid-slope (588 m) offshore Israel at the Dor Disturbance. CT scanning showed Holocene sediment evolution, capturing a shift in grain size and geochemistry, while detecting MTD units. The core from the shelf edge recorded the post glacial sea level flooding at 10-11 ka BP, with early Holocene sediments marked by coarser grains, high biogenic material, and abundant foraminifera. Sapropel S1, dated to 6-9 ka BP, is characterized by low Ti/Al, high Si/Al, and high TOC, reflecting increased Nile discharge and precipitation in the source region. Benthic foraminifera disappearance in the slope core indicated bottom water anoxia, interrupted by re-oxygenation linked to the ~8.2 ka BP cold event. Toward the mid-Holocene, increased Ti/Al and Fe ratios indicate higher weathering rates in the Nile watershed due to reduced rainfall and vegetation, correlating with regional aridification caused by orbital changes. Four MTD units with higher bulk density and reduced porosity were accompanied with higher Ca/Fe ratios. Radiocarbon dates within these units indicated the deposition of recycled older sediments from the early Holocene, while the mass transport events occurred between 6.2 and 1.8 Ka BP. Distinct changes are also observed in the benthic foraminifera community in association with the MTD including the total number of individuals per gram dry sediment (BF/g), species richness, dominance, and species composition. Furthermore, within all the MTD units a noticeable increase in broken BF shells was also documented.

Life cycle and morphogenetic differentiation in heteromorphic cell types of a cosmopolitan marine microalga

L. Bousque - laurie.bousquet@mail.huji.ac.il (1,2), S. Fainsod(1,2), J. Decelle(3), O. Murik(4), F. Chevalier (3) , B. Gallet (3), R. Templin (3), Y. Schwab (3), Y. Avrahami (1,2), G. Koplovitz (2), C. Ku (5), M. J. Frada (1,2)

1) Department of Ecology, Evolution and Behaviour, Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel;
2) The Interuniversity Institute for Marine Sciences in Eilat, Eilat, Israel;
3) Laboratoire Physiologie Cellulaire et Végétale, Univ. Grenoble Alpes, CNRS, CEA, INRAE, IRIG-DBSCI-LPCV, 38000 Grenoble, France;
4) Translation Genomics Lab and Medical Genetics Institute, Shaare Zedek Medical Center, 93722, Jerusalem, Israel;
5) Institute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan.

Gephyrocapsa huxleyi is a prevalent, bloom-forming phytoplankton species in the oceans. It exhibits a complex haplo-diplontic life cycle, featuring a diploid-calcified phase, a haploid phase, and a third 'decoupled' phase produced during viral infection. Decoupled cells display a haploid-like phenotype, but are diploid. Here, we investigated the fate of decoupled cells during culture observations and we compared the transcriptome profiles and the cellular ultrastructure of the three life-cycle cell types. We found that decoupled cells can revert to the calcified form in the absence of viral pressure, revealing the ability of G. huxleyi to modulate cell differentiation as a function of external conditions. Ultrastructural analyses showed distinct nuclear organisation with variations in chromatin volume. Transcriptomic analyses revealed gene expression patterns specific to each life phase. These included multiple regulatory functions in chromatin remodeling, broader epigenetic mechanisms and life cycling, likely contributing to cell differentiation. Finally, analyses of available host-virus transcriptomes support life-cycle transition during viral infection. This study provides cellular and molecular foundations for nuclear remodeling and cell differentiation in coccolithophores and the identification of gene markers for studying coccolithophore life cycles in natural populations.

Internal wave whispering gallery modes – a mechanistic explanation to energy transfer in submarine canyons

N. Bratspiess - bratspiess@mail.tau.ac.il (1), L. Maas (2), E.l Heifetz (3)
1) Department of Physics and Astronomy, Tel Aviv University
2) Utrecht University
3) Department of Geophysics, Tel Aviv University

Internal waves are an important feature of stratified fluids, both in oceanic and lake basins and in other settings. Many works have been published on internal wave trapping onto wave-attractors and super-attractors in 2&3D. However, most of these works didn’t deal with waves escaping these attractors. In this work we analytically prove in different geometries the existence of internal wave Whispering Gallery Modes (WGMs), internal waves that propagate continuously without getting trapped by attractors. We divide these attractors into three main categories. Channel walkers that exist in 2D basins stretched to a third dimension, polar WGMs that exist in basins invariant to rotation around their central axis, and other WGMs that exist in basins with no continuous symmetry. We also show that these WGMs are unstable or neutrally stable with respect to different perturbations depending on the type of WGM, thus enabling whispering gallery beams of a continuum of rays. We think that these whispering gallery beams may provide a mechanistic explanation to how energy propagates through submarine canyons without getting trapped. These WGMs may also explain the observed shear distribution of internal tides, with high shear values near the critical slope, where WGMs intensify.

The thermodynamic constants of the carbonate system in seawater desalination waste brines

D. Burd - debora.burd@mail.huji.ac.il (1,2), Y. Jacobson (2), J. Silverman (2), B. Lazar (1),
1) Fredy and Nadine Herrmann Institute of Earth Sciences, Hebrew University of Jerusalem, Jerusalem, Israel
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, P.O. Box 8030, Haifa 31080, Israel

Population growth, climate change and inefficient water usage have led to a worldwide water scarcity. As a result, many countries meet this challenge by desalinating seawater at shoreline facilities along their coasts. However, the desalination process produces waste brines with salinity of nearly twice that of seawater. The discharge of such brines to the sea may have a negative impact on the marine environment. This study aims to elucidate the thermodynamic properties of the carbonate species in these waste brines. This may provide insights into the modeling and optimization of the electrochemical precipitation process of carbonates from the brines and carbon sequestration potential. A new model is in development to estimate the first and second apparent dissociation constants of carbonic acid (K1', K2') in brine from desalination plant along the Israeli Mediterranean coastline. This model is based on alkalinity titration and least-squares fitting, evaluated with the Pitzer ion-interaction approach. We expect to determinate the thermodynamic equations necessary to characterize the carbonate system as a function of salinity and temperature and identify the main dominant factors influencing the apparent dissociation constants of carbonic acid in this waste. Furthermore, we aim to evaluate the capacity of different brine mixtures to absorb CO_2. The thermodynamic equations that will be formulated in this study will pave the way for estimating the fate of CO_2 in waste brine from desalination plants. Additionally, they will serve as valuable data for various applications, including the development of carbon capture technologies.

A rainbow trout (*Oncorhynchus mykiss*) artificial intestine platform to test new feed formulas

M. A. Chacon - marcelo.chacon@ocean.org.il (1), N. Verdile (2), F. Camin (3), R. Pasquariello (3), D. Peggs (4), R. Fontanillas (4), G. Løkka (5), T. AL Brevini (2), F. Gandolfi (3), T. M. Kortner (5), A. Tandler (1), A. Bitan (1)
1) Israel Limnological & Oceanographic Research, National Center for Mariculture, Eilat, Israel
2) Department of Veterinary Medicine and Animal Sciences, University of Milan, Milan, Italy
3) Department of Agricultural and Environmental Sciences, University of Milan, Milan, Italy
4) Skretting Aquaculture Innovation, Stavanger, Norway
5) Department of Paraclinical Sciences, Faculty of Veterinary Medicine, Norwegian University of Life Sciences, Ås, Norway

We are developing an in vitro screening platform (Fish-AI) to test the health value of novel fish feed formulas. The platform consists of a rainbow trout (RT) intestinal epithelial cell monolayer seeded on permeable membrane inserts and challenged for 72h with in vitro digested diets. RT reference diet, Soya-High diet or Feather-High diet were tested in the platform. The integrity of the cell monolayer was evaluated by monitoring digesta effect on the transepithelial electrical resistance (TEER) and on the permeability to fluorescent molecules, including a sugar, a dipeptide and a fatty acid. We found that while low digesta concentration (6%) did not cause any negative effect on the cell barrier, diets enriched in soy meal or feather meal induced a significant decrease in TEER values at higher concentrations (12% and 25%), as compared to the reference diet, which showed similar TEER values to cell monolayers incubated with medium alone. In agreement, the permeability to the fluorescent molecules was significantly increased in a concentration- and diet-dependent manner. Diets enriched with either soy meal or feather meal induced a significant increase in the permeability to all the fluorescent molecules at 12% concentration, suggesting a disruption of the cell barrier integrity; in contrast, the reference diet did not exert any significant detrimental effect. These results demonstrate that both, TEER and permeability assays can be used to discriminate and rank different diets in the Fish-AI platform.

The chemical and physical properties of suspended particles in the Red Sea: towards quantification of marine snow and the ballasting effect

A. Clarfield - aden.clarfield@mail.huji.ac.il (1,2), H. Huang (3), A. Bochdansky (3), G. Edvardson (1,4), G. Lapid (1,2), C. Flintrop (1,2), S. Amiran-Kan (1,2), A. Torfstein (1,2)

1) The Fredy & Nadine Herrmann Institute of Earth Sciences, Hebrew University of Jerusalem, Jerusalem, Israel.
2) The Interuniversity Institute for Marine Sciences, Eilat, Israel.
3) Ocean, Earth and Atmospheric Sciences, Old Dominion University, Norfolk, Virginia, USA
4) Department of Natural Sciences, The Open University of Israel, Ra'anana, Israel.

Mineral ballasting is the process of dense minerals encapsulating organic matter, thereby increasing their sinking rates and enhancing export production and the efficiency of the biological pump, yet the chemical composition of free floating (suspended) particles in the oceans and their physical characteristics are poorly known. Here, we present a study of suspended particle compositions and dynamics in the oligotrophic Gulf of Aqaba (GOA), northern Red Sea.

Vertical profiles of suspended particles were collected at station A, GOA, during 11 sampling cruises between December 2022 and February 2023, as well as one complementary cruise during August 2023. Coeval sampling of the sinking particle flux was achieved using a pelagic sediment trap mooring. The particulate matter was measured for its trace element and organic carbon content, and corresponding seawater samples were measured for macronutrient concentrations, temperature, salinity, fluorescence, and beam attenuation.

Particle dynamics were further monitored in the GOA throughout 2023 using a Focused Shadowgraph Imaging (FoSI) camera, which provided a high-resolution quantification of particle numbers, shape, volumes and orientation across the water column. The results highlight the presence of aggregates of marine snow that likely serve as ballasts enhancing POC export.

Combined, the chemical and physical properties of particulate matter in the GOA reveal the associations between the organic carbon and lithogenic and authigenic elements, as well as similarities and differences between the suspended and sinking particle fractions. The results highlight the presence of marine snow aggregates that likely serve as ballasts enhancing POC export.

Light-enhanced calcification of symbiotic, bleached, recovered and aposymbiotic corals

I. Cohen - 2itaycohen@gmail.com (1), R. Horwitz (2), Z.Dubinsky (2), J. Erez (1)
1) The Institute of Earth Sciences, The Hebrew University of Jerusalem, Jerusalem 91904, Israel.
2) Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan, 52900, Israel

Algal symbionts are believed to support coral calcification because light enhances calcification up to several-fold, a phenomenon commonly known as light-enhanced calcification (LEC). In contrast, non-symbiotic corals are considered to be unaffected by light. The unprecedented global bleaching events require an in-depth reevaluation of the role of symbionts in LEC. In this study, the symbiotic corals Acropora variabilis and Pocillopora damicornis were experimentally bleached by exposure to prolonged darkness. When re-illuminated with full visible spectrum (400-700nm), oxygen production was not detected, and calcification rates were significantly lower than those of control non-bleached colonies. However, LEC was observed in the bleached P. damicornis and A. variabilis with ratios of 1.8 and 3 times higher in the light than dark, respectively Similar ratios were observed in the control colonies. Surprisingly, the highest LEC was observed in a non-symbiotic coral, Tubastrea faulkneri (showing an L/D ratio of 4.9). Recently, blue light was shown to enhance coral calcification while photosynthesis was kept below the compensation point (Cohen et al. 2016). We demonstrate that bleached and non-symbiotic corals respond to blue light by enhancing calcification similar to the full spectrum exposure. We conclude that algal symbionts are important for maintaining high calcification rates. However, the LEC mechanism in both symbiotic and non-symbiotic corals depend on light absorption particularly on the blue part of the spectrum by the coral host.

Stable strontium and magnesium isotopes behavior in coastal aquifers during long-term seawater circulation

A. Cohen-Peretz - anael.cohen@weizmann.ac.il (1), N. Shalev (2), Y. Kiro (1)
1) Department of Earth and Planetary Sciences, Weizmann Institute of Science, Israel.
2) Department of Earth Sciences, The Hebrew University, Israel.

Groundwater-derived solute and isotope fluxes to the ocean, once deemed subordinate, have emerged as significant contributors to ocean chemistry. The chemical composition of these coastal aquifer groundwaters is affected by mixing between fresh and saline water bodies and by water-rock interactions. The latter also depend on the residence time of the intruding seawater and its flow paths. This study delves into the chemical dynamics of a carbonate-rich silicate aquifer at the Nitzanim Nature Reserve in Israel, unraveling the behavior of stable strontium and magnesium isotopes in the context of groundwater flow and water-rock interactions.

Notably, calcium, potassium, sodium, and strontium concentrations exhibit non-conservative behavior, contrasting with the conservative nature of magnesium. Our comprehensive approach integrates both magnesium and strontium isotopes, offering a holistic understanding of coastal aquifer dynamics. Strontium, akin to calcium and distinguished by its stable isotopes, enriches insights into the intricate processes governing these aquifers, contributing to a comprehensive comprehension of marine strontium dynamics.

Focusing on magnesium isotopes, our δ26Mg data (ranging from -1.46 to -0.82‰) reveals depletion compared to the conservative mixing line. Proximity to the coast mirrors seawater values, becoming more negative along the salt-water flow path from the sea into the aquifer over centuries. Estimating the contribution of long-term circulated submarine groundwater discharge (SGD) to the magnesium isotope budget emphasizes its magnitude (-2 Tmol yr-1 · ‰), comparable to rivers (-1.4 Tmol yr-1 · ‰). This underscores the necessity of linking isotope values to flows on diverse time scales within coastal aquifers, emphasizing water-rock interaction and residence time in determining the isotopic composition of terrestrially-derived solute fluxes to the ocean.

The Influence of ocean-atmosphere interaction on precipitation in the eastern Mediterranean: implications for sub-seasonal to seasonal forecasting

O. Cohen - ofer.cohen5@mail.huji.ac.il (1), O. Adam (1), A. Hochman (1)
1) Fredy and Nadine Herrmann Institute of Earth Sciences, Hebrew University, Jerusalem, Israel

The Eastern Mediterranean (EM) region is considered a global warming hotspot projected to experience increased temperatures, water shortages and droughts during summer, as well as high-intensity precipitation and flooding events during winter. These impacts, in a region already struggling with water shortages, highlight the importance of improving the skill of sub-seasonal to seasonal forecasting, as part of the ongoing adaptation efforts. Here we aim to assess the sub-seasonal to seasonal influence of ocean-atmosphere interactions on precipitation in the Levant. Specifically, we find robust statistical relations between ocean parameters such as sea surface temperature, heat content and surface energy fluxes over parts of the Mediterranean in autumn, and winter precipitation in the Levant. By employing a Self-Organizing Map (SOM) approach, we identify key patterns of variability in Mediterranean Sea fields that influence Levant precipitation. Our analysis of the hydrological balance reveals that both dynamic and thermodynamic processes play a role in linking ocean properties, cyclone behavior, and Levant precipitation. Specifically, sea-surface conditions regulate cyclone intensity and trajectories, as well as the thermodynamic characteristics of air transported by cyclones, ultimately impacting precipitation. Through simplified representations of these coupled processes, we aim to integrate them into operational forecast models, enhancing their sub-seasonal to seasonal prediction skill with minimal computational cost.

Comparative characterization of the redox-regulated chaperone HSP33 from different microalgae under oxidative stress.

Dr. N. Segal (1), M. Fhima (2) M. Cohen (2).
1) The National Center for Mariculture in Eilat (NCM), Israel.
2) BGU-Campus Eilat, Israel.

Environmental stressors like temperature and oxidative stress significantly impact organismal growth and survival by causing proteins to unfold, lose functionality, and aggregate, potentially leading to cell death. Cells respond by recruiting heat shock proteins (chaperones) to prevent protein aggregation. In *Escherichia coli*, Hsp33 is a redox-regulated chaperone activated by a four-cysteine redox switch upon zinc ion release and cysteine oxidation, which triggers structural changes and dimerization.

In Chlamydomonas reinhardtii, the green algal CrHSP33 lacks a functional redox switch due to the absence of a key cysteine, rendering it constantly active and regulated by expression levels. This study compared Hsp33 activity across different algae, including Nannochloropsis, Phaeodactylum, Porphyridium, Picochlorum, and Chlamydomonas, focusing on their redox switch.

In our study, the purified Hsp33s underwent reducing and oxidizing treatments, followed by thermal aggregation and zinc-binding assays. CrHsp33 and PorHsp33 did not efficiently bind zinc and remained active under reducing conditions during thermal aggregation. Interestingly, both retained activity despite their aggregation state. These findings emphasize Hsp33's role in managing oxidative stress, underscoring its importance for algae and marine organisms under environmental stress and the importance of further research.

Dolomite clumped isotope constraints on the Phanerozoic Ocean δ^{18}O values

S. Cooper-Frumkin - Shlomit.Frumkin@mail.huji.ac.il (1) AND Ryb U. (1)
1) The Fredy and Nadine Herrmann Institute of Earth Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel

Despite prolonged research, the δ^{18}O composition of ancient seawater remains debated. On timescales >107 years, the δ^{18}O composition of the seawater is controlled by the ratio of oxygen isotope exchange fluxes during hydrothermal alteration in mid-ocean ridges and surface weathering. Oxygen and clumped isotope analyses of carbonate minerals can be used to calculate the δ^{18}O of mineral parental-water, without assuming formation temperatures. In ancient marine carbonate rocks these waters are typically diagenetic fluids that have been modified from seawater under various water to rock ratios. Most previous studies have therefore assumed some water to rock ratio (typically zero or infinite) to calculate the original δ18O value in the ocean from carbonate oxygen and clumped isotope data – leading to ambiguity in the interpretation. Here, we overcome this challenge by relaxing the assumption of known water to rock ratios, and instead constraining the range of δ18O values of ocean water permissible by dolomite clumped and oxygen isotope data. Our dataset includes 21 published (and one unpublished) Phanerozoic records, divided to time-intervals. Modeled ranges of ocean of δ^{18}O values are overall consistent with the previously hypothesized invariant ocean δ^{18}O (2 to -2 ‰ VSMOW) during the last 400 Ma. However, in the Ordovician we find lighter composition of seawater of ≤-3.5 ‰ VSMOW, consistent with the results of a recent study that used a similar approach to constrain ocean of δ18O values from marine calcites (Thiagarajan et al., 2024). Considered together, these more conservative analyses support a shift in the balance of water-rock reactions during the Early Paleozoic, in which the oxygen exchange flux from hydrothermal alteration increased relative to that from weathering.

Can we grow salmon in the desert?

B. Dach (1)

1) AlgaeCore – SimpliiGood

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Differential grazing by salps affects microbial community composition

A. Dadon Pilosof - ayelet@ruppin.ac.il (1,2,3,4,5,6)
1)The Faculty of Marine Science, Ruppin Academic Center, Michmoret, Israel
2)Department of Ecology, Evolution & Behavior, The Hebrew University of Jerusalem, Jerusalem, Israel
3)Sorbonne Université, Laboratoire d'Océanographie de Villefranche, Villefranche-sur-Mer, France
4)Institut Universitaire de France, Paris, France
5)The Inter-University Institute for Marine Sciences, Eilat, Israel
6)Oregon Institute of Marine Biology, University of Oregon, Eugene, Oregon

Salps, gelatinous planktonic feeders, play a significant role in marine ecosystems. Their ability to filter large volumes of seawater and form dense swarms impacts phytoplankton populations and carbon cycling. Dense swarms of salps have a high grazing impact that can deplete the photic zone of phytoplankton and export huge quantities of organic matter to the deep sea. Previous studies suggested salps have a non-selective feeding strategy, with larger particles retained at higher efficiencies than small particles. To examine salp diets, we used direct in situ sampling (InEx method) of undisturbed solitary *Salpa maxima*. Aggregates ("chains") of Salpa fusiformis were studied using in situ incubations. Our findings suggest that in situ feeding rates are higher than previously reported and that cell removal is size independent with ~1 µm picoeukaryotes preferentially removed over both larger eukaryotes and smaller bacteria. The overall filtration efficiency of bacterioplankton by the two salps species was low (18%), while microbial eukaryotic cells were filtered at a much higher efficiency (68%). Differential retention was observed where some bacterial phylotypes and eukaryotic cells were captured much less efficiently than others. This variability suggests that the prey's properties play a critical role in determining its ability to avoid filtration. This selective feeding can alter microbial community composition during salps bloom. Salp swarms can suppress phytoplankton blooms and outcompete other grazers, contributing to the oceanic carbon pump through efficient carbon export. Understanding salp grazing and its impact on microbial communities is crucial for marine food web dynamics.

A novel marine bacterium as a probiotic supplement to improve health, feed digestion, and resilience of the gilthead seabream (*Sparus aurata*)

A. Dake (1,2), K. Kashkush (2), L. Guttman (1,2)
1) Israel Oceanographic and Limnological Research, The National Center for Mariculture, Eilat, 8811201, Israel
2) Department of Life Sciences, Ben Gurion University of the Negev, Be'er Sheva, 8410501 P.O Box 653, Israel

Improving productivity in aquaculture demands maintaining the well-being of the cultured organisms. For this purpose, probiotics have become common in culture setups to enhance fish growth, health, and resilience. The current study examined a novel marine bacterium for its feasibility in improving the growth, digestibility, and health performances of gilthead seabream Sparus aurata. For this aim, a feeding trial was performed over 12 weeks in which fish were fed commercial aquafeed with different inclusion rates of the probiotic bacterium of 108, 1010, and 1012 CFU/Kg feed compared to a probiotic-free diet. Fish growth, feed digestibility, immune response, and microbial community composition were measured throughout the culture period. Results indicated no effect of probiotic treatment on fish growth performances, but protein and lipid digestion was improved when the probiotic was supplemented at 1010 CFU/Kg group, proposing an improved absorption of these macronutrients. The probiotic supplement at 1010 CFU/Kg also induced an increase in antiprotease activity, while myeloperoxidase activity increased only during the first six weeks. Probiotic supplementation influences microbial community composition, indicating their resilience to varying treatments. Ultimately, the probiotic treatment improved fish survival after challenging them with Streptococcus agalactiae, with highest survival rate of 70% in the probiotic supplementation level of 1012 CFU/Kg. Overall, the novel probiotic bacterium efficiently improves feed digestion and fish health. The origin of such bacterium, from the gut of an algivorous sea urchin, proposes further study concerning the contribution to fish in feed digestion and energy gaining under diets with high plant or algal ingredients.

Co-extraction of pigments, phenolic compounds and polysaccharides from the green seaweed *Ulva*

N. David - davno@post.bgu.ac.il (1, 2) G. Klin (3), D. Lewitus (3) and E. Salomon (1)
1) Israel Oceanographic and Limnological Research, The National Center for Mariculture,
Eilat, Israel
2) The Department of Life Sciences, Ben- Gurion University of the Negev Eilat Campus, Israel
3) The Department of Polymer Materials Engineering, Shenkar College, Ramat Gan, Israel

More than just a food source, seaweeds contain an abundance of metabolites that can be used as active materials for the science, medical and beauty industries. Metabolites such as pigments or phenolic compounds (PC) are antioxidant, some with promising antibacterial and anti-cancer activities. Seaweed polysaccharides are commonly used as gelling, thickening or emulsifying agents in many industries. Recently, the possibility of using these materials for production of renewable, degradable bioplastic has emerged. The high economical and industrial value of these materials raises an interest in developing optimal extraction protocols, for efficient utilization of seaweed stocks. Our aim was to develop a biorefinery protocol for consecutive extraction of pigments, phenolic compounds and polysaccharides from the widely spread and fast-growing green seaweed Ulva. The biorefinery process is comprised of pigment and phenolic compounds extraction using methanol, followed by hot water extraction of polysaccharides. The extracted polysaccharide fraction is then purified using ethanol precipitation. Several extraction times and solvent-to-algae ratios were tested to optimize the extraction process. Optimal polysaccharides, pigments and PC yields were achieved with a preliminary 1:10 algae to methanol ratio, two hours hot water extraction with a 1:10 algae to water ratio, followed by precipitation with 1:5 algae to ethanol ratio. The polysaccharide fraction was successfully used to produce thin, flexible, semi-transparent, plastic-like films. These results demonstrate the possibility of using a common, fast-growing seaweed as an ultra-sustainable source for high value products, such as bioactive secondary metabolites and building blocks for producing bioplastics.

Community composition and seasonal dynamics of microplastic biota in the eastern mediterranean sea

K. Davidov - keren5180797@gmail.com (1), K. S. Marsay (1), S. Itzahri (1), M. Rubin-Blum (2), P. Sobral (3), C. F. Kranzler (4), M. Oren (1)

1) Department of Molecular Biology, Ariel University, Ariel, Israel.
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, Haifa, Israel.
3) MARE - Marine and Environmental Sciences Centre & ARNET - Aquatic Research Network Associated Laboratory, NOVA School of Science and Technology, NOVA University of Lisbon, Lisbon, Portugal,
4) The Mina and Everard Goodman Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan, Israel.

Marine plastic pollution poses a growing environmental threat, with microplastics accumulating in the global oceans. This study profiles the seasonal dynamics and taxonomic composition of the plastisphere, the microplastic ecosystem, in the Eastern Mediterranean Sea. Using long-read 16S and 18S metabarcoding, we analyzed offshore microplastic and whole seawater samples across each season over a two-year period. The analysis revealed a higher richness of prokaryotic communities on microplastics compared to seawater, which was predominantly composed of Proteobacteria and Bacteroidota and exhibited notable seasonal variability. Benthic eukaryotes were enriched on microplastics compared to the surrounding seawater. Diatoms (Bacillariophyceae), in particular, showed significant enrichment within the microplastic eukaryotic community with primarily pennate diatoms of Amphora, Navicula, and Nitzschia genera, whereas the seawater included mostly centric diatoms. Seasonal fluctuations were less pronounced in the microplastic communities than in seawater, highlighting the relative stability of this new human-made ecosystem. These findings underscore the unique ecological niche of microplastic-associated communities in marine environments.

Sediment and water column sources of marine carbonyl sulfide identified by their sulfur isotopes

C. Davidson - chen.davidson@mail.huji.ac.i (1), A. Angert (1), Y. Avidani (1), S. T. Lennartz (2), A. Amrani (1)
1) The Institute of Earth Sciences, The Hebrew University of Jerusalem
2) Institute of Chemistry and Biology of the Sea, The University of Oldenburg

Oceanic emissions of carbonyl sulfide (COS), act as important precursors for stratospheric sulfate aerosols, which regulate Earth's radiation budget. COS is also used as a proxy for terrestrial plants' removal of atmospheric CO_2, which regulates Earth's climate. The oceans are the largest natural source of COS. Yet, large uncertainties are associated with the magnitude and location of oceanic COS emissions. Thus, better constraints on the COS budget are needed for reliable climatic models. Sulfur isotope measurements of COS were recently used to constrain tropospheric COS budget estimates. However, published measurements of S isotopes of aquatic COS are currently scarce. We present here, a comprehensive data set of S isotope (δ34S) measurements of marine COS from the Atlantic Ocean, the Mediterranean Sea, the Red Sea, the Wadden Sea, and the North Sea. We used a water-air equilibrator to sample COS in the gas phase, and preserved them in Silitek-treated canisters for later analysis in the lab, using a GC/MS-ICPMS. The COS in surface water shows $\delta^{34}S$ values in the range of -4 to 20‰. We use the spatial and temporal changes in S isotopes of COS to identify the isotopic values of different sources of COS, including the production of COS in the sediment, photoproduction, light-independent production, and hydrolysis. These new findings will help to constrain the ocean-atmosphere COS flux and create an improved COS budget isotopic mass balance for COS-based GPP models and stratospheric sulfate models.

Can we use aeolid nudibranchs to find cryptic jellyfish polyps at sea?

H. Dror - hila.dror@gmail.com (1), T. Lotan (2), D.Angel (1)

1) Department of Maritime Civilizations & The Leon Recanati Institute for Maritime Studies, University of Haifa, Mt. Carmel, Haifa 3103301, Israel

2) Marine Biology Department, The Leon H. Charney School of Marine Sciences, University of Haifa, Mt. Carmel, Haifa 3103301, Israel

Scyphozoa possess specialized organelles called nematocysts, venom-filled capsules equipped with ejectable tubules, which they use to sting prey. Aeolid nudibranchs are marine gastropods, known to prey on various cnidarian animals. Not only are they not deterred by their prey's sting, but nudibranchs can isolate and store nematocysts in their cerata (dorsal appendages) for their own defense. Scyphozoan polyps are regarded as the driving force behind jellyfish outbreaks. However, they are cryptic and their location in the marine environment remains unknown for most species.

We explored interactions between aeolid nudibranchs and scyphozoan polyps in common eastern Mediterranean species. Our goal was to find nudibranch species that feed on scyphozoan polyps, and use the specific nematocysts stored in their cerata as a means to locate the polyps in the field. We tested two nudibranch species (*Phidiana militaris* and *Flabellina affinis*) in the laboratory to see if they feed on scyphozoan polyps (*Rhopilema nomadica*, *Cassiopea andromeda*, *Phyllorhiza punctata*, and *Aurelia* sp.), and whether polyps could serve as their sole food source for extended periods. We then induced the nudibranchs to expel their nematocysts and measured how long it took to incorporate new ones from the polyps. Our results show that, while F. affinis avoids scyphozoan polyps, P. militaris consumes all tested polyp species and can subsist on them for long periods (≤ 255 d). Feeding rates varied among prey species tested, ranging from 4.4 to 53.4 polyps day^{-1}. However, *P. militaris* does not store scyphozoan nematocysts in its cerata, rendering it ineffective for tracking polyps in nature.

Copepod-associated, rather than seawater microbial communities reflect the spatial and environmental heterogeneity of the Mediterranean Sea

X. Velasquez - ximvel@ocean.org.il (1, 2), T. Ozer (1), M. G. Mazzocchi (3), F. Carlotti (4), M.Pujo-Pay (5), T. Guy-Haim (1)

1) National Institute of Oceanography, Israel Oceanographic and Limnological Research (IOLR), Haifa, Israel
2) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Israel
3) Integrative Marine Ecology Department, Stazione Zoologica Anton Dohrn, Villa Comunale, Naples, Italy
4) Aix-Marseille Université, Université de Toulon, CNRS/INSU, IRD, Mediterranean Institute of Oceanography (MIO), Marseille, France
5) Sorbonne Université, CNRS, Laboratoire d'Oc´eanographie Microbienne, LOMIC, F-66650 Banyuls-sur-Mer, France

The pronounced west-to-east environmental gradients across the Mediterranean Sea (MS) and the ubiquity of pelagic copepods provide an optimal setting to study the mechanisms shaping zooplankton-associated microbial communities. We used 16S rRNA gene amplicon sequence variants (ASVs) obtained from dominant copepod taxa (*Oncaea*, *Farranula*, *Clausocalanus*) and seawater collected during Mediterranean Sea expedition (PERLE 4). We sampled epipelagic mesozooplankton in 16 sites from the Tyrrhenian to the Levantine basins by vertical net hauls (0–250 m), and seawater from corresponding depths by Rosette sampler. Our results revealed greater horizontal microbial community dissimilarity in the copepod hosts than in the seawater, dividing the copepod microbiota into two main clusters—a western region including the Tyrrhenian and western Ionian basins, and an eastern region consisting of the eastern Ionian, Cretan and Levantine basins. Selection under heterogeneous environmental conditions and limited host dispersal due to mesoscale features may explain the microbial dissimilarity in the hosts between the western and eastern MS regions. In contrast, the seawater microbial communities showed lower spatial variability, displaying more similar microbial composition between regions. However, bacterial community distribution significantly shifted vertically, indicating that distinct water layers harbor different microbial communities. The relative abundance of dominant microbial taxa in the copepods (opportunist copiotrophs) varied strongly with spatial distribution, showing similar patterns in basins with homogeneous environmental conditions and physical connectivity. We conclude that copepod microbiota better reflect the cross-basin spatial and environmental heterogeneity of the MS than seawater microbial communities, suggesting that they may serve as efficient environmental bioindicators.

Aerobic microbial methanogenesis and methane oxidation in *Aplysina aerophoba*

M. A. Duran Canche - marthita.duran.md@gmail.com (1), C. Conti (1), J. Milucka (2), S. Schorn (2), L. Steindler (1)
1) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Abba Khoushy Ave 199, Haifa, 3498838, Israel.
2) Department of Biogeochemistry, Max Planck Institute for Marine Microbiology, Celsiusstrasse 1, D-28359 Bremen, Germany.

Marine sponges interact with a wide range of microorganisms and are considered holobionts. A recent study using microbial metatranscriptomes from the sponge Aplysina aerophoba hypothesized that a hidden methane cycle exists within this sponge due to microbial activity. This sponge is known to thrive in shallow, fully oxygenated waters. The study suggested two potential pathways for aerobic methanogenesis: one involving Alphaproteobacteria using methyl phosphonate (MPN) as a phosphorus source, generating methane, and another involving the use of methylamine (MeA) as a nitrogen source, also producing methane. Additionally, symbionts of the phylum Binatota were suggested to have the genetic capability to oxidize the produced methane. However, this hypothesis has not yet been experimentally tested. In this study, we performed incubation experiments on three A. aerophoba specimens collected from the Gulf of Trieste (Adriatic Sea). We employed stable isotopes, specifically Carbon-13, as tracers for MPN and MeA substrates. Sponge tissue was exposed to five different treatments in airtight bottles. Seawater was sampled from the incubation bottles at 0, 3, 6, 12, and 24 hours from the start of the incubation. Additional incubations were conducted with $^{13}CH_4$ to test for methane oxidation. The samples are currently being analyzed with a methane-stable carbon isotope analyzer (Picarro). We expect to observe the production of $^{13}CH_4$ when sponge tissue is incubated with ^{13}C-MPN and ^{13}C-MeA and the production of $^{13}CO_2$ when sponge tissue is incubated with $^{13}CH_4$.

Seasonality of gelatinous zooplankton in the Israeli Mediterranean

D. Edelist - blackreefs@gmail.com (1, 2), T. Guy-Haim (3), I. Savva (1), D. L. Angel (1)
1) Department of Maritime Civilizations and Leon Recanati Institute for Maritime Studies, University of Haifa, Mount Carmel 3498838, Haifa, Israel
2) Ruppin Academic Center, Emeq Heffer, 40250000 Israel, Michmoret Campus
3) National Institute of Oceanography (IOLR), Haifa, Israel

The timing of jellyfish swarm events determines the extent of their impact on social, economic, operational and public health interests along the Israeli Mediterranean coastline. The citizen science-based Meduzot Baam website (https://www.meduzot.co.il/) has been collecting observations on the appearance of gelatinous zooplankton (GZ) since 2011, and now enables the investigation of ”arrival phenology” across the main taxa. By applying the Jellyfish Swarm Index (JSI) for every taxon, several distinct patterns were uncovered. Rhopilema nomadica remains the most prominent species, typically swarming in summer (June-July), with longer but less dense winter swarms between December and April. Several other scyphozoan taxa that may co-occur with R. nomadica in summer include *Rhizostoma pulmo*, *Phyllorhiza punctata*, *Aurelia* sp., *Cotylorhiza erythraea*, *Chrysaora pseudoocellata*, and *Marivagia stellata*. All of these species have metagenic life cycles, alternating between planktonic and benthic stages. Conversely, the holoplanktonic Pelagia noctiluca only occurs in the Levant during winter, appearing when large storms disperse it toward the Israeli coast. During late winter and spring (March-May), prior to the polyspecific summer swarms, Porpita porpita may wash ashore, and blooms of other smaller taxa abound. Prominent among these are the ctenophores *Mnemiopsis leidyi* and *Beroe ovata* and the rarer *Cestum veneris*, which are present year-round, but typically peak in spring. Salps (mainly *Thalia democratica*) also bloom in spring, followed by hydromedusae such as *Aequorea forskalea*. Finally, siphonophores are the only GZ taxon that consistently occurs in autumn.

How much zooplankton do coral-reef fish eat (in situ)?

H. Ella - hadar.ella@mail.huji.ac.il (1, 2), E. Orenstein (3), P. Roberts (4), I. Kolesnikov (1, 2), T. Shaulov (1, 2), J. S. Jaffe (5), and A. Genin (1, 2)

1) Department of Ecology, Evolution and Behavior, The Hebrew University of Jerusalem
2) The Interuniversity Institute for Marine Sciences in Eilat
3) Ocean Informatics in The National Oceanography Center
4) Monterey Bay Aquarium Research Institute in California
5) Scripps Institution of Oceanography, University of California – San Diego

Coral reefs flourish in oligotrophic seas. The unknown sources of allochthonous nutrients needed to support the reef's high productivity have puzzled researchers since the 1950's (termed the "Paradox of the Reef"). Recent studies have shown that the import of allochthonous nutrients through the consumption of plankton by reef inhabitants can resolve this enigma. However, zooplankton consumption has never been quantified in situ. Using a state-of-the-art, autonomous underwater microscope, we measured, for the first time, predation rates and prey selectivity by 3 species of common zooplanktivorous fishes in a Red Sea coral reef. Our method also allowed the assessment of the effects of current speed, water temperature, and prey density on those rates. A single group of fish removed on average 40% of the zooplankton passing through it. Such a rate contributed a considerable amount of nutrients to the reef, partly explaining the "paradox". The effects of current speed, prey density, water temperature, as well as prey selectivity greatly varied among species. The inter-specific differences can explain corresponding differences in their typical group size and geographic distribution. Our study introduces a new technique to quantify in-situ zooplankton predation, thereby contributing to the understanding of ecosystem functioning in coral reefs.

Calcium carbonate precipitation in the ocean: The role of biomineralization

J. Erez - jonathan.erez@mail.huji.ac.il (1)
1) Institute of Earth Sciences, The Hebrew University of Jerusalem, Israel

The ocean is the largest carbon reservoir in the present global carbon cycle. Calcium carbonate ($CaCO_3$) precipitation and dissolution in the ocean controls to a large extent the alkalinity budget and hence its pH and buffer capacity. Biomineralization of foraminifera, coccolithophores, sea urchins and mollusks are the most important processes responsible for $CaCO_3$ precipitation in today's ocean. Most of the $CaCO_3$ production occur above the thermocline while dissolution occurs mostly on the ocean floor and is almost entirely inorganic. Biomineralization of $CaCO_3$ is strongly perturbed by ocean acidification of the upper ocean resulting from atmospheric CO_2 increase. Most of the marine calcifyers decrease their calcification with the exception of coccolithophores that show mixed responses to ocean acidification. These confusing results can be explained by the major difference in their biomineralization mechanisms. Most groups of calcifyers, i.e., foraminifera, corals, sea urchins and others bring seawater directly to their calcification site and their calcifying fluid is simply seawater. Coccolithophores on the other hand calcify intracellularly, use specific membranal transporters to bring calcium and carbon- into their calcifying vesicle and hence are less affected by ocean acidification. In this lecture we will provide direct evidence to asses these observations and explain their consequences for the global carbon cycle.

Temporal effects on sperm motility across three echinoid species

G. Eviatar - galeviatar@gmail.com (1 ,2, 3), L. Roth (1, 2, 3) and O. Bronstein (1, 2)
1) School of Zoology, The George S. Wise Faculty of Life Sciences, Tel Aviv University, 69978, Tel Aviv, Israel
2) Steinhardt Museum of Natural History, Tel Aviv University, 69978 Tel Aviv, Israel
3) The Interuniversity Institute for Marine Sciences in Eilat, Israel

Sexual reproduction is fundamental to understanding biodiversity, biogeography, and evolution with broadcast spawners facing challenges like sperm limitation or competition due to variations in adult distributions, water flow, and spawning timing. Various aspects of sperm performance, such as sperm morphology, longevity, and motility, are directly linked to fertilization success.

This study aims to evaluate the influence of gametes age on sperm motility and ultimately assess the optimal timeframe for fertilization in three echinoid species: *Paracentrotus lividus* (commercially cultivated and wild Mediterranean population), *Echinometra* sp. EZ and *Tripneustes gratilla elatensis* (wild Red Sea species).

Sperm was collected dry during each species' peak reproductive season. Activation (motility without egg signals) was induced by dilution in sterile seawater. Hyperactivation, characterized by intensified flagellum beating in response to egg pheromones, was triggered by dilution in egg-water (obtained by incubation of 50,000 eggs ml^{-1} sterile seawater). Sperm kinematic parameters such as velocity and linearity were evaluated over three hours following spawning in 15 min intervals. Data was obtained using a Computer Assisted Sperm Analysis (Microptic, SCA, Spain) system, generating high-throughput motility profiling of individual sperm cells.

In all species, sperm velocity and motility decreased as the sperm aged in both activated and hyperactivated states. Nevertheless, the rate of decline varied significantly between species. Mean sperm velocity of cultivated *P. lividus*, was almost half of that of the wild species studied, with lower overall sperm motility. We show that sperm kinematics play a part in reproductive fitness and are directly linked to the animal’s life history."

Submesoscale horizontal stirring enhances seasonal enrichment of low-chlorophyll surface waters

Y. Fadida - yotam@ocean.org.il (1, 2), V. Verma (3), R. Barkan (3, 4), E. Biton (2), A. Solodoch (5), Y. Lehahn (1).
1) University of Haifa
2) Israel Oceanographic and Limnological Research
3) Tel Aviv University
4) Department of Atmospheric and Ocean Sciences, UCLA
5) Hebrew University of Jerusalem

The large seasonal increase in marine photosynthetic organisms - i.e., phytoplankton bloom - is a ubiquitous oceanic phenomenon that contributes to the removal of carbon dioxide from the atmosphere and that supports the growth and development of larger organisms throughout the marine ecosystem. The underlying mechanisms controlling the intensity and timing of these blooms have been proposed to be dominated by vertical transport and mixing processes that are enhanced at front and filament circulation patterns, commonly known as submesoscale currents. Here we show that the winter blooms characterizing oligotrophic waters, are also significantly intensified by horizontal transport and stirring motions induced by submesoscale currents.

Using ocean color remote sensing data and high-resolution numerical simulations in the Eastern Mediterranean Sea, we demonstrate that the energization of submesoscale currents in winter significantly increases the connectivity between the coastal waters and the ultra-oligotrophic waters in the sea interior, thereby enriching the latter with chlorophyll-rich coastal-sourced water. Multi-year observational chlorophyll time series indicates that submesoscale horizontal stirring is responsible for ∼ 25% of the seasonal surface chlorophyll increase in the region.

The contribution of fecal pellets to export production and trace element fluxes in the Gulf of Aqaba

C. M. Flintrop - clara.flintrop@gmail.com (1, 2), A. Clarfield (1, 2), S. Amiran-Kan (1, 2), A . Torfstein (1, 2)
1) Interuniversity Institute for Marine Sciences in Eilat
2) The Fredy & Nadine Herrmann Institute of Earth Sciences, Hebrew University of Jerusalem

The marine biological carbon pump is responsible for 70% of the surface-to-deep C gradient in the oceans today, making it the most important mechanism for oceanic carbon sequestration. It is driven by the export of organic matter particles, including fast-sinking zooplankton fecal pellets and phytoplankton aggregates. Yet, the quantitative contribution of different types of fecal pellets to export production, as well as their elemental composition and the effects of incorporated mineral ballast, remain poorly constrained.

We present a time series of fecal pellet compositions and fluxes from the oligotrophic Gulf of Aqaba, northern Red Sea. Fifty-five samples were collected using a sediment trap deployed at a water depth of 410 meters (total water depth 610 meters) at ~36-hour intervals over a period of three months, which captured a bottom resuspension event and the onset of the phytoplankton spring bloom. We categorized the fecal pellets according to established types and calculated type-specific number and volume fluxes from the trap samples. We further measured the trace element content of 225 pellet samples and compared it to total organic carbon and inorganic elemental composition of the bulk samples. Combined with additional environmental and oceanographic parameters, these results are used to i) quantify the organic carbon and trace element fluxes associated with fecal pellets, and ii) single out the processes controlling changes in fecal pellet composition and fluxes.

The planktonic microbiome of coral reef ecosystems

H. G. R. Steinsdóttir (1, 2, 3), D. Akkaynak (2, 3), and **M. J. Frada** - miguel.frada@mail.huji.ac.il (1, 3)
1) Department of Ecology, Evolution and Behaviour, Alexander Silberman Institute of Life Sciences, Hebrew University of Jerusalem
2) Hatter Department of Marine Technologies, Leon H. Charney School of Marine Sciences, University of Haifa
3) The Interuniversity Institute for Marine Sciences in Eilat, Israel

Coral reefs are highly diverse ecosystems comprising a variety of benthic organisms and associated symbiotic microflora. Reef activity is strongly regulated by the day-night cycle and generally consumes planktonic primary producers and modifies the biogeochemistry of its surrounding water. While microorganisms in the reefs' surrounding water are expected to carry out important ecosystem functions and interact closely with reef organisms, these microbes and their diel dynamics remain poorly characterized. To mitigate this knowledge-gap, we examined at high temporal a coral-reef in the northern Red Sea and compared its biogeochemical signatures, microbial density by flow cytometry and the microbial diversity using gene-amplicon sequencing (prokaryotic and eukaryotic) against a coastal sandy-bottom area and the open sea. We found that microbial assemblages populating the reef are distinct, presenting unique or enriched microbial genotypes less represented in other areas. Moreover, reef-associated microbial assemblages display marked diel oscillations in abundance. These oscillations are contrast to variations in the density of heterotrophic protists and the density of larger zooplankton (annelids), suggesting strong biotic control of reef-associated microflora. Our study, provides novel high-frequency detail on microbial diversity patterns and novel evidence of strong top-down controls of microbial plankton inhabiting coral reef ecosystems.

Evaluating the impact of fossil fuel pollution events on the Israeli continental shelf ecosystem

G. Gal - gal@ocean.org.il (1), E. Ofir (1), T. Islam (2), Y. Peled (1), E. Lahav (1), P. Astrahan (1), R. Bookman (3)
1) Kinneret Limnological Laboratory, Israel Oceanographic and Limnological Research
2) Centre for Policy Exploration Analysis Simulation, The Netherlands
3) The Leon H. Charney School of Marine Sciences, University of Haifa

Exploration, production and transport of fossil fuels in the marine environment come with environmental inherent risks. Pollution events often result in immediate and long-term environmental damage. These increased activities along the Israeli coast present risks that need to be evaluated. Our objective was to develop and implement tools for assessing and quantifying the possible damage to the Israeli marine ecosystem resulting from fossil fuel pollution events.

To evaluate the impact of pollution, an OpenOil model was used along with a newly developed Ecospace model of the Israeli continental shelf. Scenarios were derived from the Energean's Karish Lease Environmental document, under various weather conditions. As seabed pollution remains in the system for extended periods of time compared to pelagic water column pollution, we focused on benthic species, which are highly sensitive due to their reduced motility relative to pelagic organisms. Large uncertainties in local biota response to varying pollutant concentrations and in pollution levels hinder accurate assessment of potential impacts. We therefore incorporated novel deep uncertainty tools to account for the uncertainty.

The results indicate that deeper populations display longer-term damage and increased recovery times compared to shallow populations, intensified by higher pollutant concentrations. In addition, it was found that at relatively moderate levels of pollution, the recovery period required to reach 50% of the initial biomass was several years. Given the current and planned fossil fuel activity worldwide, this study can assist in assessing potential impacts of pollution events on the marine ecosystem.

Single-cell RNA-seq of the rare virosphere reveals the native hosts of giant viruses in the marine environment

A. Fromm - amir.fromm@weizmann.ac.il (1), G. Hevroni (1), F. Vincent (1, 3), D. Schatz (1), C. A. Martinez-Gutierrez (2), F. Aylward (2), A. Vardi (1)

1) Department of Plant and Environmental Sciences, Weizmann Institute of Science, 7610001, Rehovot, Israel
2) Department of Biological Sciences, Virginia Tech, Blacksburg, Virginia, USA
3) Developmental Biology Unit, European Molecular Biological Laboratory, 69117, Heidelberg, Germany

Giant viruses are globally distributed in marine ecosystems and play a significant role as evolutionary drivers of eukaryotic plankton and regulators of global biogeochemical cycles. The repertoire of known marine giant viruses has been significantly expanded recently, mainly through metagenomic studies. However, most of these viruses have unknown hosts, which hinders our ability to understand their lifecycle and assess their ecological importance. Our study aimed to discover the native hosts of giant viruses using a novel, ultrasensitive, single-cell metatranscriptomic approach. By applying this approach to natural plankton communities, we detected hundreds of single cells from multiple host lineages infected by diverse giant viruses. These cells included members of the algal groups Chrysophycae and Prymnesiophycae and a rare infected population of the under-studied class Katablepharidaceae, infected by a strain of giant virus from a recently defined lineage. Detection of infected Katablepharids cells enabled subsequent tracking of a high prevalence of cell-fate regulation genes in the virus that were highly expressed during infection. We further examined this host-virus dynamics in a temporal resolution and suggested that this giant virus controls the rise and demise of its host population. Our results demonstrate how single-cell metatranscriptomics is a powerful approach to linking viruses with their authentic host and studying their ecological significance in a culture-independent approach in the marine environment. We now expand the scope of our research to explore other aquatic environments, such as alpine lakes, oceanic blooms, and a diatom bloom in the Gulf of Eilat, hoping to shed light on host-virus dynamics in these ecosystems.

Unlocking carbon sequestration potential for a coral-based marine animal forest

G. Giallongo - giovanni.giallongo1994@gmail.com (1, 2, 3), N. Shashar (1), B. Rinkevich (2)
1) Ben Gurion University of the Negev
2) Israel Oceanography and Limnological Research
3) Interuniversity Institute for Marine Sciences

While the urgency for nature-based solutions for climate mitigations in the face of current climate change scenarios is evident, comprehending the carbon removal potential of marine animal forest (MAF) ecosystems, like coral reefs, remains challenging. Both ex-situ and in-situ experiments yield variable results, complicating our understanding. Further, previous ecosystem approaches presented contradicting predictions, especially concerning the calcification-to-photosynthesis ratio, identifying reefs as either carbon sources or sinks. Indeed, the complex nature of these ecosystems, encompassing vertical and lateral carbon fluxes, poses significant challenges. This study introduces a Coral-Based Marine Animal Forest Module (CBMM) as a simplified model to calculate carbon budgets and as a tool to evaluate carbon sequestration potential. The CBMM, a scalable mid-water structure, populated with Stylophora. pistillata (a model coral species) fragments, develops into a MAF. As it develops, the CBMM attracts reef-associated organisms, fostering a diverse community that could sequester carbon, along with symbiotic algal photosynthesis. This simplified model helps mitigate complexities, establishing a clear starting point (time 0, almost zero carbon) and an endpoint (mature MAF), assessing the CBMM's carbon sequestration capacity. By assessing carbon fluxes and stocks between these two community developmental stages and by considering population structures, the study aims to present a simplified modular approach and to provide a clearer understanding of carbon dynamics in coral reef ecosystems.

The role of mesoscale features in shaping microplankton dynamics in the Eastern Mediterranean Sea

M. Gilboa - mrvgilboa@gmail.com (1, 2), A. Lazar (1), I. Berman-Frank (2), T. Guy-Haim (1)

1) Israel Oceanographic and Limnological Research
2) The Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa

The abundant and persistent occurrences of mesoscale features in the Eastern Mediterranean Sea (EMS) affect the thermohaline gradients, mixing, and nutrient availability. We hypothesized that these features strongly affect the microplankton communities in the EMS. To test this hypothesis, microplankton (50 – 200 µm) was sampled using plankton net hauls at 30 stations along a Mediterranean transect between Cyprus and Sicily in January–February 2024. The cruise targeted several mesoscale features, including stations inside, outside and in the margins of three anticyclonic eddies (ACE) and two potential cyclonic eddies (CE). To understand how microplanktonic communities are affected by factors at the mesoscale (10–200 km), we examine changes in physical conditions and the abundances of corresponding microplankton functional types along the transect. High biomass (>9 mg m^{-3}) was measured in an ACE off the south-eastern coast of the Cretan Arc, with high abundances of diatoms, radiolarians and Phaeocystis, suggesting a mechanism for localised enhanced growth. We examined whether the physical shear between the moving water inside the eddy and the surrounding ocean can cause sufficient turbulence, promoting mixing between deep and surface waters and enhanced vertical mixing at the edges of the eddy. This mixing leads to the upward transport of nutrients along the eddy's edge, fostering a nutrient-rich environment that directly supports greater phytoplankton abundance and productivity. Together with direct comparison of abundances in contrasting ACEs and CE we conclude that mesoscale processes play important roles in shaping microplankton communities, with bottom-up implications to the entire food web.

Intra-seasonal oscillations in the Eastern Mediterranean: atmospheric influence and oceanic response

Y. Feliks (1), A. Solodoch (1), and **H. Gildor** - hezi.gildor@mail.huji.ac.il (1)
1) he Fredy and Nadine Herrmann Institute of Earth Sciences, The Hebrew University of Jerusalem

This study investigates the intra-seasonal oscillations (ISOs) within the Eastern Mediterranean Sea (EM) and their atmospheric drivers. Our analysis identifies persistent ISO modes of variability with periods of 44, 33, 28, 24, 22, and 19 days in the velocity of the upper water column. The modal frequencies are persistent while the modal amplitudes varying across seasons. Winter ISOs are notably more intense and faster than those observed during the summer. The ISO modes are characterized by the formation of eddies with radii of approximately 40 km, interacting with the persistent gyres of the basin. Despite their relatively small scale, these eddies display synchronization across the basin.

In winter, the identified ISO modes exhibit nearly depth-independent flow down to 200 m, while in summer, the flow is significantly reduced in the upper 50 m and almost absent below. These seasonal differences are attributed to stronger stratification and a shallower thermocline in summer (less than 50 m) compared to winter (approximately 200 m).

Atmospheric ISOs, with periods tightly matching those in the ocean, are also identified in the 500 hPa geopotential field over the Near East, suggesting a coupling between atmospheric and oceanic ISOs. Consistently, atmospheric ISOs exhibit significantly stronger intensities during winter and are reflected in sea surface winds.

These atmospheric modes, which span 2000–4000 km, may drive the oceanic ISOs, serving as a basin-wide forcing mechanism. This coupling is analogous to a “musical composition” played out on the sea surface, where atmospheric oscillations orchestrate the oceanic response."

Viral lysis vs. nutrient starvation: effect on *Prochlorococcus* macromolecular structure and the microbial community

S. Givati - shirashgr@gmail.com (1, 2), D. Aharonovich (1), O. Weissberg (1), N. Belkin (2), Q. Zeng (3), E. Rahav (2) and D. Sher (1)

1) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel;
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Haifa, Israel.
3) Department of Ocean Science, Hong Kong University of Science and Technology. Hong Kong SAR, China.

In marine environments, cyanobacteria supply organic carbon to heterotrophic bacteria not only as they grow and photosynthesize but also as they die. We hypothesized that different types of mortality, for example phage lysis and nutrient starvation, will have contrasting effects on the macromolecular structure of the cyanobacterial cell, and that the subsequent release of organic matter will drive the activity and growth of different heterotrophic bacteria. To test these hypotheses, *Prochlorococcus* MED4 was infected by a phage (P-HM2) to examine the effect of infection on host macromolecular composition, compared to natural death by nitrogen starvation. We observed that RNA and DNA quotas increased for the infected *Prochlorococcus*, while protein quotas decreased in the nitrogen starved *Prochlorococcus*. Then, spent media and lysate from the dying cells was added to surface seawater collected from the Eastern Mediterranean collected in and autumn and spring. In both experiments dark primary production (DPP) significantly increased in the treatments added with spent media from starved Prochlorococcus. Surprisingly, no major differences were observed in the resulting community structure (as assessed by 16S rRNA and rDNA amplicon sequencing). However, metagenomic analysis suggests that the elevated DPP results from heterotrophic CO_2 fixation, involving enzymatic processes such as anaplerosis and amino acid degradation. It identifies potential contributors, including Pelagibacterales, Flavobacteria, and Oceanospirillales. Thus, we propose that the functional differences in response to different forms of mortality is due to a shift in community function towards heterotrophic CO_2 fixation.

P3 and P4 Appendages in Daphnia are not Filters

M. Gophen - Gophen@Migal.org.il (1), J.R. Strickler (2)
1) Migal-Galilee Scientific Research Institute; POB 831, Kiryat Shmone
2) The University of Texas at Austin Marine Science Institute Port Aransas Texas 78373

The feeding mechanism of *Daphnia* is essentially extracting, assembling and packing of particles such as algal cells from a micro-fluid maintain not by sieving, as considered throughout more than 100 years. Moreover, sorting cells in a microflow, and adding small concentraetions of info-chemicals to create a minute chemical landscape in the flow, is a current research topic. Daphnia magna, features four pairs of trunk limbs (P3, P4) that move at around 10 Hz and generate an in/out-current system to extract food particles. The long history of limnological sciences accepted functional definition of the P3 and P4 as filtering. Cinematographic (250 frames per second) analysis with tracer particles and dyes defined P3 and P4 as creators of internal water circulation supporting gas exchange (respiration), motility and feeding. Slow-motion tape projection and magnified solid photos did not confirm water migration through the P3 and P4 combs. Consequently, feeding mechanism comprised of particle extraction, assembling and packing is carried out not by sieving. Straining action requires energy and saving it is a profit. The P3 and P4 solid walls flapping function enhance resiliency whilst avoiding ecological weakness by saving the filtration energy. *Daphnia* is an ecologically successful self-contained “microfluidic devices”.

A recipe for regeneration- Investigation of wound healing in the solitary tunicate Ciona robusta

T. Gordon - tgordon611@gmail.com (1, 2, 3), T. Levy (1, 2), L. Manni (3), I. L. Weissman (2), A. Voskoboynik (1, 4)
1) Hopkins Marine Station, Stanford University, Pacific Grove, CA, USA
2) Institute for Stem Cell Biology and Regenerative Medicine, Stanford University School of Medicine, Stanford, CA, USA
3) Department of Biology, University of Padova, 35121, Padova, Italy
4) Department of Biology, Stanford University, Stanford, CA, USA

Ciona robusta is an invertebrate chordate that presents robust regeneration abilities. Following bisection along the anterior-posterior axes only the posterior body part regenerates all missing organs, while the anterior part fails to regenerate and eventually dies. The mechanistic basis for this variation in Ciona's regeneration abilities remains unknown. The current study uses Ciona partial regeneration as a model to compare the cellular and molecular events that led to regenerative versus non-regenerative outcome.

The immune response, proliferation rate and gene expression profile of both anterior and posterior body parts were studied at several time points during the regeneration process. Preliminary results suggest that, initially, specific injury-induced events occur in both body parts, yet, later, a unique expression profile was observed only in regenerating tissues.

To better characterized the cell types that mediate regeneration in this model, tissue samples were dissociated, cells were stained with non-species-specific stem cell markers and analyzed using flow cytometry. Putative stem-cell-enriched populations were isolated followed by single-cell RNA sequencing using the 10X pipeline. To validate the function of these specific populations in regeneration, these cells were transplanted into naïve animals that were injured 24hr following injections. One month following transplantation, the cells were tracked in-vivo and found within the tissues of the recipients.

The isolation of these cells allows a better understanding of the cell types that mediate regeneration and exploring the key factors that enable regeneration response.

Near zero waste biofloc-based RAS – overview

A. Gross - amgross@bgu.ac.il, Z. Zhu, O. Rachamim, S. Nayak, Y. Kpordzaxor, U. Yogev, A. Ronen, D. Zilberg
ZIWR, Jacob Blaustein Institutes for Desert Research, Ben Gurion University of the Negev, Midreshet Ben Gurion 84990, Israel.

Significant amounts of nutrients from fish feed are released into the fish tank water as dissolved and solid excretions resulting in environmental pollution. As an alternative to the conventional nitrification followed by water exchange or denitrification, assimilation-based biofloc technology (BFT) may be used to in-situ convert aquaculture excretions (with an additional external carbon source) into protein-rich microbial biofloc. We have suggested employing BFT within a side assimilation reactor. This reactor relies on activated sludge under microaerophilic conditions, with the fish-rearing water and solid excretion continuously circulating through it. To address the challenge of high outflowing turbidity, we introduced a submerged ultrafiltration membrane bioreactor (MBR), which led to an average turbidity in the fish of less than 25 NTU. The system offers numerous advantages including exceptional water reuse rates >99%, energy conservation, and minimal waste generation. Notably, the biofloc displays a protein content of approximately 40%, a substantial increase compared to aerobically based BFT systems which typically contain around 20% protein.

Dry microbial biofloc was utilized as a fish feed ingredient, replacing 15%-25% of the original feed, to examine its impact on fish growth, survival, and disease resistance. Across all groups, fish survival reached 100%. While the control group exhibited slightly higher weight gain (~15%) compared to the biofloc-fed group. Interestingly, the latter demonstrated significantly superior survival rates post-bacterial challenge of 89% vs. 58%. Variations in immunity were also observed based on the origin of the external carbon source. An economic analysis underscored the potential advantages of implementing biofloc commercially.

Invasional meltdown: How jellyfish facilitate non-indigenous fish dominance?

T. Guy-Haim - tamar.guy-haim@ocean.org.il (1, 2), A. R. Morov (1), G. Sisma-Ventura (1), N. Stern (1)
1) National Institute of Oceanography, Israel Oceanographic and Limnological Research, Tel Shikmona, P.O.B. 2336, Haifa 3102201, Israel
2) Department of Life Sciences, Ben-Gurion University of the Negev, Beer Sheva 84105, Israel

Jellyfish are generally assumed as voracious zooplanktivores, predating on fish eggs and larvae and competing with fish for zooplankton, significantly impacting pelagic food webs. The most prominent jellyfish in the Eastern Mediterranean Sea (EMS) is the invasive rhizostome Rhopilema nomadica, forming massive swarms. Previous study showed that the guts of R. nomadica medusae collected during summertime contain mostly microzooplankton. Here, we aimed to determine the trophic position and dietary sources of R. nomadica and co-occurring jellyfish species in the EMS using stable isotope analysis.

Scyphomedusae, including R. nomadica, were collected in the EMS during summer and wintertime. Potential prey items, including phytoplankton, microzooplankton, copepods, and native and non-indigenous fish larvae, were collected seasonally. Mean δ15N values of R. nomadica were 14.94 ± 4.69‰ and 7.43 ± 1.89‰ in the winter and summer, respectively, indicating seasonal succession and temporal dietary shift from high (winter) to low (summer) trophic levels. Bayesian mixing models showed a contribution of 34% of fish larvae to the diet of R. nomadica in the winter and <5% in the summer.

Seasonal trophic shifts were previously shown in several jellyfish species and are considered an inherent scyphozoan ontogenetic trait. Nonetheless, such shifts in R. nomadica have far-reaching implications for the EMS biodiversity. During the winter, larvae and eggs of native fish only are present in the EMS waters, whereas non-indigenous fish reproduce during spring and summertime. Therefore, R. nomadica potentially exerts higher predatory pressure on native fish, facilitating the dominance of non-indigenous fish, through an invasional meltdown process."

Hydrodynamic modulations of sea-clutter in coastal environment

N. Haim - nirhaim@tauex.tau.ac.il (1), V. Grigorieva (1), Y. Toledo (1)
1) School of Mechanical Engineering, Faculty of Engineering, Tel Aviv University

Marine X-band radars are becoming invaluable tools for ocean and coastal monitoring, offering high-resolution observations of spatial and temporal sea surface variations. These radars provide maps of surface currents, gravity waves, and winds by detecting the back-scatter of microwave electromagnetic waves from capillary waves via Bragg diffraction. This back-scatter, commonly referred to as sea clutter, is influenced by various factors, with short gravity waves (within the wind-wave range) being particularly significant. A common approach to isolating these wave fields involves linear regression of the root square of the signal-to-noise ratio: $Hs = m\sqrt{SNR} + n$. While this method is easy to implement, its simplicity overlooks many factors that also affect the SNR signature, potentially leading to inaccuracies in the interpretation of radar data.

An oceanographic radar station equipped with a WaMoSII system and FURUNO navigational radar (Far 2117 XN-24AF) was installed on the cliffs of Tsuk Beach, Tel Aviv (32°07’46.1”N 34°47’12.6”E). Over the past five years, this station has collected data on the nearshore zone, extending up to 4 km offshore, where water depths reach approximately 50 meters. However, comparisons between radar-derived significant wave heights and simultaneous in-situ measurements have revealed significant discrepancies, due to the influences of coastal hydrodynamic processes on sea clutter, such as tidal oscillations and edge waves. Understanding these biases will help refine the use of marine radars for coastal applications and presents a novel opportunity to observe coastal dynamics through sea clutter analysis.

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

A. A. Hamoud - alhanab.sweetie@gmail.com (1), R. Bar-Shalom (1), T. Perez (1), D. J. Repeta (2), and L. Steindler (1)
1) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa
2) Woods Hole Oceanographic Institution, Woods Hole, MA, USA (2)

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 food web. 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.

Biological filtration and digestion: impact on polystyrene and polylactic-acid microplastics particles in marine ecosystems

E. Harel - edenharel@mail.tau.ac.il (1), I. Zucker (2, 3 *), N. Shenkar (1, 4 *)

1) School of Zoology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv, 69978, Israel.
2) School of Mechanical Engineering, Faculty of Engineering, Tel Aviv University, Tel Aviv 69978, Israel.
3) Porter School of the Environment and Earth Sciences, Faculty of Exact Sciences, Tel Aviv University, Tel Aviv 69978, Israel.
4) The Steinhardt Museum of Natural History and National Research Center, Tel Aviv University, Tel Aviv, 69978, Israel.

Plastic pollution, a widespread environmental challenge, significantly impacts marine ecosystems. The degradation of plastic under environmental conditions results in the generation of microplastic (MP; <5 mm), frequently ingested by marine organisms across various trophic levels, including filter-feeders such as ascidians (Chordata, Ascidiacea). These organisms are integral to benthic-pelagic coupling, transporting MP from the water column through the marine food web.

Ascidians, sessile marine invertebrates, are highly efficient at capturing minute particles. Their filtering capabilities, sedentary nature, and their ability to thrive in both pristine and polluted waters, make them ideal models for studying interaction of plastic debris with marine organisms. Here, we investigated the influence of filtration and digestion by the solitary ascidian Styela plicata on the fate of MP in the marine environment, with a focus on contrasting two distinct plastics, polystyrene (PS) and the biodegradable polylactic-acid (PLA).

Within two hours of filtration, the ascidians efficiently cleared particles sized between 2-5 µm. Post digestion and secretion, PS concentrations increased, while PLA levels remained constant. Notably, the prevalence of smaller particles after digestion suggested potential fragmentation of PLA. Some MPs were egested repackaged within fecal pellets, which substantially increased the pellets' drag force and sinking velocity. Raman spectroscopy revealed notable alterations in the spectral characteristics of digested MPs, due to coating by organic substances.

These findings highlight the role of ascidians — and other filter-feeders— in modifying the structure of MP in their environment. Research into such modifications is essential to further understand the MP cycle and its broader ecological implications.

Sustainable seas: Cultivating the future

Dr. Orna Harel (1)
1) Sea2Cell

Imagine a world where fish are plentiful, but none are caught from the ocean. That's the promise of cultivated fish – grown from cells, not nets. It's climate-smart: no trawling, no ocean damage, and much lower emissions, giving our warming planet a bit of breathing room. Plus, it tackles food security head-on, providing a steady, sustainable protein source without overfishing. Cultivated fish isn’t just a lab experiment; it's a potential lifeline in the fight against climate change and hunger, swimming in the right direction.

Proposed biomineralization model for hyaline foraminifera based on the incorporation of minor and trace elements

H. Hagar - hagar.hauzer@mail.huji.ac.il (1,2), E. David (3), E. Jonathan (1)

1) The Fredy & Nadine Herrmann Institute of Earth Sciences, The Hebrew University of Jerusalem, The Edmond J. Safra Campus - Givat Ram Jerusalem 9190401, Israel
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, Haifa 3109701, Israel
3) School of Ocean and Earth Science, University of Southampton, European Way, Southampton, SO14 3ZH

Foraminifera biomineralization is under debate – two broad mechanisms have been proposed for the transport of ions to the site of calcification: (1) transmembrane transport (TMT) model – transport of mainly Ca^{2+} against H^+ to form the $CaCO_3$ shell, best represented by coccolithophores that calcify their shells intracellularly (2) seawater vacuolization (SWV) model – endocytosis of seawater as the main source of Ca and trace elements. The vacuoles are modified to elevated pH and DIC using alkalinity transporter to precipitate their calcite. Here we compare the partition of trace elements in foraminifera, coccolithophores, and inorganic calcite as a function of carbonate chemistry to shed light on their biomineralization mechanisms. In biogenic carbonates (foraminifera and coccolithophores) the distribution coefficient of Li (DLi) is much higher than most inorganic calcites, suggesting a strong biological control on this element. We propose that both DNa and DLi are higher due to activity of Na^+/H^+ ATPase as shown for coccolithophores, and Li is leaking through the Na transporter. Large difference in DLi and DNa between high and low-Mg foraminifera was observed perhaps indicating an effect of high-Mg on the partition of alkali elements in calcite. Low-Mg foraminifera (planktic and benthic) show DMg ~20 times lower than inorganic calcite, which supports a Mg-removal mechanism in low-Mg species. Coccolithophore DSr is higher than all foraminiferal species, implying that foraminifera do not utilize Ca^{2+} transport through which $_{Sr2}^{+}$ leaks. The biomineralization process in high-Mg foraminifera may include an amorphous calcium carbonate (ACC) precursor.

The effect of carbonate chemistry on the incorporation of trace elements into shells of benthic foraminifera

H. Hagar - hagar.hauzer@mail.huji.ac.il (1, 2), E. David (3), M. Wolfgang (4, 5), R. Yair (6), E. Jonathan (1)

1) The Fredy & Nadine Herrmann Institute of Earth Sciences, The Hebrew University of Jerusalem, The Edmond J. Safra Campus - Givat Ram Jerusalem 9190401, Israel
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, Haifa 3109701, Israel
3) School of Ocean and Earth Science, University of Southampton, University Road Southampton SO17 1BJ, UK
4) Institute of Geosciences, Goethe University Frankfurt, Riedberg Campus Altenhöferallee 1 Frankfurt Am Main 60438, Germany
5) FIERCE, Frankfurt Isotope & Element Research Center, Johann Wolfgang Goethe-Universität Frankfurt am Main, Altenhöferallee 1, 60438 Frankfurt am Main, Germany
6) Department of Marine and Coastal Sciences and Department of Earth and Planetary Sciences, Rutgers University, 71 Dudley Road, New Brunswick NJ 08901, USA

The sodium-to-calcium ratio (Na/Ca) of biogenic $CaCO_3$ has recently been introduced as a proxy for past seawater Ca^{2+} concentrations ($[Ca_2+sw]$) as demonstrated by a positive correlation between seawater and shell Na/Ca. Here, the effect of carbonate chemistry on the Na/Ca proxy was investigated culturing the large benthic species *Operculina ammonoides* under set of experiments independently varying pH and the dissolved inorganic carbon (DIC). In addition to Na+, the incorporation of Li^+, Mg^{2+}, and Sr^{2+} into the shells of this high-Mg calcitic foraminifer under constant DIC (~2170 µmol kg^{-1}) with varying pH (7.5-8.4 NBS), and under varying DIC (830-2470 µmol kg^{-1}) with constant pH (~7.9).

Na/Ca_{shell} and Li/Ca_{shell} in *O. ammonoides* are positively correlated with seawater carbonate chemistry (CO_3^{2-} and Ω), while Sr/Ca_{shell} and Mg/Ca_{shell} are much less sensitive to these factors. Given that past changes in surface ocean water Ω were probably small relative to changes in $[Ca_2^+{}_{sw}]$, the correction for this secondary effect over the Cenozoic is likely to be small. Therefore, we conclude that *O. ammonoides* Na/Ca sensitivity to the carbonate system is unlikely to compromise the use of this proxy to reconstruct past $[Ca_2^+{}_{sw}]$. Applying the Na/Ca proxy in the Cenozoic extinct Nummulites can be utilized for past Ca^{2+} reconstructions. Furthermore, coupling this information with the partition coefficients of other elemental and isotopic systems (e.g., Li^+, Sr^{2+}, Mg^{2+}, K^+, B, $\delta^{11}B$) may allow the reconstruction of wider aspects of past ocean chemistry.

An active-matter model for the formation of jellyfish swarms

E. Heifetz - eyalh@tauex.tau.ac.il (1), E. Gengel (1), Z. Kuplik (1), D. Angel (2)
1) Tel Aviv University
2) Haifa University

Jellyfish form large swarms showing a complex succession of active and passive movements. We present an active matter model for those swarming phenomena which considers counter-current swimming, avoidance of strong shear and coastlines and swarm recruitment. We model the jellyfish as active Brownian particles in the overdamped limit with directional preferences for flow direction, turbulence and a self-induced signaling tracer. The tracer corresponds to pressure fluctuations associated with the bell oscillation of jellyfish and pheromones. Jellyfish and tracer get advected by the background flow. Our analysis suggests that dense swarms are the result of a phase transition process which involves an interplay of flow and behavioral responses. In particular, we find that it in certain situations weak persistent recruitment is enough to initiate spontaneous emergence of swarms. Our numerical simulations show a high sensitivity of emergent structures to parameters, emphasizing the need for further model-based experiments.

Atmospheric microbial viability and nutrition in the oligotrophic east mediterranean sea

B. Herut - barak@ocean.org.il (1, 2), B. Ankri (1, 2), X. Dubinsky (1) and E. Rahav (1, 3)
1) Israel Oceanographic and Limnological Research, Haifa, Israel.
2) Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel.
3) Department of Earth and Environmental Sciences, Ben Gurion University of the Negev, Beer Sheva, Israel.

We present the coupling between leachable fluxes of atmospheric inorganic nitrogen and phosphorus (LIN and LIP, respectively) and surface water primary production and nutrient concentrations/pool during a full annual cycle at the oligotrophic Southeastern Mediterranean Sea. It was estimated that dry aerosols leachable fluxes of LIN can support between 2-4% of the surface primary production and between 1-19% of the NO_3 concentration in the seawater mixed layer, enhanced mainly during the stratified period and dust events. In addition, we investigated the viability of airborne prokaryotes over the eastern Mediterranean Sea. Airborne prokaryotes in sea-spray contained 5-34% of viable cells (median 21%), with an apparent E-W gradient between Cyprus/Crete (~10%) westwards to Sicily (~25%). Aerosols at ~20 m above the sea surface, reflecting cells with longer atmospheric transport, displayed a patchier distribution, with higher microbial viability in easternmost locations south of Cyprus and west of Crete (~25%).

Influence of tropical sea surface temperatures on sub-seasonal precipitation in the middle east

A. Hochman - assaf.hochman@mail.huji.ac.il (1), N. Shachar (1), H. Gildor (1)

Understanding the dynamics of sub-seasonal precipitation is vital for improving climate predictions, especially in regions vulnerable to water scarcity, like the Middle East. This study explores how tropical sea surface temperatures, specifically through the lens of two major climate drivers—the El Niño Southern Oscillation (ENSO) and the Indian Ocean Dipole (IOD)—affect sub-seasonal precipitation variability and predictability across the region. Focusing on the critical month of October, a key period for water resource management, we highlight the significant influence of ENSO and IOD events on rainfall patterns.

Our analysis reveals that simultaneous El Niño and positive IOD events lead to a striking 50% increase in precipitation compared to La Niña and negative IOD phases. We delve into the mechanisms behind these differences, including shifts in water vapor transport and changes in the frequency of essential rain-bearing systems. Notably, we find that El Niño, when paired with a positive IOD, paradoxically increases the frequency of Eastern Mediterranean cyclones, known as 'Cyprus Lows'—a counterintuitive result that we will explain in detail.

Despite these insights, the interaction between ENSO and IOD introduces significant challenges for sub-seasonal precipitation forecasting in the Middle East. Our findings enhance our understanding of the complex relationships between tropical sea surface temperatures and precipitation patterns and highlight the ongoing difficulties in forecasting sub-seasonal to seasonal weather in this climate-sensitive region.

Parasites in gelatinous zooplankton

A. Iakovleva - ctenophorana@gmail.com (1, 2), A. R. Morov (1), D. L. Angel (2), and T. Guy-Haim (1)
1) National Institute of Oceanography, Israel Oceanographic and Limnological Research, Tel Shikmona, P.O.B. 2336, Haifa 3102201, Israel
2) Department of Maritime Civilizations, University of Haifa, Mount Carmel, Haifa 3498838, Israel

Being an integral part of marine food webs, diverse gelatinous zooplankton species serve as hosts to a broad range of parasites. Studying these parasites is crucial, as they can affect host population dynamics and impact marine ecosystems and their functions. Host-parasite interactions are particularly intriguing when non-native species invade new regions, such as during Lessepsian migration, a common phenomenon in the Eastern Mediterranean Sea. As non-native species spread, they can transmit parasites to native host populations (parasitic spillover) or get infected with native parasites (parasitic spillback). In this study we describe host-parasite interactions in the gelatinous zooplankton of the Mediterranean and Red Seas.

We detected parasites in three species of scyphozoan medusae – *Rhopilema nomadica*, *Rhizostoma pulmo*, and *Aurelia solida*, inside the ctenophore *Mnemiopsis leidyi*, and inside the chaetognath *Flaccisagitta enflata*. Morphological examinations and molecular genetic analyses were used to determine the identity of the parasites. Identified parasites belong to a diverse group of animal taxa, including cnidarian planulae, and parasitic flatworms and roundworms – platyhelminthes (cestodes and trematodes) and nematodes. Here, we show for the first time a spillover of a burrowing sea anemone Edwardsiella carnea to the Mediterranean native barrel jellyfish R. pulmo and the invasive Indo-Pacific nomad jellyfish *R. nomadica*. We propose that *E. carnea planulae*, which are common parasites of *M. leidyi* in East Atlantic waters, were introduced with their host to the Mediterranean Sea, reaching the Southeastern Mediterranean. Future research is planned to examine potential implications of these parasites in controlling the populations of their gelatinous hosts.

Exploring fungal plasticity: phenotypic and genetic responses of marine aspergillus niger-like isolate to the presence of plastic polymers

S. S. Itzhari - shelizbio@gmail.com (1), K. Davidov (1) & M. Oren (1)
1) Department of Molecular Biology, Ariel University, Science Park, 40700 Ariel, Israel.

Plastic pollution in marine ecosystems is a global environmental concern. Due to their high abundance, endurance and other traits, plastic debris has become ideal surfaces for the colonization of a variety of marine microorganisms, including fungi. We found that an Aspergillus niger-like fungus from the Mediterranean Sea develops different phenotypic morphotypes in the presence of plastic, including attachment to pristine and UV-treated PET. To elucidate the molecular mechanisms underlying the PET-dependent morphotypes, we employed RNA-Seq using long-read nanopore MinION platform. The transcriptomic analysis revealed unique gene expression signatures that are associated with the interactions of this fungus with pristine and/or UV-irradiated PET polymers compared to the free-living fungus and identify genes that may be involved in attachment to the PET surface or its degradation. Our findings contribute to the understanding of the intricate interplay between fungi and plastic polymers at sea and suggest that fungi have developed new adaptations to this new type of man-made material.

Utilizing fatty acid ethyl esters from biological waste and natural sources as a treatment against parasitic diseases in fish

A. **Jawaji** - arunn.1016@gmail.com (1), I. Khozin Goldberg (1) and D. Zilberg (1)
1) The French Associates Institute for Agriculture and Biotechnology of Drylands, J. Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev.

Parasites are ubiquitous in aquaculture and have devastating effects with serious socioeconomic, ecological and animal welfare consequences. *Gyrodactylus turnbulli* (Monogenean) and *Trichodina* sp. (Protozoan) parasites of fish are of particular problem as currently there is no effective and permitted treatment for these diseases. Traditional chemical treatments are often toxic, may negatively affect the environment and are banned in many parts of the world, highlighting the need for alternatives. In our previous studies, we identified anti-parasitic effect of fatty acids and fatty acid ethyl esters (FAEEs), produced from the microalga Phaeodactylum tricornutum and its residue material. To expand the potential application of FAEEs, we investigated the effect of a broad range of FAEEs against G. turnbulli and Trichodina sp. and proposed additional natural sources, including coconut oil & and black soldier fly larvae (BSFL). We investigated a range of FAEEs against these parasites in guppies and barramundi, encompassing in-situ and ex-vivo tests, followed by toxicity assessments and in vivo efficacy studies on infected fish. FAEE prepared from P. tricornutum residue has effectively treated *Trichodina* sp. infection in barramundi. Of the most effective tested FAEEs, ethyl laurate (C12) emerged as a non-toxic, effective treatment against both parasites. This fatty acid is present at high levels in both coconut oil and BSFL, the latter produced from agricultural waste. The efficacy of preparation from these sources against *G. turnbulli* will be presented.

Cell-to-cell heterogeneity drives host-virus coexistence in a bloom-forming alga

N. Joffe - nir.joffe@weizmann.ac.il (1), C. Kuhlisch (1), G.Schleyer (1, 2), A.Shemi (1) and A.Vardi (1)*
1) Department of Plant and Environmental Sciences, Weizmann Institute of Science, 7610001 Rehovot, Israel
2) Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute, 07745 Jena, Germany

Algal blooms drive global biogeochemical cycles of key nutrients and serve as hotspots for biological interactions in the ocean. The massive blooms of the cosmopolitan coccolithophore *Emiliania huxleyi* are often infected by the lytic *E. huxleyi* virus (EhV), triggering bloom demise. This multi-annual "boom and bust" pattern of E. huxleyi blooms suggests that host-virus coexistence is essential for these bloom dynamics. To investigate host-virus coexistence, we developed a new model system from an *E. huxleyi* culture that recovered from viral infection. The recovered population coexists with the lytic virus, as host cells continue to divide in parallel to viral production. By applying single-molecule fluorescence in-situ hybridization (smFISH), assessing infection-specific lipid biomarkers, and generating clonal strain collections using single-cell sorting, we quantify the fraction of actively infected cells and phenotype the susceptibility of individual cells to EhV infection. We show that host population heterogeneity drives the host-virus coexistence. Our results unraveled substantial cell-to-cell heterogeneity across a continuum of susceptibility to resistance, highlighting that infection outcomes may vary depending on the individual cell. These results add a new dimension to our understanding of the complexity of host-virus interactions, commonly assessed in bulk and described by binary definitions of resistance or susceptibility. In addition, we explored the ecological consequences of coexistence with the lytic virus and found an existing advantage and tradeoff for the host. Finally, we present promising results for future anti-viral strategies of E. huxleyi using a comparative genomics approach on cells with distinct resistant phenotypes and identical genetic backgrounds.

Israel National Culture Collection of Algae (INCCA): Expanding the collection and the services provided

R. N. Kaplan Levy - ruth@ocean.org.il (1), A. Alster (1), E. Arogety Ben-Orr (1), N. Segal (2), D. Sade (3), M. Frada (4) and D. Avni (5)

1) Israel National Culture Collection of Algae (INCCA), Kinneret Limnological Laboratory, Israel Oceanographic & Limnological Research (IOLR), Israel.
2) The National Center for Mariculture in Eilat, Israel Oceanographic & Limnological Research, Israel.
3) Department of Life Sciences Core Facility, Environmental microbiome, Weizmann Institute of Science, Rehovot, Israel.
4) The Interuniversity Institute for Marine Sciences in Eilat & Department of Ecology, Evolution and Behavior, Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel.
5) Department of Natural Compound, Nutrition, and Health, MIGAL, Kiryat Shmona, Israel.

The Israel National Culture Collection of Algae (INCCA) was founded in 2020 at the Kinneret Limnological Laboratory, IOLR, with the aim of preserving Israel’s microalgae biodiversity. This abstract outline the recent expansions in the collection and the enhanced services now available to researchers and industry professionals. Over the past two years, INCCA has significantly increased its repository, incorporating over 250 strains of algae and cyanobacteria from diverse aquatic environments across Israel. The mono-algae isolated strains undergo morphological and molecular taxonomy including their microbiome identification. This expansion not only broadens the genetic diversity within the collection but also enhances the potential for discovering novel bioactive compounds and biotechnological applications.

In addition to the culture collection expansion, INCCA has upgraded its service offerings. The collection now provides the following services: live strains culture, classical and molecular taxonomy, potential of cyanotoxins production, toxicity tests and examination of bioactive molecules, scientific consultant and upscaling of cultures. Additional services are currently under development, including cryopreservation of strains, isolation of strains by demand, strain deposits and educational outreach programs.

Furthermore, INCCA has implemented a user-friendly online database (https://incca.org.il/), allowing for seamless access to strain information, research data, and ordering services. This digital transformation ensures that researchers worldwide can efficiently utilize the collection for their scientific endeavours. By expanding its collection and enhancing its services, INCCA continues to play a pivotal role in advancing algal research and promoting sustainable solutions to global challenges.

Nutrient supplemented carbonized aerogels for adsorption and enhanced biodegradation of hydrocarbons in aqueous environments

D. L. Karsagi Byron - danitlis@post.bgu.ac.il (1), H. Barak (1), B. Halpern (2), E. Kramarsky-Winter (2), L. Shelly (3), N. Azaria (3), S.l Hayun (3), A. Sivan (2) and A. Kushmaro (2, 4, 5)

1) Department of Civil and Environmental Engineering, Ben-Gurion University of the Negev, Beer-Sheva 84105, Israel
2) Avram and Stella Goldstein-Goren Department of Biotechnology Engineering, Ben-Gurion University of the Negev, Beer-Sheva 84105, Israel
3) Department of material engineering, Ben-Gurion University of the Negev, Beer-Sheva 84105, Israel
4) Ilse Katz Center for Nanoscale Science, Ben-Gurion University of the Negev, Beer-Sheva 84105, Israel
5) School of Sustainability and Climate Change, Ben-Gurion University of the Negev, Beer-Sheva 84105, Israel

Oil and petroleum spills are destructive environmental hazards contaminating water or soil and damaging the ecological balance of these environments. Since oil is composed of substances that are highly persistent and extremely toxic to the ecosystem there is ongoing search for efficient and sustainable remediation technologies. Of these technologies, the use of hydrophobic sorbents (i.e., aerogels) has recently become recognized as an ideal method for specific absorbance of hydrocarbons from aqueous environments.

Moreover, natural occurrence of oil biodegradation via microorganisms found in the environment, is also favored due to the conversion of hazardous constituents of oil into forms that are less toxic. However, the rate and range of biodegradation is limited due to the low concentrations of the necessary micro-nutrients in the environment and the low contact with oil components.

To increase oil remediation via in-situ adsorption and biodegradation in aqueous environments, we combined selective physical adsorption of hydrocarbons with a method to enhance biodegradation of the adsorbed oil using Nutrient Supplemented Carbonized Aerogels (NSCA). This is carried out through a novel technique for supplementation of critically nessecary nutrients on to the aerogel. This NSCA is characterized by high hydrophobicity (139°), high surface area (1035 m2/g), low bulk density (6 mg/cm3), and has a high adsorption capacity for hydrocarbons (78 g crude oil/g NSCA). To confirm the NSCA contribution to the enhanced biodegradation we deploy NSCA into an oil contaminated medium for a period of 21 days. We found that oil degradation was more efficient by two-fold when using NSCA as compared with oil degradation when using nutrient free Carbonized Aerogel (CA).

Alcanivorax, a genus of marine bacteria with varied tastes for hydrocarbons

A. Kartha - aishwaryakartha@gmail.com (1), Keren Davidov (1), Sheli-Shlomo Itzhari (1) and Matan Oren (1)
1) Department of Molecular Biology, Ariel University, Science Park, 40700 Ariel, Israel.

Over the past few decades, marine pollution has become a major global concern. Two significant pollutants that pose a constant risk to the marine environment are petroleum and its products, and plastic debris from various land and marine sources. Both types of materials are composed of hydrocarbons and originate from crude oil. We have isolated different strains of hydrocarbon-degrading bacteria of the genus Alcanivorax from marine plastic debris. These strains were tested for their ability to metabolize various liquid and solid hydrocarbons, including crude oil. The Alcanivorax strains were categorized into 3-4 groups based on their hydrocarbon metabolism profiles, which correlated with their colonization ability on different plastic polymer types. To understand the molecular basis of these findings, we obtained the full genomes of the strains and conducted a comprehensive screen for hydrocarbon-degrading gene candidates. The leading candidates will be further tested for their function using a knockout approach and through the expression and purification of relevant enzymes.

Methane gas in sediments of Lake Kinneret: a multiannual acoustic investigation and correlation analysis

B. Katsnelson - bkatsnels@univ.haifa.ac.il (1), R. Katsman (1), E. Uzhansky (1), A. Lunkov (1)
1) University of Haifa

Methane (CH_4) gas content is accommodated in discrete bubbles in shallow aquatic sediments. The bubble dynamics there are controlled by a diversity of physical, mechanical and biogeochemical processes that vary spatially and temporally over the aquatic ecosystem. In this study, a multiannual (2015–2021) acoustic database on gas content in sediments of Lake Kinneret, Israel is compiled. Gas content is evaluated by acoustic applications based on the sound speed inferred from the reflection coefficient. A multivariate linear regression is fitted and a closed form expression of gas content dependence on the following predictors, which change spatially and temporally over the lake, is obtained: 1) water depth; 2) short-leaving CH_4 production rate peaks fueled by punctuated phytoplankton bloom crashes; and 3) CH_4 bubble dissolution rates. Multidisciplinary analysis indicates that short-leaving CH_4 production peaks act as major controls on sediment gas content in Lake Kinneret, where the hydrodynamic regime and sloping bottom transport the autochthonous organic matter toward the profoundly lake zone. In contrast, the water depth predictor has the least significance, which is explained mainly by lack of ebullition in the deepest part of the lake. Process-based correlation analysis enables quantification and prediction of gas content dynamics in sediments. Modeling could be extended to other marine and lacustrine ecosystems with different predictors and temporal variability. Predicting CH_4 gas content dynamics is important for accurate evaluation and even reduction of a long-persisting uncertainty related to CH_4 flux from aquatic sediments and for assessment of sediment load-bearing capabilities affected by gas presence.

The first moored station at the deep eastern Levantine basin (DEEPLEV) – new insights from multi-annual synchronized measurements since 2016

T. Katz - timor@ocean.org.il (1), R. Alkalay (1, 2), Y. Weinstein (2), I. Berman-Frank (3) and B. Herut (1)

1) Israel Oceanographic & Limnological Research, Israel
2) Bar-Ilan University, Department of Geography and Environment, Israel
3) University of Haifa, Leon H Charney School of Marine Sciences, Israel

The eastern Levantine Basin (ELB) of the Mediterranean Sea is of great importance for its surrounding population and is arguably the most oligotrophic and anthropogenically impacted province in the ocean. The deployment of the first moored station at the ELB (DEEPLEV, since 2016), at 1500 m water depth, ~50 km offshore Haifa, aimed at generating synchronized, time-series measurements along the water column. The measurements, carried out by an array of sediment traps and sensors (measuring physical, chemical, and biological attributes), provide a better understanding of the system functioning. Indeed, about 10 scientific papers were already published providing new perceptions on the ELB system. We will briefly present a compilation of new insights derived from several years of DEEPLEV operation. These comprises reference to the carbon pump and the coastal-deep sea organic carbon and lithogenic particulate conveyor; relationships between lateral and vertical transport/fluxes; particulate sources; seasonal dynamics; currents and waves and more. This (ongoing) endeavor by a conglomerate of researchers from the Israel Oceanographic & limnological research (IOLR), Bar Ilan University, University of Haifa, Tel Aviv and the Hebrew universities, produced invaluable new knowledge.

Coral refuge in the Gulf of Aqaba to common reef-building corals during the 2024 global coral bleaching event

N. R. Kochman - naama-rose.kochman@mail.huji.ac.il (1, 2) and M. Fine (1, 2)
1) Department of Ecology, Evolution & Behavior, Silberman Institute of Life Sciences, The Hebrew University of Jerusalem
2) The Interuniversity Institute for Marine Science in Eilat, P.O.B 469 Eilat 88103, Israel

Intensifying and more frequent marine heatwaves (MHWs) pose an existential threat to coral reefs globally. Of the coral communities surviving consecutive MHWs, some communities undergo sensitization, while others experience acclimatization. Gulf of Aqaba (GoA) corals are renowned for their remarkable thermal resilience. This study investigated the effect of recurrent and intensifying MHWs on the survival, bleaching proxies and host and symbionts stored energy content (proteins, carbohydrates, and lipids) in Stylophora pistillata and Pocillopora damicornis in the Gulf of Aqaba/Eilat (GoA) over 4.5 years, including the fourth global coral bleaching event of 2024. During summer 2024, GoA corals experienced unprecedented thermal stress, with temperatures peaking at 32°C and cumulative heat stress reaching 30 Degree Heating Weeks (DHWs) – the highest DHWs worldwide during the 2024 global coral bleaching event and the 5th highest on record. While even milder conditions (DHW>20) typically result in extensive coral mortality (>80%), none of the tagged colonies exhibited mortality or bleaching, notably throughout summer 2024. Moreover, algal densities were similar, and chlorophyll levels were higher in peak summer 2024 compared to 2021 despite experiencing higher maximal temperatures (31.9°C vs 30.9°C) and almost 4-fold higher DHWs (27 vs 8). While the coral hosts demonstrated metabolic resilience across summer 2024, their symbionts showed reduced protein and stored energy, suggesting an enhanced nutrient translocation to the host to answer its higher energetic demand. This study contributes ecologically relevant evidence to the remarkable thermal resilience of corals from the GoA while emphasizing their global significance when facing an uncertain future for coral reefs.

Genetic adaptations of *Synechococcus* in the Red Sea

K. Kondratyeva - kirako@campus.technion.ac.il (1), M. Carlson (1, 2), M. Peleg (1, 3), I. Pekarsky (1) and D. Lindell (1)
1) Faculty of Biology, Technion - Israel Institute of Technology, Haifa, Israel
2) Department of Biological Sciences, California State University, Long Beach, CA, USA
3) Azrieli Technion Genomics Center, Technion - Israel Institute of Technology, Haifa, Israel

This project investigates the gene content of *Synechococcus*, a key primary producer in the Red Sea and the world's oceans, to understand its adaptations to varying physical, biochemical conditions, and microbial community fluctuations. The study includes an extensive collection of Red Sea Synechococcus isolates from different seasons and depths over two consecutive years, 2015 (n=798) and 2016 (n=783). Draft genomes (>2 Mb) were obtained for 1129 isolates. This dataset was complemented by Red Sea metagenomics samples (2015, n=40; 2016, n=45). The phylogenetic diversity of *Synechococcus* isolates was classified into clade, subclade, and phylotype levels using the petB genetic marker. Similar patterns of distribution were observed in both isolated and metagenomic samples, despite the latter showing a greater variety of phylogenetic groups. For instance, subclade IIa peaked in mid-spring across all depths but declined towards June, when subclades IIb and IIc became more prominent. Clade X also increased in abundance at the end of the mixing season. Among the draft genomes, clades II and X were predominant. Preliminary analysis identified accessory genes specific to certain phylogenetic groups, with 722 *Synechococcus* isolates being annotated. Their coding DNA sequences (CDSs) were clustered into gene families based on nucleotide identity, revealing correlations between gene families and Synechococcus subclades and phylotypes. This ongoing study aims to further explore the diversification of Synechococcus phylogenetic groups and their genetic and ecological specializations, providing deeper insights into their roles and adaptations in marine ecosystems.

Spatial and temporal distribution of physicochemical parameters and microbial communities in integrated multi-trophic aquaculture (IMTA) for sustainable mariculture

Y. Kpordzaxor - kpordzax@post.bgu.ac.il (1, 2), D. Nguyen (1, 2), S. Michael (3), L.M. Streb (3), A. Ben Zvi (4) and L. Guttman (2, 4)

1) Life Science Department, Ben Gurion University of the Negev, Eilat Campus, Eilat, Israel.
2) Israel Oceanographic and Limnological Research. National Center for Mariculture, Eilat, Israel.
3) Helmholtz Zentrum München – Deutsches Forschungszentrum für Gesundheit und Umwelt (GmbH), Munich, Germany.
4) Life Science Department, Ben Gurion University of the Negev, Be'er-Sheva Israel.

Bacteria are pivotal players in the aquaculture environment by determining water quality and cultured organisms' growth, health, and resilience. Hence, understanding the dynamics of microbial communities under different conditions is vital for improving aquaculture sustainability through bacterial management. The current study focused on the dynamics of microbial communities in water and different host organisms in an integrated multi-trophic aquaculture (IMTA) system where sea urchins (*Paracentrotus lividus*), mullet fish (*Mugil cephalus*), and green seaweed (*Ulva fasciata*), are cultured in line to improve culture productivity, sustainability, and cost-effectiveness. Over twelve weeks, the physicochemical parameters and growth performances were monitored in the different culture units, while 16S rRNA analyses characterized the dynamics in microbial communities' composition and functionality along time and space (i.e., culture units and hosts). The results revealed distinct microbial compositions across the different culture units, with significant variations in alpha and beta diversity influenced by environmental factors. Flavobacteriales were higher in the in-situ waters as compared to the organisms and most abundance in the *Ulva* unit. Enterobacterales were most abundance in fish gut than other sample sources. Pseudomonadales and Synechococcales were higher in the sea urchin water than other units. Vibrio were significantly lower in the *Ulva* unit than sea urchin than fish unit. The *Ulva* thallus maintained stable microbial diversity throughout the experiment demonstrating its role as a biofilter filter. Temporal changes in microbial communities, especially in later weeks, were linked to fluctuations in physicochemical parameters. For example, the fish unit is particularly influenced by total nitrogen, temperature, and ammonia. The clustering of the *Ulva* community is also influenced by similar factors, but more responsive to total phosphorus and BOD. Week zero communities were much influenced by DO and TOC for fish and Ulva units. Alpha diversity was highest in the sea urchin water, indicating a dynamic microbial environment, while the Ulva unit maintained a more balanced microbial community. Significant functionality diversity was observed in the sea urchin and Ulva units for the in-situ waters. Sea urchin gut and *Ulva* thallus, fish gut and *Ulva* thallus were significantly different for their alpha diversities. Ammonia shows a strong positive correlation with multiple microbial orders such as Lactobacillalles, Enterobacterales, Pseudomonadales, and Rhodobacterales in the sea urchin unit. Temperature and total phosphorus also correlate positively with several microbial orders, including Corynebacteriales, Pseudomonadales, and Synechococcales. Dissolved Oxygen and total organic carbon generally show negative correlations with microbial orders, especially with Erysipelotrichales and Corynebacteriales in the sea urchin unit. In the fish unit, Enterobacterales and Rhodobacterales show strong positive correlations with temperature. Enterobacterales, Flavobacteriales, and Corynebacteriales also exhibit positive correlations with ammonia. Total suspended solids and Biochemical Oxygen Demand have more moderate correlations with microbial orders, such as Pseudomonadales and Flavobacteriales. Phosphorus shows moderate correlations with Rhodobacterales, Pseudomonadales, and Lactobacillales. Enterobacterales and Chitinophagales exhibit significant positive correlations with ammonia in the *Ulva* unit in-situ waters. Synechococcales show moderate positive correlations with temperature and TSS. Rhodobacterales also show a positive correlation with temperature and BOD. DO shows strong negative correlations with Enterobacterales and Flavobacteriales. These findings contribute to our understanding of microbial management in aquaculture, offering valuable insights for enhancing the productivity and sustainability of IMTA practices.

Development of tractable coral models for understanding their biology

E. Kramarsky Winter - Esti.winter@gmail.com (1), A. Kushmaro (1)
1) Ben Gurion University, Department of Biotechnology Engineering

Coral reef systems are important complex living environments that play a role in oceanic wellbeing. Stony corals, keystone reef organisms, form the solid structure and backbone of these reefs. Many members of this evolutionarily basal class are known to produce biologically active compounds or biologically unique organelles making them not only important from an environmental point of view but also important in their use as source of bioactive materials. In recent decades, incidences of mass coral mortality due to disease, and pollution have increased, driven by a combination of anthropogenic and natural causes. This has raised the worldwide concern for coral well being, and the environmental and societal services they provide. Consequently there arose a need for a tractable model system to better understand coral biology, and their response to specific stressors. Over the last decade we have developed miniaturized coral tissue model lines that can be shared and utilized by researchers from a variety of laboratories offering an important advantage for studying dynamic complex processes such as those occurring in reef environments. We provide a proof of concept for their usefulness in numerous research endeavours ranging from examining calcification at a microscale, to assessing toxicological effects of suspected micro pollutants on coral physiological health providing us a better understanding of their biology and resilience.

Rhopilema nomadica in the Mediterranean: molecular evidence for migration and ecological hypothesis regarding its proliferation

Z. Kuplik - zafrirkuplik@tauex.tau.ac.il (1), H. Dror (2), K. Tamar (1), A. Sutton (3), J. Lusana (4), B. Lugendo (4) and D.L. Angel (2)

1) The Steinhardt Museum of Natural History, Tel Aviv University, Tel Aviv, Israel
2) Recanati Institute for Maritime Studies and the Department of Maritime Civilizations, University of Haifa, Israel
3) Seaunseen, Tanzania
4) Department of Aquatic Sciences and Fisheries Technology, University of Dar es Salaam, Tanzania

Since it was first observed in Israel in the 1970s, *Rhopilema nomadica* has established a reputation as one of the worst invasive species in the Mediterranean Sea. It was assumed to originate in the Red Sea, or in the Indo-Pacific region, but in the absence of additional reports of live specimens outside the Mediterranean, its origins remained a mystery. Here, via molecular analysis, we present the first verified results of the existence of *R. nomadica* in the Western Indian Ocean. Moreover, using additional evidence from *Cassiopea andromeda* and *R. nomadica*, we propose that the construction of the Aswan High Dam may have led to the proliferation of *R. nomadica* in the Levantine Basin.

Detecting microplastics in the ocean: unveiling spectral signatures for enhanced identification

G. Kurtser - gili.kurtser@mail.huji.ac.il (1), C. Haspel (1)
1) The Fredy and Nadine Herrmann Institute of Earth Sciences, Hebrew University of Jerusalem, Jerusalem, Israel

The increase of microplastics in marine ecosystems presents a growing ecological threat, affecting aquatic life through ingestion, entanglement, and the release of harmful toxins. Accurate detection of these pollutants is crucial for understanding their distribution and impact. Traditional methods of assessing plastic pollution primarily rely on in situ sampling, which is time-consuming, labor-intensive, and costly. However, remote sensing offers a more efficient, scalable alternative. In this study, we introduce a novel approach in three stages: (1) using unsupervised machine learning, we identify the common types of plastics found in the ocean and examine the characteristics that influence their reflectance; (2) using a single scattering model with measured size distributions and measured refractive indices as input, we perform realistic, high resolution calculations of the Mueller matrix elements of microplastics in seawater; (3) using the multiple scattering model OSOAA (Ordres Successifs Océan Atmosphère Avancé; Advanced Successive Orders Ocean Atmosphere), we simulate the spectral reflectance of an ocean-atmosphere system in which the ocean contains varying microplastic concentrations, considering all orders of scattering, absorption, reflection, and transmission in the coupled atmosphere-ocean system. Thus, we simulate the unique spectral signatures of microplastics in seawater as observed from satellite altitudes. Utilizing these spectral signatures, our results can help inform the designs of satellite-based remote sensing algorithms for real-time monitoring of microplastics across vast oceanic regions, significantly reducing the need for laborious field sampling.

Sialic acid modification attenuates viral infection in a cosmopolitan alga

B. Labbel - ben.labbel@weizmann.ac.il (1), D. Schatz (1), S. Ben-Dor (2), O. Dym (2), F. Sanchez (3), S. Yau (3), and A. Vardi (1)

1) Departments of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, Israel.
2) Life Sciences Core Facilities, Weizmann Institute of Science, Rehovot, Israel.
3) Observatoire Oéanologique de Banyuls-sur-Mer, France.

The relationship between microalgae and their viruses profoundly influences primary production in marine ecosystems and global biogeochemical cycles. Despite this critical importance, our understanding of algal defense mechanisms against viral infections remains limited, and these mechanisms hold significant biotechnological potential for applications such as crop protection. This study unveils a novel anti-viral defense mechanism employed by the cosmopolitan green alga *Ostreococcus tauri*. We elucidate that this defense mechanism involves the regulation of sialic acids (Sias), mediated by the gene cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMAH). Sias are known to be crucial in pathogen recognition and specificity in animals, where they often serve as receptors for viral entry. Our results demonstrate that Sias undergo significant alterations in *O. tauri* during infection and recovery through CMAH expression, leading to an increase in N-glycolylneuraminic acid (Neu5Gc) in resistant cultures. Through genetic engineering, we demonstrate that overexpression of the CMAH gene in a susceptible *O. tauri* strain led to a remarkable enhancement in defense against viral infection. Acquired resistance was attributed to decreased viral particle adsorption to the cell, resulting in a delayed active viral infection, as quantified using single-molecule fluorescence in situ hybridization (smFISH). Furthermore, phylogenetic and structural analyses reveal that the distribution of CMAH is highly selective among marine protists. These findings indicate strong evolutionary conservation of the functional role of Sias in host-pathogen interactions, extending from animals to algae, and balanced by high selective evolutionary pressure in marine ecosystems.

Monitoring ecological shifts in Israeli marine reserves: impact of enforcement

O. F. Landau - orif@npa.org.il (1), E. Guk(1) and R. Yahel(1)
1) Science division, Israel Nature and Parks Authority

In recent years, enforcement within marine reserves in Israel has increased. Consequently, it is essential to determine whether enhanced enforcement has led to an improvement in the ecological status of the community within the reserves. To address this question, a comprehensive index is needed to assess ecosystem status over time and space. This study follows ECOfast index, an integrative ecological tool for ecosystem-based assessment of Shallow Rocky Reefs. The index uses rapid, non-destructive SCUBA diving surveys documenting fish, invertebrates and algae in the eastern Mediterranean Sea. The index integrates information on key species such as the size of individuals, commercial value, the presence of non-indigenous species and the IUCN status of species. Using this index, we assessed changes in the ecological status of Israel's marine nature reserves based on extensive local surveys conducted since 2015, which included visual identification of fish, invertebrates, and algae. Preliminary results show an overall improvement in the ecological status of the community since 2015, highlighting the recovery of biodiversity hotspots within the reserves. These changes are visualized using maps illustrating shifts over time and across spatially interpolated areas. The ECOfast index is a powerful tool for marine reserve management, enabling spatial and temporal tracking of ecosystem status in response to changes in management regulations. By evaluating ecological status, the index identifies areas within reserves that are particularly sensitive due to higher biodiversity. Integrating survey data into a single framework will help managers prioritize conservation efforts and protect biodiversity in Israel’s marine nature reserves.

Demystifying heterotrophic diazotrophy in streambeds

R. Lander - Landerr@post.bgu.ac.il (1), E. Geisler (1), C. Villamarin (1), S. Arnon (1), A. Gafni (1), H. Siebner (1), E. Bar-Zeev (1)

1) Zuckerberg Institute of Water Research, Ben-Gurion University of the Negev, Sde Boker"

Aquatic heterotrophic N_2 fixation plays an important role in primary and secondary production. However, freshwater environments pose a challenge in determining the role of heterotrophic diazotrophy due to ecological heterogeneity. Here, we investigate diazotrophy along freshwater subsurface layers, focusing on two lifestyles: biofilm-associated cells attached to sediment and planktonic cells in porewater. Samples were collected from aerobic and anaerobic layers of the subsurface in the Jordan river and incubated in microcosms for 24h with ^{15}N under ambient conditions. After, samples were analyzed for diversity of the different lifestyles, abundance, and N_2 fixation rates. Confocal scanning laser microscopy unveiled the isochronal presence of phototropic (cyanobacterial) diazotrophs in aerobic sediment biofilms and a more abundant dispersal of diazotrophs in anaerobic biofilms. Immunolabelling the nitrogenase enzyme coupled with flow-cytometry indicated that aerobic sediment had a greater quantity of diazotrophs and higher proportion of diazotrophs to total bacteria than the anaerobic layer (10%, 4%, respectively). Nevertheless, most proportions of diazotrophs to bacteria ranged from 1% to 11%. Furthermore, significantly higher N_2 fixation rates were measured in anaerobic porewater in the summer than the winter with a mean difference of 0.4 nmol N $L^{-1}d^{-1}$ and in anaerobic sediment along this same trend with a mean difference of 18 nmol N $g^{-1}d^{-1}$. Preliminary DNA sequencing identified the dominancy of Desulfobacterota and Pseudomonadota in the anaerobic pore water. Altogether, our results and corresponding insights intimate the immense importance of subsurface diazotrophy to the N cycle in freshwater environments considering its seasonal, temporal, and eco-stoichiometric vicissitudes.

Sea surface microlayer mediates microbial flux between the atmosphere and Pacific ocean

A. C. Tastassa (1, 2), Y. Dubowski (1), O. Argaman-Meirovich (1), I. Kuzmenkov (1), **N. Lang-Yona** - naama.ly@technion.ac.il (1)

1) Civil and Environmental Engineering, Technion – Israel Institute of Technology, Haifa, Israel
2) Department of Chemical Engineering and Applied Chemistry, University of Toronto, Toronto, Ontario, Canada

Marine-atmosphere microbial exchange plays a significant role in global nutrient cycling, gene transfer, and marine ecology, though mechanisms are poorly understood. To better understand this process, we investigated the role of the sea-surface microlayer (SML) in mediating marine emissions of bioaerosols. We analyzed the 16S rRNA gene and transcript sequences from surface seawater (SW), SML, and marine atmosphere samples, collected across a gradient of latitudes between the North Gyre and Equator in the Pacific Ocean. Genomic signature varied diurnally and spatially in all environments, where the SW community is the most consistent and air the most variable. Interestingly, the SML genomic community variability clusters directly between SW and air, much like its environmental position. The 16S rRNA transcript signature, used as a proxy for microbial activity and viability, showed tight clustering in the air and SML suggesting selective control of the active microbial community in these environments compared to SW. Further, the transcriptional community composition in the air clustered between the SML and SW, pointing to viable non-SML-mediated exchange. Abundant taxa from air-associated and marine-associated phyla show a gradient of presence through the three environments of interest, suggesting an exchange of key organisms through the SML. This study contributes to improving clarity in the role of the SML in the exchange of marine bioaerosols, advancing our understanding of how microbial communities travel and best utilize their environment.

The source to sink signal transfer of particulate matter in the Gulf of Aqaba, northern Red Sea

G. Lapid - gil.lapid@mail.huji.ac.il (1, 2), A. Torfstein (1, 2)
1) Institute of Earth Sciences, Hebrew University of Jerusalem
2) Interuniversity Institute for Marine Sciences of Eilat

Deep sea sediments record the history of the oceans and of the atmosphere through the ongoing accumulation of the sinking particle flux on the seafloor. Nevertheless, the accumulating sediments might experience significant compositional shifts during their journey from source to sink, including weathering of atmospheric dust or fluvial material, scavenging or reverse-scavenging of chemical elements in seawater, and the formation of authigenic phases on or within sinking particles. Thus, the interpretation of deep sea sediments is not straightforward and warrants careful examination and evaluation.

Here, we investigate the source to sink signal transfer in the Gulf of Aqaba, northern Red Sea by studying two overlapping time series of atmospheric dust, collected between 2009-2019, and sinking particulate matter collected using a sediment trap deep mooring between 2015-2018. The samples were sequentially leached such that five (dust) or four (marine particles) mineralogic phases in each sample were separated, and the uranium isotopic composition (234U/238U) and inorganic elemental abundances were determined. The results are used to characterize the geochemical fingerprint of the different components of the samples, their provenance, and the variations between the atmospheric and marine particle flux composition. Moreover, the (234U/238U) composition of the silicate minerals can be used to assess the relative timeframe of sediment transport from source to sink, and we explore this by developing a conceptual model for the evolution of (234U/238U) over time.

Spatial association between jellyfish and phytoplankton at the sub-kilometer scale

O. Lapidot - Lapidot4@gmail.com (1), P. Gray (2, 3), I. Berenshtein (1), T. Lotan (1), D. Sher (1), E. Boss (3) and Y. Lehahn (2)

1) Department of Marine Biology, Charney School of Marine Sciences, University of Haifa, Haifa, Israel
2) Department of Marine Geosciences, Charney School of Marine Sciences, University of Haifa, Haifa, Israel
3) School of Marine Sciences, University of Maine, Orono, Maine

Marine ecosystems have complex networks of relationships between species. These relationships can manifest in the spatial patterns of different populations, yet spatial associations of populations across trophic levels are rarely explored. Jellyfish are a ubiquitous and increasing component of global marine ecosystems, consume zooplankton, and provide food for many predators. They are a vector for carbon export, which, in turn, affects phytoplankton community structure. In high densities, jellyfish swarms may help distinguish water masses of different origins which may create ecological boundaries of different phytoplanktonic species. Despite their important role in marine biogeochemical cycles, the impacts of jellyfish swarms are poorly understood, particularly at small scales (<1 km). In this study, we mapped out jellyfish density using ship and aerial survey techniques, collected water samples inside and outside aggregations of nomad jellyfish (Rhopilema nomadica), and analyzed the picophytoplankton composition (Synechococcus, Prochlorococcus, nano and pico-eukaryotes) and heterotrophic bacteria. We used ship-based radiometry and satellite-based chlorophyll-a measurements, together with the flow cytometry counts to spatially cluster the phytoplankton communities inside and outside the swarms. Our observations, from July of 2022, are the first quantitative evidence for jellyfish patches in scales of ~300 meters. We report on patchiness around the swarm with significant differences inside and outside. Our results shed new light on jellyfish-phytoplankton spatial association at very small scales and contribute to our understanding of the role of jellyfish in marine and coastal ecosystems, especially in uncertain future of globally gelatinous-dominated ocean.

Feeding fish alcohol?

A. Laskavi (1), E. Poverenov (1), S. Harpaz (2)
1) Center for Agro-Nanotechnology, Institute of Postharvest and Food Sciences, Agricultural Research Organization the Volcani Center
2) Department of Poultry and Fisheries, Institute for Animal Research, Agricultural Research Organization the Volcani Center

Fish, especially carnivorous fish, require a high level of protein in their food. The enzymatic degradation of protein is carried out in the fish intestine mainly by the digestive enzymes trypsin and chemo-trypsin. The activity of these enzymes in small fish is low and improves as the fish grow. In past experiments, alcohol has been shown to enhance protein-digesting enzymes of fish (in-vitro) and significantly improves their activity. Different alcohols were examined and a clear association was found between the structure of the alcohol and the intensity of the activity improvement. The alcohol must be brought to the site of activity i.e. the fish intestine. Normally, most of the alcohol added to food will be absorbed in the stomach and will not reach the intestine. One way to protect alcohol on its way to the intestine is by using microcapsules in which the alcohol will pass through the stomach and then reach the intestine. However, such microcapsules are very expensive. Therefore, several other possible alternatives to protect the alcohol were examined. It was found that by supplementing the feed with 1% propanol and/or butanol alcohol, it is possible to obtain better growth of the European sea bass (*Dicentrarchus labrax*) and the Asian sea bass (*Lates calcarifer*) also known as Barramundi.

Navigating innovation: building scalable sales strategies in the aquaculture market

A. Lavi - aranl@atlantium.com (1)
1) Global Aquaculture at Atlantium Technologies

In today's rapidly evolving aquaculture market, even the most innovative technologies can fail if they are not supported by effective sales, marketing and BD strategies. One of the biggest challenges for start-ups, often overlooked by entrepreneurs, is not the next sale, but rather developing a systematic, reliable and scalable sales process under the contestants of both resources and time. I will discuss the unique challenges start-ups face in the technologically saturated market and how innovative approaches to sales and marketing can help navigate these complexities, build a sustainable sales process and effectively make the transition from innovation to growth.

Aerobic methane production in nitrogen-depleted oceanic regions

Lázaro García J.A - lgjaimeabdiel@gmail.com (1), A. Hamoud (1), R. Bar Shalom (1), D. Repeta (2) Sosa O. (3), L. Steindler (1).

1) Department of Marine Biology, Leon H. Charney School of Marine Science, University of Haifa, Haifa, Israel
2) Woods Hole Oceanographic Institution, Massachusetts, USA
3) University of Puget, Tacoma, Washington USA.

Phosphorus (P) and nitrogen (N) are common limiting elements for primary and secondary production in aquatic environments. Interestingly, important amounts of the potent greenhouse gas methane are produced under the depletion of these inorganic nutrients. It has been demonstrated that the utilization of dissolved organic nutrient compounds can result in methane emissions. Specifically, under P-limiting conditions, the utilization of methylphosphonates (MPn) as a phosphorus source by marine bacteria leads to methane release. Moreover, it has been suggested that methylamine and other methylated compounds, such as dimethylsulfoniopropionate (DMSP), may result in methane emissions under N-depletion. While methane production via the degradation of MPn has been studied in relative depth, little is known about the specific metabolism, genes, and microbial groups involved in methylamine and DMSP-related aerobic methane production. This research aims to identify whether methylated organic compounds, like methylamine and DMSP, can be utilized as nitrogen and sulfur sources by marine bacteria through the aspartate aminotransferase pathway (AAT) and the DMSP lyase pathway (dddD), respectively, while releasing methane. In this study, we investigate the potential for methane release by marine bacterial isolates that are abundant members of the natural marine microbial community, such as members of the SAR11 clade. The results from this research will enhance our understanding of the sources of methane that contribute to the typical methane supersaturation observed in surface oceanic waters.

Air-sea interactions in stable atmospheric conditions: lessons from the desert semi-enclosed Gulf of Eilat (Aqaba)

S. Abir (1, 2), H. A. McGowan (3), Y. Shaked (1,4), H. Gildor (1), E. Morin (1), and **N.G. Lensky** - Nadavl@gsi.gov.il (1, 2)

1) Institute of Earth Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel
2) Geological Survey of Israel, Jerusalem, Israel
3) Atmospheric Observations Research Group, The University of Queensland, Brisbane, Australia
4) Interuniversity Institute for Marine Sciences, Eilat, Israel

Accurately quantifying air-sea heat and gas exchange is crucial for comprehending thermoregulation processes and modeling ocean dynamics; these models incorporate bulk formulae for air-sea exchange derived in unstable atmospheric conditions. Therefore, their applicability in stable atmospheric conditions, such as desertenclosed basins in the Gulf of Eilat/Aqaba (coral refugium), Red Sea, and Persian Gulf, is unclear. We present 2-year eddy covariance results from the Gulf of Eilat, a natural laboratory for studying air-sea interactions in stable atmospheric conditions, which are directly related to ocean dynamics. The measured mean evaporation, 3.22m yr^{-1}, approximately double that previously estimated by bulk formulae, exceeds the heat flux provided by radiation. Notably, in arid environments, the wind speed seasonal trend drives maximum evaporation in summer, with a minimum winter rate. The higher evaporation rate appears when elevated wind, particularly in the afternoon, coincides with an increase in vapor pressure difference. The inability of the bulk formulae approach to capture the seasonal (opposite from our measurements) and annual trend of evaporation is linked to errors in quantifying the atmospheric boundary layer stability parameter. Most of the year, there is a net cooling effect of surface water (-79Wm^{-2}), primarily through evaporation. The substantial heat deficit is compensated by the advection of heat via northbound currents from the Red Sea, which we indirectly quantify from energy balance considerations. Cold and dry synoptic-scale winds induce extreme heat loss through air-sea fluxes and are correlated with the destabilization of the water column during winter and initiation of vertical water-column mixing.

CO_2 sequestration by $CaCO_3$ dissolution: Laboratory experiments, kinetics and implications

A. Levi - adam.levi@mail.huji.ac.il (1), D. Avnir (2), J. Erez (1)
1) Institute of Earth Sciences, The Hebrew University of Jerusalem, Israel
2) Institute of Chemistry, The Hebrew University of Jerusalem, Israel

Carbon dioxide (CO_2) increase in the atmosphere is the major contributor to the greenhouse effect, global warming, and climate change. Removing CO_2 from the atmosphere, its capture and sequestration are of great importance for global environmental remediation. Here we present a method for CO_2 sequestration by its use for the dissolution of calcium carbonate ($CaCO_3$), with or without carbonic anhydrase (CA) catalysis. By this process, CO_2 is captured by its conversion to dissolved HCO_3^{2-} according to $CO_2+H_2O+CaCO_3$ -> $2HCO_3^{2-}+Ca^{2+}$ the solution of which can be safely discarded to the ocean. This approach is in contrast to many studies that propose $CaCO_3$ precipitation for CO_2 sequestration. A series of closed system batch experiments were conducted with coral aragonite in distilled water with various concentrations of CO_2 at constant temperature (25°C). The effect of $CaCO_3$ particles size (i.e., surface area), reaction time and presence of CA were investigated. Measurements of alkalinity and pH were used to evaluate the dissolution rates and the CO_2 sequestration capabilities of the system. The results show removal efficiency of CO_2 ranging from 30% to 95% depending on the initial CO_2 concentration (0.04% to 100%). Sequestration rate was largely affected by particles size and CO_2 concentration. CA catalysis increased the rates by a factor of 2 to 5, depending on the CA and CO_2 concentrations. This experimental system can remove large amounts of CO_2 in a relatively short time and CA catalysis accelerates sequestration rate. Modeling the results show high efficiencies even at relatively low CO_2 concentrations of 800 ppm to 2000 ppm.

Wave climate along the Mediterranean coast of Israel

A. Levin - lanna@technion.ac.il (1), M.Sladkevich (1), D. Bar (1), A. Zavadsky (1)
1) Coastal and Marine Engineering Research Institute, Technion City, Haifa 32000, Israel

The wave measurements along the Israeli Mediterranean Coast consist of three major datasets: (1) visual observations at Ashdod (1957-1975); (2) combined instrumental and visual measurements at Ashdod: wave heights and periods were measured by a Datawell waverider buoy, directions were estimated visually (1976-1991); (3) instrumental measurements of all wave parameters by the directional Datawell waverider buoys at Ashdod since 1992 (95.7% coverage) and at Haifa – since 1993 (94.6% coverage). The buoys are moored at about 24 m depth (~2 km offshore).

The study presents long-term analysis (annual, seasonal, monthly) of main wave parameters (significant wave height H_m0, mean wave direction MWD, peak wave period T_p, wave energy P_w) during 29 hydrographic years (01.04.1994-31.03.2023). The maximum recorded Hm0 is 6.82 m at Ashdod and 7.35 m – at Haifa. The dominant wave direction is WNW at both locations. Long-term trends in changes in wave heights and energy were not detected.

Wave storm events were specified and analysed. The storms were divided based on their energy, into five classes: weak, moderate, significant, severe, extreme. During the considered period 752 storms were revealed in Ashdod and 680 – in Haifa. At both locations the stormiest month is February during which the maximum wave energy was obtained.

Extreme wave analysis reveals that waves with Hm0=7.7 and 8.4 m can be expected once per 100 years at Ashdod and Haifa, respectively. No such waves were recorded during the considered period. According to our analysis the return period of the recorded maximum wave heights is 20 years.

Mercury levels in loggerhead and green sea turtle eggshells from nests along the Mediterranean coast of Israel

O. Levin - orin.levin@mail.huji.ac.il (1), M. Asfur (1), Y. Levi (2), O. Rybak (2), A. Shachnai (3), J. Silverman (3)
1) Faculty of Marine Sciences, Ruppin Academic Center, Mikhmoret, Israel
2) Israel's Sea Turtle Rescue Center, Nature & Parks Authority, Mikhmoret, Israel
3) National Institute of Oceanography (IOLR), Tel Shikmona, Haifa, Israel

Sea turtles roam vast regions of the Mediterranean Sea throughout their lives, during which they accumulate mercury, primarily as a function of their tropic level and age. This study examined the spatial distribution of mercury in hatched eggshells of loggerhead sea turtles (caretta caretta, n=180) and green sea turtles (chelonia mydas, n=40) from nests along the Mediterranean coast of Israel. This was done to determine spatial trends of mercury exposure on a regional scale in nesting females, assuming that eggshell mercury levels are related to the mother's mercury burden. Ten eggshells were sampled from each nest during the nesting seasons of 2022, and 2023 (n=22).

Some of the nests were transferred to protected enclosures after the eggs were laid. In general, mean mercury levels in each nest varied greatly between nests from the same enclosures and between different shores in both species. As expected, the mean mercury level in loggerhead eggshells was significantly higher than green sea turtle eggshells (8±1 and 1.0±0.5 ppb (mean±SE), respectively, $p<0.0001$). Furthermore, mercury in loggerhead eggshells decreased from the northern to the southern region of Israel from 10±1 ppb (n=100) to 5.4±0.3 ppb (n=80), respectively. Finally, mercury levels in loggerhead eggshells are substantially higher and more robust (much higher sample size of eggs and nests in this study) than previously reported values from other regions in the Mediterranean Sea and globally. This result suggests that eastern Levantine sea-turtles are more exposed to mercury pollution than other marine areas of the Mediterranean Sea and globally.

Monthly trace element patterns and Inter Chamber Variability (ICV) in planktic foraminifera species (*Globigerinoides ruber albus* and *Turborotalita clarkei*) from the Gulf of Aqaba

N. Levy - noy.levy2@mail.huji.ac.il (1, 2), A. Torfstein (1, 3), R.Schiebel (2), N. Chernihovsky (1, 3), K. P. Jochum (2), U. Weis (2), B. Stoll (2), G.H. Haug (2, 4)

1) The Fredy & Nadine Herrmann Institute of Earth Sciences, Hebrew University of Jerusalem, Jerusalem 91904, Israel.
2) Max Planck Institute for Chemistry, Hahn-Meitner-Weg 1, 55128 Mainz, Germany.
3) Interuniversity Institute for Marine Sciences, Eilat 88103, Israel.
4) Department of Earth Sciences, ETH Zurich, Sonneggstrasse 5, 8092 Zurich, Switzerland

Environmental and biological factors influence the trace element composition (element/Ca) of planktic foraminifer shells, making these measurements useful for reconstructing past oceanic and climatic conditions. Recent analytical advances that enable single shell analyses warrant a better understanding of variance in trace element systematics between species, individual shells, and single shell chambers.

Here, we present element/Ca ratios in planktic foraminifer shells from the Gulf of Aqaba (June 2014 – June 2015), using laser ablation ICP-MS on single shells and chambers of Globigerina ruber albus and Turborotalita clarkei. Shells were collected from sediment traps at five depths (120-570 m) and a proximal core top (~720 m).

Results reveal species- and element-specific trends. Turborotalita clarkei showing generally higher element/Ca values than G. ruber albus. Significant element/Ca excursions (e.g., Na/Ca, Mg/Ca), particularly in T. clarkei, along with a relative increase in inter-chamber variability (ICV), occurred around March-April 2015 during maximum water column mixing. Furthermore, the final chamber (F0) of G. ruber albus shows different element/Ca patterns compared to earlier chambers (F-1, F-2). For example, while Mg/Ca and B/Ca in G. ruber albus trace seawater temperature and pH, we find that the optimal signal is obtained from pooled means of Mg/Ca and B/Ca in F-1 and F-2. By contrast, Al/Ca, which is assumed to trace the terrigenous fraction, displays significant differences between water column and core top shells, and warrants further investigation.

This study highlights the complexity of element/Ca variability between species and chambers and offers insights into their application in the study of downcore records.

Unveiling the hidden depths: multi-markers for investigating plastic debris on the Southeastern Mediterranean seafloor

X. Li - edmeesparrow@gmail.com (1, 2) Y. Segal (2) and R. Bookman (1)
1) Leon H. Charney School of Marine Sciences (CSMS), University of Haifa, Haifa, Israel
2) Israel Oceanographic and Limnological Research, Haifa, Israel

Marine macro-litter (> 2.5 cm) accumulation on the seafloor represents an escalating environmental concern that requires accurate information for understanding and management of marine plastic pollution. Bottom-litter were collected from depths ranging from 200 to 1300 meters in the Levant basin. A three-tier, multi-label categorization system was developed to classify plastic bag and packaging (PBP), comprising between 89.9% and 93.0% of the total macro-litter on the seabed. The first two tiers classified PBP by primary source and physical characteristics, such as shape, size, and integrity. The third-tier quantified surface-attached organic and inorganic matter and degradation markers. Most PBP consisted of fragments ranging from 2.5 to 10 cm in size, posing challenges for source identification. For PBP larger than 10 cm, take-out consumer plastics dominated on the continental shelf and slope (81.8% and 83.3%, respectively), while industrial packaging became more pronounced in the abyssal plain (41.9%). At the same time, an increased prevalence of PBP with distinctive features, such as handles was observed in area proximate to the coastline. Moreover, the distribution of PBP was influenced by bio-ecological drivers, with a notable decline in its surface attachment observed from continental areas to deep-sea basins. Similarly, the degradation indices for carbonyl groups and carbon-oxygen single bonds were lower in the deep-sea samples, suggesting slower degradation in this environment. This combination of spatial and chemical analysis provides deeper insights into the PBP behaviour and degradation across different marine zones, supporting better management of plastic litter and its impacts on the marine ecosystem.

The role of ocean processes in future Northern Hemisphere mid-latitude winter precipitation changes

N. Liberty-Levi - noga.liberty@weizmann.ac.il (1)
(1) Weizmann Institute of Science

In response to anthropogenic emissions, winter net precipitation (precipitation minus evaporation) in the Northern Hemisphere mid-latitudes is projected to considerably intensify by the end of this century. Previous studies argued for the importance of surface quantities in setting local precipitation changes. Thus, to elucidate the future changes in precipitation, it is crucial to examine the changes in ocean processes, as they play a fundamental part in the surface response to anthropogenic emissions. In this study, we use a hierarchy of ocean coupling simulations to quantify the relative roles of the ocean, and its dynamic and thermodynamic components, in the projected intensification of Northern Hemisphere mid-latitude winter net precipitation. We find that the increase in mid-latitude net precipitation over land and the Pacific Ocean stems from thermodynamic ocean processes, which mostly act to warm the surface, increase the meridional moisture gradient, and thus the moisture flux convergence by mid-latitude eddies. In contrast, over the Atlantic Ocean, dynamic ocean processes modify the zonal moisture gradient, therefore increasing the convergence of moisture over that region. Our results highlight the importance of better investigating and monitoring ocean-atmosphere coupling processes to improve our preparedness for future large-scale climate change.

An integrated approach to measure photosynthetic performance provides deeper insights into thermal tolerance in *Microcystis aeruginosa*

O. Liran - oded.liran@ocean.org.il (1)
1) Yigal Alon Kinneret Limnological Laboratory, Israel Oceanographic and Limnological Research, P.O.Box 447, Migdal 14950, Israel

Thermal tolerance in phytoplankton have gained renewed attention due to increasing temperature fluctuations caused by climate change. In some conditions, abrupt temperature changes exceeding 10°C difference occur and pose significant challenges to aquatic microorganisms. In order to gain deeper insights into photosynthetic performance under stress, we developed an integrated system for simultaneous measurement of gas exchange, chlorophyll fluorescence and redox reactions of photosynthesis. This setup combines a quadrupole mass spectrometer for CO_2 and O_2 exchange measurements and a Joliot type spectrophotometer/fluorometer. The metabolic chamber houses both gas exchange entry point and optic modules, allowing direct correlation between the two techniques. By synchronizing these measurements, we can better understand the relationship between electron transport, oxygen evolution, and overall phytoplankton photosynthesis responses to stress. In this study, we compared the response of two Microcystis aeruginosa strains to heat shock – international standard PCC7806 and local strain in Lake Kinneret C-1004. Our findings revealed differences in photosynthetic performance between the two strains in their response to extreme heat stress conditions. Our findings suggest potential differences in adaptation to sudden temperature increases between the two strains. The combined approach, in addition to standard biochemical and biological examinations, enhances our understanding of aquatic photosynthesis under varying environmental conditions and we envision that it will become an important tool in climate change research. Future studies will focus on investigating the genetic basis of heat tolerance in M. aeruginosa and examining long-term acclimation potential to better predict and mitigate the impacts of climate change on aquatic ecosystems.

Assessing inland tsunami sediments within archaeological contexts at caesarea Israel

E. S. Lottner - eslottner@gmail.com (1)
1) University of Haifa

Identifying ancient inland tsunami deposits is important for recognizing tsunami risk today. In Israel, 8th century AD sediments preserved in an ancient warehouse near the coast of Caesarea were interpreted as tsunami-related; but because these findings have not been substantiated elsewhere there is little understanding of the lateral extent, scale, or magnitude of the event. During recent archaeological excavations, similar deposits were found in locations beyond the warehouse, including 1.5km inland above a Byzantine (4-5th AD) crypt. These newly exposed deposits can be assessed to determine their origin, and whether they could be associated to the same event. Within a collaboration with the Israel Antiquities Authority, sediment samples were collected to be analyzed for marine content (e.g. foraminifera/shelly inclusions), grain size and XRF; with the aim to decipher the mechanism and time of deposition. Preliminary results have not yet negated the hypothesis. If evidence supporting tsunami deposits far from the coastline is recognized, it will broaden our understanding of the scope of these past events, and guide policy regarding everyday coastal planning as well as disaster preparedness.

Characterizing organic matter availability and its potential link to the methane cycle in thermokarst lakes

O. Magori Cohen - orenmag@post.bgu.ac.il (1), A. Pellerin (2), K. Walter-Anthony (3), N. Hasson (3), E. Eliani-Russak (1) and O. Sivan (1)

1) Department of Earth and Environmental Sciences, Ben-Gurion University
2) institute of Marine Sciences (ISMER-UQAR), Quebec
3) University of Alaska Fairbanks

In northern latitudes, permafrost soil thawing leads to thermokarst lakes formation. Beneath and around these lakes, a thawed zone (talik) is formed, in which anoxic conditions prevail. Under such conditions, methane, a potent greenhouse gas, is produced by microorganisms (methanogenesis). Organic matter (OM) serves as a substrate in one of the two methanogenesis pathways. OM can also facilitate thermodynamically preferable metabolic pathways and methane oxidation by serving as an electron acceptor or an electron shuttle, thus mitigating methane emissions.

The goal of this research is to characterize organic matter's availability for microbial degradation in thermokarst settings and to examine its potential relation to the methane cycle.

To accomplish this, 5-m cores were extracted from three sites in a thermokarst lake's talik: (1) lake's sediments, (2) lake's margin and (3) lake's terrace. Porewater was extracted from the cores for geochemical and dissolved organic matter (DOC) analysis. Sediment was collected for soil organic carbon (SOC) analysis, as well as incubation experiments, to determine methane accumulation rates. DOC was described using optical indices, and SOC was described based on pyrolysis and combustion, using Rock-Eval. In all sites, methanogenesis is dominant in depths greater than 2m. In shallower depths, it is only dominant in the lake sediments, with higher methane accumulation rates. We suggest that the DOC pool is dominated by leaching of SOC, while hydrological advection is negligible. In shallow depths in the lake's margin, roots excretions could contribute to a ""fresher"" DOC pool, and provide oxygen, which suppresses methanogenic activity.

Interspecies metabolic interactions drive Palmahim cold seep prokaryotic communities

S. Malavin - stas.malavin@gmail.com (1, 2), M. Rubin Blum (2, 3)
1) Zuckerberg Institute for Water Research, Ben-Gurion University of the Negev, Sede Boker Campus 84990, Israel
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, P.O. Box 8030, Haifa 31080, Israel
3) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, 199 Abba Khoushy Ave, Mount Carmel, Haifa 3103301, Israel

The deep hydrosphere hosts diverse and understudied biota that provide essential ecosystem services. In cold seep ecosystems like the Palmahim hydrocarbon seeps, 60 km offshore Israel at 1150 meters depth, natural hydrocarbon discharge supports chemosynthetic communities. These ecosystems play a significant role in global geochemical cycles by transferring carbon from seabed reservoirs to the hydrosphere and potentially the atmosphere. Microbes, particularly anaerobic methane-oxidizing archaea (ANME) and sulfate-reducing bacteria (SRB), act as a biological filter, preventing methane emissions from reaching the water column. The well-known symbiosis with bacteria allows multicellular animals, such as clams and tube worms, to thrive in deep-sea chemosynthetic ecosystems. However, interactions inside the prokaryotic community and their ecosystem role are considerably understudied.

At Palmahim seep sediments, we found rich microbial communities including bacteria, archaea, microeukaryotes, and viruses. Amplicon-based metabarcoding and genome-resolved metagenomics show stratification of ANME and SRB by depth, with ANME-2 clades inhabiting more shallow sediments than ANME-1. Co-abundance network analysis revealed several clusters associated with ANME archaea. Genomic analysis indicated that in most abundant bacterial phyla, the ANME-2-associated cluster is a hotspot of main transporter genes, such as the ATP-binding cassette (ABC) and the major facilitating superfamily (MSF) transporters. On the contrast, the ANME-1-associated genomes demonstrated much smaller number of transporters. These results indicate that the ANME-2-associated prokaryotic community may host diverse metabolic interactions. Community-level metabolic modeling also suggests that the ANME-2-associated community of Palmahim cold seeps benefits from metabolite sharing between its members.

Spatio-temporal patterns of water flow in pulsating corals

D. Malul - malolds@gmail.com (1, 2), R. Holzman (2, 3), and U. Shavit (1)
1) Civil and Environment Engineering - Technion Israel Institue of Technology
2) The Interuniversity Institue for Marine Sciences in Eilat
3) School of Zoology - Tel Aviv University

Pulsating corals from the Xeniidae family exhibit a unique periodic pulsation of their tentacles that generates a steady current, shown to expel waste products from photosynthesis and enhance the process by up to tenfold. This same flow likely facilitates the supply of nutrients from the environment, which is believed to be the primary source of sustenance for these corals and may explain why pulsation persists during the night. However, little is known about the flow approaching the polyp, carrying these nutrients, or the flow near the tissue where mass-transfer occurs. Here we used Particle Image Velocimetry on single polyps, combined with a Lagrangian analysis of tracers, to measure the flow field in the polyp's vicinity. Our measurements revealed substantial flow between the tentacles of pulsating corals, roughly equal in volume to the water expelled from the polyp, amounting to 36 liters per day (~36,000 polyp volumes). Of this volume, about 15 liters per day originated from below the polyp, accounting for 75% of the total interception of previously unencountered water. Most of these new water interceptions occurred during the downward stroke of pulsation, primarily at the distal half of the tentacles. Our findings represent a first step in understanding the potential role of pulsation in nutrient uptake.

A kinematic model for meddies

S. Maor - sagi.maor@weizmann.ac.il (1), O. Saporta-Katz (1), H. Gildor (2), V. Rom-Kedar (1)
1) Weizmann Institute of Science
2) Hebrew University of Jerusalem

We present a novel kinematic model of Mediterranean eddies (meddies) that replicates the intricate vortex dynamics associated with the Mediterranean Outflow Water (MOW). This model is designed for integration into the existing kinematic-dynamic framework [1], which was developed to study the Atlantic Meridional Overturning Circulation (AMOC) under advective processes. The original model [1] combines a density box approach that modulates AMOC amplitude with the advection of temperature and salinity fields, driven by both AMOC and a time-dependent kinematic velocity field. However, in [1], the velocity field was represented as an oscillating double gyre without incorporating meddies.

Preliminary results from the new model, which integrates the double gyre configuration, the novel kinematic representation of meddies, and a fixed-amplitude AMOC, demonstrate westward and northward transport with chaotic dynamics. These findings suggest that the model holds potential for alignment with observational data [2]. Further tuning of the kinematic meddies model may offer new insights into the role of meddies in regional circulation, potentially advancing our understanding of their influence on large-scale oceanic flows.

Rapid dynamic color change in the grouper *Variola louti* is associated with interspecies interactions and camouflage

S. Marom - marom.sagi@gmail.com (1, 4), M. Kiflawi (2, 4), D. Akkaynak (3, 4), R. Holzman (1, 4, 5)
1) School of Zoology, Faculty of Life Sciences, Tel Aviv University, Tel Aviv 69978, Israel.
2) Department of Life Sciences, Ben Gurion University, Beer Sheva 8410501, Israel.
3) Hatter Department of Marine Technologies, Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, 3103301, Israel.
4) The Inter-University Institute for Marine Sciences, PO Box 469, Eilat 88103, Israel.
5) Steinhardt Museum of Natural History, Tel Aviv University, Tel Aviv, Israel.

Among fish, rapid dynamic color change is primarily known for intraspecific communication or camouflage, while examples of rapid color change in interspecific contexts are rare. In this research we studied dynamic color changes and their associated behaviors in the grouper *Variola louti*. Using underwater videography and color-calibrated photography, we recorded the natural behavior and measured the body colors of *V. louti* in a coral-reef environment. We found that *V. lout*i exhibited a range of pattern displays, which transformed within seconds in coordination with behavioral changes. A head stripe pattern was observed when *V. louti* engaged in agonistic interspecific interactions. Interestingly, this pattern was absent when hunting alone or in cooperation with moray eels. The fish's body color brightness and body patches contrast were associated with their swimming behavior. Darker body colors and high-contrast body patches were expressed when the fish were resting on the bottom, whereas bright and uniform body colors were displayed when swimming higher above the reef. Our results suggest that *V. louti* utilizes these dynamic color displays for camouflage and interspecific communication in agonistic and competitive interspecies interactions. These findings highlight the significance of dynamic color changes and provide valuable insights into the behavioral ecology of animals.

A T6SS in the coral pathogen *Vibrio coralliilyticus* secretes an arsenal of anti-eukaryotic effectors and contributes to virulence

S. Mass -shirmass@mail.tau.ac.il (1), H. Cohen (1), R. Podicheti (2), D. B. Rusch (3), M. Gerlic (1), B. Ushijima (4), J. C. van Kessel (3), E. Bosis (5), and D. Salomon (1)

1) Department of Clinical Microbiology and Immunology, School of Medicine, Faculty of Medical and Health Sciences, Tel Aviv University, Israel.
2) Center for Genomics and Bioinformatics Indiana University, Bloomington, Indiana, USA.
3) Department of Biology, Indiana University, Bloomington, Indiana, USA.
4) Department of Biology and Marine Biology, University of North Carolina Wilmington, Wilmington, NC, USA.
5) Department of Biotechnology Engineering, Braude College of Engineering, Karmiel, Israel.

Vibrio coralliilyticus (Vcor) is a pathogen of coral and shellfish, leading to devastating economic and ecological consequences worldwide. Although rising ocean temperatures correlate with increased Vcor pathogenicity, the specific molecular mechanisms and determinants contributing to virulence remain poorly understood. Here, we systematically analyzed the type VI secretion system (T6SS), a contact-dependent toxin delivery apparatus, in Vcor. We identified two omnipresent T6SSs that are activated at temperatures in which Vcor becomes virulent; T6SS1 is an antibacterial system mediating interbacterial competition, whereas T6SS2 mediates anti-eukaryotic toxicity and contributes to mortality during infection of an aquatic model organism, Artemia salina. Using comparative proteomics, we identified the T6SS1 and T6SS2 toxin arsenals of three Vcor strains with distinct disease etiologies. Remarkably, T6SS2 secretes at least nine novel anti-eukaryotic toxins comprising core and accessory repertoires. We propose that T6SSs differently contribute to Vcor's virulence: T6SS2 plays a direct role by targeting the host, while T6SS1 plays an indirect role by eliminating competitors.

Marine periphyton biofilter in recirculating aquaculture system for intensive fish farming

S. Meiroz-Yagur - shaiyag@post.bgu.ac.il (1)*, G. Banet (1), and L. Guttman (1)
1) Department of Life Sciences, Ben Gurion University of the Negev Eilat Campus, Beer-Sheva 84105, Israel

Sustainable and inexpensive technologies for treating mariculture effluents can significantly reduce the construction and operation costs of recirculating aquaculture systems (RAS) for intensive fish farming. Marine periphyton has been shown to remove excess nutrients in the stream of fishpond effluent while converting waste into edible biomass. Still, the technology has not been developed commercially. Toward this goal, we developed and examined the performances of a marine periphyton-based biofilter in RAS for intensive culture of gilthead sea bream (*Sparus aurata*). Three RAS were operated for 5 months in a recirculating mode using a minimal water discharge of 10% day^{-1}. Each RAS was initially introduced with fish at a different stocking density of 40, 60, or 80 kg m^{-3}. All systems were monitored 24/7 for temperature, pH, and oxygen levels. Samples for water quality measurements were taken every 2-4 hours from the fish tanks and biofilters, considering levels of the dissolved inorganic N forms of total ammonia nitrogen, toxic ammonium (NH_3-N), nitrite (NO_2-N), Nitrate (NO_3-N), as well as dissolved phosphorus (PO_4-P). In addition, the growth performances of fish and periphyton and their biochemical content were measured.

Fish stocking density in RAS was successfully increased to ~170 Kg m^{-3}. Temperature, pH, and oxygen levels in the culture tanks were at acceptable ranges for fish culture of 19.4 – 28.5° C, 6.6 – 8.5, and 60 – 170%, respectively. Despite the high stocking density of fish, the level of NH_3-N was kept below 0.05 mg L-1 (i.e., non-harmful level), even when the level of total ammonia nitrogen reached >4.5 mg L^{-1}. It is assumed that such low levels of NH_3-N were achieved due to the diurnal synchronization between fish N excretion and periphyton photosynthesis. Besides maintaining high-quality water for fish culture, periphyton grew at an acceptable rate while assimilating the excess N in culture water and reaching levels of cell protein in the dry biomass between 30-48%. Hence, it is sufficient to utilize the harvested periphyton biomass in fish diets to reduce the content of costly animal or plant protein (e.g., fishmeal).

Rapid succession of diatoms and viruses within a dramatic spring bloom event

J. Mellijor - jasminlynnmellijor@gmail.com (1), Y. Tennenbuam-Azulai (1), D. Spungin (1), Y. Avrahami (2, 3), A. Vardi (4), M. Frada (2, 3) and C. Kranzler (1)

1) The Mina and Everard Goodman Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan, 5290002, Israel
2) Department of Ecology, Evolution and Behavior, Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Jerusalem, 91904, Israel
3) The Interuniversity Institute for Marine Sciences in Eilat, Eilat, Israel
4) Department of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, 7610001, Israel

Diatoms are a globally distributed and diverse group of phytoplankton that contribute ~20% of primary productivity on the planet and substantial carbon export in the ocean. These aquatic, unicellular eukaryotes are characterized by high growth rates and dominance within seasonal phytoplankton bloom events. While viruses are considered key players in phytoplankton bloom demise, little is known about the prevalence and patterns of virus infection within a diatom bloom. To better understand how viruses might shape diatom bloom dynamics we used quantitative metatranscriptomics analysis of the diatom and virus community at high temporal resolution during an outstanding spring bloom event in the Gulf of Aqaba/Eilat (GoA/E), in the northern Red Sea. Throughout our sampling period, that captured both the peak of the spring bloom and the initiation of its demise, we observed three distinct transitions in active diatom genera, shifting between Skeletonema, Pseudo-nitzchia and Leptocylindrus dominance, indicating rapid and dynamic turnover of diatom taxa within a single diatom bloom event. In addition, we identified multiple cell-associated viruses, with near full-length genomes and close homology to known diatom-infecting Marnaviridae. Intriguingly, temporal fluctuations in the abundance of several dominant viruses corresponded with the observed turnover in diatom taxa, raising the possibility that viruses may drive both the succession of taxa within a diatom bloom and orchestrate its ultimate collapse. Together, these observations suggest a dynamic interplay between diatoms and viruses within a single bloom event and provide additional insight into the role that viruses play in shaping diatom community structure in the ocean.

Behavioral responses of larval fish to marine oil pollution

Y. Merlis (1) - Merlis.Yael@gmail.com

1) University of Haifa

To reach the mature reproductive stage, developing larval fish need to adapt and exhibit behavioral responses to survive. It is known that larval fish face many challenges to complete connectivity and dispersion, yet it remains unclear whether they can perform avoidance responses to oil pollution, which is increasingly prevalent. This research seeks to understand whether larval fish can detect and avoid oil-polluted areas, thereby exhibiting avoidance behavior in response to oil pollution. Additionally, it aims to explore how swimming speed and orientation are influenced by exposure to oil pollution, both of which are crucial for the survival and dispersal of larval fish. The difficulty in this research stems from tracking their behavior in their natural environment and the wide variety of pollution types and concentrations in the marine environment. Additionally, research in this area is relatively limited and focuses mainly on adult fish rather than larval stages.

In this study, laboratory experiments were conducted in choice cells with a clean and a polluted cell, as well as in a SWIM FLUME to measure the swimming speeds of the larvae in the presence of oil pollution and in clean waters. This was done to understand whether larval fish can detect oil pollution and to assess the impact of pollutants on their swimming speed. In the field, we used a seine to recruit fish larvae in conditions of pollution and without, to understand the larvae's behavior in their natural environment.

Preliminary results show no preference of the larvae for polluted or clean cells, suggesting that larval fish may not be able to detect pollution encounters and therefore cannot perform an avoidance response. Studying the response of larval fish to oil pollution is vital due to its impact on species dispersion and population connectivity at the larval stage, which is essential for maintaining the health of the marine ecosystem and ensuring ecological balance

Observational insights into kinetic energy distribution and circulation dynamics in sub-mesoscale eddy of the East Mediterranean

L. Michaeli - lironmi@mail.huji.ac.il (1) A. Solodoch (1)
1) The Hebrew University of Jerusalem

Eddies (aka vortices) are a common phenomenon in all oceans and seas. They appear on various scales, interact with the ambient surface currents, and strongly influence marine material dispersion. Mesoscale eddies (<100km) have been an active target of research since the 1960s and are well known as the dominant reservoir of kinetic energy in the ocean. For Sub Mesoscale Eddies (<10km), their small size presents an observational challenge which has greatly limited their in-situ measurement. In this work, we leverage a rich multi-platform dataset collected within a single sub mesoscale eddy, including a dozen surface drifters to shed light on the surface circulation within the eddy. We apply spectral analysis techniques in a novel fashion to understand the various modes of circulation variability and their distribution within the eddy. Our results offer a first look at the kinetic energy profile of a small-scale eddy. The quantitative results show a lower frequency of sub-inertial kinetic energy in the center of sub mesoscale vortices and at a higher amplitude. We additionally study the modulation of wind-driven inertial oscillations within the eddy, as well as the temporal evolution and eventual eddy dissipation. The novel observations and analysis tools are expected to provide a unique verification source for theoretical understanding and numerical representation of eddies in models, and for understanding marine material retention within eddies.

The origins of death at sea: Characterizing conserved cell death genes in distant algae

A. Mizrachi - avia.mizrachi@weizmann.ac.il (1), M. Sadeh (1), S. Ben-Dor (2), O. Dym (2), J. K. Brunson (3 ,4), A. E. Allen (3, 4), R. E. Jinkerson (5), D.Schatz (1), and A. Vardi (1).

1) Department of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, Israel.
2) Department of Life Sciences Core Facilities, Weizmann Institute of Science, Rehovot, Israel.
3) Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA, USA.
4) Environmental Genomics, J. Craig Venter Institute, La Jolla, CA, USA
5) Department of Chemical and Environmental Engineering, University of California, Riverside, CA, USA.

Phytoplankton drive global primary production and form vast blooms in aquatic ecosystems. Bloom demise and phytoplankton rapid turnover fuel marine microbial life and are suggested to involve programmed cell death (PCD) induced by environmental stress. However, the algal PCD machinery remains elusive. Here, we identified novel PCD-related and stress survival genes through transcriptomics of sensitive and resilient subpopulations of the diatom Phaeodactylum tricornutum exposed to oxidative stress. Comparison with a mutant screen in the green alga Chlamydomonas reinhardtii identified functionally conserved PCD gene candidates, including the cysteine protease cathepsin X/Z (CPX). CPX mutants in P. tricornutum and C. reinhardtii exhibited resilience to oxidative stress and infochemicals, supporting a conserved role in PCD. Phylogenetic and structural analyses showed high similarity between algae and human CPX proteins. CPX is widely expressed in the oceans and correlates with upcoming demises during toxic diatom blooms. Elucidating algal PCD components sheds light on the evolutionary origin of PCD in microorganisms and their strategies to cope with stressful conditions.

Seasonal dynamics of mercury associated with zooplankton in Haifa Bay

E. S. Mizrahi - esmizrahi@hotmail.com (1, 2, 3) R. Bookman (1), N. Teutsch (2), T. Guy-Haim (3)
1) Charney School of Marine Sciences, The Department of Marine Geosciences
2) Geological Survey of Israel
3) Israel Oceanographic & Limnological Research

Heavy metals can have devastating environmental and health impacts, as evidenced by the Minamata Bay disaster in the 1950s, where mercury pollution caused widespread diseases and mortality. This study investigates mercury accumulation in marine zooplankton, focusing on Haifa Bay, Israel, a region historically impacted by industrial pollution, particularly from the Kishon River and underground water sources. Between 2020 and 2022, seven plankton sampling surveys were conducted across 10 stations, using horizontal zooplankton net tows to collect samples. Zooplankton samples were sorted by taxonomic groups and digested with nitric acid to measure total mercury (THg) concentrations. The study expanded in June 2023 to include day and night sampling, capturing diel variations in zooplankton communities. THg concentrations varied considerably, with the highest recorded value (117 ng/g) found in September 2021 at the ST2→ST4 transect near Haifa Port, while ST9→ST10 transect in the outer bay consistently had the lowest concentrations. Although demersal taxa showed slightly higher mercury levels than non-demersal taxa, no significant difference was found. This research emphasizes the importance of measuring mercury in lower trophic level organisms like zooplankton to better understand the spatial and temporal patterns of contamination in marine ecosystems and to inform future pollution management and conservation efforts.

Sulfur, rare earth elements and sharks

Eitan S. Newman(1,2), Dan Tchernov(1,2), Natascha Wosnick(3), Rachel Ann Hauser-Davis(4), Aviad Schenin(1), **Danny Morick** - dmorick@univ.haifa.ac.il(5, 1)
1)Morris Kahn Marine Research Station, University of Haifa, Sdot Yam, Israel
2)Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Israel
3)Programa de Pós-Graduação em Zoologia, Universidade Federal do Paraná, Curitiba, Brazil
4)Laboratório de Avaliação e Promoção da Saúde Ambiental, Instituto Oswaldo Cruz (Fiocruz), Rio de Janeiro, Brazil
5)Department of Blue Biotechnologies and Sustainable Mariculture, Leon H. Charney School of Marine Sciences, University of Haifa Israel

Focusing on apex predators as bio-indicators enables a glimpse into the whole marine ecosystem. The objective of this research is to better understand and quantify the pollutants that are present in the environment of the southeastern Mediterranean Sea. Apex predator's bio-accumulate, bio-magnify and bio-transfer elements present in their environment. In this research sharks were sampled from an aggregation at the Orot-Rabin power plant and desalination plant in Hadera, Israel. Blood was analyzed using ICP-MS and an extensive report was created of 37 elements that were detected in the blood sampled. Arsenic (mean=327 ppm, max=4114 ppm), mercury (mean=1.82 ppm, max=10.78 ppm), and lead (mean=1.09 ppm, max=27.05 ppm) have exhibited concentrations higher in relation to other locations from literature and much higher than the recommended consumption rates for humans and in concentrations that might impair physical health and might be indicative of the state of other organisms in the ecosystem. Sulfur has presented very high concentrations (mean=12676 ppm, max=66704 ppm). High sulfur concentrations might impair physiological processes and requires further investigation into the physiological standards. The group of rare earth elements (REE) has presented a very high Spearman correlation (X>0.9) that is indictive of accumulation of these elements as a group, indicating a source of pollution in the area that is associated with new technology such as car batteries. This research, describing the prevalent of elements that marine organisms are exposed to in the Eastern Mediterranean Sea (EMS) and a call for mitigation procedures and further monitoring of elements, metals and rare earth elements that animals are exposed to in the Eastern Mediterranean Sea.

Integrated pest management in aquaculture using monosex prawn biocontrol agents: the Emek HaMa’ayanot case study between 2017-2023

S. Moscovitz - moscovis@post.bgu.ac.il (1), A. Emanuel (2), H. Glassner (2), E. D. Aflalo (1, 3), O. Ovadia (1, 4), and A. Sagi (1, 5)

1) Department of Life Sciences, Ben Gurion University of the Negev, Israel
2) Eden Research Farm, Emek HaMa’ayanot, Israel
3) Department of Life Sciences, Achva Academic College, Israel
4) Goldman Sonnenfeldt School of Sustainability and Climate Change, Ben-Gurion University of the Negev, Israel
5) National Institute for Biotechnology in the Negev, Ben Gurion University of the Negev, Israel

Integrated Pest Management (IPM) using monosex freshwater prawns is a sustainable solution for fish farmers, offering multiple benefits: prawns predate on snails that transmit parasitic trematodes, such as Centrocestus formosanus, reducing fish infection rates while minimizing pesticide use. Additionally, prawns serve as an extra protein product, increasing farmers’ financial security and total pond yield without the need for additional feed. Globally, this practice also supports job creation in prawn hatcheries processing and sales.

From 2017-2023 we conducted observations over the use of Macrobrachium rosenbergii prawns in polyculture systems with base fish (tilapia, carp) and quality fish (bass, seabream) in Emek HaMa’ayanot, Israel. We compared prawn-IPM implementation between base and quality fishponds, mapping prawn demand and distribution, assessing the prawn-IPM and fish interface, the change in fish infection during the season with prawn-IPM, prawn survival, yield, and potential extra profits for farmers.

The findings show an increase in prawn demand over the years, reflecting growing farmer confidence in prawn-IPM. There was no significant difference in fish infection changes between base and quality fishponds, indicating that prawns provided similar biological control for both. Prawn yields were higher in base fish fishponds, resulting in greater potential economic benefits, however this was heavily affected by the pond operational interface.

Broader use of prawn-IPM is expected to provide both ecological and economic advantages for aquaculture. The interface of prawn-IPM can be optimized, focusing more on ecological benefits in quality fish fishponds, while enjoying both ecological and economic benefits in base fish fishponds.

Mic-RAS: A photomembrane bioreactor-based recirculating aquaculture system where fish waste becomes a product

M. Moshkovitz - moshkovm@post.bgu.ac.il (1), Y. Siboni(1), A. Ronen(2), I. Khozin-Goldberg(1), D. Zilberg(1)

1) The French Associates Institute for Agriculture and Biotechnology of Drylands, The Jacob Blaustein Institutes for Desert Research, Ben Gurion University of The Negev, Israel.

2) The Zuckerberg Institute for Water Research, The Jacob Blaustein Institutes for Desert Research, Ben Gurion University of The Negev, Israel.

Conventional Recirculating Aquaculture Systems (RAS) rely on nitrification and water exchange to remove solids and nitrate, leading to nutrient waste and environmental impact. Microalgae are a source of bioactive compounds such as polyunsaturated fatty acids (PUFA). Microalgae require a steady supply of nutrients for biomass production, primarily carbon, nitrogen, and phosphorus, all of which are found in fish excretions. The freshwater microalga selected for this study belongs to the Eustigmatophytes, known for their high levels of omega-3 PUFA and is temporarily named BZ. We aimed to evaluate the use of BZ in a microalgae-integrated RAS (mic-RAS) to assimilate soluble (mainly ammonia) and solid fish excretions, thereby maintaining high water quality and producing BZ biomass as a valuable byproduct.

A small-scale mic-RAS comprised of a 10 L fish aquarium and a 10 L microalgal photo-membrane-bioreactor was established. A microfiltration membrane facilitated the circulation of clean permeate from the photo-bioreactor back to the fish aquarium, while retaining the microalgal biomass. Water was analysed for nitrogenous compounds and total organic carbon (TOC), and microalgal growth was assessed. The system was continuously operated with different fish stocking densities. Feed was applied at 2% body weight. Results revealed that nitrogenous compounds were maintained at low levels over time at fish stocking densities of up to 8 g/L and TOC:TN ratio remained constant over time. Microalgal concentrations gradually increased over time.

This study highlights the potential of the mic-RAS using BZ and a sustainable approach for water treatment in aquaculture.

Lack of physiological impact but increased antibiotic-resistant gene accumulation in *Brachidontes pharaonis* from a polluted coastal site

A. Mukaila - alhassanmu1766@uds.edu.gh, A. Kovalev, M. Rubin-Blum, and G. Rilov

1) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Abba Khoushy Ave 199, Haifa, 3498838, Israel
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, P.O. Box 8030, Haifa 31080, Israel

Understanding the combined impacts of multiple stressors on marine species and communities is critical, as most stressors do not act in isolation. For example, exposure to pollution can affect species resilience to global warming. We tested this hypothesis using the invasive mussel *Brachidontes pharaonis* on the Israeli Mediterranean coast. Localized coastal pollution, beyond normally increasing heavy metals and organic load, often includes antibiotic-resistant bacteria that may lead to the accumulation of antibiotic-resistant genes (ARGs) in marine ecosystems. This study assessed the combined effects of pollution and thermal stress on physiological parameters (oxygen consumption, survival, and condition index) and the presence of ARGs in B. pharaonis from polluted (Qiriyat Yam in the industrial Haifa Bay) and pristine (Neve Yam) sites in a laboratory experiment. Before acclimation, five mussels from each population were tested for ARGs using qualitative PCR. Following this, 100 mussels from each population were transferred to an intertidal chamber and exposed to increasing temperatures (34°C, 37°C, and 39°C). The results indicated no significant difference in survival, condition indices and metabolic functioning between populations, except on day 9 of exposure at 39°C. PCR results revealed that both sites harbored the blaTEM, blaCTX-M32, and sul1 ARGs, with blaTEM being the most prevalent, followed by sul1, and blaCTX-M32 being the least common. ARGs were more frequently observed in mussels from the polluted site. Our findings suggest that B. pharaonis may not serve as a reliable bioindicator for pollution stress. However, the increased prevalence of ARGs in mussels from the polluted site highlights a potential link between pollution and ARG accumulation.

How does a coral dance? A neurobiological study of soft coral pulsation

E. Nadir - elinornadir@mail.tau.ac.il (1), T. Lotan (2), and Y. Benayahu (1)
1) School of Zoology, Faculty of Life Sciences, Tel Aviv University, Tel Aviv 6139001, Israel
2) Department of Marine Biology, the Leon H. Charney School of Marine Sciences, University of Haifa, Haifa 3498838 Israel

Some soft corals in the family xeniidae exhibit a unique constant pulsation motion rivaled only by jellyfish pulsation. However, the neural mechanism of repetitive pulsation in these animals is still unknown. Repetitive motion in animals is controlled by central pattern generators or pacemakers, though these are understudied in basal metazoans. As such, Xenia umbellata, a fast-growing Red Sea octocoral, was developed as a laboratory model to explore the mechanism of pulsation in xeniid octocorals. Using amputation experiments, regeneration, transcriptomics and spatial analysis, we explored the distribution and molecular makeup of the pacemakers in X. umbellata pulsation. Our research revealed that the molecular elements in X. umbellata pulsation are conserved, but the distribution of pacemakers is unique to these corals.

Epiphytic bacterial communities of *Asparagopsis taxiformis*: seasonal, spatial, and host genetic variations

O. Nahor - nahoro27@gmail.com (1, 2) and Á. Israel (2), N. Barger (1), and T. Luzzatto-Knaan (1)
1) Department of Marine Biology, The Charney School of Marine Sciences, University of Haifa, Israel
2) Israel Oceanographic & Limnological Research, Tel Shikmona, Haifa, Israel

The relationships between epiphytic bacteria and marine macroalgae are intricate, yet our understanding of these bacterial communities' structure, interactions, and functions remains limited. This study aims to explore the epiphytic bacterial communities associated to Asparagopsis taxiformis, a non-native red seaweed from the Israeli Mediterranean Sea (IMS). We analyzed 80 samples of A. taxiformis which were collected bi-monthly over two years from two distinct sites in the IMS. 16S rRNA gene amplicon sequencing revealed a positive correlation between microbial alpha diversity and seawater temperature. Further analysis showed that bacterial community composition was temperature-dependent, reflecting seasonal changes. Samples from different sites and time points exhibited greater similarity in bacterial communities when the algal host was genetically closer. This study strongly suggests that epiphytic bacterial communities associated with A. taxiformis undergo seasonal shifts and are influenced by the host's genetic background.

This study is part of a broader project exploring the metabolomic profile and antimicrobial bioactivity of Asparagopsis extracts. It aims to uncover the relationship between epiphytic bacteria, and algal extract bioactivity.

The reduction of forage fish for fishmeal harms both the fish consumers and the marine ecosystem

A. Neri -aneori@gmail.com (1, 2) and M. Agami (3)

1) Morris Kahn Marine Research Station, Marine Biology Department, The Leon H. Charney School of Marine Sciences, The University of Haifa, Haifa 3498838, Israel

2) The Interuniversity Institute for Marine Sciences in Eilat, Eilat 8810302

This talk briefly examines the impacts of directing much of the global small fish catch to the aquafeed industry rather than to direct human consumption, raising fish prices and interfering with the coastal marine food web. Forage fish are a crucial source of nutrition in developing countries and an essential link in the coastal marine food web. Unfortunately, forage fish are captured in large quantities and primarily reduced to fishmeal and aquafeed production for aquaculture. This practice raises fresh fish prices locally, disrupts the ecosystem, diminishes the populations and catch of forage fish consumers, including larger fish (such as mackerel), and marginalizes local artisanal fishermen. The practice’s impact on fish prices costs consumers hundreds of millions of US dollars globally and tens of millions of US dollars nationally per year while harming the nutrition of low-income fish consumers. The higher fish prices are unfair because they burden financially and nutritionally disadvantaged societies.

Modeling the controls on microbial iron and manganese reduction in methanic sediments

R. Neumann Wallheimer - neumanra@post.bgu.ac.il (1), I. Halevy (2) and O. Sivan (1);
1) Ben Gurion University of the Negev
2) Weizmann Institute of Science

Microbial iron and manganese respiration in deep methanic sediments challenges traditional models of microbial respiration in aquatic environments. However, there is limited understanding of these processes in the methanic zone. Here, we quantify both the thermodynamic and the kinetic controls of potential iron and manganese respiration processes in the methanic sediments of lacustrine and marine sites – Lake Kinneret (LK) and the Southeastern Mediterranean Sea (MedS). Using theoretical bioenergetic methods, we develop a nominal model to calculate catabolic rates and biomass growth rates. Then, we estimate the microbial community sizes of expected iron and manganese reducers. A Monte Carlo simulation addresses uncertainties, enabling the estimation of total reaction rates for various metabolic processes.

Our results reveal that the type of oxide consumed significantly influences bioreaction rates more than its concentration. Notably, bioreactions with amorphous manganese oxides are more favorable than those with highly reactive iron oxides. In both environments, manganese oxide reduction by ammonium and methane oxidation are expected to be significant, while manganese oxide reduction by hydrogen and acetate oxidation are expected to be considerable only in LK. The most probable iron oxide reduction process in LK is hydrogen oxidation, followed by methane oxidation. In the MedS iron oxide reduction is most probably coupled to the oxidation of ammonium (Feammox) to molecular nitrogen, and in a few cases may be coupled to methane oxidation. These findings improve our understanding of the thermodynamic and kinetic controls on the composition of microbial communities and their effect on the geochemistry of methanic sediments.

Species sorting by seaweed *Ulva* and marine periphyton governs microbial community assembly along effluent treatment

D.Nguyen - nguyth@post.bgu.ac.il (1, 2), O. Ovadia (3, 4), M. Masasa (1, 2), A. Tarnecki (5), N. P. Brennan (6), N. R. Rhody (6), K. L. Main (6), and L. Guttman (2, 3*)

1) Marine Biology and Biotechnology Program, Department of Life Sciences, Ben-Gurion University of the Negev, Eilat Campus, Eilat, Israel
2) Israel Oceanographic and Limnological Research, The National Center for Mariculture, P.O. Box 1212, 8811201, Eilat, Israel
3) Ben-Gurion University of the Negev, Department of Life Sciences, P.O.B. 653, 8410501, Beer-Sheva, Israel
4) The Goldman Sonnenfeldt School of Sustainability and Climate Change, Ben-Gurion University of the Negev, Beer Sheva 84105, Israel
5) Auburn University Shellfish Lab, Auburn University, Dauphin Island, Alabama, USA
6) Marine & Freshwater Aquaculture Research, Mote Marine Laboratory, Sarasota, Florida, USA

Plant-based biofilters with seaweeds or periphyton efficiently remove the excess nitrogen in mariculture effluent while forming a protein-rich biomass. Yet, little is known about the microbial assemblies in such biofilters. Metacommunity theory, the study of communities spatially connected via dispersal, is among the central pillars of microbial ecology. It evaluates which of the four paradigms of patch dynamic, species sorting, mass effects, or neutral model best explains community dynamics. While theoretical research endorsed the neutral model in aquatic environments, empirical studies primarily support mass effects and species sorting paradigms. Here, we study metacommunity theory in a two-step biofilter with *Ulva fasciata* for ammonia removal and a sequenced marine periphyton biofilter for polishing and nitrate removal. During five weeks, microbial assemblies in the three patches of *Ulva*, periphyton, and water were analyzed following 16S rRNA gene amplicon sequencing. Our results of community structure, diversity, and functionality support the argument that species sorting, operating through environmental heterogeneity, is the central force that drove microbial community dynamics in all three habitats. Determinism was a leading force across all patches, highest in *Ulva*, medium in the ambient water, and lowest in periphyton. This trend coincides with community diversity, suggesting that a less diverse environment tends to impose a more selective force and vice versa. Function-wise, genes related to nitrogen and sulfur metabolisms were higher in periphyton than in the water and *Ulva* assemblies. Our results proved against the common thinking that in such a small-scale aquatic system, mass effects would overrule.

Adaptive protocol for model assessments and environmental protection of brine discharge from desalination plants

H. Gildor (1) **O. Nir** - oritnir.eco@gmail.com (2, 3)

1) The Institute of Earth Sciences, The Hebrew University, Jerusalem.
2) Orit Nir Environmental consulting
3) The Israeli Planning Administration

Desalination is crucial for addressing Israel's growing water scarcity due to its increasing population and arid natural conditions. To mitigate the environmental effects of brine discharge, specifically on sensitive habitats and the intake pipe of the desalination plants themselves, it is necessary to (1) choose an optimal location for the discharge outfall and (2) optimize the design of the outfall structure to achieve maximum dilution. These are both determined using numerical model simulations to assess the spreading of brine discharged from the marine outfall. Models are carried out according to an ad hoc protocol written by the Ministry of Environmental Protection (MOEP) and the Committee for Planning National Infrastructure, which promotes and approves the plans.

After the desalination plants are operational, as part of MOEP regulation, they are required to have yearly monitoring plans that measure, among other parameters, the salinity around the outfall, intake, and additional sampling stations. Long-term analysis of monitoring data revealed that the far-field model assessment underestimated the brine spread under operating conditions. The modeling protocol, being an adaptive document, was reassessed and improved with input from advisors from the academy. Changes to the protocol include, for example, the requirement to collect a year's data of currents, in the proposed location of the outfall for later use in model calibration and validation; an additional control phase involving a calibration and validation report that the regulator must approve before advancing to model predictions.

Measurement of oil slicks thickness using interferometry

J.-P. Obeid jeanp.obeid@gmail.com (1, 2), A. Shalabney (1), E. Rahav (3), A. Solodoch (4), T. Treibitz (5), Y. Lehahn (2)

1) Lab of Nanophotonics and Light-Matter Interaction, Braude College of Engineering,Karmiel, Israel.
2) Department of Marine Geosciences, University of Haifa, Israel.
3) Department of Marine Biology, Israel Oceanographic and Limnological Research (IOLR), Israel
4) Institute of Earth Sciences The Hebrew University of Jerusalem, Israel.
5) Department of Marine Technologies, University of Haifa, Israel.

Having severe ecological and economical consequences, ocean oil spills - the human-induced release of liquid petroleum hydrocarbons into the marine environment are of great concern worldwide.

The ability to efficiently respond to oil spill events and mitigate their negative impact depends on the ability to collect reliable information on the thickness of the resulting oil slicks, which is essential to accurately estimating the amount and environmental impact of the floating oil, model spreading and evaporation processes, and optimize countermeasures such as in-situ burning and chemical dispersion.

Here we show results from a project aimed at developing an optical system for in-situ measurements of oil slicks thickness using reflective spectroscopy. Leveraging the multiple reflections of light from the air-oil interface and from the oil-water interface, our apparatus forms an interference pattern between them. The spectral dependence of this interference pattern is utilized to compute the thickness of the oil product layer floating above the seawater.

We tested the ability of the system to accurately measure the thickness of floating layers from two different and common types of oil products, namely condensate and crude oil. In lab conditions, we are able to estimate geometrically the oil layers thickness as a reference measurement for validation of our optical apparatus. Over a wide range of oil product thicknesses, we found an average accuracy of 95% in optical thickness retrieval, compared to the geometrical measurement. We are now working on making the system usable in sea conditions."

Bioremediation potential of *Alcanivorax*: exploring hydrocarbon colonization and degradation strategies

K. Davidov (1), A. Kartha (1), S.-S. Itzhari and **M. Oren** - matanok@gmail.com (1)
1) Department of Molecular Biology, Ariel University, Science Park, Ariel 40700, Israel

Marine hydrocarbon pollution, intensified by oil spills, industrial discharges, and plastic waste, poses a significant threat to ocean ecosystems. Liquid and solid hydrocarbon pollutants are toxic to many marine organisms; however, certain microbial genera, such as Alcanivorax, utilize hydrocarbons as a rich nutritional source. These microbes play a crucial role in degrading hydrocarbon pollutants, providing a natural solution for mitigating pollution and supporting ecosystem recovery. In this research, we investigated 11 isolated and purchased Alcanivorax strains, assessing their ability to colonize and metabolize crude oil, alkanes, and plastic polymers. We sequenced and assembled their genomes, identifying relevant hydrocarbon-degrading genes. Alcanivorax bacteria form thick biofilms around alkane droplets, emulsifying and internalizing microdroplets that are gradually consumed and mineralized by the cells. The presence of flagella in some Alcanivorax strains appears crucial for the rapid colonization of solid plastic surfaces, though it is less significant for crude oil and saturated shorter alkanes. Additionally, we found that UV weathering affects Alcanivorax colonization and potentially their biodegradation capabilities. In light of our findings and existing knowledge, we propose that Alcanivorax holds great promise for developing bioremediation solutions in both industrial settings and natural environments.

Ecological succession on 3D printed ceramic artificial reefs

A. Oren - asao@post.bgu.ac.il (1 ,2), O. Berman (3, 4), R. Neri (1, 2), M. Edery-Lutri (1, 2), N. Chernihovsky (1), E. Tarazi (3), N. Shashar (1)
1) Eilat Campus, Department of Life Sciences, Ben Gurion University of the Negev
2) Interuniversity Institute for Marine Sciences in Eilat
3) Design-Tech Lab, Industrial Design Department at the Faculty of Architecture and Town Planning, Technion
4) Matter of Tech Lab, Cornell Tech

The global degradation of natural coral reefs requires innovative approaches to their conservation and restoration. This study investigates the efficacy of using parametric tools in 3D software and 3D printed terracotta structures, towards artificial reefs (ARs) design. Three ARs were deployed in the northern Gulf of Eilat\Aqaba in 2019. Seven months post deployment the ARs were consolidated to one location. Consecutive monitoring, conducted from June 2019 to March 2022, examined the recruitment and settlement of fish, coral, and other marine organisms on the ARs. The ARs hosted complex communities, with fish populations reaching equilibrium approximately one year after deployment. Soft corals were first observed 4.5 months post deployment, and stony corals 5.5 months post deployment, with neither reaching a steady state within the study period. Additionally, we found that uniting dispersed ARs units into a single complex significantly increased fish abundance but did not affect species richness. This study contributes to our understanding of effective artificial reef design, spatial distribution and implementation, as well as to the understanding of marine ecological succession processes in the Gulf of Aqaba.

Assessing the nutritional value of biofloc produced in a RAS as a feed ingredient using *Artemia* as a model organism

V. Pandey - vandanapandeyeee@gmail.com (1) and D. Zilberg (1)
1) The French Associates Institute for Agriculture and Biotechnology of Drylands, Jacob Blaustein Institutes for Desert Research, Ben Gurion University of the Negev, Israel; Email: vandanap@post.bgu.ac.il, 055-260-4822

Feed cost, availability, sustainability and nutritional value is important in aquaculture development. Biofloc, a microbial biomass generated through the assimilation of fish excretions (ammonia and solid waste), has emerged as a promising sustainable feed ingredient in aquaculture. Studies by Yogev and Gross (2019) demonstrated that integrating microaerophilic bioreactors with recirculating aquaculture systems (RAS) can produce biofloc, which contains around 40% protein and has potential as a sustainable feed ingredient, as shown in Nayak et al. (2023).

Fish feeding trials are lengthy, complex and have problems with growing restriction due to animal ethics issues. Brine shrimp (*Artemia*), a non-selective filter-feeding crustacean having, short life cycle, easy accessibility and previous use as a model for host-pathogen interactions make it ideal for small-scale trials (Norouzitallab et al., 2014). Therefore, we proposed the use of artemia model for fish/shrimp feeding trials to evaluate the effect of feed formulations on health and growth.

Artemia were fed diets supplemented with varying biofloc inclusion levels (10%,15%, 25%, 50%, and 100%) combined with commercial fish feed. Results showed that feeding with 25% biofloc improved Artemia growth and survival following bacterial challenge compared to control and other inclusion levels. While 100% biofloc reduced growth rates, this aligns with previous findings in barramundi (*Lates calcarifer*), where biofloc supplementation (20%), enhanced immunity but slowed growth. However, unlike in barramundi, Artemia growth was elevated when 25% biofloc inclusion was applied.

First study of marine litter on the coasts of Eilat in the Gulf of Aqaba

G. Pasternak (1)

1) The Recanati Institute for Maritime Studies, University of Haifa, 199 Aba-Khoushi Avenue, Mount Carmel, Haifa 3498838, Israel.

The Gulf of Aqaba-Eilat, the home of the northernmost coral reefs in the world, is threatened by anthropogenic pressure such as tourism and manmade pollutions, including the recently growing problem of marine litter (ML), especially plastic due to its wide distribution, durability, and low biodegradability. Many coral reefs are polluted with plastics such food and beverage packages, abandoned fishing gear, vehicle tyre fragments. Plastics impact includes entanglement, physical damage, substrate coating, blockage of oxygen, food and energy. ML on Eilat's coast was studied for the first time as part of a nationwide coastal ML study conducted between November 2020 and February 2023, to understand ML composition and sources, and find ways to prevent it and its arrival to the sea. The beaches of Eilat which serve tourists throughout the year and are cleaned several times a day, were found clean according to “Clean Coast Index” (ICC) during the entire study. The density of ML found in Eilat was 6.37±1.5 items per 100m^2 which is lower than in other studies in the Red Sea, and similar to that found on the Israeli beaches of the Mediterranean Sea. More than half of the ML found in Eilat were cigarette butts, which with other small items found, indicates that Eilat's beaches are not cleaned thoroughly. With prevailing northern winds in the Gulf of Aqaba, ML is more likely to arrive from land to the sea, and the coasts of Eilat can be a major source of ML to the Red Sea's coral reef.

The sea urchin *Diadema setosum* invasion on the Israeli mediterranean rocky reefs: thermal resilience and potential ecological impacts under ocean warming

I. Preiss - irispreiss@gmail.com (1,2), Prof. G. Rilov (1,2), Prof. I. Berman-Frank (1)
1) Marine Biology Department, The Leon H. Charney School of Marine Sciences, University of Haifa, 199 Aba Khoushy Ave. Mt. Carmel, Haifa 31905, Israel
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, P.O. Box 8030, Haifa 31080, Israel

Climate change, and bioinvasions are major drivers of ecosystem change. The Israeli Mediterranean Sea coastal reef biodiversity is greatly impacted by both drivers being severely transformed with increasing loss of native species, and expansion of thermophilic invasive populations. Over the last 3 years, the invasive Indo-Pacific urchin, *Diadema setosum*, has become abundant along the Israeli coastline. Our study aimed to quantify the distribution of *D. setosum*, define its thermal tolerance to seawater temperatures, and assess its potential ecological impacts through grazing. Our coastal surveys, over the last three years, revealed highly clustered populations with hundreds of individuals in some locations but absence in others. Thermal vulnerability was evaluated by temperature performance experiments conducted at the IOLR flowthrough mesocosm system over a 16-36°C temperature range. Oxygen consumption and food assimilation by the urchins were used as proxies for thermal stress levels. Gonad-Somatic Index (GSI), and gonad histology analyses were used to assess impact on reproduction potential. Performance increased from 16°C to peak at ~ 28-30°C above which we observed some decline but mortality occurred only at 36°C. The impact of temperatures on *D. setosum* grazing rates were assessed at two densities in a flowthrough mesocosm system at ambient, and ambient +3°C temperatures. Boulders with higher density at both temperatures were grazed to bare rock within one month. Field caging experiments showed similar results. These findings indicate that the tropical invasive urchin is resilient to current and future climate warming and has the potential for severely impacting the Mediterranean coastal reef communities.

The synergistic effects of chronic gas-condensate pollution and warming on the survival and performance of the mussel *Brachidontes pharaonis*

N. Pressman Tal - nogalita.p@gmail.com (1, 2), P. Astrahan (3), T. Guy-Haim (1)
1) National Institute of Oceanography, Israel Oceanographic and Limnological Research, Haifa, Israel
2) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Israel
3) Israel Oceanographic and Limnological Research, The Yigal Alon Kinneret Limnological Laboratory, Israel

Ocean warming and oil pollution are regarded as two of the most widespread and pressing environmental stressors, raising significant concerns for the future of marine ecosystems. While each of these stressors can have independent impacts, several studies have showed synergistic impacts of the combined effects, posing series threats to the marine environment. While numerous studies have evaluated the impacts of crude oil and warming on the marine environment, only a few assessed the effects of gas-condensate, a hydrocarbon by-product of the natural gas production, and none tested the combined effects of warming and gas-condensate pollution.

Here we aimed to test the interactive effects of chronic exposure to gas-condensate and warming using the Indo-Pacific mussel Brachidontes pharaonis. The mussels were continuously exposed to five concentrations of gas-condensate in two temperatures, ambient and warmed (+3°C), over a period of 77 days. Mussel mortality was negligible across treatments, confirming that the concentrations used were sublethal. Clearance rates decreased with increasing gas-condensate concentrations in both temperature levels, but were consistently lower in the warmed treatment compared to the ambient temperature. Respiration rates decreased significantly with increasing condensate concentrations in the warmed treatment and were significantly higher in the ambient temperature. Malformations and histological alterations were observed in the gills and digestive glands of the mussels, including hepatic tubules with disintegrated epithelial cells and infiltrated basophilic cells at the higher gas-condensate concentrations compared to the control. These effects were more pronounced under warmed conditions, consistent with the observed physiological responses.

Development of microaerophilic-membrane-based assimilation aquaculture system

O. Rahamim - orelra@post.bgu.ac.il*, Z. Zhu (1), A. Ronen (1), E. Aflalo (2), D. Zilberg (1), A. Gross (1)
1) ZIWR, BIDR, Ben Gurion University of the Negev
2) Achva Academic College

Aquaculture is expanding rapidly to meet increasing global fish demand (FAO, 2022). A significant challenge is the high cost of fish feed, which typically contains 30-50% protein. However, only 20-30% of this protein is converted into fish biomass, with the remainder excreted as toxic ammonia and solids. Biofloc technology (BFT) was developed to manage total ammonia nitrogen while producing protein-rich microbial flocs. However, limitations including poor water quality and high energy demands for aeration have restricted BFT to specific fish species and small-scale operations.

To address these challenges, Yogev and Gross (2019) proposed a microaerophilic bacterial assimilation process that focuses on biomass production over nitrification. This approach used a side reactor to convert ammonia, fish solid waste, and external carbon sources into protein-rich biofloc. High total suspended solids (TSS), averaging ~127 mg/L, posed a challenge for integrating BFT with recirculating aquaculture systems (RAS). To mitigate this, a hollow-fiber ultrafiltration membrane treatment was introduced.

In a pilot-scale RAS with barramundi (Lates calcarifer) cultured at a density of ~20 kg/m^3, a 100% survival rate and a feed conversion ratio (FCR) of 1.5 were achieved. Approximately 45% of nitrogen from uneaten feed was assimilated into microbial protein, indicating effective nutrient reuse. Water quality was significantly improved, with TSS reduced by 74% to 33 mg/L. These findings demonstrated the potential of this system to enhance nutrient recycling and water quality, advancing intensive aquaculture practices.

Impact of combined seawater warming and triazine-type herbicide pollution on the physiology and potential toxicity of the dinoflagellate *Alexandrium minutum*

E. Rahav - eyalrahav@gmail.com (1, 2) and B. Herut (1)
1) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Haifa, Israel
2) Department of Earth and Environmental Sciences, Ben-Gurion University of the Negev

Coastal phytoplankton communities are often exposed to multiple anthropogenic stressors simultaneously. Here, we experimentally examined how temperature increase (20-26 °C) and triazine-type herbicides pollution (500 ng terbutryn L^{-1}), both recognized as emerging stressors, affect the abundance, physiology and selected saxitoxin gene expression in the toxic dinoflagellate Alexandrium minutum. The results show that A. minutum is more susceptible to terbutryn pollution with increasing temperatures, resulting in a significant decline in its abundance (~80%) and photosynthetic activity (~40%), while saxitoxin gene expression increased (1.5-2.5-fold). This suggests that in warming polluted coastal areas where A. minutum is often found, saxitoxin poisoning may occur even in the absence of a massive bloom. Our results recommend the development of science-based monitoring practices for algal dissolved toxins in coastal waters and estuaries, supporting environmental policies under warming and contaminated coastal regions.

Investigating the gene expression modulation in *Paenibacillus dendritiformis* in response to surfactin

O. Rainish (1), N. Barger (1), T. Luzzatto-Knaan (1)

1) Department of Marine Biology, The Charney School of Marine Sciences, University of Haifa, Haifa, Israel

Natural products are chemical compounds produced by organisms to interact with their environment, and among them surfactin, a cyclic lipopeptide produced by Bacillus subtilis, plays a pivotal role in biofilm formation, motility, and microbial antagonism. Remarkably, Paenibacillus dendritiformis not only displays attraction to surfactin but also actively degrades it. This study aims to unravel how surfactin modulates gene expression in P. dendritiformis, with a particular focus on identifying the peptidases involved in surfactin degradation and broader gene expression changes influenced by its presence. Our preliminary data suggest that growth in the presence of surfactin prolongs the bacterial lag phase, followed by later augmented growth. Based on our previous studies in B. subtilis, which demonstrated surfactin's impact on cell division and DNA replication, we selected relevant genes (including *minD*, *recA*, *dnaN*, *dnaA*, *dnaG*, *gyrA*, *gyrB*, *ftsZ*, and *minC*) for further exploration. Protease genes were identified through the MEROPS database, with their secretion potential validated using SignalP-6.0, leading to the selection of 10 proteins of interest. Through the antiSMASH platform, we targeted genes associated with the production of natural products, including Isochorismate synthase, Bacitracin synthetase 3, and L-ectoine synthase. Using RNA sequencing and quantitative PCR (qPCR) we aim to capture the impact of surfactin on the regulation of cell cycle, natural products expression and degradation mechanism in P. dendritiformis.

How corals make reefs: a geochemical perspective of coral biomineralization

S. Ram - sharon.ram@mail.huji.ac.il (1) and J. Erez (1)
(1) The Fredy and Nadine Herrmann Institute of Earth Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel

Coral reefs ecosystems depend on biomineralization of the reef framework for their existence. We studied biomineralization of hermatypic corals by the incorporation trace and minor elements into their skeletons (El/CaCoral) by changing the Ca concentrations (CaSW) in the experimental seawater. The partition of six cations (Li, Na, Mg, K, Sr and Ba) into nine corals skeletons species. The cations to Ca ratios in the skeletons (El/CaCoral) correlated linearly with their ratios in seawater (El/CaSW), revealing consistent and species-specific partition coefficients (DCoral). For Li, Mg, Na, and K, the partition coefficients were lower than one but higher than the inorganic aragonite values (DInorg) while for Sr and Ba DCoral, were higher than one but lower than DInorg values. Notebly, DCoral for the elements with DEl<1, showed inter-species systematic values, with the highest DCoral for *Acropora lamarcki*, corresponding to its highest calcification rates, whereas *Pocillopora damicornis* showed the lowest DCoral values, consistent with its lowest calcification rates. Opposite systematic trend was observed for the elements with DEl >1. These results suggest species-specific physiological control indicating skeleton precipitation from a semi-closed seawater (SW) reservoir. This extracellular calcifying fluid (ECF=SW) follows Rayleigh distillation with respect to all the measured trace and minor elements. The level of Ca utilization (1-f) and the degree of isolation of the calcifying system from external seawater, control the efficiency and rate of the calcification. The deviations from DInorg values (so called "vital effect) are governed mainly by the pH and DIC elevation in the ECF. The present study provides a strong basis for utilizing multi-elemental proxies in fossil corals, for reconstructing past ocean chemistry and climate reconstructions.

Do marine protected areas provide marine fish protection against metal pollution?

D. Ramon - Debiramon@gmail.com (1, 2), P. Croot (3), T. Zaquin (4), D. Morick (1,2), M.Lalzar (1), A. Scheinin (1, 2), E. Shemesh (1,2), D. Tchernov (1, 2), N. Davidovich (1, 2, 5), M. Britzi (6)

1) Department of Marine Biology, Charney School of Marine Sciences, University of Haifa
2) Morris Kahn Marine Research Station, University of Haifa
3) Earth and Ocean Sciences, School of Natural Science and Ryan Institute University of Galway
4) Bioinformatics Service Unit, University of Haifa
5) Israeli Veterinary Services
6) National Residue Control Laboratory, Kimron Veterinary Institute

Chemical pollutants, like metals, are a major threat to marine health. While much research has been placed on bioaccumulation of metals and the human exposure via consumed seafood, there are still large knowledge gaps regarding the impacts of metals to the health of the marine environment. Particularly, there have been very few studies assessing the ability of marine protected areas (MPAs) to provide protection for fish against chemical threats. This study aims to address this knowledge gap by assessing the accumulation of mercury, arsenic, cadmium, and lead in fish of ecological and economic importance collected along the Israeli coastline. To do this, four main sites are described: an area of high anthropogenic influence, a relatively pristine area, a highly trawled fishing area, and a no take MPA. We take advantage of numerous species caught within the MPA, including local species like highly prized keystone groupers as well as migratory species, to characterize the metal accumulation patterns within the MPA and compare them to those outside. Comparisons were made using individual parameters including species, weight, length, trophic position, location, maturity, migratory/local, and BMI. In addition, a general additive mixed effect (GAM) model was developed for mercury and arsenic accumulation, incorporating all parameters simultaneously. The GAM model shows elevated mercury accumulation within the MPA as a factor of fish maturity. This study therefore addresses both ecological concerns and potential human impacts by providing context to species-specific accumulation, human health risks, and abilities of MPA to fend off chemical pollution.

Methanic sediments near the deep-sea brine pools hold an untapped biotechnological potential

L. Ratinskaia - ratinskaialina@gmail.com (1, 2), M. Rubin-Blum (1, 2) and T. Luzzatto- Knaan (2)
1) The Department of Marine Biology, Israel Oceanographic and Limnological Research
2) The Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa

Life flourishes in the absence of light-driven photosynthesis in deep-sea chemosynthetic environments, such as hydrocarbon seeps. Poorly studied organisms fuel productivity in these extreme habitats and produce a wealth of largely unexplored secondary metabolites – a potential untapped biotechnological resource. To address this knowledge gap, we study the diversity of secondary metabolites and their producers in euxinic and methanic sediments adjacent to the deep-sea brine pools at Palmahim Disturbance, the Eastern Mediterranean Sea. Using omics, we link microbial taxonomy and the potential to produce secondary metabolites, that is, natural products. Metagenome-assembled genome investigations have predicted that microbial communities can produce antimicrobial ranthipeptides, versatile terpenes, and complex thiopeptides, highlighting the biotechnological potential of these microbial metabolites. We found that the elusive Ca. Zixibacteria encoded the highest richness of biosynthetic gene clusters (BGCs). The understudied Desulfobacterota, Caldatribacteriota, and Chloroflexota were also enriched with BGCs. The function of these clusters varied among phyla, e.g. ~40% and only 2% of BGCs encoded terpene biosynthesis, in Chloroflexota and Desulfobacterota, respectively. In Desulfobacterota, ~32% of BGCs were linked to the production of ribosomally synthesized and post-translationally modified peptides (RiPPs), such as thiopeptides and ranpeptides. Metabolomics using liquid chromatography-mass spectrometry (LC-MS) identified circa 800 molecules, often with undefined structures, hinting at the presence of novel or understudied compounds. The ongoing work focuses on linking omics datasets, aiming to trace key compounds, from genotype to chemotype. This study will uncover novel bioactive compounds and enhance our understanding of deep-sea ecosystems' metabolic diversity and adaptation mechanisms.

Chemoautotrophic and photoautotrophic inorganic carbon fixation rates in the oligotrophic Eastern Mediterranean Sea and Northen Red Sea.

T. Reich - reichtom@gmail.com (1, 2), N. Belkin (1), G. Sisma-Ventura (1), I. Berman-Frank (2) and E. Rahav (1)
1) National Institute of Oceanography, Israel Oceanographic and Limnological Research, Haifa, Israel
2) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel

We investigated the spatiotemporal variability of photosynthesis and dark inorganic carbon fixation (DCF) in the photic and aphotic layer of the eastern Mediterranean Sea (EMS), as well as monthly photosynthetic and DCF rates from the photic layer of the northern Gulf of Aqaba (GOA) collected over a decade between 2010-2020. Our results show that the contribution of DCF to the total primary productivity was generally low in the EMS coastal area (typically ~2-4%) and higher at the offshore water (often ~11% in the EMS and ~43% in GOA).

Moreover, we show that the contribution of DCF to primary productivity was higher during the oligotrophic summer when heterotrophic microbial metabolism prevails than in the winter period when photo-autotrophy is more dominant in both seas. This resulted in an annual integrated contribution of ~5 g C m^{-2} y^{-1} attributed to DCF alone in the photic zone of the EMS (180m) and ~34.6 g C m^{-2} y^{-1} integrated through the whole water column.

In the GOA DCF contributed ~6% to the particulate organic carbon flux during the winter and ~30% during summertime. Complimentary nutrient-enrichment bioassays of seawater from 5m show that dissolved organic nutrient enrichment (P and C based) significantly elevates DCF, whereas addition of dissolved inorganic nutrients (PO_4^{3+}, NO_3^- or both) significantly increased photosynthesis but to a lesser extent DCF.

Taken together, our results suggest that DCF may be an important biochemical process in oligotrophic seas, and thus should be incorporated into oceanic carbon production estimates."

Automated reef fish monitoring with high-resolution video and AI

V. Rina - victor.china@gmail.com (1, 2)
1) Dead Sea-Arava Science Center
2) Ben Gurion University

Traditional reef fish monitoring methods, relying on manual expert surveys, limit temporal and spatial data resolution. This study introduces an innovative automated pipeline leveraging high-resolution video footage and deep learning to monitor reef fish in the Red Sea, addressing these limitations through a three-step process:

Fish Detection: A fine-tuned YOLOv10 model, trained on 15,000 pre-labeled fish images from public sources, processes high-resolution video in 640x640 pixel subframes. This approach preserves fine details while overcoming computational limitations of full-frame analysis.

Unsupervised Clustering: KMeans clustering groups visually similar fish images, extracting representative centroids for each cluster. This step efficiently summarizes data and identifies potential outliers representing rare species.

Species Identification: We evaluate three different approaches: manual expert review, a custom-trained CNN model, and a multimodal LLM approach.

Our scalable, high-resolution reef fish monitoring pipeline significantly enhances temporal and spatial data collection capabilities. Through efficient processing of extensive video datasets, this approach has the potential to revolutionize marine biodiversity research and conservation efforts.

A kinematic-dynamic 3D Model for density-driven ocean flows

O. Saporta-Katz - vered.rom-kedar@weizmann.ac.il (1), E. S. Titi (1, 2, 3), H. Gildor (4), and V. Rom-Kedar (1)
1) The Weizmann Institute.
2) University of Cambridge, UK.
3) Texas A& M University, USA.
4) The Hebrew University.

Kinematic models, in which passive scalars are advected by a predetermined velocity field, can exhibit intricate behaviors of scalar fields, often associated with chaotic advection phenomena. Potential temperature and salinity fields are active tracers that determine the ocean's potential density; their distribution significantly influences the density-driven component of the velocity field, while the overall flow affects their distribution. We introduce an intermediate-complexity model of this fundamental non-linear process [1]. In this hybrid kinematic-dynamic model, the velocity field is a sum of a time-dependent mode that is externally induced and a mode with an amplitude that depends on density differences between boxes. In one limit, the model simplifies to an oceanic box model, including a bi-stable regime, while in another limit, it approximates a kinematic model of oceanic chaotic advection. Several open problems related to this model are discussed, including its relevance to the Atlantic Meridional Overturning Circulation and its dependence on the Mediterranean outflow waters.

Exploring couplings between iron reducing bacteria and methanotrophs in methanogenic sediments.

A. Rosenblatt - adirosen@post.bgu.ac.il (1), M. Rubin (2), A. Gafni (3), O. Sivan (1)

1) The Department of Earth and Environmental Sciences, Ben-Gurion University Of the Negev, Beer Sheva, Israel
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Haifa, Israel
3) The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sede Boqer, Israel

Background and Aims: Microbial methane oxidation (methanotrophy) plays a crucial role in mitigating the release of this important greenhouse gas methane from aquatic systems. Interestingly, we found aerobic methanotrophic activity below the oxic-anoxic zone in highly reduced methanogenic lake sediments. Concomitantly, obligate anaerobic microbes, such as methanogens and iron reducers, were observed there. However, the co-existence of these aerobic and anaerobic microbes, the link between the processes, and the oxygen requirement for the bacterial methanotrophs have remained unclear. This study aims to examine the interactions between these microbial populations in the sedimentary zone of the Sea of Galilee, focusing on the methanotrophic bacteria Methylomonas and the iron-reducing bacteria Desulfuromonas. These populations may serve as regulators of methane emissions from sediments to the aquatic environment and subsequently, the atmosphere.

Methods: A series of incubation experiments were performed with enriched cultures and their mixture close to natural conditions. and the changes in iron and methane concentrations in their media were monitored, as well as small metabolites

Results: Our data show significant difference in the measured parameters in the mixture compared to each of the population alone.

Conclusions: The results indicate an interaction between the two populations, which changes the measured parameters and enabled both survive in this hypoxic environment. The outcome of this study is expected to enhance our understanding of microbial interactions that affect methane dynamics. The knowledge of this microbial interactions is essential for the mitigation of this greenhouse gas emissions.

Computer-assisted sperm analysis – a novel approach to study sperm behavior across marine invertebrates broadcast spawners

Lachan Roth - lachanroth@gmail.com (1, 2, 3), Gal Eviatar(1, 2, 3) and Omri Bronstein(1, 2)
1) School of Zoology, The George S. Wise Faculty of Life Sciences, Tel-Aviv University, 69978, Tel-Aviv, Israel.
2) Steinhardt Museum of Natural History, Tel Aviv University, 69978 Tel Aviv, Israel.
3) The Inter-University Institute for Marine Sciences in Eilat, Israel.

Inter-specific breeding, i.e., reproduction between individuals of different species, is often avoided to prevent the formations of sterile, low fitted hybrids and maintain genetic diversity. The biological mechanisms underlying inter-specific breeding avoidance are poorly understood in marine invertebrates. Broadcast spawning is a widespread sexual reproduction strategy within marine invertebrates, that involves shedding gametes into the water column, facilitating external fertilization, yet increasing the potential for inter-specific gamete encounters. Motility of benthic marine invertebrate species is often limited or completely absent in sessile species. As a result, pre-copulation behavior and mate-choice control are significantly challenged, and sperm transport relies primarily on sperm kinematics and water movement. Here, we examine whether inter-specific breeding avoidance is driven by sperm behavior. We tested the effects of egg derivatives from six sea urchin species (Echinodermata: Echinoidea) and two fire coral species (Cnidaria: Hydrozoa) on sperm behavior and kinematics. We used Computer-Assisted Sperm Analysis (CASA) to accurately measure sperm motility parameters (e.g., velocity and linearity) and examined the sperm behavior in the presence of female derivatives of all eight species. Our results reveal that sperm was effectively activated by signals from all eggs, regardless of species assignment, and imply an equal fertilization potential with no relation to the phylogenetic distance. As sea urchins are key aquaculture species, elucidating fundamental mechanism underlying their sexual reproduction is essential for optimizing breeding practices and sustainability. Furthermore, these findings highlight the potential of CASA systems in aquaculture breeding efficiency, allowing higher potential fertilization success in bred species.

Morphodynamics of the shallow seafloor during the course of a storm: high-resolution direct observations

N. Rozen - noga.rozen@mail.huji.ac.il (1, 2), T. Katz (3), N. Lensky (1, 2), O. Crouvi (1), O. Katz (1), A. Mushkin (1), A. Agnon (2)

1) Geological Survey of Israel, 32 Yesha'ayahu Leibowitz St. Jerusalem, Israel
2) The Fredy & Nadine Herrmann Institute of Earth Sciences, The Hebrew University, The Edmond J. Safra Campus - Givat Ram, Jerusalem, Israel
3) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Haifa, Israel

Studying seabeds during storms is crucial for coastal management, yet intra-storm morphology and sediment transport remain understudied due to challenges in obtaining data amid harsh wave conditions. Here we present direct observations of sediment and seafloor morphodynamics during a high-wave event. We analyzed data from two observation stations deployed at ~6.5 m water depth, about 500 m offshore the Ne’urim beach-stretch (north of Netanya), focusing on one storm between 3-12 March 2023. One station was equipped with current and wave meters, and the second with an underwater camera capturing videos of the seafloor. Video observations yield two distinct behaviors: on grain movement scale we distinguish stagnation, creep, saltation, suspension; on seafloor morphology level we distinguish five categories from calm to intense water motion. Observations revealed gradual seafloor changes, from biological control through different types of ripples correlated with the rise in significant wave height, leading to smoothing at the storm's peak. Sediment dynamics evolved from stagnation to a combination of creep, saltation, and suspension at peak conditions. Post-storm, seafloor morphology alternated between ripple types, with slow return to pre-storm state even after achieving initial wave height. Sediment dynamics remained stable as the storm declined, combining creep, saltation, and suspension until substantial wave height reduction, then gradually reached stagnation at storm end. Turbidity increased rapidly, peaking with maximal wave height, then gradually declined to pre-storm levels. Our analysis highlights a link between seafloor morphodynamics and storm progression, indicating changes during storm-rise occur faster than the return to the original state.

A step forward towards sustainable aquaculture

G. Rubinstein - guyr@moag.gov.il (1)

1) Ministry of Agriculture

The increasing demand for fish consumption, alongside increasing in the awareness of environmental protection, creating new and harder conflicts between aquaculture and the environment.

In order to reduce as much as possible, the negative impact on the environment, and continue to raise fish, economically, adjustments must be made to the new situation. In Israel, with the help of government tools, we are working to promote solutions that minimize the environmental damage, increase the ecological system services that the open fish ponds can provide to the natural environment, alongside maintaining the economic viability of the fish farm.

The actions include a broad environmental reform to regulate the interface of releasing the water from fish ponds to the environment. Collaborate with farmers, and environmental organizations, accompanied by government support in financing the necessary expenses, and improving the grow out facilities accordingly.

In addition, creation of ecological natural habitats, that are not disturbed by hazards, as an integral part within the areas of the fish ponds, which will be ecological habitats for the various animals without harming the agricultural activity.

Studying the molecular mechanisms underpinning thermotolerance in diatoms acclimation to marine heat waves

M. Sadeh - mai.sadeh@weizmann.ac.il (1)*, S. Ben-Dor (2), G. Friedlander (2) D. Schatz (1), A. Vardi (1)
1) Department of Plant and Environmental Sciences, Weizmann Institute of Science, Rehovot, Israel
2) Life Science Core Facilities, Weizmann Institute of Science, Rehovot, Israel

Marine heat waves (MHW) are extreme climate events in which ocean temperature rises for days to months and can expand over thousands of kilometers. IPCC predictions show that MHW frequency is increasing worldwide along with climate change. Little is known about the impact of MHW on marine microbial life and, specifically, on algal blooms. Our goal is to decipher molecular mechanisms underpinning thermotolerance of diatoms during bloom succession. We first investigated metacaspases (MC), cystine proteases that share structure similarity to caspases, and were initially suspected to be involved in cell-fate regulation during bloom demise. Surprisingly, we revealed that MCs have a vital role in heat stress acclimation, possibly by protein aggregates clearance, as recently discovered in plants and yeast. Using CRISPR-Cas9, we generated a triple knock-out mutant of the MC genes in the model diatom Phaeodactylum tricornutum. Mutants were exposed to HW treatment for 72 hours and then transferred back to pre-treatment conditions. Triple MC mutants showed increased sensitivity to HW treatment compared to WT, and cell death peaked days after returning to lower temperatures. Samples from this setup were taken to proteomics analysis and revealed more crucial proteins involved in thermotolerance. In addition, we examined the response of different diatom isolates from the Gulf of Aqaba (GoA) to heat treatment and discovered HW tolerance is species-specific. We also sampled the GoA annual diatom spring bloom and exposed natural populations to MHW treatment. We will specifically look for MC expression and activity as a heat stress biomarker. We aim to reveal the molecular strategies employed by marine diatoms to cope with MHW and hope to shed light on the MHWs ecological impact, specifically during diatom blooms.

From lab to plate

A. Sagi (1)

1) Ben Gurion University of the Negev

The world of transferring academic research knowledge to industry is complex and challenging. This topic is of considerable interest on a global level. Various models enable the industrial application of knowledge derived from academic research. Israel has success stories, yet the economic potential remains significant. The contribution can be mutual, and creating an advanced industrial environment could directly or indirectly benefit academic research, even at its basic level.

We propose achieving this not through sporadic, disconnected actions but by adopting flexible implementation mechanisms. This includes concentrating efforts on building a technology-based industry near the university, supported by private investments that recognize the advantages of proximity to the university and ongoing dialogue with its faculty and students.

The green seaweed *Caulerpa nummularia* as a potential source for food and antioxidants

E. Salomon - eitansol@ocean.org.il (1)

1) Israel Oceanographic and Limnological Research, National Center for Mariculture, Eilat, P.O. Box 1212, Eilat 8811201, Israel

Seaweeds have been used as food for thousands of years. They are considered as a good source for proteins, minerals, and health promoting substances such as phenolic compounds and antioxidants. Seaweeds are known for their strong umami flavors, which makes them desirable for many people, yet deter many others from consuming them. Currently, only a limited number of seaweed species are commercially grown for food or food supplements. In the Far East, several species of the green seaweed genus *Caulerpa* are commercially grown and sold fresh or dried for human consumption. The current study focuses on the potential of *Caulerpa nummularia*, local to the Gulf of Eilat, to serve as a nutritional source. *C. nummularia* was isolated from fish tanks in the National Center for Mariculture, transferred for indoor cultivation, and its nutritional values were measured. *C. nummularia* cuttings were able to propagate and grow asexually in open-flow aquarium systems. *C. nummularia* has a slightly salty but neutral flavor. It had 23±0.4 % protein and 54.2±0.4 %, carbohydrate content (DW). Its mineral values included 18 mg magnesium, 37 mg calcium, 17 mg potassium, 0.6 mg iron and 0.08 mg C. zinc, per 5 g dry seaweed. These values are similar to those of other seaweeds and constitute between 1-5% of the recommended daily intake (Europe). Additionally, ~5 mg of phenolic compounds were measured per 1 gram of dry seaweed. The suitability of clonal growth, its neutral taste and nutritional values, suggest *Caulerpa nummularia* as a promising new mariculture crop plant.

Northbound transport of the mediterranean outflow and the role of time-dependent chaotic advection

O. Saporta-Katz - orikatz.ok@gmail.com (1), N. Mantel (2), R. Liran (2), V. Rom-Kedar (1), H. Gildor (2)
1) Department of Computer Science and Applied Mathematics, Weizmann Institute of Science
2) The Institute of Earth Sciences, Hebrew University of Jerusalem

The Mediterranean Sea releases approximately 1 Sv of water into the North Atlantic through the Gibraltar Straits, forming the saline Mediterranean Outflow Water (MOW). Its impact on large-scale flow and specifically its northbound Lagrangian pathways are widely debated, yet a comprehensive overview of MOW pathways over recent decades is lacking. We calculate and analyze synthetic Lagrangian trajectories in 1980–2020 reanalysis velocity data. Sixteen percent of the MOW follow a direct northbound path to the sub-polar gyre, reaching a 1,000 m depth crossing window at the southern tip of Rockall Ridge in about 10 years. Surprisingly, time-dependent chaotic advection, not steady currents, drives over half of the northbound transport. Our results suggest a potential 15–20 years predictability in the direct northbound transport. Additionally, monthly variability appears more significant than inter-annual variability in Lagrangian mixing and spreading the MOW.

Strategic plan for aquaculture in Israel - 2050

A. Savaya (1)
1) Mariculture Division at the Ministry of Agriculture and Food Security, Israel

Fish consumption is on the rise, both in Israel and worldwide. Today, however, over 90% of the fish consumed in Israel is imported. The Ministry of Agriculture and Food Security is leading a strategic plan for the aquaculture sector in Israel for the coming 25 years. The presentation will expose the current and future development directions for the sector to achieve 3 main goals:

1. Food security
2. Economic viability of sector
3. Israel as global leader in technologies development and application

Periods of halite deposition/dissolution in the late-glacial to early Holocene Dead Sea as documented in Na/Cl ratios of soluble salts extracted from the DSDDP deep core

P. Schimmer-Pick - pamela.schimmer@mail.huji.ac.il (1, 2), B. Lazar (1), G. Sharabi (2), O. Khalifa (1), M. Stein (1, 2)
1) Institute of Earth Sciences, The Hebrew University of Jerusalem, Israel
2) The Geological Survey of Israel, 32 Yesha'yahu Leibowitz St., Jerusalem, Israel

The modern Dead Sea is a terminal lake that evolved from a series of ancient lakes since the late Neogene time. Water-rock interactions and the hydrologic regime along the Dead Sea Basin dictated the salinity and composition of the brines that filled these lakes and the sedimentary sequences they deposited. These processes resulted in a brine with a Ca-chloride composition, which has been evolving during the lake's history. The chemical compositions of soluble salts within the Dead Sea sediments were obtained from the DSDDP 5017-1-A core for the time interval of ~ 15-9 ka. Na/Cl ratios declined to low values at the end of the last glacial period (~15-14.5 ka), indicating halite deposition (at core depth of 92.8 m), followed by a sharp incline that marks a period of halite dissolution. This dissolution period was again followed by massive halite deposition at ~ 14 ka (88.48 m in the core), followed by halite dissolution during the Younger Dryas (12.9-11.6 ka). A second interval of massive halite deposition over the entire lake commenced at ~11 ka. The halite dissolution/deposition temporal pattern in the lake is chronologically associated with rapid (a few hundred years) changes in the regional hydroclimate (lake level) regime. These changes are related to the climate-oceanographic conditions in the North Atlantic. The massive halite deposition periods in the late glacial-early Holocene Dead Sea coincided with pulses of freshwater inputs to the North Atlantic due to glacial melting: MWP 1a at ~14.5- 13.8 ka and MWP 1b at ~11-10 ka.

Transgene Expression Regulation in Marine Algae

N. Segal (1)
1) National Center for Mariculture, Israel Oceanography and Limnology.

Microalgae are a diverse group of single-cell photosynthetic organisms that can adapt to extreme habitats and produce various essential biological and high-value products. Throughout the years, much effort has been made to improve Microalga product quality and yield. These efforts have been made by manipulating growth conditions or actively transforming foreign genes and using metabolic engineering. However, the use of microalgae as 'heterologous systems' for transgene expression, a term referring to introducing genes from one species into the genome of another, has yet to fulfill its potential. In *Chlamydomonas reinhardt*ii, it has been demonstrated that the epigenetic mechanism regulates transgene expression by randomly mutating the CrSRTA gene of the Sirtuin protein family. This gene is homologous to the human SIRT6 and is part of the sirtuin protein family that functions as Histone Deacetylase. This discovery provides a new method of studying the effect of the epigenetic mechanism on transgene expression in different microalgae and understanding the mechanisms that regulate it.

Mutating the same gene in other Microalgae might improve the transgene expression and ratio of expression colonies in different marine microalgae. Generating a more solid and reliable system will increase the use of microalgae as an expression system.

Effects of off-axis hydrothermal systems on the oceanic Mg budget

N. Shalev - netta.shalev@mail.huji.ac.il (1) and D. S. Ramos (2)
1) Fredy & Nadine Herrmann Institute of Earth Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel
2) Department of Marine and Coastal Sciences, Rutgers University, New Brunswick, NJ, USA

The chemistry of the ocean and its variations throughout time are controlled by the oceanic budgets (the sum of input and output fluxes) of various elements. Hydrothermal reactions of seawater with the oceanic crust at mid-ocean ridge flanks play a fundamental role in determining the ocean's chemical (and isotope) composition. The water flux through these systems is on the same order of magnitude as the river discharge to the ocean, and approximately three orders of magnitude higher than that of on-axis systems. Thus, understanding and quantifying the reactions occurring at ridge flanks are essential for studies that use the oceanic budgets of elements and their isotopes to understand the modern Earth's surface environment and its variations over time. However, our current knowledge of such reactions is limited mainly due to system heterogeneity and challenges in sampling.

Here, we focus on the importance of these off-axis systems for our understanding of the oceanic magnesium (Mg) budget. We modeled the oceanic Mg budget and its stable isotopes (δ26Mg) over the last 20 Myr for two endmember scenarios: 1) where off-axis hydrothermal systems act solely as a sink for Mg; and 2) where Mg exchange occurs between seawater and crust in these systems (i.e., Mg sink flux = Mg source flux). The results show that these two scenarios lead to different outcomes, mainly for the off-axis hydrothermal, dolomite, and groundwater Mg fluxes. These findings highlight the need for further research into Mg (and Mg isotope) dynamics in the hydrothermal systems at ridge flanks.

Elucidating the sensitivity of ocean deoxygenation to the macromolecular composition of marine primary producers

S. Sharoni - ssharoni@mit.edu (1), K. Inomura (2), S. Dutkiewicz (1), O. Jahn (1), G. Britten (3), and M. Follows (1).
1) Department of Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology
2) Graduate School of Oceanography, University of Rhode Island
3) Department of Biological Oceanography, Woods Hole Oceanographic Institution

The oceans are currently losing their oxygen and are expected to lose more in the future due to human-induced climate changes. However, the uncertainty associated with the magnitude and extent of future ocean deoxygenation is still large. A source of uncertainty associated with ocean deoxygenation is related to the consumption of oxygen during bacterial respiration. The amount of oxygen consumed during organic matter respiration relative to carbon, i.e., the respiration quotient, depends on its macromolecular and elemental composition. Despite significant global variations in phytoplankton elemental composition, the respiration quotients of the organic matter are constant in models that assess the impact of climate change on oceanic oxygen. This likely results in a misrepresentation of the rates of deoxygenation. Here, we calculated the respiration quota of organic matter in the ocean by explicitly simulating the macromolecular composition of phytoplankton in a 3D global ocean using the MIT ocean general circulation model (MITgcm). In these simulations, the MITgcm is coupled to a model that resolves the cellular allocation to protein, carbohydrates, lipids, chlorophyll, and storage molecules. Using the model, we show that there are global variations in the respiration quotient of the organic matter driven by variations in cellular allocation to major macromolecules in response to environmental conditions. We further test the effect of variations in the respiration quotients on ocean oxygen budget. Our results provide a mechanistic understanding of the factors influencing the respiration quotients of organic matter in the ocean and their impact on the global oxygen cycle.

Drugs in the sea: pharmaceutical contamination along the coasts of Israel

G. Navon - shenkarn@tauex.tau.ac.il (1), O. Nordland (2), A. Kaplan (2), D. Avisar (2), N. Shenkar (1 ,3)
1) School of Zoology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv, 69978, Israel.
2) The Water Research Center, Porter School of the Environment and Earth Sciences, Raymond and Beverly Sackler Faculty of Exact Sciences, Tel Aviv University, Tel Aviv, 69978, Israel.
3) The Steinhardt Museum of Natural History and National Research Center, Tel Aviv University, Tel Aviv, 69978, Israel.

Global increase in the use of pharmaceutically-active compounds (PhACs), and their insufficient removal in wastewater treatment plants, have resulted in their continuous release into the marine environment. Unlike other pollutants, pharmaceuticals are designed to induce physiological and hormonal changes in organisms, even at low concentrations. This study aims to assess the extent and impact of pharmaceutical pollution along Israel's Mediterranean and Red Sea coasts. Solitary ascidians (Chordata, Ascidiacea) were used as biological indicators, while stony corals from the Gulf of Eilat were analyzed for coral reef contamination. The objectives were: 1) Develop new analytical tools to detect and quantify pharmaceutical residues in marine samples; 2) Identify high-risk contamination zones along the Mediterranean coast; 3) Examine pharmaceutical residues in coral tissues from shallow and deep sites in Eilat. Three pharmaceuticals—carbamazepine (CBZ), bezafibrate (BZF), and diclofenac (DCF)—were detected at multiple Mediterranean sites, while 10 out of 18 common drugs were found in coral tissues from Eilat, with higher concentrations at shallow sites and on the northern shore. The findings highlight the urgent need for further research into pharmaceutical pollution, to better understand its scale and potential effects on marine life, alongside valuable data on regional pollution levels and recommendations for managing pharmaceutical discharge.

From viral to bacterial control: the impact of elevated temperature on algal bloom demise

N. Shima - noa.shima@weizmann.ac.il (1), A. Isbi (1), N. Albocher Kedem (1), D. Schatz (1), A. Vardi (1)
1) Department of Plant & Environmental Sciences, Weizmann Institute of Science

Phytoplankton are unicellular photosynthetic microorganisms that form the basis of the marine food web. Marine heterotrophic bacteria have complex interactions with phytoplankton, ranging from mutualism to pathogenicity. Phytoplankton blooms of the cosmopolitan coccolithophore Emiliania huxleyi cover vast oceanic areas and have important roles in the global carbon and sulfur cycles. While the main known cause leading to bloom termination is viral infection by the Emiliania huxleyi virus (EhV), recent evidence showed that pathogenic bacteria are also involved in bloom demise. In the current study, we aim to determine the yet unknown impact of temperature on bacterial and viral virulence toward *E. huxleyi*. This question is timely and ecologically important, as the oceans get warmer due to climate change, with already observed impacts on *E. huxleyi* blooms dynamics and biogeographic distribution. Preliminary results show that co-culturing *E. huxleyi* with several marine bacteria or with EhV at an elevated temperature led to changes in host susceptibility. Elevated temperature hastens bacterial-induced algae mortality while reducing viral-induced cell death. By developing several sensitive approaches to assess bacteria virulence combined with single cell analysis of viral infection at elevated temperatures, this study will expand our understanding regarding the relative contribution of viral infection versus bacterial pathogenicity to algal bloom demise in a warming ocean.

Underwater radiated noise pollution from vessel activity – characterization and mitigation options

M. Shipton - mshipton@campus.haifa.ac.il (1, 2)
1) Department of Marine Technology, Haifa University, 199 Abba Khoushy Ave., Haifa
2) The Institute for Maritime Policy and Strategy, Ha-Namal St 21, Haifa

Underwater radiated noise (URN) pollution from vessel activity has been recognized as one of the most severe threats to the health of the global marine ecosystem.

Due to the rapid attenuation of light in the water column, marine fauna (e.g., fish, crustaceans, and marine mammals) rely heavily on the acoustic channel to navigate, communicate, locate food, and avoid predators. In this regard, various research frameworks have shown that URN from vessel activity leads to adverse effects among marine fauna, such as heightened stress symptoms and significant behavioral changes.

Despite the subject's graveness, little has been done to address or attempt to mitigate the harmful effects of URN. This primarily stems from two fundamental shortcomings in the current research agenda: the incoherent characterization of URN and the lack of any viable policy options to mitigate it.

Characterization of URN from vessels is paramount in order to estimate the nominal noise levels of vessels and understand how the physical attributes of the vessel (type, size) or operating conditions (e.g., speed of the vessel) affect noise levels. The characterization of URN from vessels could then act as an empirical basis for constructing policy and regulatory initiatives aimed at mitigating URN.

To this end, I have constructed a statistical model of URN levels based on thousands of acoustic recordings of vessels conducted in the Adriatic and Mediterranean Seas. Based on this data, I propose several viable policy options that can be implemented to mitigate the effects of URN pollution from vessels near coastal waters.

Nanoflagellates and ciliates dominate the Palmahim cold seep protist community, parasitic Syndiniales follow

L. Shmakova - lushmakova@gmail.com (1), S. Malavin (1, 2), M. Rubin Blum (1, 3)
1) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, P.O. Box 8030, Haifa 31080, Israel
2) Zuckerberg Institute for Water Research, Ben-Gurion University of the Negev, Sede Boker Campus 84990, Israel
3) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, 199 Abba Khoushy Ave, Mount Carmel, Haifa 3103301, Israel

In cold hydrocarbon seep areas like the Palmahim hydrocarbon seeps, 60 km offshore Israel at 1150 meters depth, natural hydrocarbon discharge supports rich chemosynthetic ecosystems. A syntrophic consortium of anaerobic methane-oxidizing archaea (ANME) and sulfate-reducing bacteria (SRB) constitutes their core. Multicellular animals, such as tube worms, molluscs, and decapods, thrive in cold seeps, mostly in symbiosis with bacteria. Unicellular eukaryotes (protists) are also abundant, but much lesser studied.

We analyzed the protist fauna of the Palmahim seep sediments using rDNA-based metabarcoding. The analysis revealed 343 OTUs of protists and fungi from 8 supergroups, namely Alveolata, Apusomonada, Breviatea, Chlorophyta, Metamonada, Opisthokonta (non-Metazoan), Rhizaria, and Stramenopiles. The three most abundant groups were (in order of decreasing abundance) Stramenopiles, Ciliophora, and Dinoflagellata. Dinoflagellates were the most diverse (80 OTUs), followed by Stramenopiles (59 OTUs), and then ciliates (29 OTUs). Parasitic Syndiniales (61 OTUs) dominated Dinoflagellata. The fourth most abundant group was Prasinophyta (Chlorophyta). This may be attributed to non-motile organic-walled resting cysts (phycomata), that are known to concentrate in oxygen-depleted sediments. Ciliates were represented by eight classes with the distribution dependent on the distance from the brine pool. Armophorea and Colpodea were mostly found in the core taken in the vicinity of the brine pool, while Prostomatea and Spirotrichea were observed exclusively at a two-meter distance from the brine pool. Litostomatea and Oligohymenophorea were present in both samples but in bigger amounts in the core close to the brine pool. Further investigation is needed to determine the driver of the observed protist communities.

Annual dynamics of cyanophage abundances and their infection in the Sargasso Sea

C. Shopen Gochev - camelia@campus.technion.ac.il (1) and D. Lindell (1)
1) Faculty of Biology, Technion – Israel Institute of Technology

Viruses are the most abundant entities in the oceans and affect bacterial distribution. This study investigates the annual dynamics of cyanophages, viruses infecting cyanobacteria. Focusing on the Bermuda Atlantic Time-series (BATS) station, monthly samplings over two years unveil fluctuations in cyanophage abundances and infection of the dominant cyanobacterium, Prochlorococcus. As known for this region, we observed distinct seasonal patterns in cyanobacterial abundances. Prochlorococcus peaked in late summer deep in the photic zone and Synechococcus reached its peak in spring at the surface. The T7-like cyanophages dominated the cyanophage community at BATS, different to other regions studied thus far, outnumbering T4-like cyanophages by two-fold on average. Abundances of T4-like and T7-like cyanophages peaked in fall with maximum abundances at 80-100 meters. These annual dynamics were consistent for both years. Infection of Prochlorococcus was generally greater at depth than at the surface throughout the seasonal cycle. However, infection levels were highest by far in fall, deep in the photic zone. Interestingly, seasonal infection patterns were different for the two cyanophage groups, with infection by T7-like cyanophages greater than by T4-like cyanophages in most months. T4-like cyanophage infection was low at the surface (0-2.5%), with maximal infection in subsurface waters in summer and fall (3.5-5%). Infection of Prochlorococcus by T7-like cyanophages was relatively low in surface waters (0-4%), reaching 20-26% in the fall at depth. These findings suggest seasonal differences in the impact of cyanophages on their cyanobacterial hosts. This further suggests that the seasonality of these two cyanophage groups are attributed to distinct responses to biotic and abiotic seasonal changes.

The relation of extra-tropical advected ocean heat anomalies and ENSO

M. Shourky Wolff - maya.shourky@mail.huji.ac.il (1) Ori Adam (1)
(1) Fredy and Nadine Herrmann Institute of Earth Sciences, Hebrew University, Jerusalem, Israel

Despite substantial progress over the past few decades in understanding El Niño and the Southern Oscillation (ENSO), the origin of the subsurface ocean heat anomalies that mature into ENSO events in the equatorial Pacific remains uncertain. in this study, we perform a Lagrangian back trajectory analysis using ocean reanalysis data to assess the contribution of extra-tropical advected heat anomalies to Equatorial Pacific SST variability in the region commonly used to quantify ENSO variations (Niño3.4 region). The above relation is studied using two physical paradigms: remotely advected (i) temperature anomalies, and (ii) spiciness anomalies. Our findings indicate that heat anomalies associated with ENSO have significant contributions from extra-tropical regions, which have been identified in previous studies as contributing to Equatorial SST variability on decadal or longer timescales. We map the probability of regions poleward of 10° to act as source regions for upwelled water in the Niño 3.4 region. We then define effective advected heating (EAH) as the product of this probability and the temperature or spiciness difference from the mean value in the Niño 3.4 region. EAH is found to be positively correlated with the mean temperature tendency in the Niño3.4 region, for both temperature and spiciness anomalies. An analysis of the mixed layer heat budget corroborates this result Temperature and spiciness EAH are generally similar, with main differences in the subtropical south-eastern Pacific. Both the 'temperature anomaly' and 'spiciness anomaly' paradigms show potential predictive power of ENSO variability.

Strong climate control on the millennial-scale dust variability and sediment provenances in the equatorial indian ocean inferred from sr-nd isotopes

A. Shukla - arvindshukla.au@gmail.com (1, 2)* and S. Kumar Singh (1)
1) CSIR-National Institute of Oceanography, Panjim, Goa, India-403003
2) School of Earth, Ocean and Atmospheric Sciences, Goa University, Taleigão, Goa, India
* Fredy & Nadine Herrmann Institute of Earth Sciences, The Hebrew University, Edmond J. Safra Campus, 91904, Jerusalem, Israel (Present address).

Ocean sediments archive information on their provenances, erosion, transport, and deposition history. They provide insights into erosional patterns of surrounding land masses, variations in aeolian fluxes, and records of climate and sea-level changes that influence these processes. In this regards, major & trace elements and Sr-Nd isotopes of the silicate fraction of a sediment core raised in the Equatorial Indian Ocean, were used to reconstruct the variation in the sediment provenance over the past ~38 ka. 87Sr/86Sr (0.71978 to 0.72491), ƐNd (-14.8 to -21.9), and few source diagnostic elements display profound variability over the depositional time scale. Primary potential sources of sediments at the core site are (i) Peninsular Gneissic Complex (PGC), (ii) Deccan Basalt, (iii) the aeolian dust from Africa, the Arabian Peninsula, and the Thar desert. Higher aeolian dust fluxes from the Sahara, South Africa, Arabian, and Thar deserts, along with sediment from the Deccan Basalt contribute significantly to the core site during the cold/arid events like HS1- 4, LGM, YD, 8.2 ka, 5.2 ka, and 1.1 ka. Conversely, warm/humid events like Early Deglacial (ED), Bølling- Allerød (B-A), and Holocene Intense Monsoon (HIM) show more PGC sediment contribution to the core site. The present investigation underscores the significant role of climate, mainly the aridity, in modulating the dust fluxes and erosion intensity and the strong coupling between Indian monsoon and North Atlantic climatic oscillations and further demonstrates minimal time delay between the production and transport of sediment from source to sink.

The influence of fresh submarine groundwater discharge on seawater acidification along the northern mediterranean coast of Israel

J. Silverman - jacobs1@ocean.org.il (1), S. Strauch-Gozali (2), M. Asfur (3)
1) Israel Oceanographic and Limnological Research (IOLR), Haifa, Israel
2) Faculty of Marine Sciences, Ruppin Academic Center, Mikhmoret, Israel

In the oligotrophic Southeastern Mediterranean Sea (SEMS), it has been shown that dissolved inorganic nutrient (DIN) from fresh submarine groundwater discharge (FSGD) enhance primary production in coastal waters. In this study pH, Total Alkalinity (TA) and DIN of seawater and fresh water in a sea-cave in the northern part of the Israeli Mediterranean coast and a nearby contact spring, respectively, were measured during October 2018–March 2020. The results show gradients of measured salinity, TA, pH and DIN along the cave axis year-round, suggesting that they are influenced by FSGD. The seawater near the back of the cave was supersaturated with respect to atmospheric CO_2 nearly year-round and there is a strong positive divergence from its regional open-water thermal dependence, which suggests that FSGD is also a source of atmospheric CO_2 in this region. Comparison of TA, salinity and pCO_2 from the back of the sea cave to their corresponding values from an abrasion platform monitoring site, ca. 3 km south of the cave, suggests that FSGD is occurring along the entire shoreline in this region. Thus, despite the increased productivity due to FSGD mediated nutrient enrichment of adjacent coastal waters of the oligotrophic SEMS, they are still a source of atmospheric CO_2 nearly year-round. Finally, the apparent trends of seawater acidification ($\Delta pH/\Delta t = -0.006\ yr^{-1}$) and pCO_2 increase (+8 ppmV yr^{-1}) observed at the nearby monitoring site since 2013 are explained by increased groundwater recharge and resulting FSGD total alkalinity compared to dissolved inorganic carbon inputs ($\Delta TA/\Delta DIC$ = 1:1.2).

Deconvolving the age and sediment provenance of the Levant Channel, eastern Mediterranean Sea

L. Sivan - Lea.sivan@mail.huji.ac.il (1), A. Torfstein A. (1, 2), O. Hymes-Kaphzan (3), M. Kanari (4), O. Katz (3)
1) Institute of Earth Sciences, Hebrew University of Jerusalem, Israel
2) interuniversity Institute for Marine Sciences, Eilat, Israel
3) Geological Survey of Israel, Jerusalem, Israel
4) Israel Oceanographic and Limnological Research, Tel Shikmona, Haifa, Israel

Submarine channels in the Levant Basin, eastern Mediterranean, are significant geological features that reveal crucial insights into sedimentary processes and basin evolution. These northwards trending channels, formed by turbidity currents and other sediment transport mechanisms, play a key role in shaping the basin's morphology and stratigraphy. Of these, the most prominent channel is the “Levant Channel” (LC), which is more than 150-km-long. Nevertheless, we still lack knowledge on when the LC was formed, whether it is active or not, where it originates from, and what is the source of the sediments.

Here, we aim to address these knowledge gaps by extracting and sampling a series of downcore records along and nearby the LC. For this purpose, the age model of two cores is determined based on radiocarbon dating of benthic foraminiferal shells. The cores’ elemental and radiogenic isotopes chemistry, mineralogy, and grain size distributions are used to preliminarily characterize the provenance and sediment transport mechanisms of the LC sediments. Particularly, this is achieved by using mixing models of the chemical and radiogenic isotope (εNd and 87Sr/86Sr) composition, assuming two primary end members in this system: the Nile River sediments and Sahara Desert dust. Our results provide insight into sediment transport dynamics and provenance, and their change over time.

Surfactin expression in *E. coli* as a platform for production of natural products from marine bacteria

B. Snir - bsnir@campus.haifa.ac.il (1), N. Barger (1), T. Luzzatto-Knaan (1)
1) Department of Marine Biology, The Charney School of Marine Sciences, University of Haifa, Haifa, Israel

Natural products are chemical compounds produced as metabolites by various organisms, with marine natural products (MNPs) playing a crucial role in this area of research. The marine environment, characterized by immense biodiversity, presents significant challenges for studying and producing MNPs, particularly because many marine microorganisms remain uncultured. Even when culturing is feasible, it is often more efficient to produce these compounds in heterologous hosts rather than manipulating the natural biosynthetic pathways. This highlights the need for a simpler system for scalable MNPs production. In this study, we present a platform aimed at addressing this challenge, using the srfA operon from Bacillus subtilis as a case study. The srfA operon encodes enzymes responsible for the biosynthesis of surfactin, a cyclic lipopeptide with potential applications as a biosurfactant. We plan to construct a plasmid containing the entire operon under an inducible promoter and transform the large plasmid (~40 kb) into Escherichia coli. To amplify the operon, we employed long and accurate PCR (LA-PCR). Additionally, we introduced the sfp gene, which supports the functionality of the enzymes. We also working on design both single- and dual-plasmid systems for sfp expression, comparing their efficiency in supporting surfactin production in the host organism. This platform provides insights into the heterologous expression of MNP biosynthetic pathways and presents a potential strategy for scalable production of valuable marine-derived compounds.

Death at sea: the dynamics of *Prochlorococcus* mortality due to nutrient starvation across genomic and geographic diversity

Y. Soussan-Farhat - yarasoussan@gmail.com (1), O. Weissberg (1) and D. Sher (1)
1) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Israel

The death of marine microbes plays a major role in nutrient cycling at sea. Natural cell death, for example as a result of UV damage or nutrient starvation, might be common in the oceans yet is not widely studied. Here, we investigate natural cell death caused by nutrient starvation in *Prochlorococcus*, a globally abundant marine cyanobacterium. We characterized the dynamics of mortality due to Nitrogen (N) and phosphate (P) starvation in 15 strains of *Prochlorococcus*, which were isolated from different oceanic locations and represent much of the genetic diversity of this clade. We asked whether the mortality phenotype depends on the nutrient stress most common where each strain was isolated from, its genetic background, or its phylogeny.

We defined sensitivity based on the mortality rate (testing also other death features such at maximum yield and number of peaks during stationary phase).

Surprisingly, the nutrient stress where the strains were isolated from, as well as the complement of genes known to be involved in N or P uptake and utilization, do not explain whether the strain is more sensitive to N or P starvation. Instead, genes related to cell quality control on the protein level were found to be more present in strain which are more sensitive to P starvation, while DNA quality control genes were tied to N sensitivity.

This is the first study to quantitatively assess mortality across strains and conditions in abundant marine microbe, refuting core hypotheses and pointing to new survival pathways.

Dynamics of shallow groundwater in Lake Kinneret during level change

S. Stein - shakedstein@ocean.org.il (1), Y. Beeri-Shlevin (1), G. Sharabi (2), T. Zilberman (2), E.Levy (2)
1) Israel Oceanographic and Limnological Research, the Kinneret Limnological Lab, Migdal, Israel
2) Geological Survey of Israel, Jerusalem, Israel

Lake Kinneret is an important freshwater source in the region. It is characterized by a relatively high salinity (~260 mgCl/L) which poses problems for agriculture and other applications. Moreover, since the lake water is used for drinking in both Israel and Jordan, it is crucial to maintain low salinity levels. Salts enter the lake through onshore and offshore saline springs (point sources) as well as through the sediment around the lake (non-point sources). Throughout the year, changes in the lake level and the groundwater level alter the hydraulic gradient, which in turn affects the Lacustrine Groundwater Discharge (LGD) regime. However, little is known about how these hydraulic changes impact LGD, its quality, and sources along the lake shores. To address these issues, shallow monitoring wells (~1 m depth) were dug on the shore of the Kinneret Limnological Laboratory. Groundwater was monitored at high frequency (every 15 minutes) using sensors, and at lower frequency (once every two weeks) using water sampling. Results indicate that during winter, the hydraulic gradient between the shallow groundwater and the lake increases, which enhances the LGD. Additionally, as the hydraulic head rises, groundwater salinity also increases, suggesting that winter may be a period of higher salt inflow into the lake. Water isotopes reveal that prior to winter, the primary source of groundwater was lake water. However, during and after winter, fresh groundwater replaced lake water. This monitoring method can be applied in various locations around lakes to differentiate between water sources and LGD regimes.

Determine the role of Sir2 on transgene silencing in the diatom *Phaeodactylum tricornutum*.

R. Steinmetz-Walther (1) Dr. N. Segal (1)

1) Department of Microalgae, Israel Oceanographic and Limnological Research (IORL) in Eilat

Microalgae, diverse unicellular organisms capable of photosynthesis, are valuable in biotechnology. Research aims to develop algae as heterologous expression systems. In Chlamydomonas reinhardtii, transgene silencing occurs through chromatin structure changes at insertion sites. Mutations in CrSRTA, a Sir2 Class IV sirtuin with NAD+ dependent histone deacetylase activity, significantly increased transgene expression. This study focuses on the Phaeodactylum tricornutum (*P. Tricornutum*) homolog of CrSRTA, aiming to determine its role in transgene silencing through CRISPR knockout. P. tricornutum showed sensitivity to zeocin. Transformant colonies grew on selective media, but GFP was undetectable via fluorescent microscopy, indicating low expression. In vitro assays confirmed CRISPR/Cas9 RNP complex efficacy in digesting target DNA. Primer functionality was verified through colony PCR. The work strategy was to generate Sir2 knockout lines in P. tricornutum by transforming Cas9-gRNA RNP complexes alongside a linearized zeocin-resistance plasmid. Compare transgene expression in mutated colonies to wild-type P. tricornutum. Initial findings suggest P. tricornutum silences transgenes. CRISPR gRNA successfully cleaves the SIR2 gene at the desired position. Right now, we continue with a phase involves in vivo CRISPR experiments in P. tricornutum, followed by analysis of successful transformations for transgene expression. This research may uncover mechanisms to enhance transgene expression in microalgae, advancing their use in biotechnology.

Seiche-induced fish-kills in the Sea of Galilee may explain the biblical miraculous catch of fish

E. Strobach - udistr@gmail.com (1), Y. Amitai (2), S. Assouline (1), D. Hamilton (3), A. Nishri (2), T. Zohary (2)
1) Volcani institute
2) Kinneret Limnological Laboratory
3) Griffith University

On May 31, 2012, thousands of dead fish were found along the north-western shore of the Sea of Galilee. Analysis of fish gill tissue revealed no evidence of poisoning, and the fish looked healthy. This event adds to reports of similar fish kills at the same location, from the early 1990s, from May 2007, and a subsequent event on June 27, 2012, a month after the May 31 event. The common hypothesis for the massive kill suggests that a seiche induced by strong winds caused the upwelling of colder and anoxic hypolimnetic water along the western shores of the lake. Still, this hypothesis has not yet been tested.

The WRF (The Weather Research and Forecasting) atmospheric model was recently coupled with the ocean model MITgcm (MIT general circulation model). The coupled model was named SKRIPS (Scripps–KAUST Regional Integrated Prediction System). The two SKRIPS model components (WRF and MITgcm) are well-tested at high resolution, allowing us to investigate the physical mechanism of the fish-kill event in an interactive system. To test the hypolimnetic water upwelling hypothesis for the massive fish-kill, we have set up and integrated the SKRIPS model for the May 31, 2012, event at a horizontal grid resolution of 400 square meter, both for the atmospheric and lake component of the model.

In this talk, I will present results from a high-resolution coupled atmosphere-lake regional simulation indicating an upwelling of cold anoxic hypolimnetic water into the surface during the event. The upwelling of cold water is increased close to the shore. The discussion will be supplemented by field data of temperature and oxygen concentrations, collected before, during, and after the fish-kill event. Our simulation results agree with the field observations, adding confidence to the anoxic hypolimnetic water upwelling hypothesis. Such fish-kill events may explain the biblical ‘miraculous catch of fish’ and the ‘miracle of the loaves and fish’. Also, it may provide a possible seasonal time frame (spring) for their occurrence in the past.

Influence of mixed layer depth on the seasonal cycle of the tropical rain belt

S. Sudheendran - sreerag.sudheendran@mail.huji.ac.il (1) and O. Adam (1)
1) The Hebrew University of Jerusalem

This study explores how variations in the spatial distribution of the ocean mixed layer depth (MLD) influence the seasonal cycle of the tropical rain belt, and in particular single- vs. double-intertropical convergence zone (ITCZ) states. The study utilizes the Community Earth System Model version 2 (CESM2) in both aquaplanet and realistic-land slab ocean model (SOM) configurations, alongside data from models participating in phases 5 and 6 of the Coupled Model Intercomparison Project (CMIP5/6). To leading order, the influence of the MLD on the tropical rain belt can be explained by how it controls sea surface temperature (SST) variations, which, in turn, affect precipitation. Specifically, we find that increasing MLD damps the extent of seasonal migrations for single ITCZs, and narrows the separation between double ITCZs; the intensity of the ITCZs increases with the sharpness of SST peaks, which generally gets damped with increasing MLD. To leading order, the dependence described above captures the differences between marine and terrestrial ITCZs in realistic land simulations. Variations across CMIP models indicate that the effect of MLD on the extent of ITCZ migrations is more pronounced in the Atlantic than in the Pacific, due to differences in ocean circulation. Energetic constraints on the sensitivity of the seasonal cycle of the tropical rain belt to MLD are proposed. Our findings have implications for systematic precipitation biases in modern climate models, associated with biases in MLD representation.

Metagenomic assembly and characterization of marine plasmids: Depth-dependent distribution of plasmids and resistance genes

L. Androsiuk (1, 2, 3), **S. Tal** - shay.tal@ocean.org.il (2)

1) Marine Biology and Biotechnology Program, Department of Life Sciences, Ben-Gurion University of the Negev, Eilat Campus, Israel
2) Israel Oceanographic & Limnological Research Ltd., National Center for Mariculture, Eilat, Israel
3) Department of Life Sciences, Ben-Gurion University of the Negev, Beer-Sheva, Israel

Plasmids play a significant role in the environmental dissemination of various functional genes, especially antibiotic resistance genes. Yet, plasmids isolated from marine environments are underrepresented in plasmid databases. Studies of environmental marine plasmids suggest that while some are very common and found across different environments, depths, and large distances, they differ from known terrestrial and freshwater plasmids. In recent years, many metagenomic studies from various environments (including marine environments) have been performed; however, these studies have typically focused on bacterial populations rather than plasmid populations. The metagenomic data collected in these studies is publicly available but is assumed to contain limited information about plasmids as it was not enriched for plasmid detection.

Here, we report the use of a pipeline for de novo assembly of plasmids in marine environments by analyzing available metagenomic sequencing data. Using data from different marine environments, we identified hundreds of novel plasmid candidates. The candidates were analyzed in terms of their distribution and gene content. We have shown that candidates' distribution corresponds to physical environmental conditions, particularly depth and temperature. Moreover, antibiotic and metal resistance genes were clustered in specific locations. Surprisingly, the diversity of resistance genes is higher in the mesophotic and deep-water regions compared to shallow water.

Candidate stem cell isolation and transplantation in Hexacorallia

S. Talice - shanital@post.bgu.ac.il (1, 2), I. Kozlovski (3), S. K. Barkan (1), G. A. Snyder (4), S. Oisher (1), T. Levy (5), U.Hadad (6), C. Davis (1), Y. Moran (3), O. Gershoni-Yahalom (1), N. Traylor-Knowles (4), B. Rosental (1, 2).

1) The Shraga Segal Department of Microbiology, Immunology, and Genetics. Faculty of Health Sciences. Center for Regenerative Medicine and Stem Cells. Ben Gurion University of the Negev, Beer Sheva, Israel
2) School of Sustainability and Climate Change, School of Sustainability and Climate Change. Ben Gurion University of the Negev, Beer Sheva, Israel
3) Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences, Faculty of Science, The Hebrew University of Jerusalem, Jerusalem, Israel
4) Rosenstiel School of Marine, Atmospheric, and Earth Science, University of Miami, Miami, FL, United States of America
5) Institute for Stem Cell Biology and Regenerative Medicine, Stanford University School of Medicine, Hopkins Marine Station, Stanford University, Pacific Grove, CA, USA
6) Ilse Katz Institute for Nanoscale Science and Technology, Ben-Gurion University of the Negev, Beer Sheva, Israel

This study investigates stem cell characteristics in Hexacorallia using the sea anemone Nematostella vectensis as a model organism. We identified a subpopulation of cells exhibiting key stem cell properties, including self-renewal, differentiation potential, and long-term survival. These cells successfully integrated into recipient organisms and demonstrated therapeutic potential in chemotherapy rescue experiments.

Using aldehyde dehydrogenase (ALDH) activity as a marker, we enriched the candidate stem cell population and confirmed their properties through machine learning analysis and bulk RNA sequencing. The ALDH-high population was predominantly located in the mesenteries, suggesting a potential stem cell niche.

Cell transplantation experiments revealed clear differentiation between pre- and post-transplantation stages, indicating successful engraftment and differentiation of transplanted cells. This research establishes a foundation for stem cell studies in Hexacorallia and opens avenues for potential cell therapy approaches in corals, addressing issues related to heat tolerance and survival in the context of global warming. Our findings provide a valuable model for future research in coral conservation and regenerative medicine in marine invertebrates, potentially leading to novel strategies for preserving and restoring coral reef ecosystems.

Mesophotic rocky reefs provide refuge for shallow fish assemblages of a semi-tropical sea.

A. Tsemel - atsemel@univ.haifa.ac.il (1), S. Martinez(1), S. Einbinder(1), H. Nativ(1), I. Izhaki(2) and D. Tchernov(1)
1) Morris Kahn Marine Research Station, Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa
2) Department of Evolutionary and Environmental Biology, University of Haifa

The ‘deep-reef refugia’ hypothesis was raised in light of global climatic changes. This hypothesis suggested that a deeper suitable habitat would allow reef-forming corals to experience the evolutionary alterations needed to adapt to the changing climatic conditions (Glynn, 1996). This study is the first to test the hypothesis in the Mediterranean Sea.

Fish census data from 2015-2022 at 10m (23% (±11) of 1m PAR), 25m (8% (±4) of 1m PAR), and 45m (3% (±2) of 1m PAR) depths and light were collected using closed-circuit re-breather systems. Temperature and complexity data were also analysed. Fish species and trait diversity were calculated using R.

Our data show that 1) depth generalist species dominate the metacommunity and deep reefs host the same species as the shallow reefs; 2) gamma diversity (Effective and True Diversity) is higher in the 25m community ; 3) alpha diversity at the shallow 10m depth is reduced compared with 25m; 4) depth specific beta diversity increases with depth; 5) Turnover is the dominant overall characteristic, and nestedness weaker at the deeper reefs; 6) functional diversity of the shallow reefs is contained within that of the deeper reefs.

These fish community characteristics at 25m depth align with theoretical criteria proposed by Medeiros et al. (2021) to test the validity of depth as a refuge for fish communities, apart from turnover (instead of nestedness) being the dominant characteristic. The 25 m rocky reefs, at the mesophotic, seem to provide a refuge for the fish community of the Israeli coast.

On the difficulty of a rapid attribution of extreme events to anthropogenic climate change

P. Sherman (1), **E. Tziperman** - eli@eps.harvard.edu (1, 2) and P. Huybers (1, 2)
1) School of Engineering and Applied Sciences, Harvard University
2) Department of Earth and Planetary Sciences, Harvard University

Increases in extreme weather events are an important possible consequence of anthropogenic climate change (ACC), yet it is famously difficult to attribute individual events to ACC. We are motivated by recent attribution studies by the ""World Weather Attribution Project"" (WWAP) based on fitting the observed record to extreme value distribution functions and making the distribution parameters a function of the observed global mean surface temperature (GMST). We show that this attribution analysis can lead to false-positive results. Specifically, the effects of natural variability modes such as ENSO on the GMST make it difficult to confidently attribute extreme events to ACC. We re-examine three attribution cases, suggesting modifications that may increase our confidence in the meaningfulness of the attribution results. [With Peter Sherman and Peter Huybers]

Adapting to the future: Salinity and temperature tolerance of the non-indigenous ascidian *Phallusia nigra*

A. Unger - amitunger98@gmail.com (1), N. Shenkar (1, 2)
1) School of Zoology, George S. Wise Faculty of Life Sciences, Tel-Aviv University, Tel Aviv, Israel
2) The Steinhardt Museum of Natural History and Israel National Center for Biodiversity Studies, Tel-Aviv University, Tel Aviv, Israel

Ascidians play a key role in fouling communities globally, often adapting to diverse environmental conditions. However, they can cause significant ecological and economic damages, including competition for space and resources, which may lead to the displacement of native species and a reduction in endemic biodiversity. *Phallusia nigra* is a widely distributed solitary ascidian native to the Red Sea, and considered non-indigenous in the Mediterranean Sea and Singapore. This study compared the adaptability of native and non-native populations of *P. nigra* to changing environmental conditions. We conducted artificial fertilizations to culture juveniles from all populations under laboratory conditions, a protocol designed for this study, followed by a month-long multi-factorial stress experiment. The experiment tested three salinities (35, 40, 43 PSU) and three temperatures (16, 25, 31 °C). Survival was monitored three times per week, with blood-flow current direction measured weekly as a stress indicator. Results revealed that salinity significantly affected the Mediterranean population, while temperature was the primary factor for the Red Sea population. The Singapore population showed notable survival at 25 and 31 °C across all salinities. None of the populations survived at 16 °C, and low temperatures inhibited larval development, indicating a reproductive barrier. A model predicting P. nigra's present and future distribution suggests range expansion and enhanced survival under future conditions. These findings highlight *P. nigra*'s adaptability, its potential for global spread, and the need to mitigate the impacts of invasive species on marine ecosystems in a changing climate.

Initial insights and challenges from studying a diverse library of heterotrophic marine bacteria.

V.K. Waseem Bashir - wvaliyak@campus.haifa.ac.il (1), C. Alejandra Martinez Gutierrez (2), H. Scott (3), E. Forchielli (3), M. Osborne (3), K. Sampath (3), L. Zoccarato (4), K. Herbst (3), H.-P. Grossart (5), D. Segrè (3), D. Sher (1)

-1) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel.
2) Department of Earth Science, University of California at Santa Barbara, Santa Barbara, CA, USA
3) Department of Biology, Boston University, Boston, MA, USA
4) Institute of Computational Biology, University of Natural Resources and Life Sciences, Vienna, Austria
5) LeibnizInstitute for Freshwater Ecology and Inland Fisheries (IGB), Neuglobsow, Germany.

Microbial ecologists use various approaches such as monoculture and co-culture models, controlled microbiomes, and mesocosms to understand the complexity of the larger bacterial ecosphere. A bacterial monoculture library is an approach which allows the comparison of one bacterial model to that of other strains, bridging the gap between studying monocultures and bacterial communities. This study provides valuable insights into establishing and testing a heterotrophic marine bacterial library as a tool for studying marine bacterial ecology and physiology. We assembled a library of heterotrophic marine bacteria, which were selected based on an extensive genome comparison to represent as many functionally and phylogenetically distinct groups of bacteria as possible. Genome resequencing revealed important information on Single Nucleotide Polymorphisms that could imply changes in the physiology of some strains in the library compared to ancestral ones. We characterized some basic bacterial physiological traits such as biochemical phenotypes, biofilm formation, motility, antibiotic susceptibility, nutritional requirements, and optimal growth temperature, assessing the library as a research tool. For instance, we used the crystal-violet assay to check for biofilm formation, showing that alpha and gamma-proteobacteria produce the most biofilms on plastic surfaces, whereas other known biofilm forming bacterial isolates likely require a different assay. Similarly, we observed differences in motility between two assays (plate swarming and stab), possibly related to the ability to grow aerobically. This study offers important insights into how microbial traits are partitioned across diversity, as well as tools for users to address challenges associated with working with a diverse heterotroph library.

The rotation of fish eggs relative to the surrounding water and its implication to mass transfer

M. van Gelder - m.van-gelder@campus.technion.ac.il (1, 2), R. Holzman (2, 3), U. Shavit (1)
1) Civil and Environmental Engineering, Technion IIT, Haifa, 32000, Israel.
2) The Inter-University Institute for Marine Sciences, Eilat, 88103, Israel.
3) School of Zoology, Faculty of Life Sciences, Tel Aviv University, Tel Aviv 69978, Israel

Pelagic fish eggs rely on mass transfer with the surrounding water for oxygen supply. Past studies assumed no relative motion between the egg and the surrounding water, implying that diffusion is the only process that governs oxygen transfer.

The distribution of density within fish eggs is non-uniform, with the heavy embryo at the bottom and light oil globule at the top. We hypothesize that this internal structure acts as an internal restoring moment that balances the external torque applied on the egg by the flow. This mechanism allows the egg to maintain a vertical orientation, while the water rotates around it, resulting in a relative motion between the egg and the surrounding water. This motion can enhance the flux of oxygen into the egg by stimulating advection mechanisms in addition to diffusion.

Here, we measured the orientation of fish eggs under increasing rotational velocities, which applied external torque on the egg in the range experienced in the ocean. We show that eggs maintain a constant orientation within each rotational velocity, while the water rotates around them. Eggs inclined further towards a horizontal orientation as the velocity increased, up to a critical velocity in which they started tumbling. A theoretical model we developed shows that this behavior can result from the non-uniform distribution of the mass within the eggs under increasing torque.

The relative motion of the eggs under waves and turbulence was not considered nor implanted in previous models of oxygen transfer rates into fish eggs, thus, likely been underestimated.

The eastern Mediterranean boundary current: stability and spiral formation

V.Verma - vickyverma@mail.tau.ac.il, R. Barkan, A. Solodoch., H. Gildor, & Y. Toledo.

The Eastern Mediterranean (EMED) boundary current is an important constituent of the general circulation in the basin. Although a basin-scale feature, the boundary current is only tens of kilometers wide and a few hundred meters deep, making it challenging for a numerical model to resolve its dynamics adequately. In this presentation, we discuss a realistic regional model of the EMED, with nested grids, that resolves a wide range of motions, from basin-scale down to submesoscale (100 m – 10 km), and enables a detailed investigation of the boundary current dynamics. Seasonal changes in the boundary current will be discussed. We show that the boundary current becomes unstable year-round and spawns submesoscale anticyclonic eddies (spirals), elucidate the spiral formation process, and highlight the role of bottom drag in instigating the instabilities. Furthermore, an eddy kinetic energy generation analysis reveals that a mix of barotropic and baroclinic instabilities is responsible for the spiral formation.

Field validation of the all-female monosex biotechnology in the freshwater prawn *Macrobrachium rosenbergii*

M. Wahl - wahlm@post.bgu.ac.il (1), E. D. Aflalo (1, 2), K. Hongrath (3), A. Shechter (3) and A. Sagi (1, 4)
1) Department of Life Sciences, Ben-Gurion University of the Negev, P.O.B. 653, Beer-Sheva 84105, Israel.
2) Department of Life Sciences, Achva Academic College, Arugot 7980400, Israel.
3) Enzootic Ltd., 1 Coleman Street #10-10, The Adelphi, Singapore, 179803, SG.
4) National Institute for Biotechnology in the Negev, Ben-Gurion University of the Negev, P.O.B. 653, Beer-Sheva 84105, Israel.

A major drawback in the freshwater prawn Macrobrachium rosenbergii aquaculture is its complex social structure, characterized with bimodal growth and wide size distribution, limiting stocking densities (typically up to $4/m^2$) and the ability to reach industrialized yields. Manipulations of the androgenic gland hormone-sexual switch (IAG-switch) enabled the development of monosex biotechnologies. Recently, using parental cell transplantation, a non-GMO WW-based biotechnology for all-female monosex production was established. Here, we report the first large-scale field validation of the above all-female M. rosenbergii biotechnology, investigating a range of high stocking densities from 10 to $20/m^2$ with different nursery practices. The all-female populations resulted in higher yields (up to 4,474 kg/ha) compared to previous prawn culture records. Moreover, the all-female culture produced medium-sized specimens characterized by high size uniformity (CV 3.8% to 12.2%) with an average weight of 31.5 to 54.8 g depending on stocking density and nursery practice. The high rate of actively reproductive females at harvest (above 80%) suggests the potential for higher growth if energy were not invested in vitellogenesis and a potential shortening of the growout period. This study demonstrates the feasibility and advantages of the all-female biotechnology. Its global potential in the industry will be discussed in light of the effects of the major culture parameters studied on yields.

Genome editing for improved crustacean aquaculture: Achievements and challenges

H. Wattad - haninw@post.bgu.ac.il (1), J. Molcho (1), R. Manor (1, 2), S. Weil (1), E. D. Aflalo (1, 3), V. Chalifa-Caspi (4), M. Pimenta Leibowitz (5), A. Sagi (1, 2)

1) Department of Life Sciences, Ben-Gurion University of the Negev, P.O. Box 653, Beer-Sheva 84105, Israel
2) The National Institute for Biotechnology in the Negev, Ben-Gurion University of the Negev, P.O. Box 653, Beer-Sheva 84105, Israel
3) Department of Life Sciences, Achva Academic College, Mobile Post Shikmim 7980400, Israel
4) Bioinformatics Core Facility, Ilse Katz Institute for Nanoscale Science & Technology, Ben-Gurion University of the Negev, Beer-Sheva, Israel
5) Colors farm LTD, Central Arava Branch, Moshav Hatzeva 86815, Israel

The CRISPR/Cas technology typically enables accurate genomic editing. It has been applied to many model and non-model organisms for functional genomic studies and agricultural applications. For genome editing in the widely cultured prawn Macrobrachium rosenbergii, our laboratory recently established two CRISPR platforms: the first through electroporation of primary embryonic cell culture and the second via microinjection into early-stage embryos. Nevertheless, the CRISPR/Cas genome editing approach in non-model organisms poses challenges that arise from the lack of comprehensive information, as well as genetic variations, including a high frequency of single nucleotide polymorphisms, differences in sex chromosomes, and repetitive sequences that can lead to off-target events. Next-generation sequencing analysis demonstrated a high frequency of genetic variations in genes on both autosomal and sex chromosomes, which have been shown to affect the accuracy of editing analyses. Furthermore, mapping a specific tag that integrates into double-strand break sites enabled identifying off-target sites, which is essential for addressing future aquaculture-related regulatory issues. By overcoming the above challenges and understanding the genetic landscape, we were able to improve the efficiency and precision of genome editing by devising a roadmap for selecting optimal guides with high certainty. Notably, using our suggested roadmap for a de-novo genome-annotation approach that enables accurate gene prediction and guide design for knock-outs, we succeeded in editing a specific non-lethal phenotype-related early-acting scarlet gene through the microinjection platform, which showed an apparent change in eye pigmentation in edited embryos and larvae.

Radium isotope insight into the stratification history of the meromictic Lake Kivu

Y. Weinstein - weinsty@biu.ac.il (1), R. Alkalay (1)
1) Bar-Ilan University

The research of ‘killer lakes’, which are meromictic lake that accumulate large inventories of harmful gases in their deep water, is of very high importance due to their possible severe impact on human life and well-being. This was unfortunately demonstrated in Lake Monum and Lake Nyos (1984 and 1986, respectively). Lake Kivu is a deep (485m) meromictic lake, located along the western branch of the East African Rift (Rwanda-DRC), at the foot of the highly active Nyiragongo volcano, with a population of >2 million people occupying its shores. It has a shallow mixolimnion (~65 m) and a deeper monimolimnion, which is subdivided into separate water layers by several picnoclines, with the most prominent at 260m and a secondary one at ~320-330m. The deep lake holds very large volumes of both CO2 and CH4. Lake stratification is maintained via deep hydrothermal discharge at depth. In Sept. 2022, we conducted a water column radium profile, as well as an onshore hydrothermal spring. Considering the high concentration of the 226Ra in the hydrothermal water (15.5 dpm/l) and the limited lake water volume at depth, the relatively low activities in the >330m water (2 dpm/l) suggests that the deep stratification is quite recent (<40-50 years), which further suggests that the hydrothermal discharge probably varies on a multi-annual time scales. The data also insinuate that there might be a wide variety of Ra activities in sub-lacustrine springs, which may provide insights into aquifer residence times. Future sampling of sub-lacustrine springs could further constrain meromixis history.

Unveiling the mechanisms behind positive and negative interactions in marine microbial communities: a mathematical exploration of *Prochlorococcus* - heterotroph interactions

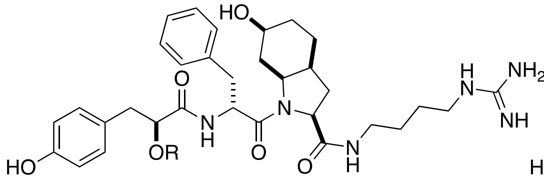
O. Weissberg - osnat.weissberg@gmail.com (1), Z. Wu (2), M. J. Follows (2) and D. Sher (1)
1) Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa
2) Department of Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology, Cambridge, MA, USA

Phytoplankton drive the marine food web through carbon fixation, but their success relies on intricate bacterial partnerships. This study explores the mechanisms governing interactions between the cyanobacterium *Prochlorococcus* and co-occurring marine heterotrophic bacteria, using mathematical models. We ask whether mathematical models explicitly representing four putative mechanisms of interaction (overflow metabolism, mixotrophy, exoenzymes and detoxification) are able to recapitulate the results of laboratory co-cultures. Our results reveal two key mechanisms where heterotrophs support *Prochlorococcus*: i) Cross-feeding, whereby Prochlorococcus supplies fixed carbon to heterotrophs, while heterotrophs recycle essential nitrogen through exoenzymes or overflow metabolism, creating a mutually beneficial loop; ii) Detoxification, whereby heterotrophs detoxify harmful byproducts (e.g., reactive oxygen species) produced by Prochlorococcus, leading to a positive interaction. These mechanisms differ in the overall productivity of the co-culture system. Finally, the models are able to capture also negative interactions, but these are very rare within the range of growth parameters tested, suggesting that negative interactions observed in laboratory cultures are likely due to additional mechanisms not represented in these models, such as antibiotic production.

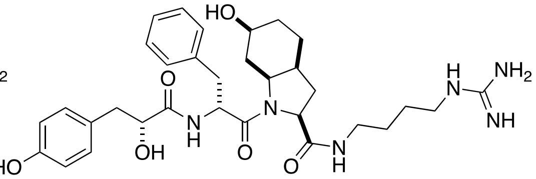
Studies toward understanding the ecological role of *Microcystis* spp. modified peptides

S. Weisthal-Algor (1), R. Hasan-Amir (1), A. Sukenik (1) and S. Carmeli (1).
1) School of Chemistry, Raymond and Beverly Sackler Faculty of Exact Sciences, Tel Aviv University, 69978 Tel Aviv, Israel.

During our thirty years study of secondary metabolites of water-bloom-forming cyanobacteria in Israeli water bodies, we noticed that these strains produce arrays of structurally similar modified peptides. While studying the chemical content of a massive bloom of a brown *Microcystis* sp. collected during the Spring of 2012 in Lake Kinneret, Israel, we isolated relatively large amounts of aeruginosins KT608A, KT608B and KT650 and decided to study their influence on the growth of *Microcystis* cell lines propagated from the 2013 bloom material. The effect of aeruginosins KT608A, KT608B on the growth of some of these cell lines and the roll of some other modified peptides isolated from the 2016 bloom material, will be presented.



Aeruginosin KT608A R=H
Aeruginosin KT650 R=Ac



Aeruginosin KT608B

Can we engineer firmicutes for production of natural products?

H. Winckler Aharoni - hadari.wi@gmail.com (1), N. Barger (1), T. Luzzatto Knaan (1)
1) The Department of Marine Biology, Leon H. Charney School of Marine Sciences, University of Haifa

Firmicutes are a phylum of bacteria, primarily gram-positive known to be ubiquitous in soil and marine environments. *Bacillus subtilis*, model bacterium from this phylum produces a surface-active compound called Surfactin. Surfactin also has an antibiotic property against other bacteria and is already used in agriculture as a plant growth promoter. CRISPR, a method of genetic engineering discovered in bacteria's protection system, makes it possible to form local DNA breaks and make a specific modification, such as inserting or removing a gene and point mutations. Other methods, such as plasmids transformation, are more abundant, yet do not provide an extensive and simple solution like the CRISPR method. Although CRISPR has not been widely used in bacterial systems, recent studies have successfully applied it in Bacillus subtilis, demonstrating its potential for targeted gene editing. So far, we have successfully inserted the designated plasmid into the bacterium and confirmed its successful insertion using markers of antibiotic resistance. Therefore, this research aims to setup a CRISPR-based genetic engineering system for the use of Firmicutes bacteria, aiming to manipulate the production of their natural products. To setup a working system of CRISPR-cas9, the first step is to make changes in the genome of Bacillus subtilis in order to influence the production of Surfactin. By refining this method, we aim to create a versatile and efficient tool for manipulating the genetic pathways of Firmicutes, ultimately leading to increased yields of valuable natural compounds.

Spatiotemporal dynamics of metabolic functioning of Halophila stipulacea in the Northern Gulf of Aqaba

G. Winters - wintersg@adssc.org (1), M. Kaminer (1), N. Lipkin (1, 2, 3), S. Zilberman (2), G.Raanan (2), J. Silverman (2), H. Manh Nguyen (1, 4), R. Sirota (1, 5, 6) , Z. Lavie (5,7), Gilad Antler (5, 7) and G.Rilov (2, 3)

1) The Dead Sea and Arava Science Center (DSASC), Masada National Park, Mount Masada, Israel
2) Israel Oceanographic and Limnological Research, National Institute of Oceanography, Tel Shikmona, P.O. Box 8030, Haifa 31080, Israel
3) Department of Marine Biology, Charney School of Marine Science, University of Haifa, Israel;
4) Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Be'er Sheva, Israel
5) The Zuckerberg Institute for Water Research (ZIWR), Ben-Gurion University of the Negev, Eilat, Israel
6) Department of Geological and Environmental Sciences, Ben-Gurion University of the Negev, Be'er Sheva, Israel.
7) The Interuniversity Institute for Marine Sciences, Eilat, Israel

Seagrass meadows are highly productive ecosystems that provide important ecosystem services and significantly contribute to carbon sequestration. Quantifying the productivity of seagrass meadows is important for calculating their contribution as a carbon sink and to estimate the ecological and economical consequences of their worldwide decline. To investigate the spatio-temporal dynamics of the metabolic functioning of Halophila stipulacea in the northern Gulf of Aqaba and assess their contribution to the water column carbon budget turnover in the region, we measured the productivity of the seagrass in-situ using benthic chambers over multiple years during summer and Winter (Feb and July of 2023, 2024), at two different depths (3 and 12m) in two sites characterized by distinctly different sedimentary compositions (North Beach and the South Beach). Custom-made benthic incubation chambers were used in-situ to measure oxygen production/uptake, carbon uptake/production and calcification/CaCO3 dissolution rates under light and dark conditions, respectively. This allows to calculate net photosynthesis (NP), gross photosynthetic rates (GP) and respiration (R) rates, net primary production (NPP), gross primary production (GPP), net community calcification (G) and $CaCO_3$ dissolution (D) as a function of the time dependent changes in the measured parameters at the beginning and end of the incubations. Overall, we did not find significant differences between depths, seasons or sites. However, during a strong heatwave in the summer of 2024, the deep North Beach meadow demonstrated weak net respiration instead of photosynthesis. Our calculations show that Eilat’s seagrass meadows are able to uptake at least 44,000 Kg of CO_2 per year.

Extreme surface latent heat flux in the tropical and subtropical oceans governed by extratropical atmospheric dynamics

T. Yaari-Sadeh - tsruya.yaari@wezimann.ac.il (1), S. Raveh-Rubin (1)
1) Weizmann Institute of Science

Evaporation from the tropical and subtropical oceans is key for the global energy and hydrological cycles, through air-sea heat exchange and moisture supply to the atmosphere. Previous studies mainly characterized the variability of ocean evaporation on climate time scales in these regions, not accounting for extreme transient evaporation ‘hotspots’. Here we aim to quantify the variability of ocean evaporation on the daily-weekly timescale which hosts the extreme episodes and understand its drivers. By analyzing turbulent latent heat flux data in ERA5 for 1979-2020 we first highlight the occurrence of evaporation hotspots - regionally exceeding 250 W/m2 and lasting for few days - which build up the long-term climatology. We then show indications for the role of midlatitude dynamics in governing this variability, and especially the extreme evaporation hotspots. In this extratropical-tropical interaction, dry air intrusions from the wake of extratropical cyclones reach low latitudes and dominate the occurrence and variability of intense latent heat flux in these regions. The dominance of this mechanism varies across different tropical regions and seasons. The influence of dry intrusions on ocean surface sensible heat flux is, however, more complex. Our results suggest that the variability and extremes of tropical latent heat flux are governed by extratropical dynamics on the synoptic scale. Thus, this extratropical-tropical interaction may affect downstream tropical precipitation variability and ocean dynamics and thermodynamics.

Allochthonous groundwater microorganisms affect coastal seawater microbial abundance, activity and diversity

K. Yanuka-Golub - keren@gal-soc.org(1, 5), N. Belkin (2), N. Weber (3), M. Mayyani (3), Y. Levy (4), I. J. Reznik (4), M. Rubin-Blum (2), E. Rahav (2), Y. Kiro (3).

1) The Institute of Applied Research, The Galilee Society, ShefaAmr, Israel.
2) Israel Oceanographic and Limnological Research, National Institute on Oceanography, Haifa, Israel.
3) Department of Earth and Planetary Sciences, Weizmann Institute of Science, Rehovot, Israel.
4) Geological Survey of Israel, Jerusalem, Israel.
5) The Institute of Evolution (IoE), Haifa University, Haifa, Israel.

Submarine groundwater discharge (SGD) is a globally important process supplying nutrients and trace elements to the coastal environment, thus playing a pivotal role in sustaining marine primary productivity. Along with nutrients, groundwater also contains allochthonous microbes that are discharged from the terrestrial subsurface into the sea. Currently, little is known about the interactions between groundwater-borne and coastal seawater microbial populations, and groundwater microbes' role upon introduction to coastal seawater populations. Here, we investigated seawater microbial abundance, activity and diversity in a site strongly influenced by SGD. In addition, through laboratory-controlled bottle incubations, we mimicked different mixing scenarios between groundwater and seawater. Our results demonstrate that the addition of 0.1 µm filtered groundwater stimulated heterotrophic activity and increased microbial abundance compared to control coastal seawater, whereas 0.22 µm filtration treatments induced primary productivity and Synechococcus growth. 16S rRNA gene sequencing showed a strong shift from a SAR11-rich community in the control samples to Rhodobacteraceae dominance in the <0.1 µm treatment, in agreement with Rhodobacteraceae enrichment in the SGD field site. These results suggest that microbes delivered by SGD may affect the abundance, activity and diversity of intrinsic microbes in coastal seawater, highlighting the cryptic interplay between groundwater and seawater microbes in coastal environments, which has important implications for carbon cycling.

Foraminifera as bioindicators for monitoring heavy metal distributions in the Gulf of Aqaba-Eilat

O. Yehoshafat (1, 2), S. Abramovich (1), S. Ashckenazi-Polivoda (4), A. Torfstein (2, 3)
1) Department of earth and environmental science, Ben Gurion University of the Negev
2) Interuniversity Institute for Marine Sciences of Eilat (IUI)
3) Institute of Earth Sciences, Hebrew University of Jerusalem, Israel
4) Dead sea & Arava Science center, Mount Masada, Israel

Global anthropogenic activities and industrial growth significantly impact and transform marine environments, particularly in coastal areas where human activities intersect with the ocean. These vulnerable regions face severe ecological imbalances due to various human-induced stressors, such as the continuous discharge of Heavy Metals (HMs) into the marine environment. Yet documenting real-time seawater heavy metal contents is extremely challenging logistically and analytically. Recent research has shown that foraminiferal shell chemistry could serve as a reliable proxy for detecting HMs enrichment in marine environments, even at trace concentrations.

This study focuses on monitoring the spatial and temporal variability of heavy metal concentration in benthic foraminifera shells from the Gulf of Aqaba-Eilat (GoA), a relatively isolated marine ecosystem in the northern Red Sea. Living specimens of the three most common large benthic foraminifera taxa *(Amphistegina lessonii, Peneroplis pertusus, Soritid)* were seasonally collected from six locations along the northern GoA coast, representing both polluted and natural habitats. The results of this study will characterize the distribution of HMs along the northern GoA coastline and identify areas of increased anthropogenic pressure and their potential sources. Furthermore, the results of this study will aim to establish the use of foraminifera as a reliable biomonitoring tool for marine environment health worldwide.

HF radar observations collected over 4 years in the southern Israeli coast

J. Zaken - jacobzkn@gmail.com (1) and Izhaq-Yaron Toledo (1)
1) Tel-Aviv University

Among the various instrumentations available for measuring sea characteristics, high-frequency (HF - between 3 to 30MHz) radars show some unique advantages. These systems operate by sending a vertically polarized electromagnetic signal on the sea surface, where waves (with half the radar's wavelength) cause Bragg scattering, reflecting towards the radar's receiver. This reflected signal is shifted in a certain Doppler frequency, due to the wave's velocity towards the radar's receiver, thus, enabling the calculation of the current's velocity. The returning signal's second-order sidebands are proportionate to the wave height spectrum and are analyzed to calculate it. These shore-based remote-sensing systems enable monitoring of surface currents, waves and winds, allowing for large measurement coverage areas, in a resolution varied from hundreds of meters to few kilometers. However, despite the HF radar's advantages, these systems have not been used in the Levantine basin for the study of currents and waves. In this study, we have gathered observations of currents and waves using a HF radar (8.3 MHz) in Israel's southern coast for the past four years. These observations can cover up to 180 km from the coast, in a resolution of 1.5 km, every 20 minutes. The observation provided by our radar can be used for future oceanographic studies, operational drift calculations, and mitigation of oil contaminations. We present here our validation of the radar's observation using Acoustic Doppler current profiler, the first radar observed currents and waves, and typical patterns that appear along the Israeli southern coast.

Constraints on the Dead Sea levels based on Mg^{2+} budget since the last deglaciation

J. Zhao - jie.zhao@weizmann.ac.il (1), Yael Kiro (1)
1) Department of Earth and Planetary Sciences, Weizmann Institute of Science, 234 Herzl St., Rehovot 7610001, Israel

The Levant region of the Eastern Mediterranean is projected to experience increased drought due to rising greenhouse gas emissions. Proxy-based paleoclimate reconstructions are crucial for understanding natural hydroclimate variability, which is essential for constraining future hydroclimate changes in response to a globally warmer climate. Here, we reconstruct the lake levels of the Dead Sea in the southern Levant based on conservative pore-fluid Mg^{2+} concentrations from the Dead Sea Deep Drilling Project since the last deglaciation. Our Mg^{2+}-deduced lake levels are significantly higher (by 70–100 m) than the values from the lake level curve based on onshore records during ~16 to 8 ka, indicating a missing Mg^{2+} inventory in the Dead Sea Basin, which currently consists of a deep north basin (~300 m) and a shallow south basin (~10 m). After reevaluating the conservative behavior of Mg^{2+}, a dual Mg^{2+} inventory model is developed to address this discrepancy, where the south basin was much deeper during ~16 to 8 ka and served as an important Mg^{2+} reservoir. Considering this dual inventory scenario, we were able to constrain both the depth of the southern basin at the beginning of the Holocene, and the lake levels. The corrected Mg^{2+}-deduced lake levels reflect a dry Bølling-Allerød interstadial with the lake level likely below 457 meters below sea level (mbsl), and a relatively wet Younger Dryas with the lake level rising to ca. 417 mbsl. Around 9 ka, in the early Holocene, the lake levels were around 320–330 mbsl. Our findings provide geochemical quantitative insights into the periods of low stands and rapid lake level changes, which previously had large uncertainties due to limited exposure of shorelines and beach deposits.

Coupling anaerobic digestion with aquaponics to promote the circular economy in arid zones

Z. Zhu - ze@post.bgu.ac.il (1), U. Yogev (2), H. Karanja (1), A. Gross (1)
1) Zuckerberg Institute for Water Research, Jacob Blaustein Institutes for Desert Research, Ben Gurion University of the Negev, Midreshet Ben Gurion 84990, Israel.
2) National Center for Mariculture, Israel Oceanographic and Limnological Research Institute, Eilat 88112, Israel

Aquaponics (integration of aquaculture and hydroponics) is increasingly viewed as a sustainable method to enhance food security. Despite its potential, constraints such as nutrient imbalances and inefficient waste management hinder its widespread adoption. An effective approach to address these issues is the onsite treatment of aquaponic wastes to recycle nutrients (e.g., nitrogen and phosphorus), recover energy, and reuse water. Our study explores the integration of anaerobic digestion (AD) with aquaponics to enhance system efficiencies in nutrient recycling, water usage, and energy consumption. We examined three systems: a traditional aquaponics system (DAP), a coupled aquaponics system (CAP), and a novel zero-discharge off-grid aquaponics system enhanced with UASB (CAP-AD) at a desert-based facility in Midreshet Ben-Gurion, Israel. Over four months, we monitored nutrient, water, and energy balances and assessed crop yields and resource use efficiency. Results showed that the CAP-AD system recovered an additional 33% of the total input nitrogen and 37% of the phosphorus from fish sludge, with total nutrient utilization efficiencies of 76% for nitrogen and 80% for phosphorus. This system also demonstrated 1.6 times increase in plant productivity per area, 2.1 times lower water usage, and 16% lower energy consumption per kilogram of feed compared to DAP and CAP. Additionally, biogas production supported approximately 84% of the operational energy requirements, while CO2 sequestration was significantly higher than feed carbon, reducing the carbon footprint by 64%. This study underscores the benefits of integrating anaerobic digestion with aquaponics, particularly in arid regions, promoting a circular economy through efficient waste treatment and resource reuse.

Sub-sampling method for analyzing chemical composition of marine surface microlayer

A. Ziner - aviya.z@campus.technion.ac.il (1), I. Kuzmenkov (1), Y. Dubowski (1)
1) Technion, Israel Institute of Technology

The marine surface microlayer (SML) is distinct from subsurface water by physical, chemical and biological properties. Due to its location at the air-water interface, SML regulates mass transfer between ocean and overlying atmosphere. Any alteration in such fluxes can have significant impact considering that most of the globe's surface is covered by oceans. Marine emissions of volatile and semi-volatile organic compounds (VOCs/SVOCs) are of special interests due to their potential role in aerosol formation and resulting impact on the Earth's radiation balance. Yet, our current knowledge regarding these complex fluxes is highly lacking.

SML sampling is technically challenging, especially in high seas and when using large research vessels. These limitations may introduce biases in the available database and resulting scientific conclusions. Here we present a new approach to study SML chemical composition, using water sub-sampling combined with application of membrane filter followed by SPME-GC-MS analysis. The new method allows quantitative analysis of VOCs/SVOCs profile of the SML, with higher efficiency and accuracy than traditional methods, as well as the ability to sample in variety of sea conditions.

Applying this new methodology in field campaigns conducted near Herzliya and in Haifa-Bay revealed clear spatial and temporal variations in the chemical composition of the SML, both on diurnal and seasonal scales. The obtained data indicates that SML composition is affected by both biological and anthropogenic sources. Furthermore, complimentary atmospheric VOCs measurements in the marine boundary layer suggests that its is affected by the chemical composition of the SML.

Assessing the impact of aquifer heterogeneity on coastal groundwater flow dynamics and salinity under tidal sea level changes

A. Zonshine - adam-shalom.zonshine@weizmann.ac.il (1), Y. Kiro (1)
1) Weizmann Institute of Science, Department of Earth and Planetary Sciences Herzl St 234, Rehovot

Coastal aquifers are crucial water resources that support both human populations and coastal ecosystems. Understanding the interactions between fresh and saline groundwater and the driving forces behind submarine groundwater discharge (SGD) and saltwater intrusion, is essential in managing these resources. This research investigates through simulations the effects of transient sea level and aquifer heterogeneity on groundwater flow and solute transport in coastal aquifer.

Using FEFLOW, a finite-element groundwater flow and solute transport model, we conduct 2D simulations, in a Monte Carlo work frame to analyse subsurface flow and salt transport under tidal sea-level fluctuations and changing heterogeneity properties. We used object-based modelling, as well as geostatistical realizations utilizing sequential indicator simulation (SISIM) algorithm, through the Stanford Geostatistical Modeling Software (SGeMS) program.

Our preliminary results reveal transient responses in both fresh and saline groundwater flow paths, that is different to equivalent homogeneous models, such as reduced circulation of saline water in models with higher connectivity measures of heterogeneity, and the formation of preferential flow paths.

By comparing heterogeneous and homogeneous models, we assess the effects of different lithological units and their connectivity on flow patterns and volumes, solute transport, etc. The results provide insights into how heterogeneity affects preferential flow paths, and salinity distribution, offering information for future coastal aquifer management.

Virulence, resistance and coexistence: understanding host-virus infection dynamics in marine diatoms

O. Zucker - ori.zucker@biu.ac.il (1), D. Spungin (1), C. Kranzler (1)
1) Bar-Ilan University

Diatoms are among the most widespread groups of phytoplankton in the ocean, contributing ~40% of the marine primary production. Virus infection in phytoplankton is considered a major conduit of ecological and biogeochemical transformation in the ocean, yet little is known about virus infection dynamics in diatoms. Using the bloom-forming, centric diatom, Chaetoceros tenuissimus and the RNA virus, CtenRNAV, we are exploring virus life history traits and the mechanisms that underscore resistance. Limited exposure to CtenRNAV (1.5 h), at a multiplicity of infection (MOI) of 10, was sufficient to generate culture demise with the onset of virus-mediated mortality apperent at ~4 days post infection (dpi). We used fluorescence-activated cell sorting (FACS) to determine the percentage of infected cells throughout the time course of infection. Surprisingly, despite an MOI of 10, the majority of cells were still uninfected at 1.5 hpi, with <1% of cells exhibiting clear signs of viral infection. Increasing the MOI to 1000 led to a moderate 10-fold increase in initial infection, suggesting that a large majority of cells were not susceptible to virus infection. In addition, both competitive inhibition experiments with inactive viruses and inhibition of endocytosis led to a reduction in virus replication. These data provide insight into the factors regulating successful virus infection in C. tenuissimus, advancing our understanding of how this biogeochemically critical group of marine microeukaryotes might resist and survive virus predation in the global ocean.

Coral bleaching in the Gulf of Aqaba/Eilat - reefs on the verge of a tipping point?

A. Zvuloni - zvuloni@npa.org.il (1), M. Fine (2), Y. Shaked (2)
1) South District, Israel Nature and Parks Authority, Israel
2) The Hebrew University of Jerusalem, Israel; The Interuniversity Institute for Marine Sciences in Eilat, Israel

In mid-August 2024, a significant coral bleaching event was recorded for the first time in the northern Gulf of Aqaba/Eilat (GoA). This event, triggered by extreme environmental changes, most notably elevated sea temperatures, highlights the fragility of coral ecosystems. When water temperatures exceed a critical threshold, the symbiotic relationship between corals and their zooxanthellae breaks, causing the expulsion of the algae. While corals initially survive this process, they suffer from severe nutrient depletion, and prolonged exposure can lead to widespread mortality.

GoA corals are known for their exceptional heat tolerance, developed over millennia through natural selection in the warmer waters of the southern Red Sea. However, the summer of 2024 brought unprecedented heat stress, with temperatures peaking at 31.9°C and daily maximums remaining above 30°C for two consecutive months. The DHW index (Degree Heating Week), which measures accumulated heat stress on corals, reached 30°C-weeks - well beyond the 8°C-weeks threshold for severe/mass bleaching events.

Despite the remarkable natural resilience of corals in the GoA, this bleaching event raises concerns that the reefs are approaching a tipping point. Studies show that local stressors, such as water pollution and nutrient enrichment, are exacerbating the vulnerability of these corals to thermal stress and bleaching. Although this year's bleaching did not result in catastrophic damage, it raises critical questions about the long-term resilience of GoA corals and underscores the urgent need for targeted conservation efforts to mitigate local threats.

Inundated Tamarix forest – a novel, climate change-induced littoral habitat in Lake Kinneret

T. Zohary - tamarz@ocean.org.il (1), A. Alster (1), D. Cummings (1, 2), A. Dolev (3), W. Eckert(1), G. Gal(1), A. Gasith (4), E. Guk (2,5), E. Leibovici (1), E. Ofir (1), S. Varulker (1), Y. Be'eri-Shlevin (1)
1) Kinneret Limnological Laboratory, Israel Oceanographic & Limnological Research
2) WA Dept. of Fish and Wildlife, Ridgefield, WA 98642, USA
3) Israel Nature and Parks Authority
4) School of Zoology, Faculty of Life Sciences, Tel Aviv University, Israel
5) Department of Geography, The Hebrew University of Jerusalem, Israel

Dense, impassable forests of Tamarix jordanis developed on exposed shores of Lake Kinneret during an unusually long drought of five consecutive years, with declining annual mean water level. Then, rapid refilling during two sequential high-rainfall winters inundated the forests, creating a novel aquatic habitat. Our objectives were to investigate the environmental conditions and biota in this new littoral habitat, quantify its spatial and temporal distribution, and assess the need for management actions. We sampled monthly along transects through two dense forest sites and a control no-vegetation littoral site. Shortly after inundation, the conditions among the trees resembled those of shaded swamps: decomposing organic matter, subdued circulation and low light intensity which led to hypoxia, low pH, high particulate organic matter and nutrients, and to unique phytoplankton and zooplankton assemblages. With time of ongoing inundation, the extreme conditions dissipated, although most trees survived 3-4 years continuous flooding. After the environmental conditions relaxed, the inundated trees, live and dead, comprised a preferred fish habitat. Using satellite (Sentinel-2) imagery we mapped the spatial distribution of live inundated vegetation and how it diminished over time of continuous flooding. To prevent the recurrence of impassable forests clogging the shores, we proposed proactive management: reducing the amplitude of water level fluctuations and removing T. jordanis sprouts shortly after emergence. Understanding the dynamics of such novel habitats is crucial for effective ecosystem management and conservation. Lake Kinneret serves as a valuable case study for addressing similar challenges in other freshwater systems worldwide.

אפיון העדפות משפחת Soritidea בסביבת עשב הים במפרץ אילת

(1) yarden2709@gmail.com - **ירדן כהן**

1) המחלקה למדעי כדור הארץ והסביבה, אוניברסיטת בן גוריון בנגב

סוריטידים הם קבוצה מאוד נפוצה של פורמיניפרים בנטונים גדולים עם סימביוזה תוך תאית עם אצות חד תאיות מטיפוס דינופלגלטה הנקראות (*Symbiodinium*) שמצויות גם באלמוגים. סוגים של משפחה זו מאפיינים בתי גידול של מים רדודים וחמים בסביבות הטרופיות הסובטרופיות. במפרץ אילת נציגים של המשפחה נפוצים בעיקר על עשבי הים שמהווה סביבה מועדפת עליהם .

פורמיניפרים בנטונים ומשפחת הסוריטידים רגישים מאוד לשינויים סביבתיים כך שמחקר עליהם יכול לגלות המון על הסביבה.

מטרות המחקר:

1. אפיון ההבדלים בין האוכלוסיות של סוריטידים כתלות בעומק בית הגידול על עשבי הים ובעונתיות. האפיון התבצע על ידי אומדן: כמות הפרטים לסמ""ר, גודל הפריטים והתרומה ביחס לכלל מאסף הפורמיניפרים.
2. אפיון החותמת הגיאוכימית בשלדי הסוריטידים ככלי פוטנציאלי לניטור ריכוזי מתכות אנטרופוגניות ואפיון הרכב השלד.